

FUNGI ASSOCIATED WITH COFFEE IN YUNNAN AND CHIANG RAI PROVINCES AND WORLDWIDE CHECKLIST

LI LU

DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE

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THIS DISSERTATION IS A PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY IN BIOLOGICAL SCIENCE

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ABSTRACT

Yunnan, China, and Chiang Rai, Thailand, are located in the northern part of the Greater Mekong Subregion (GMS), are characterized by their warm climate and rich ecological diversity, offering a unique habitat for diverse fungal communities. These environmental conditions not only support the growth of *Coffea arabica*, one of the region's most economically important cash crops, but also favor the proliferation of fungi, increasing the crop's vulnerability to fungal infections during both cultivation and post-harvest periods. Thus, a comprehensive study was conducted to investigate the fungi associated with the economic crop coffee in Yunnan, China, and Chiang Rai, Thailand. To address this challenge and contribute to sustainable agricultural development, a comprehensive study was conducted to investigate the fungi associated with coffee in Yunnan, China, and Chiang Rai, Thailand. A total of 360 saprobic fungal collections were obtained from eight locations—Baoshan, Dali, Dehong, Jinghong, Lincang, Nujiang, and Pu'er in Yunnan in China and Chiang Rai in Thailand. Initial ITS analyses revealed that these collections represent seven classes, 37 orders, 83 families, and 137 genera. The life modes of these taxa were interpreted based on previously published studies, and fungal diversity across the eight locations was compared and discussed.

From the total collections, 139 well-preserved samples with abundant fruiting bodies and mature morphological structures were selected for detailed morphological and multi-locus phylogenetic analyses. These collections span four classes, 27 orders, 69 families, and 87 genera, resulting in the identification of six new genera, 77 new species, one novel DNA sequence, 47 new records, and four additional collections. Notably, four

species (*Acrocalymma daliense*, *Pseudohelminthosporium clematidis*, *Tubeufia coffeae,* and *Menisporopsis dinemasporioides*) were documented in both their sexual and asexual morphs on natural substrates. In addition, 235 fungal endophytes were isolated from 270 leaf segments of *Coffea arabica* collected from four coffee plantations in Yunnan. All isolates were identified through ITS sequencing, revealing their classification within Ascomycota, distributed across two classes, 10 orders, and 17 families. To assess their potential for biological control, 61 endophytes were evaluated in dual-culture assays against four known plant pathogens. Notably, *Nigrospora* sp. XCE-7 and *Daldinia* sp. ME-9 inhibited *Alternaria alternata* with over 70% growth suppression. Likewise, *Daldinia* sp. ME-9, *Nigrospora* sp. T5E-7, and *Daldinia* sp. T5E1-3 effectively inhibited *Penicillium digitatum*, also exceeding 70% inhibition rates. A new species of sooty mold, *Trichomerium puerense*, was also described and confirmed through pathogenicity testing as a pathogen of *Coffea arabica* in Yunnan.

Furthermore, this study compiled a global checklist of fungi associated with *Coffea* species, encompassing 1,295 records, including 987 species across 90 orders, 181 families, and 370 genera. Each entry includes geographical distribution, host plant, isolation source, taxonomic classification, and reference literature. This database provides an invaluable resource for advancing mycological and plant pathological research on coffee crops.

Overall, this work reveals the extensive diversity of microfungi associated with coffee plants in southern China and northern Thailand. The discovery of new taxa and geographic records enhances biodiversity inventories, while the identification of bioactive endophytes offers promising avenues for environmentally friendly disease management strategies. These findings support sustainable agricultural practices, promote biodiversity conservation, and contribute to innovation in plant health management.

Keywords: 360 Saprobic Collections, 77 New Species, 6 New Genera, 235 Endophytic Collections, Biocontrol Agent, Coffee Fungal Checklist, Fungal Diversity, Phylogeny, Sooty Mold Fungi, Taxonomy

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ABBREVIATIONS AND SYMBOLS

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

CHAPTER 1

INTRODUCTION

1.1 Background and Rationale

1.1.1 Overview of Coffee Plants in Worldwide

Coffee plants are evergreen shrubs or small trees characterized by glossy leaves, fragrant white flowers, and red cherries that contain the coffee beans (Anzueto et al., 2005). They belong to the genus *Coffea* within the family Rubiaceae and are generally believed to have originated in Ethiopia, where *Coffea arabica* was first discovered (Amamo, 2014). Today, coffee is cultivated in more than 80 countries across tropical and subtropical regions, supporting the livelihoods of over 25 million families worldwide (Lu et al., 2020b; Cassamo et al., 2023).

Coffee, renowned as the second most traded and preferred commodity after oil worldwide and consumed for centuries, has a rich historical and cultural significance, connecting people across the globe through a shared tradition of consumption (Adhikari et al., 2020; AL-Asmari et al., 2020), contains over 1,000 compounds, particularly flavonoids, which help prevent high-fat diet-induced non-alcoholic fatty liver disease (Gao et al., 2023). *Coffea* comprises over 100 species, but only *Coffea arabica*, *C. canephora*, and *C. liberica* are used for beverage production; among these three species, *C. arabica* and *C. canephora* represent approximately 70% and 30% of global production, respectively, while *C. canephora* represents less than 1% (Davis et al., 2006; Duong et al., 2020; de Sousa et al., 2022). Due to its unique flavor, aroma, and low caffeine content, arabica coffee is the best-selling coffee worldwide (Lu et al., 2022a; Raimondo, 2022). Other *Coffea* species are caffeine-free from seeds or have a very low content level that is not suitable for beverage production (e.g., *C. boiviniana*, *C. jumellei*, *C. sakarahae*, and *C. pervilleana*), or the presence of secondary purine alkaloids such as theophylline and theobromine (e.g., *C. racemosa* and *C. sessiliflora*). These chemical compounds may affect the flavor or the overall drinking experience, potentially reducing their suitability for coffee beverage production (Hamon et al., 2025). Since

2022, coffee has ranked as the world's 104th most traded product, with a total trade value of $45.4 billion, playing a significant role in the global economy (https://oec.world/en/profile/hs/coffee).

1.1.2 Importance of Coffee in Southern China and Northern Thailand

In mainland China, the first coffee plants (arabica coffee—*Coffea arabica*) were planted in Zhukula Village, Binchuan County, Dali City, Yunnan Province in 1982 (Zhang et al., 2014). Since the climatic conditions are ideal in Yunnan Province, arabica coffee has long been the predominant coffee type (Rigal et al., 2020). China's coffee cultivation areas are mainly distributed in Yunnan and Hainan provinces, while Yunnan's coffee planting area, production, and agricultural output value account for more than 98% of the country's total (Palanza, 2018; Lu et al., 2022a). Thus, it became the third largest agricultural export in Yunnan, and is mainly cultivated in Baoshan, Dali, Dehong, Honghe, Lincang, Pu'er, Wenshan, and Xishuangbanna, and these regions feature strong but not bitter taste, fragrant but not hard smell and slightly fruity flavor (Zhang et al., 2021). China's total coffee production ranks 13th in the world (2024), and the annual production of coffee reaches 1.9 million 60-kilogram bags of coffee, with 95% of coffee products produced by Yunnan Province (http://apps.fas.usda.gov/psdonline/psdQuery.aspx). From 2021 to 2022, the coffee planting area was around 92,860 hectares in Yunnan Province, with an output of 108,700 tons, and the output value of the whole coffee industry chain was around $44.23 billion (Huang et al., 2022).

In Thailand, the demand for coffee is steadily rising, and tourism plays a significant role in this growth. The coffee plantations in northern regions (Chiang Rai, Chiang Mai, Mae Hong Son, and Lampang provinces) have not only become integrated into tourist destinations but also serve as a testament to the global appeal of Thai coffee, attracting both domestic and international visitors (Smith et al., 2019). Chiang Rai, for instance, is renowned for its ideal climate conditions for growing Arabica coffee in northern Thailand (Sitikarn et al., 2022). Similarly, Chumphon, Nakhon Si Thammarat, Surat Thani, and Yala in southern Thailand are also important coffee planting areas, each contributing to the story of Thailand's coffee industry (Maluleem, 2022). Thailand's total production of coffee ranks 20th in the world (2024), and the annual

production of coffee reaches 0.7 million 60-kilogram bags (http://apps.fas.usda.gov/psdonline/psdQuery.aspx).

1.1.3 Importance of Microfungi in Coffee and Ecosystem Functioning

Coffee-growing areas provide a suitable environment for the emergence of diverse organisms, many of which are closely associated with coffee plants (Carvalho et al., 2019). Fungi, in particular, are among the most common and extensively studied microorganisms in coffee plantations, present throughout various stages of growth and processing (De Bruyn et al., 2017). As essential microorganisms, fungi play vital roles in nutrient cycling, organic matter decomposition, and symbiotic interactions with plants (Corbu et al., 2023). Their contributions to ecological balance and agricultural productivity are significant, and their diverse metabolic capabilities make them invaluable in numerous industrial and medical applications, showcasing their potential to inspire innovation and progress (Zhang et al., 2024). However, fungi also have detrimental effects; certain species cause plant diseases, leading to substantial agricultural losses (Zhang et al., 2024), while others infect humans and animals, presenting treatment challenges (Hyde et al., 2018). Furthermore, some fungi produce mycotoxins that contaminate food supplies, posing health risks to humans and animals (Hyde et al., 2018).

The first mention of the microorganisms associated with *Coffea* plants dates from the 19th century, which was about the description of the arbuscular mycorrhizal fungi (AMF) colonizing the roots of *C. arabica* and *C. liberica* (Janse, 1897). Fungi associated with coffee exist in different life modes, including endophytes, pathogens, and saprobes (Duong et al., 2020; Lu et al., 2022b). The highest number of fungal species has been documented from *Coffea arabica* (Table 5.1).

Coffee can easily be infected by pathogenic fungi during growth, post-harvest handling and storage, and processing (Varga et al., 2010). One of the most virulent diseases is ‘coffee rust’ caused by *Hemileia vastatrix,* which wiped out coffee 150 years ago and continues to cause problems in coffee plantations worldwide (McCook et al., 2006). Fungal diseases in coffee can be divided into two types: diseases in pre-harvest and diseases in post-harvest (Coates et al., 1997; Roberto et al., 2019). Many post-harvest coffee pathogens are infected shortly before harvest, are generally not found at harvest, and feature low activity; moreover, poor storage conditions during post-harvest favour their development

(Coates et al., 1997). Fungal invasions before harvest are mainly induced by the interaction between the plant host and other organisms (such as insects), while fungal infections after harvest are controlled by nutrient availability, temperature, humidity and biological factors (insects) (Ismaiel et al., 2015). Another pathway is that endophytic fungi in coffee beans change their life modes to saprobic/pathogenic after the beans are harvested, becoming postharvest pathogens (Huang et al., 2020). Most postharvest fungi produce toxins as secondary metabolites *viz* ochratoxin-A, which is a mycotoxin mainly produced as a result of secondary metabolism of many species of *Aspergillus* and *Penicillium* and is the most common mycotoxin present in agricultural commodities (Miller, 1994). Toxin-producing fungi can be isolated from coffee beans both pre-harvest and post-harvest, while the risk of fungal growth and mycotoxin production after harvest is higher in high temperature areas (Alvindia et al., 2016). These toxins can cause host infections and reduce coffee bean quality (Proctor et al., 2018) and can be carcinogenic, hepatotoxic, hematotoxic, nephrotoxic and neurotoxic for humans (Khan et al., 2019). Silva et al. (2000) isolated ochratoxin-A from damaged coffee beans, and ochratoxin-A was shown to cause coffee quality and yield losses. Studies have shown that the main toxigenic fungal genera comprise *Aspergillus*, *Penicillium* and *Fusarium*, which are natural coffee contaminants (Bokhari, 2007), and they can infect hosts in both farms and warehouses (Rezende et al., 2013).

The potential of coffee endophytes as biocontrol agents has been extensively investigated, including their ability to produce growth-promoting metabolites, insect and pest repellents, and antimicrobials to combat plant pathogens, as well as their role in protecting plants in stressful environments (Quesada-Moraga et al., 2014; Monteiro et al., 2020; Lu et al., 2022c). Endophytes usually live inside the host without causing injury or obvi-ous symptoms, and this association can provide a better living environment for both the host and fungus (Torres-Mendoza et al., 2020). Huang et al. (2020) screened potential antagonistic endophytes that prevent and control post-harvest diseases.

Saprobes can be both beneficial and harmful to the host; they act as decomposers, breaking down dead organic matter and releasing essential nutrients, thereby facilitating a sustainable environment for cohabiting plants (Hyde et al., 2007). Additionally, some saprobic fungi inhibit the growth of pathogenic fungi, while others can produce harmful mycotoxins, contaminating 20–25% of global crops (Eskola et al., 2020). Although Masaba (1993) showed the potential of using the saprobic microflora

isolated from coffee berry surfaces to manage coffee berry disease (Gichuru, 2005), only a few studies on coffee saprobes have been carried out worldwide (Lu et al., 2022b). There were few reports on coffee saprobic fungi in China and Thailand before 2020. This highlights the need for more research in this area.

1.2 Significance of the Study

Research on fungi associated with coffee can be traced back to the 19th century, until early 20th-century studies, with few publications and primarily focused on pathogens and endophytes, with significant neglect of saprobic fungi (Lu et al., 2022a, 2022b, 2022c, 2022d, 2024, 2025).

Pathogens are the most widely studied fungi in coffee, as their infection can impact coffee production and quality (Lu et al., 2022b). Pathogens represent the primary limiting factors in coffee production, accounting for approximately 26% of global annual coffee losses due to diseases, which threaten the livelihoods of nearly 125 million people worldwide (Maghuly et al., 2020). Therefore, discovering and examining new pathogens is crucial for understanding disease dynamics, developing effective management strategies, and safeguarding coffee production against future threats.

Some research has shown that saprobes *Phialomyces macrosporus* isolated from leaf litter has the potential to be used in the management of coffee halo blight in seedlings and produced volatile or non-volatile compounds that can inhibit the growth, sporulation, and viability of the causative agent of the coffee brown eye-spot, *Cercospora coffeicola* (Botrel et al., 2018; Laborde et al., 2019). Therefore, saprobes have the potential as a biological control agent to manage diseases. In China and Thailand, a very few studies have been carried out on saprobes associated with coffee.

In addition, the study of endophytes on coffee plants may play a crucial role in promoting the growth of coffee plants, enhancing their disease resistance, and improving coffee yield and coffee bean quality (Lu et al., 2022c). Since Rayner's pioneering study in 1948 (Rayner, 1948), numerous investigations have explored coffee endophytes, revealing their antimicrobial and antagonistic properties, including *Beauveria bassiana* for coffee berry borer resistance, *Trichoderma* spp. for *Fusarium* wilt control, and other genera (e.g.

Acremonium, *Muscodor*, *Simplicillium*) with antibacterial and antifungal activities (Posada et al., 2007; Fernandes et al., 2009; Mulaw et al., 2013; Monteiro et al., 2017; Gomes et al., 2018). Therefore, identify and examine the antagonistic abilities against pathogens of endophytic fungi associated with coffee is necessary for coffee ecosystems.

1.3 Research Questions

1.3.1 What is the diversity of saprobic fungi associated with *Coffea* in Yunnan, China and Chiang Rai, Thailand?

1.3.2 Can endophytic fungi from *Coffea* be developed as potential biocontrol agents against common plant pathogens?

1.3.3 What are the ecological roles of saprobic or endophytic fungi in *Coffea* agroecosystems, and how might they interact?

1.4 Research Objectives

1.4.1 To identify and describe novel/known fungal taxa associated with coffee from Yunnan, China, and Chiang Rai, Thailand based on morphology and multigene phylogeny.

1.4.2 To isolate, identify, analyze the diversity, and screen the endophytic fungi with antagonistic abilities against pathogenic fungi/bacteria.

1.4.3 To provide an updated checklist of fungi associated with coffee worldwide.

1.5 Expected Outcomes

1.5.1 A diversity analyses of saprobes associated with coffee.

1.5.2 Novel species, host/geological records of saprobes associated with coffee from Yunnan, China, and Chiang Rai, Thailand.

1.5.3 Identify coffee-associated endophytic fungi with antagonistic activity against pathogenic fungi/bacteria in Yunnan, China and analyze the diversity.

1.5.4 A checklist of fungi associated with coffee worldwide.

1.6 Research Contents

This study focuses on the diversity, taxonomy and phylogeny of saprobes associated with coffee plants in southern China and northern Thailand; also isolate, identify, analyze the diversity, and screen the endophytes with antagonistic abilities against pathogens in southern China, comprising six chapters.

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

Chapter 2 provides the diversity, taxonomy and phylogeny of coffee saprobes. In this chapter, we analyzed 360 samples diversity which collected from Yunnan, China, and Chiang Rai, Thailand. Based on morphological comparisons and multigene phylogenetic analyses, we introduce six new genera, 76 new species, 47 new records, four known species and one novel sequence data. The description and illustrations for each taxon are provided.

Chapter 3 emphasis on endophytic fungi associated with coffee leaves in China. This chapter also provides data on invitro antagonism against fungal and bacterial pathogens.

Chapter 4 provides a new sooty mold fungi associated with coffee. Details regarding fungal taxonomic positions, morphological characterization, and pathogenicity testing are provided.

Chapter 5 provides a checklist for all fungi associated with coffee. Details regarding fungal taxonomic positions, varieties of coffee, source of isolation and known distributions are provided.

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

CHAPTER 2

DIVERSITY, MORPHOLOGY AND PHYLOGENY OF MICROFUNGI ON COFFEE IN SOUTHERN CHINA AND NORTHERN THAILAND

2.1 Introduction

Coffea (Rubiaceae) is the world's 124th most-traded product and the second most popular beverage worldwide (Adhikari et al., 2020; Al-Asmari et al., 2020). The coffee industry is a powerhouse, contributing to the economies of both exporting and importing countries. Its annual income is estimated to exceed $200 billion, providing livelihoods for around 100 million families (Adugna, 2024; Freitas et al., 2024). The genus *Coffea* boasts over 120 species, but only two, Arabica coffee (*Coffea arabica*, 75%) and Robusta coffee (*Coffea canephora*, 25%), hold significant economic importance, making them the key players in the industry (Lu et al., 2022a; Gole & Seyoum, 2024). In 2024, China ranks 13th in global coffee production and is the largest coffee market in East Asia, while Thailand ranks 20th and is the third-largest market in the region (http://apps.fas.usda.gov/psdonline/psdQuery.aspx).

There are an estimated 2.5 million species of fungi, but only about 165,000 have been described thus far (Niskanen et al., 2023; Kraisitudomsook et al., 2024; https://www.indexfungorum.org accessed on 12 January 2025). Coffee is susceptible to microfungi during pre-harvest and post-harvest processing, especially pathogenic fungi, which can affect coffee tree growth, fruit yield, and quality (Waller, 1985; Lu et al., 2022b). The first coffee-associated microorganism described was the arbuscular mycorrhizal fungi (AMF) colonising the roots of Coffea arabica and *C. liberica* Hiern (Janse, 1897). Fungi associated with coffee exist in different life modes, including endophytes, pathogens and saprobes (Duong et al., 2020; Lu et al., 2022b). Several surveys of the literature also show that a few studies have been conducted on saprobes associated with coffee worldwide (Arias et al., 2014). Most of the studies focus on pathogens, as pathogenic fungal infections reduce coffee yield and quality, and thus

affect farmers' income and consumers' health (Pimenta et al., 2018; Dos Santos et al., 2021). Some research has shown that saprobes have the potential as a biological control agent to manage diseases. In China, a very few studies have been carried out on fungi associated with coffee and also few studies in Thailand. In addition, coffee is one of the most important economic crops; thus, isolation and identification of coffee saprotrophic fungi based on morphology and multigene phylogeny are useful for future studies on the secondary metabolites of coffee fungi.

In this study, I provide and compare the diversity analyses for 360 collections associated with coffee in southern China and northern Thailand. In addition, I introduced 127 species with full (macro and micro characteristics) descriptions, illustrations, and a phylogenetic tree that shows the phylogenetic position of these taxa. All species illustrated below are in alphabetical order. They represent 86 genera in 58 families, 26 orders and three classes in Ascomycota.

2.2 Materials and Methods

2.2.1 Sampling Collection, Examination, and Isolation

Decaying coffee twigs of *Coffea* sp. or *C. arabica* were collected from the tropical to subtropical regions, Yunnan Province in China (Baoshan, Dali, Dehong, Jinghong, Lincang, Nujiang, and Pu'er cities) and Thailand (Chiang Rai Province) from 2020 to 2024. After the collection information was recorded (Longitude, latitude, altitude) (Rathnayaka et al., 2024), the specimens were brought to the mycology laboratory at Qujing Normal University, Yunnan, China, and Mae Fah Luang University, Chiang Rai, Thailand, for examination. Morphological observations and single spore isolations followed the procedures outlined in Senanayake et al. (2020). During single spore isolation, each germinated spore is carefully selected and transferred to a fresh PDA plate to establish a pure culture. Different pure cultures were used for DNA extraction and PCR, which represent two culture collection numbers for each strain. Morphological characteristics were observed using a Leica DM2500 compound microscope and photographed with a Leica DMC4500 camera fitted onto the microscope. The scanning electron microscope (SEM, QUANTA 450) (Hitachi,

Ibaraki, Japan) was used to observe the ultrastructure of peridium and spores for future reference. The measurements were processed in Tarosoft (R) Image Frame Work v. 0.9.7, and photographic plates were made in Adobe Photoshop CC 2018. The pure cultures were deposited in the culture collection of the Zhongkai University of Agriculture and Engineering (ZHKUCC) or the Mae Fah Luang University Culture Collection (MFLUCC), Chiang Rai, Thailand. Specimens were deposited at the Mycological Herbarium of Zhongkai University of Agriculture and Engineering (MHZU) or the herbarium of Mae Fah Luang University (MFLU) Chiang Rai, Thailand. Faces of fungi (FoF) numbers and Index Fungorum (IF) numbers were obtained as explained in Jayasiri et al. (2015) and Index Fungorum (2025). All taxonomic information will be deposited in the Greater Mekong Subregion fungal database (Chaiwan et al., 2021).

2.2.2 Molecular Studies

Fresh fungal mycelia grown on potato dextrose agar (PDA) or fruiting bodies from substrate were scraped off and transferred to a 1.5 ml microcentrifuge tube for genomic DNA extraction. Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, China) was used to extract DNA following the manufacturer's instructions. For the fungi that could not be germinated, DNA was directly extracted from the fruiting bodies using the same Kit. The polymerase chain reaction (PCR) employed a total volume of 25 µl, which contained 12.5 µl of 2xMaster Mix, 1 µl of each primer (10 pM) (forward and reverse), 2 µl genomic DNA template, and 8.5 µl ddH2O. The PCR thermal cycle program and primers are given (Table 2.1). The PCR products were sent for sequencing at SinoGenoMax, Shanghai, China.

2.2.3 Phylogenetic Analyses

To clarify the taxonomic status of potential new taxonomic units of interest in this study, ITS sequences were used for initial identification through BLASTn searches in GenBank. Phylogenetic analyses were conducted using multi-gene markers recommended in recent publications. The relevant sequence data and newly generated DNA sequences were combined, and automatic alignment and editing were completed using OFPT (Zeng et al., 2023). Afterward, all datasets were concatenated into fasta files format; the alignments were checked visually and improved manually where necessary in the AliView program (Larsson, 2014). Phylogenetic analyses were

referred to Dissanayake et al. (2020) and conducted with maximum likelihood (ML) and Bayesian posterior probability (BYPP) algorithms on the CIPRES Science Gateway portal (https://www. phylo.org/). Maximum likelihood analysis was performed by RAxML-HPC v.8, with rapid bootstrap analysis, followed by 1,000 bootstrap replicates with the GTRGAMMA substitution model. The Bayesian analyses were performed by MrBayes 3.2.7a, and the best nucleotide substitution model for each data partition was evaluated by MrModeltest 2.2 (Nylander, 2004). The Markov Chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (BYPP) (Rannala & Yang, 1996). Six simultaneous Markov chains were run for 2 million generations, and trees were sampled every 1,000th generation. The first 20% of trees, representing the burn-in phase of the analyses, were discarded, and the remaining trees were used for the BYPP value in the majority rule consensus tree. The phylogenetic trees were viewed by FigTree (v 1.4.2) (Rambaut, 2014) and edited using Microsoft Office PowerPoint (2020) and Adobe Illustrator CS6 (Adobe Systems Inc., USA). The bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes.

2.2.4 Genealogical Concordance Phylogenetic Species Recognition Analysis

The level of recombination among closely-related species was assessed using Genealogical Concordance Phylogenetic Species Recognition (GCPSR) analysis, specifically employing the Pairwise Homoplasy Index (PHI) test (Bruen et al., 2006). Data analysis was conducted using SplitsTree v. 4 software (Bruen et al., 2006; Huson & Bryant, 2006). Relationships among closely-related taxa were visualized through split graphs generated from concatenated datasets using the LogDet transformation and split decomposition options. A PHI test value of $\Phi w \leq 0.05$ indicates significant recombination within the dataset, providing crucial evidence to support species justification.

2.2.5 Diversity Analysis Methods

Sample isolation and DNA extraction were conducted as outlined below. BLASTn searches in NCBI of ITS sequences for 360 collections were performed, and the results were statistically analyzed by class, order, family, and genus levels. The ITS tree was conducted by the website of iTOL 6.9.1 (Letunic & Bork, 2024). Bar charts, pie charts, line charts, and chord diagrams were generated using statistical software,

including Tableau 2022 (Lessy et al., 2022), Origin 2022 (Shi, 2022), and Office 365, and subsequently edited using Adobe Photoshop CC 2018. Fungal diversity and evenness were assessed using the Shannon diversity index (H'), Simpson's diversity index (D) (Li et al., 2016), and Pielou's evenness index (J') (Bråthen et al., 2015) for each collection site; the formula is as follows:

$$H^{\wedge}{}' = -\sum(p_i \ln(p_i)), p_i = N_i/N_t$$

$$D = 1 - \sum(p_i^2)$$

$$J' = H' / \ln(S)$$

where Ni represents the number of isolates of each genus obtained by the collection sites, Nt is the total number of isolates obtained by the collection sites, and S is the total number of genera in the collection sites.

Table 2.1 Details of genes/loci with PCR primers and protocols used in this study

Order, Family, or Genus	Loci	PCR primers (forward/reverse)	Reference
Class Dothideomycetes			
Pleosporales, Rhizodiscinaceae,	ITS	ITS5/ITS4	White et al. (1990)
Pleurotremataceae, Hysteriaceae,	LSU	LR0R/LR5	Vilgalys and Hester (1990)
Muyocopronaceae, Patellariaceae,	SSU	NS1/NS4	White et al. (1990)
Patellariaceae, Acrocalymmaceae,	*TEF*1-α	983F/2218R	Rehner (2001)
Barriopsis	*RPB*2	fRPB2-5F/fRPB2–7cR	Liu et al. (1999)
Dothiorella, *Lasiodiplodia*,	ITS	ITS5/ITS4	White et al. (1990)
Neofusicoccum	LSU	LR0R/LR5	Vilgalys and Hester (1990)
	*TEF*1-α	728F/986R	Carbone and Kohn (19990
	*RPB*2	fRPB2-5F/fRPB2–7cR	Liu et al. (1999)
	*TUB*2	Bt2a/Bt2b	Glass and Donaldson (1995)
Class Lecanoromycetes			
Stictidaceae	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys and Hester (1990)
	*RPB*2	fRPB2-5F/fRPB2–7cR	Liu et al. (1999)
	mtSSU	mrSSU1/mrSSU3R	Zoller et al. (1999)

Table 2.1 (continued)

Order, Family, or Genus	Loci	PCR primers (forward/reverse)	Reference
Class Sordariomycetes			
Chaetosphaeriaceae, Coniochaetaceae,	ITS	ITS5/ITS4	White et al. (1990)
Conlariaceae, Nitschkiaceae,	LSU	LR0R/LR5	Vilgalys and Hester (1990)
Scortechiniaceae, Cytosporaceae,	SSU	NS1/NS4	White et al. (1990)
Erythrogloeaceae, Distoseptisporaceae,	*TEF*1-α	983F/2218R	Rehner (2001)
Plectosphaerellaceae, Stachybotryaceae,	*RPB*2	fRPB2-5F/fRPB2–7cR	Liu et al. (1999)
Bionectriaceae, Pleurotheciaceae,	*ACT*	ACT512F/ACT783R	Carbone and Kohn (1999)
Pseudodactylariaceae,	*cmdA*	CAL228F/CAL2Rd	Groenewald et al. (2013)
Helminthosphaeriaceae, Podosporaceae,	*TUB*2	Bt2a/Bt2b	Glass and Donaldson (1995)
Sporidesmiaceae, Hypoxylaceae,			
Leptosilliaceae			
Nectriaceae	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys and Hester (1990)
	*RPB*2	fRPB2-5F/fRPB2–7cR	Liu et al. (1999)
	*TUB*2	T1/T22	O'Donnell and Cigelnik (1997)
	ACT	ACT512F/ACT783R	Carbone and Kohn (1999)
Xylariaceae	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LR0R/LR5	Vilgalys and Hester (1990)
	*RPB*2	fRPB2-5f/fRPB2–7cR	Liu et al. (1999)
	*TUB*2	T1/Bt2b	O'Donnell and Cigelnik (1997)

2.3 Results

2.3.1 Diversity Analyses

In this study, a total of 360 saprobic fungal collections associated with coffee collected from eight places in Yunnan Province, China, and Chiang Rai, Thailand, were primarily analyzed based on employing a BLASTn search in GenBank using ITS sequences. The primary results revealed 360 saprobic fungal collections belonging to seven classes (Agaricomycetes, Arthoniomycetes, Dothideomycetes, Eurotiomycetes, Lecanoromycetes, Orbiliomycetes, and Sordariomycetes), 37 orders, 83 families, and 137 genera (Figures 2.1–2.3). In terms of class, Dothideomycetes was the largest class containing the most collections (255, 70.83%), followed by Sordariomycetes (91, 25.28%), Eurotiomycetes (six, 1.67%), and Lecanoromycetes (five, 1.39%). The other three classes are Agaricomycetes, Arthoniomycetes, and Orbiliomycetes, containing

the least collections (one collection each, 0.28%) (Figure 2.1). Our results, which are consistent with those for *Chromolaena odorata* (Siam weed), *Hevea brasiliensis* (Para rubber) and *Tectona grandis* (teak), with Dothideomycetes and Sordariomycetes as the dominant classes (Doliom et al., 2017; Mapook et al., 2020a; Senwanna et al., 2021), reveal both overlap and divergence in fungal assemblages. We identified several genera, such as *Colletotrichum, Diaporthe, Dothiorella, Fusarium, and Rhytidhysteron*, that were commonly found across all hosts, indicating a group of generalist fungi capable of colonizing both native and introduced plants (Doliom et al., 2017; Mapook et al., 2020a; Senwanna et al., 2021; This study). The discovery that *C. odorata* (coffee), and *H. brasiliensis* (rubber) share a substantial number of fungal taxa (*Montagnula*, *Muyocopron*, *Nigrograna*, *Neomassarina*, *Patellaria*, *Torula*) is particularly significant, suggesting that introduced plants may contribute to fungal spillover within ecosystems (Mapook et al., 2020a; Senwanna et al., 2021). Further, *the observation that Tectona grandis*, a native species, also shares several fungal taxa with coffee, such as *Barriopsis*, *Lasiodiplodia*, *Neooccultibambusa*, *Paradictyoarthrinium*, *Tubeufia*, and *Longiostiolum* (Doliom et al., 2017), indicates that these overlapping fungi may possess host-jump ability, demonstrating strong environmental adaptability and the ability to survive and reproduce on different hosts. This phenomenon suggests that the origin of plants (native vs. introduced) may influence fungal diversity and host specificity, with introduced hosts potentially acting as reservoirs or bridges for fungal transmission. The need for further comparative analyses that incorporate the ecological traits of shared fungi to provide deeper insights into fungal adaptation and host range expansion is urgent, underscoring the importance of our research.

In terms of order, class Sordariomycetes showed the highest number of orders (19 orders, 51.35%), followed by Dothideomycetes (12 orders, 32.43%), Lecanoromycetes (two orders, 5.41%) and the other four classes, Agaricomycetes, Arthoniomycetes, Eurotiomycetes and Orbiliomycetes showed the lowest number of orders each comprising one order, 2.7% (Figure 2.2a). Meanwhile, Pleosporales (Dothideomycetes) was the most prevalent order, comprising 34 families (40.96%), followed by Hypocreales and Xylariales (Sordariomycetes), which were the second prevalent orders, each comprising four families (4.81%), and the third most prevalent order, Diaporthales (Sordariomycetes), comprising three families (3.61%) (Figure 2.2b). The top three

families with the most genera were Botryosphaeriaceae, Diatrypaceae and Didymosphaeriaceae, all comprised six genera each (4.37%) (Figure 2.2c).

In terms of the genus, *Nigrograna* (16 collections, 4.44%), *Acrocalymma* (15 collections, 4.17%), *Rhytidhysteron* (11 collections, 3.06%), *Colletotrichum* (10 collections, 2.78%), and *Paraconiothyrium* (10 collections, 2.78%) were the top five genera with the highest number of collection obtained, while other 24 genera shown 4–9 collections (1.00–2.5%) namely, *Botryosphaeria*, *Brunneofusispora*, *Crassiparies*, *Diaporthe*, *Distoseptispora*, *Dothiorella*, *Fusarium*, *Helminthosporium*, *Lasiodiplodia*, *Leucaenicola*, *Longiostiolum*, *Massarioramusculicola*, *Medicopsis*, *Melomastia*, *Menisporopsis*, *Montagnula*, *Neomassaria*, *Neooccultibambusa*, *Paradictyoarthrinium*, *Phaeosphaeria*, *Pseudochaetosphaeronema*, *Sporidesmium*, *Stephanonectria* and *Tubeufia* (Figure 2.3). Additionally, we conducted a statistical analysis of the life modes reported for species within each genus, drawing on data from previous studies. The results indicated that most collections belong to the genera previously reported as only saprobes, comprising 158 collections (43.89%), followed by 148 collections (41.11%) belonged to the genera previously were reported as saprobes, endophytes, and pathogens, and then 32 collections (8.89%) belonged to the genera previously were reported as both saprobes and endophytes. The fewest collections belonged to genera reported as both saprobes and pathogens, totaling 22 collections (6.11%) (Figures 2.1, 2.3).

All strains were collected from seven sites in China (Yunnan: Baoshan, Dali, Dehong, Jinghong, Lincang, Nujiang, and Pu'er City) and one site in Thailand (Chiang Rai). According to the results (Figures 2.1, 2.4a), Pu'er City (Yunnan, China) comprises 90 collections across 59 genera, 44 families, and 22 orders, followed by Jinghong City (Yunnan, China) comprises 52 collections across 39 genera, 30 families, and 14 orders, Baoshan City (Yunnan, China) comprises 50 collections across 41 genera, 33 families, and 14 orders, Chiang Rai (Thailand) comprises 41 collections across 33 genera, 27 families, and 15 orders, Lincang (Yunnan, China) also comprises 41 collections across 30 genera, 25 families, and 10 orders, Dali City (Yunnan, China) comprises 36 collections across 24 genera, 19 families, and six orders, Dehong City (Yunnan, China) comprises 27 collections across 20 genera, 16 families, and 11 orders, Nujiang City (Yunnan, China) had the lowest strain count, with 23 strains spanning 18 genera,

15 families, and four orders. In these eight collection sites, unique strains were identified in each area; each individual chord in Figure 2.4b illustrates the overlap of genera among the regions. Sorted by the number of non-overlapping genera from highest to lowest, Pu'er City has 23 genera (38.98%), Chiang Rai (Thailand) has 12 genera (36.36%), Dali City has 11 genera (45.83%), Jinghong City has nine genera (23.08%), Baoshan and Lincang City has six genera (14.63% and 20.00%, respectively), Dehong City has five genera (25.00%), and Nujiang City has three genera (16.67%) (Figure 2.4b).

The diversity of saprobic fungi associated with coffee in Yunnan, China, and Chiang Rai, Thailand, was evaluated using the Shannon Diversity Index (H′), Simpson's Diversity Index (D), and the Evenness Index (J') (Lu et al., 2022c).

The Shannon index (H′) was used to quantify fungal diversity within communities, with higher values indicating greater ecological diversity (Strong, 2016). Simpson's index (D), which highlights both species richness and distributional evenness within sample sites, complements the Shannon index, the values range from 0 (dominance by a single species) to 1(maximum diversity), with high values indicating that species are distributed evenly (Faith and Du 2018). The Evenness Index (J') evaluates the uniformity of species abundance, high evenness (J' close to 1) typically indicates a balanced community where no single species dominates, while low evenness (J' close to 0) may result from environmental stressors, competitive exclusion, or the presence of a dominant species (Zhang et al., 2021b). According to Table 2.2, Pu'er City in Yunnan, China, shows the highest values for the Shannon Diversity Index (H' = 3.9258) and Simpson's Diversity Index (D = 0.9763), but with the lowest Evenness Index (J' = 0.9628), indicating a high fungal diversity and a few dominant species prevail in the ecosystem; in contrast, most other species exist in smaller numbers, resulting in an uneven species distribution in this region. In contrast, Baoshan City in Yunnan, China, exhibits high values across all three indices (H' = 3.6416, D = 0.9712, J' = 0.9806), suggesting a healthy ecosystem with rich and well-distributed diversity. The diversity indices of the remaining six regions tended to be relatively stable, Dali City in Yunnan, China, are H' = 3.0778, D = 0.9491, J' = 0.9685, Dehong City in Yunnan, China, are H' = 2.8977, D = 0.9383, J' = 0.9673, Jinghong City in Yunnan, China, are H' = 3.5478, D = 0.9667, J' = 0.9684, Lincang City in Yunnan, China, are H'

= 3.3034, D = 0.9590, J' = 0.9712, Nujiang City in Yunnan, China, are H' = 2.8114, D = 0.9338, J' = 0.9727, Chiang Rai, Thailand, are H' = 3.4176, D = 0.9637, J' = 0.9774. Among these, the lower values in Dehong and Nujiang Cities indicate that fungal diversity in these regions is low and species distribution is uneven, which may predict an ecological imbalance in these areas. Since diversity data is available for only one site in Thailand, a direct comparison of fungal diversity between China and Thailand is not feasible. However, the data suggest that fungal diversity at the Thailand site is moderate, which may indicate a relatively stable ecological environment with a balanced species distribution. However, due to the limited nature of the data and the broad distribution of coffee-growing regions in Thailand, our data cannot fully reflect the diversity of coffee-growing environments across the country. Further data from multiple sites across Thailand would be necessary to draw more comprehensive conclusions about the country's coffee-associated fungal diversity and make more meaningful comparisons with the Chinese sites.

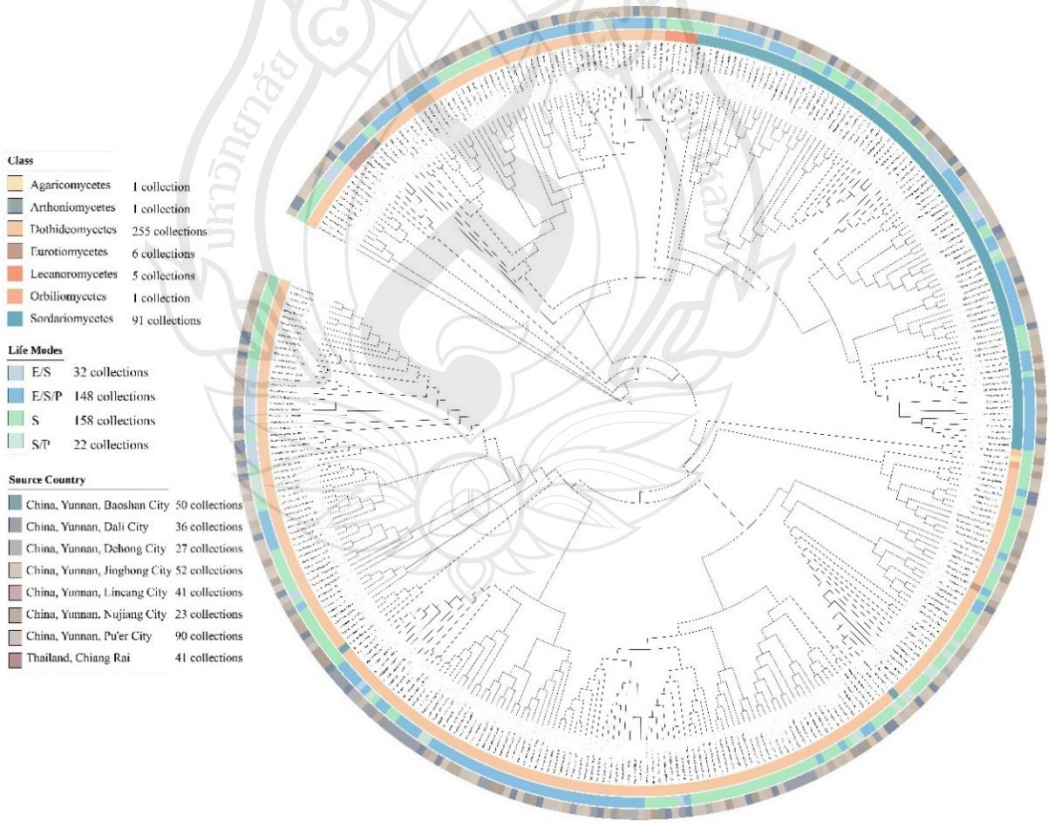


Figure 2.1 Phylogenetic tree of 360 coffee collections obtained from coffee based on ITS sequences

Figure 2.1 From the inside to the outside, the first layer of color represents the distribution (class level) of the fungus species, the second layer of color represents its corresponding life modes of the genus, and the third layer of color represents its corresponding location where the strain was collected.

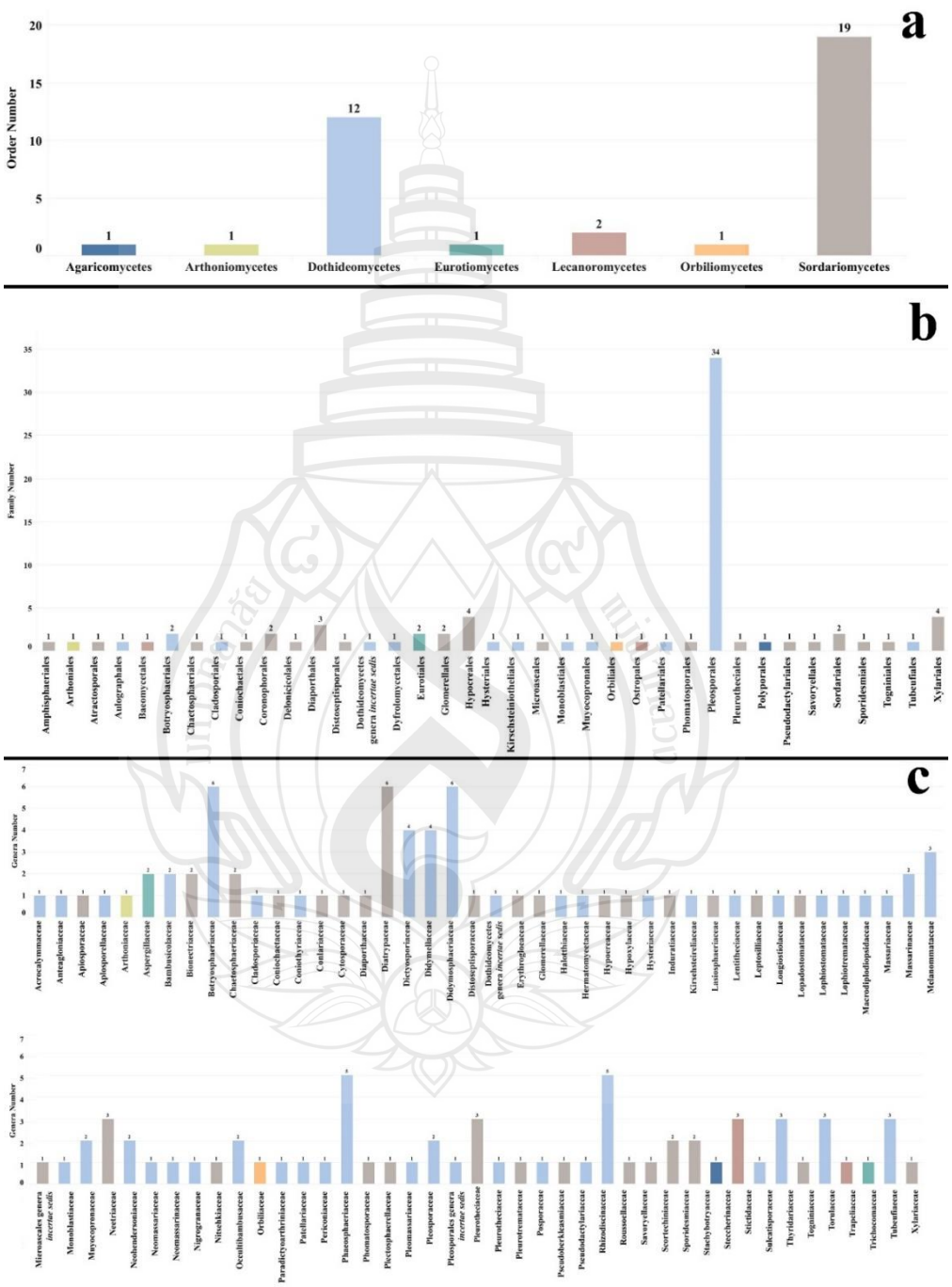


Figure 2.2 Bar graph showing the diversity distribution of 360 strains by class, order, and family

Figure 2.2 (a) The number of orders within seven classes. (b) The number of families within 37 orders. (c) The number of genera within 83 families. Each color indicates that it belongs to the same class.

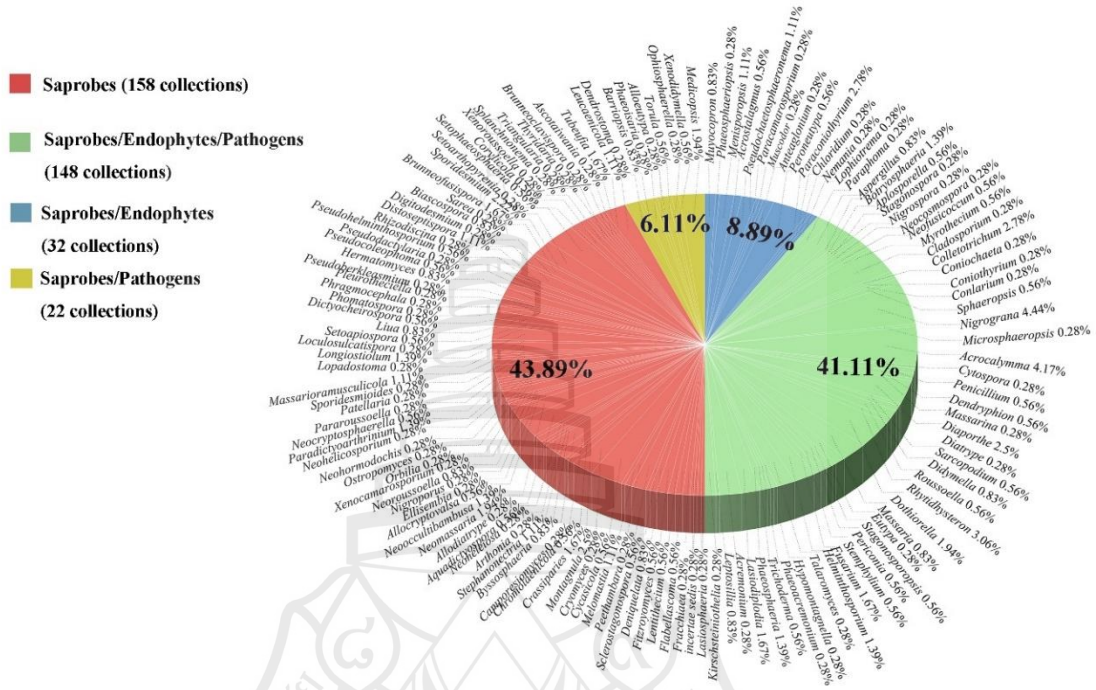


Figure 2.3 A pie charts display the percentage distribution of 360 collections across 137 genera and their corresponding life modes

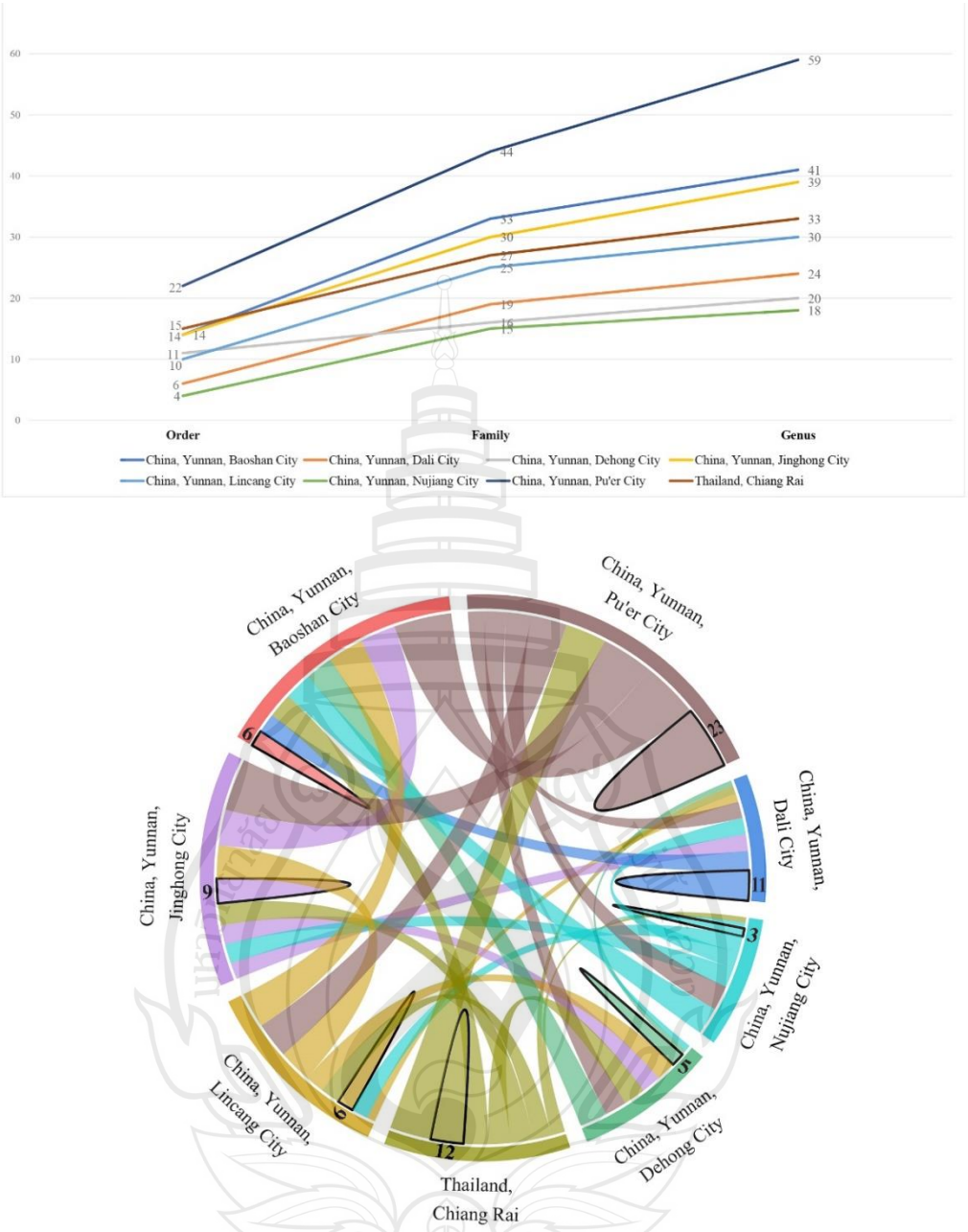


Figure 2.4 Diversity of coffee-associated saprobic fungi across eight collection sites

Figure 2.4 (a) Line chart showing taxonomic diversity (order, family, and genus) across different collection sites. (b) Chord diagram illustrating genus-level overlap and unique fungal distributions among the eight collection sites (Numbers indicate the number of unique genera in each region).

Table 2.2 Fungal diversity analyses of saprobic fungi associated with coffee hosts from different population sites

Collection sites	H'	D	J'
China, Yunnan, Baoshan City	3.6416	0.9712	0.9806
China, Yunnan, Dali City	3.0778	0.9491	0.9685
China, Yunnan, Dehong City	2.8977	0.9383	0.9673
China, Yunnan, Jinghong City	3.5478	0.9667	0.9684
China, Yunnan, Lincang City	3.3034	0.9590	0.9712
China, Yunnan, Nujiang City	2.8114	0.9338	0.9727
China, Yunnan, Pu'er City	3.9258	0.9763	0.9628
Thailand, Chiang Rai	3.4176	0.9637	0.9774

Note H' = Shannon's diversity index, D = Simpson's Diversity Index, and J' = Pielou's evenness index

2.3.2 Taxonomy

2.3.2.1 Dothideomycetes

Aulographales Crous, Spatafora, Haridas & I.V. Grig., Studies in Mycology 96: 151 (2020)

Rhizodiscinaceae Crous, Spatafora, Haridas & I.V. Grig., Studies in Mycology 96: 151

Rhizodiscina Hafellner, Beih. Nova Hedwigia 62: 195 (1979)

Notes: Rhizodiscina was proposed by Hafellner (1979) with the type species *R. lignyota*. The species was initially described as *Peziza lignyota* by Fries (1822). Hafellner (1979) re-examined and revised *Pe. lignyota*, then designating the strain M 0177903 (CUP-D 110-43) from Germany as the type specimen of *R. lignyota.* Kutorga and Hawksworth (1997) reported that many characteristics of *R. lignyota* are similar to *Poetschia* in different shapes and sizes of asci and spores, as well as in the structure of the epithecium. However, a distinguishing feature between *Poetschia* and *Rhizodiscina* is the massive exciple in *R. lignyota*, which occupies nearly half of the ascoma, unlike *Po. andicola* (Yacharoen et al., 2015). Presently, five species are listed in this genus and only reported from the sexual morph (Johnston, 2022; Index Fungorum, 2025), and

among those, only two species contain sequence data (*R. lignyota* and *R. rimosa*) (Johnston, 2022). In this study, we introduce the first asexual morph of *Rhizodiscina* from coffee in Yunnan Province, China.

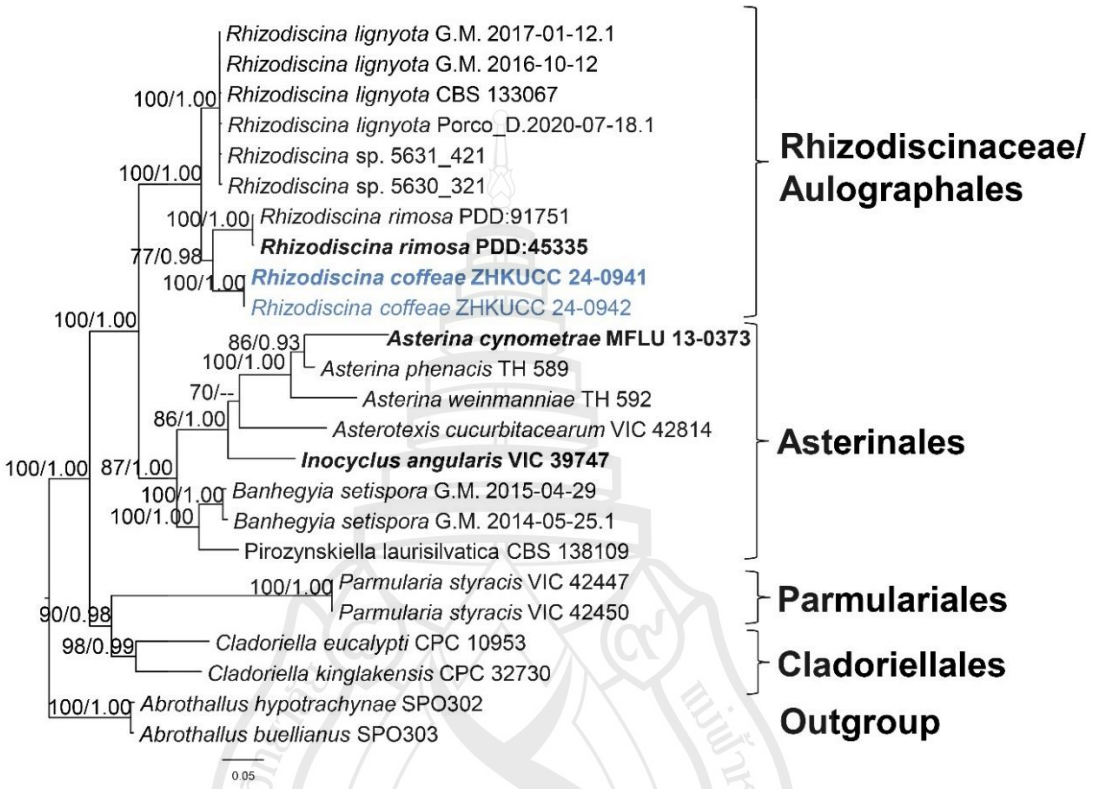


Figure 2.5 Phylogenetic tree of *Rhizodiscina*

Figure 2.5 Phylogram generated from maximum likelihood analysis based on a combined ITS and LSU sequence dataset. Twenty-four strains are included in the combined sequence analysis, which comprises 1,242 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Abrothallus buellianus* (SPO303) and *Abrothallus acetabuli* (SPO308).

Rhizodiscina coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903644; *Facesoffungi number*: FoF 17551; Figure 2.6

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0517

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Coelomycetous. *Conidiomata* 100–180 µm high × 100–180 µm diam. ($\overline{x}$ = 128 × 126 µm, n = 15), apothecial, superficial, subglobose, in small groups or scattered on the bark, exposing a black velvety hymenium at maturity, crenulated and rising above at the rim, convex in outline, with black anchoring base, unilocular, thick-walled. *Conidiomata wall* 15–20 µm wide ($\overline{x}$ = 17.5 µm, n = 20) wide, density, outer layer composed of 2–4 layers, brown colour cells of *textura angularis* to *textura globulosa*, inner layer thin, hyaline colour cells of *textura angularis*. *Conidiophores* inconspicuous or micronematous, formed from the innermost layer of wall cells, often reduced to conidiogenous cells. *Conidiogenous cells* 7–11 × 2–4 µm ($\overline{x}$ = 8.5 × 2.9 µm, n = 25), holoblastic, subglobose or cylindrical or obpyriform, hyaline, smooth, some branched, with a rounded tip, producing a single conidium at the tip. *Conidia* 2.5–3.5 × 1.5–2 µm ($\overline{x}$ = 3.1 × 1.7 µm, n = 25), 1-celled, oblong or cylindrical, rounded at both ends, hyaline, aseptate, granulates, smooth-walled, without a mucilaginous sheath. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 35–40 mm in one month at 25°C, circular, umbonate, with entire margin, rough surface with aerial mycelium, flossy, velvety, from above olivaceous-green and below olivaceous green to black.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 2 February 2024, Li Lu, XAZC-2-7 (MHZU 24-0517, holotype), ex-type ZHKUCC 24-0941, other living culture ZHKUCC 24-0942.

GenBank numbers: ZHKUCC 24-0941: ITS = PQ608192, LSU = PQ608029; ZHKUCC 24-0942: ITS = PQ608193, LSU = PQ608030.

Notes: Based on the phylogenetic analyses of combined ITS and LSU sequence, our isolates form a lineage sister to *Rhizodiscina rimosa* strains (PDD 91751

and PDD 45335, ex-type) with statistical bootstrap support (77 ML/0.98 BYPP) (Figure 2.5). In a BLASTn search, our collection's ITS and LSU sequences showed 97% and 99% similarity to *R. lignyota* (OP763100 and OP763385), respectively. In morphologically, only the sexual morph of *Rhizodiscina* species is known (Yacharoen et al., 2015; Johnston, 2022; Yao et al., 2023). Unfortunately, we were unable to obtain the sexual morph for our species which makes it not possible to compare morphology. While the fruiting body morphology of our species is similar to other *Rhizodiscina* species by superficial, crenulated and arising above at the rim, with a convex outline, with black anchoring base (Yacharoen et al., 2015; Johnston, 2022; Yao et al., 2023; Figure 2.6). We, therefore, identified our collection as a new species *R. coffeae*, which is for the first time isolated from coffee plants in China and represents the asexual morph of *Rhizodiscina*.

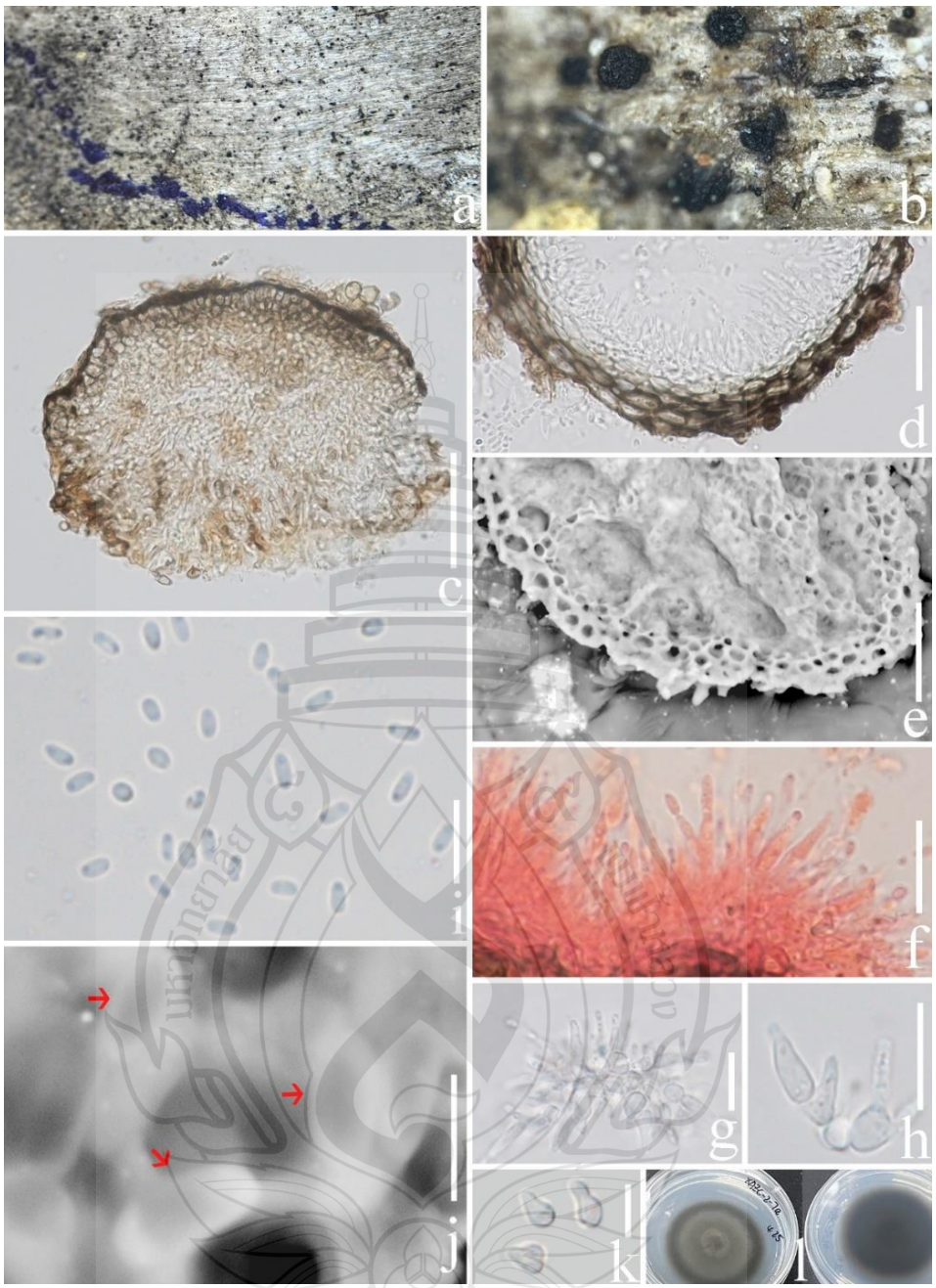


Figure 2.6 *Rhizodiscina coffeae* (MHZU 24-0517, holotype)

Figure 2.6 a, b Conidiomata on a decaying branch of *Coffea arabica.* c Longitudinal section of conidioma. d, e Conidioma wall (e: SEM microphotographs of conidioma wall). f–h Conidiogenous cells with conidia (f: stained with Congo red reagent). i, j Conidia (j: SEM microphotographs of conidia showing smooth perispore). k Germinated conidia. l Culture on PDA from above and below. Scale bars: c = 50 µm, d, e = 20 µm, f–i, k = 10 µm, j = 2 µm.

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2006)

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

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

Notes: Based on the morphological and phylogenetic distinction from other genera in Botryosphaeriaceae, *Barriopsis* was introduced by Phillips et al. (2008), with the type species *Barriopsis fusca*. The species had initially been described as *Physalospora fusca* by Stevens (1926). *Barriopsis* is one of the less well-known genera in the family Botryosphaeriaceae (Jayawardena et al., 2019a). There are only five species reported for this genus, *viz*. *B. archontophoenicis*, *B. fusca* (= *Barriopsis stevensiana*), *B. iraniana*, *B. tectonae*, and *B. thailandica* (Hyde et al., 2024a; Wang et al., 2024b). Members of *Barriopsis* are distributed in Cuba, Iran and Thailand from different hosts, and it is known from both sexual and asexual morphs (Phillips et al., 2008; Abdollahzadeh et al., 2009; Doilom et al., 2014; Tibpromma et al., 2017). The sexual morph of *Barriopsis* is characterised by pseudothecia ascomata, hyaline and septate pseudoparaphyses, bitunicate, clavate and stipitate asci with ellipsoid to ovoid ascospores (Phillips et al., 2008; Tibpromma et al., 2017). *Barriopsis* has a Lasiodiplodia-like asexual morph with conidia that are initially hyaline, aseptate and thick-walled, becoming dark brown and septate with irregular longitudinal striations (Stevens, 1926; Phillips et al., 2008). In this study, a new species exhibiting asexual morphs is introduced from a coffee host in China. This is the first report of a *Barriopsis* species isolated from coffee in China.

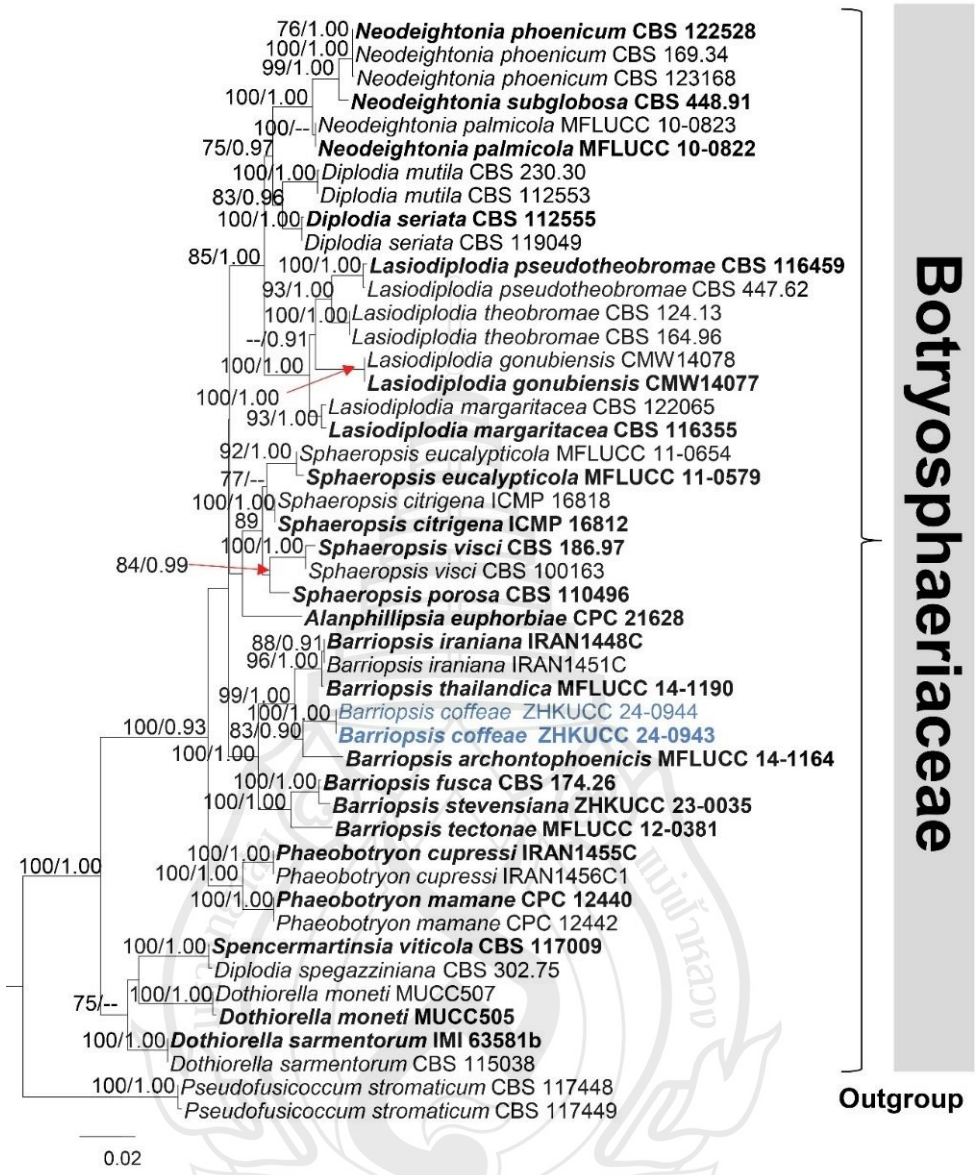


Figure 2.7 Phylogenetic tree of *Barriopsis*

Figure 2.7 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU SSU, and *TEF*1-α sequence data. Forty-seven strains are included in the combined sequence analysis, which comprises 3,366 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Pseudofusicoccum stromaticum* (CBS 117448 and CBS 117449).

Barriopsis coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903603; *Facesoffungi number*: FoF 17552; Figure 2.8, Figure 2.9

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0518

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Coelomycetous. *Conidiomata* 150–280 ×15– 300 µm diam. ($\overline{x}$ = 210 × 199 µm, n = 10), stromatic, pycnidial, superficial, dark brown to black, solitary, subglobose or oval, uniloculate, thick-walled, ostiolate. *Ostioles* central, circular, epapillate. *Peridium* 25–40 µm wide ($\overline{x}$ =33 µm, n = 20), composed of outer layers of brown to black, thick-walled, cells of *textura globulosa* or *textura agularis*, inner layers hyaline and thin-walled. *Hamathecium* arising from the conidiogenous layer, up to 70 µm long, 3 µm wide, extending above the level of developing conidia, hyaline, usually aseptate and unbranched, and tip rounded, paraphyses. *Conidiophores* absent. *Conidiogenous cells* 6–10 × 3–6 µm ($\overline{x}$ = 8 × 4.7 µm, n = 30), holoblastic, cylindrical or ovoid, slightly swollen at the base, hyaline, thin and smooth-walled. *Conidia* 25–35 × 13–16 µm ($\overline{x}$ = 30 × 14 µm, n = 30), hyaline, solitary, oblong or oval, aseptate, thick-walled, sometimes with small guttules, with longitudinal striations. **Asexual morph in culture**: *Mycelium* 3–7 µm broad ($\overline{x}$ = 4.8 µm, n = 30), pale brown to brown, septate and branched. *Chlamydospores* intercalary, catenate, light brown to brown, smooth and thick-walled, formed within the PDA medium around three months. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours and germ tube produced from one end of the ascospore. Colonies on PDA reaching 9 cm diam. after one month at 25°C, with appressed mycelial mat and fluffy aerial mycelium on the surface, becoming dull green to olivaceous-black from above, hyphae septate, branched, smooth. Dull green to black from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC-1 (MHZU 24-0518, holotype), ex-type ZHKUCC 24-0943, other living culture ZHKUCC 24-0944.

GenBank numbers: ZHKUCC 24-0943: ITS = PQ608194, LSU = PQ608031, SSU = PQ607921, *TEF*1-α = PQ602085; ZHKUCC 24-0944: ITS = PQ608195, LSU = PQ608032, SSU = PQ607922, *TEF*1-α = PQ602086.

Notes: In the present phylogenetic analysis, *Barriopsis coffeae* formed a sister lineage to *B. archontophoenicis* with 83% ML and 0.90 BYPP statistical support (Figure 2.7). Based on the molecular sequence comparison, our isolate (ZHKUCC 24-0943, ex-type) differs from *B. archontophoenicis* (MFLUCC 14-1164, type) by 9/455 bp for ITS (2%, without gaps), 20/989 bp (2%, without gaps) for LSU, 3/1018 bp (0.2%, without gaps) for SSU, and 3/340 bp (0.8%, without gaps) for *TEF*1-α. In morphology, long hamathecium and hyaline conidia of *B. coffeae* with longitudinal striations can be distinguished from hyaline to brown conidia of *B. archontophoenicis* (Konta et al., 2016; Figure 2.8) and other *Barriopsis* species (Abdollahzadeh et al., 2009; Doilom et al., 2014; Tibpromma et al., 2017). Therefore, *Barriopsis coffeae* is introduced here as a new species.

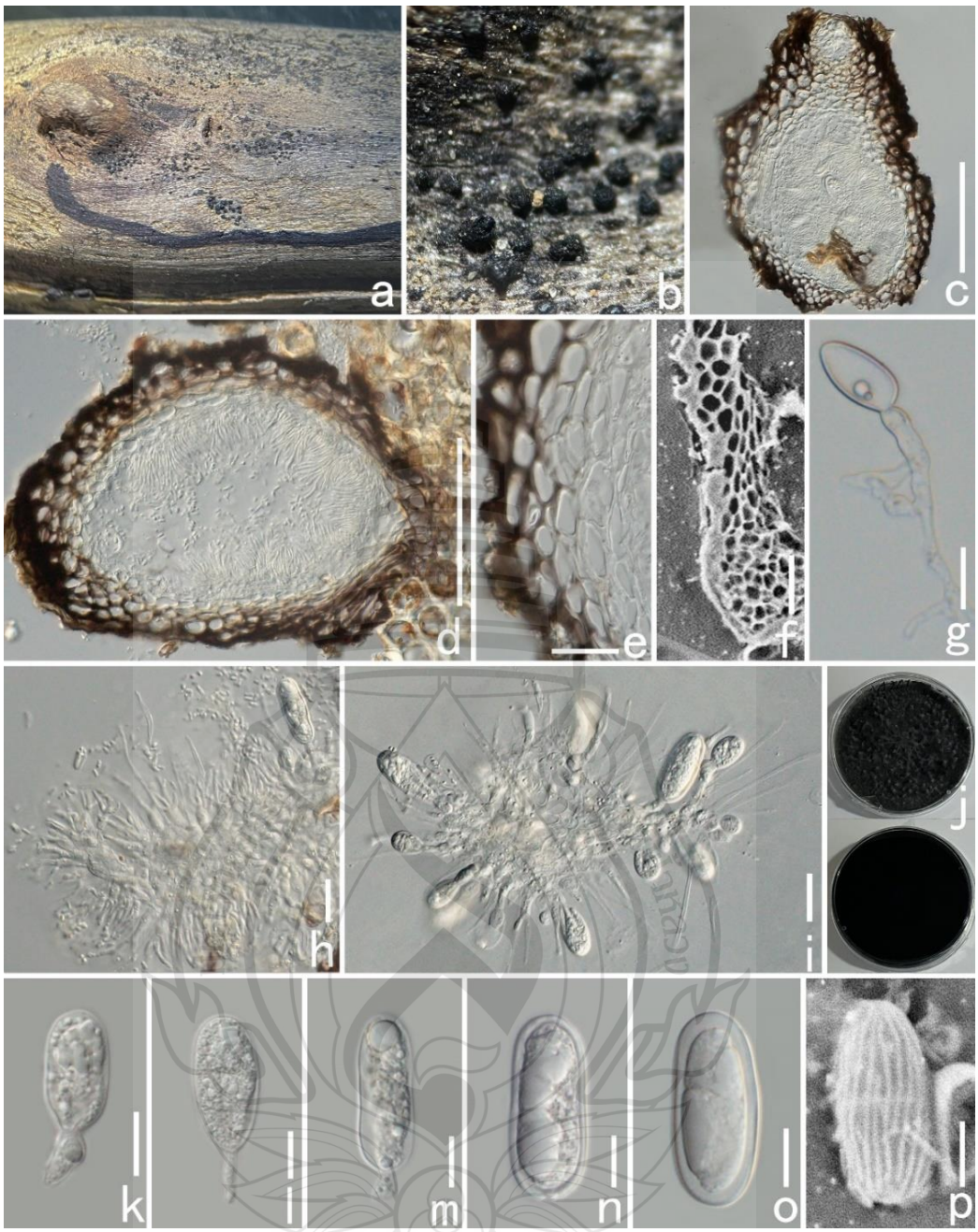


Figure 2.8 *Barriopsis coffeae* (MHZU 24-0518, holotype)

Figure 2.8 a, b Conidiomata on a decaying branch of *Coffea arabica*. c, d Longitudinal section of conidiomata. e, f Peridium (f: SEM microphotographs of peridium). h Paraphyses. i Conidiogenous cells with conidia. j Germinated conidium. k–p Conidia (p: SEM microphotographs of conidia show the longitudinal stripes). i Culture on PDA from above and below. Scale bars: c, d = 100 µm, f–i = 20 µm, k–p = 10 µm.



Figure 2.9 *Barriopsis coffeae* (ZHKUCC 24-0943, ex-type living culture on PDA)

Figure 2.9 a–c Mycelium. d–f Catenulate chlamydospores (d: Chain formations; e, f: Intercalary formations). Scale bars: a–f = 10 μm.

***Dothiorella* Sacc., Michelia 2 (6): 5 (1880)**

Notes: Dothiorella was introduced by Saccardo (1880), with *D. pyrenophora* as the type species. There are 422 epithets in Index Fungorum (2025). However, *Dothiorella* encountered a series of revisions as many species in this genus have been reduced to synonymy (Dissanayake et al., 2021; Zhang et al., 2021). Zhang et al. (2021) made a systematic revision of *Dothiorella* by synonymizing 15 known species, which reduced the number of *Dothiorella* members and established a more stable systematic relationship. Based on phylogenetic analyses of combined ITS, LSU, *TEF*1-α, and *TUB*2, presently only 44 species are accepted in this genus (Wu et al., 2021; Li et al., 2023; Wu et al., 2023). *Dothiorella* has often been confused with *Diplodia* in morphological characterizations. The type species, *Dothiorella pyrenophora* differs from *Diplodia* by conidia that are brown and 1-septate early in their development, while they are attached to the conidiogenous cells (Phillips et al., 2005). Sexual morphs of *Dothiorella* have erumpent or superficial ascomata and clavate asci with septate ascospores (Wu et al., 2021; de Farias et al., 2023). However, the sexual morph of the species is rarely found in nature and has never been reported in culture. Here, we introduce a new species (*D. coffeae*) and two new records (*D. acericola* and *D. camelliae*) of *Dothiorella* isolated from Yunnan Province, China. Besides, this is the first report of a *Dothiorella* species on coffee plants.

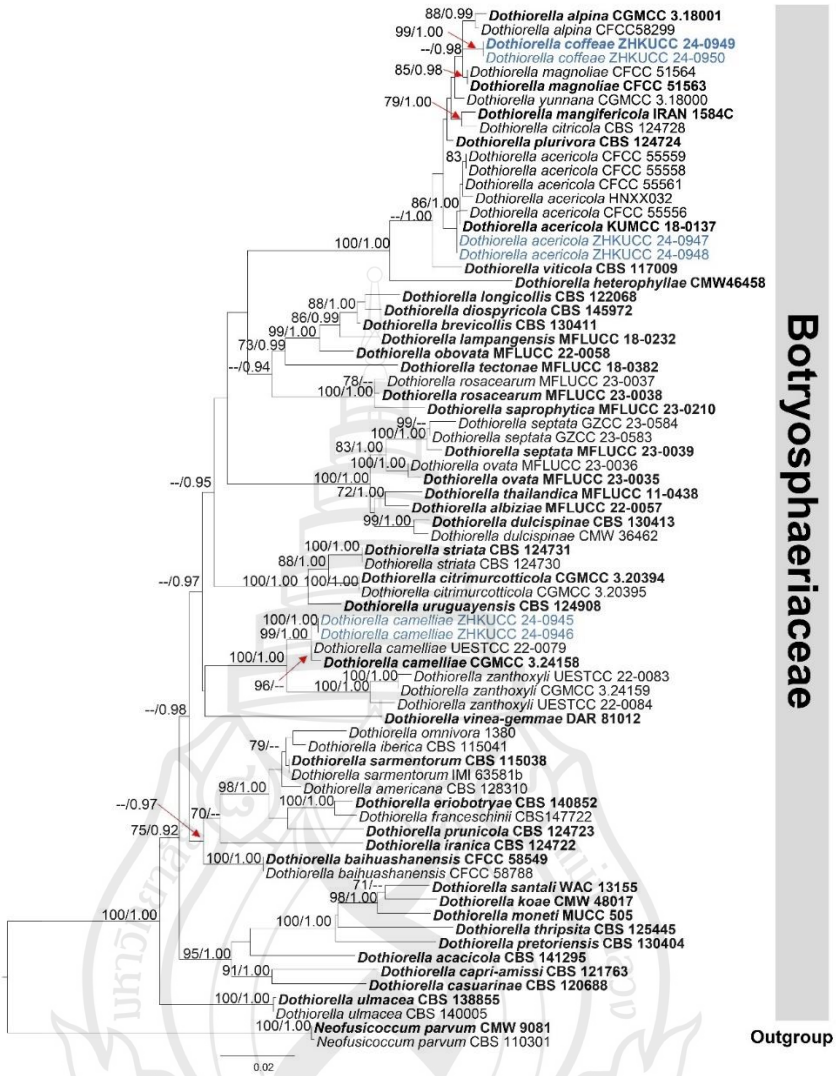


Figure 2.10 Phylogenetic tree of *Dothiorella*

Figure 2.10 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *TEF*1-α, and *TUB*2 sequence data. Seventy-four strains are included in the combined sequence analysis, which comprises 2045 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Neofusicoccum parvum* (CBS 110301 and CMW 9081).

Dothiorella acericola Phookamsak, Tennakoon & K.D. Hyde, Fungal Diversity 95: 78 (2019) (BS1-C1)

Index Fungorum number: IF 556178, *Facesoffungi number*: FoF 05711; Figure 2.11

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 150–230 × 200–250 μm ($\bar{x}$ = 179 × 218 μm, n = 10), immersed, moderately erumpent in the bark at maturity, dark brown to black, globose to subglobose, ostioles papillate, central. *Peridium* 25–35 μm wide ($\bar{x}$ = 32 μm, n = 30), composed of *textura globulosa* or *textura angularis* cells, outer layer dark brown thick-walled, inner layer subhyaline to hyaline, thinner-walled cells. *Hamathecium* of 3–6 μm wide ($\bar{x}$ = 4.8 μm, n = 30), hyaline, unbranched, septate, slightly constricted at the septum, pseudoparaphyses, *Asci* 80–140 × 20–25 μm ($\bar{x}$ = 116 × 22 μm, n = 30), 2–8-spored, clavate, bitunicate, well-developed apex-bearing chamber, rounded at apex, irregularly biseriate. *Ascospores* 17–22 × 10–13 μm ($\bar{x}$ = 20 × 11.8 μm, n = 30), subglobose, oblong, ovoid to sub-clavate, 0–1-septate, slightly or constricted at the septum, with a dark brown band at the septa, pale brown and later become dark brown at maturity, smooth-walled, straight, cells obtuse or acute towards ends. **Asexual morph**: See Phookamsak et al. (2019).

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching up to 9 cm diam. at 25°C after one month, circular, slightly raised, margin diffuse, sparse, at first white, later becoming dark greenish olivaceous from above, olivaceous to black from below.

Known hosts: Acer palmatum (Phookamsak et al., 2019); *Ziziphus jujuba* (Pan et al., 2021); *Euonymus japonicus* (Lin et al., 2023); *Coffea* sp. (This study).

Known distribution: China (Phookamsak et al., 2019; Pan et al., 2021; Lin et al., 2023; This study).

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (1053 m), 30 July 2022, Li Lu, BS1-C1 (MHZU 24-0520), living culture ZHKUCC 24-0947, other living culture ZHKUCC 24-0948.

GenBank numbers: ZHKUCC 24-0947: ITS = PQ608198, LSU = PQ608035, *TEF*1-α = PQ602089; ZHKUCC 24-0948: ITS = PQ608199, LSU = PQ608036, *TEF*1-α = PQ602090.

Notes: Dothiorella acericola was discovered on various plants as saprobes and pathogens from China and is only known from its asexual morphs (Phookamsak et al., 2019; Pan et al., 2021; Lin et al., 2023; Pem et al., 2024). In this study, our new collection is reported the sexual morph for the first time (Figure 2.11). Based on phylogenetic analyses, our isolates grouped together with other strains of *D. acericola* (CFCC 55556 and KUMCC 18-0137 ex-type) with a ML/BI = 86/1.00 statistical support (Figure 2.10). We were unable to observe the asexual morph from our collection; hence, the morphology could not be compared. However, based on the phylogenetic analyses, we identify our collection as *D. acericola*. Thus, we introduce it here as a new host record from coffee plants, and this represents the sexual morph of *D. acericola* for the first time.

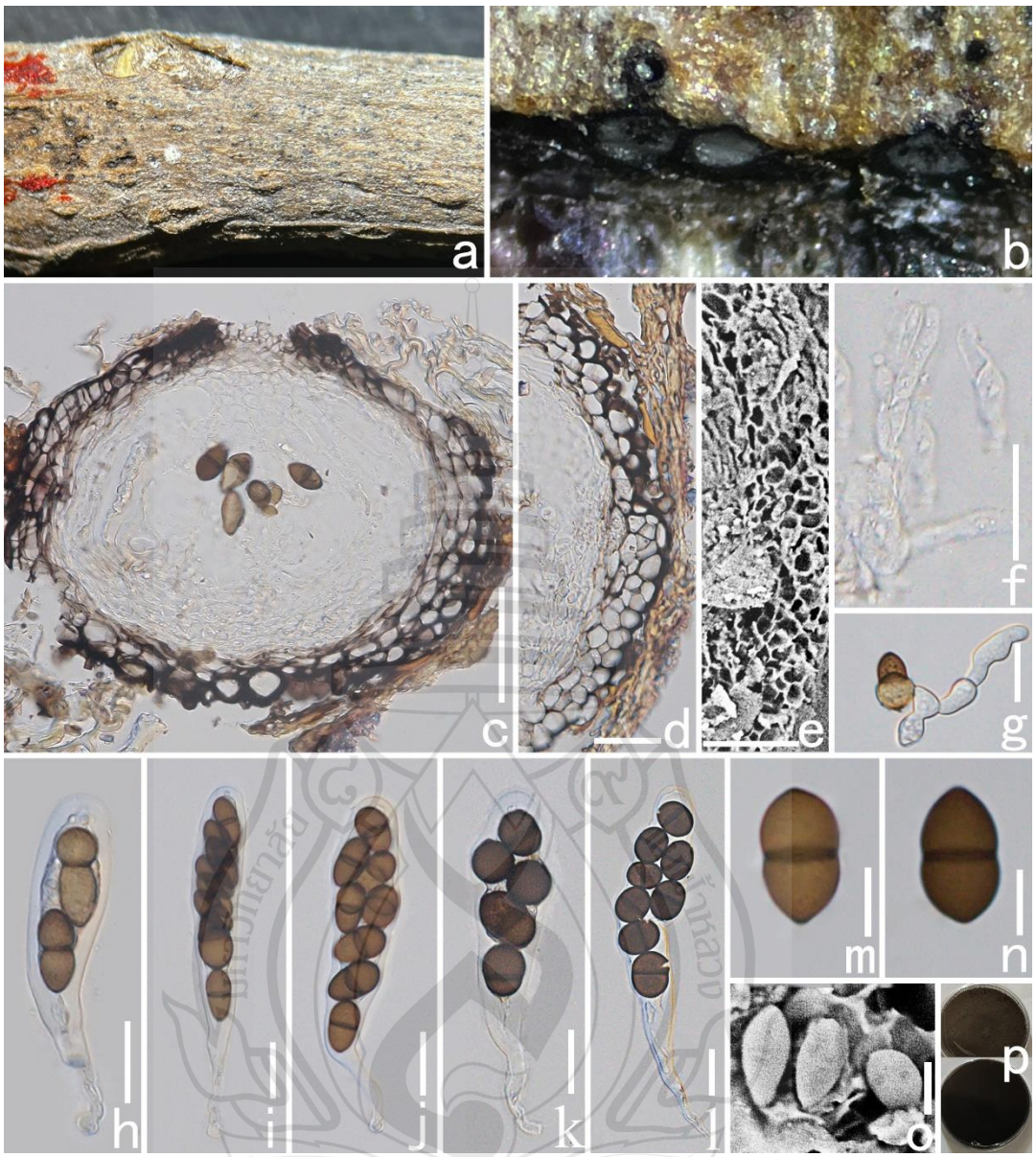


Figure 2.11 *Dothiorella acericola* (MHZU 24-0520, new host record)

Figure 2.11 a, b Appearance of ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g Germinated ascospore. h–l Asci. m–o Ascospores (o: SEM microphotographs of ascospores). p Culture on PDA from above and below. Scale bars: c = 50 µm, d, e = 30 µm, f–l = 20 µm, m–o = 10 µm.

Dothiorella camelliae L.W. Li & Jian K. Liu, MycoKeys 97: 94 (2023) (JHMH8)

Index Fungorum number: IF 847167; *Facesoffungi number:* FoF 14572; Figure 2.12

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 150–240 × 180–280 µm ($\bar{x}$ = 210 × 235 µm, n = 10), semi-immersed, partly erumpent at maturity, solitary or gregarious, dark brown to black, subglobose, multilocular, with ostiole. *Peridium* 30–45 µm wide ($\bar{x}$ = 37 µm, n = 10), thick-walled, outer layers composed of 2–4 layers dark brown cells of *textura angularis*, becoming hyaline towards the inner region. *Hamathecium* of 3–5 µm wide ($\bar{x}$ = 4.1 µm, n = 10), hyaline, frequently aseptate, pseudoparaphyses. *Asci* 70–110 × 18–25 µm ($\bar{x}$ = 91 × 24.7 µm, n = 30), 6–8-spored, clavate, short-stalked with club-like, thick-walled, bitunicate, irregularly biseriate. *Ascospores* 19–25 × 10–12 µm ($\bar{x}$ = 22.6 × 11 µm, n = 30), oblong or oval, 0–1-septate, slightly constricted at the septum, hyaline to dark brown, moderately thick-walled, straight, cells obtuse or acute towards ends. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on PDA reaching 90 mm diam. after two months at 25°C, circular, effuse, raised, fluffy, with entire to slightly undulate edge. Surface initially white and later turning dark olivaceous from the surrounding of the colony and dark brown to black from below.

Known hosts: Camellia oleifera (Li et al., 2023), *Coffea* sp. (This study).

Known distribution: China (Li et al., 2023; This study).

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (1672 m), 12 September 2021, Li Lu, JHMH8 (MHZU 24-0519), living culture ZHKUCC 24-0945, other living culture ZHKUCC 24-0946.

GenBank numbers: ZHKUCC 24-0945: ITS = PQ608196, LSU = PQ608033, *TEF*1-α = PQ602087, *TUB*2 = PQ572175; ZHKUCC 24-0946: ITS = PQ608197, LSU = PQ608034, *TEF*1-α = PQ602088, *TUB*2 = PQ572176.

Notes: Dothiorella camelliae was isolated as saprobes on the decaying branches of *Camellia oleifera* in China (Li et al., 2023). In the multi-gene phylogenetic analysis, our new collection clustered with the ex-type strain of *D. camelliae* (CGMCC 3.24158) with 99% ML and 1.00 BYPP statistical support (Figure 2.10). The BLASTn searches of the ITS, LSU, *TEF*1-α, and *TUB*2 sequence of our species resulted in 99.5%

matches with *D. camelliae*. The morphology is almost identical with *D. camelliae* in Li et al. (2023) by having a similar shape of the asci and ascospore (Li et al., 2023; Figure 2.12). Therefore, herein we report the first record of *D. camelliae* isolated from coffee.

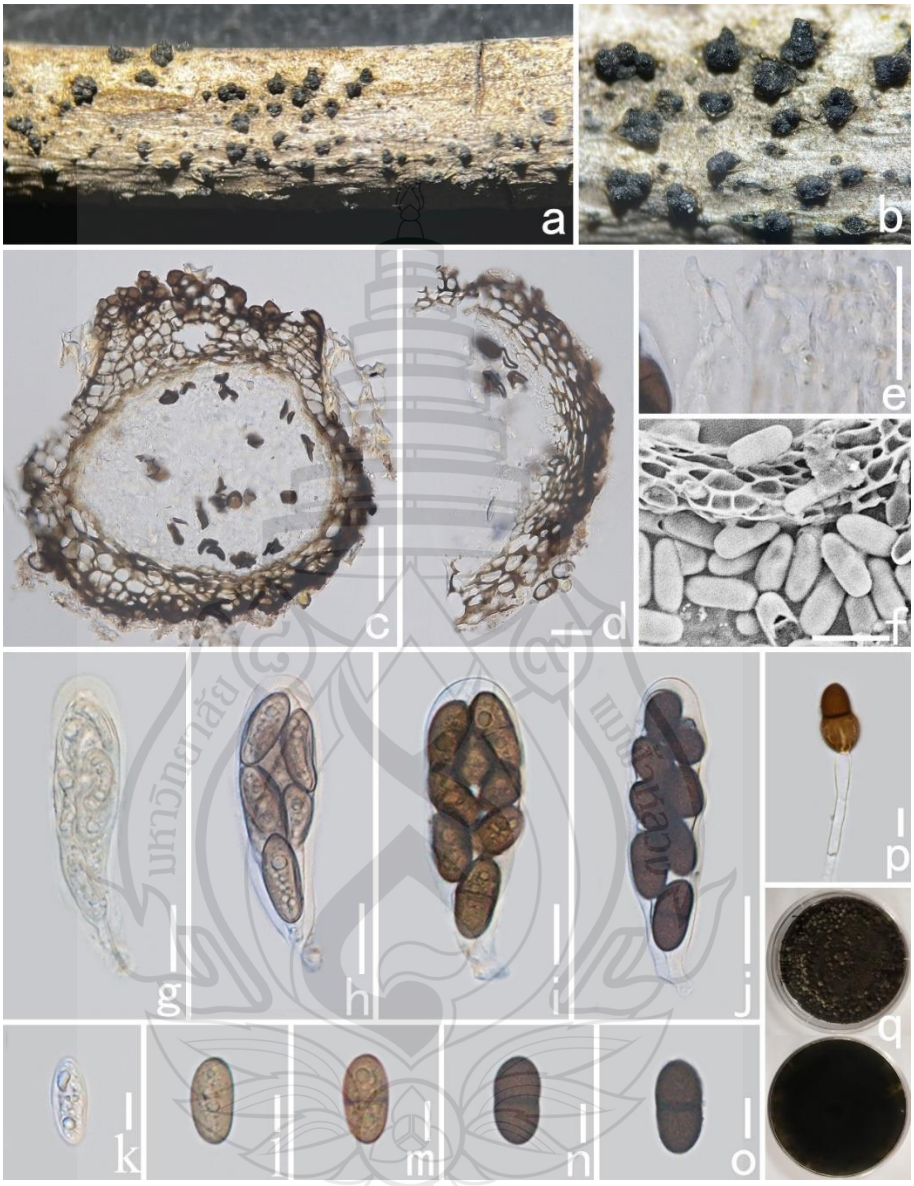


Figure 2.12 *Dothiorella camelliae* (MHZU 24-0519, new host record)

Figure 2.12 a, b Appearance of ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d Peridium. e Pseudoparaphyses. f: SEM microphotographs of peridium and ascospores. g–j Asci. k–o Ascospores. p Germinated conidium. q Culture on PDA from above and below. Scale bars: c = 50 µm, d = 30 µm, e–j = 20 µm, k–p = 10 µm.

Dothiorella coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903611; *Facesoffungi number*: FoF 17553; Figure 2.13

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0521

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 200–300 × 180–250 μm ($\bar{x}$ = 234 × 210 μm, n = 10), semi-immersed to superficial or erumpent, solitary to gregarious, globose to subglobose or irregular shape, dark brown to black, unilocular or multilocular, spores scattered outside the fruiting body, without ostiolar neck. *Peridium* 30–45 μm wide ($\bar{x}$ = 36 μm, n = 30), comprising 2–4 layers of thick-walled, dark brown to hyaline cells arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 3.5–6.5 μm ($\bar{x}$ = 7.5 × 5 μm, n = 30), holoblastic, phialidic, discrete, ellipsoid or ampulliform, hyaline, smooth, proliferating at the same level giving rise to periclinal thickenings, or rarely proliferating percurrently to form one or two close, indistinct annellations. *Conidia* 18–24 × 9–11 μm ($\bar{x}$ = 21 × 10 μm, n = 30), subglobose to ellipsoid, cylindrical when mature, with rounded ends, initially hyaline or brown and aseptate, becoming dark brown and 1-septate when mature, slightly constricted at the septum, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours and germ tube produced from one end of the ascospore. Colonies on PDA reaching 9 cm diam. after one month at 25°C, with appressed mycelial mat and fluffy aerial mycelium on the surface, becoming olivaceous-black from above. Dull green to black from below.

Material examined: China, Yunnan Province, Nujiang City, on a decaying branch of *Coffea* sp., 18 March 2023, Li Lu, C-29 (MHZU 24-0521, holotype), ex-type ZHKUCC 24-0949, other living culture ZHKUCC 24-0950.

GenBank numbers: ZHKUCC 24-0949: ITS = PQ608200, LSU = PQ608037, *TEF*1-α = PQ602091, *TUB*2 = PQ572177; ZHKUCC 24-0950: ITS = PQ608201, LSU = PQ608038, *TEF*1-α = PQ602092, *TUB*2 = PQ572178.

Notes: In the present phylogenetic analysis, *Dothiorella coffeae* formed an independent branch between *D. alpina* (CFCC58299 and CGMCC 3.18001, type) and *D. magnoliae* (CFCC 51564 and CFCC 51563, type) with 99% ML and 1.00 BYPP statistical support (Figure 2.10). Based on nucleotide comparisons, *D. coffeae* (ZHKUCC 24-0949, ex-type) is different from *D. alpina* (CGMCC 3.18001) by 8/487 bp (1.6%, without gaps) of the ITS and 4/264 bp (1.5%, without gaps) of the *TEF*1-α, while it is different from *D. magnoliae* (CFCC 51563) in 5/449 bp (1%, without gaps) of the ITS and 3/265 bp (1.1%, without gaps) of the *TEF*1-α. While *D. alpina* and *D. magnoliae* only have ITS and *TEF*1-α genes (You et al., 2017; Hyde et al., 2020). In morphology, the conidia of *D. coffeae* are subglobose to ellipsoid, cylindrical when mature, 1 septate, constricted at the septum, the upper and lower cells are long and cylindrical, while *D. alpina* are oblong conidia, 1-septate and without constricted at the septum (Hyde et al., 2020), and *D. magnoliae* having verruculose conidia and upper and lower cells are short and subglobose (You et al., 2017). In addition, the PHI test results (Figure 2.14) revealed no significant recombination relationships between *D. coffeae* and its phylogenetically related taxa within the dataset. Therefore, *D. coffeae* is introduced here as a new species isolated from *Coffea* sp. in China.

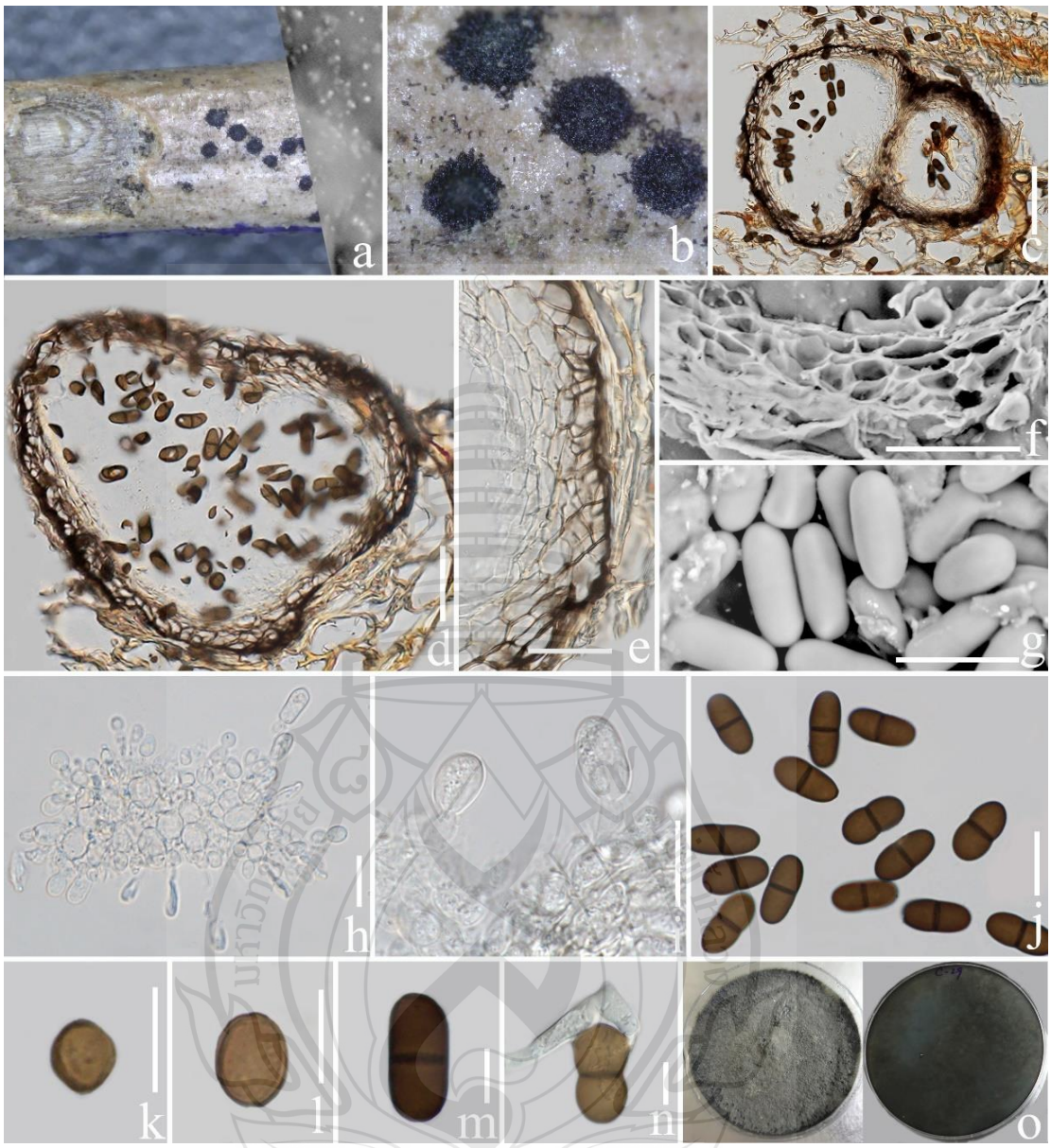


Figure 2.13 *Dothiorella coffeae* (MHZU 24-0521, holotype)

Figure 2.13 a, b Conidiomata on a decaying branch of *Coffea* sp. c, d Longitudinal section of conidiomata. e, f Peridium (f: SEM microphotographs of peridium). h, i Conidiogenous cells with conidia. g, j–m Conidia (g: SEM microphotographs of conidia). n Germinated conidium. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, e, f = 30 µm, g–j = 20 µm, k–n = 10 µm.

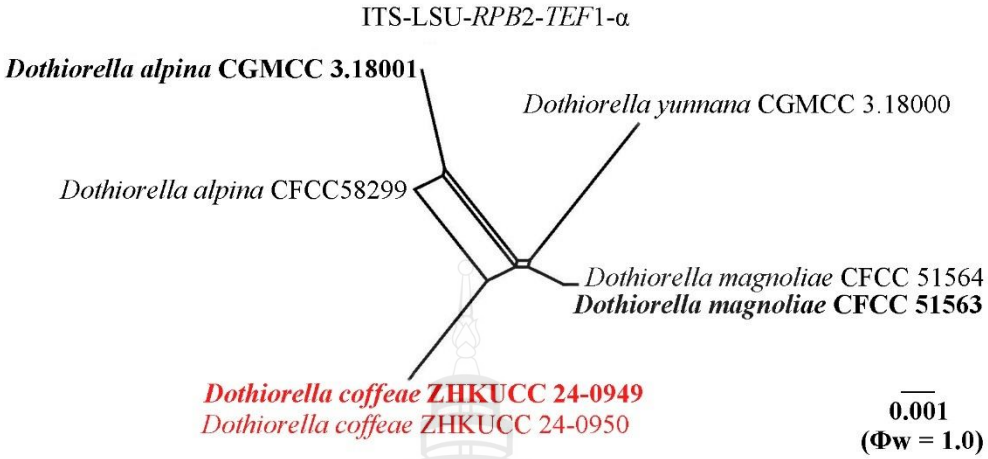


Figure 2.14 Split graphs of *Dothiorella coffeae*

Figure 2.14 Split graphs showing the results of the pairwise homoplasy index (PHI) test of the new taxa, *Dothiorella coffeae*, and closely-related taxa using LogDet transformation and splits decomposition. The PHI test result P-value (Φw) ≤ 0.05 indicates that there is significant recombination between the isolates included in the alignment. The new taxa are in red, bold indicate the type species and PHI test value and scale bars are given in the bottom right corner.

Lasiodiplodia Ellis & Everh., in Clendenin, Bot. Gaz. 21: 92 (1896)

Notes: Lasiodiplodia was established by Clendenin (1896) with *L. theobromae* as the type species. *Lasiodiplodia* is a pluralistic genus distributed in tropical and subtropical areas, and most members of this genus are plant pathogens that causes a variety of diseases, including cankers, dieback, fruit or root rot, branch blight, stem end rot and gummosis on a wide range of woody and fruit trees (Freire et al., 2011; Ismail et al., 2012; Coutinho et al., 2017; Tibpromma et al., 2018; Jayawardena et al., 2019a; Zhang et al., 2021; El-Ganainy et al., 2022; Tian et al., 2024). *Lasiodiplodia* species have subglobose or oval conidia, smooth, thick-walled, initially hyaline that become dark brown and striated when matured (Phillips et al., 2013; Wu et al., 2021). The typical features of sexual morphs are globose to subglobose ascomata, often with 4–5 individual locules, clavate and stipitate asci with hyaline to dark brown aseptate ascospores (Phillips et al., 2013; Wu et al., 2021). *Lasiodiplodia* has accepted 89 species (Index Fungorum, 2025; Tian et al., 2024; Zhou et al., 2024). In this study, we introduce a new species (*L. coffeae*) and a new collection (*L. pseudotheobromae*) in this genus from coffee in China.

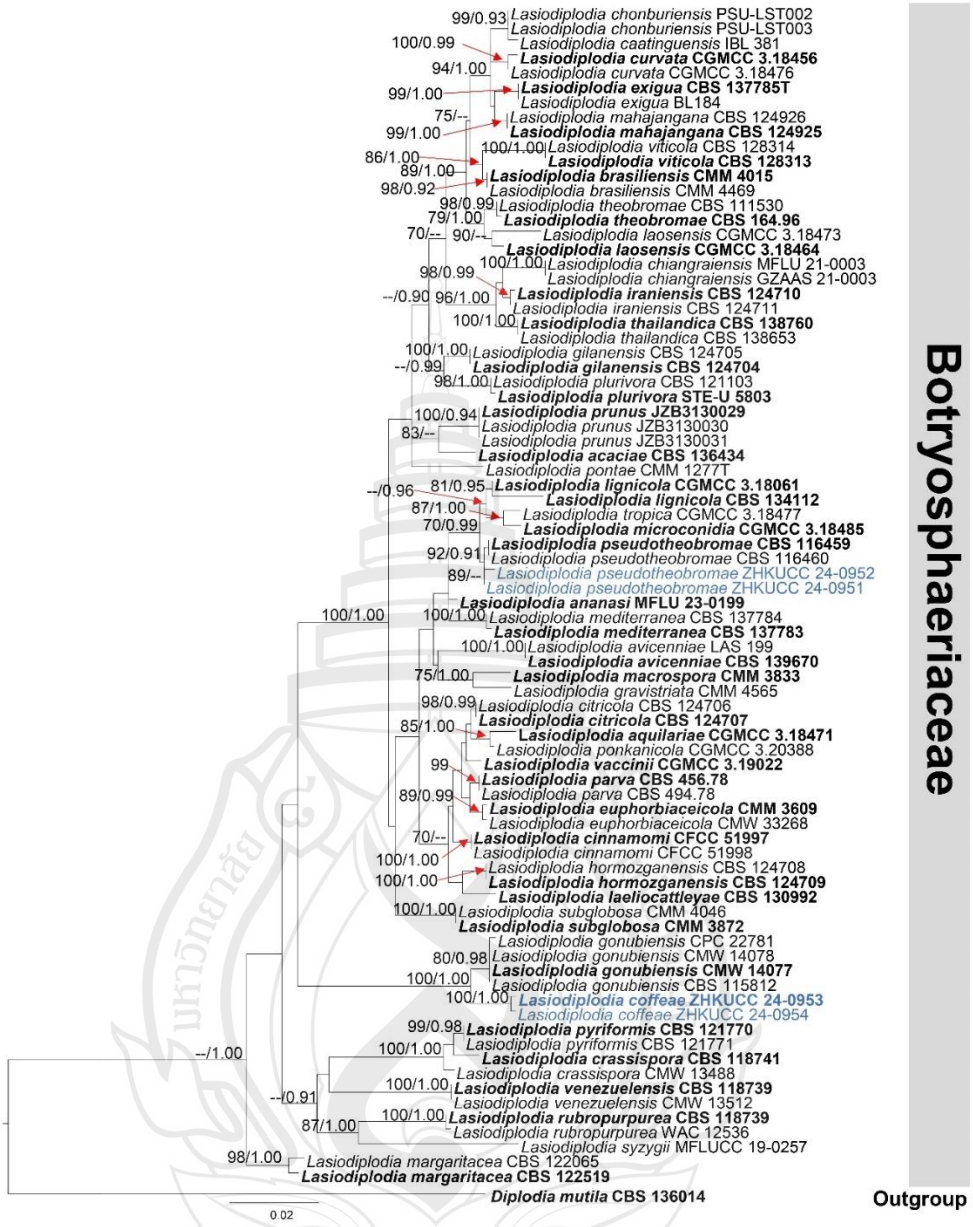


Figure 2.15 Phylogenetic tree of *Lasiodiplodia*

Figure 2.15 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, *TEF*1-α, and *TUB*2 sequence data. Eighty-one strains are included in the combined sequence analysis, which comprises 1331 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Diplodia mutila* (CBS 136014).

Lasiodiplodia coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903615; *Facesoffungi number*: FoF 17554; Figure 2.16

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0523

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 150–200 × 160–260 µm ($\bar{x}$ = 178 × 215 µm, n = 15), immersed to semi-immersed, raised, scattered, solitary, uni-loculate, globose to subglobose, pale brown to dark brown, with inconspicuous ostiole. *Peridium* 15–22 µm wide, composed of several layers of thick-walled, dark brown to pale brown cells of *textura angularis*. *Hamathecium* inconspicuous in a hyaline gelatinous matrix, pseudoparaphyses. *Asci* 100–170 × 22–32 µm ($\bar{x}$ = 142 × 28 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, long pedicel, apically rounded, with ocular chamber. *Ascospores* 30–35 × 10–15 µm ($\bar{x}$ = 33 × 13.9 µm, n = 30), bi-seriate, fusiform, aseptate, straight to curved, thin- and smooth-walled, hyaline with granular. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on PDA after four weeks at 25–27°C, raised in center, velvety, circular, white from above, pale yellow from below.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH4-2 (MHZU 24-0523, holotype), ex-type ZHKUCC 24-0953, other living culture ZHKUCC 24-0954.

GenBank numbers: ZHKUCC 24-0953: ITS = PQ608204, *TEF*1-α = PQ602095, *TUB*2 = PQ572179; ZHKUCC 24-0954: ITS = PQ608205, *TEF*1-α = PQ602096, *TUB*2 = PQ572180.

Notes: Based on phylogenetic analysis, *Lasiodiplodia coffeae* (ZHKUCC 24-0953 and ZHKUCC 24-0954) forms a sister lineage to *L. gonubiensis* (CPC 22781, CBS 115812, CMW 14078 and CMW 14077, ex-type) with 100% ML, 1.00 BYPP statistical supports (Figure 2.15). Based on the molecular sequences comparison, our isolates (ZHKUCC 24-0953, ex-type) deviates from *L. gonubiensis* (CMW 14077, type) by 0/479 bp for ITS (0%, without gaps), 7/244 bp (2.86%, without gaps) for *TEF*1-α, and 7/459 bp (1.5%, without gaps) for *TUB*2, and differs from other strain

L. gonubiensis (CMW 14078) by 0/479 bp for ITS (0%, without gaps), 4/244 bp (1.63%, without gaps) for *TEF*1-α, and 4/422 bp (0.95%, without gaps) for *TUB*2. Our isolates exhibit sexual morph characteristics similar to *L. gonubiensis* (CPC 22781), including clavate asci and fusiform ascospores. However, our species is different from *L. gonubiensis* by long pedicellate asci, 8-spored, aseptate ascospores, hyaline and with granular. *Lasiodiplodia gonubiensis* has (4–)6–8-spored asci, hyaline to pale brown ascospores, becoming 1–2-septate when mature (Trakunyingcharoen et al., 2015; Figure 2.16). Therefore, we introduced *L. coffeae* as a new species from coffee from China.

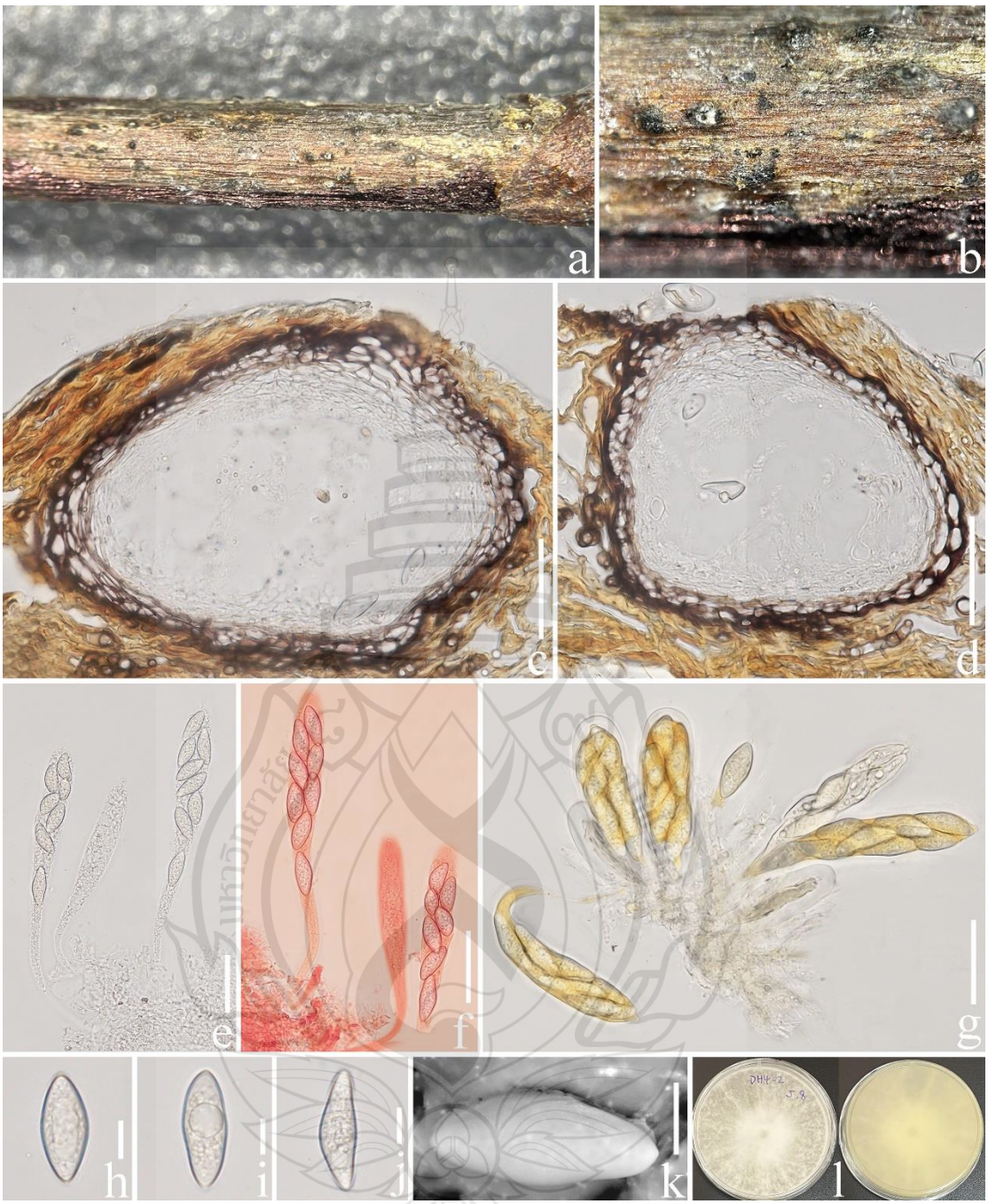


Figure 2.16 *Lasiodiplodia coffeae* (MHZU 24-0523, holotype)

Figure 2.16 a, b Ascomata on the host surface. c, d Section of ascomata with peridium. e Asci with water. f Asci with Congo red reagent. g Asci with iodine solutions. h–k Ascospores (k: SEM microphotographs of ascospore). l Culture on PDA from above and below. Scale bars: c–g = 50 µm, h–k = 10 µm.

Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous, Fungal Diversity 28: 8 (2008)

Index Fungorum number: IF 510941; *Facesoffungi number*: FoF 00166; Figure 2.17

Saprobic on a decaying of *Coffea* sp. **Sexual morph**: See Tennakoon et al. (2016). **Asexual morph**: Coelomycetous. *Conidiomata* 120–260 × 150–300 µm ($\bar{x}$ = 191 × 232 µm, n = 15), pycnidial, scattered, solitary, immersed, unilocular, obpyriform, dark brown to black. *Pycnidial wall* 35–50 µm wide ($\bar{x}$ = 42 µm, n = 20), composed of several layers of thick-walled, dark brown to pale brown cells of *textura angularis*. *Paraphyses* 1.5–3 µm wide ($\bar{x}$ = 2.5 µm, n = 20), filamentous to cylindrical, unbranched, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–12 × 4–6 µm ($\bar{x}$ = 10 × 4.8 µm, n = 20), holoblastic, cylindrical, thick-walled, hyaline, smooth, and slightly swollen at the base. *Conidia* 25–30 × 12–16 µm ($\bar{x}$ = 28 × 15 µm, n = 30), ellipsoid, apex and base rounded, aseptate, hyaline, thick-walled, with granular content.

Culture characteristics: Conidia germinating on PDA within 10 h. Colonies on PDA after four weeks at 25–27°C, raised, velvety, circular, with entire edge, black from above and below.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (1053 m), 30 July 2022, Li Lu, BS1-C17 (MHZU 24-0522), living culture ZHKUCC 24-0951, other living culture ZHKUCC 24-0952.

GenBank numbers: ZHKUCC 24-0951: ITS = PQ608202, *TEF*1-α = PQ602093; ZHKUCC 24-0952: ITS = PQ608203, *TEF*1-α = PQ602094.

Known hosts: *Acacia mangium*, *Citrus aurantium*, *Coffea* sp., *Gmelina arborea*, *Rosa* sp. (Alves et al., 2008; This study), *Acacia confusa*, *Albizia falcataria*, *Mangifera sylvatica*, *Paulownia fortune*, *Eucalyptus* spp. (Zhao et al., 2010), Grapes (Dissanayake et al., 2015), *Bouea burmanica*, *Cananga odorata*, *Osmanthus fragrans*, *Hevea brasiliensis*, *Persea americana*, *Psidium* sp., *Coffea arabica*, *Dimocarpus longan*, *Ficus racemosa*, *Syzygium samarangense*, *Phyllanthus acidus*, *Juniperus chinensis* (Trakunyingcharoen et al., 2015; Freitas-Lopes et al., 2020), Walnut (Li et al., 2016), *Mangifera indica* (Kwon et al., 2017), *Vachellia karroo*, *Senegalia mellifera*, *Pterocarpus angolensis*, *Adansonia digitata*, *Syzygium cordatum*, *Terminalia catappa*,

T. sericea, *Sclerocarya birrea* subsp. *caffra* (Jami et al., 2017); Postharvest fruit (Pipattanapuckdee et al., 2019), Chinese hackberry (Liang et al., 2020), *Citrus* (Chen et al., 2021), *Calamus* sp. and *Panicum* sp. (Rathnayaka et al., 2023), *Ananas comosus* (Tian et al., 2024).

Known distribution: Brazil (Freitas-Lopes et al., 2020), China (Zhao et al., 2010; Dissanayake et al., 2015; Li et al., 2016; Liang et al., 2020; Chen et al., 2021; This study), Costa Rica, Netherlands, Suriname, Zaire (Alves et al., 2008), South Korea (Kwon et al., 2017), South Africa (Jami et al., 2017), and Thailand (Trakunyingcharoen et al., 2015; Pipattanapuckdee et al., 2019; Tian et al., 2024).

Notes: *Lasiodiplodia pseudotheobromae* was introduced by Alves et al. (2008), and later, many strains were introduced from various hosts worldwide. It has been reported as a pathogen associated with coffee dieback disease (Freitas-Lopes et al., 2020). Our strain shares similar morphology to *L. pseudotheobromae* (CBS-H 19916, holotype) in having holoblastic, hyaline, cylindrical, slightly swollen at the base conidiogenous cells, ellipsoid, apex and base rounded, aseptate, hyaline, thick-walled conidia (Figure 2.17). And our strain formed a sister lineage to *L. pseudotheobromae* (CBS 116459, ex-type) with 92% ML and 0.91 BYPP statistical support (Figure 2.15). Thus, we identified our strain as *L. pseudotheobromae*, based on morphological characters and phylogenetic analyses. Our strain *L. pseudotheobromae* (MHZU 24-0522) is introduced as a new collection, which was isolated from *Coffea* sp. in China.

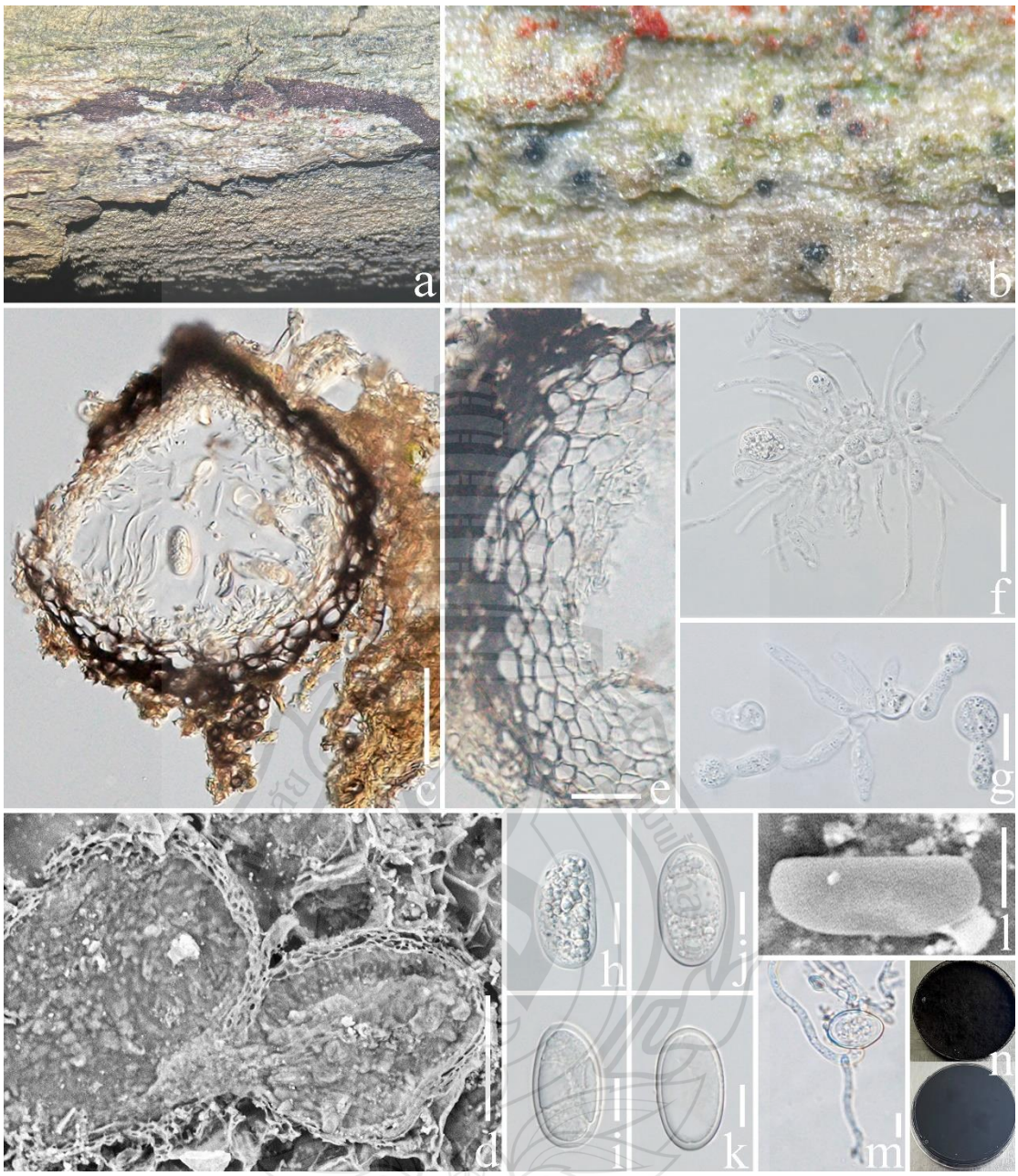


Figure 2.17 *Lasiodiplodia pseudotheobromae* (MHZU 24-0522, new collection)

Figure 2.17 a, b Conidiomata on the host surface. c Section of conidioma. d Section of conidiomata under the SEM. e Pycnidial wall. f, g Paraphyses, conidiogenous cells with conidia. h–l Conidia (l: SEM microphotographs of conidium). m Germinated conidium. n Culture on PDA from above and below. Scale bars: c, d = 50 µm, e, f = 20 µm, g–m = 10 µm.

Neofusicoccum Crous, Slippers & A.J.L. Phillips

Notes: Neofusicoccum was reported by Crous et al. (2006) with the type species *N. parvum*. *Neofusicoccum* is a genus of saprobes, endophytes, and pathogens in the family Botryosphaeriaceae, which is known for causing dieback symptoms and cankers in woody hosts (Jayawardena et al., 2019b; Tennakoon et al., 2021; Xu et al., 2022).

In the past several years, *Neofusicoccum* species were frequently reported to cause plant diseases, e.g. *N. parvum*, *N. luteum*, *N. batangarum*, and *N. mangiferae* (Feng et al., 2020; Tapia et al., 2020; Wan et al., 2020; Chen et al., 2021; Diniz et al., 2021; Seddaiu et al., 2021). *Neofusicoccum* has accepted 71 epithets (Index Fungorum, 2025). In this study, two new host records (*N. podocarpi* and *N. sichuanense*) from coffee are introduced.

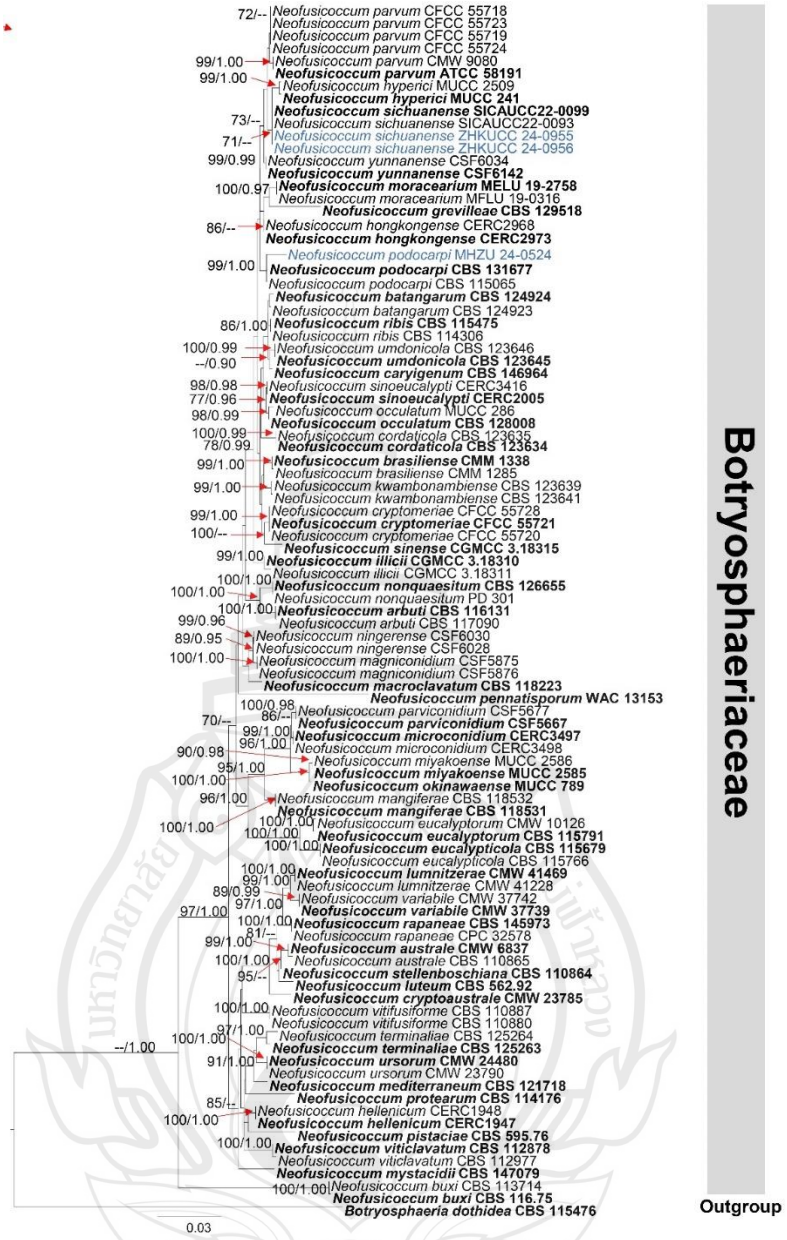


Figure 2.18 Phylogenetic tree of *Neofusicoccum*

Figure 2.18 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, *RPB*2, *TEF*1-α, and *TUB*2 sequence data. Ninety-six strains are included in the combined sequence analysis, which comprises 2259 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Botryosphaeria dothidea* (CBS 115476).

Neofusicoccum podocarpi W. Zhang & Crous, Persoonia 46: 102 (2021)

Index Fungorum number: IF 838096; *Facesoffungi number*: FoF 17555; Figure 2.19

Saprobic on a decaying of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 150–200 × 200–250 µm ($\bar{x}$ = 171 × 219 µm, n = 10), pycnidial, solitary, globose to irregular, dark brown to black, immersed to semi-immersed, unilocular. *Pycnidial wall* 20–30 µm wide ($\bar{x}$ = 26 µm, n = 20), comprising several layers dark brown to hyaline cells of *textura angularis*. *Paraphyses* not observed. *Conidiophores* reduced to conidiogenous cells, or forming a supporting cell. *Conidiogenous cells* 4–8 × 2.5–5 µm ($\bar{x}$ = 6.4 × 3.9 µm, n = 20), holoblastic, discrete, hyaline, cylindrical, phialidic with periclinal thickening. *Conidia* 15–25 × 5–7 µm ($\bar{x}$ = 20 × 6.3 µm, n = 30) fusiform, hyaline, thin-walled, straight to slightly curved, smooth with granular contents, aseptate, base subtruncate to bluntly rounded.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp., 16 September 2021, Li Lu, puer 4-12 (MHZU 24-0524).

GenBank numbers: MHZU 24-0524: ITS = PQ608206, *RPB*2= PV186799, *TUB*2 = PQ572181.

Known hosts: Diseased twigs of *Podocarpus henkelii* (Zhang et al., 2021); dead branch of *Coffea* sp. (This study).

Known distribution: South Africa (Zhang et al., 2021); China (This study).

Notes: *Neofusicoccum podocarpi* was introduced from diseased twigs of *Podocarpus henkelii* by Zhang et al. (2021). Morphologically, our isolate (MHZU 24-0524) matches well with the asexual morph description of *N. podocarpi* (Zhang et al., 2021) in having holoblastic, discrete, hyaline, cylindrical, phialidic conidiogenous cells with periclinal thickening and hyaline, thin-walled, smooth with granular contents, aseptate conidia (Figure 2.19). In the phylogenetic tree (Figure 2.18), our isolate forms a close lineage to *N. podocarpi* (CBS131677, ex-type) with statistical support of 99% ML, 1.00 BYPP. Thus, we introduce our isolate as *N. podocarpi*, the first report as a saprobe from a dead branch of *Coffea* sp. from China.

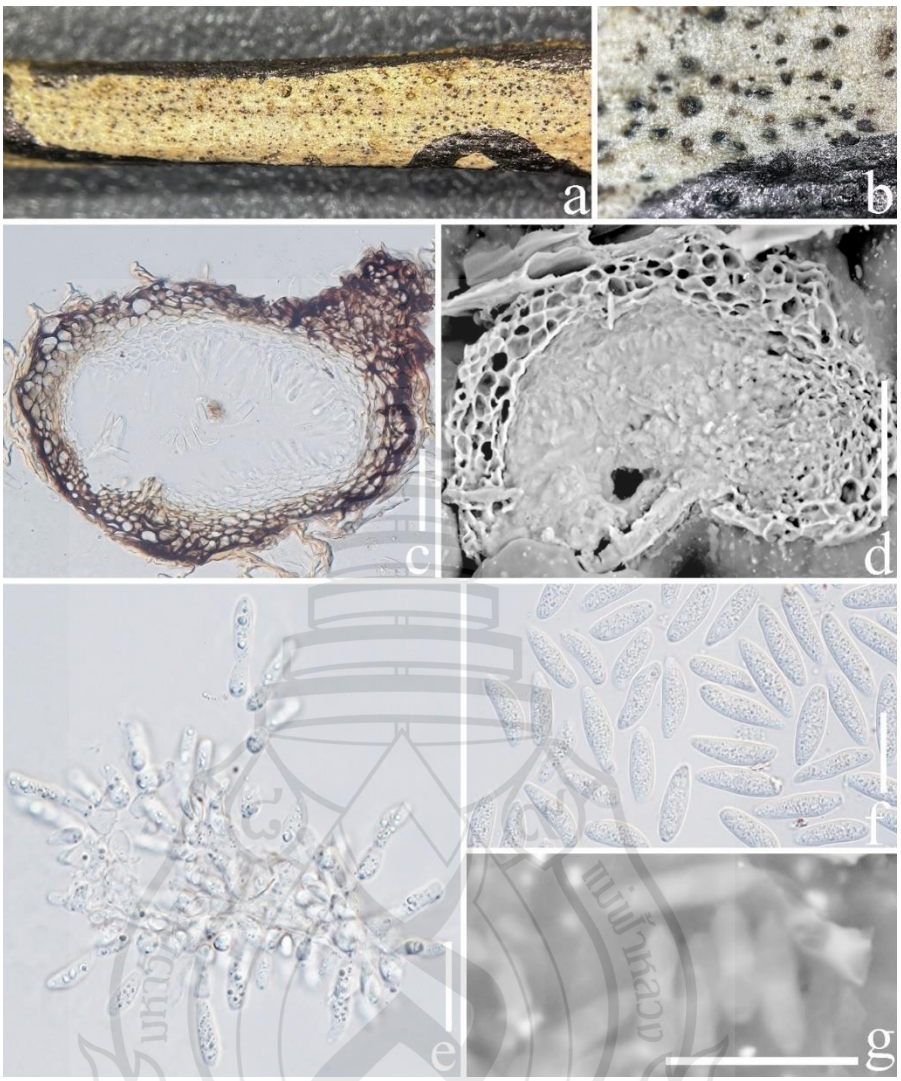


Figure 2.19 *Neofusicoccum podocarpi* (MHZU 24-0524, new host and country record)

Figure 2.19 a, b Conidiomata on the host surface. c, d Section of conidiomata and pycnidial wall (d: SEM microphotographs of conidioma). e Conidiogenous cells with conidia. f, g Conidia (g: SEM microphotographs of conidia). Scale bars: c, d = 50 µm, e–g = 20 µm.

Neofusicoccum sichuanense X.L. Xu & C.L. Yang, Frontiers Microbiol. 13 (no. 1016548): 13 (2022)

Index Fungorum number: IF 845074; *Facesoffungi number*: FoF 16289; Figure 2.20

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 150–220 × 200–250 µm ($\bar{x}$ = 181 × 210 µm, n = 15), immersed to semi-immersed, scattered, solitary, subglobose, pale brown to brown. *Peridium* 25– 35 µm wide ($\bar{x}$ = 30.5 µm, n = 20), comprising several layers of *textura angularis*, outer region of brown cells, and inner region of hyaline cells. *Hamathecium* of 3–4.5 µm wide ($\bar{x}$ = 3.6 µm, n = 20), filiform, septate, branched, pseudoparaphyses. *Asci* 70–110 × 18–22 µm ($\bar{x}$ = 82 × 18.8 µm, n = 20), 8-spored, bitunicate, clavate, hyaline, with thin-walled, short pedicel, apically rounded. *Ascospores* 20–25 × 6–10 µm ($\bar{x}$ = 22 × 8.4 µm, n = 30), fusoid to ellipsoid, sometimes with tapered ends, usually broadest in the middle, hyaline to yellowish, aseptate, thin and smooth-walled, granular. **Asexual morph**: See Xu et al. (2022).

Known host: *Juglans regia* (Xu et al., 2022); *Coffea* sp. (This study).

Known distribution: China (Xu et al., 2022; This study).

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS2-C21 (MHZU 24-0525), living culture ZHKUCC 24-0955, other living culture ZHKUCC 24-0956.

GenBank numbers: ZHKUCC 24-0955: ITS = PQ608208, *TEF*1-α = PQ602097, *RPB*2 = PV186801; ZHKUCC 24-0956: ITS = PQ608209, *TEF*1-α = PQ602098, *RPB*2 = PV186802.

Notes: *Neofusicoccum sichuanense* was isolated from a dead twig of *Juglans regia* in China (Xu et al., 2022) with both asexual and sexual morphs. In the phylogenetic tree (Figure 2.18), our new collection forms a close lineage to *N. sichuanense* (SICHUCC22-0093 and SICHUCC 22-0099, ex-type) with bootstrap support (71% ML). Based on pairwise nucleotide comparisons of ITS, *TEF*1-α, and *RPB*2, there are no to minute base pair differences among our isolate (ZHKUCC 24-0955) and *N. sichuanense* (SICHUCC 22-0099). Morphologically, the morphological characteristics of our isolate (ZHKUCC 24-0955) resembles the sexual morph description of *N. sichuanense* (Xu et al., 2022; Figure 2.20). Thus, we introduce our

isolate as *N. sichuanense* and this is first time this species is collected from a dead branch of *Coffea* sp. in China.

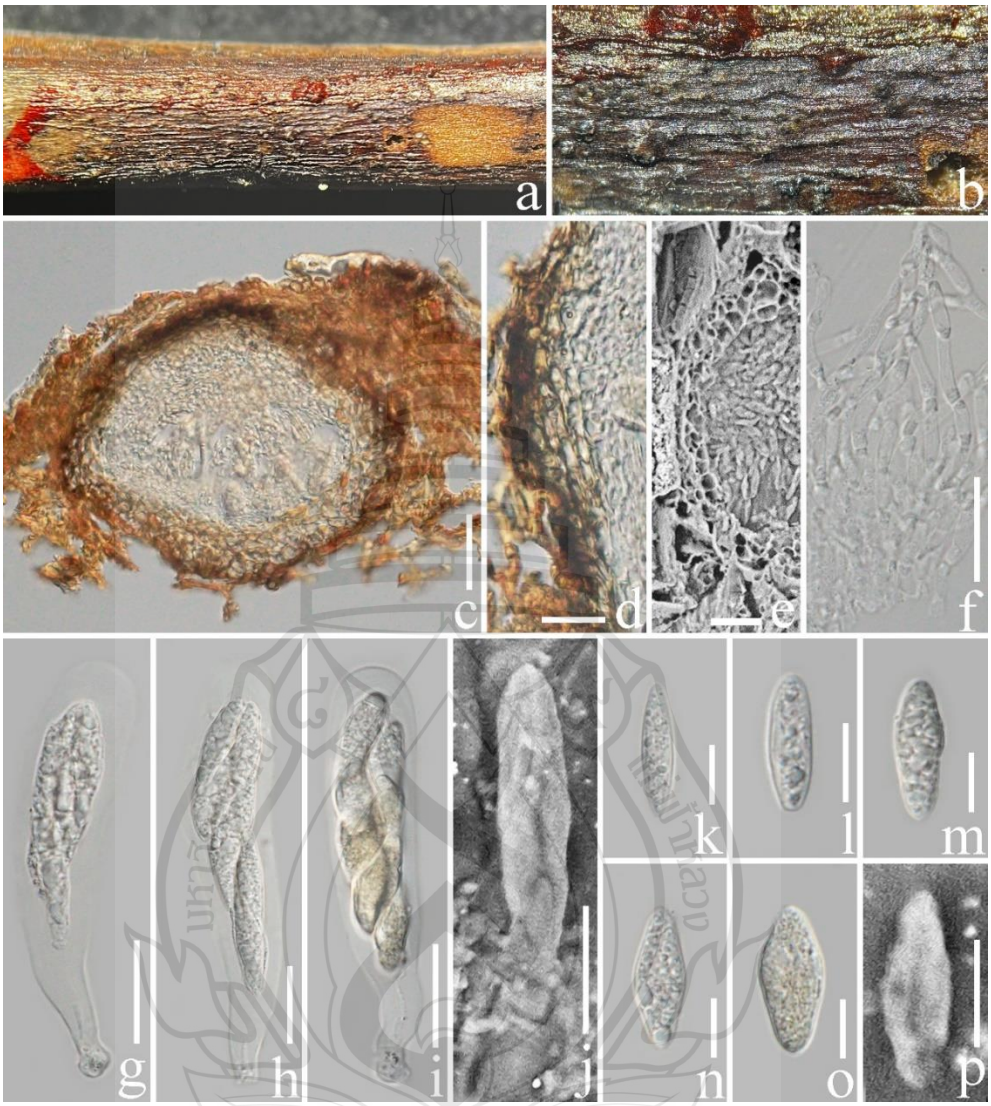


Figure 2.20 *Neofusicoccum sichuanense* (MHZU 24-0525, new host record)

Figure 2.20 a, b Ascomata on the host surface. c Section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g–j Asci (j: SEM microphotographs of ascus). k–p Ascospores (j: SEM microphotographs of ascospore). Scale bars: c = 50 µm, d–j = 20 µm, k–p = 10 µm.

Dyfrolomycetales K.D. Hyde & Hongsanan

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

Melomastia Nitschke ex Sacc., Atti Soc. Veneto-Trent - Sci. Nat., Padova, Sér. 4: 90 (1875)

Notes: *Melomastia* was introduced by Saccardo (1875) with *M. friesii* as the type species, which was later synonymized under *M. mastoidea* by Schröter (1894). In addition, Norphanphoun et al. (2017) demonstrated that *M. italica* and *Dyfrolomyces maolanensis* clustered into distinct lineages within Pleurotremataceae, subsequently synonymizing *D. maolanensis* under *Melomastia maolanensis* and transferring *Melomastia* to Pleurotremataceae based on morphology and multi-gene phylogeny. Furthermore, Li et al. (2022) synonymized 11 species of *Dyfrolomyces* under *Melomastia* based on morpho-molecular studies. Phylogenetic analysis results revealed that two species, *M. chromolaenae* and *M. tiomanensis*, form a distinct clade and were thus reinstated into *Dyfrolomyces* (Kularathnage et al., 2023). *Melomastia* is characterized by immersed, globose, black ascomata with an erumpent apex, cylindrical asci with a J-, subapical ring, and 2-septate ascospores with or without a gelatinous sheath (Barr, 1994; Kang et al., 1999; Norphanphoun et al., 2017; Li et al., 2022). There are 67 species listed under *Melomastia* in Index Fungorum (2025), and the genus is widely distributed across Africa, China, Germany, Italy, Japan, Poland, and the USA (Norphanphoun et al., 2017; Dayarathne et al., 2020; Li et al., 2022; Kularathnage et al., 2023). Most species are saprobes from woody substrates in various habitats, including terrestrial, freshwater, and marine environments (Norphanphoun et al., 2017; Phukhamsakda et al., 2020; Li et al., 2022; Kularathnage et al., 2023; Naziazeno & Aptroot, 2023). Despite the close relationship between *Melomastia* and *Dyfrolomyces*, their exact relationship remains uncertain (Xu et al., 2024). The asexual morph of *Melomastia* is not reported (Norphanphoun et al., 2017; Li et al., 2022; Kularathnage et al., 2023). This study introduces two host records (*M. puerensis* and *M. thamplaensis*) from coffee based on morphology and phylogeny.

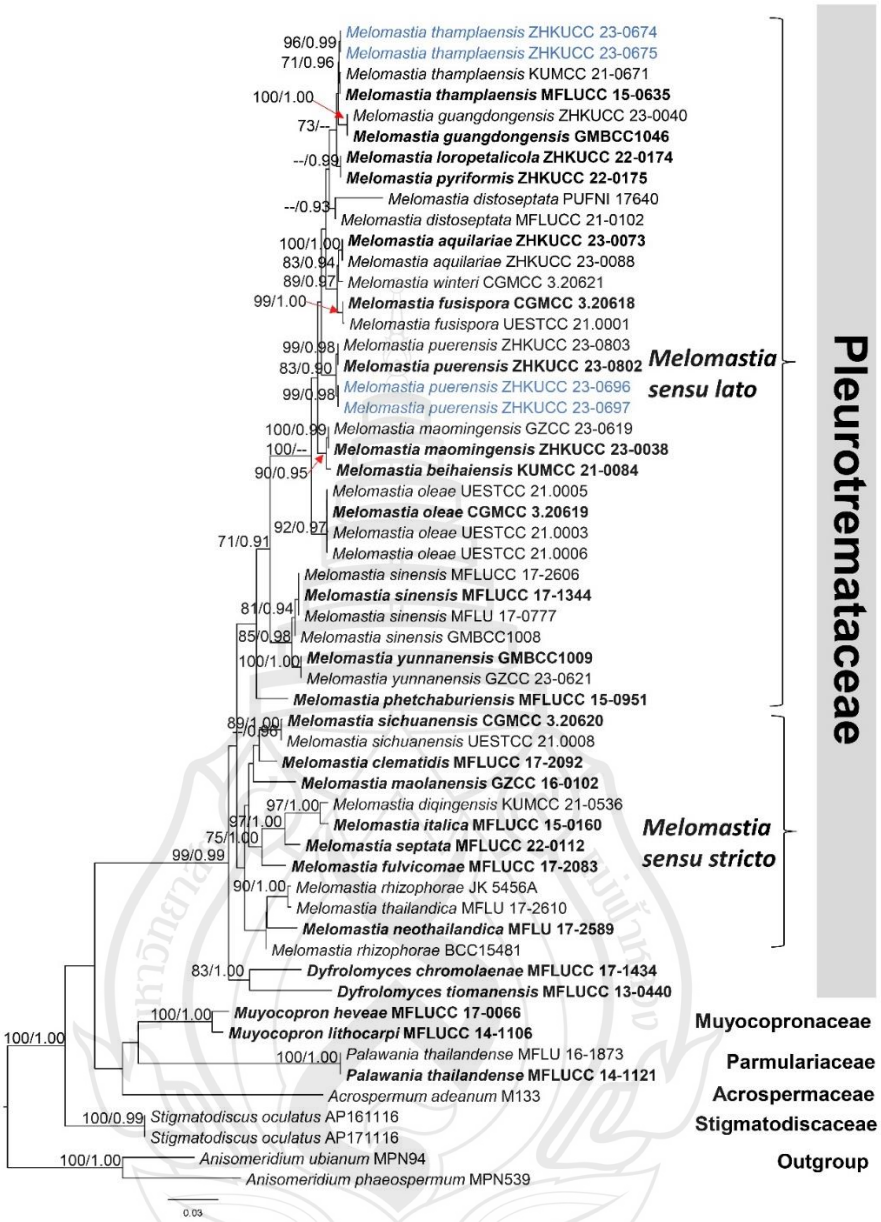


Figure 2.21 Phylogenetic tree of *Melomastia*

Figure 2.21 Phylogram generated from maximum likelihood analysis based on a combined dataset of LSU, SSU, and *TEF*1-α sequence data. Fifty-six strains are included in the combined sequence analysis, which comprises 2,601 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Anisomeridium phaeospermum* (MPN539) and *A. ubianum* (MPN94).

Melomastia puerensis R.F. Xu & Tibpromma, MycoKeys 103: 75 (2024)

Index Fungorum number: IF 901419; *Facesoffungi number*: FoF 15195; Figure 2.22

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 300–500 × 400–500 µm ($\bar{x}$ = 422 × 460 µm, n = 20), scattered or gregarious, immersed, raised dark spots on the host surface, black, subglobose to obpyriform, carbonaceous, ostiolate, papillate. *Papilla* bluntly conical, ostiolar canal internally covered by filiform periphyses. *Peridium* 30–50 µm wide ($\bar{x}$ = 42 µm, n = 20), composed of several layers of pale brown cells of *textura angularis*, becoming hyaline towards inner side and fusing with tissue on outer side. *Hamathecium* of 2.5–4 µm wide ($\bar{x}$ = 2.9 µm, n = 20), comprising numerous, unbranched, hyaline, septate, guttulate, pseudoparaphyses, attached at the base and between the asci, embedded in a gelatinous matrix. *Asci* 90–180 × 6–8 µm ($\bar{x}$ = 142 × 6.9 µm, n = 20), 8-spored, long-cylindrical, smooth-walled, bitunicate, fissitunicate, short-pedicellate, apically rounded with an apical ring. *Ascospores* 20–32 × 6–8 µm ($\bar{x}$ = 28 × 7 µm, n = 30), overlapping-uniseriate, typically 3-septate, 1–2-septate when young, fusiform with acute angular ends, constricted at the septum, hyaline, smooth-walled, with a prominent guttules in each cell. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, raised at the center, irregular, undulate at the margin, felty, white from above and a yellowish ring in the middle, brownish from below.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS2-C13 (MHZU 23-0093), living culture ZHKUCC 23-0696, other living culture ZHKUCC 23-0697.

GenBank numbers: ZHKUCC 23-0696: LSU = PQ608059, SSU = PQ607927, *TEF*1-α = PQ602112; ZHKUCC 23-0697: LSU = PQ608060, SSU = PQ607928, *TEF*1-α = PQ602113.

Known hosts: Hevea brasiliensis (Xu et al., 2024), *Coffea* sp. (This study).

Known distribution: China (Xu et al., 2024; This study).

Notes: *Melomastia puerensis* was collected from *Hevea brasiliensis* from China and introduced by Xu et al. (2024). Phylogenetically, our isolates form a sister

lineage basal to *M. puerensis* (ZHKUCC 23–0803 and ZHKUCC 23–0802, ex-type) with statistical support of 83% ML and 0.90 BYPP (Figure 2.21). Based on nucleotide comparisons, our isolates (ZHKUCC 23-0696) are almost similar to *M. puerensis* (ZHKUCC 23–0802) by 6/903 bp (0.6%, without gaps) in *TEF*1-α and identical in LSU and SSU. Our collection aligns well with the description of *M. puerensis* (Xu et al., 2024; Figure 2.22). Based on both phylogenetic and morphological evidence, we identify our collection as a new host record from coffee host.

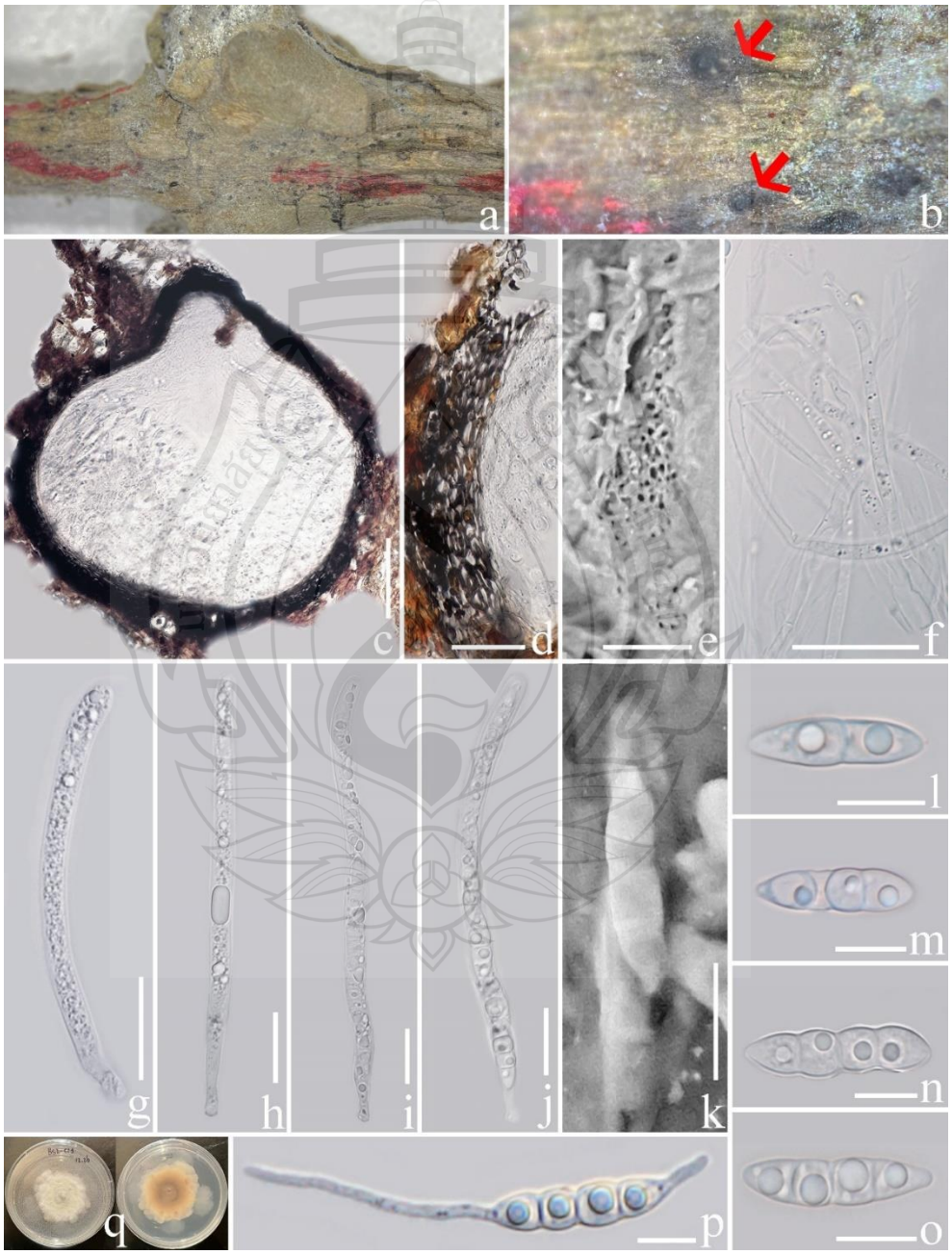


Figure 2.22 *Melomastia puerensis* (MHZU 23-0093, new host record)

Figure 2.22 a, b Colonies on substrate (arrow indicates the Papilla). c Vertical cross section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g–j Asci. k–o Ascospores (k: SEM microphotographs of ascospore). p Germinated ascospore. q Culture on PDA from above and below. Scale bars: c = 100 μm, d, e = 30 μm, d–j = 20 μm, k–p = 10 μm.

Melomastia thamplaensis J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, Phytotaxa 313 (3): 271 (2017)

Index Fungorum number: IF 52496; *Facesoffungi number*: FoF 02612; Figure 2.23

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph**: *Ascomata* 400–600 × 400–700 μm ($\bar{x}$ = 480 × 525 μm, n = 20), scattered or gregarious, visible as dark, raised spots on the host surface, black, semi-immersed, clypeate, subglobose to obpyriform, some with a broad, flattened base, coriaceous to carbonaceous, ostiolate. *Ostioles* central, papillate. *Clypeus* extending outwards around the ascomata, thicker around the papilla, composed of dense, melanized cells. *Peridium* 35–50 μm ($\bar{x}$ = 40 μm, n = 20), consisting of three layers: an outer layer of pale brown, dense, amorphous, thick-walled cells fusing with host tissue, a middle layer of thick-walled black cells of *textura angularis*, and an inner layer of thin-walled black cells of *textura angularis*. *Hamathecium* of 1.5–2.5 μm wide ($\bar{x}$ = 2.2 μm, n = 20), numerous, filiform, septate, sometimes branched, hyaline, pseudoparaphyses, attached at the base and between the asci, embedded in a gelatinous matrix. *Asci* 100–170 × 6–8 μm ($\bar{x}$ = 143 × 6.7 μm, n = 20), 8-spored, long-cylindrical, short-pedicellate, apically rounded with an apical ring. *Ascospores* 20–26 × 5–6 μm ($\bar{x}$ = 24 × 5.4 μm, n = 30), overlapping-uniseriate, hyaline, fusiform with acute angular ends, typically 3-septate, constricted at the septum, smooth-walled, containing several guttules when young. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, raised at the center, circular, irregular at the margin, felty, gray from above, brownish from below.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp., 12 July 2022, Li Lu, XTBG-C3 (MHZU 23-0082), living culture ZHKUCC 23-0674, other living culture ZHKZUCC 23-0675.

GenBank numbers: ZHKUCC 23-0674: LSU = PQ608061, SSU = PQ607929, *TEF*1-α = PQ602114; ZHKUCC 23-0675: LSU = PQ608062, SSU = PQ607930, *TEF*1-α = PQ602115.

Known hosts: Limestone outcrops (Zhang et al., 2017), *Coffea* sp. (This study), *Millettia leptobotrya* (Ren et al., 2024).

Known distribution: Thailand (Zhang et al., 2017), China (Ren et al., 2024; This study).

Notes: *Melomastia thamplaensis* was introduced by Zhang et al. (2017) and collected from a corticate decaying branch among limestone outcrops in Thailand. In the phylogenetic tree, our isolates (ZHKUCC 23-0674 and ZHKZUCC 23-0675) clustered with *M. thamplaensis* (KUMCC 21-0671 and MFLUCC 15-0635, ex-type), with 71% ML and 0.96 BYPP support (Figure 2.21). Based on nucleotide comparisons, our isolates (ZHKUCC 23-0674) almost overlap with *M. thamplaensis* (MFLUCC 15-0635, ex-type) by 4/919 bp (0.4%, without gaps) in *TEF*1-α and identical in LSU and SSU. Morphologically, our collection fits well with the *M. thamplaensis* description in Zhang et al. (2017) (Figure 2.23). Combining both phylogeny and morphological evidence, our isolates are identified as *M. thamplaensis*, and herein, we report *M. thamplaensis* from coffee for the first time.

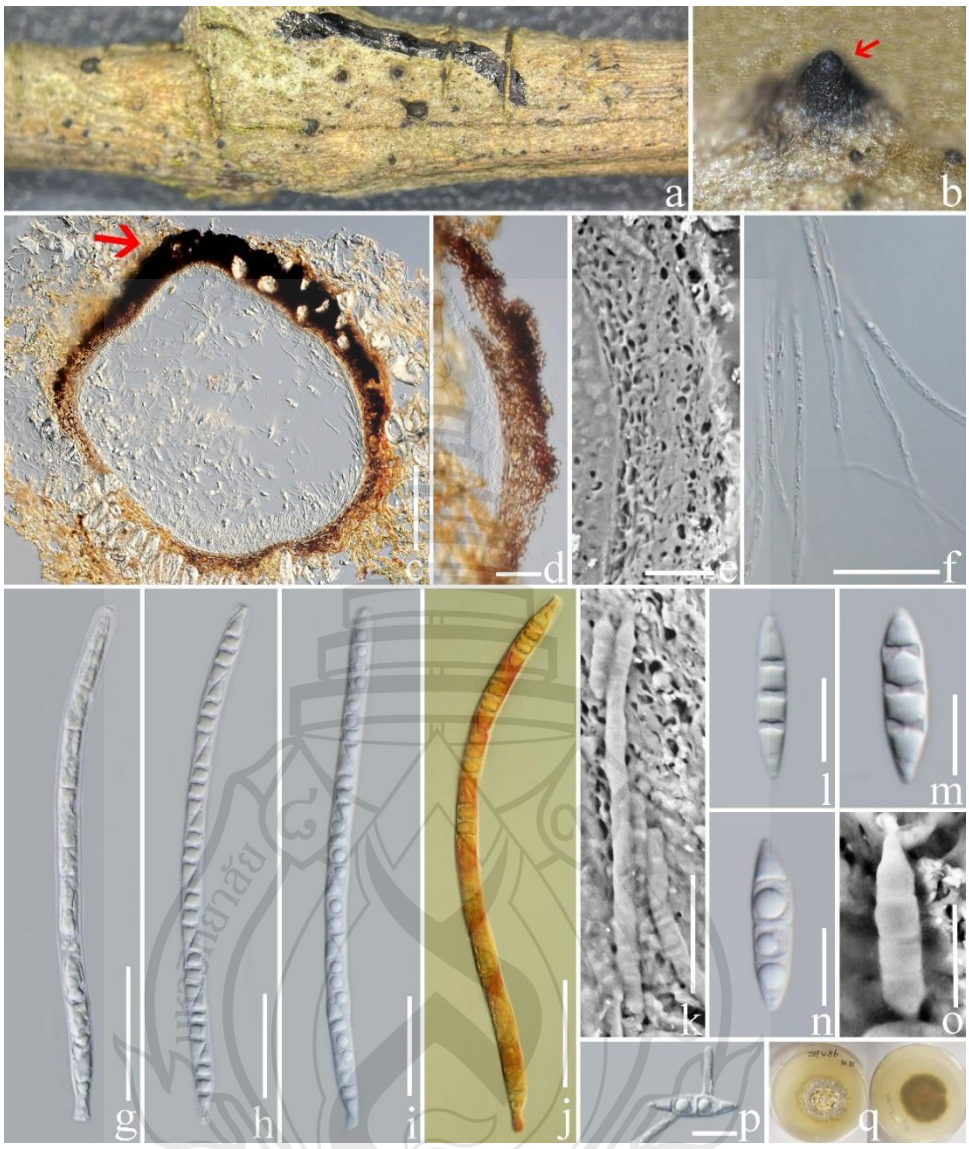


Figure 2.23 *Melomastia thamplaensis* (MHZU 23-0082, new host record)

Figure 2.23 a, b Colonies on substrate (arrow indicates the Papilla). c Vertical cross section of ascoma (arrow indicates the Clypeus). d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g–j Asci (j: Asci stained with Lugol's iodine). k SEM microphotographs of asci and ascospore. l–o Ascospores (o: SEM microphotographs of ascospore). p Germinated ascospore. q Culture on PDA from above and below. Scale bars: c = 100 µm, d–k = 30 µm, l–p = 10 µm.

Hysteriales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 265 (1897)

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

Rhytidhysteron Speg., Anales de la Sociedad Científica Argentina 12 (4): 188 (1881)

Notes: Rhytidhysteron was introduced by Spegazzini (1881) to accommodate *R. brasiliense* and *R. viride*, without defining a type species. Later, Clements and Shear (1931) designated *R. brasiliense* as the type species. *Rhytidhysteron* was previously placed in the Patellariaceae, which was later transferred to the Hysteriaceae by Boehm et al. (2009) based on multi-gene phylogeny analyses. There are 43 species of *Rhytidhysteron* listed in the Index Fungorum (2025). Members of *Rhytidhysteron* are distributed on various plants worldwide and can be found as saprobes, endophytes, and weak pathogens on woody plants in both terrestrial and marine habitats, and some are rarely found as human pathogens (Du et al., 2023). A new collection (*R. coffeae*) is introduced in this study.

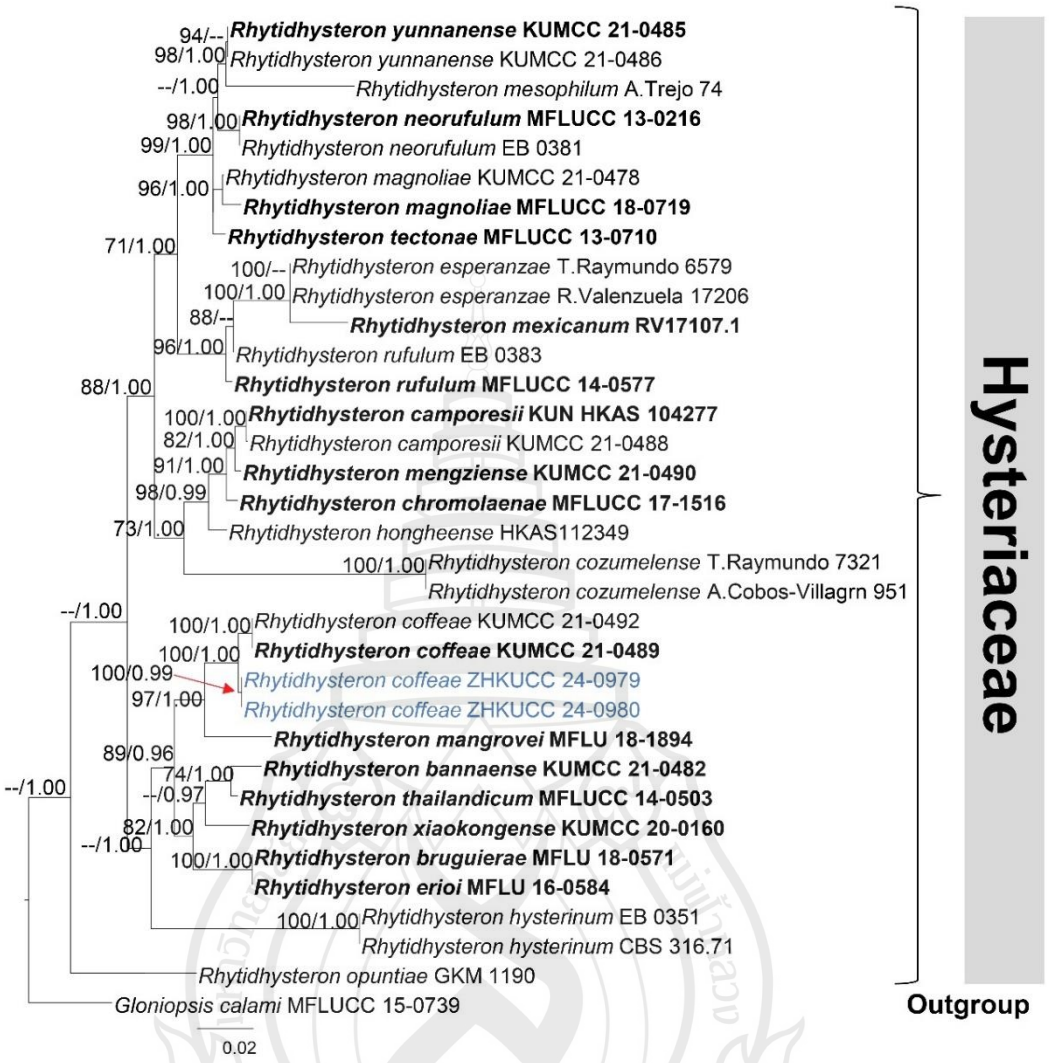


Figure 2.24 Phylogenetic tree of *Rhytidhysteron*

Figure 2.24 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *TEF*1-α sequence data. Thirty-four strains are included in the combined sequence analysis, which comprises 2,928 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Gloniopsis calami* (MFLUCC 15-0739).

Rhytidhysteron coffeae T.Y. Du & Tibpromma, J. Fungi 9 (2, no. 148): 10 (2023)

Index Fungorum number: IF 846000; *Facesoffungi number:* FoF 12958; Figure 2.25

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 1000–1600 × 400–600 µm ($\bar{x}$ = 1300 × 534 µm, n = 15), hysterothecial, solitary, superficial, base is embedded in the plant tissue, navicular, black, apothecioid, rough, perpendicular striae, elongate and depressed, compressed at apex, and opening through a nearly circular longitudinal slit, reddish brown at the center. *Exciple* 80–120 µm wide ($\bar{x}$ = 94 µm, n = 30), composed of two walls, outer layer brown to dark brown, inner layer pale brown to hyaline, thick-walled cells of *textura angularis*. *Hamathecium* of 2–3 µm wide ($\bar{x}$ = 2.2 µm, n = 30), dense, hyaline, septate, branched, cellular pseudoparaphyses. *Asci* 150–190 × 10–13 µm ($\bar{x}$ = 170 × 11.5 µm, n = 30), 8-spored, bitunicate, cylindrical, short pedicel with club-like, rounded at the apex, with an ocular chamber, and J-, apical ring. *Ascospores* 22–28 × 8.5–10 µm ($\bar{x}$ = 25.5 × 9.2 µm, n = 30), uni-seriate, slightly overlapping, ellipsoidal to fusoid, hyaline to yellowish, 1-septate when immature, becoming brown to reddish brown, 3-septate when mature, constrict at the septa, rounded to slightly pointed at both ends, guttulate, smooth-walled, without a mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm in one month at 25°C, flossy, velvety, flat, circular, and undulate margin, with aerial mycelium, white from above and yellowish from below.

Material examined: China, Yunnan Province, Pu'er City, Mojiang County, Jinggongcoffee plantation, 101◦44′20″ E, 23◦15′15″ N, decaying wood of *Coffea* sp. L. (Rubiaceae), 23 December 2020, L. Lu, MJC2 (holotype, HKAS 122700, ex-type living culture, KUMCC21-0489); Yunnan Province, Pu'er City, Qixiang coffee plantation, 101◦20′47″ E, 22◦42′15″N, on decaying wood of *Coffea* sp. (Rubiaceae), 25 December 2020, L. Lu, QXC8 (HKAS122701 paratype, ex-paratype culture, KUMCC 21-0492); Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp. (100°96 E, 22°66 N, 1073 m), 2 April 2024, Li Lu, XAZC-2-10 (MHZU 24-0537), living culture ZHKUCC 24-0979, other living culture ZHKUCC 24-0980.

GenBank numbers: ZHKUCC 24-0979: ITS = PQ608238, LSU = PQ608072, SSU = PQ607933, *TEF*1-α = PQ602120; ZHKUCC 24-0980: ITS = PQ608239, LSU = PQ608073, SSU = PQ607934, *TEF*1-α = PQ602121.

Known hosts: Coffea sp. (Du et al., 2023, this study).

Known distribution: China (Du et al., 2023, This study).

Notes: Rhytidhysteron coffeae was isolated as saprobic on *Coffea* sp. in Yunnan Province, China (Du et al., 2023). In our phylogenetic analysis, our strains group with *R. coffeae* (KUMCC 21-0489, ex-type) with 100% ML and 1.00 BYPP statistical support (Figure 2.24). In addition, the morphology of our collection is identical or similar to the ex-type morphology by having hysterothecial ascomata and ellipsoidal to fusoid ascospores (Du et al., 2023; Figure 2.25). We, therefore, identified our collection as *R. coffeae*, which is a new collection from *Coffea* sp. in China. We provide SEM pictures of the exciple and ascospores of this species for future reference.

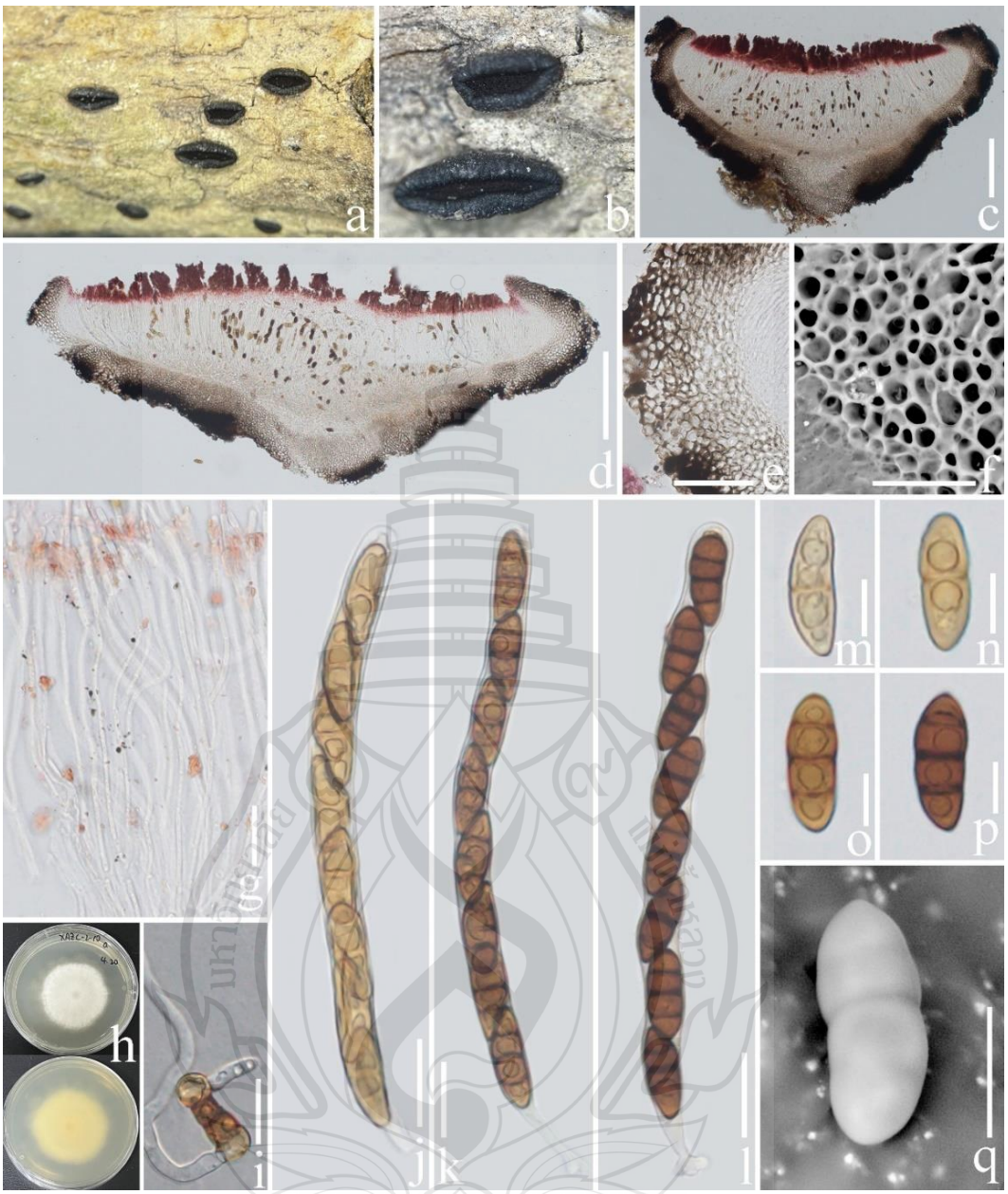


Figure 2.25 *Rhytidhysteron coffeae* (MHZU 24-0537, new collection)

Figure 2.25 a, b Hysterothecia on a decaying branch of *Coffea* sp. c, d Vertical section through hysterothecium. e, f Exciple (f: SEM microphotographs of exciple hole). g Epithecium mounted in water and pseudoparaphyses. h Culture on PDA from above and below. i Germinated ascospore. j–l Asci. m–q Ascospores (q: SEM microphotographs of ascospore). Scale bars: c, d = 200 µm, e = 50 µm, f, g, i–l= 20 µm, m–q= 10 µm.

Kirschsteiniotheliales Hern.-Restr., R.F. Castañeda, Gené & Crous, Studies in Mycology 86: 72 (2017)

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

Kirschsteiniothelia D. Hawksw., Botanical Journal of the Linnean Society 91: 182 (1985)

Notes: Kirschsteiniothelia introduced by Hawksworth (1985) was typified by *Kir. aethiops*. Thirty-three *Kirschsteiniothelia* epithets are listed in Index Fungorum (2022). *Kirschsteiniothelia* is widespread in tropical regions and commonly occur on dead wood (Mehrabi et al., 2017). The sexual morph of *Kirschsleiniothelia* is characterized by brown or black, globose to subglobose ascomata with or without central papilla, a thick-walled peridium, filiform and hyaline pseudoparaphyses, cylindrical-clavate with 8-spored asci and ellipsoidal, brown to dark brown ascospores (Hawksworth, 1985, Boonmee et al., 2012, Hyde et al., 2013, Mehrabi et al., 2017). Boonmee et al. (2012) found that the type species of *Kirschsteiniothelia* (*Kir. aethiops*) grouped with the type species of *Dendryphiopsis* (*D. atra*) in their phylogenetic analyses, and this shows that *Dendryphiopsis* represents the asexual morph of *Kirschsteiniothelia*. The connection was confirmed by Hawksworth (1985), and accepted by Boonmee et al. (2012), Hyde et al. (2013) and Wijayawardene et al. (2014). In this study we introduced one new species in *Kirschsteiniothelia,* and this is the first report of *Kirschsteiniothelia* from coffee.

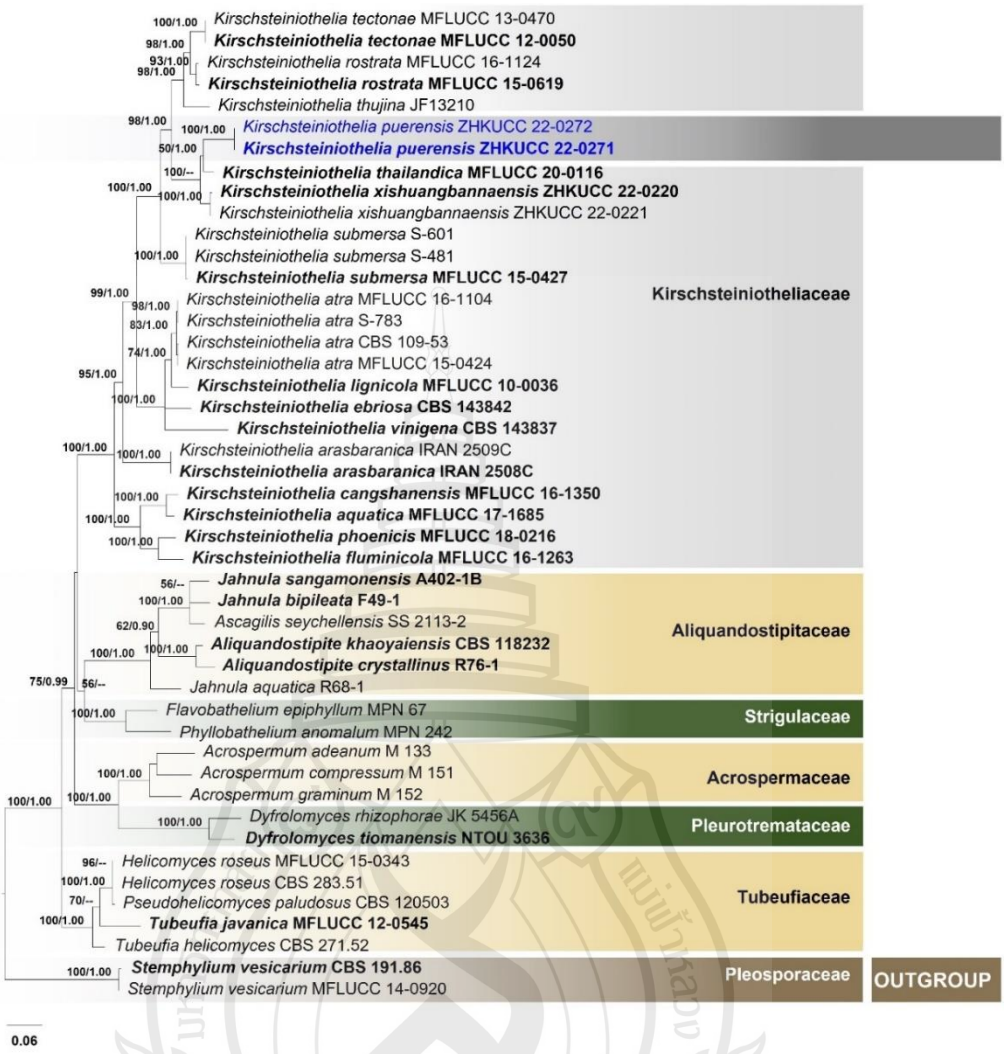


Figure 2.26 Phylogenetic tree of *Kirschsteiniothelia*

Figure 2.26 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, and SSU sequence data. Fourty-six strains are included in the combined sequence analysis, which comprises 2,406 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Stemphylium vesicarium* (CBS191.86, MFLUCC 14-0920).

Kirschsteiniothelia puerensis L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559884; *Facesoffungi number:* FoF 12893; Figure 2.25

Etymology: In reference to the host location, "Pu'er" City, where the holotype was collected.

Holotype: ZHKU 22-0142

Saprobic on decaying coffee wood. Sexual morph: Undetermined. Asexual morph: *Colonies* scattered on coffee wood, hairy, solitary or clustered, black, conspicuous on surface. *Mycelium* exposed on the surface of the substrate except for the roots. *Conidiophores* 100–250 × 5–12 μm, ($\bar{x}$ = 148.5 × 9 μm, n = 20), macronematous, mononematous, solitary or caespitose, cylindrical, straight or slightly flexuous, smooth, dark brown, unbranched, slightly swollen at the base, 7–15 septate. *Conidiogenous cells* 15–25 × 5–10 μm, ($\bar{x}$ = 19 × 8 μm, n = 20) monoblastic, dark brown to black, terminal and smooth. *Conidia* 60–140 × 5–20 μm ($\bar{x}$ = 98 × 14 μm, n = 20), acrogenous, solitary, obclavate, 5–12 septate, invagination in the septate, hyaline when immature and become pale-brown to brown, straight or curved, pale-brown at the apex, truncate at base, tapering towards apex, sometimes has long stipes up to 73 μm, some with a hyaline sheath around the tip (some two globose sheaths).

Culture characteristics: Conidia germinated within 12 hours on PDA. Colonies on PDA reaching 40 mm diam, after two months at room temperature (22°C). Circular, dark green, with aerial mycelium, dense and fluffy on the surface, sparse on the edge, black in reverse.

Material examined: China, Pu'er, Yunnan Province, on a dead wood of *coffea* sp., 23th Dec. 2020, L. Lu, MJ-C3 (holotype ZHKU 22-0142, **ex-type living culture** ZHKUCC 22-0271 = ZHKUCC 21-0272).

GenBank numbers: ZHKUCC 22-0271 = ITS: OP450977, LSU: OP451017, SSU: OP451020; ZHKUCC 22-0272 = ITS: OP450978, LSU: OP451018, SSU: OP451021.

Notes: In the phylogenetic tree, *Kirschsteiniothelia puerensis* formed a well-separated clade sister to *Kir. thailandica* (MFLUCC 20-0116) with moderate statistical support (50% ML/1.00 BYPP, Figure x), while both taxa are sister to *Kir. xishuangbannaensis* (ZHKUCC 22-0220) with 100% ML bootstrap support. Based

on the blast results, ITS and SSU gene sequences showed 90% and 98% similarities to *Kir. thailandica* (MT985633) and (MT984280) respectively. The LSU sequence showed 93.5% similarity to *Kir. rostrata* (NG_059790). In morphology, *Kir. puerensis* also has similar morphological features to *Kir. rostrata*, *Kir. thailandica* and *Kir. xishuangbannaensis* (Hyde et al., 2017, Sun et al., 2021, Fang et al., 2022). However, *Kir. puerensis* conidiophores (110–240 × 6–12 μm, 7–12 septate) are longer than *Kir. thailandica* (55–93 × 7–10 μm), but shorter than *Kir. rostrata* (190–450 × 9–15 μm, 7–24 septate). In addition, conidia of *Kir. puerensis* are 5–12 septate, while in *Kir. thailandica* they are 6–8-septate, 8–13-septate in *Kir. rostrata*, and 3–8-septate in *Kir. xishuangbanaensis* (Hyde et al., 2017; Sun et al., 2021; Fang et al., 2022). Hence, based on both morphology and phylogeny, we introduce *Kir. puerensis* as a new species.

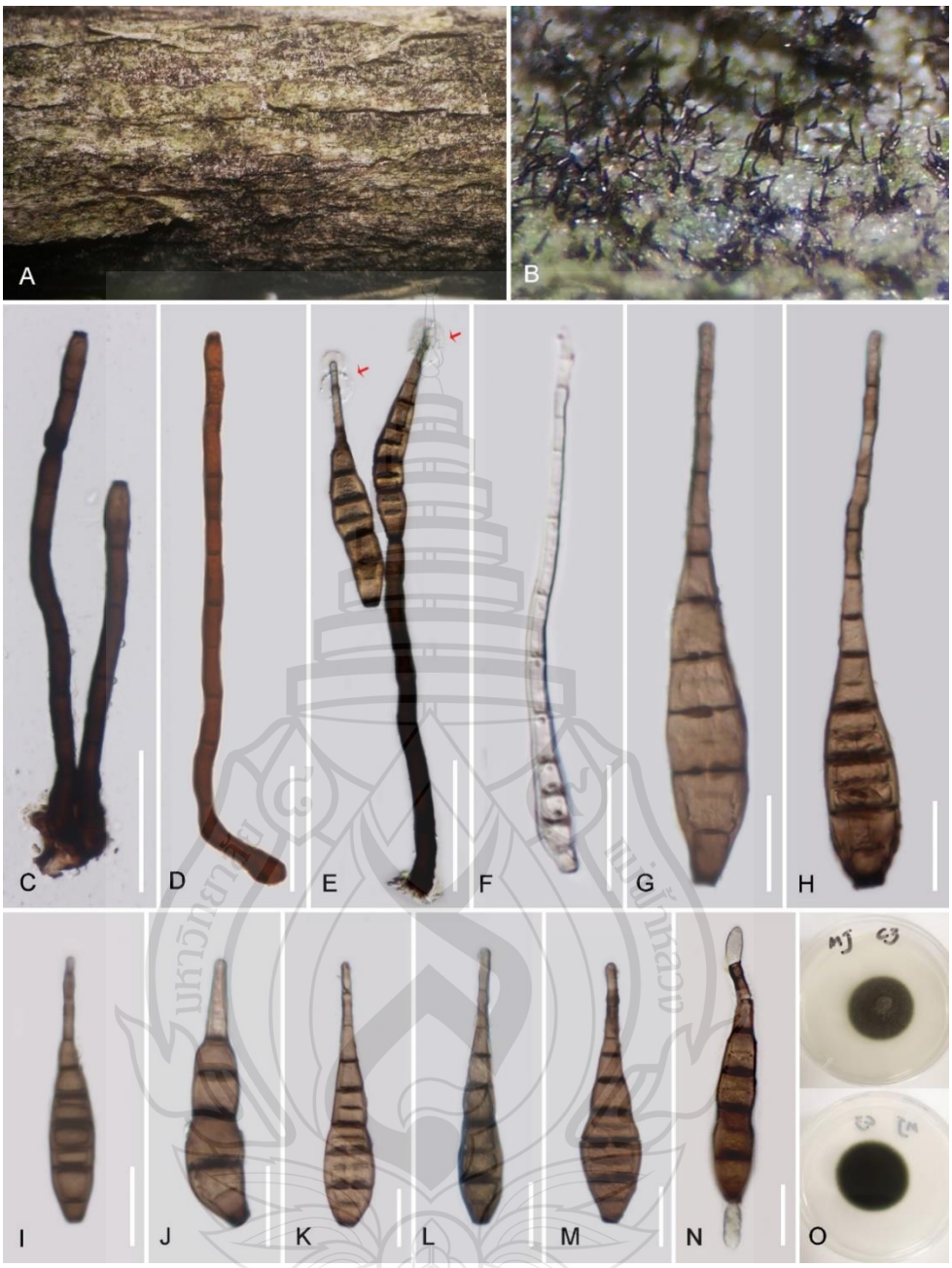


Figure 2.27 *Kirschsteiniothelia puerensis* (holotype ZHKU 22-0142)

Figure 2.27 A, B. Colonies on the host. C, D. Conidiophore. E. Conidiophore with conidia and sheaths (red arrows indicate mucilaginous sheaths). F–M. Conidia. N. Germinated conidium. O. Culture on PDA from above and reverse. Scale bars: C–E = 50 μm; F–N = 20 μm.

Muyocopronales Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 230 (2016)

Muyocopronaceae K.D. Hyde, Fungal Diversity 63 (1): 164 (2013)

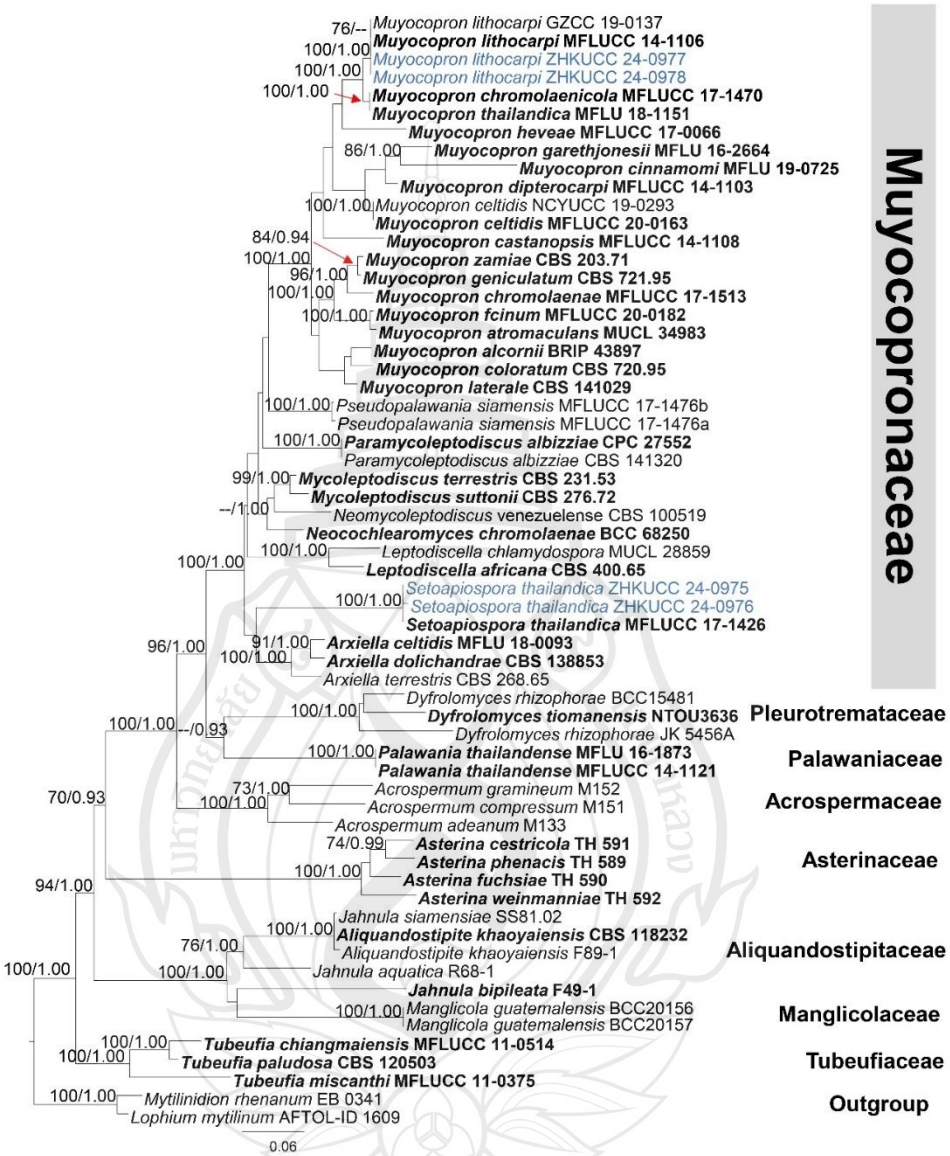


Figure 2.28 Phylogenetic tree of Muyocopronaceae

Figure 2.28 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *TEF*1-α sequence data. Sixty-one strains are included in the combined sequence analysis, which comprises 3,030 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are

given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Lophium mytilinum* (AFTOL-ID 1609) and *Mytilinidion rhenanum* (EB 0341).

Muyocopron Speg., Anales Soc. Ci. Argent. 12 (3): 113 (1881)

Notes: Muyocopron was introduced by Spegazzini (1881) with the type species *M. corrientinum*. Members of the *Muyocopron* species have been distributed worldwide and are associated with various plants (Mapook et al., 2016a; Tibpromma et al., 2016; Senwanna et al., 2019). It occurs as saprobes, pathogens and endophytes, containing both sexual and asexual morphs (Mapook et al., 2023). The sexual morphs of *Muyocopron* species are characterized by superficial, subcarbonaceous ascomata, without mycelium, bitunicate, 8-spored asci, and ellipsoidal, hyaline ascospores (Spegazzini, 1881; Luttrell, 1951; Hyde et al., 2013; Mapook et al., 2016). The asexual morphs are characterized by irregular sporodochium-like conidiomata, enteroblastic, monophialidic conidiogenous cells, and fusiform or fusoid-ellipsoid, aseptate or septate conidia with terminal and/or lateral appendages, with or without dark brown appressoria (Hernández-Restrepo et al., 2019). Eighty-one *Muyocopron* species are listed in Index Fungorum (2025), and we introduce a new record, *M. lithocarpi* from *Coffea* sp. from China.

Muyocopron lithocarpi Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 235 (2016)

Index Fungorum number: IF 551618; *Facesoffungi number:* FoF 01890; Figure 2.27

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 80–120 × 150–220 µm ($\bar{x}$ = 105 × 187 µm, n = 5), superficial, coriaceous, solitary or scattered, appearing as circular, flattened, brown to dark brown spots, covering the host, without a subiculum, with a poorly developed basal layer and an irregular margin. *Ostiolar* central. *Peridium* 10–25 µm wide ($\bar{x}$ = 15.6 µm, n = 20), widest at the sides, outer layer comprising dark brown to black pseudoparenchymatous, occluded cells of *textura epidermoidea*, inner layer comprising light brown cells of *textura angularis*. *Hamathecium* of 1.5–3.5 µm wide ($\bar{x}$ = 2.6 µm, n = 20), cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 60–100 × 20–30 µm ($\bar{x}$ = 82 × 25 µm, n = 20), 8-spored, bitunicate, saccate or obpyriform, pedicellate, with small ocular chamber

when young. *Ascospores* 17–22 × 10–14 µm ($\bar{x}$ = 20 × 12 µm, n = 20), irregularly arranged, overlapping in the ascus, oval to obovoid with obtuse ends, hyaline, aseptate, with granular appearance. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm in one month at 25°C, irregular, white, flat, with entire margin, dark brown to light brown from below, from the center of the colony with white margin.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH4-3 (MHZU 24-0536), living culture ZHKUCC 24-0977, other living culture ZHKUCC 24-0978.

GenBank numbers: ZHKUCC 24-0977: ITS = PQ608240, LSU = PQ608074, SSU = PQ607935, RPB*2* = PV186817; ZHKUCC 24-0978: ITS = PQ608241, LSU = PQ608075, SSU = PQ607936, RPB*2* = PV186818.

Known hosts: On dried twigs of *Dipterocarpus tuberculatus* (Dipterocarpaceae) (Mapook et al., 2016); on dead twigs of *Mangifera indica* (Anacardiaceae) (Jayasiri et al., 2019); on decaying pod septum of *Delonix regia* (Fabaceae) (Jayasiri et al., 2019); on dead leaves and decaying twig of *Celtis formosana* (Cannabaceae) (Tennakoon et al., 2021; Chethana et al., 2021); on dead twigs of *Zanthoxylum fagara* (Rutaceae) (Mapook et al., 2023); *Coffea* sp. (Rubiaceae) (This study).

Known distribution: Thailand (Mapook et al., 2016; Jayasiri et al., 2019; Mapook et al., 2023), China (Tennakoon et al., 2021; Chethana et al., 2021; This study).

Notes: Based on the multigene phylogenetic analyses, our strains grouped with *M. lithocarpi* (GZCC 19-0137 and MFLUCC 14-1106, ex-type) (Figure 2.26). In morphology, our new collection (MHZU 24-0536) also confirmed to share similar morphological characters with the type material (MFLU 15–1133, holotype) by having coriaceous and flattened ascomata, bitunicate, saccate or obpyriform asci, and ascospores that are oval to obovoid, and aseptate (Mapook et al., 2016; Figure 2.27). This is the first report of *M. lithocarpi* on *Coffea* sp. in China.

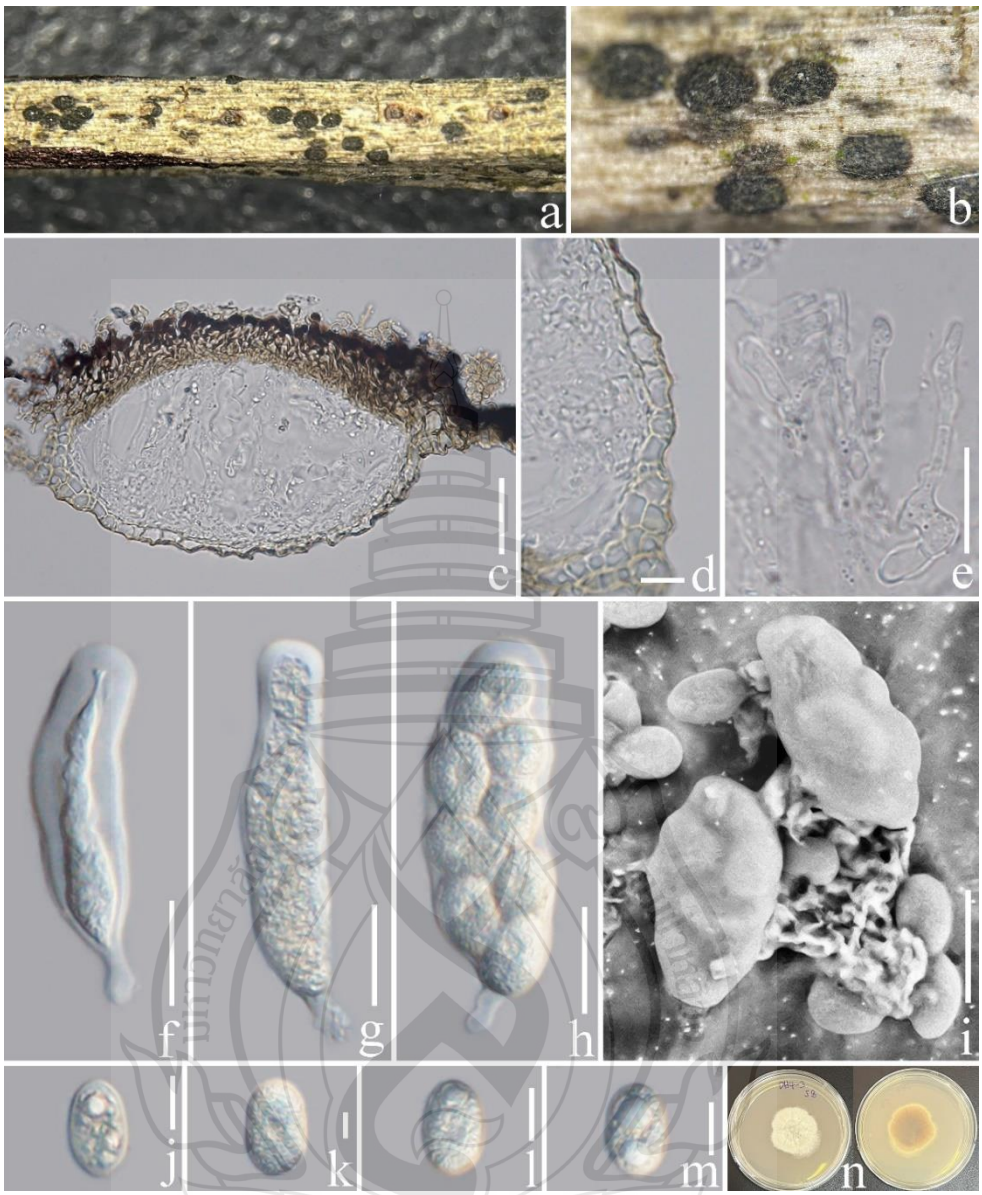


Figure 2.29 *Muyocopron lithocarpi* (MHZU 24-0536, new host record)

Figure 2.29 a, b Appearance of ascomata on *Coffea* sp. c Vertical section of ascoma. d Peridium. e Pseudoparaphyses. f–i Asci (i: SEM microphotographs of asci and ascospores). j–m Ascospores. n Culture on PDA from above and below. Scale bars: c = 30 µm, f–i = 20 µm, d, e, j–m = 10 µm.

Setoapiospora Mapook & K.D. Hyde, Fungal Diversity 100: 134 (2020)

Notes: Based on the phylogenetic analyses of combined LSU, ITS, and SSU sequence data, *Setoapiospora* was introduced with the type species *S. thailandica* by Hyde et al. (2020). The saprobic fungus *S. thailandica* was isolated from dead branches from Thailand with the sexual morph. The sexual morph is characterized by carbonaceous ascomata, appearing as dark brown to black spots, with ostioles and external dark brown setae, comprising dark brown cells of *textura epidermoidea* peridium, hamathecium cylindrical to filiform, septate, pseudoparaphyses, bitunicate asci, cylindrical, 8-spored, pedicellate, with an ocular chamber, ellipsoid to broadly fusiform ascospores, hyaline, 1-seriate, 1-septate, constricted at the septum, with a small lower cell and a large upper cell, widest at the centre and tapering towards the ends, granular (Hyde et al., 2020). No further species have been introduced to this genus since its establishment. In this study, we introduce a new host and new country record of *S. thailandica* from coffee plants from China.

Setoapiospora thailandica Mapook & K.D. Hyde, Fungal Diversity 100: 135 (2020)

Index Fungorum number: IF 556906; *Facesoffungi number:* FoF 06794; Figure 2.28

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 200–350 × 300–450 µm ($\bar{x}$ = 251 × 384 µm, n = 15), semi-immersed to superficial, solitary or scattered, carbonaceous, appearing as black spots, with a poorly developed basal layer and an irregular margin. *Setae* dark brown, tapers toward the top. *Ostiole* central. *Peridium* 20–30 µm wide ($\bar{x}$ =22 µm, n = 20), comprising dark brown cells of *textura epidermoidea*, tightly connected to the substrate. *Hamathecium* of 1.5–3 µm wide ($\bar{x}$ = 1.9 µm, n = 30), filiform, septate, branched, pseudoparaphyses. *Asci* 100–150 × 15–20 µm ($\bar{x}$ = 126 × 17 µm, n = 30), 8-spored, bitunicate, cylindrical, short pedicellate, straight or slightly curved, with an ocular chamber. *Ascospores* 20–25 × 10–12 µm ($\bar{x}$ = 23 × 11 µm, n = 30), 1-seriate or partially bi-seriate, ellipsoid to broadly fusiform, hyaline, 1-septate, constricted at the septum, with a small lower cell and a large upper cell, widest at the centre and tapering towards ends, granular. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, circular, white, flat, filamentous margin, pale brown to brown from below, from the center of the colony, creamy white at margin.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp., 16 September 2021, Li Lu, puer1-3 (MHZU 24-0535), living culture ZHKUCC 24-0975, other living culture ZHKUCC 24-0976.

Known hosts: on dead branches of wood (Hyde et al., 2020), *Coffea* sp. (This study).

Known distribution: Thailand (Hyde et al., 2020), China (This study).

GenBank numbers: ZHKUCC 24-0975: ITS = PQ608242, LSU = PQ608076, SSU = PQ607937, *TEF*1-α = PQ602122; ZHKUCC 24-0976: ITS = PQ608243, LSU = PQ608077, SSU = PQ607938, *TEF*1-α = PQ602123.

Notes: The phylogeny based on a combined LSU, ITS, SSU and *TEF*1-α sequence dataset showed that our strains clustered together with the ex-type of *Setoapiospora thailandica* (MFLUCC 17-1426) (Figure 2.26). Based on pairwise nucleotide comparisons, there are no to minute base pair differences among our isolate (MHZU 24-0535) and *S. sichuanense* (MFLUCC 17-1426). Our new collection (MHZU 24-0535) and the type material (Hyde et al., 2020; Figure 2.28) share very similar morphologies. Based on both morphology and phylogeny herein, we provide the first report of *S. thailandica* on *Coffea* sp. in China.

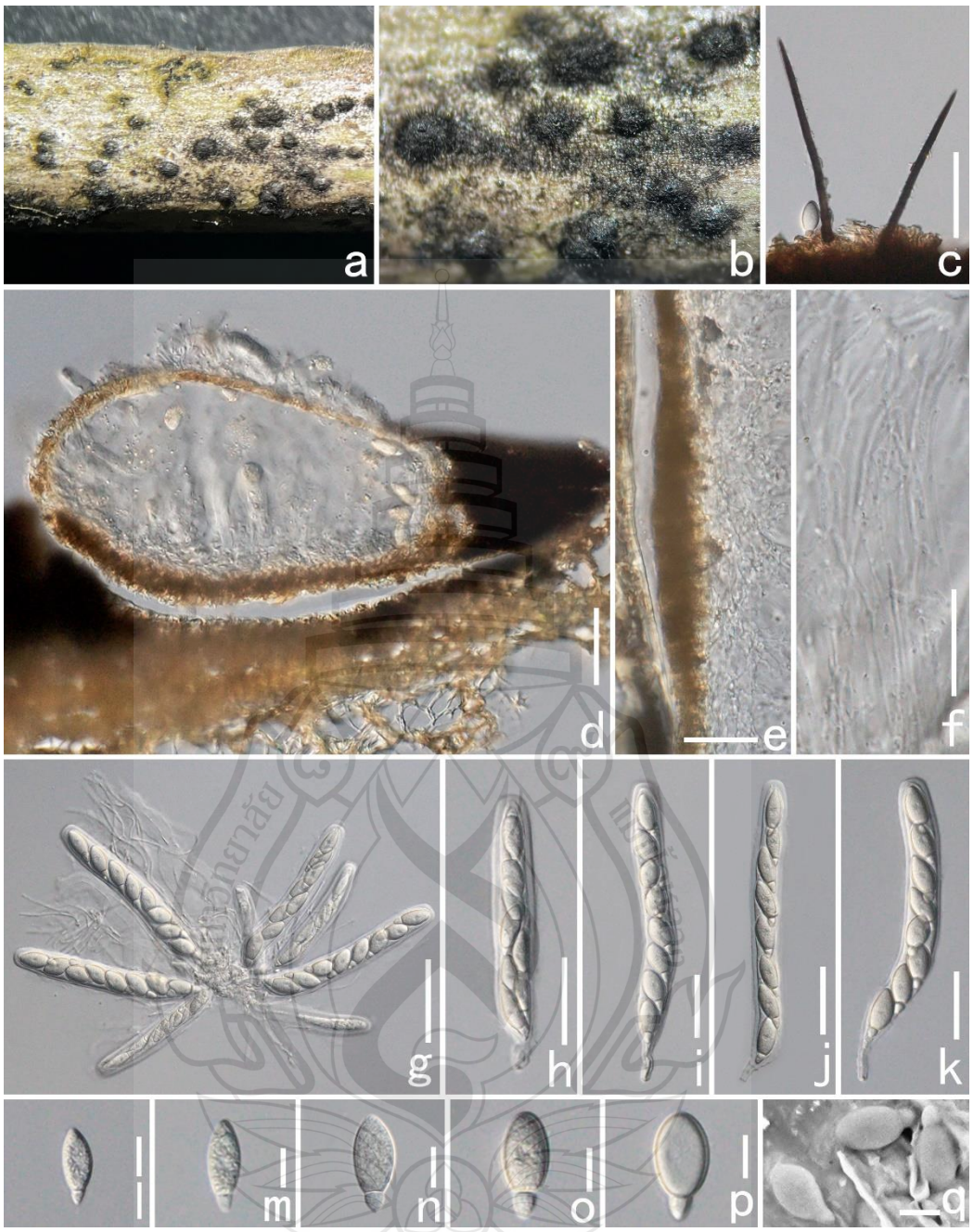


Figure 2.30 *Setoapiospora thailandica* (MHZU 24-0535, new host and country record)

Figure 2.30 a, b Appearance of ascomata on *Coffea* sp. c Setae. d Vertical section of ascoma. e Peridium. f Pseudoparaphyses. g–k Asci. l–q Ascospores (q: SEM microphotographs of ascospores). Scale bars: c, d, g = 50 µm, e, f = 20 µm, h–k = 30 µm, l–q = 10 µm.

Patellariales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 181 (1986)

Patellariaceae Corda, Icones fungorum hucusque cognitorum 2: 37 (1838)

Patellaria Fr., Syst. mycol. (Lundae) 2(1): 158 (1822)

Notes: Patellaria was described by Fries (1822) to accommodate *P. atrata* (the type species). *Patellaria* species show the difference in the number of asci, spore sizes, and number of ascospores within the asci have been documented by Kutorga and Hawksworth (1997), and they suggested that this variation has to be studied carefully to assess any taxonomic significance (cryptic species) within the genus. Almost all *Patellaria* species have been reported as sexual morphs, which are characterized by superficial, black, apothecioid ascomata, with a greenish-black epithecium formed from the branched and swollen paraphyses, bitunicate, fissitunicate asci, and hyaline, clavate to cylindrical, up to more than 5-phragmo-septate ascospores (Kutorga & Hawksworth, 1997; Yacharoen et al., 2015; Maharachchikumbura et al., 2021). The asexual morph of *Patellaria* was unknown until phoma-like species; *Patellaria quercus* was described by Hernandez-Restrepo et al. (2016). Maharachchikumbura et al. (2021) synonymized *P. quercus* under *P. atrata* based on phylogenetic analyses. There are 1420 epithets recorded in Index Fungorum (2025), but most species have been transferred to another genus, and only a few species' sequence data are available (Suetrong & Jones, 2006; Schoch et al., 2009; Suetrong et al., 2009; Dayarathne et al., 2020). In this study, we introduce a new species, *Patellaria coffeae*, which is the first *Patellaria* species collected from coffee in China.

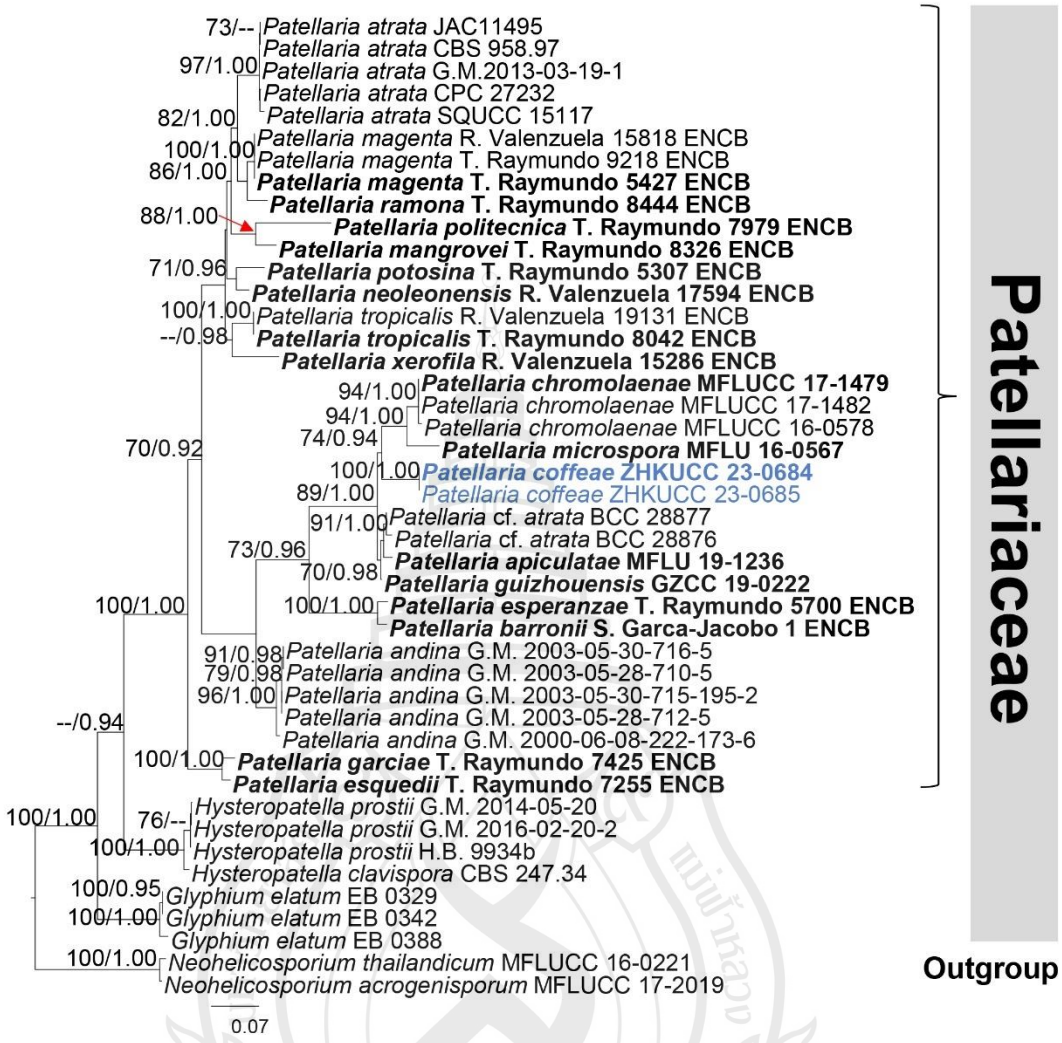


Figure 2.31 Phylogenetic tree of *Patellaria*

Figure 2.31 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, and SSU sequence data. Forty-four strains are included in the combined sequence analysis, which comprises 1,529 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Neohelicosporium acrogenisporum* (MFLUCC 17-2019) and *N. thailandicum* (MFLUCC 16-0221).

Patellaria coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903637; *Facesoffungi number:* FoF 17556; Figure 2.30

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 23-0087

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Apothecia* 500–600 × 100–200 µm ($\bar{x}$ = 550 × 167 µm, n = 10), superficial, arising singly or in small groups, sessile, erumpent from the substrate, longitudinally wide, exposing the dark hymenium at the centre, elliptical, fattened, with a carbonaceous rim, black.

Ectal excipulum 15–30 µm wide ($\bar{x}$ = 24 µm, n = 20), 3–4 cells deep, thick, dark brown cells of subglobose to subangularis. *Medullary excipulum* 10–20 µm wide ($\bar{x}$ = 15 µm, n = 20) composed of *textura globulosa to textura angularis* cells, thin-walled, hyaline to brownish. *Epithecium* green. *Hamathecium* of 2–3 µm wide ($\bar{x}$ = 2.3 µm, n = 20), hyaline, numerous, filiform, septate, branched and swollen at the apex, apices glued together to form epithecium, paraphyses. *Asci* 70–110 × 10–20 µm ($\bar{x}$ = 90 × 14 µm, n = 30), 8-spored, bitunicate, fissitunicate, short pedicellate, cylindric to clavate, rounded at the apex, with an ocular chamber. *Ascospore*s 25–35 × 6–9 µm ($\bar{x}$ = 31 × 7.5 µm, n = 40), uni- to bi-seriate, hyaline, clavate to obovoid, slightly curved, 0–6-septate, septate not distinct, with obvious guttules, smooth-walled, distinctly more tapered towards the distal end. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, flat, irregular and entire margin, cottony to woolly texture, or powdery, density, from above white, and from below reddish brown in center.

Material examined: China, Yunnan Province, Dali City, Zhukula coffee plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C24 (MHZU 23-0087, holotype), ex-type ZHKUCC 23-0684, other living culture ZHKUCC 23-0685.

GenBank numbers: ZHKUCC 23-0684: ITS = PQ608246, LSU = PQ608079, SSU = PQ607939; ZHKUCC 23-0685: ITS = PQ608247, LSU = PQ608080, SSU = PQ607940.

Notes: Based on the phylogenetic analyses of combined LSU, ITS and SSU data, the results showed that *Patellaria coffeae* forms a separate lineage below *P. chromolaenae* (MFLU 16-0578, MFLUCC 17-1482, MFLUCC 17-1479, type) and *P. microspora* (MFLU 16-0567, type) (Figure 2.29). Besides, our collection shares similar apothecia of *P. chromolaenae* and *P. microspora* introduced by Hongsanan et al. (2020a); however, *P. coffeae* can be distinguished from them by clavate to obovoid ascospore, 0–6-septate, with distinct guttules (Figure 2.30), while *P. chromolaenae* has allantoid ascospores, regularly seven septate, and *P. microspora* has ellipsoid ascospores, regularly eight septa (Hongsanan et al., 2020a). We, therefore, identified *P. coffeae* as a new species.

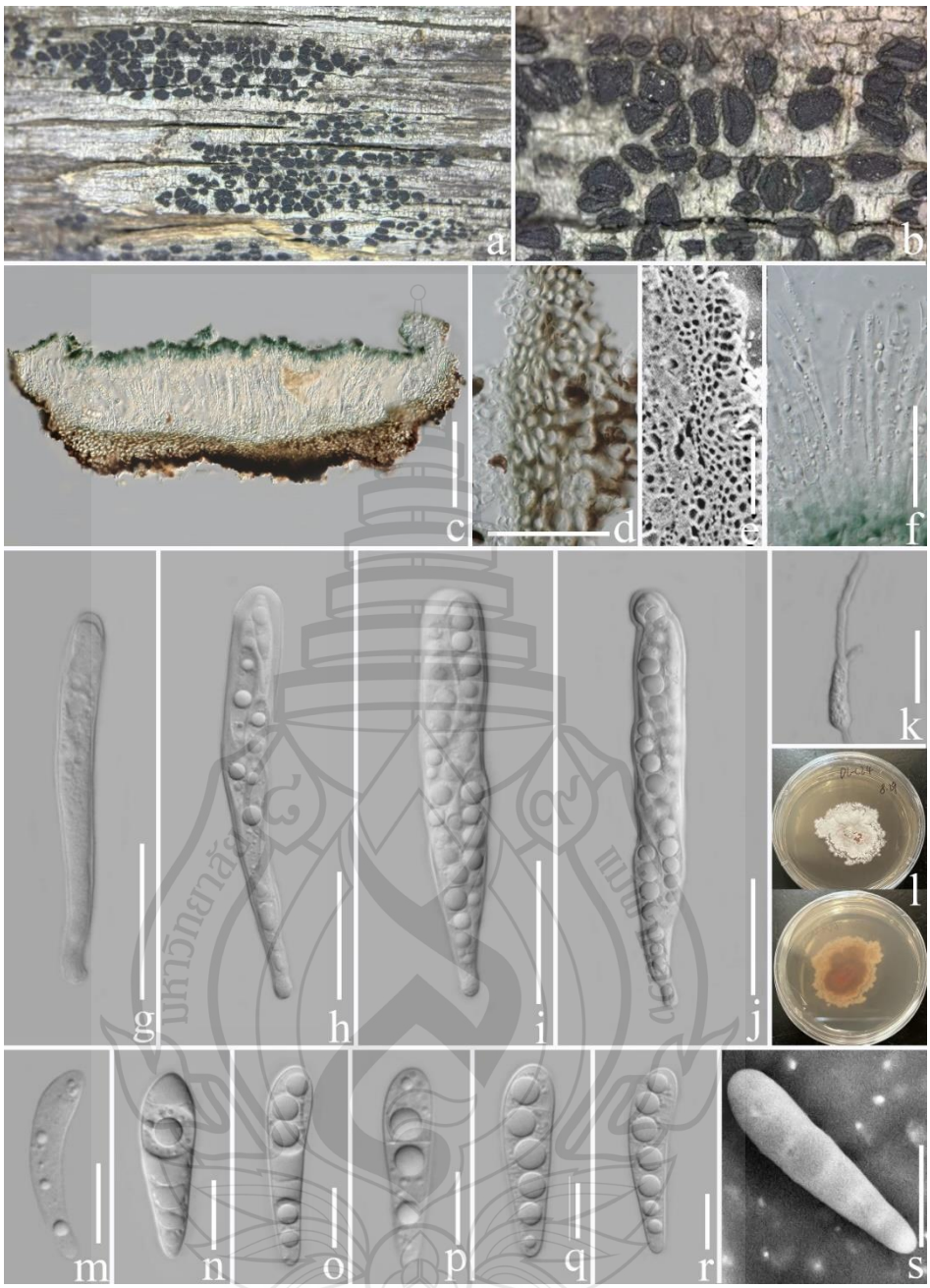


Figure 2.32 *Patellaria coffeae* (MHZU 23-0087, holotype)

Figure 2.32 a, b Apothecia on a decaying branch of *Coffea* sp. c Longitudinal section of an apothecium. d, e Excipulum wall (e: SEM microphotographs of the excipulum). f Filiform paraphyses. g–j Asci. k Germinating ascospore. l Culture on PDA from above and below. m–s Ascospores (s: SEM microphotographs of ascospore). Scale bars: c = 100 μm, d–k = 30 μm, m–s = 10 μm.

Pleosporales Luttr. ex M.E. Barr, Prodr. Cl. Loculoasc. (Amherst): 67 (1987).

Acrocalymmaceae Crous & Trakun.

Acrocalymma Alcorn & J.A.G. Irwin

Notes: Acrocalymma was introduced by Alcorn and Irwin (1987) to accommodate root and foliar rot pathogen *A. medicaginis* on *Medicago sativa* in Australia. At present, there are 18 species identified in different countries from diverse sources and habitats under this genus (Das et al., 2020; Pem et al., 2024; Index Fungorum, 2025). The sexual morph of *Acrocalymma* is characterized by globose and immersed ascomata, with ostiole, textura angularis cells of peridium, cylindrical and bitunicate asci with fusiform and septate ascospores, with a sheath. The asexual morph is characterized by solitary, papillate, and globose pycnidia; determinate, discrete conidiogenous cells; and holoblastic, aseptate, cylindrical, and hyaline conidia with a helmet-shaped mucilaginous appendage at each end (Trakunyingcharoen et al., 2014; Tennakoon et al., 2021). In this study, three new species (*A. coffeae, A. daliensis,* and *A. jinghongensis*) and one new record (*A. walkeri*) are introduced from a coffee host in China, and this is the first report *Acrocalymma* species collected from coffee.

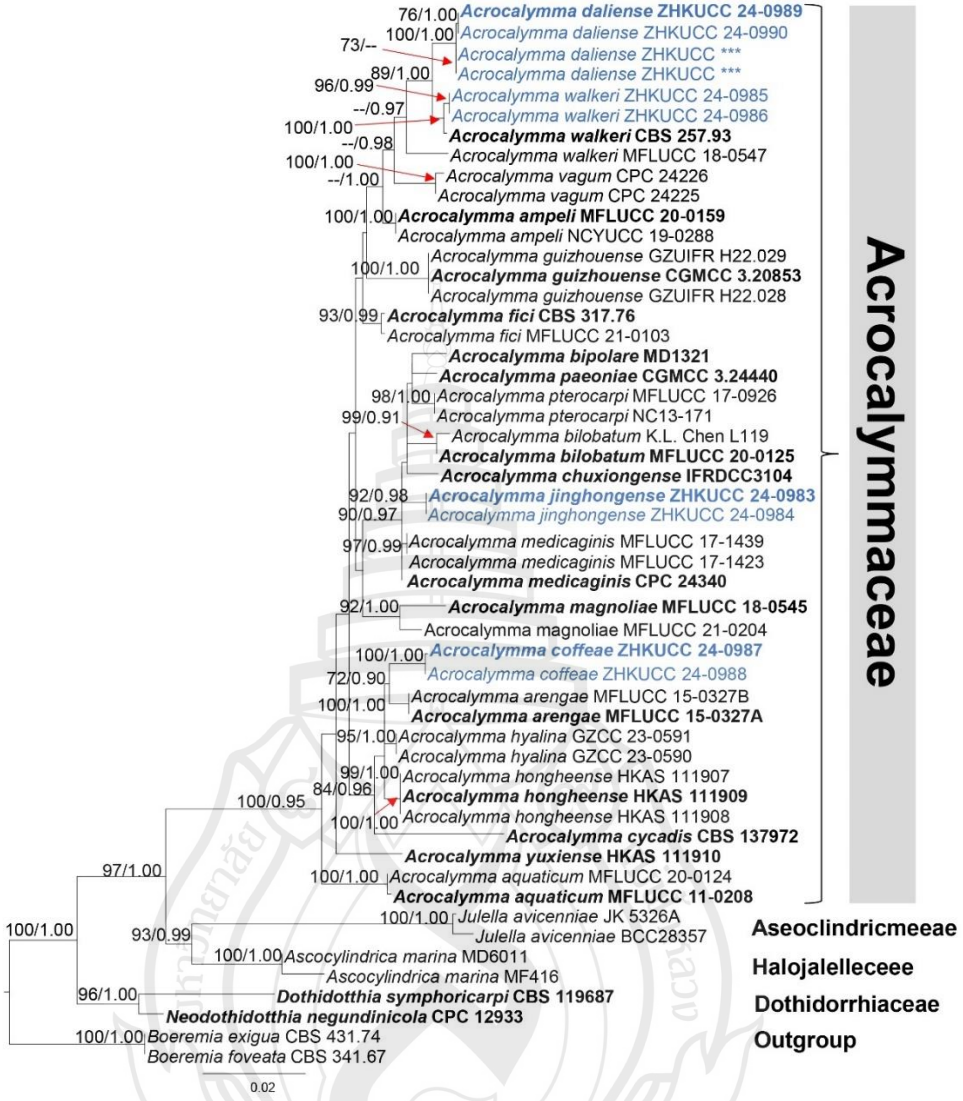


Figure 2.33 Phylogenetic tree of *Acrocalymma*

Figure 2.33 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, and SSU sequence data. Fifty-three strains are included in the combined sequence analysis, which comprises 2,543 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Bocremis exigua* (CBS 431.74) and *B. foveata* (CBS 341.67).

Acrocalymma coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903599; *Facesoffungi number:* FoF 17557; Figure 2.32

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0541

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** Not observed. **Asexual morph:** Coelomycetous. *Conidiomata* 150–200 × 180–250 µm ($\bar{x}$ = 170 × 198 µm, n = 10), pycnidial, globose or subglobose or ampulliform, brown, immersed, solitary, some with ostiole. *Pycnidia* wall 15–25 µm wide, inner layer composed of 2–3 layers of hyaline to light yellow cells, arranged in a *textura angularis*, outer layer darker, fusing cells and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–10 × 5–8 µm ($\bar{x}$ = 8 × 6 µm, n = 20), holoblastic, lining the inner cavity, oval or subcylindrical, solitary, hyaline, smooth, proliferating percurrently at apex, with prominent periclinal thickening at the apex. *Conidia* 35–45 × 7–10 µm ($\bar{x}$ = 42 × 8.5 µm, n = 20), hyaline, cylindrical to fusoid, guttulate, smooth and thin-walled, straight, apex obtuse, unicellular, aseptate, mucilaginous appendage absent.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 40–50 mm in two months at 25°C, colonies from above: circular, white, margin filamentous, dense, slightly raised, cottony to fairy fluffy appearance; from below: cream at the margin, pale brown to dark brown in the center.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp., 16th September 2021, Li Lu, puer 4-15 (MHZU 24-0541, holotype),

ex-type ZHKUCC 24-0987, other living culture ZHKUCC 24-0988.

GenBank numbers: ZHKUCC 24-0987: ITS = PQ608266, LSU = PQ608099, SSU = PQ607957; ZHKUCC 24-0988: ITS = PQ608267, LSU = PQ608100, SSU = PQ607958.

Notes: Phylogenetically, *Acrocalymma coffeae* (ZHKUCC 24-0987, ex-type and ZHKUCC 24-0988) forms a distinct lineage basal to *A. arengae* (MFLUCC 15-0327A, ex-type and MFLUCC 15-0327B) with 72% ML and 0.90 BYPP statistical

support (Figure 31). *Acrocalymma arengae* is lacks of asexual morph, hence a comparison in morphology is unfeasible (Konta et al., 2023). Based on nucleotide comparisons, our isolate (ZHKUCC 24-0987, ex-type) is different from *A. arengae* (MFLUCC 15-0327A, ex-type) by 18/837 bp (2.2%, without gaps) in ITS, 5/896 bp (0.6%, without gaps) in LSU and 11/1030 bp (1.1%, without gaps) in SSU. The morphological characteristics of our isolates fit with *Acrocalymma* asexual morph by having hyaline, cylindrical, or subcylindrical, guttulate conidia (Farr et al., 1998; Trakunyingcharoen et al., 2014; Mortimer et al., 2021; Figure 2.32). In addition, morphologically, our isolate are similar to *A. hyalina* (isolates GZCC 23-0590), but the shape of the conidia is different (oblong to subcylindrical vs. cylindrical to fusoid), besides, the conidial size of *A. coffeae* (35–45 × 7–10 μm, L/W = 3.5–6.43) is larger than that of the ex-type *A. hyalina* (30–38 × 5–9 μm, L/W = 3.33–7.6) (Chethana et al., 2023). Both phylogenetic analyses and morphological characteristics support *A. coffeae* as a distinct new species in *Acrocalymma*.

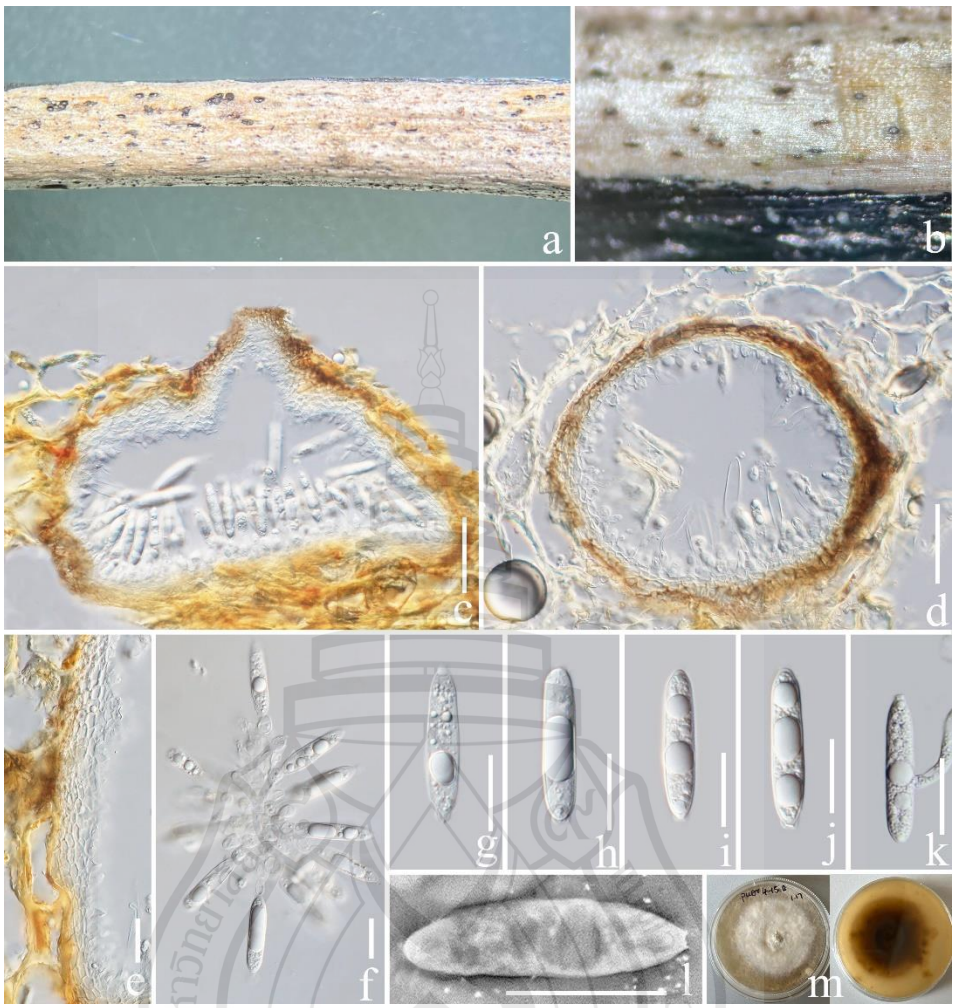


Figure 2.34 *Acrocalymma coffeae* (MHZU 24-0541, holotype)

Figure 2.34 a, b Appearance of immersed conidiomata on substrate. c, d Vertical sections through conidiomata. e Cells of pycnidia wall. f Conidiogenous cells with conidia. g–j Conidia. k Germinated conidium. l SEM microphotographs of conidium. m Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–l = 20 µm.

Acrocalymma daliense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903600; *Facesoffungi number*: FoF 17558; Figure 2.33, Figure 2.34

Etymology: The species epithet refers to the type location "Dali", China.

Holotype: MHZU 24-0542

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph (Figure 2.33)**: *Ascomata* 160–200 × 200–250 µm ($\bar{x}$ = 175 × 216 µm, n = 10), solitary, semi-immersed to immersed, erumpent through the substrate, globose to subglobose, dark brown to black, ostiolate. *Ostioles* central. *Peridium* 15–25 µm wide ($\bar{x}$ = 18 µm, n = 20), composed of 3–5 layers, cells towards the inside hyaline to lightly pigmented, brown at the outside, composed of *textura angularis* to *textura prismatica* cells. *Hamathecium* comprises numerous, 2–3 µm wide, hyaline, filamentous, branched, septate, pseudoparaphyses. *Asci* 80–110 × 10–17 µm ($\bar{x}$ = 95 × 13 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical or clavate, with a short furcate pedicel, and a small ocular chamber. *Ascospores* 20–25 × 5–7 µm ($\bar{x}$ = 23 × 6 µm, n = 20), biseriate, fusiform, 1-septate, slightly constricted at the septum, with wider upper cell, hyaline, acute at both ends, smooth-walled, guttulate, surrounded by a thick mucilaginous sheath. **Asexual morph (Figure 2.34)**: Coelomycetous. *Conidiomata* 120–180 × 120–200 µm ($\bar{x}$ = 140 × 160 µm, n = 10), solitary, immersed, partially erumpent when mature, dark brown to black, subglobose to globose, uniloculate, *Ostiole* central, papillate. *Peridium* 15–20 µm wide, composed of 3–5 layers, with outer 2–3 layers light brown, thick-walled cells of *textura angularis* and inner 1–3 layers hyaline, thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–10 µm long × 3–5 µm wide ($\bar{x}$ = 8 × 4 µm, n = 20), phialidic, cylindrical or oval, hyaline. *Conidia* 20–30 × 4–6 µm ($\bar{x}$ = 27 × 5.3 µm, n = 20), oblong to fusoid, or irregular, straight, hyaline, 0–4 septate, guttulate, some slightly constricted at the middle, without mucilaginous appendage.

Culture characteristics: Ascospores germinating on PDA within 12 h, colonies on PDA after one month attaining a diam of 30 mm at 25°C, fluffy, white, circular, flat, entire margin, with aerial mycelium, from below yellowish to light brown from edge to center, wrinkled. Conidia germinating on PDA within 12 h, colonies growing on PDA, reaching 25–30 mm in one month at 25°C, circular, white, margin

filamentous, dense, slightly raised, cottony to fairy fluffy appearance; from below: cream at the margin, pale brown to dark brown in the center.

Material examined: China, Yunnan Province, Dali City, Zhukula coffee plantation, on a decaying branch of *Coffea arabica* (1416 m), 25 July 2022, Li Lu, DL-C5 (MHZU 24-0542, holotype), ex-type ZHKUCC 24-0989, other living culture ZHKUCC 24-0990; *ibid.* DL-C32 (MHZU 24-0829, paratype), ex-paratype ZHKUCC ***, other living culture ZHKUCC ***.

GenBank numbers: ZHKUCC 24-0989: ITS = PQ608268, LSU = PQ608101, SSU = PQ607959; ZHKUCC 24-0990: ITS = PQ608269, LSU = PQ608102, SSU = PQ607960. ZHKUCC ***: ITS = PQ608270, LSU = PQ608103, SSU = PQ607961. ZHKUCC ***: ITS = PQ608271, LSU = PQ608104, SSU = PQ607962.

Notes: Multigene phylogenetic analyses showed that our collections (DL-C5, DL-C32) clustered together and formed a distinct lineage sister to *Acrocalymma walkeri* (ZHKUCC 24-0985, ZHKUCC 24-0986 and CBS:257.93, isotype) with 89% ML and 1.00 BYPP statistical support (Figure 2.31). Morphologically, our collection (MHZU 24-0542, holotype) is similar to *A. walkeri* (CBS:257.93, isotype) in having cylindrical and short pedicellate asci with fusiform ascospores, but our strain can be distinguished from *A. walkeri* by longer asci (80–110 × 10–17 µm, L/W = 4.7–11 vs. 50–80 × 8–11 µm; L/W = 4.5–10) and distinct sheath of ascospores (Shoemaker & Babcock, 1991; Chethana et al., 2023; Figure 2.33). Based on the morpho-molecular evidence, we introduce our isolates as a new species and named *A. daliense* from *Coffea arabica* in China with sexual and asexual morphs (Figure 2.33, Figure 2.34).



Figure 2.35 Sexual morph of *Acrocalymma daliense* (MHZU 24-0542, holotype)

Figure 2.35 a, b Ascomata on arabica coffee twig surface. c A vertical section through ascoma. d Peridium. e Pseudoparaphyses. f–h Asci. i–m Ascospores (l: stained with Indian ink, m: SEM microphotographs of ascospores). n Germinated asci. o Culture on PDA from above and below. Scale bars: c = 50 µm, d = 30 µm, e–h = 20 µm, i–n = 10 µm.

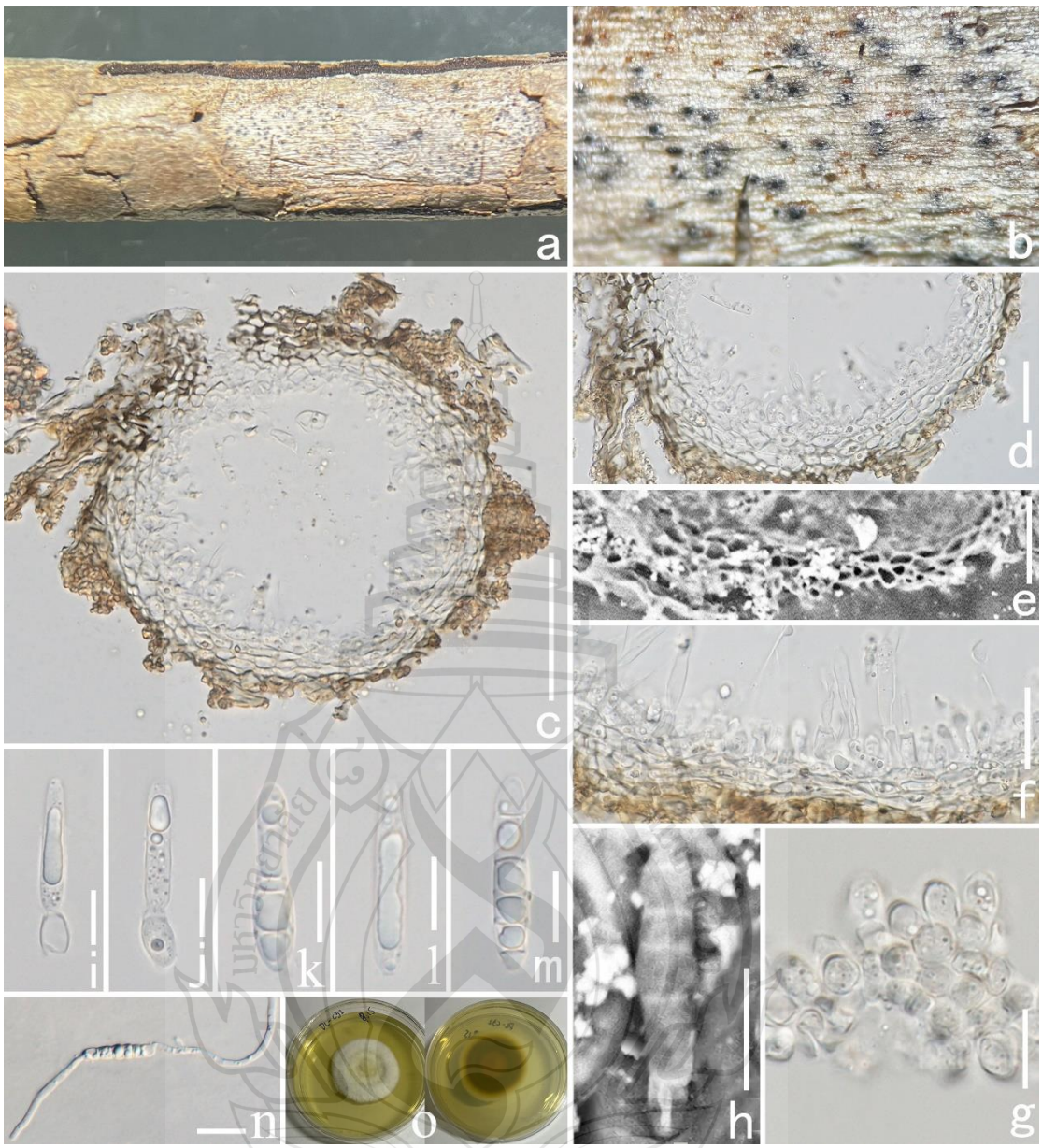


Figure 2.36 Asexual morph of *Acrocalymma daliense* (MHZU 24-0829, paratype)

Figure 2.36 a, b Appearance of conidiomata on substrate. c A vertical section through conidioma. d, e Cells of pycnidia wall (e: SEM microphotographs of peridium). f, g Conidiogenous cells. h SEM microphotographs of the conidium. i, j Conidiogenous cells with conidia. k–m Conidia. n Germinated conidium. o Culture on PDA from above and below. Scale bars: c = 50 µm, d–f, n = 10 µm, g–m = 10 µm.

Acrocalymma jinghongense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903601; *Facesoffungi number*: FoF 17559; Figure 2.35

Etymology: The species epithet refers to the type location "Jinghong", China.

Holotype: MHZU 24-0539

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 120–240 × 160–300 µm ($\bar{x}$ = 154 × 183 µm, n = 15), globose or subglobose, dark brown, semi-immersed to immersed, solitary, ostiole at centre, with minute papilla. *Pycnidia wall* 12–20 µm wide, composed of 2–3 layers of small, fattened, brown to dark brown and arranged in *textura angularis* cells, in the outer layer, darker, fusing cells and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 5–6 µm ($\bar{x}$ = 6 × 5 µm, n = 20), holoblastic, hyaline, smooth, pyriform or cylindrical, guttulate, proliferating with visible periclinal thickening at apex. *Conidia* 16–20 × 4–5.5 µm ($\bar{x}$ = 18 × 4.8 µm, n = 40), solitary, cylindrical to fusoid, apex obtuse, hyaline, guttulate, thin and smooth-walled, straight, unicellular, with faring mucoid apical appendage at lower end, visible in water.

Culture characteristics: Colonies on PDA, 30–40 mm diam. after six weeks, colonies from above: circular, flat, slightly raised in the middle, dense, surface smooth with filiform edge, fluffy to velvety with smooth aspects, off-white to greyish in the center, brown at the margin, from below: dark brown to black.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (1672 m), 12th September 2021, Li Lu, JHMH 16 (MHZU 24-0539, holotype), ex-type ZHKUCC 24-0983, other living culture ZHKUCC 24-0984.

GenBank numbers: ZHKUCC 24-0983: ITS = PQ608262, LSU = PQ608095, SSU = PQ607953; ZHKUCC 24-0984: ITS = PQ608263, LSU = PQ608096, SSU = PQ607954.

Notes: Phylogenetically, *Acrocalymma jinghongensis* (ZHKUCC 24-0983, ex-type and ZHKUCC 24-0984) forms a distinct lineage basal to *A. chuxiongense* (IFRDCC3104, ex-type) (Figure 2.31). *Acrocalymma chuxiongense* was reported as a sexual morph (Liu et al., 2022); however, our isolates show only the asexual morph, and we were unable to get a sexual morph from the culture. Based on nucleotide

comparisons, our isolate (ZHKUCC 24-0983, ex-type) is different from *A. chuxiongense* (IFRDCC3104, type) by 9/430 bp (2.0%, without gaps) in ITS and 4/864 bp (0.5%, without gaps) in LSU. Only ITS and LSU gene regions are available for *A. chuxiongense*. Furthermore, the morphology of our isolate is similar to *Acrocalymma* asexual species by having hyaline and cylindrical to fusoid conidia (Alcorn & Irwin, 1987; Tennakoon et al., 2021; Figure 2.35). Therefore, we introduce our isolate as a new species isolated from coffee plants.

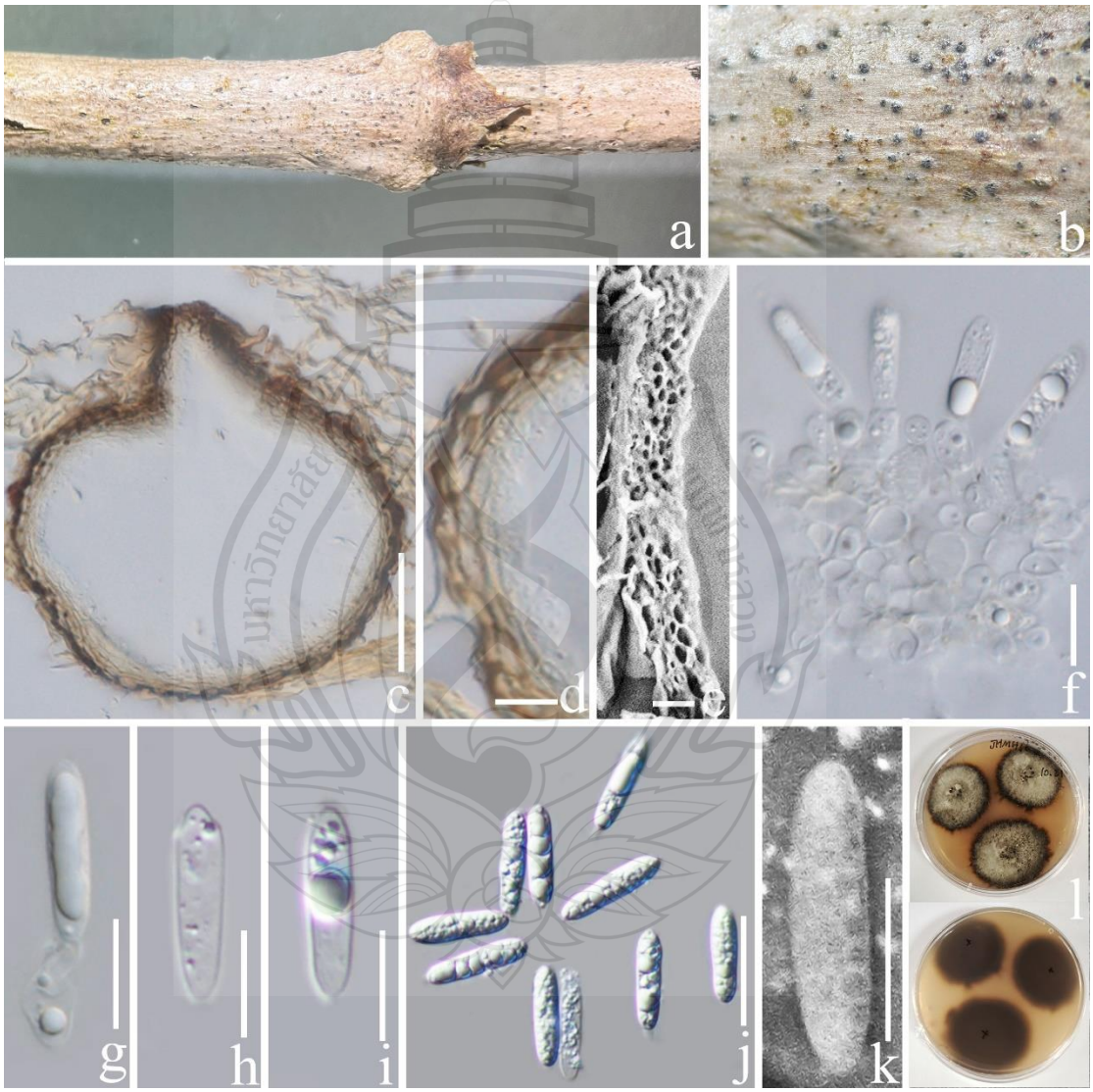


Figure 2.37 *Acrocalymma jinghongense* (MHZU 24-0539, holotype)

Figure 2.37 a, b Appearance of immersed conidiomata on substrate. c A vertical section through conidioma. d, e Cells of pycnidia wall (e: SEM microphotographs of peridium). f, g Conidiogenous cells with conidia. h–k Conidia (k: SEM microphotographs of the conidium). l Culture on PDA from above and below. Scale bars: c = 50 μm, d–k = 10 μm.

Acrocalymma walkeri (Shoemaker, C.E. Babc. & J.A.G. Irwin) Crous & Trakun., IMA Fungus 5(2): 407 (2014)

Index Fungorum number: IF 810840, *Facesoffungi number*: FoF 12929; Figure 2.36

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 120–180 × 120–160 μm ($\bar{x}$ = 132 × 135 μm, n = 10), solitary or scattered, immersed, globose or subglobose, dark brown to black, ostiole visible in surface view, elongated neck, ostiolate. *Peridium* 10–15 μm wide ($\bar{x}$ = 12 μm, n = 10), composed of thin-walled, flattened, brown to dark brown pseudoparenchymatous cells, cells towards the inside hyaline to lightly pigmented, arranged in a *textura angularis* to *textura prismatica*, at the outside, darker, fusing and indistinguishable from the host tissues. *Hamathecium* composed of 2–4 μm wide, hyaline, numerous, filamentous, branched, septate, some constricted at the septa, pseudoparaphyses. *Asci* 50–75 × 10–12 μm ($\bar{x}$ = 62 × 11 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, with a short furcate pedicel, and with a small ocular chamber. *Ascospores* 18–24 × 5–8 μm ($\bar{x}$ = 20 × 6 μm, n = 30), biseriate, hyaline, fusiform with acute ends, 1-septate when young and become 3-septate when mature, constricted at the septum, guttulate, smooth-walled, surrounded by a thin mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on PDA reaching 50 mm diameter after two months at 25°C, colonies from above: circular, margin filiform, dense, flattened, with fairy fluffy appearance, light yellow; from below: cream to reddish brown at the margin, dark brown to black in the center.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (22°31'18", 101°2'44", 856.89 m), 15 September 2021, Li Lu, JHPW 15 (MHZU 24-0540), living culture ZHKUCC 24-0985, other living culture ZHKUCC 24-0986.

GenBank numbers: ZHKUCC 24-0985: ITS = PQ608264, LSU = PQ608097, SSU = PQ607955; ZHKUCC 24-0986: ITS = PQ608265, LSU = PQ608098, SSU = PQ607956.

Known hosts: Medicago sativa (Trakunyingcharoen et al., 2014); *Magnolia* sp. (de Silva et al., 2022); dead stems of *Tithonia diversifolia* (Chethana et al., 2023); the branch of *Diospyros kaki* with canker symptoms (Atashi et al., 2024); *Coffea* sp. (This study).

Known distribution: Australia (Trakunyingcharoen et al., 2014); Thailand (de Silva et al., 2022; Chethana et al., 2023); Iran (Atashi et al., 2024); China (This study).

Notes: Acrocalymma walkeri was introduced by Crous and Trakunyingcharoen (2014). It was reported from *Medicago sativa* (Australia) and dead twigs attached to *Magnolia* sp. (Thailand) (Shoemaker et al., 1991; de Silva et al., 2022). The morphological characteristics of our collection (MHZU 24-0540) resembles *Acrocalymma walkeri* in having cylindrical asci and hyaline, fusiform, 1 or 3-septate ascospores (Shoemaker et al., 1991; de Silva et al., 2022; Figure 2.36). Multi-gene phylogeny also indicates that our species clustered with *A. walkeri* (CBS 257.93, isotype) with 100% ML, 1.00 BYPP support (Figure 2.31). Therefore, based on morphology and phylogeny evidence, we report our species as a new host and country record of *A. walkeri* from coffee in China.

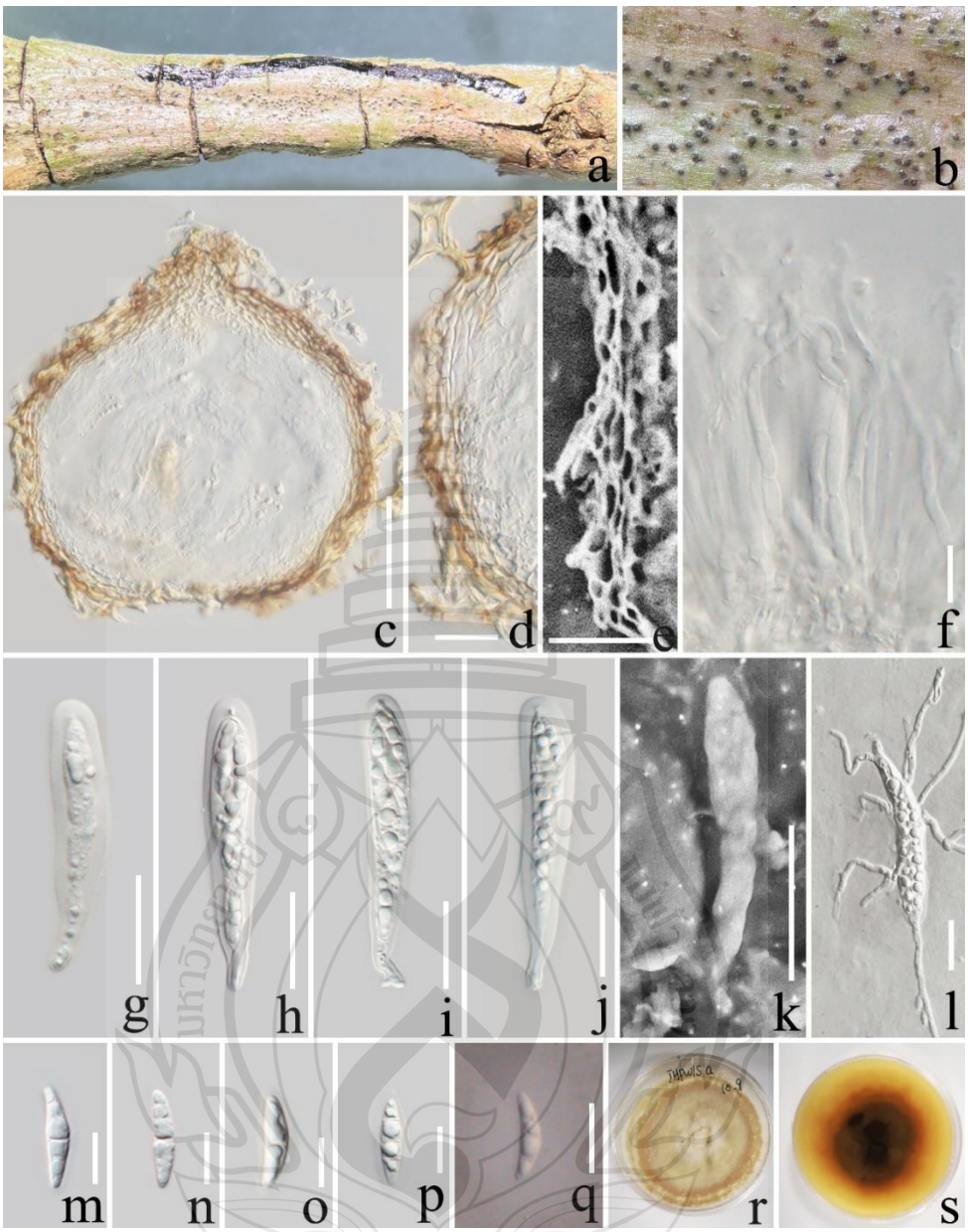


Figure 2.38 *Acrocalymma walkeri* (MHZU 24-0540, new host and country record)

Figure 2.38 a, b Ascomata on arabica coffee twig surface. c A vertical section through ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g–k Asci (k: SEM microphotographs of ascus and ascospore). l Germinated ascus. m–q Ascospores (q: Ascospore stained with Indian ink). r, s Culture on PDA from above and below. Scale bars: c = 50 µm, d–f = 15 µm, g–l = 20 µm, m–q = 10 µm.

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

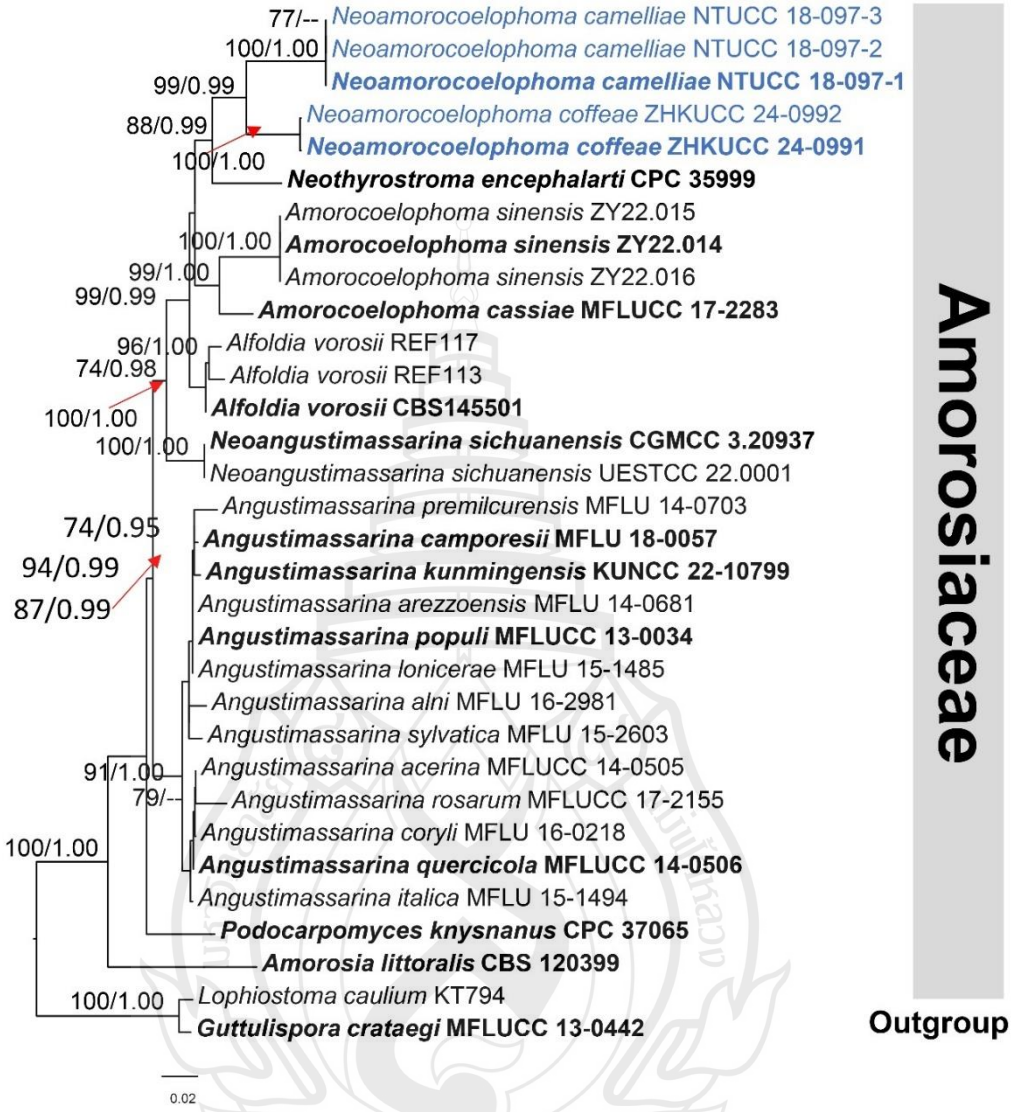


Figure 2.39 Phylogenetic tree of *Neoamorocoelophoma*

Figure 2.39 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Thirty-two strains are included in the combined sequence analysis, which comprises 4,239 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Lophiostoma caulium* (KT794) and *Guttulispora crataegi* (MFLUCC 13-0442).

Neoamorocoelophoma L. Lu, K.D. Hyde & Tibpromma, *gen. nov.*

Index Fungorum number: IF 903627; *Facesoffungi number*: FoF 17560

Etymology: The genus name refers to the similarity to the genus "*Amorocoelophoma".*

Type species: *Neoamorocoelophoma coffeae*

Saprobic on dead or decaying plants. **Sexual morph:** *Ascomata* solitary or scattered, semi-immersed to immersed, becoming erumpent when mature, coriaceous, brown to black, globose to subglobose or conical, uniloculate, ostiolate. *Ostiole* central, rounded, cylindrical, papillate, well-developed, with a pore-like opening when mature. *Peridium* comprising several layers of dark brown to lightly pigmented cells of *textura angularis* to *textura prismatica*. *Hamathecium* comprising numerous, cellular, septate, branched, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 6–8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate and club-like, rounded at the apex, with an ocular chamber. *Ascospores* 1–2-seriate or overlapping, fusiform with narrow, rounded ends, hyaline, some light brown when mature, 1-septate, constricted at the septum, upper cell is wider and longer than the lower cell, guttulate, surrounded by a mucilaginous sheath. **Asexual morph:** Chlamydosporous. *Hyphae* pale brown, septate, branched or unbranched, smooth-walled. *Chlamydospores* mostly in chains, pale brown, subglobose or oval or cylindrical, septate, constricted at the septa, smooth and thick-walled, formed within the PDA medium.

Notes: *Neoamorocoelophoma* formed an independent lineage in Amorosiaceae with 88% ML and 0.99 BYPP statistical support (Figure 2.37). In morphology, *Neoamorocoelophoma* shows the sexual morph genetic description of Amorosiaceae (Thambugala et al., 2015; Yu et al., 2022). However, it can be distinguished by having cylindrical to clavate asci, short pedicellate and club-like, 6–8-spored, fusiform, and 1-septate ascospore, with rounded ends (Figure 2.38). *Neoamorocoelophoma* produced the asexual morph from culture which is similar to *Angustimassarina* species (Thambugala et al., 2015). However, it differs from *Angustimassarina* by its branched conidiophores and subglobose to ellipsoidal conidia with 0–1 septa (Figure 2.38). Both morphological and molecular evidence collectively support the classification of *Neoamorocoelophoma* as a distinct genus in Amorosiaceae.

Neoamorocoelophoma camelliae (Ariyawansa, I. Tsai & Thambugala) L. Lu, K.D. Hyde & Tibpromma, *comb. nov.*

Basionym: *Amorocoelophoma camelliae* Ariyaw., I. Tsai & Thambug., Sci. Rep. 10 (no. 12762): 15 (2020)

Index Fungorum number: IF 903628; *Facesoffungi number*: FoF 17616

Notes: *Amorocoelophoma camelliae* was introduced as a new species based on its smaller conidia (2–3 × 1–2 μm, L/W = 1–3 vs. 9–11 × 2–3 μm, L/W = 3–5.5) when compared with the type species in *Amorocoelophoma* (*A. cassia*) (Jayasiri et al., 2019; Ariyawansa et al., 2020). In our phylogenetic analyses, *Amorocoelophoma camelliae* always formed a separate branch from other *Amorocoelophoma* species and was sister to *Neoamorocoelophoma*. In addition, the findings of Yu et al. (2022) and Zhang et al. (2024) also demonstrated that *Amorocoelophoma camelliae* forms an independent lineage from other *Amorocoelophoma* species (Figure 2.37). Unfortunately, morphological comparisons were not possible as the new genus *Neoamorocoelophoma* exhibits the asexual morph observed from culture, while *A. camelliae* was observed from natural host by having ellipsoidal to cylindrical, hyaline to pale brown, aseptate conidia (Ariyawansa et al., 2020). Based on nucleotide comparisons, *Amorocoelophoma camelliae* (NTUCC 18-097-1, ex-type) differs from the type species *A. cassia* (MFLUCC 17–2283, ex-type) by 68/469 bp (15%, without gaps) in ITS and 97/716 bp (14%, without gaps) in *RPB*2. Differs from the type species *N. coffeae* (ZHKUCC 24-0991, ex-type) by 47/505 bp (9%, without gaps) in ITS and 66/719 bp (9%, without gaps) in *RPB*2. Another three genes, LSU, SSU, and *TEF*1-α, all exhibit lower differentiation among these three species. This result shows that *A. camelliae* is more closely related to *Neoamorocoelophoma*. Hence, we transferred *A. camelliae* to *N. camelliae*. In addition, we propose that *A. camelliae* may represent the asexual morph of *Neoamorocoelophoma* in its natural hosts.

Neoamorocoelophoma coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903629; *Facesoffungi number*: FoF 17561; Figure 2.38

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0543

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 100–230 × 120–230 µm ($\bar{x}$ = 152× 168 µm, n = 15), solitary or scattered, semi-immersed to immersed, becoming erumpent when mature, coriaceous, brown to black, globose to subglobose or conical, uniloculate, ostiolate. *Ostiole* central, rounded, cylindrical, papillate, well-developed, with a pore-like opening when mature. *Peridium* 15–25 µm wide ($\bar{x}$ = 21 µm, n = 20), comprising several layers of dark brown to lightly pigmented cells of *textura angularis* to *textura prismatica*. *Hamathecium* of 2–3 µm wide ($\bar{x}$ = 2.6 µm, n = 30), comprising numerous, cellular, septate, branched, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 60–80 × 12–20 µm ($\bar{x}$ = 71 × 15.3 µm, n = 30), 6–8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate and club-like, rounded at the apex, with an ocular chamber. *Ascospores* 18–22 × 5–7 µm ($\bar{x}$ = 20.9 × 6.2 µm, n = 30), 1–2-seriate or overlapping, fusiform with narrow and rounded ends, hyaline, some light brown when mature, 1-septate, constricted at the septum, upper cell is longer than the lower cell, guttulate, surrounded by a thick mucilaginous sheath. **Asexual morph**: *Mycelium* 2–4 µm wide ($\bar{x}$ = 2.9 µm, n = 20), pale brown, septate, branched. *Chlamydospores* produced after three months of growth on PDA at 28°C, mostly in chains, pale brown, subglobose or oval or cylindrical, septate, constricted at the septa, smooth and thick-walled.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 50 mm in one month at 25°C, surface rough, slightly raised, cottony, circular with filamentous margin, from above, brown, from below, dark brown to black.

Material examined: China, Yunnan Province, Nujiang City, on a decaying branch of *Coffea* sp. (25.80 N, 98.85 E, 1005 m), 22 April 2023, Li Lu, C-04 (MHZU 24-0543, holotype), ex-type ZHKUCC 24-0991, other living culture ZHKUCC 24-0992.

GenBank numbers: ZHKUCC 24-0991: ITS = PQ608248, LSU = PQ608081, SSU = PQ607941, *RPB*2 = PV186821, *TEF*1-α = PQ602124; ZHKUCC 24-0992: ITS = PQ608249, LSU = PQ608082, SSU = PQ607942, *RPB*2 = PV186822, *TEF*1-α = PQ602125.

Notes: Based on the phylogenetic analysis of combined LSU, ITS, SSU, *TEF*1-α, and *RPB*2 sequence data, *Neoamorocoelophoma coffeae* forms a separate branch with 99% ML and 0.99 BYPP statistical support (Figure 2.37). In morphology, the sexual morph of *N. coffeae* is similar to *Angustimassarina italica* (holotype) (Tibpromma et al., 2017) and *Neoangustimassarina sichuanensis* (holotype) (Yu et al., 2022). However, it can be distinguished from the two species by 6–8-spored asci, short pedicellate and club-like, and fusiform ascospores with distinct guttules (Thambugala et al., 2015; Yu et al., 2022; Figure 2.38). Herein we introduce *N. coffeae* as a new species based on both morphological comparison and phylogenetic analyses.



Figure 2.40 *Neoamorocoelophoma coffeae* (MHZU 24-0543, holotype)

Figure 2.40 a, b Ascomata on host surface. c Longitudinal section of ascoma. d Peridium. e Hamathecium. f–i Asci. j–o Ascospore (j: SEM microphotographs of ascospores). p Ascospore stained with Indian Ink. q Culture on PDA from above and below. r Mycelium. s–u Chlamydospores growing from hyphae. Scale bars: c = 50 µm, d–i = 20 µm, j–p, r–u = 10 µm.

Anteagloniaceae K.D. Hyde & A. Mapook, Fungal Diversity 63 (1): 33 (2013)

Anteaglonium Mugambi & Huhndorf, Systematics and Biodiversity 7 (4): 460 (2009)

Notes: Anteaglonium was introduced by Mugambi and Huhndorf (2009a) to accommodate four hysterothecial taxa with hyaline 2-celled ascospores, *A. abbreviatum* (type species), *A. globosum*, *A. latirostrum*, and *A. parvulum*, which grouped in Pleosporales and outside the order Hysteriales. *Anteaglonium* had previously been accepted in Hysteriaceae because for its hysterothecial ascomata (Mugambi & Huhndorf, 2009a). Subsequently, Hyde et al. (2013) placed *Anteaglonium* in a new family, Anteagloniaceae, as it formed a distinct lineage in Pleosporales. There are 11 species recorded in Index Fungorum (2025), which were collected from different hosts as saprobes and are distributed worldwide (Mugambi & Huhndorf, 2009b; Almeida et al., 2014; Jaklitsch et al., 2018; Tan et al., 2022; Zhang et al., 2023). The sexual morph of *Anteaglonium* is characterized by hysterothecial, erumpent to superficial, fusiform to oblong, brown to shiny black ascomata, opening by pronounced or indistinct longitudinal slit running entire length of fruit body or apex raised and laterally compressed, cylindrical, short pedicellate, 8-spored asci and uniseriate or biseriate, fusiform to oblong, septate, hyaline or pigmented ascospores, constricted at the primary septum (Mugambi & Huhndorf, 2009a). The asexual morph is characterized by coelomycetous, pycnidial, globose, unilocular, conidiomata with ostioles, wall consisting of hyaline cells of textura angularis, long conidiophores, unbranched, hyaline, globose conidiogenous cells with oval to globose, hyaline, aseptate conidia, rounded at both ends (Jayasiri et al., 2016). In this study, we provide new host and new country records collected from coffee in China.

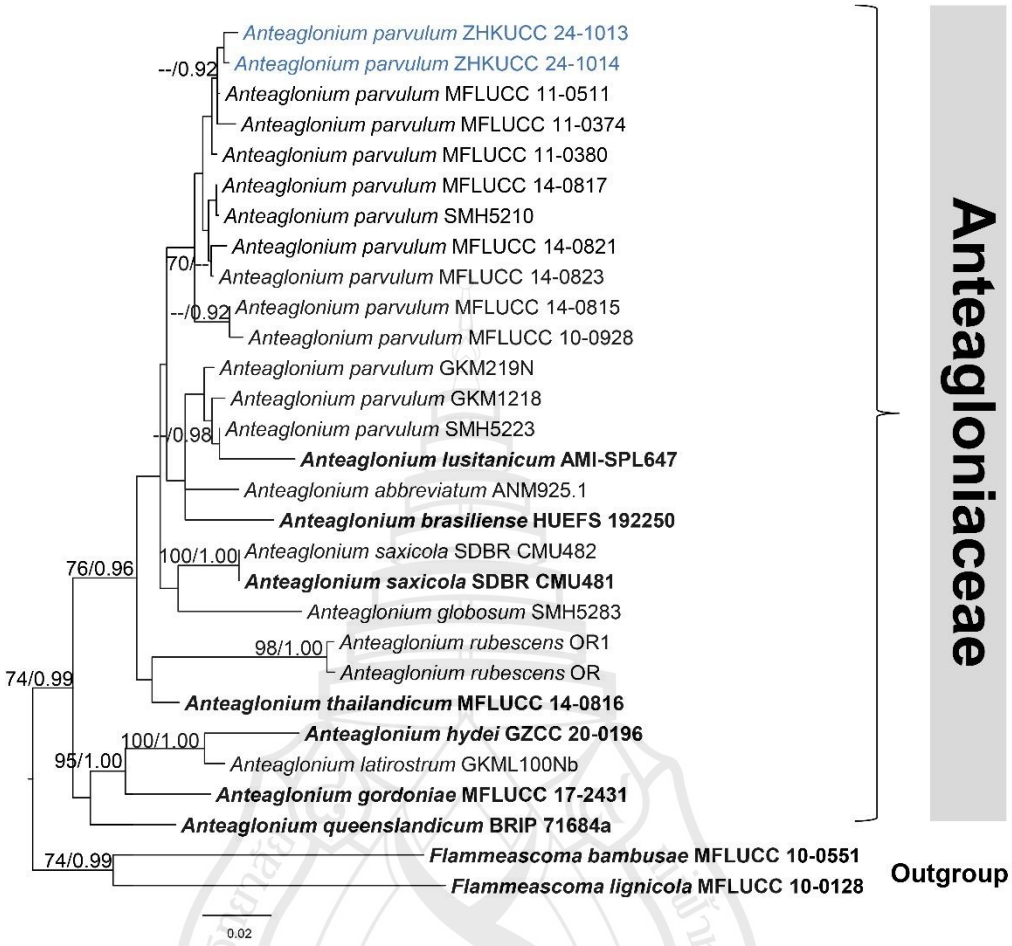


Figure 2.41 Phylogenetic tree of *Anteaglonium*

Figure 2.41 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Twenty-nine strains are included in the combined sequence analysis, which comprises 3,943 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Flammeascoma bambusae* (MFLUCC 10-0551) and *F. lignicola* (MFLUCC 10-0128).

Anteaglonium parvulum (W.R. Gerard) Mugambi & Huhndorf, Syst. Biodiv. 7 (4): 462 (2009) (LC1-C30)

Index Fungorum number: IF 543261; *Facesoffungi number:* FoF 01931; Figure 2.40

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–180 × 100–150 µm ($\overline{x}$ = 130 × 115 µm, n = 15), pycnidial, subglobose to globose, black, semi-immersed to immersed or erumpent, covered by the host periderm, raised at centre, solitary or aggregated, unilocular, thick-walled. *Conidiomatal wall* 20–25 µm wide ($\overline{x}$ = 22 µm, n = 20), outer layer composed of 4–6 layers, brown colour cells of *textura angularis*, inner layer thin, hyaline colour cells of *textura globulosa*. *Conidiophores* 20–35 × 2–3 µm ($\overline{x}$ = 28 × 2.7 µm, n = 25), upright, branched, hyaline, cylindrical, formed from the innermost layer of wall cells. *Conidiogenous cells* 8–15 × 2–3 µm ($\overline{x}$ = 11 × 2.3 µm, n = 25), phialidic, subglobose, hyaline, smooth, with a rounded tip. *Conidia* 3–4 × 2–3 µm ($\overline{x}$ = 3.7 × 2.5 µm, n = 25), 1-celled, hyaline, oval to globose, rounded at both ends, aseptate, granulates, smooth-walled. **Sexual morph**: See Jayasiri et al. (2016).

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, tightly arranged, with short, aerial mycelium, irregular with filiform margin, surface white to somewhat cottony at the center, from below white to orange at the edge, brownish at the center, wrinkled.

Material examined: China, Yunnan Province, Lincang City, on a decaying branch of *Coffea* sp., 28 July 2022, Li Lu, LC1-C30 (MHZU 24-0555), living culture ZHKUCC 24-1013, other living culture ZHKUCC 24-1014.

GenBank numbers: ZHKUCC 24-1013: ITS = PQ608272, LSU = PQ608105, SSU = PQ607963, *TEF*1-α = PQ628119, *RPB*2 = PV186831; ZHKUCC 24-1014: ITS = PQ608273, LSU = PQ608106, SSU = PQ607964, *TEF*1-α = PQ628120, *RPB*2 = PV186832.

Known hosts: On dead wood (Jayasiri et al., 2016; Hyde et al., 2020; Suwannarach et al., 2023), *Murraya exotica* (Rutaceae) (Hongsanan et al., 2020), *Coffea* sp. (This study).

Known distribution: New Zealand, Kenya (Mugambi & Huhndorf, 2009a), India (Hongsanan et al., 2020), Thailand (Jayasiri et al., 2016; Hyde et al., 2020; Suwannarach et al., 2023), China (This study).

Notes: Multi-gene phylogenetic analysis placed our two strains (ZHKUCC 24-1013 and ZHKUCC 24-1014) with other *Anteaglonium parvulum* isolates (MFLUCC 11–0374, MFLUCC 11–0380, MFLUCC 11–0511) with moderate support (Figure 2.39), and the type sequence of this species is unavailable. Most of the *A. parvulum* asexual morphs have been reported from culture, and only one record has been reported from a natural substrate (Hongsanan et al., 2020). In morphologically, our species also similar with previous records in having pycnidial conidiomata, branched conidiophores, oval to globose, aseptate and hyaline conidia (Jayasiri et al., 2016; Hongsanan et al., 2020; Figure 2.40). We, therefore, identified our collection as *A. parvulum* which is a new host and new country record from *Coffea* sp. in China.

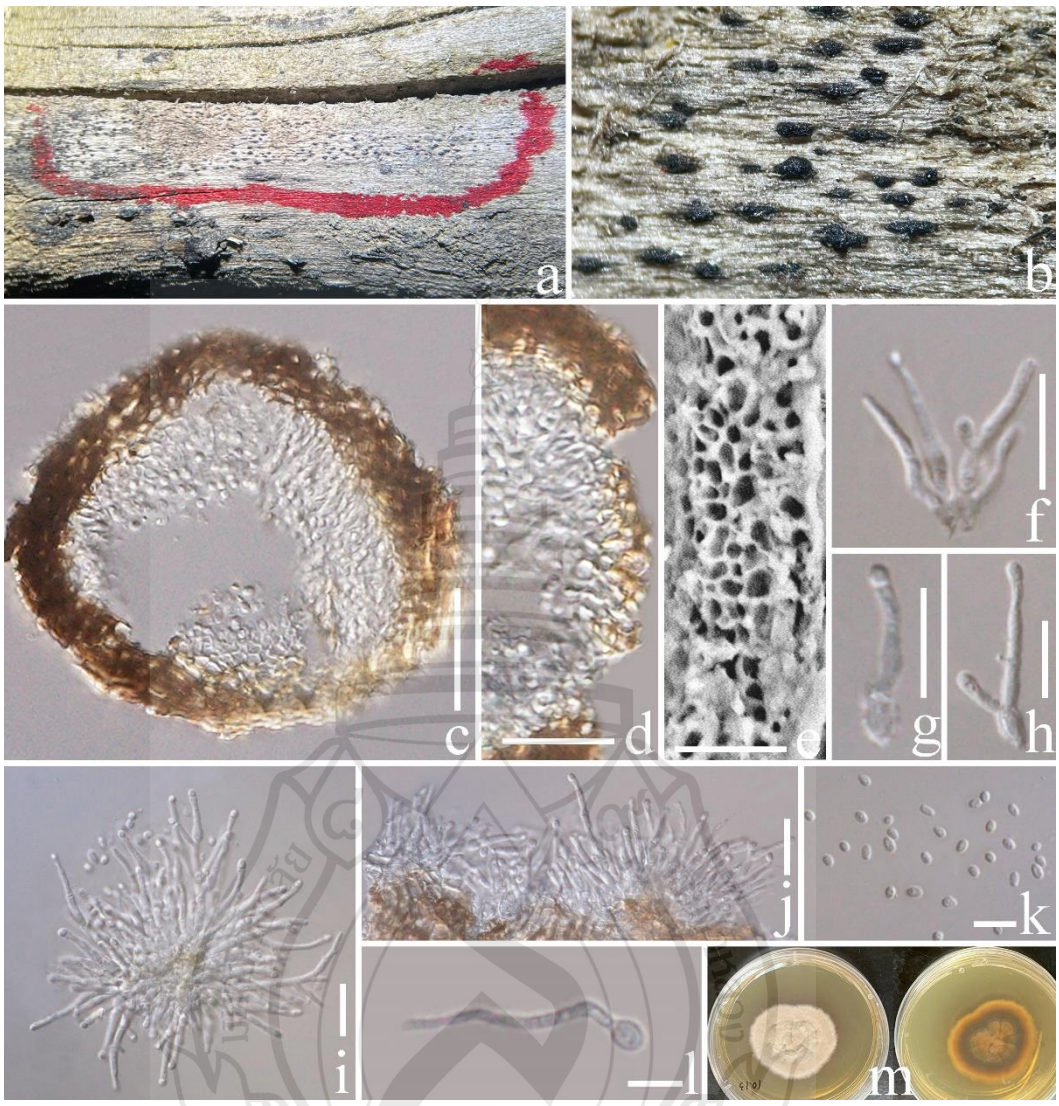


Figure 2.42 *Anteaglonium parvulum* (MHZU 24-0555, new host and country record)

Figure 2.42 a, b Appearance of conidiomata on *Coffea* sp. c Vertical section of conidioma. d, e Conidiomata wall (e: SEM microphotographs of the conidiomata wall). f–j Conidiophores, conidiogenous cells with conidia. k Conidia. l Germinated conidium. m Culture on PDA from above and below. Scale bars: c = 30 µm, d–f, i, j = 15 µm, g, h, k, l = 10 µm.

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

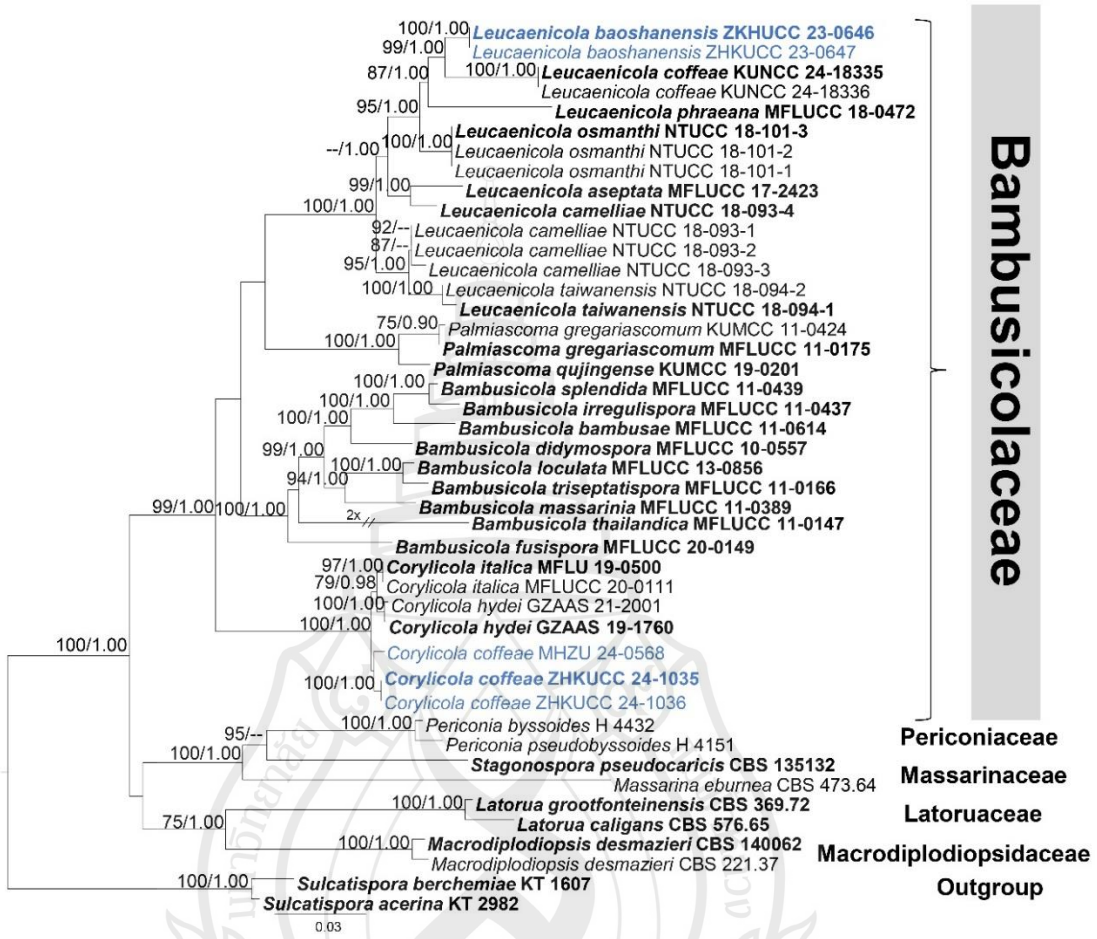


Figure 2.43 Phylogenetic tree of Bambusicolaceae

Figure 2.43 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Forty-four strains are included in the combined sequence analysis, which comprises 4,279 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Sulcatispora berchemiae* (KT 1607) and *S. acerina* (KT 2982).

Corylicola Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde, Biodivers. Data J. 8: e55957, 7 (2020)

Notes: Corylicola (Bambusicolaceae, Pleosporales) was introduced by Wijesinghe et al. (2020) to accommodate *C. italica*, which was identified as a saprobe from a dead branch of *Corylus avellana* (common hazel) in Italy (Wijesinghe et al., 2020). The second species, *C. hydei,* has been reported from a dead branch of a woody plant in China (Zhang et al., 2023). *Corylicola* can be distinguished from other genera in Bambusicolaceae by having yellowish-brown ascospore masses at the top of the ascomatal neck (Wijesinghe et al., 2020). It consists of only two species (*C. hydei* and *C. italica*) (Index Fungorum, 2025), with sexual and asexual morphs (Wijesinghe et al., 2020; Zhang et al., 2023). Herein, we introduce one new species in *Corylicola* and record the first report of *Corylicola* species from coffee plants.

Corylicola coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903608; *Facesoffungi number*: FoF 17562; Figure 2.42

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0567

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 130–200 high, 180–220 µm diam. ($\bar{x}$ = 154 × 197 µm), solitary or scattered, semi-immersed, erumpent at maturity, raised as dark spots on the substrate, sessile, globose to subglobose, coriaceous, uni-loculate with an ostiole. *Ostioles* central, papillate, lined with hyaline periphyses. *Peridium* 10–18 µm wide ($\bar{x}$ = 15 µm, n =10), thin-walled, composed of blackish to dark brown cells of *textura angularis*, fused with host tissues. *Hamathecium* of 1.5–2.5 µm wide ($\bar{x}$ = 2 µm, n =10), comprising numerous pseudoparaphyses, dense, filamentous, cellular, with distinct septa, constricted at the septa, branched. *Asci* 45–75 × 6–8 µm ($\bar{x}$ = 58 × 6.7 µm, n =20), 6–8-spored, bitunicate, fissitunicate, cylindrical, short pedicel with furcate ends or club-like, apically rounded, well-developed ocular chamber, with J-, apical ring. *Ascospores* 8–10 × 3.5–4.5 µm ($\bar{x}$ = 9.5 × 4 µm, n =40), uni to bi-seriate, fusoid to ellipsoidal, straight, hyaline or yellowish when young, becoming brown at maturity, 1-septate, constricted at the septum, rounded at both end, upper cell is wider than the lower cell, echinulate, guttulate. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, circular with filiform margin, density, slightly raised in the middle, secretion of mucus, from above white, from below white at the edge, brownish at the center, wrinkled.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* (22.6 N, 100.96 E, 1073 m), 2 April 2024, Li Lu, XAZC-2-12 (MHZU 24-0567, holotype), ex-type ZHKUCC 24-1035, other living culture ZHKUCC 24-1036; China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (22°31'18", 101°2'44", 856.89 m), 15 September 2021, Li Lu, JHPW18 (MHZU 24-0568, paratype).

GenBank numbers: ZHKUCC 24-1035: ITS = PQ608329, LSU = PQ608160, SSU = PQ608016, *TEF*1-α = PQ628174, *RPB*2 = PV357187; ZHKUCC 24-1036: ITS = PQ608330, LSU = PQ608161, SSU = PQ608017, *TEF*1-α = PQ628175, *RPB*2 = PV357188; MHZU 24-0568: ITS = PV052761, LSU = PV052763, SSU = PV052764, *TEF*1-α = PV165381, *RPB*2 = PV165380.

Notes: Corylicola coffeae is phylogenetically closer to *C. hydei* (GZAAS 19-1760, ex-type) with statistical support (100% ML, 1.00 BYPP, Figure 2.41). Morphologically, *C. coffeae* also fits the morphological profile of the genus, such as ascospores are yellowish-brown masses at the apices of ascomatal necks (Figure 2.42). However, *C. coffeae* can be differentiated from *C. hydei* by having 6–8-spored asci, a short pedicel with furcate or club-like ends, and echinulate ascospores, while those of *C. hydei* are 8-spored asci with smooth ascospores (Zhang et al., 2023; Figure 2.42). Based on nucleotide comparisons, *C. coffeae* (ZHKUCC 24-1035, ex-type) differs from *C. hydei* (GZAAS 19-1760) by 8/476 bp (1.6%, without gaps) in ITS, 2/875 bp (0.2%, without gaps) in LSU, 1/1009 bp (0.1%, without gaps) in SSU, 15/955 bp (1.6%, without gaps) in *TEF*1-α and 15/1050 bp (1.5%, without gaps) in *RPB*2. Therefore, *C. coffeae* is introduced as a new species from *Coffea arabica* in China.

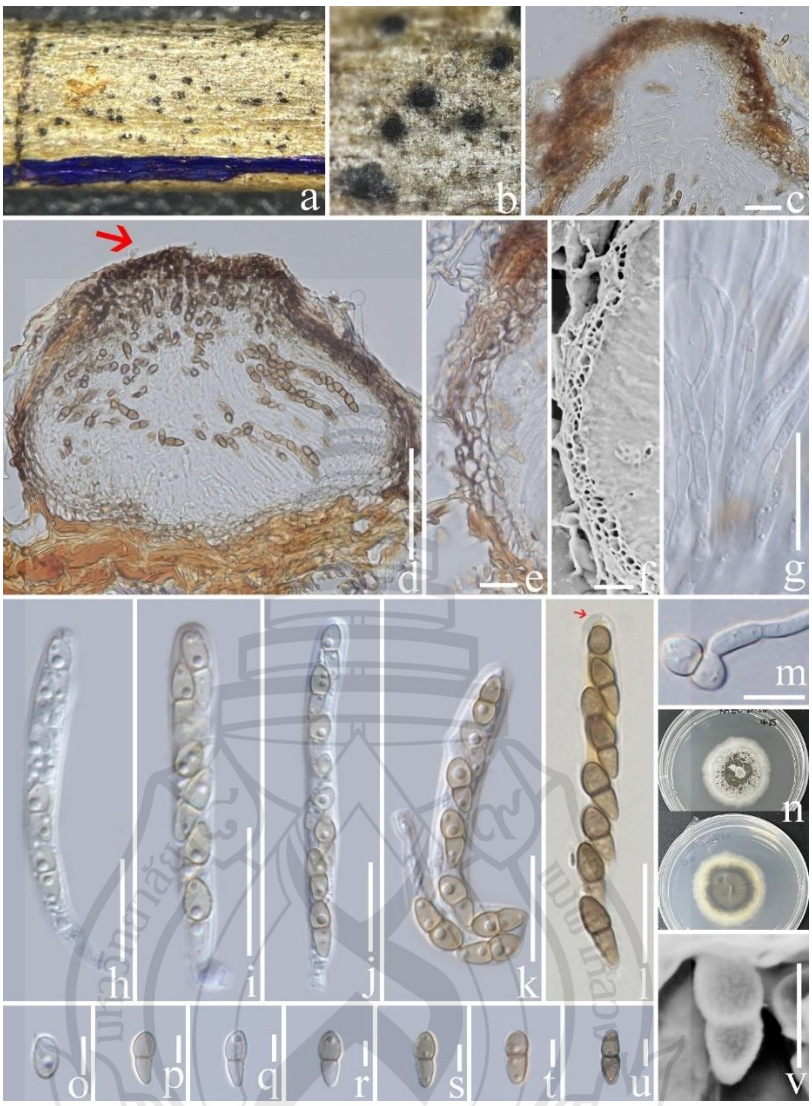


Figure 2.44 *Corylicola coffeae* (MHZU 24-0567, holotype)

Figure 2.44 a, b Appearance of ascomata on *Coffea* sp. c Ostiole. d Vertical section of ascoma (Arrow indicates ascospore masses at the apices of ascomata necks). e, f Peridium (f: SEM microphotographs of peridium). g Pseudoparaphyses. h–l Asci (Arrow indicate J-, apical ring in Melzer's reagent). m Germinated ascospore. n Culture on PDA from above and below. o–v Conidia (v: SEM microphotographs of ascospore with rough surface). Scale bars: c = 50 µm, c, d–k = 15 µm, n–u= 5 µm.

Leucaenicola Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10 (1): 37 (2019)

Notes: Leucaenicola was introduced by Jayasiri et al. (2019) to accommodate two new coelomycetous species, with *L. aseptata* as the type species. *Leucaenicola* contains six species, however, only their asexual morph has been documented (Jayasiri et al., 2019; Ariyawansa et al., 2020a, 2020b; Lu et al., 2025). *Leucaenicola aseptata* and *L. phraeana* were isolated from decaying pods of *Leucaena* sp. in Thailand (Jayasiri et al., 2019). *Leucaenicola osmanthi* has been reported to be associated with leaf lesions of *Osmanthus fragrans* in Taiwan Province of China (Ariyawansa et al., 2020a); *L. camelliae* and *L. taiwanensis* were also isolated from leaf lesions of *Camellia sinensis* in the same areas as *L. osmanthi* (Ariyawansa et al., 2020b). *Leucaenicola coffeae* have been isolated from a decaying branch of *Coffea* sp. from China (Lu et al., 2025). The genus is characterized by globose to subglobose, pycnidial, ostiolate conidiomata, enteroblastic, phialidic, globose to flask-shaped conidiogenous cells, and oblong to ellipsoidal, aseptate conidia, initially hyaline, turns brown at maturity (Jayasiri et al., 2019). Herein, we introduce *L. baoshanensis* as a new species, and this is the second *Leucaenicola* species report from coffee plants.

Leucaenicola baoshanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903617; *Facesoffungi number*: FoF 17620; Figure 2.43

Etymology: The species epithet refers to the type location “Baoshan”, China.

Holotype: MHZU 23-0068

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 120–180 µm × 120–220 µm ($\overline{x}$ = 156 × 187 µm, n = 15), subglobose to globose, black, semi-immersed to immersed, solitary or aggregated, unilocular, thick-walled, with ostiole. *Conidiomatal wall* 18–22 µm wide ($\overline{x}$ = 19 µm, n = 20), thin-walled, composed of yellowish to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–8 × 3–5 µm ($\overline{x}$ = 7.2 × 3.9 µm, n = 25), holoblastic, cylindrical to lageniform, hyaline, smooth-walled. *Conidia* 6–10 × 2.5–4 µm ($\overline{x}$ = 8 × 3.3 µm, n = 25), 1-celled, oblong to cylindrical, few reniform or inequilateral, rounded at both ends, hyaline to light brown, aseptate, granulates, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm in one month at 25°C, circular with entire margin, slightly raised, cottony, from above white, from below yellowish at the edge, brownish at the center.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (24.9 N, 98.8 E, 1209 m), 30 July 2022, Li Lu, BS2-C20 (MHZU 23-0068, holotype), ex-type ZHKUCC 23-0646, other living culture ZHKUCC 23-0647.

GenBank numbers: ZHKUCC 23-0646: ITS = PQ608292, LSU = PQ608125, SSU = PQ607979, *TEF*1-α = PQ628139, *RPB*2 = PV221296; ZHKUCC 23-0647: ITS = PQ608293, LSU = PQ608126, SSU = PQ607980, *TEF*1-α = PQ628140, *RPB*2 = PV221297.

Notes: Multi-gene phylogenetic analysis placed *Leucaenicola baoshanensis* as a sister lineage to *L. coffeae* (KUNCC 24-18335, ex-type) with moderate-support (99% ML, 1.00 BYPP, Figure 2.41). Based on nucleotide comparisons, *L. baoshanensis* (ZHKUCC 23-0646, ex-type) differs from *L. coffeae* (KUNCC 24-18335, ex-type) by 2/443 bp (0.5%, without gaps) in ITS, 81/876 bp (9%, without gaps) in LSU, 1/998 bp (0.1%, without gaps) in SSU, 6/910 bp (0.6%, without gaps) in *TEF*1-α and 24/1038 bp (2.3%, without gaps) in *RPB*2. In morphologically, *L. baoshanensis* can be distinguished from *L. coffeae* by the different shapes of conidia (oblong to cylindrical, few reniform or inequilateral vs. ellipsoidal to cylindrical), and larger conidia (6–10 × 2.5–4 μm, L/W = 1.5–4 vs. 5–6 × 2.5–3.5 μm, L/W = 1.4–2.4) (Figure 2.43; Lu et al., 2025). Therefore, *L. baoshanensis* is introduced as a new species from *Coffea* sp. in China.

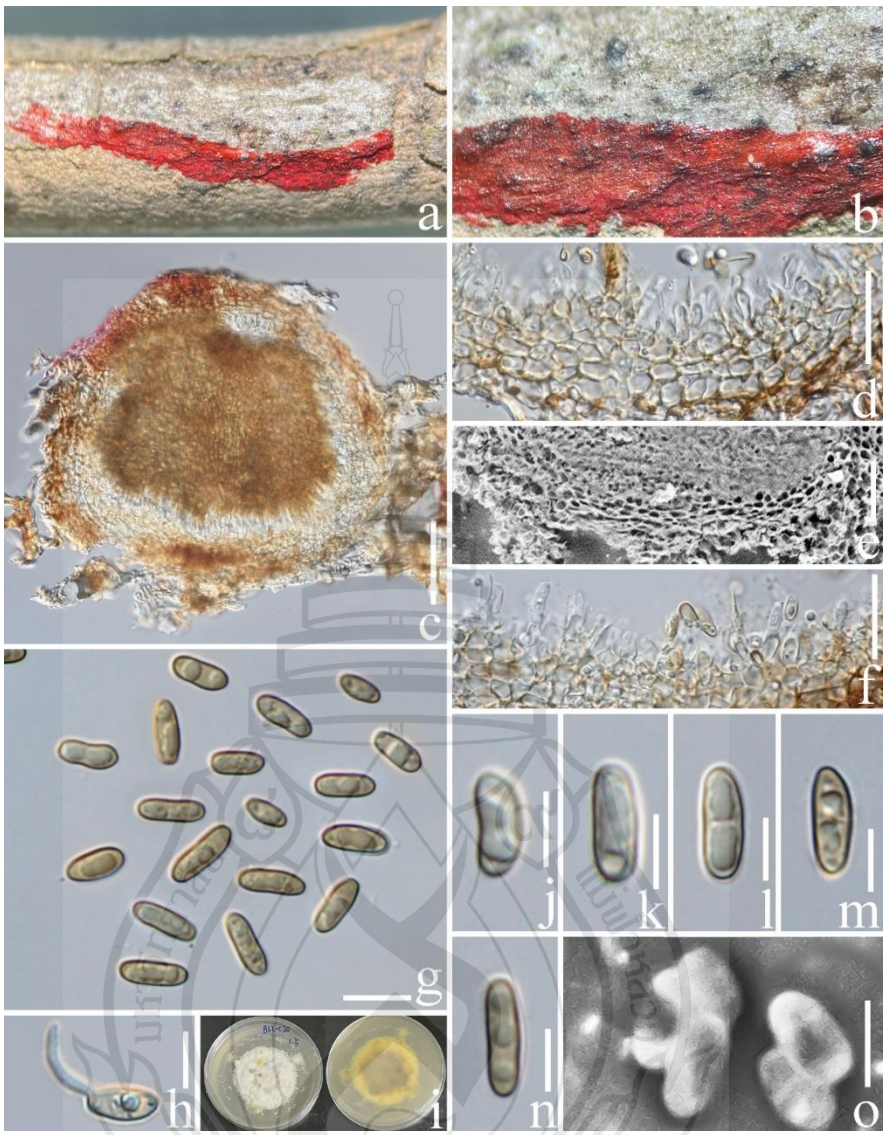


Figure 2.45 *Leucaenicola baoshanensis* (MHZU 23-0068, holotype)

Figure 2.45 a, b Appearance of conidiomata on *Coffea* sp. c Vertical section of a conidioma. d, e Conidiomata wall (e: SEM microphotographs of conidiomata wall). f Conidiogenous cells with conidia. g, j–o Conidia (o: SEM microphotographs of conidia). h Germinated conidium. i Culture on PDA from above and below. Scale bars: c = 50 µm, d–f = 20 µm, g, h = 10 µm, j–o= 5 µm.

Leucaenicola coffeae L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 900998; *Facesoffungi number*: FoF 14724; Figure 2.43

Etymology: The species epithet "coffeae" refers to the host plant genus "Coffea" from which the fungus was isolated.

Holotype: HKAS 137605

Saprobic on decaying branch of *C. arabica.* **Asexual morph**: *Ascomata* 200–350 high × 200–300 µm diam. ($\overline{x}$ = 239 × 273 µm), solitary or scattered, immersed, raised as brown to black spots on the substrate, globose to subglobose, coriaceous, uniloculate with ostioles. *Peridium* 25–35 µm wide ($\overline{x}$ = 30 µm, n = 20), thin-walled, composed of dark brown and 2–4 layers of *textura angularis* cells, with the basal part composed of thinner, hyaline, smaller cells. *Hamathecium* 1.5–3.5 µm wide ($\overline{x}$ = 2.7 µm, n = 20), dense, comprising numerous pseudoparaphyses, filamentous, hyaline, cellular, branched, with distinct septa. *Asci* 40–80 × 8–15 µm ($\overline{x}$ = 57 × 9.6 µm, n = 20), 4–8-spored, bitunicate, fissitunicate, cylindrical, long-stalked with club-shape, apically rounded, with a shallow ocular chamber. *Ascospores* 15–25 × 4–8 µm ($\overline{x}$ = 21 × 6 µm, n = 30), overlapping, uniseriate to biseriate, fusiform to ellipsoidal, straight, hyaline, mainly 1-septate, sometimes 2–3 septate, constricted at the centre septa, conical at both ends, upper cell wider than the lower cell, guttulate, mucilaginous sheath. Anamorph on PDA: *Mycelium* 1.5–2.5 µm broad ($\overline{x}$ = 2.2 µm, n = 20), hyaline, septate, branched. *Conidia* 5–6 × 2.5–3.5 µm ($\overline{x}$ = 5.6 × 3.1 µm, n = 30), ellipsoidal to cylindrical, hyaline when young, brown when mature, thin and smooth-walled, aseptate, with 1–2-guttules. **Sexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies reached 3.5 cm in diameter after one month at 25℃. Colonies circular, slightly fluffy with an entire margin, white; the reverse is white to yellowish. After four months, conidia mass formed as globose to subglobose, dark brown to black spots in culture.

Material examined: China, Yunnan Province, Pu'er, on a decaying branch of Coffea arabica (Rubiaceae) (23°43'01" N, 101°73'90" E, 1085 m alt.), 18 November 2020, LiLu, MJ-C8 (HKAS 137605, holotype), isotype MHZU 23-0058, ex-type living culture KUNCC 24-18335 = KUNCC 24-18336, ex-isotype living culture ZHKUCC 23-0626 = ZHKUCC 23-0627.

GenBank numbers: KUNCC 24-18335: ITS = OR428395, LSU = OR428417, SSU = OR428375, *TEF*1-α = OR509749, *RPB*2 = OR515519; KUNCC 24-18336: ITS = OR428396, LSU = OR428418, SSU = OR428376, *TEF*1-α = OR509750, *RPB*2 = OR515520.

Notes: Based on the multi-gene sequence analysis, *Leucaenicola coffeae* forms an independent lineage allied to *L. phraeana* (Figure 2.3). In the NCBI BLASTn searches, the ITS, LSU, SSU and *TEF*1-α sequences are similar to *L. camelliae* Ariyaw., I. Tsai & Thambugala, (MT112301, 98%), (MT071278, 90%), (MT071229, 99.9%) and (MT374091, 97%), respectively, while *RPB*2 is 97% similar to *L. osmanthi* Ariyaw., I. Tsai & Thambugala, (MN915020). *Leucaenicola coffeae* is the first species with a teleomorph known in *Leucaenicola*. The teleomorph characteristics of *L. coffeae* conform to the basic concept of *Bambusicolaceae*. The anamorph can be distinguished from *L. phraeana* by the brown and large conidia (5–6 × 2.5–3.5 µm vs. 3–4 × 1.5–2 µm) and distinct guttules (Figure 2.2; Jayasiri et al., 2019). Based on nucleotide comparisons, *L. coffeae* (ZHKUCC 23-0626) differs from *L. phraeana* (MFLUCC 18-0472) by 102/418 bp (24%, 3 gaps) in ITS, 80/844 bp (9%, without gaps) in LSU, 2/1017 bp (0.2%, without gaps) in SSU, 16/920 bp (1.7%, without gaps) in *TEF*1-α and 30/1036 bp (2.9%, without gaps) in *RPB*2; and differs from *L. osmanthi* (NTUCC 18-101-3) by 10/620 bp (1.6%, without gaps) in ITS, 78/756 bp (10%, without gaps) in LSU, 2/780 bp (0.2%, without gaps) in SSU, 21/816 bp (2.5%, without gaps) in *TEF*1-α and 26/818 bp (3%, without gaps) in *RPB*2. Therefore, we introduce *L. coffeae* as a new species in *Leucaenicola* with the first record of a teleomorph associated with the decaying branch of *C. arabica*.

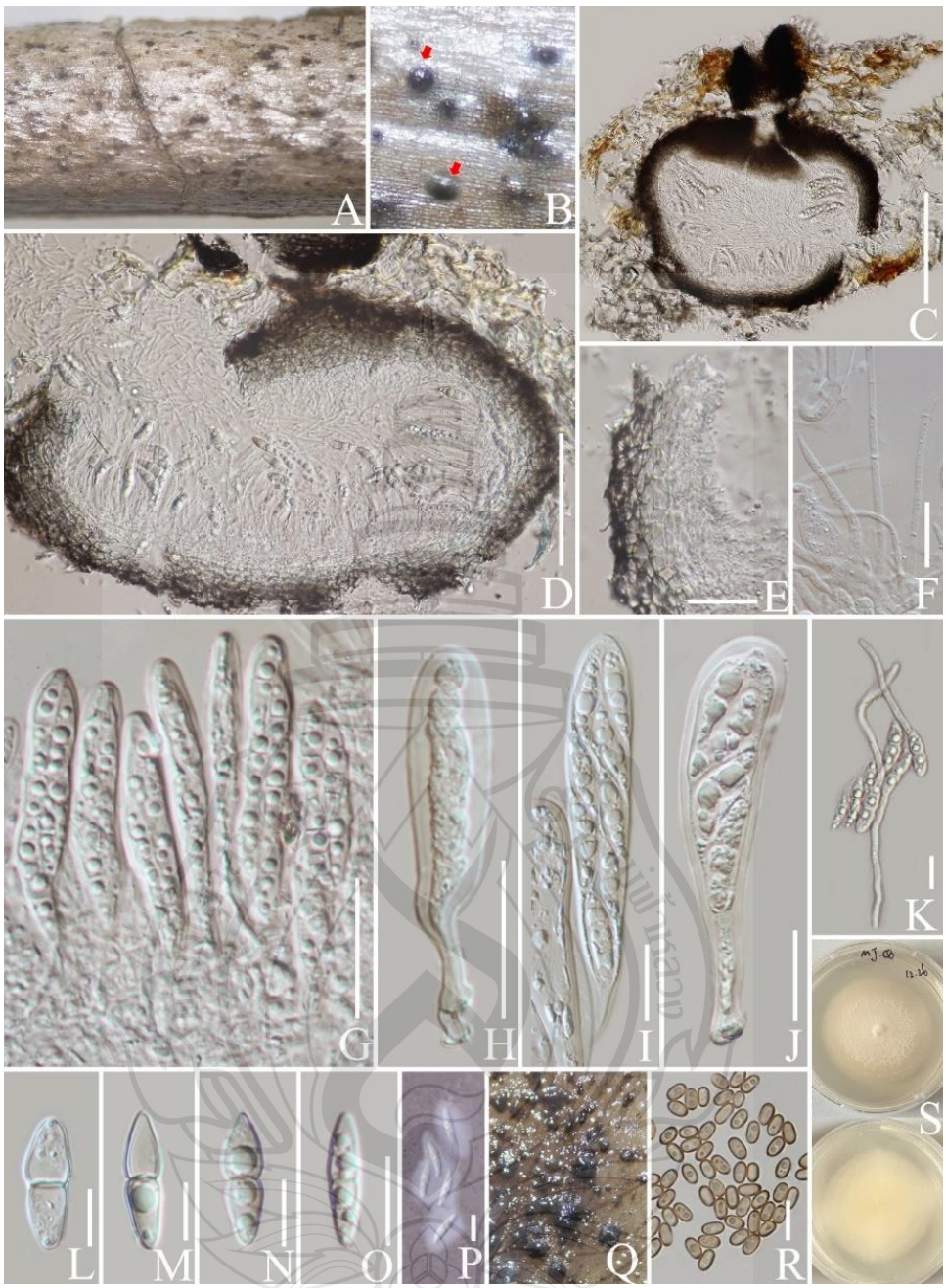


Figure 2.46 *Leucaenicola coffeae* (HKAS 137605, holotype)

Figure 2.46 A, B Appearance of ascomata on a decaying branch of *C. arabica*; C, D Longitudinal section of an ascoma; E Peridium wall; F Pseudoparaphyses; G–J Asci; K Germinated ascospores; L–O Ascospores; P Ascospores stained with Indian ink; Q Conidia mass in culture after four months; R Conidia; S Culture on PDA from obverse and reverse. Scale bars: C, D = 150 µm, E = 50 µm, F = 100 µm, G–K = 20 µm, L–P, R = 10 µm.

Cyclothyriellaceae Jaklitsch & Voglmayr, Studies in Mycology 85: 39 (2016)

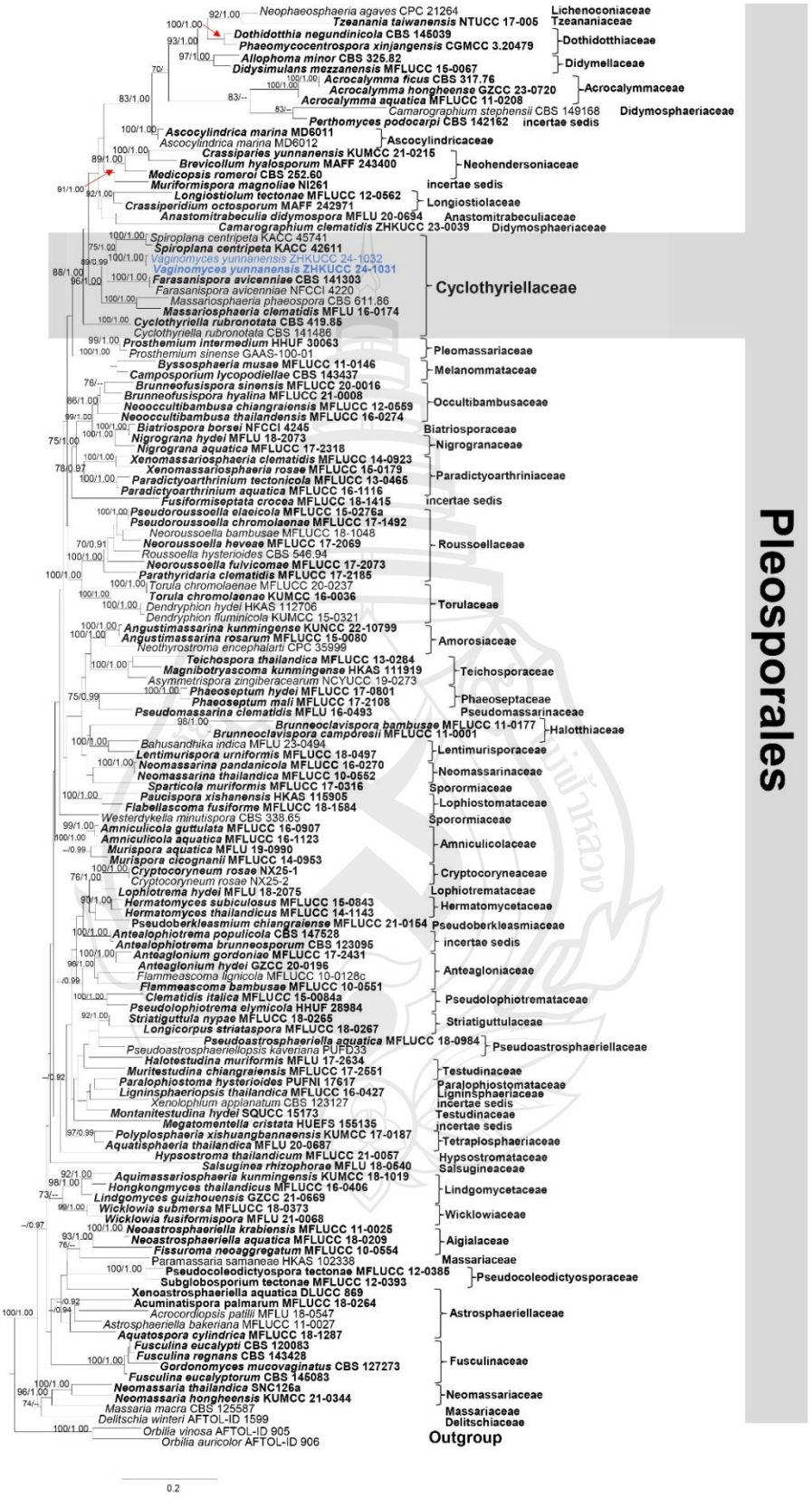


Figure 2.47 Phylogenetic tree of *Vaginomyces*

Figure 2.47 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. One hundred thirty-nine strains are included in the combined sequence analysis, which comprises 4,386 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Orbilia vinosa* (AFTOL-ID 905) and *Orbilia auricolor* (AFTOL-ID 906).

Vaginomyces L. Lu, K.D. Hyde & Tibpromma, *gen. nov.*

Index Fungorum number: IF 903655; *Facesoffungi number*: FoF 17564

Etymology: The genus name refers to the distinct mucilaginous sheath of ascospores, latin noun “vagina”.

Type species: *Vaginomyces yunnanensis*

Saprobic on dead or decaying plants. **Sexual morph:** *Ascomata* scattered to aggregated, semi-immersed to immersed, uni- to multiloculate, black spots on host surface, subglobose to globose, with ostioles. *Ostioles* central, flattened, papillate, periphyses line the inner surface of the ostiole. *Peridium* comprising several layers of gray to dark brown cells of *textura angularis*, some fusing with the host substrate. *Hamathecium* comprising numerous, cellular, septate and unbranched, psuedoparaphyses, constricted at the septa. *Asci* 6–8-spored, bitunicate, fissitunicate, clavate or long cylindrical, with short furcate pedicel, some club-like, rounded at the apex, with an ocular chamber. *Ascospores* uniseriate to biseriate, fusiform, with apical or rounded ends, 1–3-septate, constricted at the middle septum, upper cell slightly wider than others, hyaline, smooth-walled, guttulate, with a thick and distinct mucilaginous sheath. **Asexual morph on PDA:** *Mycelium* hyaline to light brown, septate and branched. *Conidiophores* formed directly on hyphae, hyaline to pale brown, septate, smooth-walled. *Conidiogenous cells* holoblastic, secession schizolytic, maturation by diffuse wall-building. *Conidia* subglobose to oval, chain of phialoconidia, hyaline when young, brown when mature, thin and smooth-walled, aseptate, guttulate.

Notes: Phylogenetic analyses based on single and multiple gene sequences reveal that *Vaginomyces yunnanensis* forms a distinct lineage within the order Pleosporales, closely related from *Spiroplana centripeta* and *Farasanispora avicenniae*

(Figure 2.44). *Spiroplana* and *Farasanispora* were placed in Pleosporales genera *incertae sedis* by Voglmayr et al. (2011) and Li et al. (2016), respectively. *Vaginomyces* is distinctly different from *Spiroplana*, which has been reported as a parasitic fungus producing hyphomycetous spores (Voglmayr et al., 2011). While *Vaginomyces* shares similar morphology with *Farasanispora* in having clavate asci with short pedicels and fusiform, 1–3-septate ascospores (Li et al., 2016). It differs from *Farasanispora* in possessing 6–8-spored asci and ascospores with a thick, distinct mucilaginous sheath and smooth-walls. Based on base pair comparison, *Vaginomyces yunnanensis* (ZHKUCC 24-1031, ex-type) differs from the type species *Spiroplana centripeta* (KACC42611, ex-type) by 54/438 bp (6.4%, without gaps) in ITS, 33/850 bp (3.8%, without gaps) in LSU; and differs from the type species *F. avicenniae* (CBS 141303, ex-type) by 48/864 bp (5.5%, without gaps) in LSU, 9/831 bp (1.1%, without gaps) in SSU; and differs from other strain of *Farasanispora avicenniae* (NFCCI-4220) by 61/461 bp (13%, without gaps) in ITS, 46/866 bp (5.3%, without gaps) in LSU, 11/1016 bp (1%, without gaps) in SSU and 83/927 bp (8.9%, without gaps) in *TEF*1-α. Therefore, *Vaginomyces* is introduced as a new genus and typified by *V. yunnanensis.*

Based on the muti-gene (Figure 44) and single-gene (Supplementary Figs 1–3) phylogenetic analyses, the taxonomic positions of *Farasanispora*, *Spiroplana*, and *Vaginomyces* are relatively stable, consistently clustering with *Massariosphaeria* within Cyclothyriellaceae. Phylogenetic analysis by Li et al. (2016) demonstrated that *Farasanispora* forms an independent branch near Ascocylindricaceae and Neohendersoniaceae. Our study also provides a similar taxonomic placement for *Farasanispora* (Figure 2.44). Furthermore, the phylogenetic position of Cyclothyriellaceae is similar to the findings of Phukhamsakda et al. (2020), indicating that the placement of this family remains stable in our study.

Based on morphological comparisons, *Farasanispora* shares similar characters with *Massariosphaeria*, including bitunicate, fissitunicate, and clavate asci, the presence of an ocular chamber, and hyaline to brown ascospores (Li et al., 2016; Phukhamsakda et al., 2020). In contrast, *Spiroplana* is only known from hyphomycetes characters, making morphological comparisons impossible. Meanwhile, *Vaginomyces* exhibits similarities with *Massariosphaeria* in having ascospores with a thick and distinct mucilaginous sheath (Phukhamsakda et al., 2020; Figure 2.45). Therefore,

Farasanispora, *Spiroplana,* and *Vaginomyces* are placed in the family Cyclothyriellaceae.

Vaginomyces yunnanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903656; *Facesoffungi number*: FoF 17563; Figure 2.45, Figure 2.46

Etymology: The species epithet refers to the type location "Yunnan", China.

Holotype: MHZU 24-0564

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 180–260 × 200–320 µm ($\bar{x}$ = 210× 260 µm, n = 15), scattered to aggregated, semi-immersed to immersed, uni- to multiloculate, black spots on host surface, coriaceous, subglobose to globose, with ostioles. *Ostioles* central, flattened, papillate, opening by an apical, lysigenous pore or dehiscence, periphyses lining the inner surface of the ostiole. *Peridium* 20–27 µm wide ($\bar{x}$ = 24 µm, n = 20), comprising two layers, with the outer layer composed of pale brown to brown, slightly flattened, thick-walled cells of *textura angularis*, fusing and indistinguishable from the host tissues. The inner layer is composed of several layers with lightly pigmented to hyaline cells of *textura angularis*. *Hamathecium* of 2–4 µm wide ($\bar{x}$ = 2.8 µm, n = 30), comprising numerous, cellular, septate and unbranched, psuedoparaphyses, constricted at the septa. *Asci* 70–140 × 15–22 µm ($\bar{x}$ = 104 × 18.8 µm, n = 30), 6–8-spored, bitunicate, fissitunicate, clavate or long cylindrical, with short furcate pedicel, some club-like, apically rounded, with an ocular chamber. *Ascospores* 35–45 × 8–12 µm ($\bar{x}$ = 39 × 10 µm, n = 30), uniseriate to biseriate, fusiform, with apical or rounded ends, 1-septate, occasionally 3-septate, constricted at the middle septum, hyaline, smooth-walled, guttulate, with a thick and distinct mucilaginous sheath. **Asexual morph on PDA:** *Mycelium* 1.5–4 µm ($\bar{x}$ = 2.2 µm, n = 30), hyaline to light brown, septate and branched. *Conidiophores* formed directly on hyphae, hyaline to pale brown, septate, smooth-walled, and loosely arranged. *Conidiogenous cells* holoblastic, secession schizolytic, slightly elongated, flask-shaped, hyaline, smooth-walled, maturation by diffuse wall-building. *Conidia* 6–10 × 3.5–6 µm ($\bar{x}$ = 7 × 5 µm, n = 30), subglobose to oval, chain of phialoconidia, hyaline when young, brown when mature, thin and smooth-walled, aseptate, guttullate.

Culture characteristics: Ascospore germinating on PDA within 24 h. Colonies growing on PDA, reaching 50 mm in one month at 25°C, surface rough, flat, circular with entire margin, velvety to slightly floccose, aerial hyphae on the surface,

from above light-brown, from below with concentric zonation visible, alternating white and brown.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April. 2024, Li Lu, DH 3-3 (MHZU 24-0564, holotype), ex-type ZHKUCC 24-1031, other living culture ZHKUCC 24-1032.

GenBank numbers: ZHKUCC 24-1031: ITS = PQ608284, LSU = PQ608117, SSU = PQ607975, *RPB*2 = PV221292, *TEF*1-α = PQ628131; ZHKUCC 24-1032: ITS = PQ608285, LSU = PQ608118, SSU = PQ607976, *RPB*2 = PV221293, *TEF*1-α = PQ628132.

Notes: Based on the muti-gene and single gene phylogenetic analysis, *Vaginomyces yunnanensis* grouped with *Spiroplana centripeta* (KACC42611, ex-type) within Pleosporales genera *incertae sedis*, with 75% ML, 1.00 BYPP statistical support (Figure 2.44). Since the morphology of the two species are quite different in the filamentous conidia of *S. centripetal* (Voglmayr et al., 2011), we cannot place them in the same genus. Herein, we introduce *Vaginomyces yunnanensis* as a new species with sexual and asexual morph (Figure 2.45, Figure 2.46) collected from a coffee host from China.

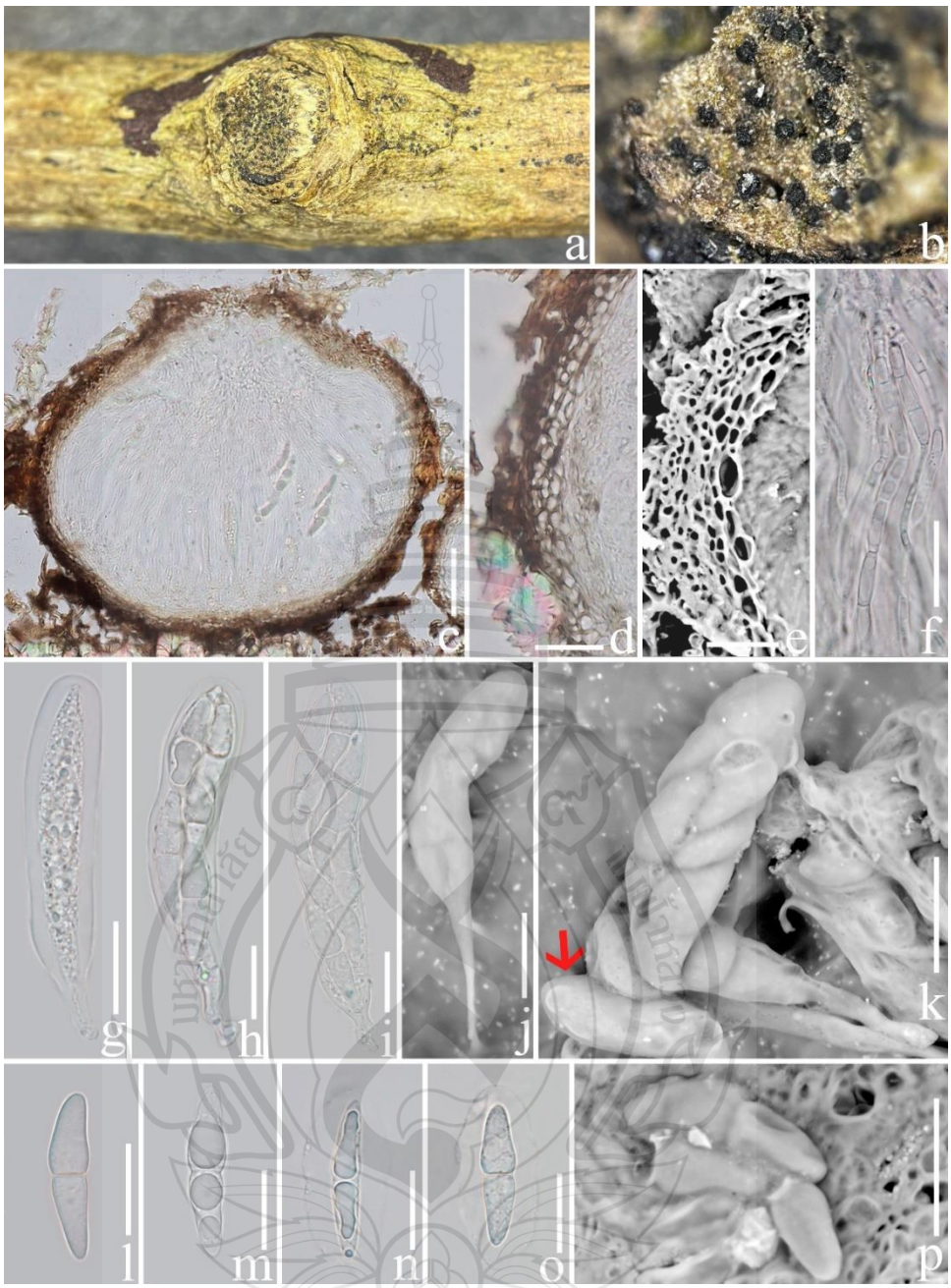


Figure 2.48 *Vaginomyces yunnanensis* (MHZU 24-0564, holotype)

Figure 2.48 a, b Ascomata on host surface. c Longitudinal section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium. g–k Asci (j, k: SEM microphotographs of asci, arrows indicate the mucilaginous sheath of ascospore). l–p Ascospores (p: SEM microphotographs of ascospores). Scale bars: c = 50 μm, d–p = 20 μm.

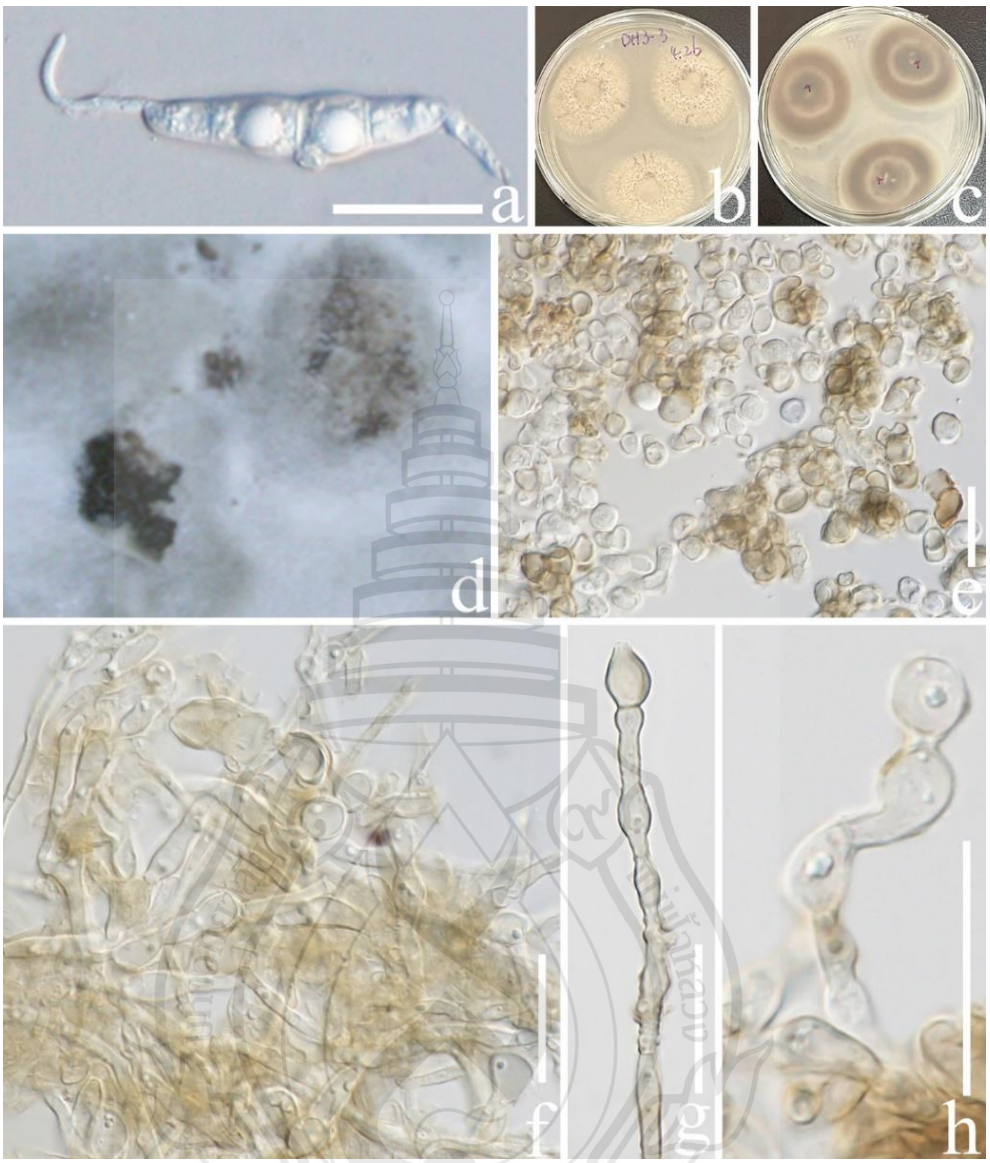


Figure 2.49 Asexual morphology of ***Vaginomyces yunnanensis*** (ZHKUCC 24-1031, ex-type)

Figure 2.49 Asexual morphology of *Vaginomyces yunnanensis* (ZHKUCC 24-1031, ex-type) on PDA culture plates. a Geminated ascospore. b, c Culture on PDA from above and below. d Conidia masse in culture after two months. e Conidia. f Mycelium. g, h Conidiogenous cells with conidia. Scale bars: a, e–h = 20 μm.

Dictyosporiaceae Boonmee & K.D. Hyde

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

Notes: Aquadictyospora was established by Li et al. (2017) with A. lignicola as the type species. Two epithets (*A. clematidis* and *A. lignicola*) listed in Index Fungorum (2024), have been found in both aquatic and terrestrial habitats as saprobes. Their distribution is not limited to a single region, as they are found in the diverse landscapes of China and Thailand (Li et al., 2017; Phukhamsakda et al., 2020). Until now, the genus has been reported only asexual morph and is characterized by superficial and scattered conidiomata, micronematous conidiophores with monoblastic conidiogenesis cells, uniformly medium brown dictyosporous and not complanate conidia with a subglobose, hyaline cell at the basal end and without appendages (Li et al., 2017; Phukhamsakda et al., 2020).

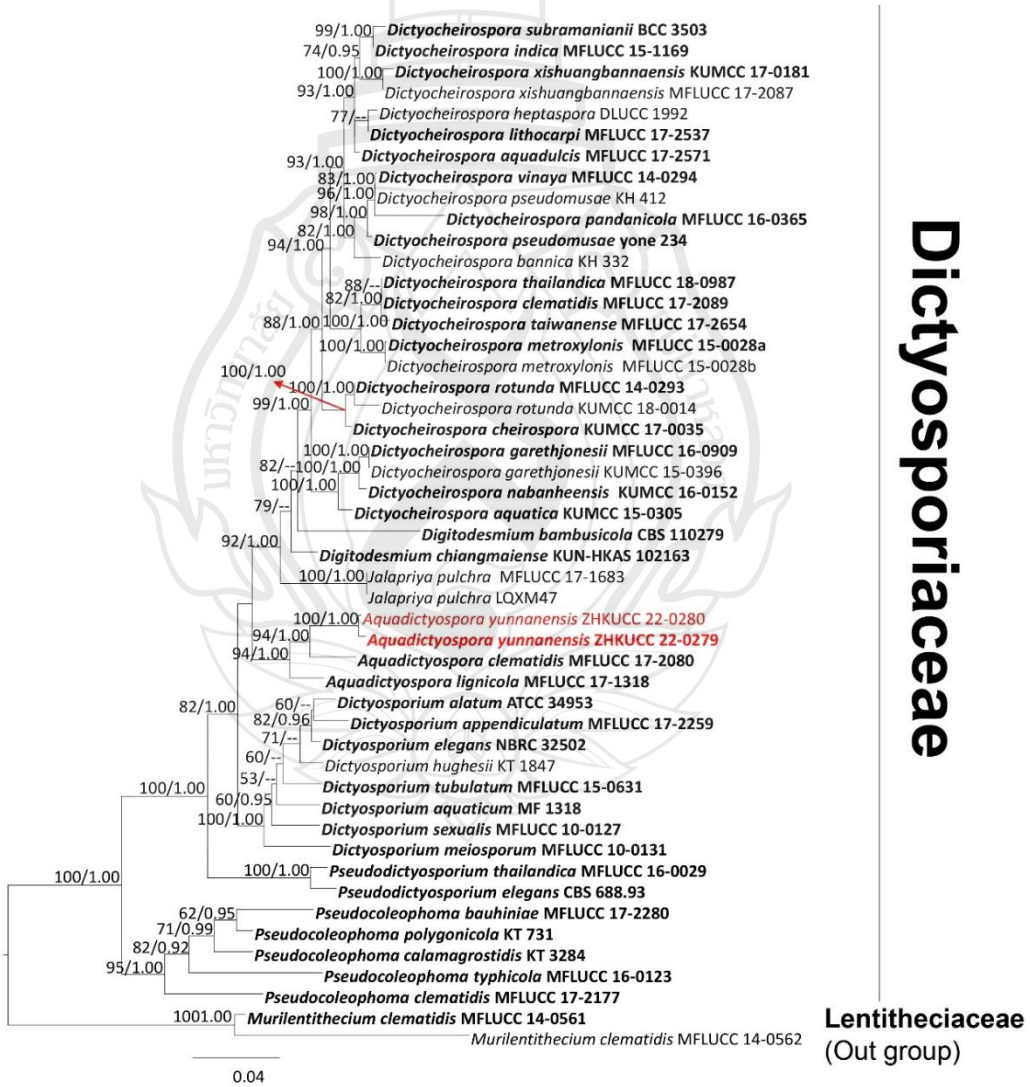


Figure 2.50 Phylogenetic tree of *Aquadictyospora*

Figure 2.50 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2 and *TEF*1-α sequence data. Forty-nine strains are included in the combined sequence analysis, which comprises 4,947 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Murilentithecium clematidis* (MFLUCC 14-0561, MFLUCC 14-0562).

Aquadictyospora yunnanensis L. Lu, M.Y. Han & Tibpromma, sp. nov.

Index Fungorum number: IF 902532; *Facesoffungi number*: FoF 16620; Figure 2.53

Etymology: The name reflects the location, "Yunnan" Province, where the holotype was collected.

Holotype: MHZU 22-0148

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph:** Not observed. **Asexual morph:** Hyphomycetous. *Colonies* on natural substrate 150–300 × 110–250 µm ($\bar{x}$ = 211 × 170 µm, n = 10), superficial, forming sporodochial conidiomata, dark brown to black, velvety, scattered, circular or subglobose in small groups, crowded and confluent when older, with base attached on surface of host plant. *Mycelium* 2–3 µm wide, immersed, septate, branched and hyaline hyphae. *Conidiophores* micronematous, reduced to conidiogenous cell, hyaline to pale brown. *Conidiogenous cells* holoblastic, solitary, determinate. *Conidia* 25–40 × 15–20 µm ($\bar{x}$ = 33 × 17.5 µm, n = 30), dictyosporous, oval to obovoid, compactly adpressed 2–4 apically rows of cells, guttulate, with hyaline and subglobose or ovoid basal cell connecting cell, 10–15 × 9–11 µm ($\bar{x}$ = 12 × 10 µm, n = 30), not complanate, secession involves splitting of the basal, without appendages or mucilaginous sheath.

Culture characteristics: Colonies on PDA reaching 50 mm diam. after two months at 25°C. Cultures from above yellow white, dense, circular, papillate with fairly fluffy, covered with white aerial mycelium; reverse dark brown at the center, edge reddish brown.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea arabica* (101°2'44" E, 22°31'18" N, 856.89 m), 15th September 2021, Li Lu, JHPW 7 ((MHZU 22-0148, holotype), ex-type ZHKUCC 22-0279, other living culture ZHKUCC 22-0280.

GenBank numbers: ZHKUCC 22-0279: ITS = OQ544398, LSU = OQ544396, SSU = OQ544400, *RPB*2 = OQ556793, *TEF*1-α = OQ556795; ZHKUCC 22-0280: ITS = OQ544399, LSU = OQ544397, SSU = OQ544401, *RPB*2 = OQ556794, *TEF*1-α = OQ556796.

Notes: In phylogeny, our new species (*Aquadictyospora yunnanensis*) formed a well-separated lineage sister to *A. clematidis* (MFLUCC 17-2080) with 94% ML/1.00 BYPP statistical support (Figure 2.1). Based on nucleotide comparisons, *A. yunnanensis* (ZHKUCC 22-0279) is different from *A. clematidis* (MFLUCC 17-2080, type) by 23/559 bp (4.1%, without gap) of the ITS, 5/838 bp (0.6%, without gap) of the LSU, 56/871 bp (6.4%, without gap) of the *RPB*2, 4/899 bp (0.4%, without gap) of the SSU and 48/913 bp (5.2%, without gap) of the *TEF*1-α. Regarding morphological characteristics, our collection is similar to *A. clematidis* in having brown conidia with a basal cell (Phukhamsakda et al., 2020). However, the difference between our new species and *A. clematidis* is that our strain has light brown conidia, is compactly adpressed, and has 2–4 apical rows of cells, while *A. clematidis* has reddish brown conidia, broadly rounded and heavily pigmented in the upper half (Phukhamsakda et al., 2020). Therefore, we introduce *A. yunnanensis* as a new species based on morphology and multigene phylogenetic analysis.

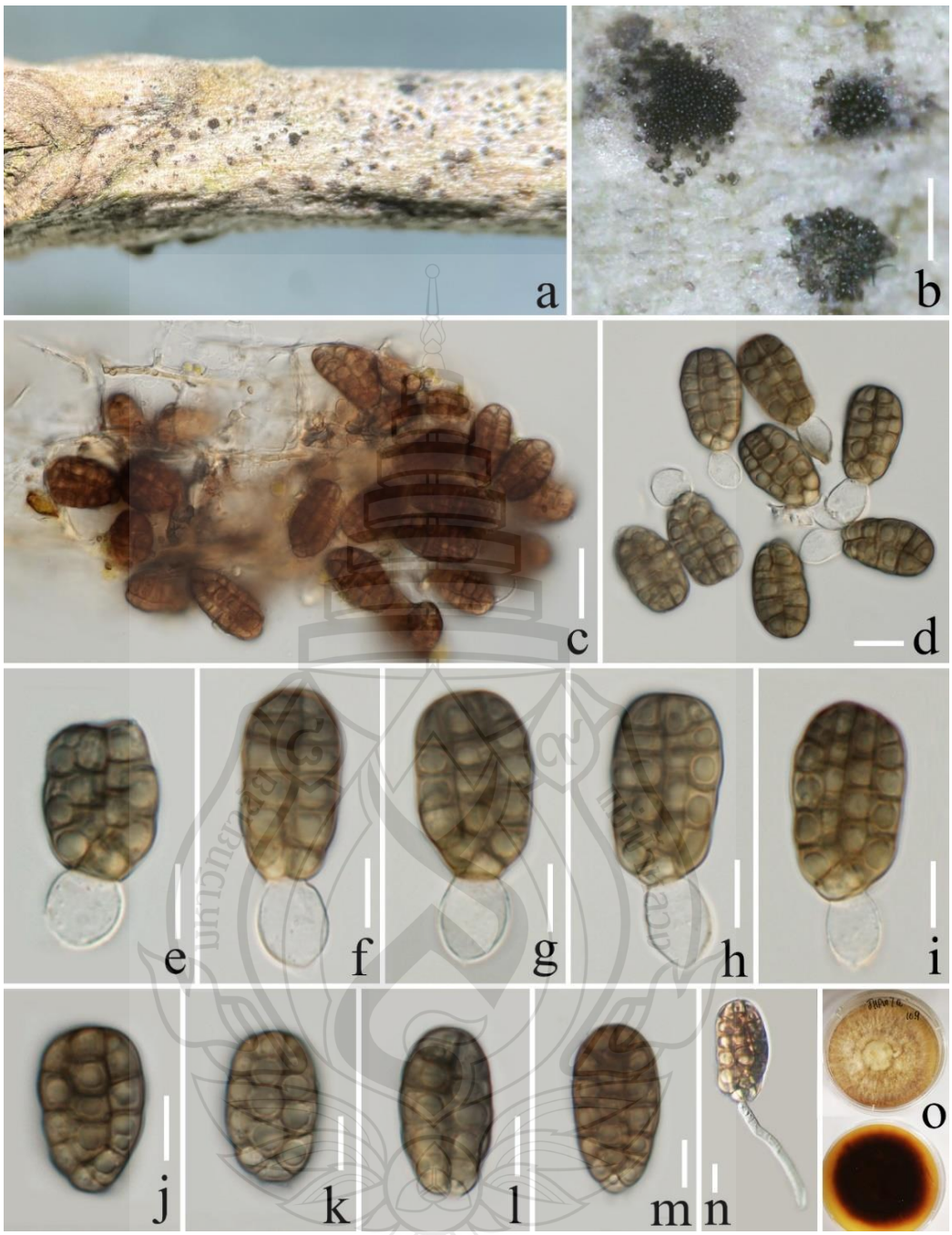


Figure 2.51 *Aquadictyospora yunnanensis* (MHZU 22-0148, holotype)

Figure 2.51 a, b. Sporodochia on natural substrate. c. Section of sporodochium. d–i. Mature conidia attached with basal cells. j–m. Mature conidia. n. Germinated conidium. o. Culture on PDA from above and reverse. Scale bars: b = 100 µm, c = 30 µm, d = 15 µm, e–n = 10 µm.

Dictyocheirospora M.J. D'souza, Boonmee & K.D. Hyde, Fungal Diversity 80: 465 (2016)

Notes: Based on phylogenetic results, *Dictyocheirospora* was introduced by Boonmee et al. (2016) to accommodates seven species, including three new species: *D. bannica*, *D. rotunda* (type species) and *D. vinaya*; and four new combinations: *D. gigantica* (= *Dictyosporium giganticum*), *D. heptaspora* (= *Dictyosporium heptasporum*), *D. pseudomusae* (= *Dictyosporium pseudomusae*), and *D. subramanianii* (= *Dictyosporium subramanianii*) (Boonmee et al., 2016). The difference between *Dictyocheirospora* and *Dictyosporium* is that in the former the conidia arms are on different planes and closely located at the apex, while in the latter, the conidia arms are closely arranged on the same plane (Boonmee et al., 2016; Shen et al., 2022). *Dictyocheirospora* is known by special morphological characteristics, such as dark sporodochial colonies and aero-aquatic cheiroid dictyospores, and they are distributed worldwide as saprobes on decaying stems, leaves, and branches (Boonmee et al., 2016; Danushka et al., 2023). In this study, two new records are introduced from a coffee host in China.

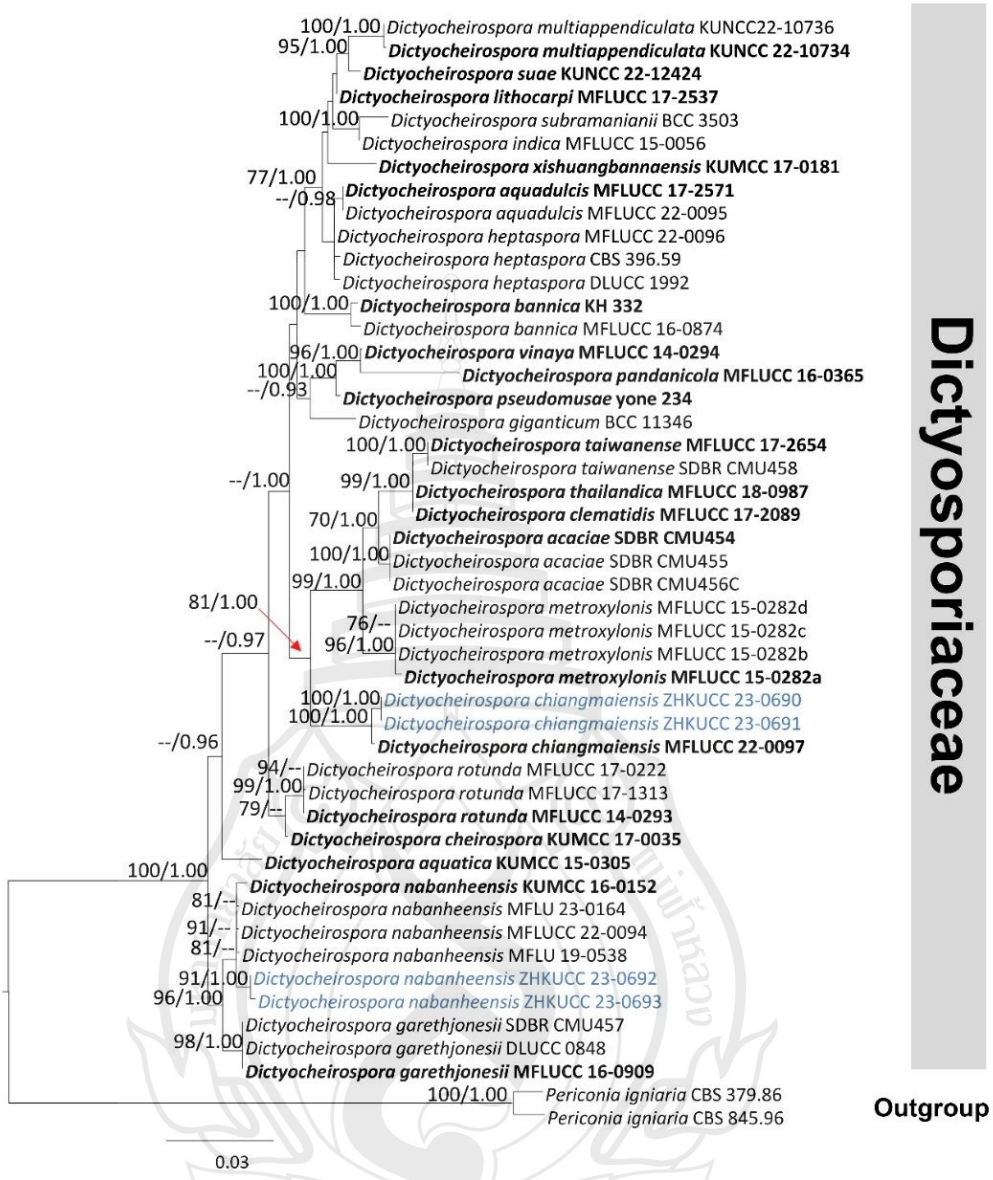


Figure 2.52 Phylogenetic tree of *Dictyocheirospora*

Figure 2.52 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, and *TEF*1-α sequence data. Forty-eight strains are included in the combined sequence analysis, which comprises 2,298 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Periconia igniaria* (CBS 379.86 and CBS 845.96).

Dictyocheirospora chiangmaiensis H.W. Shen, Boonmee & Z.L. Luo, Journal of Fungi 8 (11, no. 1200): 8 (2022)

Index Fungorum number: IF 846309; *Facesoffungi number*: FoF 17565; Figure 2.48

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* velvety, glistening, conidia readily liberated when disturbed, punctiform on a natural substrate in small groups, sporodochial, scattered and dark brown, with base attached on surface of the host plant. *Mycelium* immersed, pale brown, septate, smooth, thin-walled and branched hyphae. *Conidiophores* micronematous, mononematous, reduced to conidiogenous cell. *Conidiogenous cells* 9–15 × 3–6 µm ($\bar{x}$ = 11 × 4.7 µm, n = 10), holoblastic, cylindrical, septate, hyaline to pale brown, smooth and thin-walled. *Conidia* 42–52 × 15–20 µm ($\bar{x}$ = 47 × 17 µm, n = 30), solitary, cheiroid, ellipsoid to cylindrical, brown, not complanate, composed of 4–6 rows of cells, unseparated, with 8–10 cells per row, slightly bent inward at the apex, with a basal connecting cell, without appendages at the subapical. *Conidial secession* was schizolytic.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA growth was slow, reaching 3 cm after three months at 25°C, circular, with smooth edge, mycelium was loose, flocculent, white from above, middle mastoid, yellow to light brown from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC21 (MHZU 23-0090), living culture ZHKUCC 23-0690, other living culture ZHKUCC 23-0691.

GenBank numbers: ZHKUCC 23-0690: ITS = PQ608288, LSU = PQ608121, *TEF*1-α = PQ628135; ZHKUCC 23-0691: ITS = PQ608289, LSU = PQ608122, *TEF*1-α = PQ628136.

Known hosts: on submerged decaying wood in a stream (Shen et al., 2022), *Coffea arabica* (This study).

Known distribution: Thailand (Shen et al., 2022), China (This study).

Notes: *Dictyocheirospora chiangmaiensis* was isolated as saprobes on submerged decaying wood in freshwater habitats from Thailand (Shen et al., 2022). In a BLASTn search, the ITS and *TEF*1-α sequence of our collection showed 99%

similarity to *D. chiangmaiensis* (MFLUCC 22-0097, ex-type), and the LSU and SSU sequence showed 100% similarity to *D. chiangmaiensis* (MFLUCC 22-0097). In the present phylogenetic analysis, our strains cluster with *D. chiangmaiensis* with 100% ML and 1.00 BYPP statistical support (Figure 2.47). Morphologically, our collection fits well with the description of a holotype (MFLUCC 22-0097) in having ellipsoid to cylindrical conidia (Shen et al., 2022; Figure 2.48). We, therefore, identified our collection as *D. chiangmaiensis* which is a new host record and new country record form *Coffea arabica* in China.

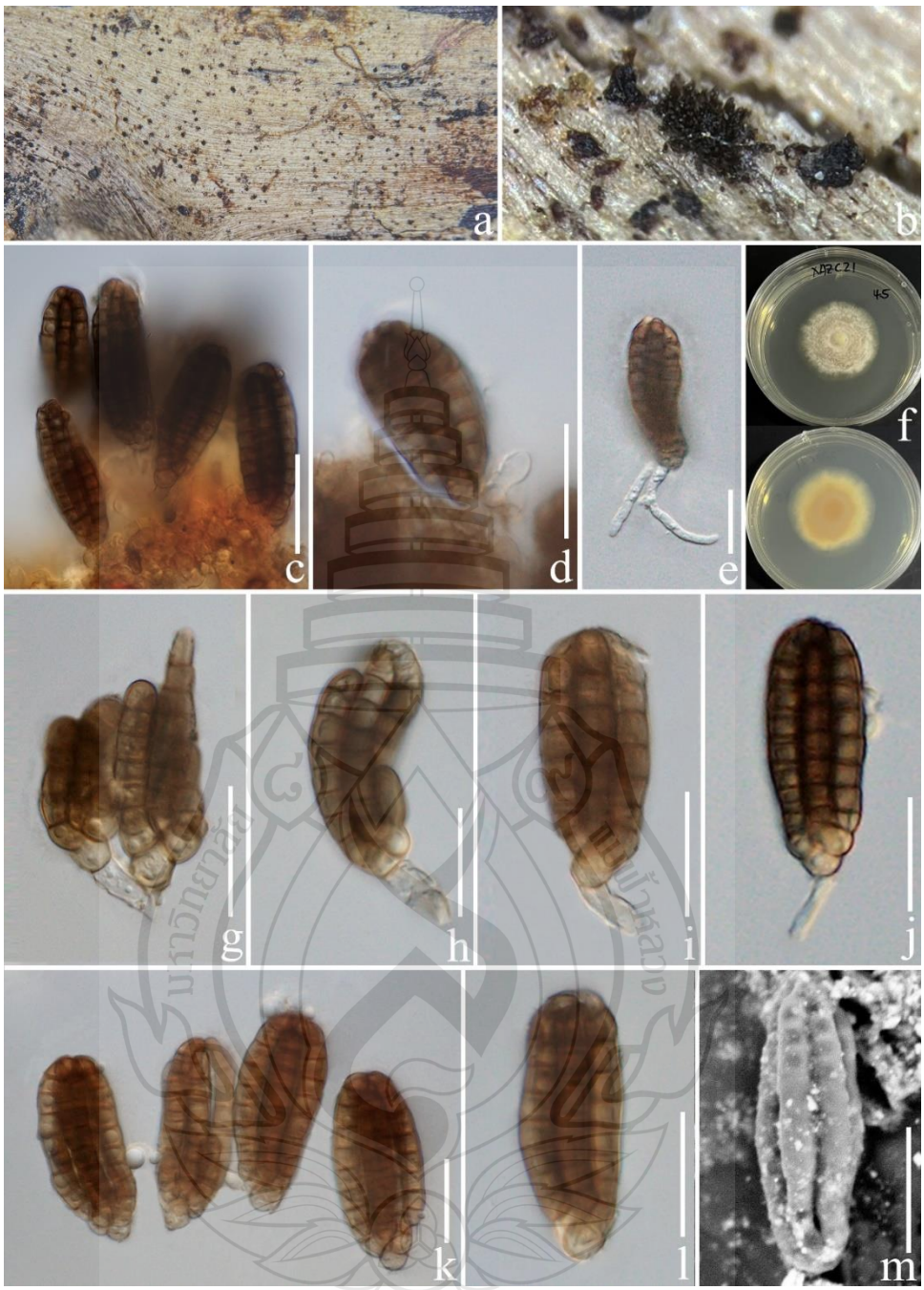


Figure 2.53 *Dictyocheirospora chiangmaiensis* (MHZU 23-0090, new host and country record)

Figure 2.53 a, b Colonies on a decaying branch of *Coffea arabica*. c, d, g-j Conidiogenous cells and conidia. e A germinating conidium. f Colonies on PDA from above and below. k-m Conidia (m: SEM microphotographs of the conidium). Scale bars: c = 30 µm, d–m = 20 µm.

Dictyocheirospora nabanheensis Tibpromma & K.D. Hyde, Fungal Diversity 93: 10 (2018)

Index Fungorum number: IF 554474, *Facesoffungi number*: FoF 04483; Figure 2.49

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* sporodochia on natural substrate in small groups, scattered, dark brown, with base attached on the surface of the host plant. *Mycelium* immersed and brown. *Conidiophores* micronematous, reduced to conidiogenous cells. *Conidiogenous cells* 9–16 × 5–7 µm ($\bar{x}$ = 13 × 5.5 µm, n = 10), holoblastic, cylindrical, wide at the top, sometimes flat at the base, hyaline, mostly remaining attached to the conidia. *Conidia* 35–50 × 15–20 µm ($\bar{x}$ = 42 × 17 µm, n = 20), solitary, oval to ellipsoid, cheiroid, not complanate, with a basal connecting cell, hyaline, smooth-walled, guttulate, individual cells discoid, arranged in 4–6 compact rows, with 8–12 cells per row; sometimes with 1–2 rounded to cylindrical appendages when young, arising from near middle of conidial rows, hyaline.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies grow on PDA, reaching 5 cm after three months at 25°C, circular, entire edge with cream margin, then white aerial mycelium, loose, flocculent in the middle, light yellow from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC25 (MHZU 23-0091), living culture ZHKUCC 23-0692, other living culture ZHKUCC 23-0693.

GenBank numbers: ZHKUCC 23-0692: ITS = PQ608290, LSU = PQ608123, *TEF*1-α = PQ628137; ZHKUCC 23-0693: ITS = PQ608291, LSU = PQ608124, *TEF*1-α = PQ628138.

Known host: *Pandanus* sp. (Tibpromma et al., 2018), *Leucaena* sp. (Jayasiri et al., 2019), *Borassus flabellifer* (Rajeshkumar et al., 2021), *Cocos nucifera* (Tian et al., 2023), *Coffea arabica* (This study).

Known distribution: China (Tibpromma et al., 2018; This study), Thailand (Jayasiri et al., 2019; Tian et al., 2023), India (Rajeshkumar et al., 2021).

Notes: In the multi-loci phylogenetic analyses, our strain (MHZUCC 23-0692 and MHZUCC 23-0693) cluster with the ex-type strain of *Dictyocheirospora nabanheensis* (KUMCC 16-0152) with 81% ML statistical support (Figure 2.47). Morphologically, our strain is similar to the holotype of *D. nabanheensis* in having oval to ellipsoid, brown conidia, and the conidial size of our collection is also similar to *D. nabanheensis* (Tibpromma et al., 2018; Figure 2.49). In a BLASTn search on NCBI GenBank, the closest matches of ITS and LSU sequences of our collection are 99% identical with *D. nabanheensis* (KUMCC 16-0152). Thus, based on the recommendations of Chethana et al. (2021), we identified our strain as *D. nabanheensis*. Our strain, *D. nabanheensis* (MHZU 23-0091), is reported as a new host record on *Coffea arabica* in China.

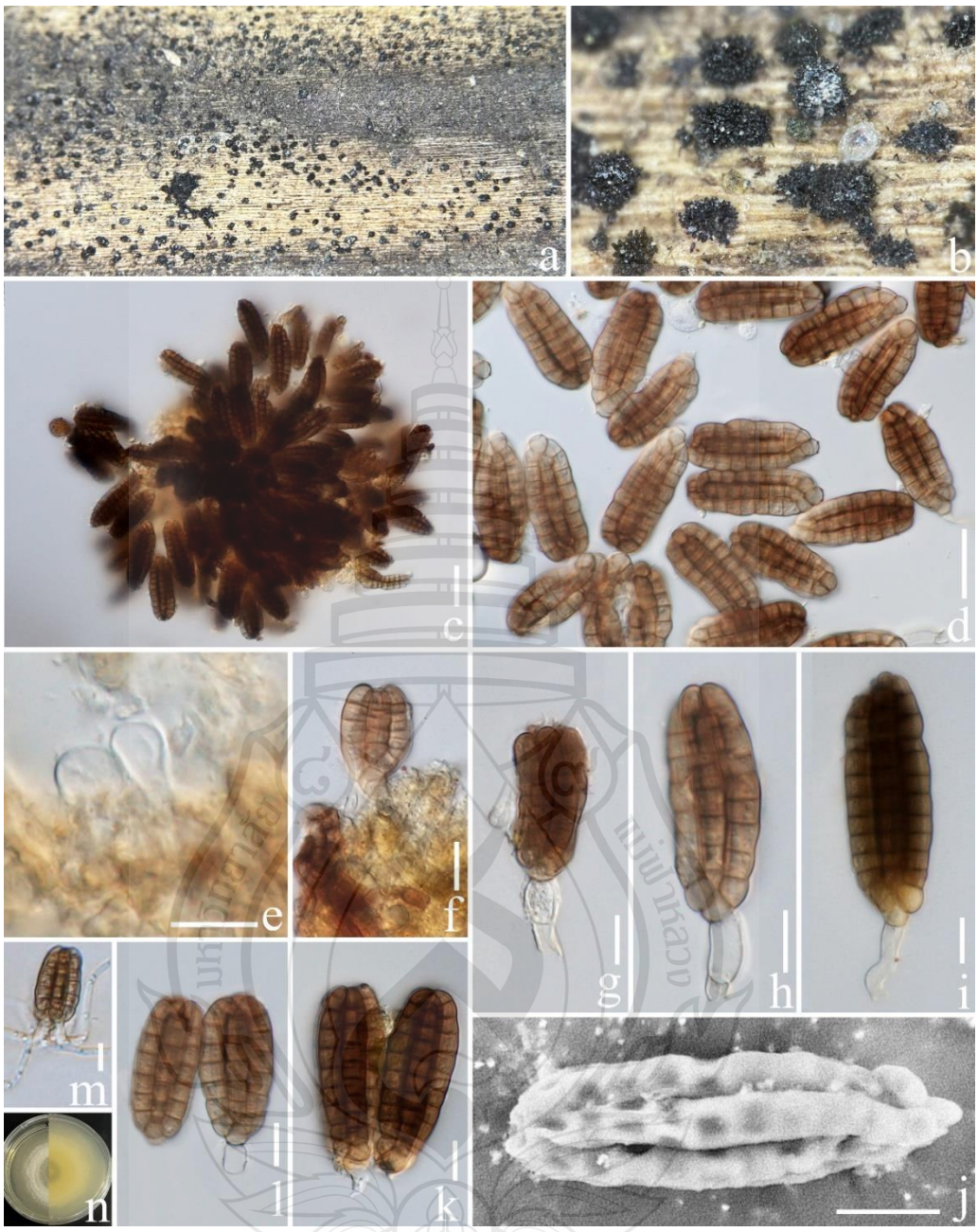


Figure 2.54 *Dictyocheirospora nabanheensis* (MHZU 23-0091, new host record)

Figure 2.54 a, b Colonies on a decaying branch of *Coffea arabica*. c Conidiomata with conidiophores. d-i Conidiogenous cells and conidia. j-l Conidia (j: SEM microphotographs of conidium). m A germinating conidium. n Colonies on PDA from above and below. Scale bars: c = 30 µm, d = 20 µm, e–m = 10 µm.

Pseudocoleophoma Kaz. Tanaka & K. Hiray., Studies in Mycology 82: 89 (2015)

Notes: Pseudocoleophoma (Pse.) was introduced by Tanaka et al. (2015) and was typified by *Pse. calamagrostidis* based on the pycnidial asexual morph which differs from *Coleophoma* (Tanaka et al., 2015). Most of the *Pseudocoleophoma* species were reported as asexual morphs (Hyde et al., 2016; Tennakoon et al., 2019; Jiang et al., 2021), but only three species have been reported for both sexual and asexual morphs viz. *Pse. bauhiniae*, *Pse. calamagrostidis*, and *Pse. polygonicola* (Tanaka et al., 2015; Jiang et al., 2021). Sexual morph is charac-terized by ostiolar ascomata, brown and polygonal to rectangular cells of peridium, numerous pseudoparaphyses, cylindrical to clavate and fissitunicate asci, fusiform, septate ascospores, with apparent sheath (Tanaka et al., 2015; Jiang et al., 2021). Asexual morph is characterized by pycnidial and subglobose conidiomata, phialidic, doliiform conidiogenous cells, and cylindrical or oblong, hyaline, aseptate, smooth-walled conidia (Tanaka et al., 2015).

In 2022, eight epithets (seven species) isolated as saprobes on different hosts and substrates from both terrestrial and freshwater habitats are listed in Index Fungorum (2022) (Tanaka et al., 2015; Hyde et al., 2016; Tennakoon et al., 2019). *Pseudocoleophoma clematidis* was transferred to Pseudocyclothy-riella by phylogenetic status and morphological distinctiveness (Jiang et al., 2021). Herein we introduce two new species in *Pseudocoleophoma*, and this is the first report of *Pseudocoleophoma* from coffee

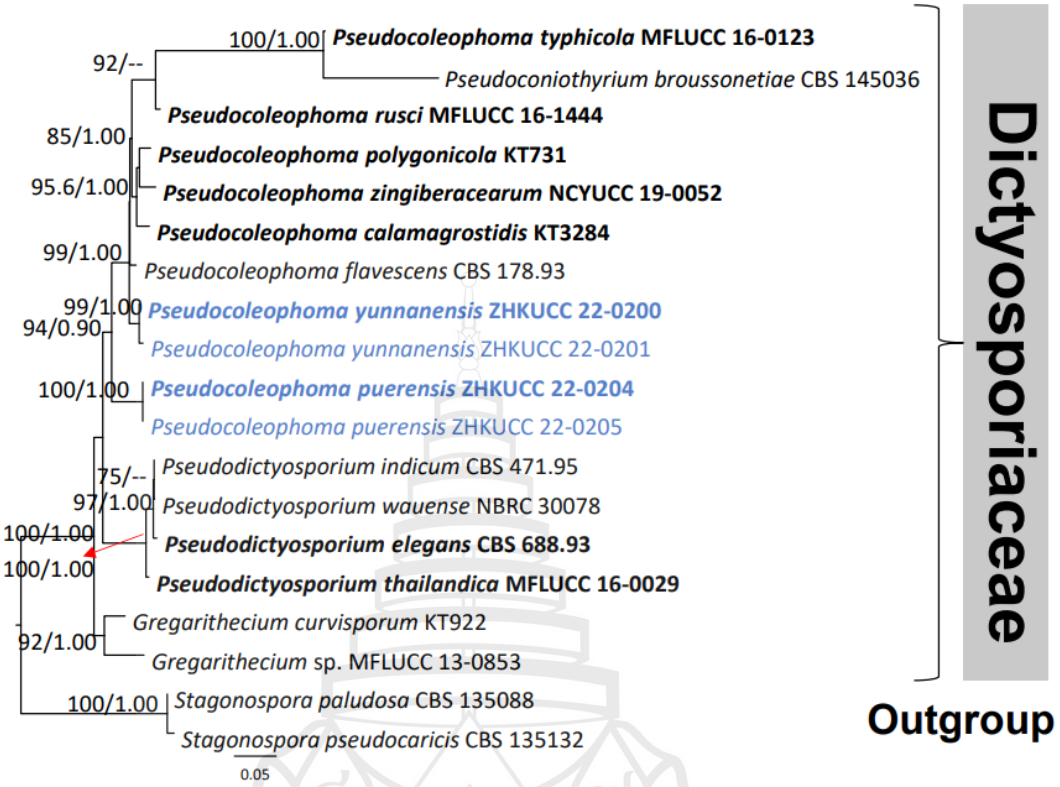


Figure 2.55 Phylogenetic tree of *Pseudocoleophoma*

Figure 2.55 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU and *TEF*1-α sequence data. Nineteen strains are included in the combined sequence analysis, which comprises 3,270 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Stagonospora paludosa* (CBS 135088) and *S. pseudocaricis* (CBS 135132).

Pseudocoleophoma puerensis L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559421; *Facesoffungi number*: FoF 12761; Figure 2.53

Etymology: Name reflects the location "Pu'er" City in Yunnan Province, where the holotype was collected.

Holotype: MHZU 22-0118

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph:**. *Saprotrophic* on decaying branch of *Coffea arabica* var. *catimor*. *Ascomata* 150–300× 170–220 µm ($\overline{x}$ = 197 × 199 µm, n = 15) (includes ostiolar neck), solitary, immersed to erumpent, brown to black, globose or subglobose. *Peridium* 14–20 µm wide ($\overline{x}$ = 17 µm, n = 20), thin, wall composed of 2–4 layers *textura angularis* cells, brown to dark brown. *Hermathecium* 1.5–3 µm wide ($\overline{x}$ = 2.3 µm, n = 20) septate, branched, numerous, hyaline, pseudoparaphyses. *Asci* 50–70 × 7–11 µm ($\overline{x}$ = 57 × 8.5 µm, n = 20), 8-spored, fissitunicate, cylindrical, rounded at the apex, with a shallow ocular chamber, long-stalked with club-like pedicel. *Ascospores* 10–15 × 3.5–6 µm ($\overline{x}$ = 11.6 × 4, n = 20), uni to biseritate, narrowly ellipsoid or oblong, 1–3 thick and dark eusepta, slightly constricted at septa, straight or slightly curved, hyaline and yellowish brown when young, turning brown when maturation, normally 4 guttulate, without sheath. **Asexual morph:** Not observed.

Culture characteristics: Colonies on PDA after two months attaining a diam of 40 mm at 25°C, above side pale-yellow, circular, flatted, margin filamentous, reverse side center brown, middle off yellowish brown and white at the margin

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* var. *catimor*, (100°56'9" E, 22°40'28" N, 1090.5 m), 16 September 2021, LiLu, Pu'er 3-2 (ZHKU 22-0118, holotype), living culture ZHKUCC 22-0204 = ZHKUCC 22-0205.

GenBank numbers: ITS: OP297799, LSU: OP297769, SSU: OP297783, tef1-α: OP321568 (ZHKUCC 22-0204, ex-type); ITS: OP297800, LSU: OP297770, SSU: OP297784, tef1-α: OP321569 (ZHKUCC 22-0205).

Notes: In the phylogenetic tree constructed based on multigene data, our isolates clustered within *Pseudocoleophoma* and formed a distinct branch basal to *Pse. typhicola* (MFLUCC 16-0123), with a fairly good statistical support (60% ML/1.00 BYPP, Figure 2.1). But *Pse. typhicola* has only been reported as an asexual morph (Hyde et al., 2016). Based on nucleotide comparisons, our isolate (ZHKUCC 22-0204) differs from *Pse. typhicola* (MFLUCC 16-0123) by 63/533 bp (11%) in ITS, 18/669 bp (2.6%) in LSU, while it lacks the SSU and *tef*1-α genes. The morphology of our isolate is similar to *Pseudocoleophoma* which was described by Tanaka et al. (2015), although we noticed that the ascospores are 1–3 septate, brown, and no sheath in ascospores.

Therefore, herein we introduce *Pse. puerensis* as a new species in *Pseudocoleophoma*.

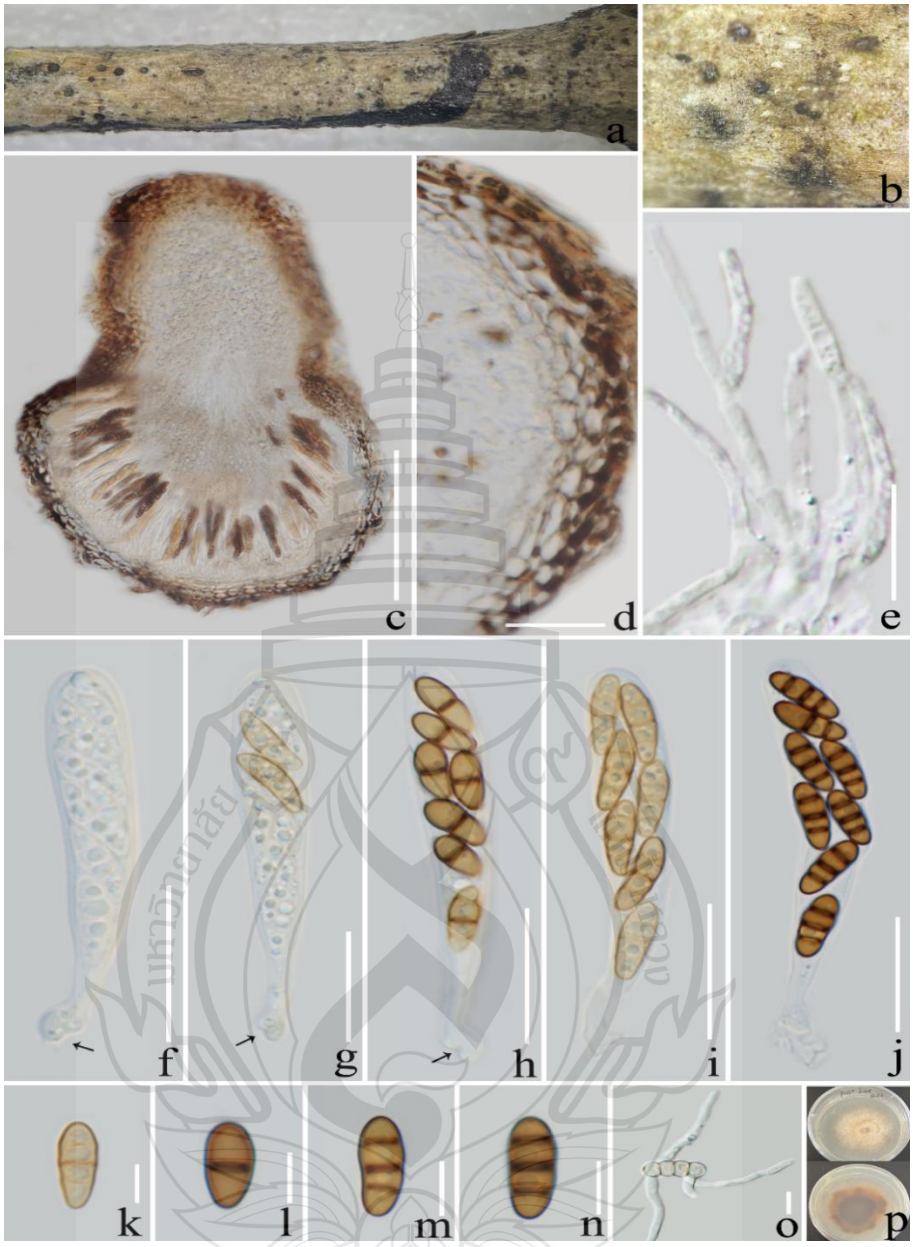


Figure 2.56 *Pseudocoleophoma puerensis* (ZHKU 22-0118, holotype)

Figure 2.56 a–b Ascomata on a decayed branch of *Coffea arabica*; c Section of an ascoma; d Peridium at side; e Pseudoparaphyses; f–j Immature and mature asci, arrows indicate club-like pedicel; k–n Ascospores; o Germinated ascospore; p,q Culture on PDA from above and reverse (60 days). Scale bars: c,e = 100 µm; f–j = 20 µm; k–n = 5 µm; (o) = 10 µm.

Pseudocoleophoma yunnanensis L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559422; *Facesoffungi number*: FoF 12762; Figure 2.53

Etymology: Name reflects the location "Yunnan" Province, where the holotype was collected.

Holotype: MHZU 22-0116

Saprotrophic on decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 160–280 × 200–280 µm ($\bar{x}$ = 216 × 243 µm; n = 15), semi-immersed to erumpent, solitary or scattered, coriaceous, subglobose to obpyriform, dark brown to black, with protruding ostiolar neck. *Peridium* 22–27 µm wide ($\bar{x}$ = 23; n = 15), outer walls comprising 2–4 layers of *textura angularis* cells, hyaline to brown, inner walls hyaline, density, several layers of *textura angularis* cells. *Hamathecium* 1.5–3 µm wide ($\bar{x}$ = 2.1 µm; n = 15), hyaline, septate, branched, pseudoparaphyses numerous. *Asci* 65–90 × 8–11 µm ($\bar{x}$ = 76 × 9 µm; n = 20), 8-spored, fissitunicate, clavate to cylindrical, some slightly curved, constricted at the upper part when mature, with an ocular chamber, short-stalked with club-shape pedicel. *Ascospores* 16–26 × 4–8 ($\bar{x}$ = 21 × 6 µm; n = 20), uni to biseriate, hyaline, fusiform, straight to slightly curved, 1-septate, 4 guttulate, smooth-walled, with distinct sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 hours, colonies on PDA after two months attaining a diam of 40 mm at 25°C, slightly raised, fluffy, white, circular, margin fila-mentous, reverse pale yellow to light brown from edge to center.

Material examined: China, Yunnan Province, Xishuangbanna, on a decaying branch of *Coffea* sp., (1672 m), 12 September 2021, LiLu, JHMH 15 (ZHKU 22-0116, holotype), living culture ZHKUCC 22-0200 = ZHKUCC 22-0201.

GenBank numbers: ITS: OP297795, LSU: OP297765, SSU: OP297779, tef1-α: OP321564 (ZHKUCC 22-0200, ex-type); ITS: OP297796, LSU: OP297766, SSU: OP297780, tef1-α: OP321565 (ZHKUCC 22-0201).

Notes: In the phylogenetic tree, our species *Pseudocoleophoma yunnanensis* formed a well-separated clade clustered with *Pse. bauhiniae* (MFLUCC 17-2280) with high statistical support (90% ML/1.00 BYPP, Figure 2.1). Based on nucleotide comparisons, our isolate (ZHKUCC 22-0200) is different from *Pse. bauhiniae* (MFLUCC 17-2280) by 13/489 bp (2.6%) in ITS, 3/833 bp (0.4%) in LSU, 9/1069 bp

(0.8%) in SSU, and 73/878bp (8.3%) in *tef*1-α. In addition, morphological features of the sexual morph *Pse. yunnanensis* can be distinguished by having constricted asci and the presence of a distinct sheath of ascospores with *Pse. bauhiniae* and other species in *Pseudocoleophoma* (Tanaka et al., 2015; Jayasiri et al., 2019). Therefore, we introduce *Pse. yunnanensis* as a new species that was isolated from coffee.

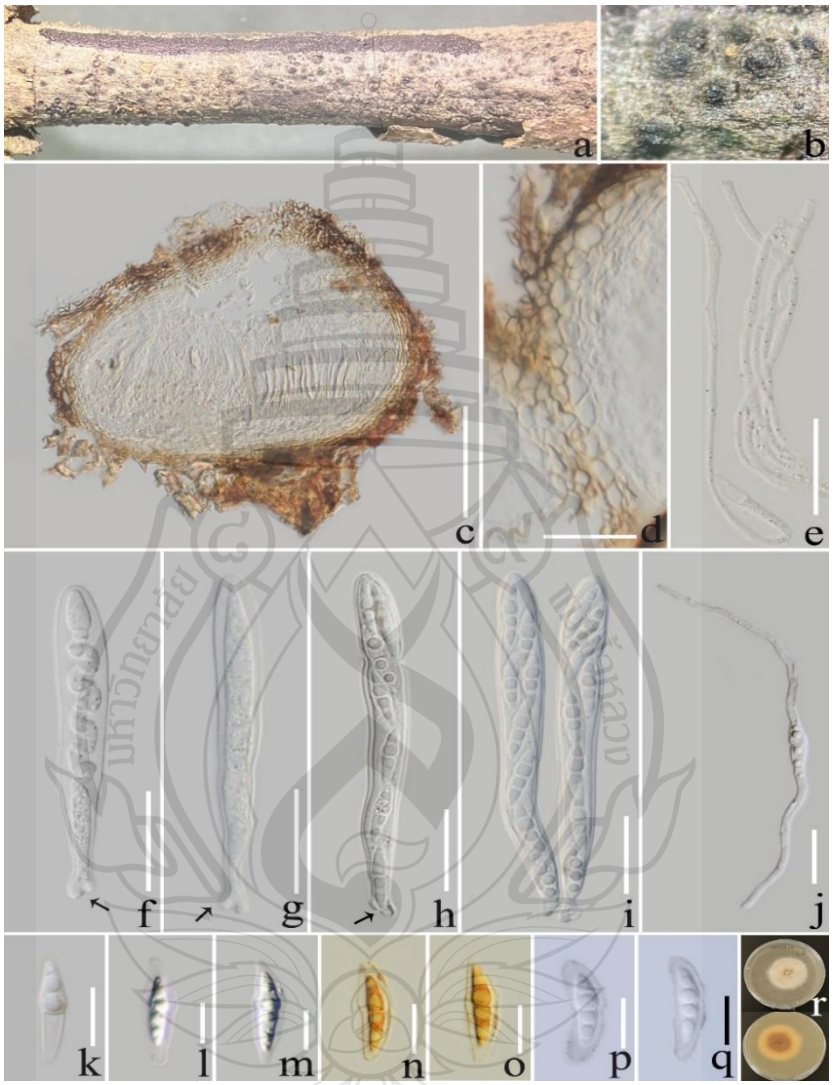


Figure 2.57 *Pseudocoleophoma yunnanensis* (ZHKU 22-0116, holotype)

Figure 2.57 a–b Ascomata on a decayed branch of *Coffea* sp.; c Section of an ascoma; d Peridium at side; e Pseudoparaphyses; f–i Immature and mature asci, arrows indicate club-shape pedicel; j Germinated ascospore; k–m Ascospores; n,o Ascospore stained with Lugol's iodine; p,q Ascospore stained with Indian ink; r Culture on PDA from above and reverse (60 days). Scale bars: c = 100 µm; d–j = 20 µm; k–q = 10 µm.

Didymosphaeriaceae Munk, Dansk botanisk Arkiv 15 (2) 128 (1953).

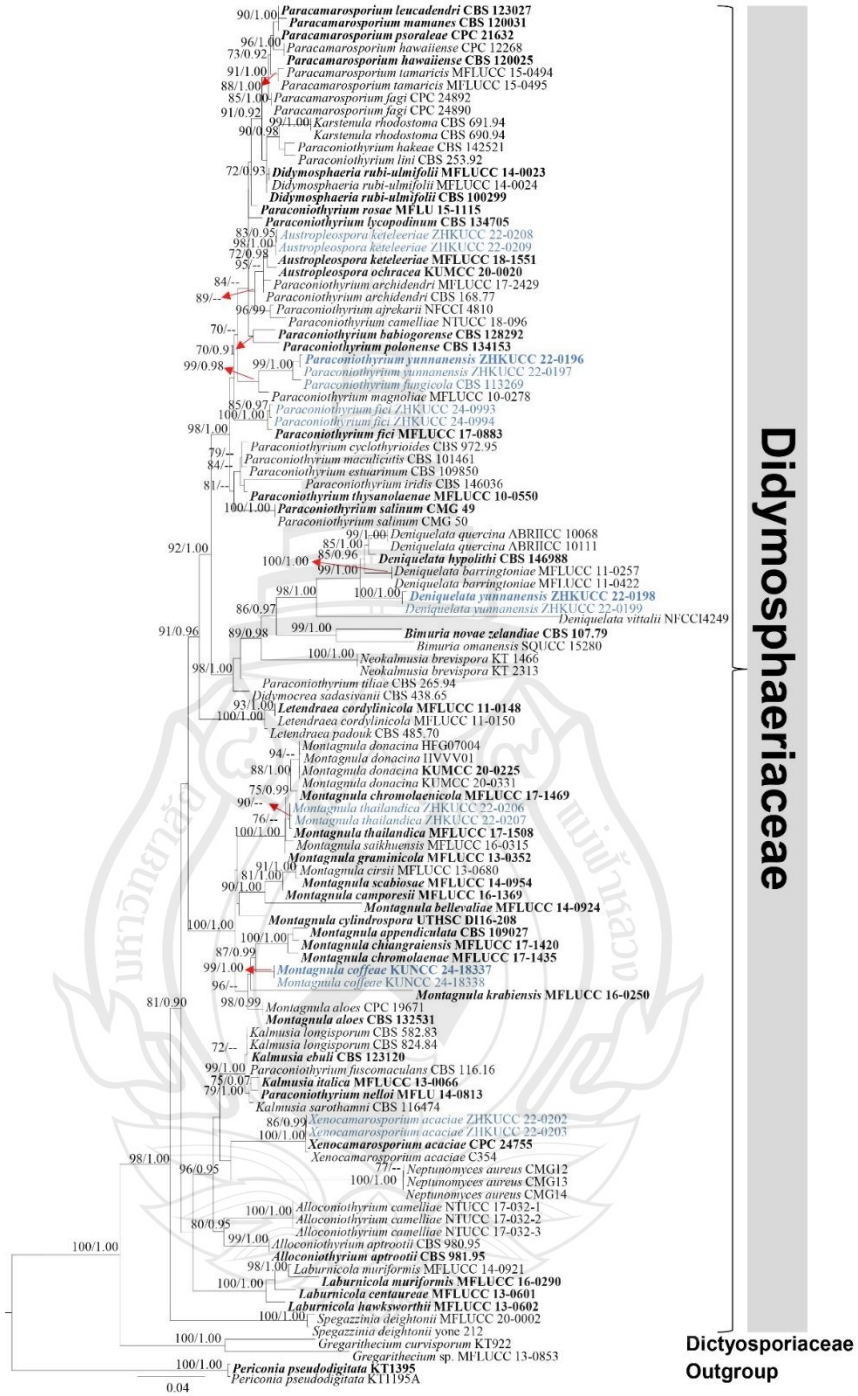


Figure 2.58 Phylogenetic tree of Didymosphaeriaceae

Figure 2.58 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2 and *TEF*1-α sequence data. One hundred eleven strains are included in the combined sequence analysis, which

comprises 5,500 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Periconia pseudodigitata* (KT1395 and KT1195A).

Austropleospora R.G. Shivas & L. Morin, Fungal Diversity 40 (1): 70 (2010)

Notes: Austropleospora (*A.*) was introduced by Morin et al. (2010), with *A. osteospermi* as the type species. This was isolated as pathogens with both sexual and asexual morphs from stems of *Chrysanthemoides monilifera* subsp. *rotundata* with dieback symptoms in Australia, but its pathogenicity has not been accurately confirmed (Morin et al., 2010). The sexual morphs are characterized by immersed and ostiolate ascomata, filamentous and septate pseudoparaphyses, bitunicate, clavate to cylindrical asci and ellipsoid, yellowish-brown ascospores. The asexual morph has coelomycetous, pycnidial, globose conidiomata, brown to reddish-brown conidiomata walls, yellowish-brown and globose to obovate conidia (Verkley et al., 2014; Ariyawansa et al., 2015; Dissanayake et al., 2021). Species of this genus have been reported as pathogenic or saprotrophic in Australia, China, and Thailand (Ariyawansa et al., 2015; Dissanayake et al., 2021). *Austropleospora* contains four epithets (three species) in Index Fungorum (2022) viz. *A. archidendri*, *A. keteleeriae*, *A. ochracea*, and *A. osteospermi*, while *A. archidendri* has been synonymized under *Paraconiothyrium* (Ariyawansa et al., 2015). Thus, we introduce the new host record *Austropleospora keteleeriae* from coffee.

Austropleospora keteleeriae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10 (1): 65 (2019)

Index Fungorum number: IF 555541; *Facesoffungi number:* FoF 05244; Figure 2.51

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Coelomycetous. *Conidiomata* 70–150 × 150–250 μm ($\overline{x}$ = 104 × 209 μm, n = 15), pycnidial, immersed, solitary, globose to obpyriform, or irregular, short ostiolate after maturity. *Conidiomata wall* 12–17 ($\overline{x}$ = 14.5 μm, n = 20), composed of 2–3 layers, inner wall composed of 1–2 layers, hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–6 × 2–4 μm ($\overline{x}$ = 4.3 × 2.5 μm, n = 20), enteroblastic, phialidic, globose to doliiform, hyaline, smooth-walled, lining the inner

wall layer of the pycnidium. *Conidia* 4–7 × 2.5–4.5 µm ($\overline{x}$ = 6 × 3.5 µm, n = 30), solitary, the color changes with different ages, hyaline when young, brown to dark-brown when maturity, subglobose to obovate, one-celled, thick and smooth-walled, aseptate, with small oil droplets. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated within 12 h on PDA, growing on PDA reaching around 40 mm after two months at room temperature (25°C). Above: White, circular, surface flocculent, with a lot of aerial mycelia. Reverse: The color gradually becomes darker from the edge to the center, white, yellowish to light brown.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* var. *catimor*, (100°56'9" E, 22°40'28" N, 1090.5 m), 16 September 2021, LiLu, Pu'er 3-9 (ZHKU 22-0120), living culture ZHKUCC 22-0208 = ZHKUCC 22-0209.

GenBank numbers: ITS: OP297801, LSU: OP297771, SSU: OP297785, *tef*1-α: OP321570 (ZHKUCC 22-0208); ITS: OP297802, LSU: OP297772, SSU: OP297786, *tef*1-α: OP321571 (ZHKUCC 22-0209).

Known hosts: Keteleeria fortunei (Jayasiri et al., 2019), *Coffea arabica* (This study).

Known distribution: China (Jayasiri et al., 2019; This study).

Notes: Austropleospora keteleeriae was isolated as saprotrophic on a decaying cone of *Keteleeria fortunei* from China (Jayasiri et al., 2019). Our new isolates form a sister clade to *A. keteleeriae* in the phylogenetic analyses with high statistical support (98 ML/1.00 BYPP, Figure 2.1). The morphological characteristics of the new isolates well fit with *A. keteleeriae* by having conidiomata consisting of textura angularis cells, phialidic, enteroblastic, hyaline and smooth conidiogenous cells, globose to obovate, one-celled, thick and smooth-walled, hyaline to brown conidia (Jayasiri et al., 2019). While ITS blast results showed that our strain is 99% similar to *A. archidendri* (*Paraconiothyrium archidendri*) (MZ855427), the results of LSU blast showed 100% similar to *Paraconiothyrium* sp. (JX496165), the results of SSU blast showed 99.9% similar to *Austropleospora* sp. (MT808321) and *tef*1-α blast showed 99.8% similar to *A. keteleeriae* (MK360045). Therefore, we introduce *A. keteleeriae* as a new host record from a decaying branch of *Coffea arabica* var. *catimor* in China based on morphology and phylogeny.

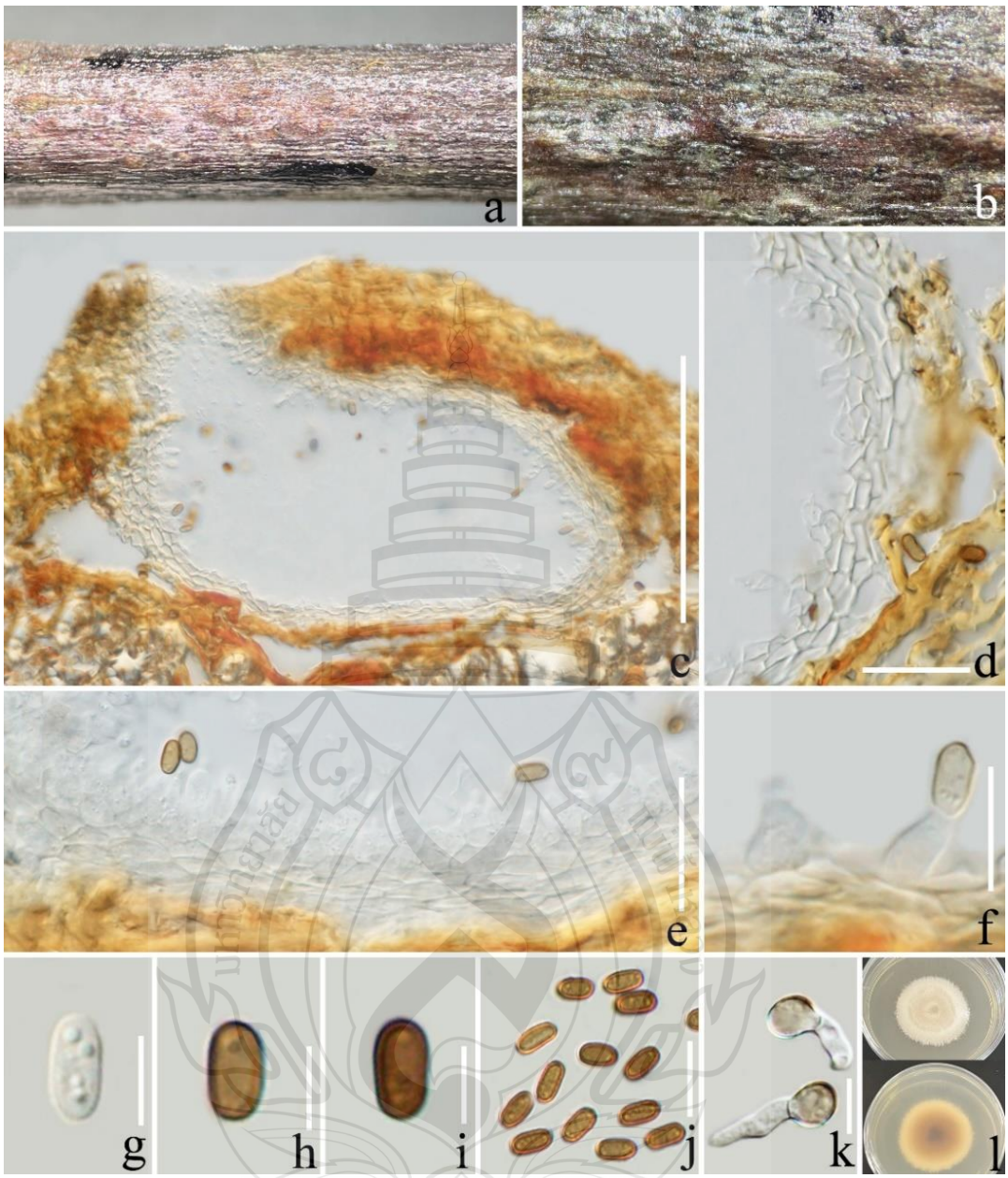


Figure 2.59 *Austropleospora keteleeriae* (MHZU 22-0120, new host record)

Figure 2.59 a–b Appearance of the conidiomata on decaying branch of *Coffea arabica* var. *catimor*; c Cross sections of a conidioma; d Pycnidial wall; e,f Conidia attached to conidiogenous cells; g–j Conidia; h Germinated conidium; l Culture on PDA from above and reverse 60 days; Scale bars: c = 100 µm; d,e = 20 µm; f,k = 10 µm; g–j = 5 µm.

Deniquelata Ariyaw. & K.D. Hyde, Phytotaxa 105 (1): 15 (2013)

Notes: Deniquelata (*D.*) was introduced by Ariyawansa et al. (2013), with *D. barringtoniae* as the type species, which was isolated as a pathogen causing leaf spots of *Barringtonia asiatica* (*Lecythidaceae*). The sexual morph of *Deniquelata* is characterized by immersed ascomata, with an ostiolar, textura angularis cells peridium, bitunicate, clavate to broadly-clavate with short furcate pedicel asci and muriform ascospores, three transverse septa and 1–2 vertical septa, without sheath (Ariyawansa et al., 2013; Alidadi et al., 2019). Asexual morph is characterized by branched and septate mycelium, conidiophores reduced to conidiogenous cells, pale brown and subcylindrical conidiogenous, subglobose to pyriform and guttulate conidia, with 1–3 transverse and 0–2 vertical septa (Crous et al., 2021). Species of this genus have been reported as pathogens, saprophytes and endophytes (Ariyawansa et al., 2013; Alidadi et al., 2019; Crous et al., 2021]. Currently, the genus *Deniquelata* contains four species in Index Fungorum (2022) viz. *D. barringtoniae*, *D. hypolithi*, *D. quercina* and *D. vittalii*. In this study, *Deniquelata yunnanensis* is introduced from coffee in Yunnan Province, China, and this is the first report of the genus *Deniquelata* from coffee.

Deniquelata yunnanensis L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 559423; *Facesoffungi number*: FoF 12763; Figure 2.53

Etymology: Name reflects the location "Yunnan" Province, where the holotype was collected.

Holotype: ZHKU 22-0115

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 140–240 × 170–240 μm ($\bar{x}$ = 187 × 209 μm, n = 20), semi-immersed, aggregated to solitary, globose to subglobose, dark brown to black, with ostiole and apex papillate to depressed. *Peridium* 12−17 μm wide ($\bar{x}$ = 14, n = 15), composed of two walls, outer wall light brown to brown, comprising 2–3 layers, cells of *textura angularis*, fused with the host cells, inner wall thin, hyaline cell. *Hamathecium* composed of dense, 1.5−3 μm wide ($\bar{x}$ = 2, n = 20), branched, hyaline, septate pseudoparaphyses, surrounding the numerous asci and enclosed in a gelatinous matrix. *Asci* 50–85 × 10–17 μm ($\bar{x}$ = 68 × 13 μm, n = 30), 8-spored, bitunicate, fissitunicate, clavate, with a short furcate pedicel. *Ascospores* 11–16 × 4–8 μm ($\bar{x}$ = 14 × 6.6 μm, n = 30), 2-seriated ascospores, partially

overlapping, muriform, hyaline when young, yellow to brown at maturity and with distinct guttulate, ellipsoidal to oblong, with 0–2 longitudinal septate in each cell, 1–3 transverse septate, constricted at the septa, slightly curved to straight, apically conical to elliptical, without a sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinated within 12 h on PDA, growing on PDA reaching around 50 mm after one month at room temperature (25°C). Surface white to light grey, circular, cottony and fluffy, slightly raised in the middle, margin filamentous, reverse yellowish to light brown.

Material examined: China, Yunnan Province, Xishuangbanna, on a decaying branch of *Coffea* sp., (1672 m), 12 September 2021, LiLu, JHMH 10 (ZHKU 22-0115, holotype), living culture ZHKUCC 22-0198 = ZHKUCC 22-0199.

GenBank numbers: ITS: OP297803, LSU: OP297773, SSU: OP297787, *tef*1-α: OP321572, *rpb*2: OP321562 (ZHKUCC 22-0198, ex-type); ITS: OP297804, LSU: OP297774, SSU: OP297788, *tef*1-α: OP321573, *rpb*2: OP321563 (ZHKUCC 22-0199).

Notes: In the phylogenetic analyses, *Deniquelata yunnanensis* formed a distinct clade sister to *Deniquelata* with strong statistical support (100 ML/1.00 BYPP, Figure 2.1). In the NCBI blast results of sequences, ITS 92.8% similar to *D. barringtoniae* (MH141242), LSU/*tef*1-α/*rpb*2 similar to *D. hypolithi* (NG_076735, 97.8%), (MZ078250, 97%) and (MZ078201, 94%) respectively, while SSU highly overlapped with *Deniquelata* sp. (MH316155) at 99%. Morphologically, our strains well fit with the generic characteristics of *Deniquelata* (Ariyawansa et al., 2013; Alidadi et al., 2019). Asexual morph of *D. hypolithi* was reported (Crous et al., 2021), while the sexual morph *D. yunnanensis* can be distinguished from *D. barringtoniae* by the color of ascospores yellow to brown at maturity and with distinct guttulate, and 1–3 transverse septa, 0–2 longitudinal septa in each ascospore, while ascospores in *D. barringtoniae* are reddish-brown, with three transverse septa and 1−2 vertical septa in each ascospore (Dissanayake et al., 2021). Both the phylogenetic analyses and morphological characteristics supported our species as a distinct new species in *Deniquelata*.

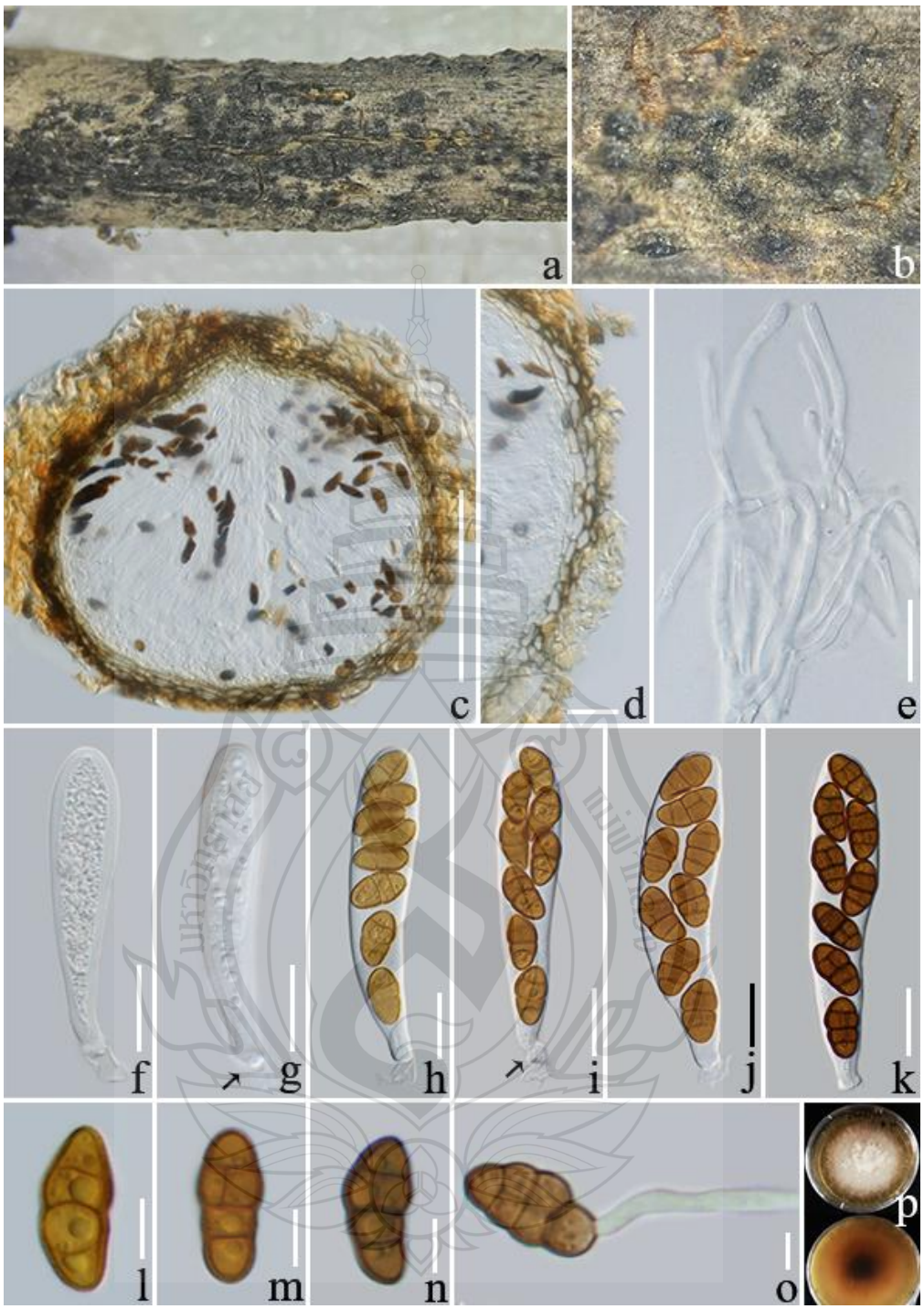


Figure 2.60 *Deniquelata yunnanensis* (ZHKU 22-0115, holotype)

Figure 2.60 a,b Ascomata on a decaying branch of *Coffea* sp.; c Vertical section of an ascoma; d Peridium; e Pseudoparaphyses; f–k Asci, arrows indicate short furcate pedicel; l–n Ascospores; o Germinated ascospore; p Culture on PDA from above and reverse (30 days). Scale bars: c = 100 µm; d–k = 15 µm; l–o = 5 µm.

Montagnula Berl., Icones Fungorum. Pyrenomycetes 2: 68 (1896)

Notes: Berlese (1896) introduced *Montagnula* typified by *M. infernalis* (Niessl) Berl. Most species of *Montagnula* have been found on dead leaves and twigs by their teleomorph with a wide geographical and host distribution (Tibpromma et al., 2018; Mapook et al., 2020; Du et al., 2021). Only *M. cylindrospora* Valenz. -Lopez, Cano, Guarro & Stchigel, has been reported as a coelomycete (Crous et al., 2020). This study introduces a novel species and a new host and country record from coffee plant in Yunnan Province, China.

Montagnula coffeae L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 900999;; *Facesoffungi number*: FoF 14725; Figure 2.53

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137611

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph:** *Ascomata* 120–180 µm high × 150–220 µm diam. ($\overline{x}$ = 150 × 183 µm, n = 15), immersed, separate beneath a clypeus or sometimes gregarious beneath fused clypei, visible as black, solitary or scattered, globose to subglobose, unilocular, black, with ostioles. *Ostioles* papillate, central. *Clypeus* brown or sometimes with a halo around the central pore, margin indistinct, consisting of dark, thick-walled hyphae in both epidermal and subepidermal cells. *Peridium* 7–11 µm wide ($\overline{x}$ = 8.8 µm, n = 15), fused with host tissue, comprising 2–3 layers of pale brown to brown cells of *textura prismatica. Hamathecium* 3–6 µm wide ($\overline{x}$ = 4 µm, n = 20) µm wide, branched, hyaline, septate, numerous pseudoparaphyses. *Asci* 60–75 × 6–10 µm ($\overline{x}$ = 65 × 8.5 µm, n = 20), bitunicate, fissitunicate, 6–8-spored, clavate, long-stalked with club-shape, straight. *Ascospores* 12–16 × 3–6 µm ($\overline{x}$ = 14 × 4.8 µm, n = 30), hyaline to yellowish when immature, brown to red-brown when mature, overlapping uniseriate or biseriate, fusiform to ellipsoid, 1-septate, guttulate, constricted at the septum, upper cell wider and shorter than lower cell and tapering towards ends, sheath drawn out to form polar appendages 4–9 µm long × 1.5–2.5 µm wide ($\overline{x}$ = 6 × 1.9 µm, n = 30), from both ends of the ascospores, straight. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h, colonies reached 3.5–4 cm in diameter after one month at 25℃. Colonies on PDA irregular, flat or slightly raised, filamentous, smooth, with undulate margin, from above, hyaline, from below, yellowish at the centre, hyaline at the edge.

Material examined: China, Yunnan Province, Lincang, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (24°17' N, 99°99' E, 960 m alt.), 28 July 2022, LiLu, LC1-C5 (HKAS 137611, holotype), isotype MHZU 23-0060, ex-type living culture KUNCC 24-18337 = KUNCC 24-18338, ex-isotype living culture ZHKUCC 23-0630 = ZHKUCC 23-0631.

GenBank numbers: ITS: OR428399, LSU: OR428421, SSU: OR428379, *TEF*1-α: OR509753, *RPB*2: OP321562 (KUNCC24-18337, ex-type); ITS: OR428400, LSU: OR428422, SSU: OR428380, *TEF*1-α: OR509754 (KUNCC24-18338).

Notes: In the concatenated phylogenetic analysis, *Montagnula coffeae* forms a distinct lineage and is basal to *M. appendiculata*, *M. chromolaenae* and *M. chiangraiensis* (Figure 2.5). Based on nucleotide comparisons, *M. coffeae* (ZHKUCC 23-0630) differs from *M. appendiculata* (CBS 109027) by 30/497 bp (6%, without gaps) in ITS and 14/833 bp (1.7%, without gaps) in LSU; differs from *M. chromolaenae* (MFLUCC 17-1435) by 24/497 bp (4.8%, without gaps) in ITS, 12/903 bp (1.3%, without gaps) in LSU and 15/1006 bp (1.5%, without gaps) in SSU; differs from *M. chiangraiensis* (MFLUCC 17-1420) by 20/498 bp (4%, without gaps) in ITS, 13/903 bp (1.4%, without gaps) in LSU and 10/1006 bp (1%, without gaps) in SSU. The morphology of *M. coffeae* is similar to *M. appendiculata* and *M. chromolaenae* in having fusiform, brown and fusiform ascospores with appendages. However, *M. coffeae* has 6–8-spored asci, while *M. appendiculata* has 8-spored asci (Figure 2.4; Aptroot, 2004). *Montagnula coffeae* have guttulate ascospores, while no guttules have been observed on the ascospores of *M. chromolaenae* (Mapook et al., 2020). *Montagnula coffeae* can be distinguished from *M. chiangraiensis* by the appendages on its ascospores (Mapook et al., 2020). The morphological differences and phylogenetic analysis results support the discovery of *M. coffeae* as a new species.

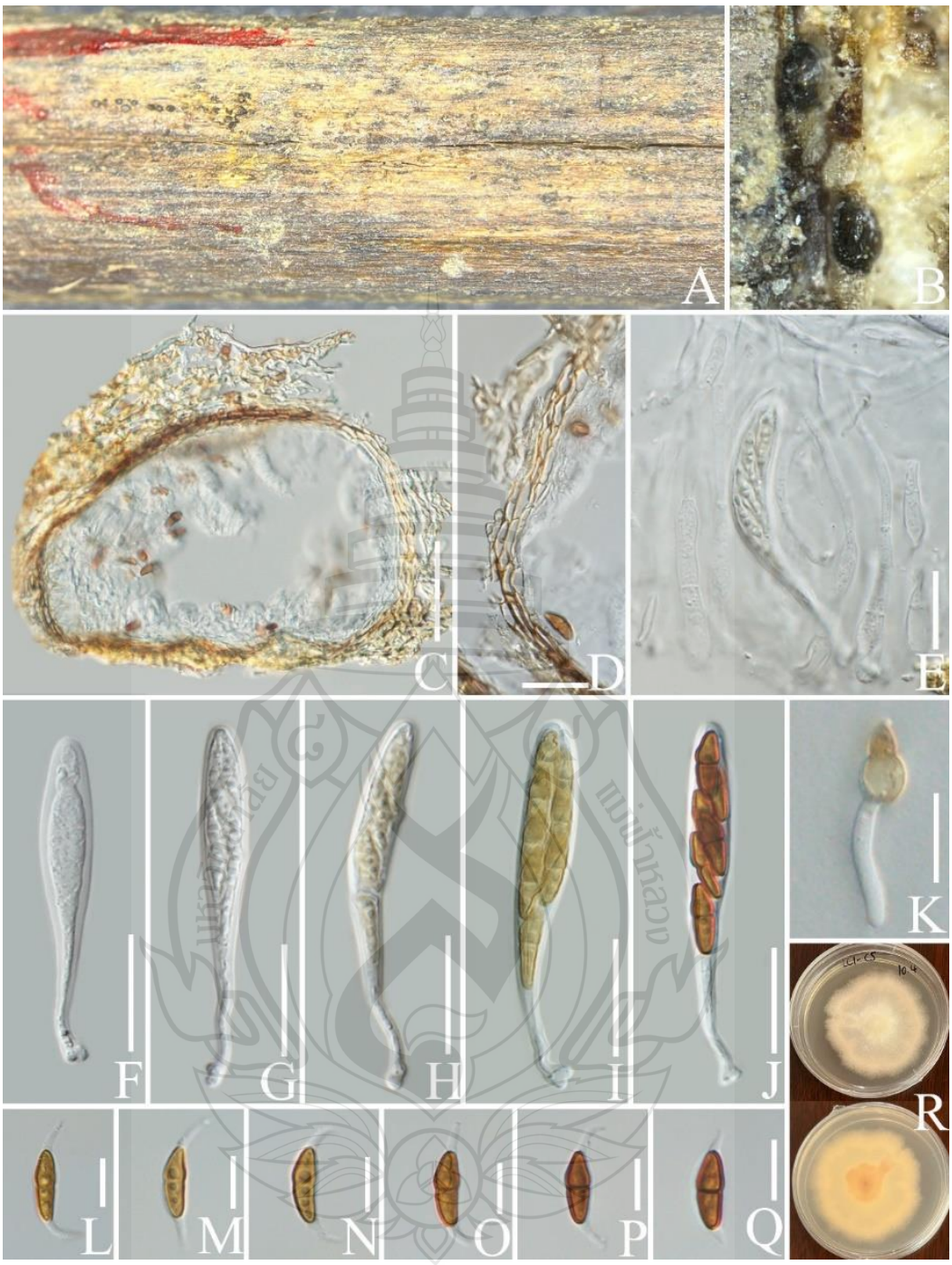


Figure 2.61 *Montagnula coffeae* (HKAS 137611, holotype)

Figure 2.61 A, B Ascomata on a decaying branch of *C. arabica*; C Longitudinal section of an ascoma; D Peridium wall; E Pseudoparaphyses; F–J Immature and mature asci; K Germinated ascospore; L–Q Ascospores; R Culture on PDA from obverse and reverse. Scale bars: C = 50 μm, D–K = 20 μm, L–Q = 10 μm.

Montagnula thailandica Mapook & K.D. Hyde, Fungal Diversity 101: 35 (2020)

Index Fungorum number: IF 557299; *Facesoffungi number:* FoF 07792; Figure 2.51

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph**: *Ascomata* 300–500 × 280–350 µm ($\bar{x}$ = 26 µm, n = 10), semi-immersed to erumpent, brown to black, spherical to obpyriform, solitary or scattered, with papillate ostiole. *Peridium* 20–30 µm wide ($\bar{x}$ = 377 × 313 µm, n = 10), comprising several layers of thin-walled, hyaline to brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyaline, cellular, branched, septate, numerous pseudoparaphyses. *Asci* 80–110 × 9–13 µm ($\bar{x}$ = 93 × 11 µm, n = 25), 6–8-spored, bitunicate, elongate-clavate, long-stalked with club-shape pedicel, slightly curved. *Ascospores* 12–16 × 5.5–6.5 µm ($\bar{x}$ = 14 × 5.8 µm, n = 25), overlapping 1–2-seriate, hyaline to yellowish-brown when immature, brown to reddish brown when mature, broadly fusiform to ellipsoid, 1-septate, constricted at the septum, slightly wider upper cell and tapering towards ends, straight or slightly curved, with 2–4 guttulate, without terminal appendages and sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h at room temperature (25°C), one month after growing on PDA it reached 60 mm, the obverse mycelium is fluffy, slightly raised, white to light brown, circular, filamentous at the margin, reverse with yellowish to dark brown from edge to center.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* var. *catimor*, (100°56'9" E, 22°40'28" N, 1090.5 m), 16 September 2021, LiLu, Pu'er 3-4 (ZHKU 22-0119), ZHKUCC 22-0206 = ZHKUCC 22-0207.

GenBank numbers: ITS: OP297807, LSU: OP297777, SSU: OP297791, *tef*1-α: OP321576 (ZHKUCC 22-0206); ITS: OP297808, LSU: OP297778, SSU: OP297792, *tef*1-α: OP321577 (ZHKUCC 22-0207).

Known hosts: Chromolaena odorata (Mapook et al., 2020), *Coffea arabica* (This study).

Known distribution: Thailand (Mapook et al., 2020), China (This study).

Notes: Montagnula thailandica was introduced as new species from dead stems of *Chromolaena odorata* from Thailand by Mapook et al. (2020) based on the morphology of sexual morph and the phylogenetic analyses. In this paper, our new isolates clustered with the ex-type strain of *M. thailandica* (MFLUCC 17-1508) with fairly good bootstrap support (ML/BI = 74/-). The morphology of the new isolate (ZHKU 22-0119) is very similar to the holotype *M. thailandica* (MFLU 20-0325) in size and color of asci and ascospores (Mapook et al., 2020). Based on blast results, ITS and *tef*1-α are 99.6% similar to *M. thailandica* (MFLUCC 17-1508), and LSU and SSU are 100% similar to *M. thailandica* (MFLUCC 17-1508). Therefore, the new isolate (ZHKU 22-0119) is identified as *M. thailandica*, and this is a new host and new country record of *M. thailandica* isolated from a decaying branch of *Coffea arabica* in China.



Figure 2.62 *Montagnula thailandica* (ZHKU 22-0119, new host and country record)

Figure 2.62 a,b Ascomata on a decaying branch of *Coffea arabica*; c Vertical section of an ascoma; d Peridium; e Pseudoparaphyses; f–j Asci, arrows indicate club-shape pedicel; k–n Ascospores; o Germinated ascospore; p Culture on PDA from above and reverse (30 days). Scale bars: c = 100 µm; d–j = 30 µm; k–n = 5 µm; o = 10 µm.

Paraconiothyrium Verkley, Studies in Mycology 50 (2): 327 (2004).

Notes: Paraconiothyrium was introduced by Verkley et al. (2004) with the type species *P. estuarinum*. In phylogeny, *Paraconiothyrium* was reported as a polyphyletic and paraphyletic genus (Lu et al., 2022), which contains 35 epithets listed in Index Fungorum (2025) and over 800 ITS sequences annotated as *Paraconiothyrium* in GenBank. Members of the *Paraconiothyrium* species were reported as pathogenic, saprobic, and endophytic that are associated with different plant hosts or substrates and have a global distribution (Ariyawansa et al., 2020; Boonmee et al., 2021; Lu et al., 2022; Tennakoon et al., 2022). The asexual morph of *Paraconiothyrium* has diverse morphology characteristics, such as eustromatic to pycnidial conidiomata, phialidic or annellidic conidiogenous cells, and hyaline to brown conidia (Verkley et al., 2004, 2014; Tennakoon et al., 2022). The sexual morph characteristics are globose or subglobose ascomata, clavate or cylindrical asci, and fusiform to ellipsoidal ascospores (Ariyawansa et al., 2014; Lu et al., 2022). In ecology, the diversity genus exhibits potential utilization as a biocontrol agent, bioreactor and antibiotic producers (Wang et al., 2021). This study introduces a new species and a new host and country record from coffee in China.

Paraconiothyrium fici Wijes. & K.D. Hyde, Fungal Diversity 10.1007/s13225-022-00502-3: [14] (2022)

Index Fungorum number: IF 559244; *Facesoffungi number:* FoF 10567; Figure 2.51

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–150 × 200–300 µm ($\overline{x}$ = 130 × 269 µm, n = 10) pycnidial, solitary or aggregated, immersed, uni- or multilocular, globose to subglobose, or irregular, black, with central ostiole. *Conidiomatal wall* 10–20 µm wide, comprising 4–5 cell layers of thick-walled, hyaline to pale brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–7 × 4–6 µm ($\overline{x}$ = 5.9 × 5.2 µm, n = 30), enteroblastic, phialidic with periclinal wall thickening or percurrent proliferations near the apex, hyaline, ampulliform or subcylindrical. *Conidia* 6–8 × 3–4 µm ($\overline{x}$ = 7 × 3.8 µm, n = 30), subglobose to cylindrical, initially hyaline, becoming pale brown to brown when mature, aseptate, thin and smooth-walled, with small guttules. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 12 h, reaching 30–40 mm in two weeks at 25°C. Colonies on PDA circular, with filiform margin, flat, smooth, superficial mycelia, velvety, from above white; from below white to pale yellow.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS1-C22 (MHZU 24-0544), living culture ZHKUCC 24-0993, other living culture ZHKUCC 24-0994.

GenBank numbers: ZHKUCC 24-0993: ITS = PQ608316, LSU = PQ608149, SSU = PQ608003, *TEF*1-α = PQ628162; ZHKUCC 24-0994: ITS = PQ608317, LSU = PQ608150, SSU = PQ608004, *TEF*1-α = PQ628163.

Known hosts: On dead twigs of *Ficus* sp. (Phukhamsakda et al., 2022), *Coffea* sp. (This study).

Known distribution: Thailand (Phukhamsakda et al., 2022), China (This study).

Notes: Paraconiothyrium fici was introduced as a saprobe on dead twigs of *Ficus* sp. in Thailand (Phukhamsakda et al., 2022). The multi-gene phylogenetic analysis of combined LSU, ITS, SSU, and *TEF*1-α sequence data revealed that our new strains form a sister lineage to the type species *P. fici* (MFLUCC 17-0883) with 100% ML and 1.00 BYPP statistical bootstrap support (Figure 2.50). The morphology of our collection is basically the same as *P. fici* (Phukhamsakda et al., 2022; Figure 2.51). Therefore, we identified our collection as *P. fici,* which is a new host record and country record form *Coffea* sp. in China.

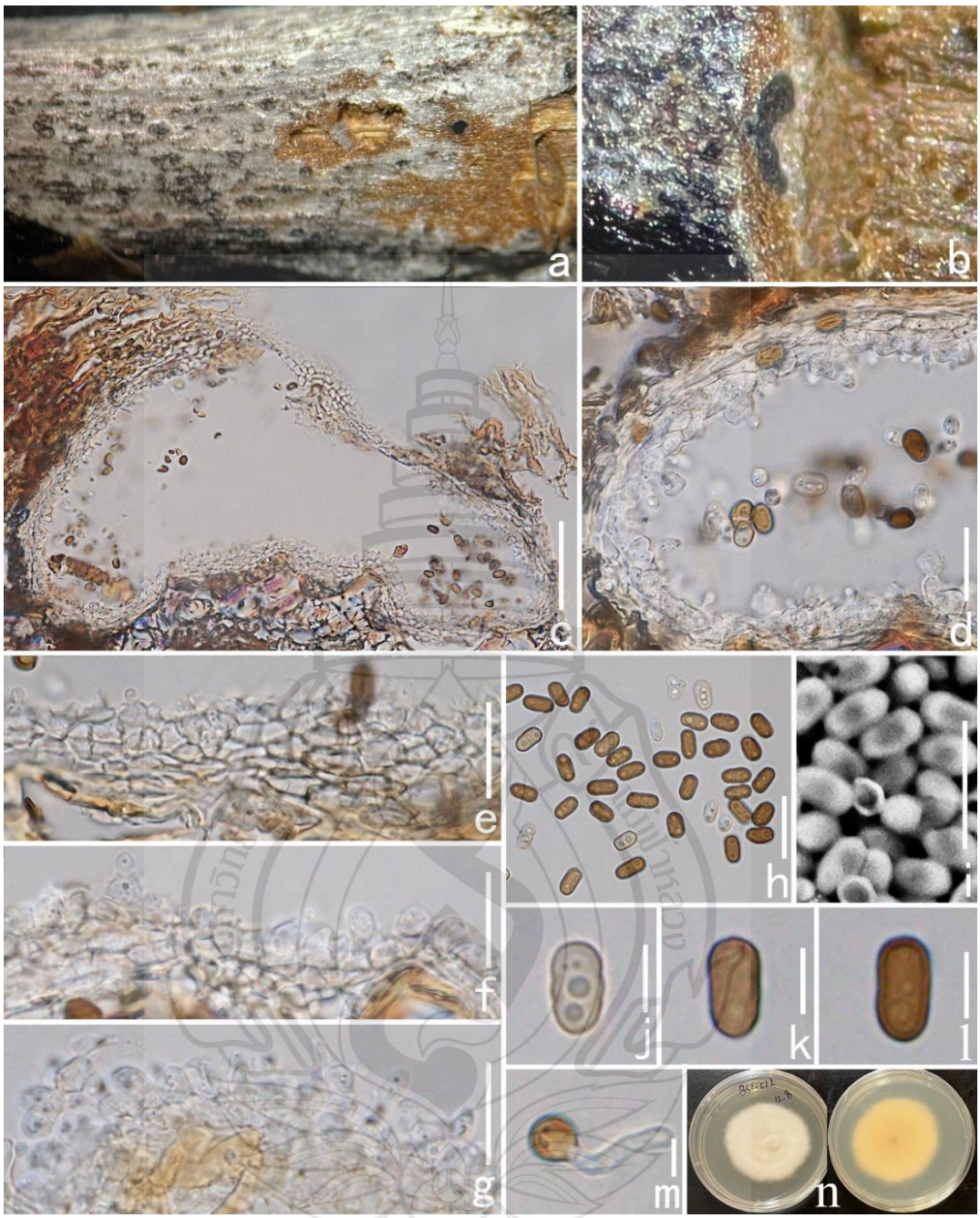


Figure 2.63 *Paraconiothyrium fici* (MHZU 24-0544, new host and country record)

Figure 2.63 a, b Conidiomata on a decaying branch of *Coffea* sp. c Longitudinal section of a conidioma. d–g Conidioma wall and conidiogenous cells. h–l Conidia (i: SEM microphotographs of conidia). m Germinated conidium. n Culture on PDA from above and below. Scale bars: c = 50 µm, d–i = 15 µm, j–m = 5 µm.

Paraconiothyrium yunnanensis L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 559424; *Facesoffungi number*: FoF 12764; Figure 2.53

Etymology: Name reflects the location "Yunnan" Province, where the holotype was collected.

Holotype: ZHKU 22-0114

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 150–250 × 160–260 μm ($\bar{x}$ = 193 × 214 μm, n = 20), solitary, scattered, immersed to semi-immersed, brown to black, globose or subglobose, coriaceous, small papilla, with small ostiole, ostiolar canal lined without hyaline periphyses. *Peridium* 16–28μm ($\bar{x}$ = 22μm, n = 20) wide, thick, composed of 4–6 layers *textura prismatica* cells, yellowish to brown. *Hamathecium* 1.5–3 μm wide ($\bar{x}$ = 2.2 μm, n = 20), hyaline, branched and septate, numerous pseudoparaphyses. *Asci* 60–110 × 8–11 μm ($\bar{x}$ = 79 × 9.3 μm, n = 30), 8-spored, bitunicate, fissitunicate, oblong or cylindrical, short-stalked, some with club-like pedicel, slightly curved. *Ascospores* 15 – 18 × 4 – 5 μm ($\bar{x}$ = 16 × 4.6, n = 30), biseritate or partially overlapping, fusiform or ellipsoidal, yellowish to light brown, 2–4-septate, smooth-walled, penultimate cell enlarged, without sheath and guttulate. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinated within 12 h on PDA, growing on PDA reaching around 40 mm after one month at room temperature (25°C). Colonies circular, filiform, mycelium raised, dark green, a lot of aerial hyphae in edges, the center of the reverse is brown with dark green edges.

Material examined: China, Yunnan Province, Xishuangbanna, on a decaying branch of *Coffea* sp., (1672 m), 12 September 2021, LiLu, JHMH 7 (ZHKU 22-0114, holotype), living culture ZHKUCC 22-0196 = ZHKUCC 22-0197.

GenBank numbers: ITS: OP297797, LSU: OP297767, SSU: OP297781, *tef*1-α: OP321566, *rpb*2: OP321560 (ZHKUCC 22-0196, ex-type); ITS: OP297798, LSU: OP297768, SSU: OP297782, *tef*1-α: OP321567, *rpb*2: OP321561 (ZHKUCC 22-0197).

Notes: Phylogenetic analyses show that *Paraconiothyrium yunnanensis* is well-separated from *Paraco. fungicola* with 100% ML, 1.00 BYPP statistical support (Figure 2.1). Based on BLAST search results of sequence data, ITS and LSU are closely

related to *Paraco. fungicola*, with similarity rates of 98.9% (MK619287) and 99.8% (JX496133), SSU is 99.8% similar to *Paraco. variabile* (KM096136), *rpb*2 is 88% (MT473955) similar to *Paraconiothyrium* sp., and *tef*1-α is 97% (LT797134) similar to *Paraco. cyclothyrioides*. In morphological characteristics, our new species is similar to *Paraco. magnoliae* in having ellipsoidal, yellowish to light brown, and septate ascospores (Tennakoon et al., 2016); However, the difference between our new species and *Paraco. magnoliae* is that ascospores have 2 or 4 septa, without sheath, and the penultimate cell is enlarged, while *Paraco. magnoliae* ascospores have three septa, a sheath, and a distinct guttule. Therefore, our isolate is described as a new species from *Coffea* sp. in China.

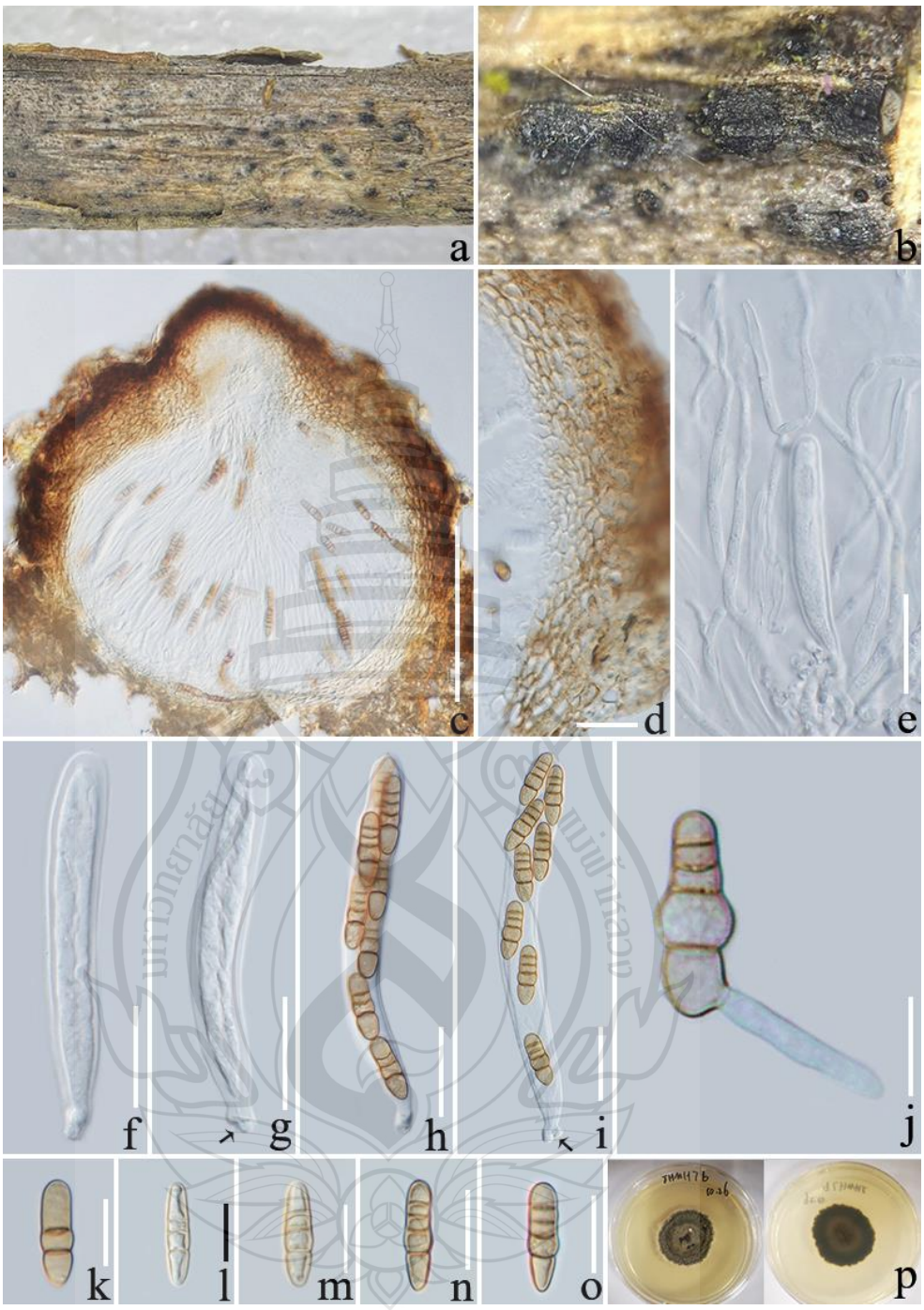


Figure 2.64 *Paraconiothyrium yunnanensis* (MHZU 22-0114, holotype)

Figure 2.64 a,b Ascomata on a decaying branch of *Coffea* sp.; c Vertical section of an ascoma; d Peridium; e Pseudoparaphyses; f–i Asci, arrows indicate club-like pedicel; j Germinated ascospore; k–o Ascospores; p Culture on PDA from above and reverse (30 days). Scale bars: c = 100 µm; d–i = 15 µm; j–o = 10 µm.

Paraconiothyrium fungicola Verkley & Wicklow, in Verkley, da Silva, Wicklow & Crous, Stud. Mycol. 50(2): 331 (2004)

Index Fungorum number: IF 500084

Synonyms: *Paracamarosporium fungicola* (Verkley & Wicklow) Wijayaw. & K.D. Hyde

Notes: Wijayawardene et al. (2016) transferred *Paraconiothyrium fungicola* (CBS 113269) to *Paracamarosporium* (*Paraca.*) as a new combination of *Paraca. fungicola* since it formed a clade with *Paraca. psoraleae* (CPC 21632) in the combined gene phylogeny of ITS, LSU and SSU. However, the phylogenetic tree of Wijayawardene et al. (2016) only contained two species of *Paraconiothyrium* viz. *Paraco. estuarinum* (CBS 109850) and *Paraco. cyclothyrioides* (CBS 432.75). However, our combined gene phylogenetic analyses of ITS, LSU, SSU, *rpb*2, and *tef*1-α included all *Paraconiothyrium* and *Paracamarosporium* species, showing that *Paraco. fungicola* still clusters within *Paraconiothyrium* and is closely related to *Paraco. magnoliae* (MFLUCC 10-0278). Our results are consistent with Wang et al. (2021). Based on nucleotide comparisons, *Paraco. fungicola* (CBS 113269) is different from *Paraca. psoraleae* (CPC 21632) by 38/552 bp (6.8%) of the ITS, 3/896 bp (0.3%) of the LSU, while different from *Paraco. magnoliae* (MFLUCC 10-0278) in 33/524 bp (6.2%) of the ITS, and 0/899 bp (0%) of the LSU. In addition, the morphology also fits with the characteristics of *Paraconiothyrium* (Tibpromma et al., 2018). Therefore, we recommend that *Paraco. fungicola* should be transferred back to the genus *Paraconiothyrium* as first reported by Verkley et al. (2004).

Xenocamarosporium Crous & M.J. Wingf., Persoonia 34: 185 (2015)

Notes: *Xenocamarosporium* (*X.*) was first proposed to include *Camarosporium* complex by Crous et al. (2015), and the type species *X. acaciae* was an asexual morph isolated from leaf spots of *Acacia mangium* in Malaysia (Crous et al., 2015). Later, the sexual morph of *X. acaciae* was introduced by Jayasiri et al. (2019) from a decaying pod of *Leucaena* sp. as a saprotrophic fungus in Thailand. The asexual characteristics of this genus are brown and globose conidiomata, brown textura angularis cells of peridium, hyaline and smooth conidiogenous cell, lining the inner conidiomatal cavity and ellipsoidal to subcylindrical, hyaline to golden-brown, verruculose, septate conidia (Crous et al., 2015). The sexual characteristics of this genus

are brown and immersed ascomata, textura angularis cells of peridium, filiform and septate hamathecium, bitunicate, cylindrical to cylindric-clavate, asci and hyaline to brown, cylindrical, septate, often enlarged at the fourth cell of ascospores (Tennakoon et al., 2019). To date, the genus consists of only one species (Tennakoon et al., 2019). Here, we introduce one new host and country record in *Xenocamarosporium* for coffee in China.

Xenocamarosporium acaciae Crous & M.J. Wingf., Persoonia 34: 185 (2015) (Figure 2.8)

Index Fungorum number: IF 812423; Facesoffungi number: FoF 05248

Saprotrophic on decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 100–200 × 110–200 µm ($\overline{x}$ = 177 × 169 µm, n = 15), immersed, subglobose, scattered, solitary, uniloculate, with short ostiole penetrating through host surface becoming brown to black spots on substrate. *Peridium* 14–19 µm wide ($\overline{x}$ = 16.9 µm; n = 20), unequal thickness, composed of 3–4 layers of hyaline to light brown, pseudoparenchymatous cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide ($\overline{x}$ = 2.1 µm, n = 20), consisting of sparse, filamentous, numerous, with a distinct constricted septum. *Asci* 60–80 × 9–11 µm ($\overline{x}$ = 71.5 × 10 µm; n = 20), bitunicate, 8-spored, cylindrical to cylindric-clavate, with short pedicellate or absent, apically rounded with an indistinct ocular chamber. *Ascospores* 13–19 × 4–5.5 µm ($\overline{x}$ = 15.8 × 4.7 µm; n = 30), uniseriate or overlapping, hyaline to brown, cylindrical, narrower and longer at the lower cell, 2–5-septate, often enlarged at the fourth cell, conical at the top. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated in PDA within 12 hours. Colonies reaching 50 mm diam. after two months at 25°C, surface yellow-gray to white, margins with aerial mycelium, circular, flatted, the reverse side is brown to light yellow.

Material examined: China, Yunnan Province, Xishuangbanna, on a decaying branch of *Coffea* sp., (101°2'44" E, 22°31'18" N, 856.9 m), 15th September 2021, Li Lu, JHPW 9 (ZHKU 22-0117), ZHKUCC 22-0202 = ZHKUCC 22-0203.

GenBank number: ITS: OP297805, LSU: OP297775, SSU: OP297789, *tef*1-α: OP321574, (ZHKUCC 22-0202); ITS: OP297806, LSU: OP297776, SSU: OP297790, *tef*1-α: OP321575, (ZHKUCC 22-0203).

Known hosts: Acacia mangium (Crous et al., 2015), *Leucaena* sp. (Tennakoon et al., 2019), *Coffea* sp. (This study).

Known distribution: Malaysia (Crous et al., 2015), Thailand (Tennakoon et al., 2019), China (This study)

Notes: In phylogeny, our strains form a clade with *Xenocamarosporium acaciae*, and the BLAST results of ITS, LSU, SSU, and *tef*1-α of our strain give 100% (MK347766), 99% (MK347983), 99.9% (MK360093) and 99.9% (MK347873) similarities with *X. acaciae*, respectively. Furthermore, the comparison of morphological characteristics of asci and ascospores shows that our isolate is highly consistent with the sexual morph of *X. acaciae* morphologically (Tennakoon et al., 2019). Therefore, in this study, *X. acaciae* (ZHKU 22-0117) is reported as a new host record and country record from coffee in China.

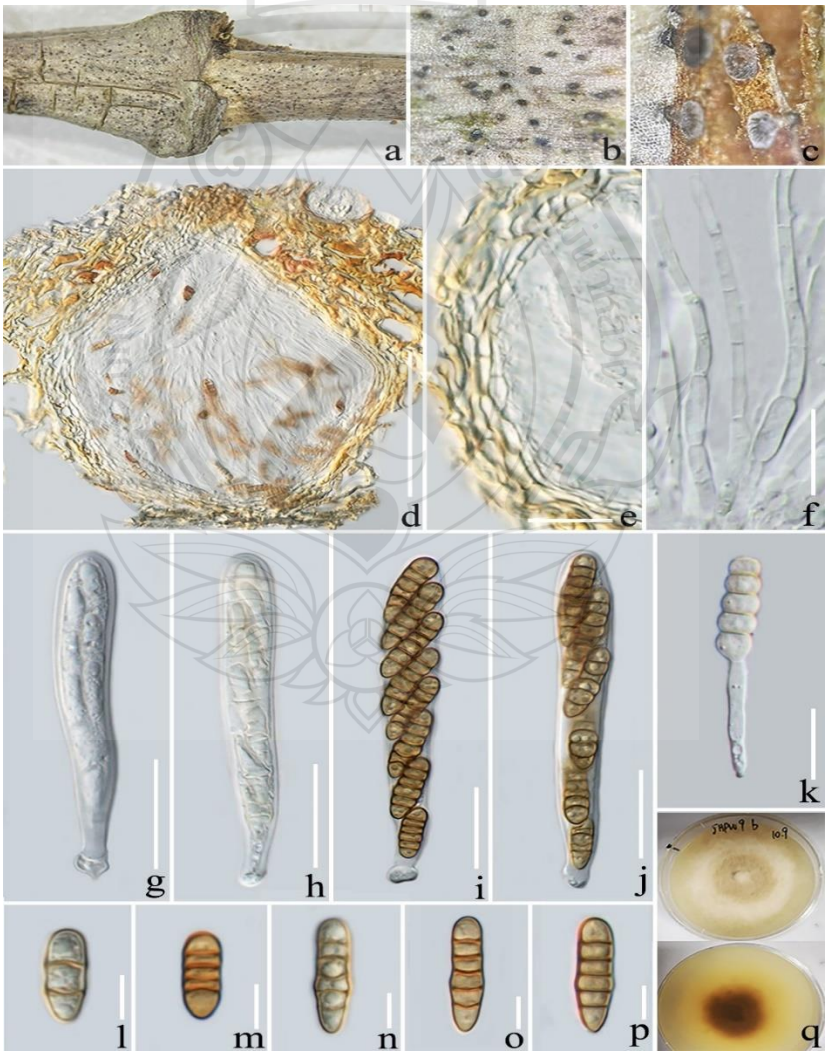


Figure 2.65 *Xenocamarosporium acaciae* (ZHKU 22-0117)

Figure 2.65 a,b Appearance of ascomata on a decaying branch of *Coffea* sp.; c–d Vertical section of an ascoma; e Peridium; f Pseudoparaphyses; g–j Asci; k Germinated ascospore; l–p Ascospores; q Culture on PDA from above and reverse (60 days). Scale bars: d = 100 µm; e–f = 15 µm; g–k = 20 µm; l–p = 5 µm.

Didymellaceae Gruyter, Aveskamp & Verkley, Mycological Research 113 (4): 516 (2009)

Xenodidymella Qian Chen & L. Cai, Stud. Mycol. 82: 205 (2015).

Notes: *Xenodidymella* typified by *X. applanate* (Niessl) Qian Chen & L. Cai, was established by Chen et al. (2015) to accommodate several phoma-like taxa. The new species, *X. coffeae*, is introduced here through phylogenetic and morphological comparisons and isolated from the Arabica coffee plant in China. This is the first *Xenodidymella* species reported from coffee.

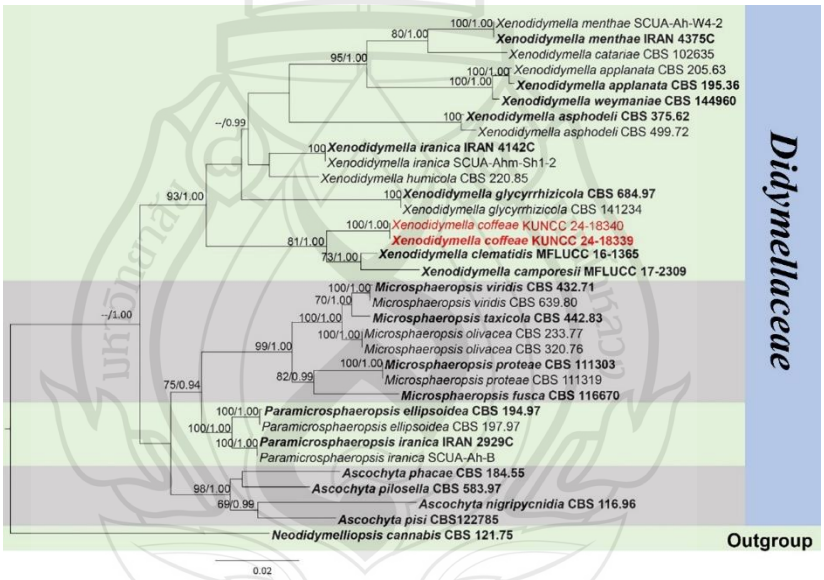


Figure 2.66 Phylogenetic tree of *Xenodidymella*

Figure 2.66 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *TUB* and *RPB*2 sequence data. Thirty-four are included in the combined sequence analysis, which comprises 2,246 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Neodidymelliopsis cannabis* (CBS 121.75).

Xenodidymella coffeae L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 901000; *Facesoffungi number*: FoF 14726; Figure 2.53

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137610

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph:** *Conidiomata* 50–80 µm high × 50–90 µm diam. ($\overline{x}$ = 62 × 70 µm, n = 20), separate or scattered, semi-immersed, black, globose to subglobose or pyriform, pycnidial, with short ostioles. *Conidiomatal wall* 6–12 µm wide ($\overline{x}$ = 9 µm, n = 30), composed of 1–3 layers of light brown to brown cells of *textura angularis*, heavily pigmented at the outer layers, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* inconspicuous or micronematous, often reduced to conidiogenous cells. *Conidiogenous cells* lining inner cavity, 4–6 × 4–7 µm ($\overline{x}$ = 5.3 × 5.4 µm, n = 30), hyaline, globose to ampulliform, enteroblastic, phialidic. *Conidia* 10–15 × 3–4 µm ($\overline{x}$ = 12 × 3.3 µm, n = 30), solitary, hyaline, oblong to cylindrical with rounded ends, aseptate, mostly straight, surface smooth or rough. **Sexual morph:** Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h, colonies reached 6 cm in diameter after two months at 25°C, filamentous, filiform margin, smooth, flat, with aerial mycelium, from above, brown at the centre, dark brown at the edge, from below, dark brown to black.

Material examined: China, Yunnan Province, Dali, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (26°09' N, 101°91' E, 1415 m alt.), 25 July 2022, LiLu, DL-C11 (HKAS 137610, holotype), isotype MHZU 23-0064, ex-type living culture KUNCC 24-18339 = KUNCC 24-18340, ex-isotype living culture ZHKUCC 23-0638 = ZHKUCC 23-0639.

GenBank numbers: KUNCC 24-18339: ITS = OR428407, LSU = OR428429, TUB = OR509743, *RPB2* = OR515527; KUNCC 24-18340: ITS = OR428408, LSU = OR428430, TUB = OR509744, *RPB2* = OR515528.

Notes: In the concatenated phylogenetic analysis, *Xenodidymella coffeae* shows a close relationship with *X. clematidis* and *X. camporesii* D. Pem, Doilom & K.D. Hyde (Figure 2.7). *Xenodidymella coffeae* conforms to the characteristics of *Xenodidymella*

by globose to ampulliform conidiogenous cells and hyaline conidia (Hyde et al., 2020). *Xenodidymella coffeae* has short ostioles and cylindrical conidia, while *X. clematidis* has long ostioles with oblong-elliptical or oval conidia (Figure 2.6; Phukhamsakda et al., 2020). Besides, the conidia of our species are larger than those of *X. clematidis* (10–15 × 3–4 µm vs. 4–8 × 2–5 µm). *Xenodidymella camporesii* has only been reported based on its teleomorph (Hyde et al., 2020). Based on nucleotide comparisons, *X. coffeae* (ZHKUCC 23-0638) is different from *X. clematidis* (MFLUCC 16-1365) by 8/482 bp (1.6%, without gaps) of the ITS, 11/786 bp (1.4%, without gaps) of the LSU; and different from *X. camporesii* (MFLUCC 17-2309) by 10/518 bp (2%, with one gap) of the ITS, 16/890 bp (1.8%, without gaps) of the LSU and 26/282 bp (9%, without gaps) of the *TUB*. This fungus is, therefore, introduced as a new species of *Xenodidymella*, following the guidelines of Chethana et al. (2021) and Pem et al. (2021).



Figure 2.67 *Xenodidymella coffeae* (HKAS 137610, holotype)

Figure 2.67 A, B Conidiomata on a decaying branch of *C. arabica*; C, D Longitudinal section of a conidioma and conidioma wall; E Conidiogenous cells with conidia; F–K Conidia; L Germinated conidium; M Culture on PDA from obverse and reverse. Scale bars: C, D, K, L = 20 µm, E–J = 10 µm.

Halotthiaceae Y. Zhang, J. Fourn. & K.D. Hyde, Mycologia 105 (3): 604 (2013)

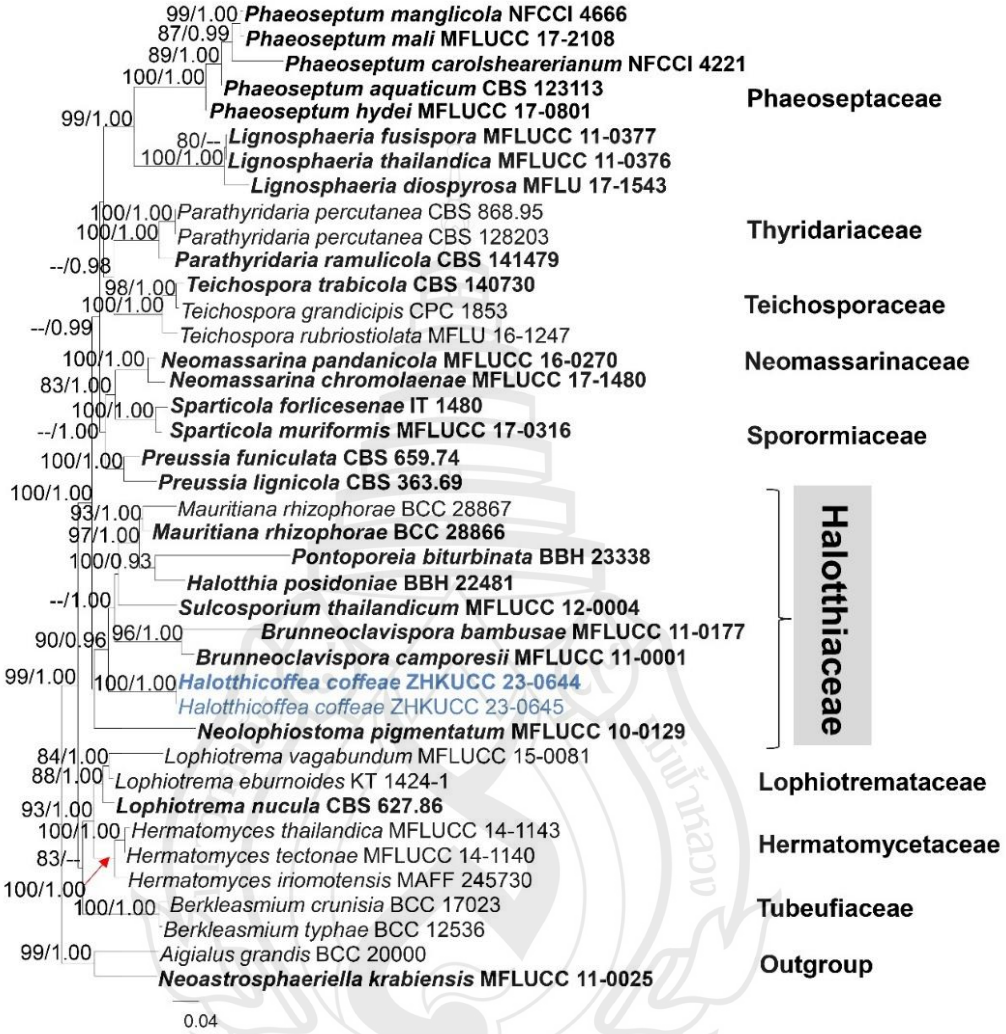


Figure 2.68 Phylogenetic tree of *Halotthicoffea*

Figure 2.68 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, and SSU sequence data. Forty strains are included in the combined sequence analysis, which comprises 2,496 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Aigialus grandis* (BCC 20000) and *Neoastrosphaeriella krabiensis* (MFLUCC 11-0025).

Halotthicoffea L. Lu, K.D. Hyde & Tibpromma, *gen. nov.*

Index Fungorum number: IF 903612; *Facesoffungi number:* FoF 17566

Etymology: The genus name refers to the host genus "*Coffea*" and family name "Halotthiaceae"

Type species: *Halotthicoffea coffeae*

Saprobic on dead or decaying plants. **Sexual morph:** *Ascomata* solitary, semi-immersed, uni-loculate, black, carbonaceous, elongate-conical with a flattened base, forming under a pseudoclypeus, with ostioles. *Ostioles* central, acute, papillate, periphyses lining the inner surface. *Peridium* comprising several layers of dark brown cells of *textura angularis*, some fusing with the substrate. *Hamathecium* comprising numerous, cellular, aseptate and unbranched, pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, long cylindrical, short pedicellate, some club-like, rounded at the apex, with an ocular chamber. *Ascospores* uniseriate to biseriate, fusiform to oblong, both ends rounded, phragmosporous, constricted at the middle septum, normally the second cell enlarged, hyaline to reddish brown, dark brown when mature, thick-walled with rough surface, guttulate, without a sheath. **Asexual morph:** Not observed.

Notes: *Halotthicoffea* formed separate branches in Halotthiaceae with 90% ML, 0.96 BYPP statistical support (Figure 2.52). In morphology, *Halotthicoffea* fits the genetic description of Halotthiaceae in having immersed ascomata, forming under a pseudoclypeus, bitunicate asci and phragmosporous, brown to dark brown ascospore (Zhang et al., 2013; Figure 2.53). It however, differs from other genera by the distinct shape of ascospore, which are fusiform to oblong, with the second cell enlarged, and thick and rough-walls (Zhang et al., 2013; Ariyawansa et al., 2015; Figure 2.53). Both morphological and molecular data confirmed *Halotthicoffea* as a distinct genus within the Halotthiaceae, with *Halotthicoffea coffeae* as the type species. This species was isolated from decaying coffee plants in China.

Halotthicoffea coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903613; *Facesoffungi number*: FoF 17567; Figure 2.53

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 23-0067

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 280–520 × 260–370 μm ($\bar{x}$ = 433× 310 μm, n = 15), solitary, immersed, uni-loculate, black, carbonaceous, elongate conical with a flattened base, forming under a pseudoclypeus, ostiolate. *Ostioles* central, papillate, periphyses line the inner surface of the ostiole. *Peridium* 15–25 μm wide ($\bar{x}$ = 19 μm, n = 20), comprising several layers of dark brown cells of *textura angularis*, some fusing with the substrate. *Hamathecium* of 2–3 μm wide ($\bar{x}$ = 2.3 μm, n = 30), comprising numerous, cellular, aseptate and unbranched, pseudoparaphyses. *Asci* 100–140 × 10–13 μm ($\bar{x}$ = 128 × 12.4 μm, n = 30), 8-spored, bitunicate, fissitunicate, long cylindrical, short pedicellate, some club-like, rounded at the apex, with an ocular chamber. *Ascospores* 17–20 × 7–10 μm ($\bar{x}$ = 18.6 × 8.9 μm, n = 30), uniseriate to biseriate, fusiform to oblong, both end rounded, 1–3-septate, constricted at the middle septum, normally the second cell enlarged, hyaline to reddish brown, dark brown when mature, thick-walled and rough surface, guttulate, without a sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospore germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm in one month at 25°C, smooth surface, slightly raised, circular with entire margin, radially furrowed at the center, velvety, from above grayish-brown, from below, dark brown to black, wrinkled.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (1672 m), 12th September 2021, Li Lu, JHMH 5 (MHZU 23-0067, holotype), ex-type ZHKUCC 23-0644, other living culture ZHKUCC 23-0645.

GenBank numbers: ZHKUCC 23-0644: ITS = PQ608250, LSU = PQ608083, SSU = PQ607943, *RPB*2 = PV165376, *TEF*1-α = PV165378; ZHKUCC 23-0645: ITS = PQ608251, LSU = PQ608084, SSU = PQ607944, *RPB*2 = PV165377, *TEF*1-α = PV165379.

Notes: Based on the phylogenetic analysis of combined LSU, ITS, and SSU sequence data, *Halotthicoffea coffeae* forms a separate lineage within Halotthiaceae (Figure 2.52). In morphology, *H. coffeae* can distinguished with other genera by fusiform to oblong, 1–3-septate, hyaline to reddish brown, thick-walled ascospores, brown when mature, and with rough surface (Zhang et al., 2013; Ariyawansa et al., 2015; Hyde et al., 2020; Figure 2.53). Herein we introduce *H. coffeae* as a new species based on both morphological comparison and phylogenetic analyses.

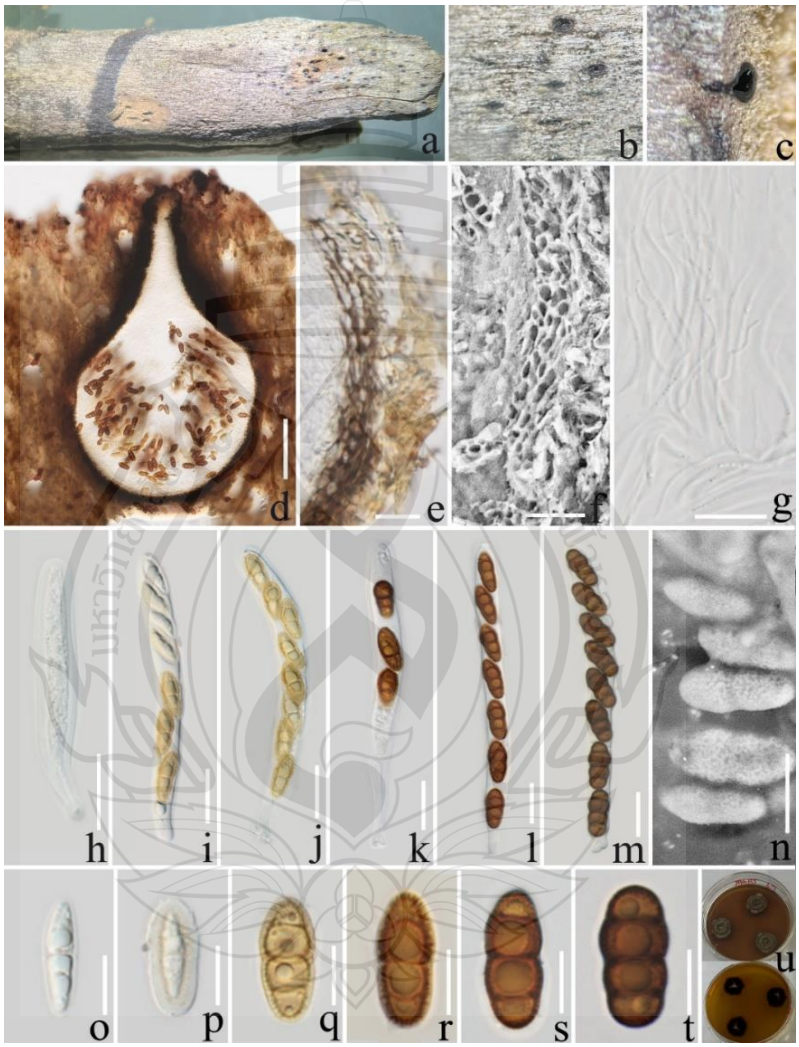


Figure 2.69 *Halotthicoffea coffeae* (MHZU 23-0067, holotype)

Figure 2.69 a, b Ascomata on host surface. c, d Longitudinal section through ascomata. e Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–m Asci. n–t Ascospore (n: SEM microphotographs of ascospores). u Culture on PDA from above and below. Scale bars: d = 100 µm, e–m = 20 µm, n–t = 10 µm.

Longiostiolaceae Phukhams., Doilom and K.D. Hyde, Fungal Diversity 102: 43 (2020)

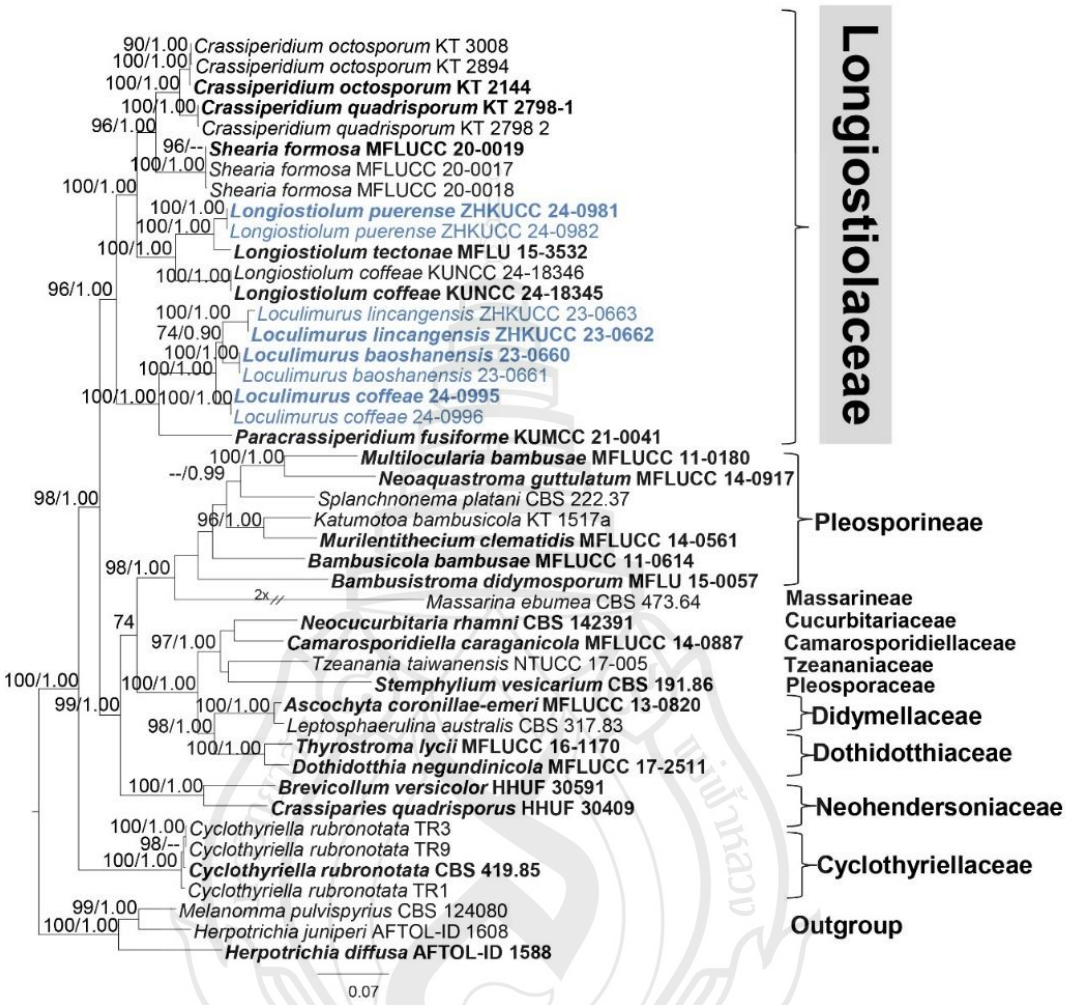


Figure 2.70 Phylogenetic tree of Longiostiolaceae

Figure 2.70 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Forty-five strains are included in the combined sequence analysis, which comprises 4,420 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Melanomma pulvispyrius* (CBS 124080), *Herpotrichia juniperi* (AFTOL-ID 1608), and *H. diffusa* (AFTOL-ID 1588).

Loculimurus L. Lu, K.D. Hyde & Tibpromma, *gen. nov.*

Index Fungorum number: IF 903618; *Facesoffungi number*: FoF 17568

Etymology: The genus name refers to the multilocular ascomata and muriform ascospores.

Type species: *Loculimurus coffeae*

Saprobic on dead or decaying plants. **Asexual morph:** Coelomycetous. *Conidiomata* solitary or aggregated, globose to subglobose, semi-immersed to immersed, multiloculate, brown to black, carbonaceous, erumpent when mature, ostiolate. *Ostioles* central, papillate. *Conidiomatal wall* comprising several layers of hyaline to brown cells of *textura angularis* or *textura globulosa*. *Conidiophores* mononematous and micronematous, or reduced to conidiogenous cells. *Conidiogenous cells* cylindrical to ampulliform. *Conidia* dictyosporous, oval to ellipsoid, muriform or obovoid, hyaline to yellowish, to brown, slightly constricted at each septate, bud scars disjunctors at base, smooth-walled, without sheath. **Sexual morph:** Not observed.

Notes: The new genus *Loculimurus* was introduced to accommodate three species collected from coffee hosts in Yunnan, China. These species were grouped and formed independent branches within the Longiostiolaceae family in the phylogenetic analysis (Figure 2.54). In morphology, *Loculimurus* fits the genetic description of Longiostiolaceae (Phukhamsakda et al., 2020); however, it differs from the other genera by multiloculate conidiomata, erumpent when mature, dictyosporous ascospores, oval to ellipsoid, muriform or obovoid (Matsumura et al., 2018; Phukhamsakda et al., 2020; Jayasiri et al., 2024; Figure 2.55). Therefore, *Loculimurus* is introduced in Longiostiolaceae with three new species, *Loculimurus baoshanensis*, *L. coffeae* (type species), and *L. lincangensis*.

Loculimurus baoshanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903619; *Facesoffungi number*: FoF 17569; Figure 2.55

Etymology: The species epithet refers to the type location “Baoshan”, China.

Holotype: MHZU 23-0075

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–180 × 100–180 µm ($\bar{x}$ = 142× 146 µm, n = 15), solitary to aggerated, globose to subglobose, immersed, multiloculate, brown to black

spots on host. *Conidiomatal wall* 10–15 µm wide ($\overline{x}$ = 12 µm, n = 20), thin-walled, comprising 2–3 layers of hyaline to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 2.5–5 µm ($\overline{x}$ = 7.7 × 3.6 µm, n = 30), enteroblastic, phialidic, determinate, pyriform to ampulliform, hyaline, smooth-walled, arising from the inner cavity of the conidiomata. *Conidia* 10–15 × 7–10 µm ($\overline{x}$ = 13 × 8.2 µm, n = 30), dictyosporous, oval to ellipsoid, muriform, with round ends, yellowish to dark brown, 1–4 transverse septate, with rounded at apex, tapering towards a slightly curved base, smooth-walled, surface smooth, without a sheath. **Sexual morph:** Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm in one month at 25°C, circular, slight raised, with filamentous edge, floccose or woolly, density, with a lot of aerial hyphae, from above, light gray, from below, cream-colored outside, brown at center, wrinkled.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS1-C15 (MHZU 23-0075, holotype), ex-type ZHKUCC 23-0660, other living culture ZHKUCC 23-0661.

GenBank numbers: ZHKUCC 23-0660: ITS = PQ608254, LSU = PQ608087, SSU = PQ607947, *RPB*2 = PV186825, *TEF*1-α = PQ602128; ZHKUCC 23-0661: ITS = PQ608255, LSU = PQ608088, SSU = PQ607948, *RPB*2 = PV186826, *TEF*1-α = PQ602129.

Notes: In our phylogeny, *Loculimurus baoshanensis* forms a separate lineage sister *L. coffeae* and *L. lincangensis* with 100% ML and 1.00 BYPP statistical support (Figure 2.54). In morphology, *Loculimurus baoshanensis* can be distinguished from *L. coffeae* and *L. lincangensis* by the thin-walled conidiomatal wall, pyriform to ampulliform conidiogenous cells, and oval to ellipsoid conidia (Figure 2.55, 2.56, 2.57). Nucleotide comparisons among the three species, *viz., L. baoshanensis* (ZHKUCC 23-0660, ex-type), *L. coffeae* (ZHKUCC 24-0995, ex-type), and *L. lincangensis* (ZHKUCC 23-0662, ex-type), are mentioned in Table 2.3. In addition, the PHI test results (Figure 2.58) revealed no significant recombination relationships between *L. baoshanensis*, *L. coffeae* and *L. lincangensis*. Therefore, *L. baoshanensis* is introduced as a new species in *Loculimurus* based on both morphological comparison and phylogenetic analyses.

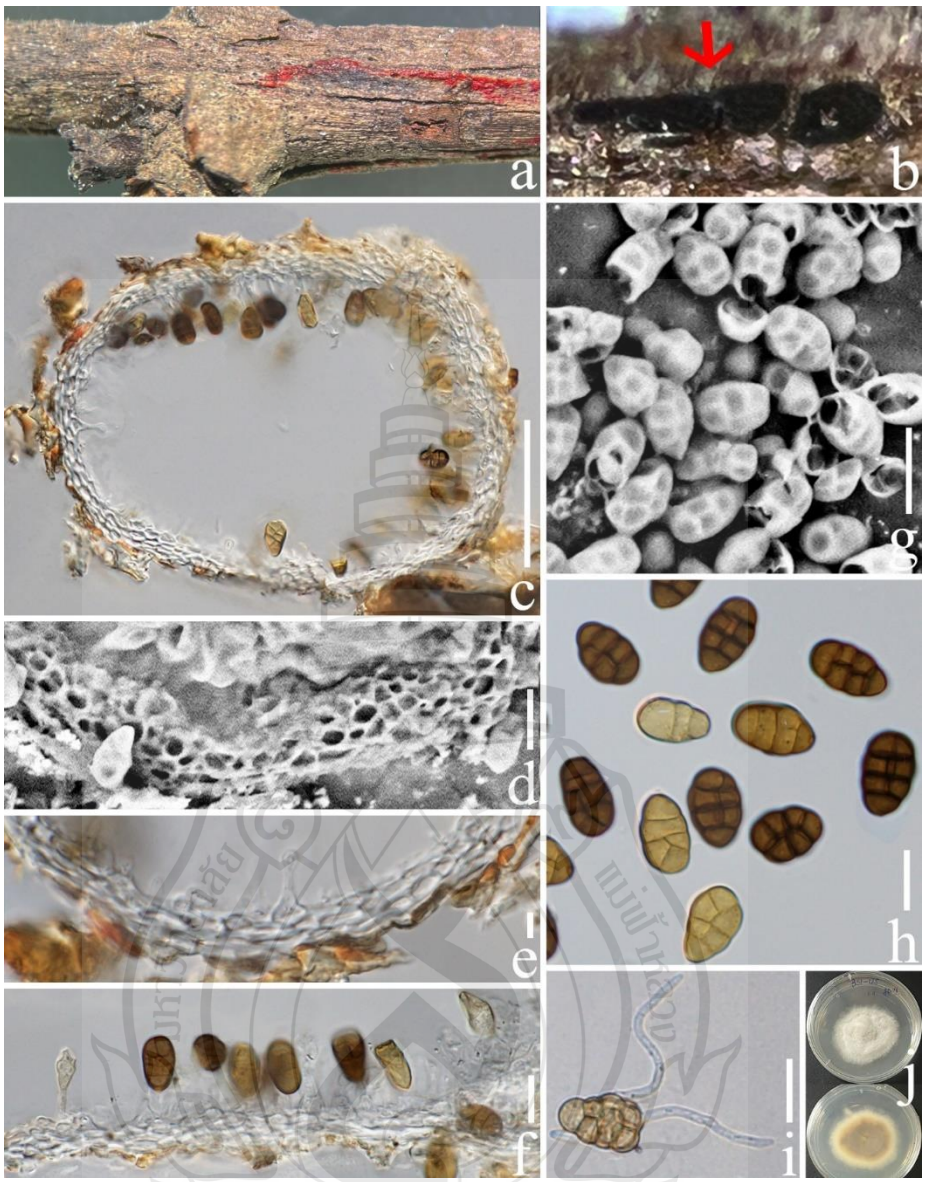


Figure 2.71 *Loculimurus baoshanensis* (MHZU 23-0075, holotype)

Figure 2.71 a, b Conidiomata on host surface (arrow indicates multilocules). c Longitudinal section through a conidioma. d SEM microphotographs of conidioma wall. e, f Conidiogenous cells with conidia. g–k Conidia (g: SEM microphotographs of conidia). l Germinated conidium. m Culture on PDA from above and below. Scale bars: c = 50 µm, d–i = 10 µm.

Loculimurus coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903620; *Facesoffungi number*: FoF 17570; Figure 2.56

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0545

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–200 × 160–240 μm ($\overline{x}$ = 140× 190 μm, n = 15), solitary, globose to subglobose, semi-immersed to immersed, erumpent when mature, multiloculate, brown to black, carbonaceous. *Conidiomatal wall* 12–18 μm wide ($\overline{x}$ = 14.5 μm, n = 20), thin-walled, comprising several layers of hyaline to brown cells of *textura angularis*, some fusing with the substrate. *Conidiophores* mononematous and micronematous, unbranched, or reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 2–5 μm ($\overline{x}$ = 7 × 2.7 μm, n = 30), enteroblastic, phialidic, hyaline, smooth-walled, subcylindrical. *Conidia* 15–20 × 7–10 μm ($\overline{x}$ = 17.2 × 8.7 μm, n = 30), dictyosporous, ellipsoid, muriform, with rounded at apex, a slightly curved or sub-acute at base, yellowish to brown, 3–5 transverse septate, slightly constricted at the septa, 0–4 longitudinal septate, surface smooth, without a sheath. **Sexual morph:** Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm in one month at 25°C, circular, flat, with filamentous margin, density, with a lot of aerial hyphae, velvety, from above white to light brown, from below, reddish brown to black.

Material examined: China, Yunnan Province, Nujiang City, on a decaying branch of *Coffea* sp. (25.80 N, 98.85 E, 1005 m), 22 April 2023, Li Lu, C-12 (MHZU 24-0545, holotype), ex-type ZHKUCC 24-0995, other living culture ZHKUCC 24-0996.

GenBank numbers: ZHKUCC 24-0995: ITS = PQ608256, LSU = PQ608089, SSU = PQ607949, *RPB*2 = PV186827, *TEF*1-α = PQ602130; ZHKUCC 24-0996: ITS = PQ608257, LSU = PQ608090, SSU = PQ607950, *RPB*2 = PV186828, *TEF*1-α = PQ602131.

Notes: Based on the phylogenetic analysis of combined LSU, SSU, *TEF*1-α, and *RPB*2 sequence data, *Loculimurus coffeae* forms a separate lineage within *Loculimurus* (Figure 2.54). In morphology, *Loculimurus coffeae* can be distinguished

from the other *Loculimurus* species by mononematous and micronematous conidiophores, longer conidia (Figure 2.56), and base pair comparison (see Table 2.3). Herein, we introduce *L. coffeae* as a new species based on both morphological comparison and phylogenetic analyses.

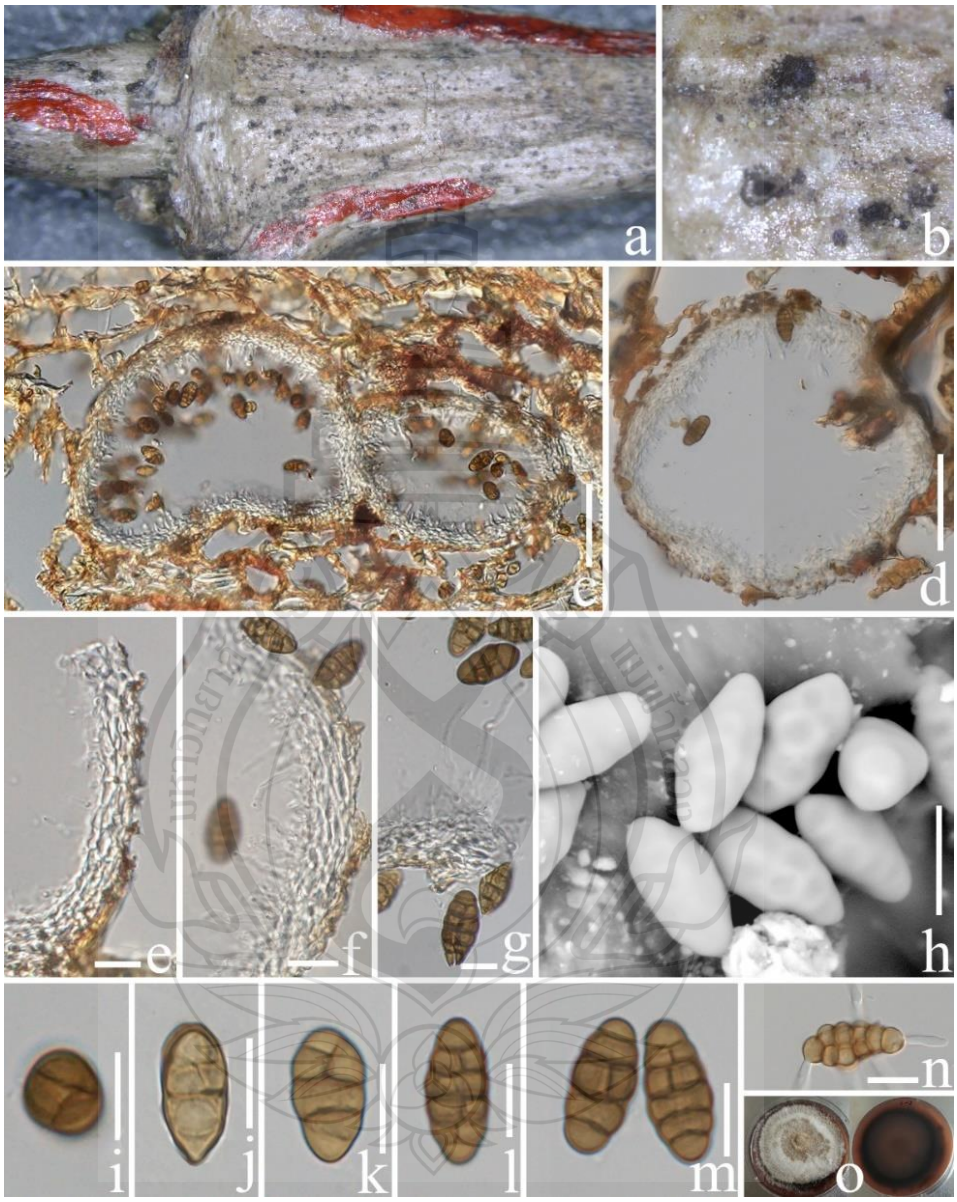


Figure 2.72 *Loculimurus coffeae* (MHZU 24-0545, holotype)

Figure 2.72 a, b Conidiomata on host surface. c, d Longitudinal section through conidiomata. e Conidioma wall. f, g Conidiophores and conidiogenous cells. h–m Conidia (h: SEM microphotographs of conidia). n Germinated conidium. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–n = 10 µm.

Loculimurus lincangensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903621; *Facesoffungi number*: FoF 17571; Figure 2.57

Etymology: The species epithet refers to the type location "Lincang", China.

Holotype: MHZU 23-0076

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–320 × 100–200 µm ($\overline{x}$ = 196× 140 µm, n = 15), solitary to aggregated, subglobose to oval, or inequilateral, semi-immersed to immersed, multiloculate, black spots on substrate, carbonaceous, ostiolate. *Ostioles* central, cylindrical. *Conidiomatal wall* 10–20 µm wide ($\overline{x}$ = 16 µm, n = 20), thin-walled, comprising several layers of hyaline to brown cells of *textura angularis*, some fusing with the substrate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–12 × 2–3.5 µm ($\overline{x}$ = 7.5 × 2.5 µm, n = 30), enteroblastic, phialidic, ampulliform to subcylindrical, determinate, hyaline. *Conidia* 10–15 × 7–9 µm ($\overline{x}$ = 13 × 7.6 µm, n = 30), dictyosporous, oval to obovoid, muriform, yellowish to brown, 1–4 transverse septate and longitudinal septate, slightly constricted at the septa, with rounded at apex, a slightly curved or sub-acute at base, surface smooth, without a sheath. **Sexual morph:** Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, circular, flat, with relatively entire margin, floccose or woolly, indicating a dense mycelial structure, especially concentrated in the center, from above, appears darker, light gray or pale brown, while the edges lighten toward the periphery, from below, cream-colored outside, brown at center, wrinkled.

Material examined: China, Yunnan Province, Lincang City, on a decaying branch of *Coffea* sp. (23.8 N, 99.4 E, 869 m), 28 July 2022, Li Lu, LC3-C6 (MHZU 23-0076, holotype), ex-type ZHKUCC 23-0662, other living culture ZHKUCC 23-0663.

GenBank numbers: ZHKUCC 23-0662: ITS = PQ608252, LSU = PQ608085, SSU = PQ607945, *RPB*2 = PV186823, *TEF*1-α = PQ602126; ZHKUCC 23-0663: ITS = PQ608253, LSU = PQ608086, SSU = PQ607946, *RPB*2 = PV186824, *TEF*1-α = PQ602127.

Notes: Based on the phylogenetic analysis of combined LSU, SSU, *TEF*1-α, and *RPB*2 sequence data, *Loculimurus lincangensis* forms a sister lineage to *L. coffeae* (Figure 2.54). In morphology, *L. lincangensis* can distinguished with the

holotype *L. coffeae* by absent mononematous and micronematous conidiophores, and oval to obovoid conidia (Figure 2.56, Figure 2.57). Nucleotide comparisons between *L. lincangensis* (ZHKUCC 23-0662, ex-type) and *L. coffeae* (ZHKUCC 24-0995, ex-type) shown in Table 2.3. Herein, we introduce *L. lincangensis* as a new species in *Loculimurus* based on both morphological comparison and phylogenetic analyses.

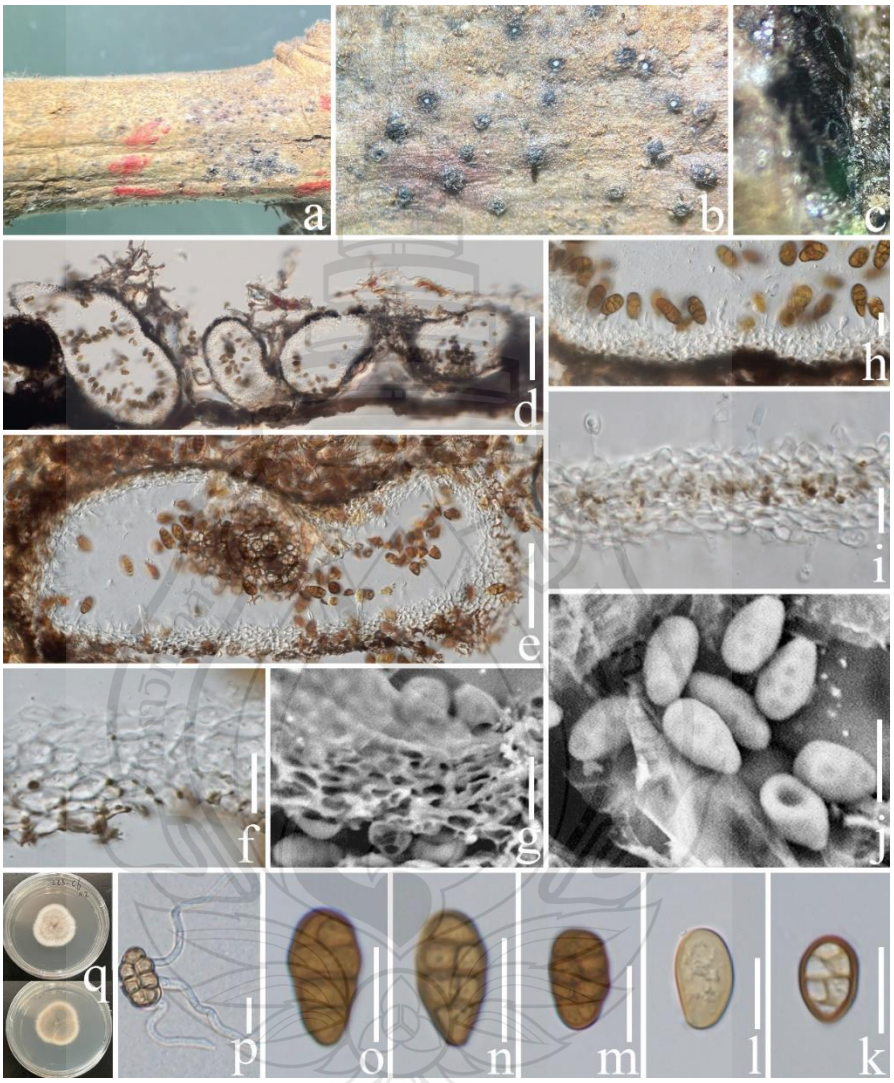


Figure 2.73 *Loculimurus lincangensis* (MHZU 23-0076, holotype)

Figure 2.73 a, b Conidiomata on host surface. c–e Longitudinal section through conidiomata. f, g Conidioma wall (g: SEM microphotographs of conidioma wall). h, i Conidiogenous cells with conidia. j–o Conidia (i: SEM microphotographs of conidia). p Germinated conidium. q Culture on PDA from above and below. Scale bars: d = 100 µm, e = 50 µm, f–p = 10 µm.

Table 2.3 Nucleotide differences in the LSU, SSU, *RPB*2, and *TEF*1-α (not trimmed sequence) of *Loculimurus* species. All sequences are without gaps

Species	LSU (%)	SSU (%)	*RPB*2 (%)	*TEF*1-α (%)
L. baoshanensis ZHKUCC 23-0660 vs. *L. coffeae* ZHKUCC 24-0995	1/853 (0.1%)	0/1029 (0%)	49/917 (5.3%)	48/957 (5%)
L. coffeae ZHKUCC 24-0995 vs. *L. lincangensis* ZHKUCC 23-0662	4/853 (0.4%)	0/1028 (0%)	48/947 (4.7%)	29/957 (3%)
L. lincangensis ZHKUCC 23-0662 vs. *L. baoshanensis* ZHKUCC 23-0660	5/860 (0.5)	0/1029 (0%)	38/925 (4.1%)	39/960 (4%)

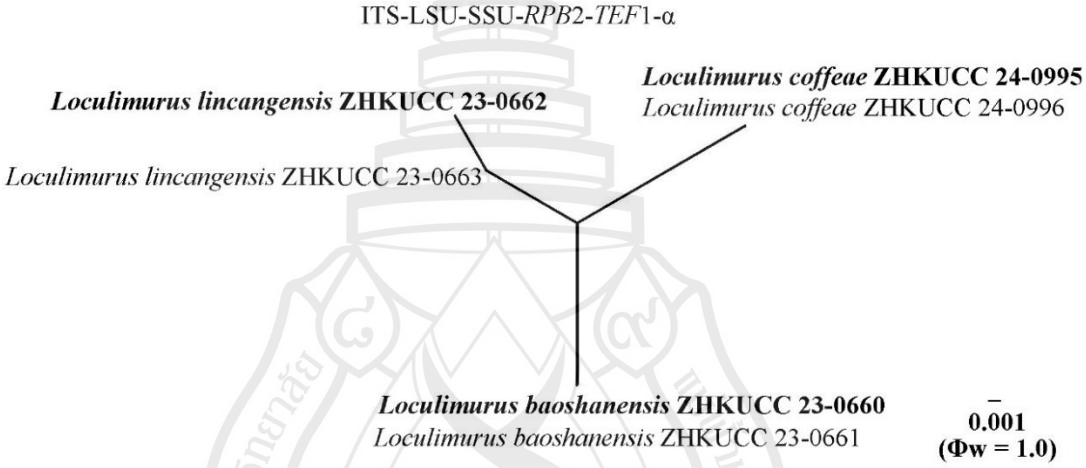


Figure 2.74 Split graphs of *Loculimurus*

Figure 2.74 Split graphs showing the results of the pairwise homoplasy index (PHI) test of three new taxa within the new genus *Loculimurus*, using LogDet transformation and splits decomposition. The PHI test result P-value (Φw) ≤ 0.05 indicates that there is significant recombination between the isolates included in the alignment. Bold strain indicates the type species, and PHI test value and scale bars are given in the bottom right corner.

Longiostiolum Doilom, Ariyaw. and K.D. Hyde, Fungal Diversity 78: 55 (2016)

Notes: Longiostiolum was introduced as a monotypic genus in the suborder Massarineae with *L. tectonae* as the type species by Li et al. (2016). Later, Phukhamsakda et al. (2020) transferred it to Longiostiolaceae based on phylogenetic analysis. Only two species are recorded in Index Fungorum (2025). The first species,

L. tectonae was collected as saprobes with sexual and asexual characteristics from the dead bark of *Tectona grandis* (Lamiaceae) from Thailand (Li et al., 2016), and the second species was isolated as saprobes on a decaying branch of *Coffea arabica* in Yunnan Province, China, with only the sexual morph (Lu et al., 2025). The sexual morph is characterized by immersed to semi-immersed ascomata, with a central ostiole, bitunicate, 8-spored, and clavate asci, with fusoid to narrowly fusoid, multi-septate ascospores. The asexual morph was found in culture and is characterized by branched, septate, and white to pale brown mycelium, conidia are produced on aerial mycelium having subglobose to ellipsoidal and without septate (Li et al.,, 2016). In this study, *L. coffeae* and *L. puerensis* are introduced from an arabica coffee plant in Yunnan, China.

Longiostiolum coffeae L. Lu & Tibpromma, sp. nov. Figure 2.10.

Index Fungorum number: IF 901002; *Facesofungi number:* FoF 14728.

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137602.

Saprobic on decaying branch of *C. arabica*. **Sexual morph**: *Ascomata* 160–280 µm high × 180–280 µm diam. ($\overline{x}$ = 212 × 238 µm, n = 15), black spots on the substrate, solitary to scattered, immersed to semi-immersed, when cut horizontally, locules visible as white contents, unilocular, globose to subglobose, with central and short ostioles. *Peridium* 20–30 µm thick ($\overline{x}$ = 23 µm, n = 15), outer layer consists of 2–4 layers of *textura angularis*, brown and thick-walled cells, inner layer consists of multi-layers of *textura angularis*, hyaline and thin-walled cells. *Hamathecium* 2–3 µm wide ($\overline{x}$ = 2.5 µm, n = 20), numerous, hypha-like, filiform, septate, branched, cellular, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 90–140 × 20–28 µm ($\overline{x}$ = 115 × 23 µm, n = 20), bitunicate, 8-spored, cylindrical to clavate, with a short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 45–55 × 8–11 µm ($\overline{x}$ = 47 × 9 µm, n = 20), overlapping uniseriate to 3-seriate, hyaline, fusoid, often enlarged at the fourth cell, with one transverse septum when young, 7–8 transverse septa when mature, constricted at the centre septa, slightly constricted at other septa, smooth-walled, sheath present. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h, colonies reached 4 cm in diameter after one month at 25℃, circular, with filiform margin, aerial, medium spare, flat or effuse, from above, hyaline, from below, hyaline to light brown at the centre, hyaline at the edge.

Materials examined: China, Yunnan Province, Lincang, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (22°8' N, 99°4' E, 870 m alt.), 28 July 2022, LiLu, LC3-C3 (HKAS 137602, holotype), isotype MHZU 23-0059, ex-type living culture KUNCC 24-18345 = KUNCC 24-18346, ex-isotype living culture ZHKUCC 23-0628 = ZHKUCC 23-0629.

GenBank numbers: KUNCC24-18345: ITS = OR428397, LSU = OR428419, SSU = OR428377, *TEF*1-α = OR509751; KUNCC24-18346: ITS = OR428398, LSU = OR428420, SSU = OR428378, *TEF*1-α = OR509752.

Notes: In the concatenated phylogenetic analysis, *Longiostiolum coffeae* formed a sister branch with *L. tectonae* (MFLU 15-3532) (Figure 2.11). Based on nucleotide comparisons, *L. coffeae* (HKAS 137602) is different from *L. tectonae* (MFLU 15-3532) by 70/480 bp (14%, without gaps) of the ITS, 13/863 bp (1.5%, without gaps) of the LSU, 4/665 bp (0.6%, without gaps) of the SSU and 75/920 bp (8%, without gaps) of the *TEF*1-α. Based on morphology, our novel taxon is similar to *L. tectonae* in the hyaline and fusoid ascospores, but differs in the sheath of ascospores, as *L. tectonae* lacks a sheath. Besides, our species has 1–8 transverse septa, while *L. tectonae* has 7–10 transverse septa (Figure 2.10; Li et al., 2016; Phukhamsakda et al., 2020). The morphological differences and phylogenetic analyses support the discovery of *L. coffeae* as a new species.

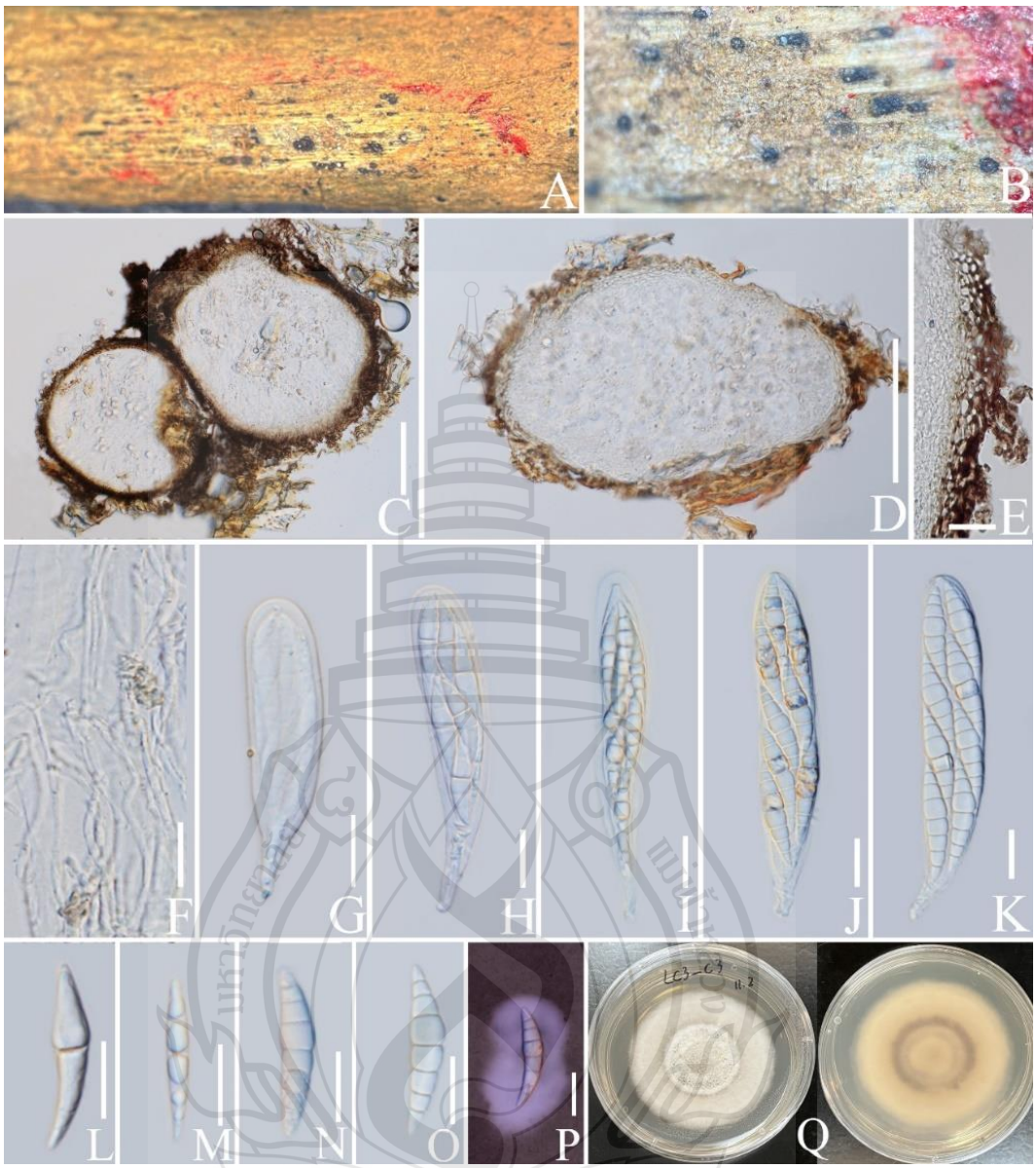


Figure 2.75 *Longiostiolum coffeae* (HKAS 137602, holotype)

Figure 2.75 A, B Ascomata on a decaying branch of *C. arabica*; C, D Longitudinal section of an ascoma; E Peridium wall; F Pseudoparaphyses; G–K Asci; L–O Ascospores; P An ascospore stained with Indian ink; Q Culture on PDA from obverse and reverse. Scale bars: C, D = 100 µm, E–P = 20 µm.

Longiostiolum puerense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.* (XAZC15)

Index Fungorum number: IF 903622; *Facesoffungi number*: FoF 17572; Figure 2.59

Etymology: The species epithet refers to the location "Pu'er", China.

Holotype: MHZU 24-0538

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 200–400 × 200–260 µm ($\overline{x}$ = 320 × 240 µm, n = 15), black spots on the substrate, solitary to scattered, semi-immersed, unilocular, subglobose to globose, with a central ostiole. *Peridium* 25–35 µm wide ($\overline{x}$ = 30 µm, n = 15), consisting of multi layers of *textura prismatica* cells, hyaline to brown. *Hamathecium* of 2–3 µm wide ($\overline{x}$ = 2.7 µm, n = 20), numerous, hypha-like, filiform, septate, branched, cellular, pseudoparaphyses, some embedded in a gelatinous matrix. *Asci* 100–180 × 20–30 µm ($\overline{x}$ = 131 × 24 µm, "n = 20), bitunicate, fissitunicate, 8-spored, cylindrical to clavate, short club-like pedicel, apically rounded, with an ocular chamber. *Ascospores* 45–60 × 8–12 µm ($\overline{x}$ = 55 × 10 µm, n = 20), overlapping uniseriate to 3-seriate, hyaline, lunate to fusoid, rounded or conical at both ends or slightly acute, often enlarged at the fourth cell, with 7–9 transverse septa, constricted at the center septum, smooth-walled, surrounded by a thick mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 4 cm diam. after one month at 25°C, white, circular, flat, undulate margin, with fluffy aerial mycelium in the surface, medium sparse. White to yellowish to brown from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC15 (MHZU 24-0538, holotype), ex-type ZHKUCC 24-0981, other living culture ZHKUCC 24-0982.

GenBank numbers: ZHKUCC 24-0981: ITS = PQ608258, LSU = PQ608091, SSU = PQ607951, *TEF*1-α = PQ602132; ZHKUCC 24-0982: ITS = PQ608259, LSU = PQ608092, SSU = PQ607952, *TEF*1-α = PQ602133.

Notes: In the phylogenetic analysis, *Longiostiolum puerense* formed a sister lineage to *L. tectonae* (MFLU 15-3532, holotype), with 100% ML and 0.99 BYPP statistical support (Figure 2.54). Based on nucleotide comparisons, *L. puerense*

(ZHKUCC 24-0981, ex-type) is different from *L. tectonae* (MFLU 15-3532, holotype) by 28/496 bp (5.6%, without gaps) of the ITS, 26/909 bp (2.8%, without gaps) of the *TEF*1-α, while LSU and SSU are mostly the same. *Longiostiolum puerense* can be distinguished morphologically from *L. tectonae* by having *textura prismatica* cells peridium, short pedicel with club-like asci and hyaline ascospores, however, *L. tectonae* has *textura angularis* cells of the peridium, asci without club-like pedicels and pale brown ascospores (Li et al., 2016; Figure 2.59). Therefore, *L. puerense* is introduced here as a new species isolated from *Coffea arabica* in China.

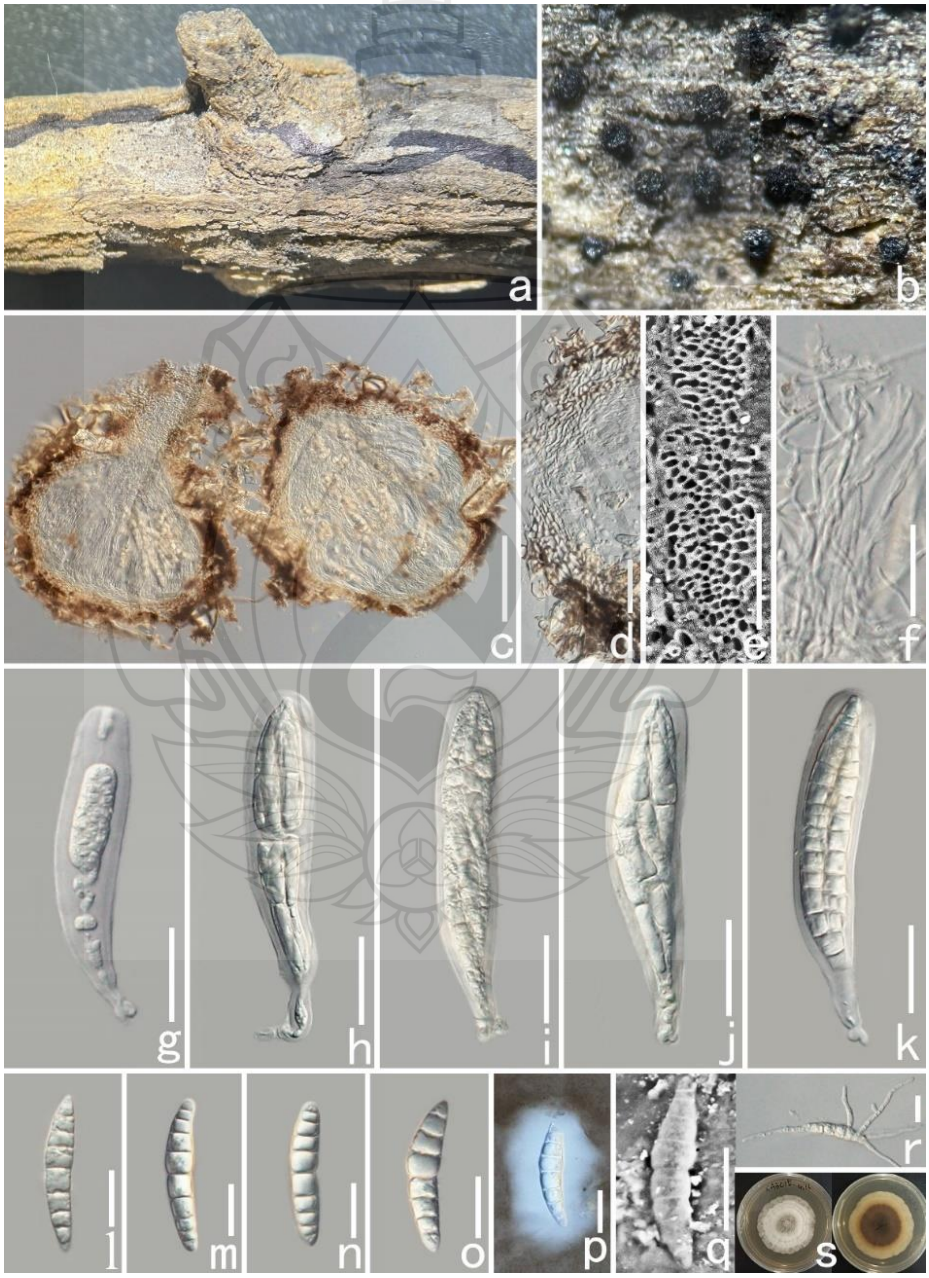


Figure 2.76 *Longiostiolum puerense* (MHZU 24-0538, holotype)

Figure 2.76 a, b Ascomata on a decaying branch of *Coffea arabica*. c Longitudinal section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Pseudoparaphyses. g–k Asci. l–o Ascospores. p An ascospore stained with Indian ink. q SEM microphotographs of ascospore. r Germinated ascospore. s Culture on PDA from above and below. Scale bars: c = 100 μm, d–k = 30 μm, l–r = 20 μm.

Lophiostomataceae Sacc., Syll. Fung. 2: 672 (1883)

Flabellascoma A. Hashim., K. Hiray. & Kaz. Tanaka, Studies in Mycology 90: 167 (2018)

Notes: Flabellascoma was proposed by Hashimoto et al. (2018) and was typified by *F. minimum*. Six species are reported in *Flabellascoma* (Index Fungorum, 2024). *Flabellascoma cycadicola*, *F. minimum*, and *F. sichuanense* were collected from terrestrial habitats (Hashimoto et al., 2018; Yu et al., 2022), while *F. aquaticum* and *F. fusiforme* were collected from freshwater habitats (Bao et al., 2019). Members of species in *Flabellascoma* are reported as saprobes and found in various hosts in China (Hashimoto et al., 2018; Bao et al., 2019; Yu et al., 2022). Asci and ascospores of different *Flabellascoma* species are very similar, and it is not easy to distinguish between them, but ascomata features and DNA data are proposed to help identify them (Bao et al., 2019; Yu et al., 2022). The sexual morph of *Flabellascoma* is characterized by subglobose to ellipsoidal ascomata, with elongated ostiolar necks, brown cells of the peridium and anastomosed pseudoparaphyses, bitunicate, fissitunicate, cylindrical to clavate asci with fusiform ascospores, hyaline, 1-septate, with a narrow bipolar sheath (Hashimoto et al., 2018). The asexual morph is characterized by pycnidial conidiomata, holoblastic conidiogenous cells, cylindrical or ampulliform and subglobose with rounded ends conidia, hyaline and aseptate (Hashimoto et al., 2018). A new species is added to *Flabellascoma* from the Arabica coffee plant in Yunnan Province, China, and this is the first report of *Flabellascoma* from coffee.

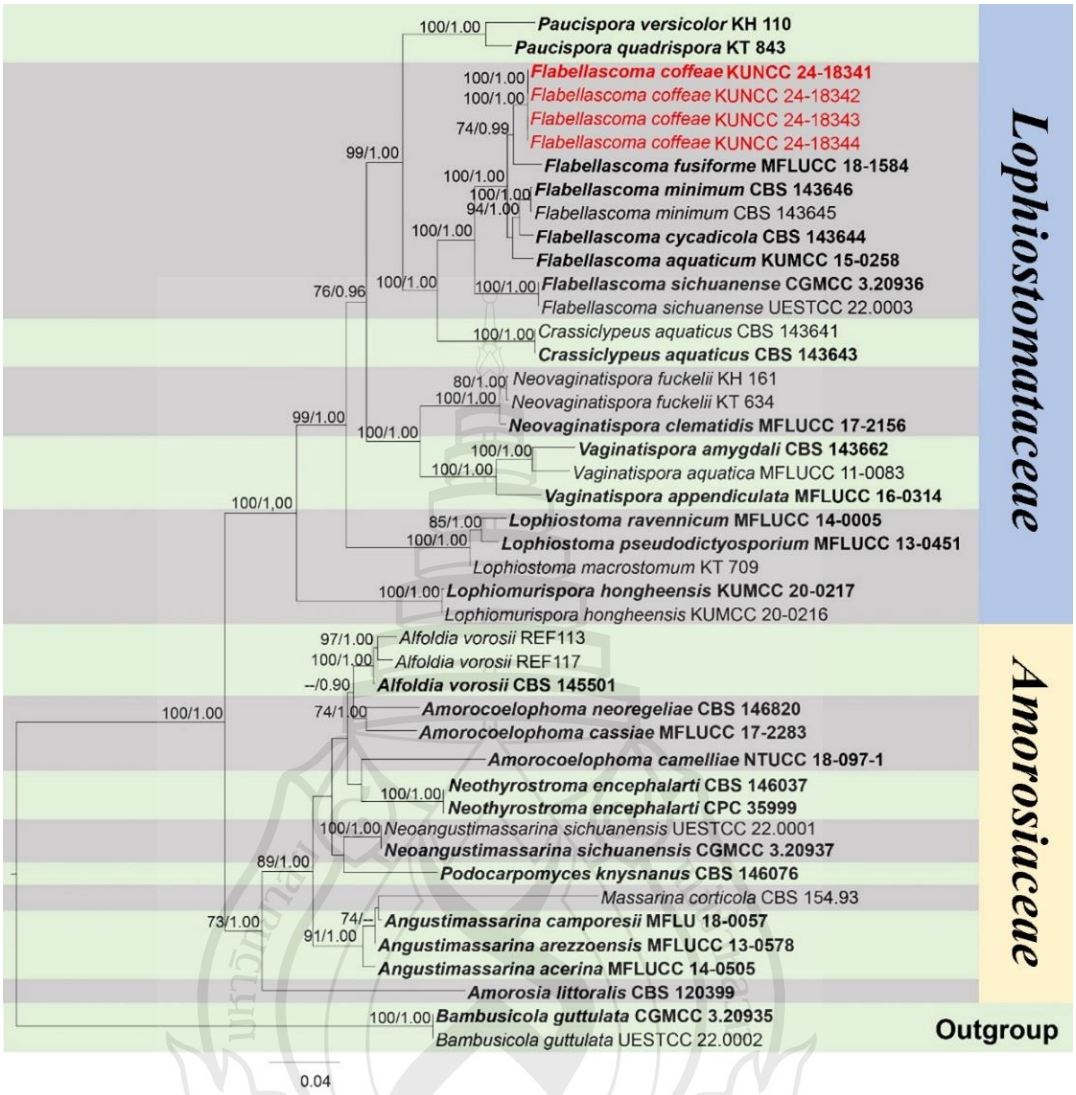


Figure 2.77 Phylogenetic tree of *Flabellascoma*

Figure 2.77 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU SSU, *RPB*2 and *TEF*1-α sequence data. Forty-four strains are included in the combined sequence analysis, which comprises 4,325 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Bambusicola guttulata* (CGMCC 3.20935 and UESTCC 22.0002).

Flabellascoma coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 901001; *Facesoffungi number*: FoF 14727; Figure 2.61

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137607

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph:** *Ascomata* 280–450 µm high × 200–280 µm diam. ($\overline{x}$ = 356 × 230 µm, n = 20) (including neck), solitary, rarely clustered, immersed, visible as black, crest-like ostiolar neck on the substrate, globose to subglobose, uniloculate. *Ostioles* central, with a pore-like opening, periphysate. *Peridium* 15–30 µm wide ($\overline{x}$ = 24 µm, n = 30), composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide ($\overline{x}$ = 2.2 µm, n = 30), hyphae-like, septate, branched, pseudoparaphyses. *Asci* 60–100 × 10–15 µm ($\overline{x}$ = 75 × 12 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight, with a short furcate sessile, apically rounded with a broad ocular chamber. *Ascospores* 20–25 × 5–7 µm ($\overline{x}$ = 22 × 6 µm, n = 30), overlapping biseriate, fusiform, hyaline, 1-septate, constricted at the septum, the upper cell slightly wider than the lower cell, guttulate, smooth-walled, with a narrow bipolar sheath. *Sheath* drawn-out at both ends, 4–7 µm long × 2–3 µm wide ($\overline{x}$ = 5.6 × 2.5 µm, n = 30), with an internal chamber at both ends of ascospores. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h, colonies reached 1.5–2 cm in diameter after twenty days at 25°C, circular, flat to umbonate, fluffy, smooth, with entire margin, from above, grey, from below, dark grey at the centre, white at the edge.

Material ex*amined*: China, Yunnan Province, Baoshan, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (24°9' N, 98°8' E, 1050 m alt.), 30 July 2022, LiLu, BS1-C3 (HKAS 137607, holotype), isotype MHZU 23-0063, ex-type living culture KUNCC 24-18341 = KUNCC 24-18342, ex-isotype living culture ZHKUCC 23-0636 = ZHKUCC 23-0637; China, Yunnan Province, Dali, on a decaying branch of *C. arabica*, (101°91' E, 26°09' N, 1416.46 m alt.), 25 July 2022, LiLu, DL-C41 (HKAS 137612, paratype), isoparatype MHZU 23-0062, ex-paratype living culture KUNCC 24-18343 = KUNCC 24-18344, ex-isoparatype living culture ZHKUCC 23-0634 = ZHKUCC 23-0635.

GenBank numbers: KUNCC24-18341: ITS = OR428405, LSU = OR428427, SSU = OR428385, *RPB*2 = OR515525, *TEF*1-α = OR509759; KUNCC24-18342: ITS = OR428406, LSU = OR428428, SSU = OR428386, *RPB*2 = OR515526, *TEF*1-α = OR509760; KUNCC24-18343: ITS = OR428403, LSU = OR428425, SSU = OR428383, *RPB*2 = OR515523, *TEF*1-α = OR509757; KUNCC24-18344: ITS = OR428404, LSU = OR428426, SSU = OR428384, *RPB*2 = OR515524, *TEF*1-α = OR509758.

Notes: The phylogenetic result, based on SSU, ITS, LSU, *RPB*2 and *TEF*1-α sequence data, showed our new collection *Flabellascoma coffeae* is close to *F. fusiforme* (Figure 2.9). *Flabellascoma coffeae* can be distinguished from *F. fusiforme* in having an internal chamber at both ends of ascospores (Figure 2.8; Bao et al. (2019)). *Flabellascoma coffeae* also fits well with the morphological characteristics of *Flabellascoma*, such as immersed ascomata with crest-like ostiolar neck, cylindrical-clavate asci and fusiform, hyaline, 1-septate ascospores with a narrow bipolar sheath (Figure 2.8; Hashimoto et al. (2018)). Based on nucleotide comparisons, *F. coffeae* (ZHKUCC 23-0636) is different from *F. fusiforme* (MFLUCC 18-1584) by 19/500 bp (3.8%, without gaps) of the ITS, 7/835 bp (0.8%, without gaps) of the LSU and 22/839 bp (2.7%, without gaps) of the *TEF*1-α. Therefore, we introduce *F. coffeae* as a new species from coffee in China, based on morphology and multigene phylogeny.

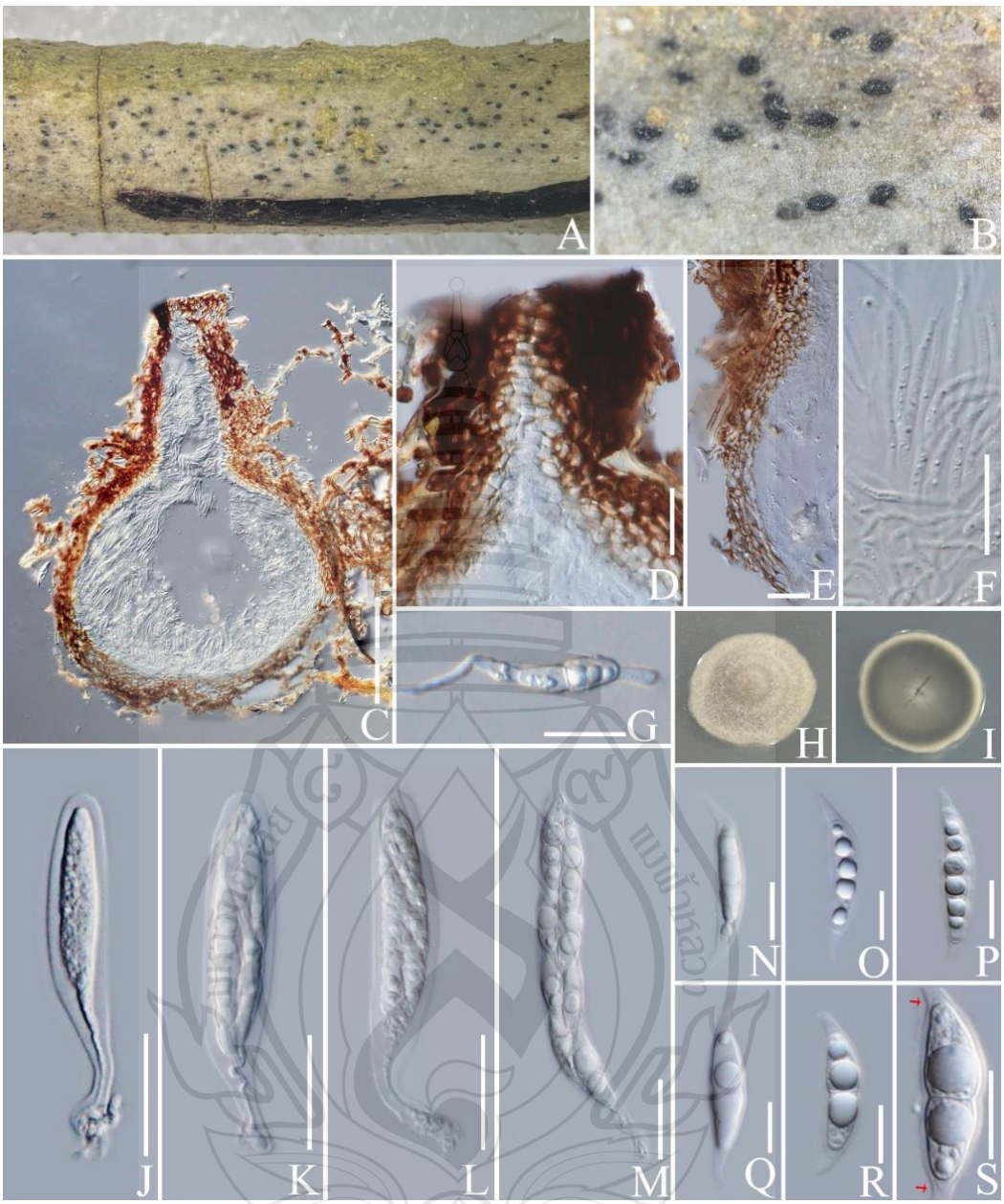


Figure 2.78 *Flabellascoma coffeae* (HKAS 137607, Holotype)

Figure 2.78 A, B Ascomata on a decaying branch of *C. arabica*; C A longitudinal section of an ascoma; D Ostioles; E Peridium wall; F Pseudoparaphyses; G Germinated ascospore; H, I Culture on PDA from the obverse and reverse; J–M Asci; N–S Ascospores (S: arrowheads indicate an internal chamber in ascospore). Scale bars: C = 100 µm, D–G, J–M = 20 µm, N–S = 10 µm.

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous, IMA Fungus 6 (1): 178 (2015)

Pseudochaetosphaeronema Punith., Nova Hedwigia 31 (1-3): 126 (1979)

Notes: Pseudochaetosphaeronema was introduced by Punithalingam (1979) with *P. larense* as the type species. Fourteen *Pseudochaetosphaeronema* species are listed in Index Fungorum (2025), as saprobes in both terrestrial and aquatic habitats, as well as endophytes and human pathogens, most of them isolated from China and Thailand, and a few from Queensland (Zhang et al., 2012; Hongsanan et al., 2020; Boonmee et al., 2021; de Silva et al., 2022; Li et al., 2023; Xu et al., 2024). Species in *Pseudochaetosphaeronema* were mainly reported as asexual morphs, and the first sexual morph species was introduced by Boonmee et al. (2021). The asexual morph of *Pseudochaetosphaeronema* is characterized by black obpyriform pycnidia with a long neck, hyaline and phialidic conidiophores, and unicellular subspherical to ellipsoidal conidia. The sexual morphology is characterized by uniloculate, black, globose to subglobose ascomata, 8-spored and bitunicate asci with hyaline, fusiform, and 1-septate ascospores. Here, we introduce two new *Pseudochaetosphaeronema* species from *Coffea* sp. in Yunnan Province, China.

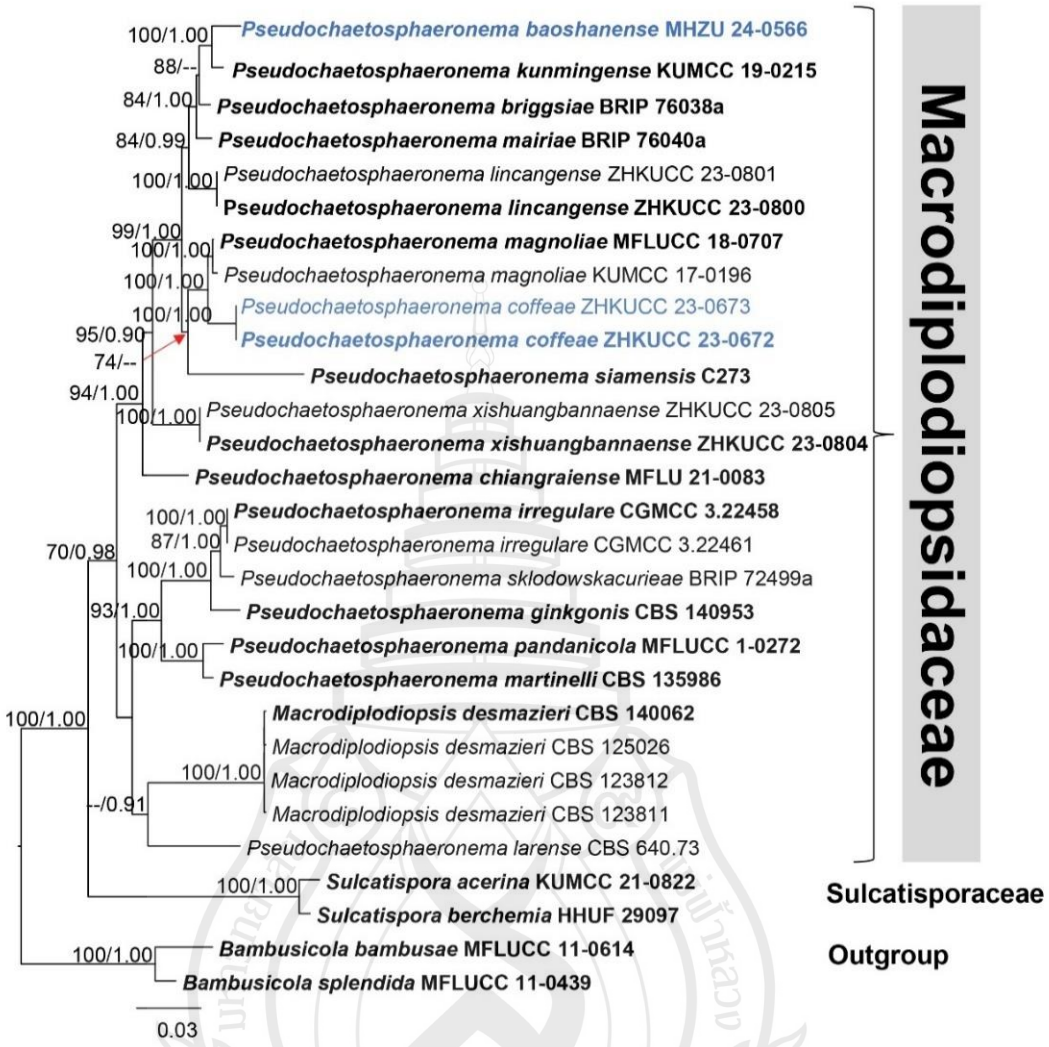


Figure 2.79 Phylogenetic tree of *Pseudochaetosphaeronema*

Figure 2.79 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU SSU, and *TEF*1-α sequence data. Twenty-nine strains are included in the combined sequence analysis, which comprises 3,234 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Bambusicola bambusae* (MFLUCC 11-0614) and *Bambusicola splendida* (MFLUCC 11-0439).

Pseudochaetosphaeronema baoshanense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903641; *Facesoffungi number*: FoF 17573; Figure 2.61

Etymology: The species epithet refers to the type location "Baoshan", China.

Holotype: MHZU 24-0566

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 100–200 × 120–220 µm ($\bar{x}$ = 153 × 160 µm, n = 15), solitary, globose to subglobose, black spots on substrate, semi-immersed to immersed, carbonaceous, unilocular. *Conidiomatal wall* 20–40 µm wide ($\bar{x}$ = 29 µm, n = 25), outer layers comprised of thick-walled, brown cells of *textura angularis* to *textura prismatica*, fusing and indistinguishable from the host tissues, inner layers comprised of hyaline, thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–9 × 3–7 µm ($\bar{x}$ = 6.9 × 3.7 µm, n = 25), monophialidic, cylindrical or ampulliform, integrated, hyaline, smooth-walled. *Conidia* 10–16 × 4.5–5.5 µm ($\bar{x}$ = 12.8 × 5 µm, n = 20), yellowish to brown, oblong to ellipsoidal, or fusoid, with rounded ends, sometimes truncated and narrow at the base, initially hyaline to yellowish, unicellular, becoming light brown before release from the pycnidia, 1–3-septate, not constricted at the septa, septal straight or bands, slightly thick-walled.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (24.9 N, 98.8 E, 1209 m), 30 July 2022, Li Lu, BS2-C14 (MHZU 24-0566, holotype).

GenBank numbers: MHZU 24-0566: ITS = PQ608323, LSU = PQ608156, SSU = PQ608010, *TEF*1-α = PQ628168.

Notes: In the concatenated gene analyses, *Pseudochaetosphaeronema baoshanense* shows a close phylogenetic affinity to *P. kunmingense* (KUMCC 19-0215, ex-type) with 100% ML and 1.00 BYPP statistical support (Figure 2.60). Based on base difference, *P. baoshanensis* (MHZU 24-0566, holotype) and *P. kunmingense* (KUMCC 19-0215, ex-type) differed by 6/509 (1%, without gaps) in ITS and 18/908 (1.9%, without gaps) in *TEF*1-α, while LSU and SSU are most the same. Morphologically, *P. baoshanensis* is similar to *P. kunmingense* in having dark brown, uni-loculate, globose to subglobose,

glabrous conidioma, monophialidic, cylindrical or ampulliform conidiogenous cells, and brown conidia. However, it differs from *P. kunmingense* in conidial morphology, *P. baoshanense* having 1–3-septate, oblong to ellipsoidal conidia, while *P. kunmingense* has 3-septate, typically fusiform or occasionally oval conidia, with round ends (Hyde et al., 2020; Figure 2.61). Thus, we introduce *P. baoshanense* as a new species.

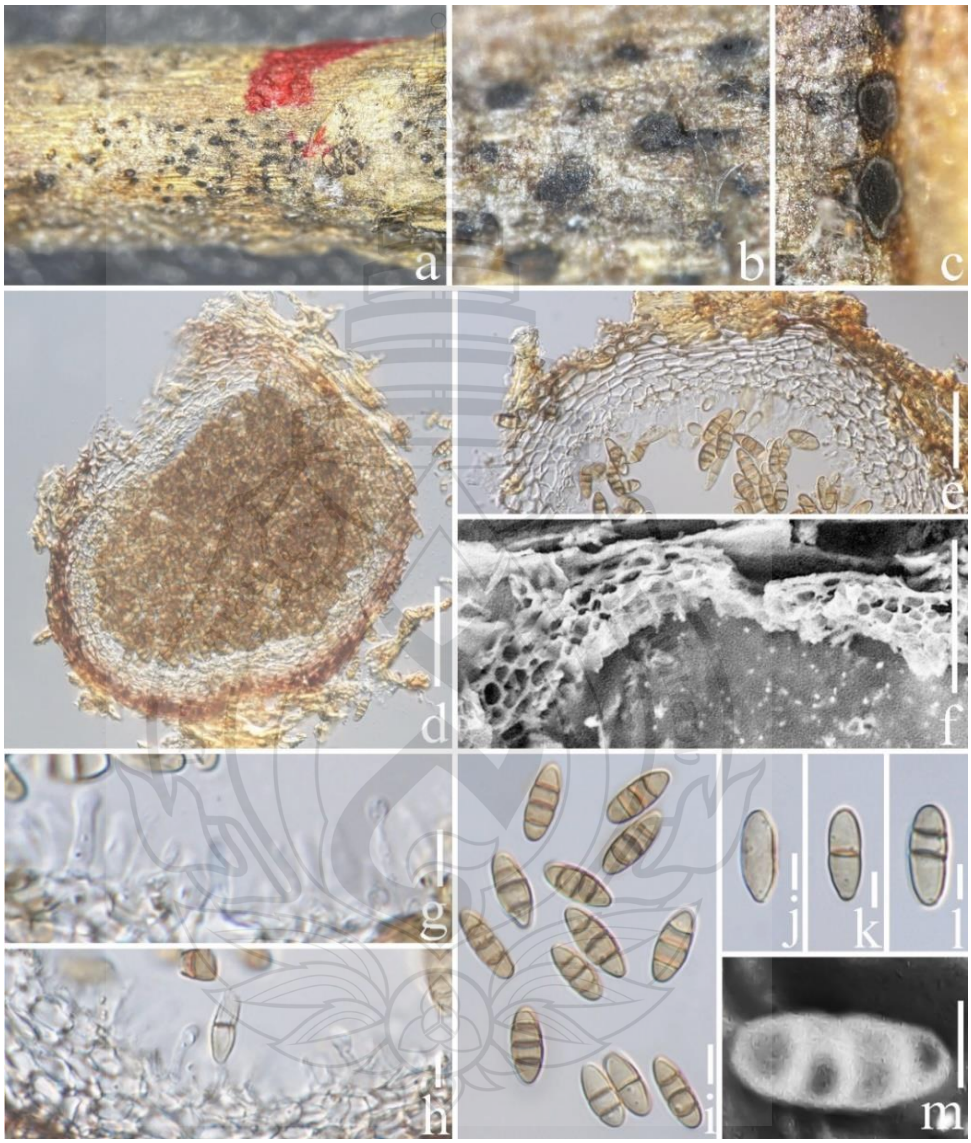


Figure 2.80 *Pseudochaetosphaeronema baoshanense* (MHZU 24-0566, Holotype)

Figure 2.80 a, b, c Appearance of conidiomata on a decaying branch of *Coffea* sp. d Longitudinal section of a conidioma. e, f Conidioma wall (f: SEM microphotographs of conidioma wall). g, h Conidiogenous cells with conidia. i–m Conidia (m: SEM microphotographs of conidium). Scale bars: d = 50 µm, e, f = 30 µm, g–m = 5 µm.

Pseudochaetosphaeronema coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903642; *Facesoffungi number*: FoF 17574; Figure 2.62

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 23-0081

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 150–190 × 180–240 µm ($\bar{x}$ = 168 × 200 µm, n = 10), solitary, globose to subglobose, dark brown to black, semi-immersed to erumpent, unilocular. *Conidiomatal wall* 20–30 µm wide, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, arranged in a *textura angularis* to *textura prismatica*. *Conidiophores* arising from the inner layers lining the conidioma, or at the base and extending part way up the side walls, sparsely septate and irregularly branched, often reduced to conidiogenous cells. *Conidiogenous cells* 6–9 × 3–6 µm ($\bar{x}$ = 7.4 × 3.7 µm, n = 20), monophialidic, cylindrical or ampulliform, integrated, hyaline, smooth-walled. *Conidia* 12–16 × 3–5 µm ($\bar{x}$ = 14 × 3.5 µm, n = 20), hyaline, cylindrical to fusoid, solitary, smooth, thin-walled, straight, 1–3-septate, constricted at the septum, without a mucilaginous sheath.

Culture characteristics: Conidium germinating on PDA within 24 h. Colonies on PDA reaching 20 mm diam. after two months at 25°C, circular, flat, with entire margin, cream, with sparse aerial mycelium. From below cream to brown, becoming brownish towards the center.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (1053 m), 30 July 2022, Li Lu, BS1-C11 (MHZU 23-0081, holotype), ex-type ZHKUCC 23-0672, other living culture ZHKUCC 23-0673.

GenBank numbers: ZHKUCC 23-0672: ITS = PQ608321, LSU = PQ608154, SSU = PQ608008, *TEF*1-α = PQ628166; ZHKUCC 23-0673: ITS = PQ608322, LSU = PQ608155, SSU = PQ608009, *TEF*1-α = PQ628167.

Notes: In the multi-gene phylogenetic analysis, our strains form an independent lineage from *Pseudochaetosphaeronema magnoliae* (MFLUCC 18-0707, ex-type) with 100% ML and 1.00 BYPP statistical support (Figure 2.60). Based on base pair difference, our strain (ZHKUCC 23-0672, ex-type) and *P. magnoliae* (MFLUCC 18-0707, ex-type) differed by 9/543 (1.6%, without gaps) in ITS, 2/864 (0.2%, without

gaps) in LSU, 5/1019 (0.5%, without gaps) in SSU, and 10/899 (1.1%, without gaps) in *TEF*1-α. The morphology of our collection is similar with *P. magnoliae* in having cylindrical to fusoid conidia (de Silva et al., 2022); however, it can be distinguished from *P. magnoliae* in having longer conidiogenous cells (6–9 × 3–6 µm, L/W = 1–3 vs. 4–5 × 2.5–3.5 µm, L/W = 1.1–2) and 1–3-septate conidia, whereas *P. magnoliae* has unicellular conidia (de Silva et al., 2022; Figure 2.62). We, therefore, introduce our collection as *P. coffeae* collected form *Coffea* sp. in China.

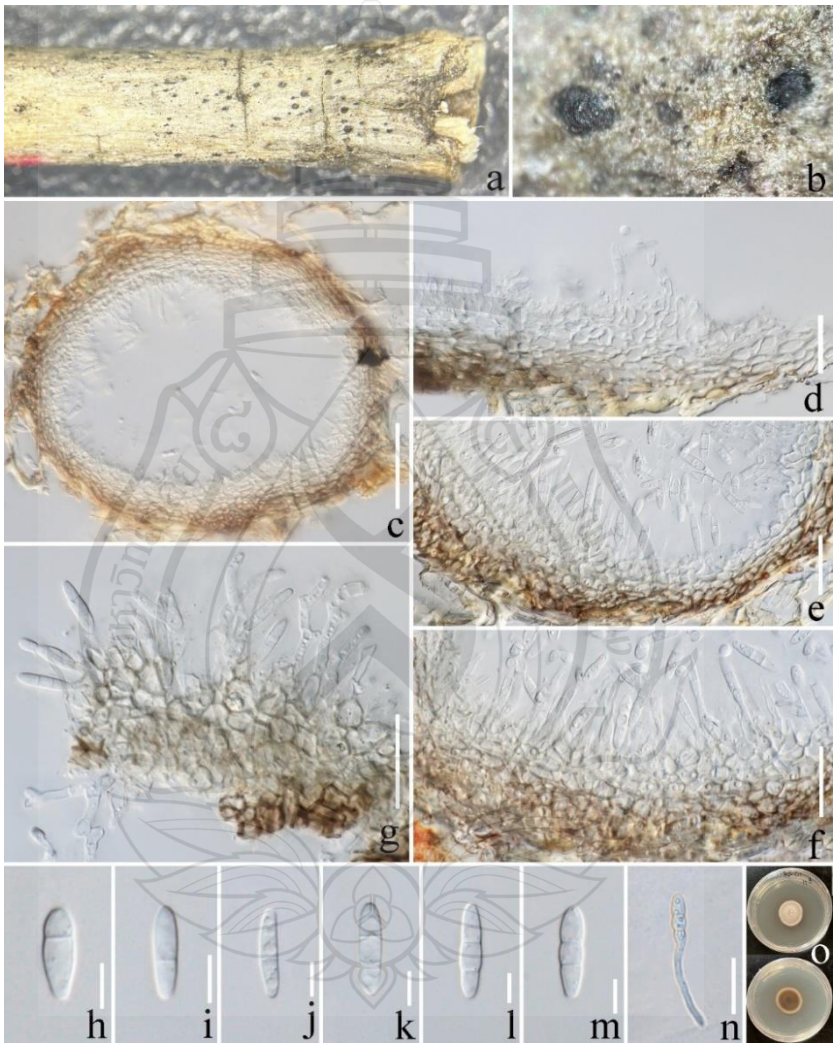


Figure 2.81 *Pseudochaetosphaeronema coffeae* (MHZU 23-0081, Holotype)

Figure 2.81 a, b Appearance of conidioma on a decaying branch of *Coffea* sp. c Longitudinal section of conidioma. d Conidioma wall. e–g Conidiogenous cells with conidia. h–m Conidia. n Germinated conidium. o Culture on PDA from above and below. Scale bars: c = 50 µm, d–g, n = 20 µm, h–m = 5 µm.

Massariaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 73 (1869)

Helminthosporium Link, Mag. Ges. Naturf. Freunde Berlin 3 (1): 10 (1809)

Notes: Helminthosporium was established by Link (1809) and typified by *H. velutinum* Link; it is a polyphyletic genus in *Massarinaceae* of *Pleosporales* (Chen et al., 2022). Members of *Helminthosporium* mainly occur as anamorphs. Little is known about the teleomorph of *Helminthosporium* (Hughes, 1953; Subramanian, 1987; Tanaka et al., 2015). Herein, we introduce *H. puerensis* as a new species with a teleomorph from the Arabica coffee plant in Yunnan, China.

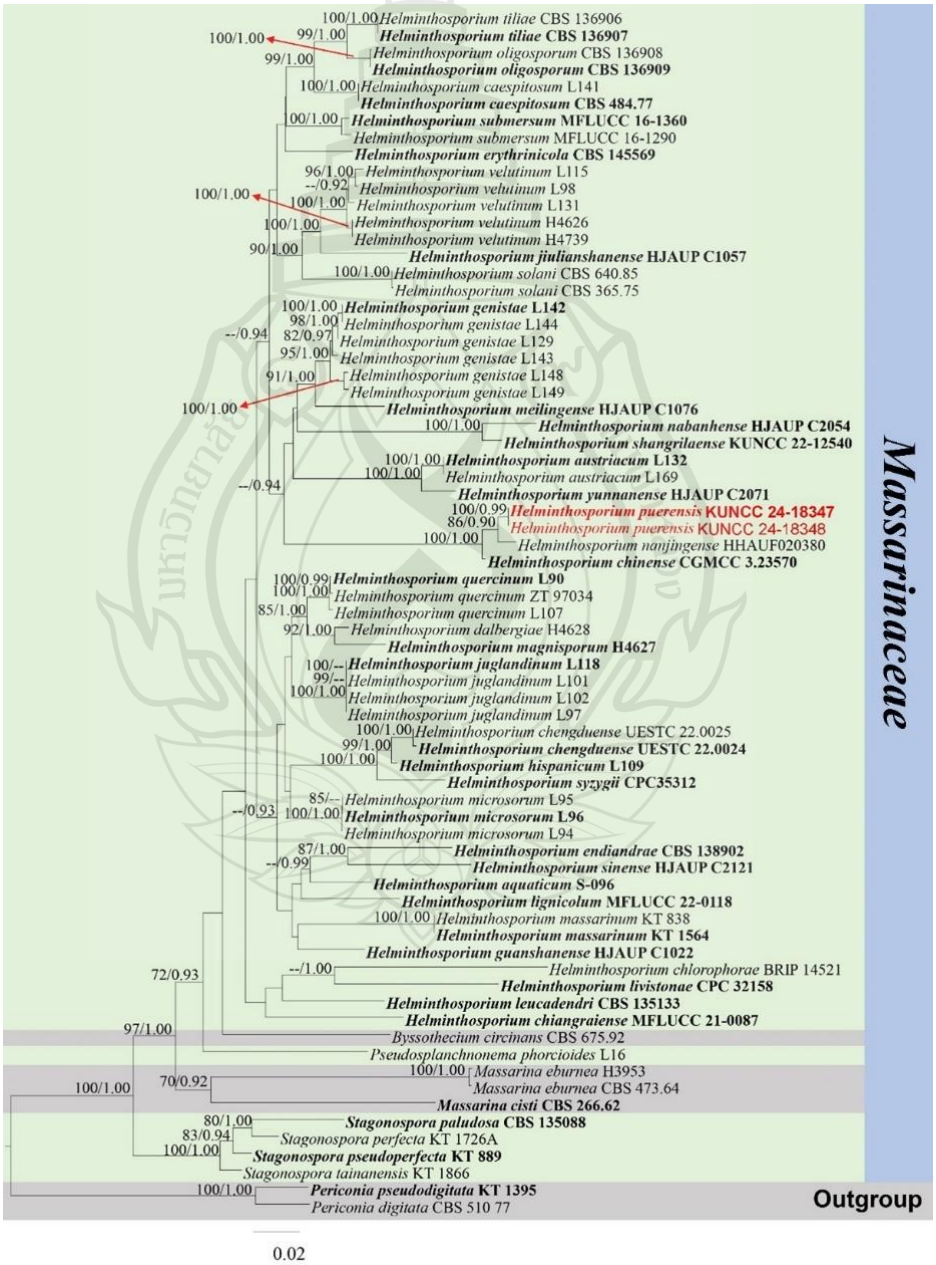


Figure 2.82 Phylogenetic tree of *Helminthosporium*

Figure 2.82 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2 and *TEF*1-α sequence data. Seventy-one strains are included in the combined sequence analysis, which comprises 4,404 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Periconia pseudodigitata* (KT 1395) and *P. digitata* (CBS 510.77).

Helminthosporium puerensis L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 901003; *Facesoffungi number*: FoF 14729; Figure 2.66

Etymology: The epithet refers to the location "Pu'er" from where the holotype was collected.

Holotype: HKAS 137606

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 250–400 × 220–400 µm ($\bar{x}$ = 320 × 310 µm, n = 15, including ostioles), solitary to scattered, immersed, visible as black dots with black hair on the host surface, globose to subglobose. *Ostiolar* neck central, cylindrical to papillate, surrounded by dark brown clypeus-like structure, without periphyses. *Peridium* 20–30 µm wide ($\bar{x}$ = 26, n = 20), composed of 4–6 layers of *textura angularis* cells, polygonal to rectangular, light brown. *Hamathecium* 2–3 µm wide ($\bar{x}$ = 2.2, n = 20), hyaline, filiform, branched, septate, pseudoparaphyses numerous. *Asci* 80–170 × 15–25 µm ($\bar{x}$ = 130 × 19 µm, n = 20), 4–8-spored, fissitunicate, bitunicate, clavate, straight, rounded at the apex, with a narrow apical chamber and faint ring, short-stalked with club-shape, sometimes with long stipes. *Ascospores* 25–30 × 7–11 µm ($\bar{x}$ = 26.5 × 9 µm, n = 30), mostly straight, 1–3-septate, constricted at the septum, asymmetric, with wider upper cell, hyaline, guttulate, smooth-walled, sheath present. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h, colonies reached 4 cm in diameter after two months at 25℃, surface smooth, circular, flat, with entire margin, from above, hyaline to light yellow, from below, dark brown at the centre, hyaline at the margin.

Material examined: China, Yunnan Province, Pu'er, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (22°70'12" N, 101°34'78" E, 900 m alt.), 6 September 2020, LiLu, QX-C7 (HKAS 137606, holotype), isotype MHZU 23-0055, ex-type living culture KUNCC 24-18347 = KUNCC 24-18348, ex-isotype living culture ZHKUCC 23-0620 = ZHKUCC 23-0621.

GenBank numbers: KUNCC24-18347: ITS = OR428391, LSU = OR428413, SSU = OR428371, *RPB*2 = OR515515, *TEF*1-α = OR509745; KUNCC24-18348: ITS = OR428392, LSU = OR428414, SSU = OR428372, *RPB*2 = OR515516, *TEF*1-α = OR509746.

Notes: Phylogenetic analyses show that *Helminthosporium puerensis* groups with *H. chinense* Y.P. Chen & Maharachch., (CGMCC 3.23570) and *H. nanjingense* Meng Zhang, Xiao J. Wang & H.Y. Wu, (HHAUF 020380) (Figure 2.13). *Helminthosporium chinense* and *H. nanjingense* were only reported as anamorphs from decaying branches of palm trees (Sichuan Province, China) and dead branches of an unidentified tree (Jiangsu Province, China), respectively. Based on nucleotide comparisons, *H. puerensis* (ZHKUCC 23-0620) is different from *H. chinense* (CGMCC 3.23570) by 18/578 bp (3%, without gaps) of the ITS, 3/749 bp (0.4%, without gaps) of the LSU, 16/780 bp (2%, without gaps) of the SSU and 8/320 bp (2.5%, without gaps) of the *TEF*1-α. In comparison, it is different from *H. nanjingense* (HHAUF 020380) in 7/454 bp (1.5%, without gaps) of the ITS (*H. nanjingense* only has ITS sequence data available). *Helminthosporium chinense* and *H. nanjingense* showed only a small difference in ITS by 7/447 (1.6%, without gaps). Based on BLASTn search results of sequence data, ITS is 97.4% similar to *H. chinense* (ON557754), LSU, SSU and *RPB*2 are closely related to *H. quercinum*, with similarity rates of 97% (KY984338), 98.8% (NG_062196) and 92.5% (KY984398), respectively and *TEF*1-α is 94% (KY984448) similar to *H. microsorum*. In terms of morphological characteristics, our species can be distinguished from *H. quercinum* and *H. microsorum* by the hyaline ascospores with inconspicuous sheath; *H. quercinum* and *H. microsorum* are hyaline to brown ascospores with conspicuous sheath (Voglmayr & Jaklitsch, 2017). Our species is most similar to the teleomorph *H. massarinum* in that it has ellipsoidal and hyaline ascospores (Figure 2.12; Tanaka et al. (2015)). Therefore, the morphological differences and phylogenetic analyses support the introduction of *H. puerensis* as a new species.

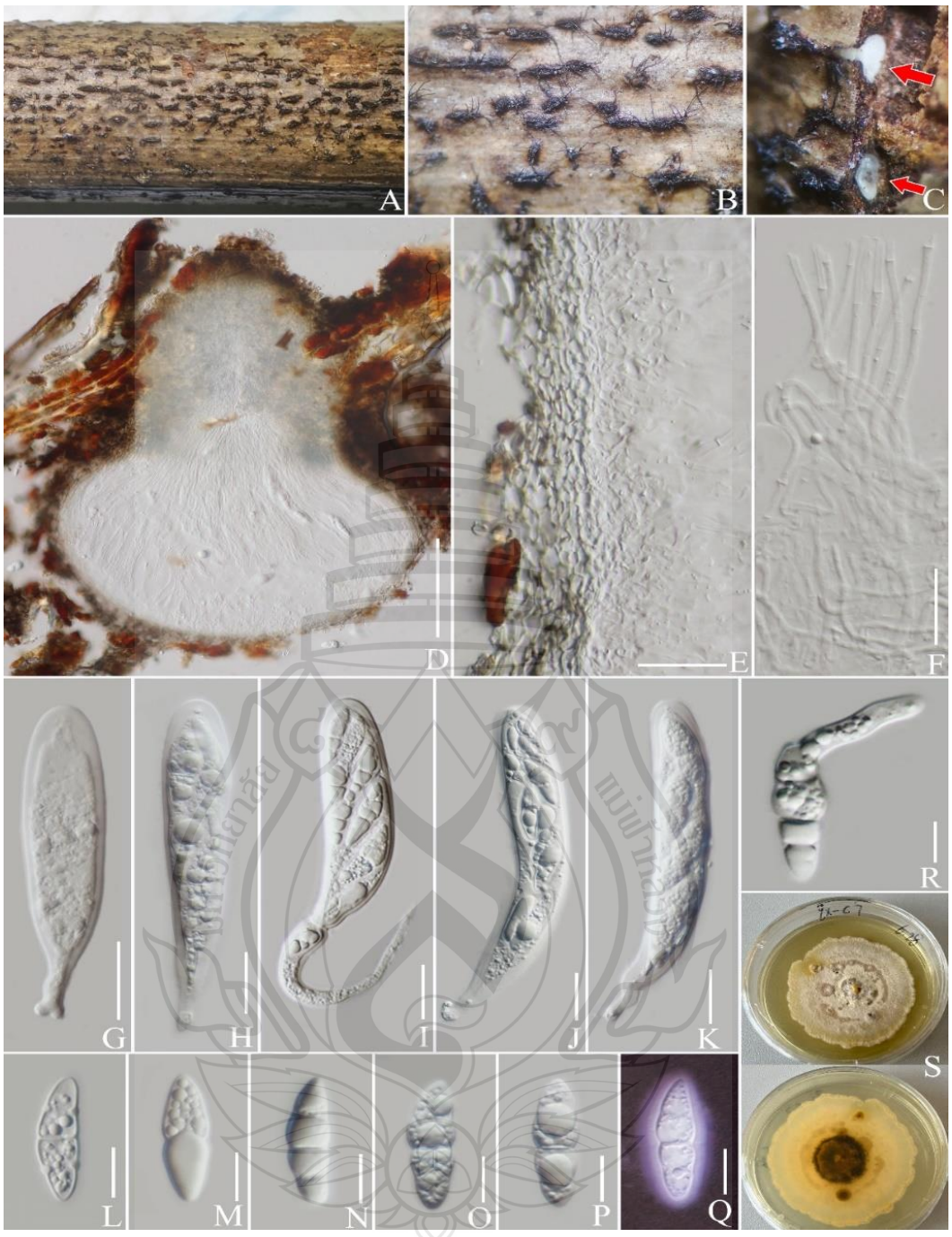


Figure 2.83 *Helminthosporium puerensis* (HKAS 137606, Holotype)

Figure 2.83 A, B Ascomata on a decaying branch of *C. arabica*; C, D Vertical section of ascoma; E Peridium wall; F Pseudoparaphyses; G–K Asci; L–P Ascospores; Q An ascospore stained with Indian ink; R Germinated ascospore; S Culture on PDA from obverse and reverse. Scale bars: D = 100 µm, E–K = 20 µm, L–R = 10 µm.

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

Notes: Based on morphological and phylogenetic analyses, Huanraluek et al. (2018) introduced *Massarioramusculicola* as a monotypic genus within Massariaceae, Pleosporales, Dothideomycetes, and it was typified by *M. chiangraiensis*. It is characterized by globose to subglobose ascomata, cylindrical, short pedicellate asci, and hyaline, fusiform, septate ascospores with a sheath (Huanraluek et al., 2018). This study introduces a new collection from a coffee host in Thailand. No further new species have been introduced to *Massarioramusculicola,* which remains monotypic (Hyde et al., 2024a). A new collection of *M. chiangraiensis*, is introduced in this study.

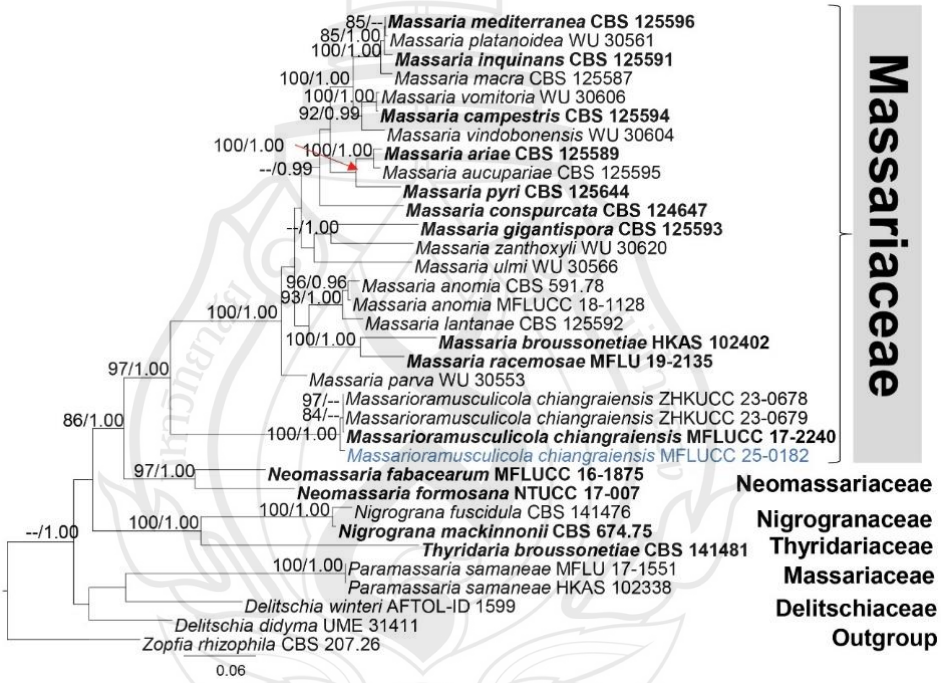


Figure 2.84 Phylogenetic tree of *Massarioramusculicola*

Figure 2.84 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU SSU, and *RPB*2 sequence data. Thirty-four strains are included in the combined sequence analysis, which comprises 4,572 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Zopfia rhizophila* (CBS 207.26).

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

Index Fungorum number: IF 554426; *Facesoffungi number*: FoF 04479; Figure 2.64

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 205–270 × 160–250 µm ($\overline{x}$ = 243 × 215 µm, n = 10), forming black spot on the host surface, globose to subglobose, semi-immersed to immersed, solitary, ostiolate. *Peridium* 15–30 µm wide ($\overline{x}$ = 22.5 µm, n = 20), composed of several black brown to hyaline cells of *textura angularis*, fusing with the host. *Hamathecium* of 1–2 µm wide ($\overline{x}$ = 1.4 µm, n = 20), numerous, cylindrical to filiform, branched, and septate, trabeculae, embedded in a gelatinous matrix. *Asci* 70–97 × 9.5–11.5 ($\overline{x}$ = 83 × 10.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, with a distinct ocular chamber at the apex of asci. *Ascospores* 20–26 × 5–6.5 ($\overline{x}$ = 22.5 × 5.7 µm, n = 20), overlapping, bi-seriate, fusiform, 0–1-septate when immature, 2–3-septate when mature, slightly constricted at the septa, rounded at both ends, guttulate, hyaline, surrounded by a thin mucilaginous sheath, smooth-walled. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm after one month at 25°C, colonies from above: circular, dense, the colour of the center is saffron, white at the margin, smooth surface; from below: brown to saffron to brown at center, white at the margin.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-11 (MFLU 25-0095), living culture MFLUCC 25-0182.

GenBank numbers: MFLUCC 25-0182: ITS = PQ608298, LSU = PQ608131, SSU = PQ607985, *RPB2* = PV221302.

Known hosts: dead twigs of unidentified host in terrestrial environments (Huanraluek et al., 2018), *Coffea* sp. (Hyde et al., 2024b; This study).

Known distribution: Thailand (Huanraluek et al., 2018; This study), China (Hyde et al., 2024b).

Notes: Phylogenetic analyses showed that our isolate (MFLUCC 25-0182) grouped with *Massarioramusculicola chiangraiensis* (MFLUCC 17-2240, ex-type; Figure 2.63), which was introduced by Huanraluek et al. (2018) and collected from decaying dead twigs of an unidentified host in Thailand. In addition, our morphological characters can fit well with the description of *M. chiangraiensis* (Huanraluek et al., 2018; Hyde et al., 2024b; Figure 2.64). Thus, our isolate was identified as *M. chiangraiensis*, and this is a new collection from a coffee host in Thailand.

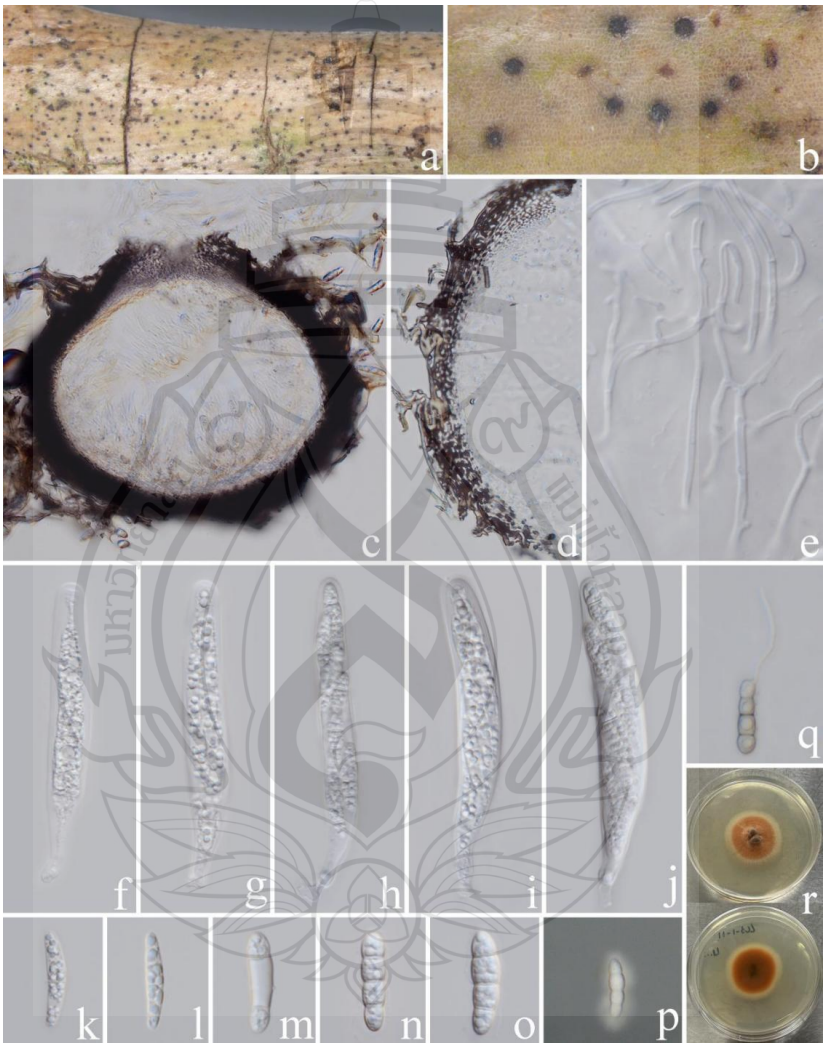


Figure 2.85 *Massarioramusculicola chiangraiensis* (MFLU 25-0095, new collection)

Figure 2.85 a, b Appearance of ascomata on host tissue. c Vertical sections through ascoma. d Peridium. e Hamathecium f–j Asci. k–o Ascospores. p Ascospore stained in Indian ink. q A germinating ascospore. r Culture on PDA from above and below. Scale bars: c = 50 µm, d–j = 20 µm, k–q = 10 µm.

Melanommataceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze - Ascomyceten, Edn 2 1(2): 220 (1885)

Byssosphaeria Cooke, Grevillea 7 (43): 84 (1879)

Notes: Byssosphaeria was introduced by Cooke and Plowright (1879) and typified by *B. keithii*. *Byssosphaeria* is a widespread genus distributed from temperate to tropical regions (Kirk et al., 1983; Hongsanan et al., 2020), with approximately 54 epithets recorded in Index Fungorum (2025). Members of species in *Byssosphaeria* were mostly reported as saprobic on decorticated wood, the bark of fallen branches, old leaves, and various other plant substrates (Hyde et al., 2013; Tennakoon et al., 2018; Xiong et al., 2023). The sexual morph of *Byssosphaeria* is characterized by superficial ascomata with bright yellow, orange, green, or red flat apices around the ostiole, with dependent hyphal appendages that merge with the subiculum below and hyaline ascospores (Barr, 1990; Zhang et al., 2012). The asexual morph has been reported from sporulated cultures as chaetophoma-like (Barr, 1984) or pyrenochaeta-like coelomycetes (Samuels & Müller, 1978). This study introduces two new *Byssosphaeria* species from coffee in China and Thailand.

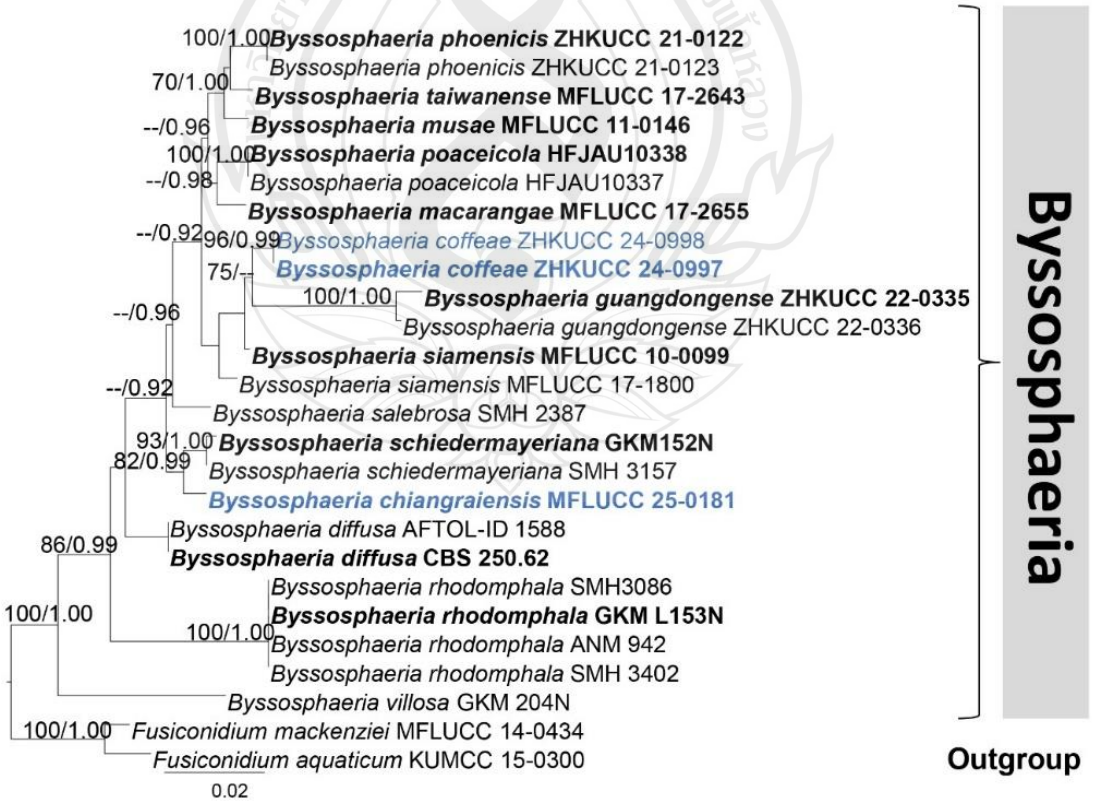


Figure 2.86 Phylogenetic tree of *Byssosphaeria*

Figure 2.86 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *TEF*1-α sequence data. Twenty-six strains are included in the combined sequence analysis, which comprises 3,861 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Fusiconidium aquaticu* (KUMCC 15-0300) and *F. mackenziei* (MFLUCC 14-0434).

Byssosphaeria chiangraiensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903606; *Facesoffungi number*: FoF 17575; Figure 2.66

Etymology: The species epithet refers to the type location "Chiang Rai", Thailand.

Holotype: MFLU 25-0094

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 300–450 × 300–450 µm ($\bar{x}$ = 389 × 400 µm, n = 10), solitary or scattered in small groups, superficial with basal subiculum anchoring on the substrate, globose to subglobose, dense black hairy, apapillate with pore-like ostiole, surrounded by an orange to light brown discoid. *Setae* 4–6 µm wide ($\bar{x}$ = 4.8, n = 20), filiform, brown to black, septate. *Peridium* 40–70 µm wide ($\bar{x}$ = 52 µm, n = 20), thick-walled, composed of several yellow to browncells, outer layer cells of *textura angularis* to *textura prismatica,* with hyaline internal cells of *textura angularis*. *Hamathecium* of 1.5–3.5 µm wide ($\bar{x}$ = 2.5 µm, n = 20), dense, hyaline, septate, branched, pseudoparaphyses, embedded in mucilage. *Asci* 90–130 × 10–15 µm ($\bar{x}$ = 112 × 13 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindro-clavate to clavate, long pedicel, club-like, the immature asci usually with furcate pedicel. *Ascospores* 30–40 × 6–9 µm ($\bar{x}$ = 34 × 7 µm, n = 20), bi-seriate, fusiform with narrow ends, slightly curved, smooth, hyaline to pale brown, 1-septate, becoming 3-septate after discharge, constrict at the middle septate, guttulate, surrounded by a thin mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h, colonies on PDA after one month attaining a diameter of 20 mm at 25°C, light yellow, circular, flat, entire margin, from below yellowish to light brown from edge to center.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-12 (MFLU 25-0094, holotype), ex-type MFLUCC 25-0181.

GenBank numbers: MFLUCC 25-0181: ITS = PQ608281, LSU = PQ608114, SSU = PQ607972, *TEF*1-α = PQ628128.

Notes: The multi-locus phylogeny generated herein indicates that *Byssosphaeria chiangraiensis* forms separate lineage (82% ML, 0.99 BYPP) basal to *B. schiedermayriana* (SMH 3157 and GKM 152N, ex-type) (Figure 2.65). Morphologically, *B. chiangraiensis* is distinct from *B. schiedermayriana* (K(M):108784, holotype) in having setaceous ascomata and an unobvious ascospore sheath, whereas *B. schiedermayriana* ascomata lack setae and ascospores have hyaline appendages at each acute to subacute end (Zhang et al., 2012; Figure 2.66). Based on nucleotide comparisons, our isolate (MFLUCC 25-0181, ex-type) differs from *B. schiedermayriana* (GKM 152N, ex-type) by 6/897 bp (0.6%, without gaps) in LSU, 15/740 bp (2%, without gaps) in *TEF*1-α. Combined with phylogeny and morphological evidence, *B. chiangraiensis* is identified as a new *Byssosphaeria* species from Arabica coffee from Thailand.



Figure 2.87 *Byssosphaeria chiangraiensis* (MFLU 25-0094, holotype)

Figure 2.87 a, b Appearance of ascomata on substrate. c Setae. d Vertical section through ascoma. e Peridium. f Hamathecium. g–i Asci. j–n Ascospores (n: Ascospores strained with Indian ink to show a sheath). o Culture on PDA from above and below. Scale bars: c, e = 50 µm, d = 100 µm, f–l = 20 µm, j–n = 10 µm.

Byssosphaeria coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903607; *Facesoffungi number*: FoF 17576; Figure 2.67

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0546

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 300–400 × 300–400 μm ($\overline{x}$ = 330 × 360 μm, n = 10), globose to subglobose, superficial, with dehiscent base, middle collapsed of the top, unilocular, black, solitary or aggregated, conspicuous at the surface, dense black hairy, with pore-like opening, surrounded discoid orange to light brown area. *Setae* 5–9 μm wide ($\overline{x}$ = 6, n = 20), filiform, numerous, brown to black, septate. *Peridium* 45–75 μm wide ($\overline{x}$ = 60, n = 20), thick-walled, composed of several brown outer layer cells of *textura globosa* to *textura angularis*, with hyaline internal cells of *textura angularis*. *Hamathecium* of 2–3 μm wide ($\overline{x}$ = 2.4, n = 20), hypha-like, branched, septate, filamentous. *Asci* 120–160 × 10–15 μm ($\overline{x}$ = 140 × 13 μm, n = 20), 8- spored, bitunicate, fissitunicate, clavate long pedicel, some club-like, rounded and without small ocular chamber at the apex of asci. *Ascospores* 30–40 × 5–7 μm ($\overline{x}$ = 33 × 6 μm, n = 30), bi-seriate, fusiform, mostly 1-septate, some 3-septate, slightly constricted at the septa, guttulate, initially hyaline, at maturity pale yellow, surrounded by a thin gelatinous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospore germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, colonies from above: circular, margin filamentous, flat, white, cottony to fairy fluffy appearance; from below: cream to yellowish.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC27 (MHZU 24-0546, holotype), ex-type ZHKUCC 24-0997, other living culture ZHKUCC 24-0998;

GenBank numbers: ZHKUCC 24-0997: ITS = PQ608282, LSU = PQ608115, SSU = PQ607973, *TEF*1-α = PQ628129; ZHKUCC 24-0998: ITS = PQ608283, LSU = PQ608116, SSU = PQ607974, *TEF*1-α = PQ628130.

Notes: In the phylogenetic tree, our strain formed a separate lineage under *Byssosphaeria guangdongensis* (ZHKUCC 22-0335 and ZHKUCC 22-0335, ex-type) with 75% ML bootstrap support (Figure 2.65). Based on nucleotide comparisons, our isolate

(ZHKUCC 24-0997, ex-type) is different from *B. guangdongensis* (ZHKUCC 22-0335, ex-type) by 27/973 bp (2.7%, without gaps) in ITS, 4/886 bp (0.4%, without gaps) in LSU and 69/1035 bp (6.6%, without gaps) in SSU. Morphologically, our species is similar to the holotype of *B. guangdongensis* in its globose to subglobose, superficial ascomata, setose, pore-like ostiole, surrounded by yellowish to orange disc, and asci with long pedicels and 8-spores. However, it can be distinguished by numerous setae of the ascomata and 1–3-septate ascospore (Xiong et al., 2023; Figure 2.67). Combining both phylogeny and morphological evidence, our species is identified as *B. coffeae.*

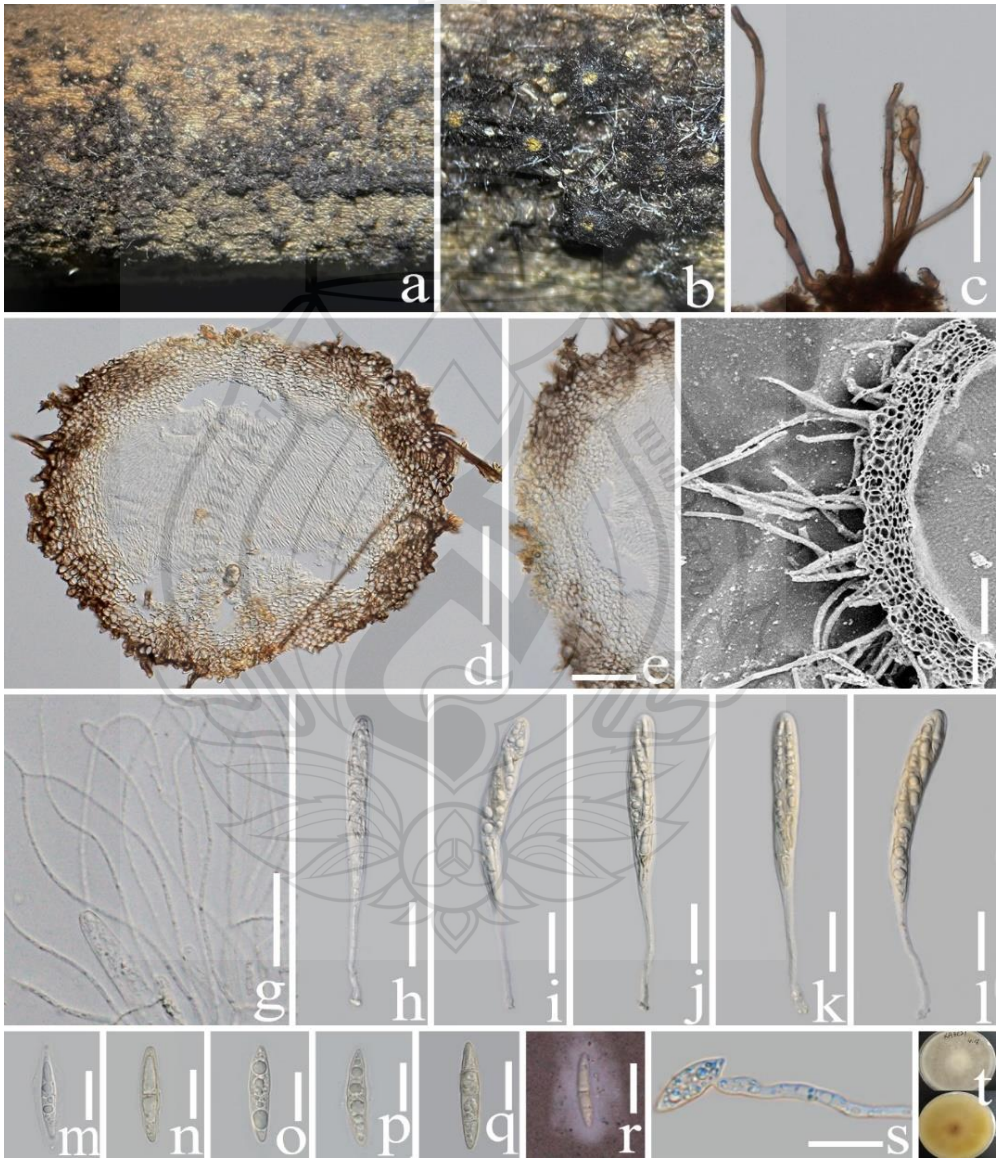


Figure 2.88 *Byssosphaeria coffeae* (MHZU 24-0546, holotype)

Figure 2.88 a, b Appearance of ascomata on substrate. c Setae. d Vertical section of ascoma. e, f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–l Asci. m–r Ascospores (r: ascospore strained with Indian ink to show a sheath). s Germinated ascospore. t Culture on PDA from above and below. Scale bars: c, e, f = 50 μm, d = 100 μm, g–l = 30 μm, m–s = 20 μm.

Phragmocephala E.W. Mason & S. Hughes, The Naturalist London 1951: 97 (1951)

Notes: The hyphomycete genus *Phragmocephala* was introduced by Mason and Hughes (1951) based on only morphological characters without phylogenetic analyses and is typified by the *P. elliptica* (Wijayawardene et al., 2012). The first phylogenetic placement of this genus was in Melanommataceae in Dothideomycetes (Su et al., 2015). *Phragmocephala* is characterized by macronematous, mononematous, erect more or less straight conidiophores that are terminated by a single integrated holoblastic conidiogenous cell, with the phragmo conidia are typically ellipsoidal, blastic, solitary, 3–6-septate, seceding with a portion of the conidiogenous cell by rupture of the wall, immediately below the base of the conidium (Mason & Hughes, 1951; Whitton et al., 2012). There are 15 species epithets in Index Fungorum (2025), while only two species with molecular data (Su et al., 2015; Hyde et al., 2021). In this study, a new record from a coffee host in Thailand is introduced, along with its morphology and molecular data.

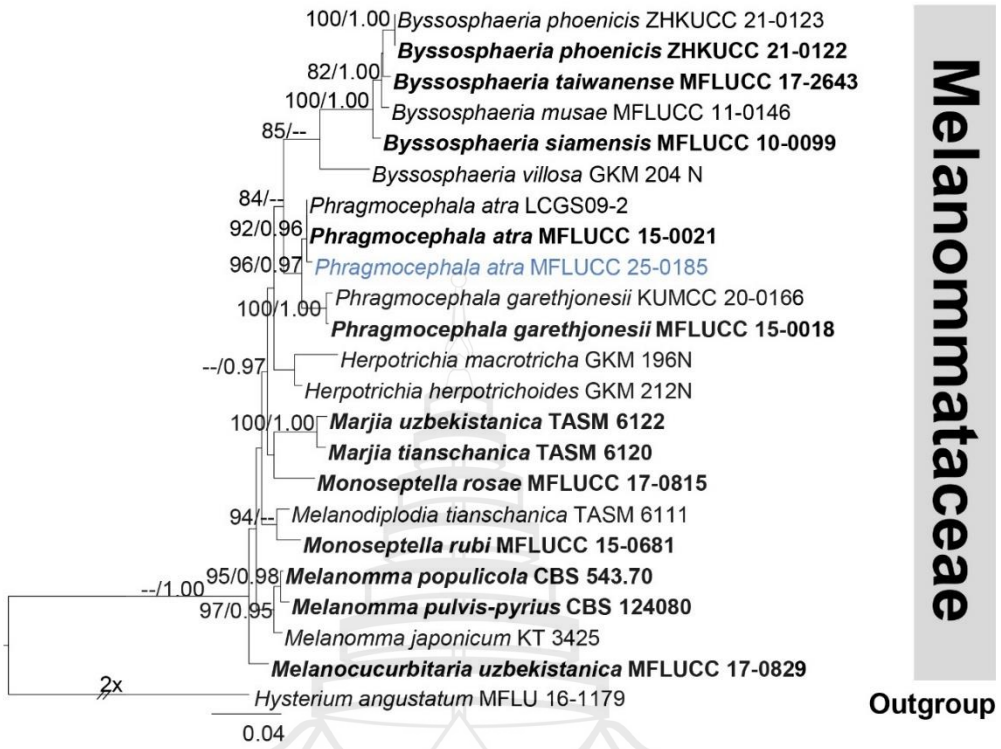


Figure 2.89 Phylogenetic tree of *Phragmocephala*

Figure 2.89 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *TEF*1-α sequence data. Twenty-three strains are included in the combined sequence analysis, which comprises 3,327 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Hysterium angustatum* (MFLU 16-1179).

Phragmocephala atra (Berk. & Broome) E.W. Mason & S. Hughes, The Naturalist London 1951: 97 (1951)

Index Fungorum: IF 303243; *Facesoffungi number*: FoF 00573; Figure 2.69

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Hyphomycetous. *Colonies* on substrate superficial, effuse, solitary to scattered, dark brown to black. *Hyphae* hyaline, filiform, branched. *Conidiophores* 120–170 × 6–9 µm ($\bar{x}$ = 169 × 7.8 µm, n = 20), synnematous, macronematous, septate, unbranched or

branched, erect, dark brown at the base, hyaline to pale brown at fertile, apex flared, sometimes proliferating, septate. *Conidiogenous cells* 17–25 × 6–9 µm ($\bar{x}$ = 20.7 × 7.9 µm, n = 20), monoblastic, terminal, integrated, elongated, hyaline to pale brown, often separating from the conidia through a break or frill below the base of conidium. *Conidia* 30–35 × 17–19 µm ($\bar{x}$ = 32.9 × 17.8 µm, n = 30), 4–6-septate, ellipsoidal to oval, pale brown at apical and basal cells, with dark brown to black central cells, with a thick dark band on the central septum, smooth-walled, rounded at apex, truncate at base, sometimes released with part of conidiogenous cell, conidial secession schizolytic. **Sexual morph**: Not observed.

Culture characteristic: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm in one month at 25℃, circular with entire margin, surface rough, density, radially striated, from above white, from below yellowish to pale brown, wrinkled.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-9 (MFLU 25-0098), living culture MFLUCC 25-0185.

GenBank numbers: MFLUCC 25-0185: ITS = PQ608331, LSU = PQ608162, SSU = PQ608018.

Known hosts: on decaying wood in a stream (Su et al., 2015); *Coffea arabica* (This study).

Known distribution: China (Su et al., 2015); Thailand (This study).

Notes: Phragmocephala atra was introduced by Mason and Hughes (1951). Su et al. (2015) identified it with DNA sequence data and morphological comparison collected from submerged wood from freshwater streams in Yunnan Province, China. In our phylogenetic analysis, our strain clusters with *P. atra* (LCGS09-2) with 92% ML and 0.96 BYPP statistical support (Figure 2.68). Our species also confirms the key morphological feature of *P. atra* in the dark brown to black central cells of the conidial, referring to the protologue and recent descriptions (Mason & Hughes, 1951; Taylor & Hyde, 2003; Su et al., 2015; Figure 2.69). We, therefore, identified our collection as *P. atra* which is a new host record and new country record from a coffee host in Thailand.



Figure 2.90 *Phragmocephala atra* (MFLU 25-0098, new host and country record)

Figure 2.90 a, b Synnemata on a decaying branch of *Coffea arabica*. c–f Squash mount of synnemata in distilled water. g–i Conidiogenous cells with conidia. j–m Conidia. n Germinating conidium. o Culture on PDA from above and below. Scale bars: c–f = 50 µm, g–n = 20 µm.

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

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

Notes: Based on the phylogenetically basal to *Massaria* species and morphologically distinct, *Neomassaria* was introduced as a novel genus in Massariaceae by Hyde et al. (2016), with *N. fabacearum* as the type species. Later, a neomassaria-like species, *N. formosana* was collected and based on phylogenetic analyses of concatenated LSU, *RPB*2, SSU and *TEF*1-α loci, and it formed a sister group with *N. fabacearum;* however, those two species formed a monophyletic and well-supported lineage with an uncertain phylogenetic placement within Pleosporales (Ariyawansa et al., 2018). Thus, the new family Neomassariaceae was proposed for the genus *Neomassaria* (Ariyawansa et al., 2018). Ten *Neomassaria* species listed in Index Fungorum (2025) and all these species have been reported as saprobes on dead branches, distributed mainly in China, Thailand, and Italy (Ariyawansa et al., 2018; Hyde et al., 2016; De Silva et al., 2022; Yang et al., 2022; Yang et al., 2023; Zhang et al., 2024; Lu et al., 2025). The sexual morph of *Neomassaria* is characterized by having immersed, subglobose to globose ascomata, central ostioles, a peridium comprising cells of *textura angularis*, pseudoparaphyses, 8-spored, bitunicate oblong to cylindrical, pedicellate asci, containing ellipsoid to fusiform, 1-septate, hyaline ascospores, with or without a gelatinous sheath (Hyde et al., 2016). The asexual morph is characterized by hyphomycetous, macronematous and mononematous conidiophores; monoblastic and holoblastic, integrated, terminal, cylindrical, and dark brown conidiogenous cells; with septate, acrogenous, solitary, obclavate, pale brown to brown conidia, hyaline towards apex (Zhang et al., 2024). In this study, five new species and two new records are introduced from the host of coffee; among them, one of the new species was collected from Thailand, and the other from China. In addition, coelomycetous asexual characteristics are introduced in *Neomassaria* for the first time.



Figure 2.91 Phylogenetic tree of *Neomassaria*

Figure 2.91 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Seventy-seven strains are included in the combined sequence analysis, which comprises 4,267 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Berkleasmium thailandicum* (MFLUCC 17-2000) and *Berkleasmium longisporum* (MFLUCC 17-1999).

Neomassaria asexualis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903632; *Facesoffungi number*: FoF 17577; Figure 2.71

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

Holotype: MHZU 24-0549

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 100–200 × 80–250 µm ($\overline{x}$ = 161 × 150 µm, n = 15), solitary to gregarious, unilocular, subglobose to irregular, immersed, small black spots on the host surface, ostioles central. *Conidiomatal wall* 12–18 µm wide ($\overline{x}$ = 14 µm, n = 15), hyaline to brown, thin, 2–4 layers, outer layer composed of brown cells of *textura angularis*, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* arising from the inner layer of conidioma, at times reduced to conidiogenous cells. *Sporodochial conidiogenous cells* 6–12 × 1.5–2.5 µm ($\overline{x}$ = 10 × 1.9 µm, n = 30), polyphialidic, lining the inner cavity, hyaline, smooth, terminal, integrated, subcylindrical to cylindrical, straight, thin-walled, with minute periclinal thickenings, collarette absent or indistinct. *Conidia* 3.5–5.5 × 1–2 µm ($\overline{x}$ = 4.4 × 1.7 µm, n = 35), hyaline, oblong, guttules, aseptate, rounded at both ends, forming conidial chains that remain attached. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours. Colonies on PDA reaching 4 cm diam. after one month at 25°C, circular, slightly raised, surface rough with transparent viscous liquid, entire edge, green, white aerial mycelium outside. Dark green from below.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp. (22°31'18", 101°2'44", 856.89 m), 15 September 2021, Li Lu, JHPW 26 (MHZU 24-0549, holotype), ex-type ZHKUCC 24-1003, other living culture ZHKUCC 24-1004.

GenBank numbers: ZHKUCC 24-1003: ITS = PQ608308, LSU = PQ608141, SSU = PQ607995, *TEF*1-α = PQ628154, *RPB*2 = PV221310; ZHKUCC 24-1004: ITS = PQ608309, LSU = PQ608142, SSU = PQ607996, *TEF*1-α = PQ628155, *RPB*2 = PV221311.

Notes: Neomassaria has been reported mainly by its sexual morph (Ariyawansa et al., 2018; Hyde et al., 2016; De Silva et al., 2022; Yang et al., 2023), only *N. thailandica* has been reported as asexual morph (hyphomycetes) (Zhang et al., 2024). In the multi-gene phylogenetic tree, our asexual species *N. asexualis* formed a separate branch under *N. livistonae* (SNC146, type) with 82% ML, 0.97 BYPP statistical support (Figure 2.70). We could not compare the morphology with the species of *Neomassaria*, as our isolates were only the asexual morph (coelomycetous) (Figure 2.71). Based on nucleotide comparisons, *N. asexualis* (ZHKUCC 24-1003, ex-type) is different from the *N. livistonae* (SNC146, type) by 23/932 bp (2.5%, without gaps) of the ITS, 12/946 bp (1.3%, without gaps) of the *TEF*1-α and 20/858 bp (2.3%, without gaps) of the *RPB*2, SSU and LSU are basically the same. Therefore, *N. asexualis* was introduced here as a new species in *Neomassaria* from *Coffea* sp. in China, which is the first coelomycetous asexual morph of *Neomassaria*.

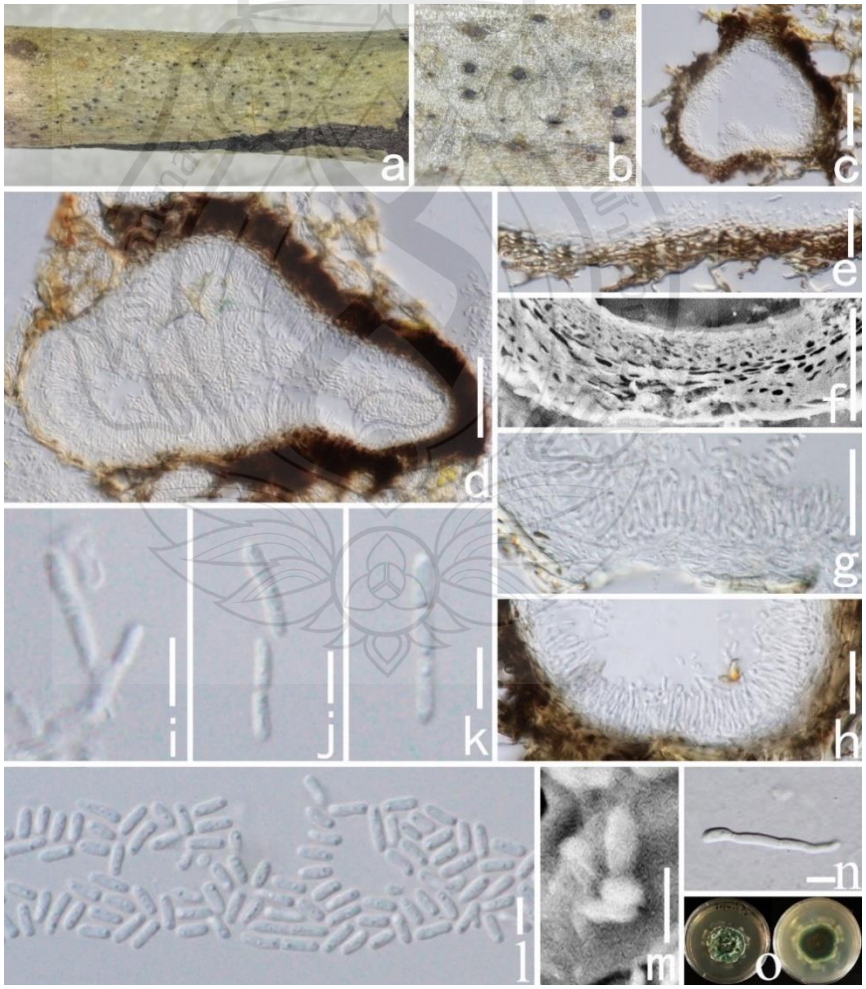


Figure 2.92 *Neomassaria asexualis* (MHZU 24-0549, holotype)

Figure 2.92 a, b Conidiomata on a decaying branch of *Coffea* sp. c, d Longitudinal section of conidiomata. e, f Conidiomata wall (f: SEM microphotographs of conidioma wall). g, h Sporodochial conidiogenous cells with conidia. i–m Conidia (m: SEM microphotographs of conidia). n Germinated conidium. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–h = 20 µm, i–n = 5 µm.

Neomassaria coloradensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903633; *Facesoffungi number*: FoF 17578; Figure 2.72

Etymology: The species epithet refers to the brown ascospores.

Holotype: MFLU 25-0096

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 250–550 µm high × 300–599 µm diam. ($\overline{x}$ = 400 × 368 µm, n = 15), scattered to gregarious, semi-immersed, coriaceous, dome-shaped, appearing as dark black raised regions on host surface, unilocular, globose or subglobose, carbonaceous, ostioles central. *Peridium* 40–80 µm wide ($\overline{x}$ = 59 µm, n = 15), multilayered, apical areas more darkened in pigments and thicker, outer layers almost disappear at base and fused with host, inner layers hyaline, comprising hyaline and thick-walled cells of *textura intricata* to *textura angularis*. *Hamathecium* of 1.5–2.5 µm wide ($\overline{x}$ = 2 µm, n = 20), anastomosing, trabecular pseudoparaphyses, hyaline, branched, numerous. *Asci* 100–130 × 8–13 µm ($\overline{x}$ = 117 × 10 µm, n = 20), 2–8-spored, bitunicate, fissitunicate, short stalked, some club-like, oblong to cylindrical, straight or slightly curved. *Ascospores* 10–18 × 6–7 µm ($\overline{x}$ = 15 × 6.4 µm, n = 30), uniseriate, hyaline to dark brown, ellipsoid to broadly fusiform, 1-septate in the middle, slightly constricted at the septum, upper and lower cells have germ slits when mature, asymmetrical, guttulate, mature ascospores have a germ slit oblique in relation to the cell axis, surrounded by a thin mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA slowly growing, reaching 1.5 cm diam. after one month at 25°C, circular, yellow, slightly raised, entire margin. Yellow to brown from below.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea* sp., 01 November 2023, Li Lu, LC3-2-2 (MFLU 25-0096, holotype), ex-type MFLUCC 25-0183.

GenBank numbers: MFLUCC 25-0183: ITS = PQ608305, LSU = PQ608138, SSU = PQ607992, *TEF*1-α = PQ628151, *RPB*2 = PV221307.

Notes: Phylogeny based on combined ITS, LSU, SSU, *TEF*1-α, and *RPB*2 sequence data (Figure 2.70) indicates that our isolate (MFLUCC 25-0183, ex-type) formed an independent branch with 93% ML, 1.00 BYPP statistical support, within *Neomassaria.* Morphologically, our new collection fits the descriptions of *Neomassaria* by having oblong to cylindrical asci with short pedicels, and 1-septate, hyaline and ellipsoid to fusiform ascospore, and a sheath (Hyde et al., 2016; Ariyawansa et al., 2018). However, our strain can be distinguished from other *Neomassaria* species by the 2–8-spored asci, brown ascospores, as well as the germ slits (Figure 2.72). Therefore, our isolate are introduced here as a new species in *Neomassaria*, named as *N. coloradensis,* which was collected from *Coffea* sp. in Thailand.

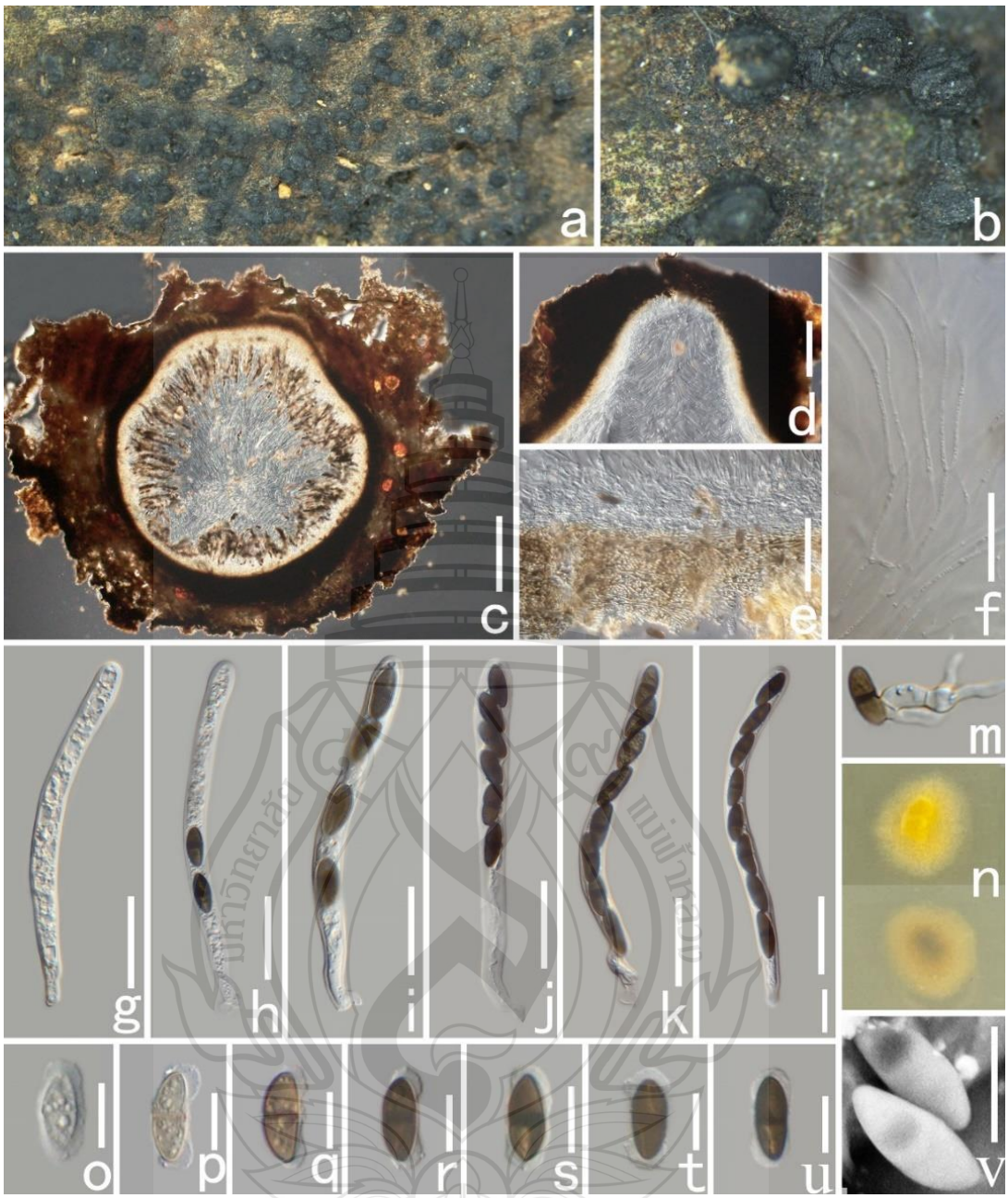


Figure 2.93 *Neomassaria coloradensis* (MFLU 25-0096, holotype)

Figure 2.93 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d Ostiole. e Peridium. f Hamathecium of trabeculate. g–l Asci. m Germinated ascospore. n Culture on PDA from above and below. o–v Ascospores (v: SEM microphotographs of ascospores). Scale bars: c = 100 μm, d, e = 50 μm, f–l = 30 μm, m, o–t = 10 μm.

Neomassaria coffeae L. Lu & Tibpromma, sp. nov. Figure 2.14.

Index Fungorum number: IF 901004; *Facesofungi number:* FoF 14730.

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137608.

Saprobic on a decaying branch of *C. arabica*. Sexual morph: *Ascomata* 150–220 µm high × 150–250 µm diam. ($\overline{x}$ = 191 × 210 µm, n = 15), solitary to gregarious, semi-immersed to immersed, coriaceous, visible as black dots on the substrate, unilocular, globose or subglobose, ostioles central. *Peridium* 10–20 µm wide ($\overline{x}$ = 14 µm, n = 15), outer walls comprising 3–4 layers of *textura prismatica* cells, brown to dark brown, inner walls thin, hyaline and density. *Hamathecium* 1.5–2.5 µm wide ($\overline{x}$ = 2 µm, n = 20), hyaline, filiform, septate, branched, cellular, numerous pseudoparaphyses. *Asci* 80–110 × 10–15 µm ($\overline{x}$ = 93 × 13 µm, n = 20), 8-spored, bitunicate, fissitunicate, oblong to cylindrical, straight, sometimes with short pedicellate, with ocular chamber. *Ascospores* 15–18 × 5–7 µm ($\overline{x}$ = 16.5 × 5.6 µm, n = 30), uniseriate to biseriate, hyaline, yellowish when mature, ellipsoid to broadly fusiform, 1-septate in the middle, constricted at the septum, guttulate, surrounded by mucilaginous sheath observed clearly when mature. Asexual morph: Not observed.

Culture characteristics: Ascospore germinating within 24 h on PDA. Colonies reached 4 cm in diameter after two months at 25°C. Colonies obverse: circular, flat to slightly raised, fluffy, with filiform margin, white; reverse: brown in centre with yellowish to white edges.

Materials examined: China, Yunnan Province, Baoshan, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (24°9' N, 98°8' E, 1210 m alt.), 30 July 2022, LiLu, BS2-C19 (HKAS 137608, holotype), isotype MHZU 23-0066, ex-type living culture KUNCC 24-18349 = KUNCC 24-18350, ex-isotype living culture ZHKUCC 23-0642 = ZHKUCC 23-0643.

Notes: According to the multi-gene phylogeny, *Neomassaria coffeae* forms a sister lineage to *N. fabacearum* (Figure 2.15). Morphologically, *N. coffeae* can be distinguished from *N. fabacearum* by having guttulate ascospores with mucilaginous sheath and *textura prismatica* peridium (Figure 2.14; Hyde et al., 2016). Based on nucleotide comparisons, *N. coffeae* (ZHKUCC 23-0642) is different from the type

species *N. fabacearum* (MFLU 16-1875) by 18/883 bp (2%, without gaps) of the LSU, 5/868 bp (0.6%, without gaps) of the SSU and 46/843 bp (5.5%, without gaps) of the *TEF*1-α. In addition, the PHI test results (Figure 2.22g) revealed no significant recombination relationships between *N. coffeae* and its phylogenetically related taxa. Therefore, based on morphological characteristics and phylogenetic analyses, we introduce our strains as a new species, *N. coffeae*.

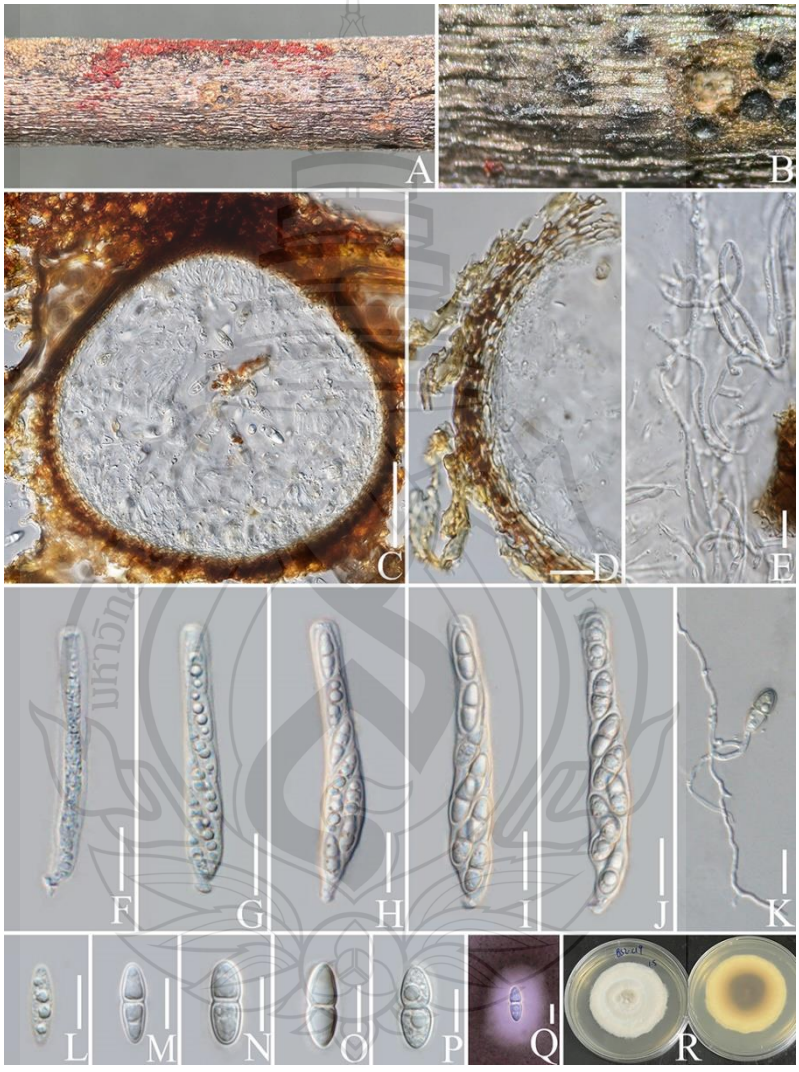


Figure 2.94 *Neomassaria coffeae* (HKAS 137608, holotype)

Figure 2.94 A, B Ascomata on a decaying branch of *C. arabica*; C Longitudinal section of an ascoma; D Peridium wall; E Pseudoparaphyses; F–J Asci; K Germinated ascospore; L–P Ascospores; Q An ascospore stained with Indian ink; R Culture on PDA from obverse and reverse. Scale bars: C = 50 μm, D, E, L–Q = 10 μm, F–K = 20 μm.

Neomassaria formosana Ariyaw., Jaklitsch & Voglmayr, Cryptog. Mycol. 39 (3): 368 (2018)

Index Fungorum number: IF 827114; *Facesoffungi number*: FoF 17579; Figure 2.73

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 250–350 × 200–360 µm ($\overline{x}$ = 285 × 296 µm, n = 15), immersed with erumpent neck, solitary, unilocular, coriaceous, globose to subglobose, brown to black, ostiole central. *Peridium* 20–30 µm wide ($\overline{x}$ = 27 µm, n = 15), hyaline to light brown, comprising 3–4 layers, relatively thick-walled cells of *textura angularis*, thinner-walled and lighter at the inner side, outside fusing with the host. *Hamathecium* of 1.5–2.5 µm wide ($\overline{x}$ = 1.7 µm, n = 20), hyaline, septate, branched, anastomosing, trabecular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 90–110 × 7–9 µm ($\overline{x}$ = 100 × 7.8 µm, n = 20), 8-spored, bitunicate, fissitunicate, oblong to cylindrical, short-stalked and club-shaped, apically rounded, straight. *Ascospores* 20–25 × 4–6 µm ($\overline{x}$ = 22 × 4.7 µm, n = 30), overlapping 1–2-seriate, hyaline, fusoid to ellipsoid, 1-septate in the middle, constricted at the septum, slightly enlarged towards the median septum, narrowly rounded at both ends, some guttulate, without a mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 3 cm diam. after one month at 25°C, irregular, white, slightly raised in the middle, filiform margin, with cottony texture, radially striated. White to dark green from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp. (856.8 m), 15 September 2021, Li Lu, JHPW10 (MHZU 24-0548), living culture ZHKUCC 24-1001, other living culture ZHKUCC 24-1002.

GenBank numbers: ZHKUCC 24-1001: ITS = PQ608303, LSU = PQ608136, SSU = PQ607990, *TEF*1-α = PQ628149, *RPB*2 = PV221305; ZHKUCC 24-1002: ITS = PQ608304, LSU = PQ608137, SSU = PQ607991, *TEF*1-α = PQ628150, *RPB*2 = PV221306.

Known hosts: dead stems of *Rhododendron* sp. (Ariyawansa et al., 2018), decaying petioles of *Trachycarpus fortunei* (Zhang et al., 2024), *Coffea* sp. (This study).

Known distribution: China (Ariyawansa et al., 2018; Zhang et al., 2024; This study).

Notes: The type species, *Neomassaria formosana* was originally described as saprobic on dead stems of *Rhododendron* sp. from China (Ariyawansa et al., 2018). In the phylogenetic tree, our collection formed a sister lineage to *N. formosana* (NTUCC 17-007, ex-type) with 100% ML, 1 BYPP statistical support (Figure 70). The blast results of LSU, SSU, *TEF*1-α, and *RPB2* genes also showed 99% similarity with *N. formosana* (NTUCC17-007 (ex-type), NTUCC17-008, and NTUCC17-009). Morphologically, the features of our strain are almost the same as the holotype *N. fabacearum* in having fusoid to ellipsoid ascospores with guttules and narrowly rounded ends (Ariyawansa et al., 2018; Figure 2.73). Therefore, our strain is introduced here as a new host record of *N. formosana* from *Coffea* sp. in China.

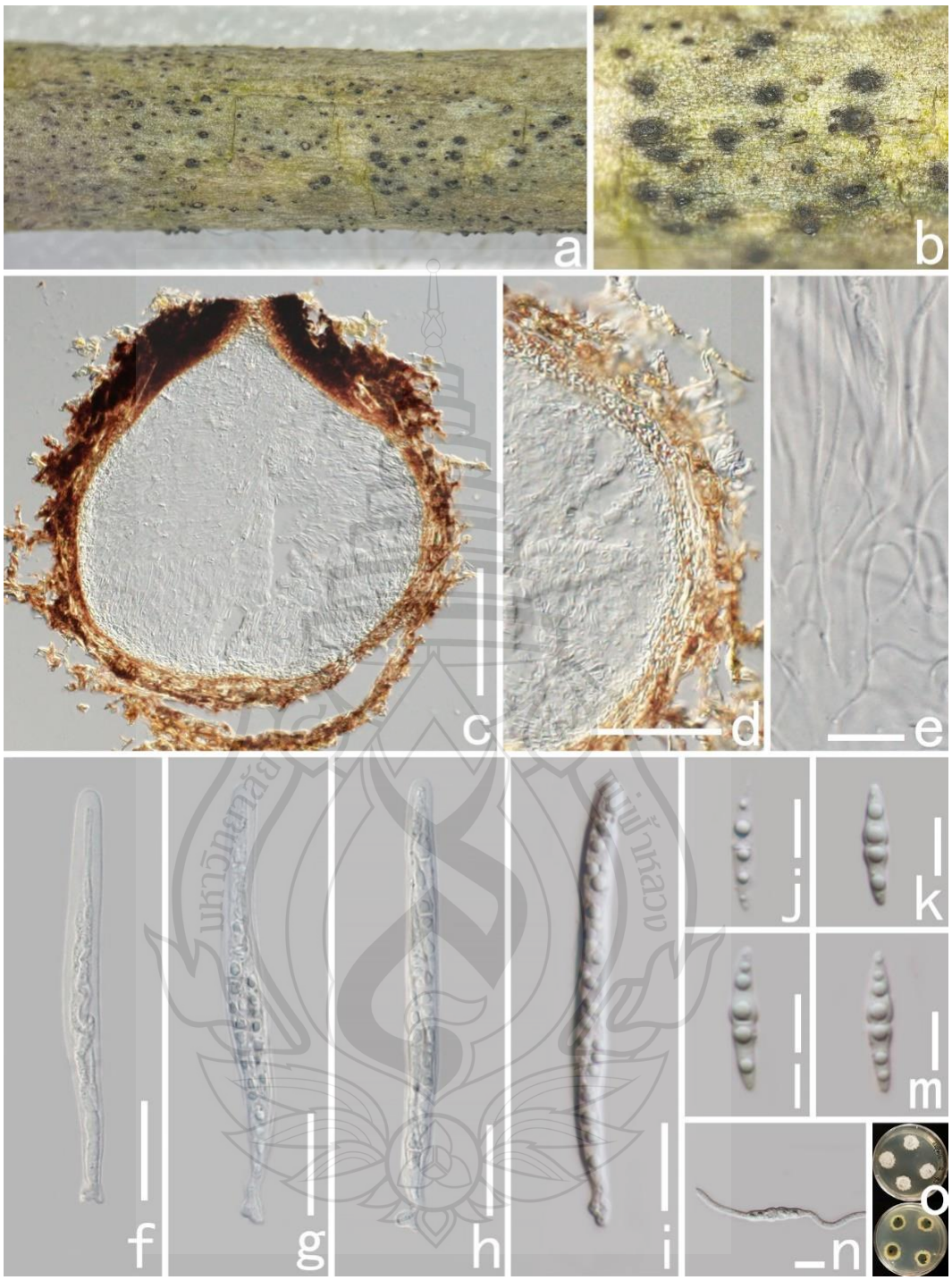


Figure 2.95 *Neomassaria formosana* (MHZU 24-0548, new host record)

Figure 2.95 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d Peridium. e Hamathecium of trabeculate. f–i Asci. j–m Ascospores. n Germinated ascospore. o Culture on PDA from above and below. Scale bars: c = 100 µm, d, e = 50 µm, f–i = 20 µm, j–n = 10 µm.

Neomassaria palmae S.N. Zhang, K.D. Hyde & Jian K. Liu, Fungal Diversity 10.1007/s13225-024-00536-9: [95] (2024)

Index Fungorum number: IF 901932; *Facesoffungi number*: FoF 15958; Figure 2.74

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 150–250 × 150–280 µm ($\overline{x}$ = 183 × 230 µm, n = 15), solitary to gregarious, semi-immersed to immersed, coriaceous, visible as black dots on the substrate, unilocular or multilocular, globose or subglobose, ostioles central. *Peridium* 10–20 µm wide ($\overline{x}$ = 15 µm, n = 15), comprising 2–4 layers of *textura globulosa* cells, brown to dark brown, some almost inseparable from the substrate. *Hamathecium* of 1.5–2.5 µm wide ($\overline{x}$ = 1.8 µm, n = 20), anastomosing, trabecular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–110 × 10–15 µm ($\overline{x}$ = 90 × 13.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, oblong to cylindrical, straight, or slightly curved, with short pedicels, and with a flat ocular chamber. *Ascospores* 17–25 × 5–7 µm ($\overline{x}$ = 21 × 6 µm, n = 30), uniseriate to biseriate, hyaline, ellipsoid to fusiform, 1-septate in the middle, constricted at the septum, guttulate, surrounded by a thick mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 4 cm diam. after one month at 25°C, surface rough, white, irregular, slightly raised, undulate margin, with fluffy aerial mycelium on the surface. White to dull green from below, wrinkled at the middle.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (98°8' E, 24°9' N, 1209 m), 30 July 2022, Li Lu, BS2-C16 (ZHKU 24-0551), living culture ZHKUCC 24-1007, other living culture ZHKUCC 24-1008.

GenBank numbers: ZHKUCC 24-1007: ITS = PQ608310, LSU = PQ608143, SSU = PQ607997, *TEF*1-α = PQ628156, *RPB*2 = PV357177; ZHKUCC 24-1008: ITS = PQ608311, LSU = PQ608144, SSU = PQ607998, *TEF*1-α = PQ628157, *RPB*2 = PV357178.

Known hosts: Rhapis excelsa (Zhang et al., 2024), *Coffea* sp. (This study).

Known distribution: China (Zhang et al., 2024; This study).

Notes: Zhang et al. (2024) introduced *Neomassaria palmae* based on a collection from decaying rachides of *Rhapis excelsa* in China. Our collection is grouped with *N. palmae* (SNC146, ex-type), which is 100% ML and has 1.00 BYPP statistical support (Figure 2.70). We recognize our collection as *N. palmae* as they share the same morphology and almost identical molecular data (Zhang et al., 2024; Figure 2.74). A new host record for *N. palmae* from a coffee plant is provided herein.

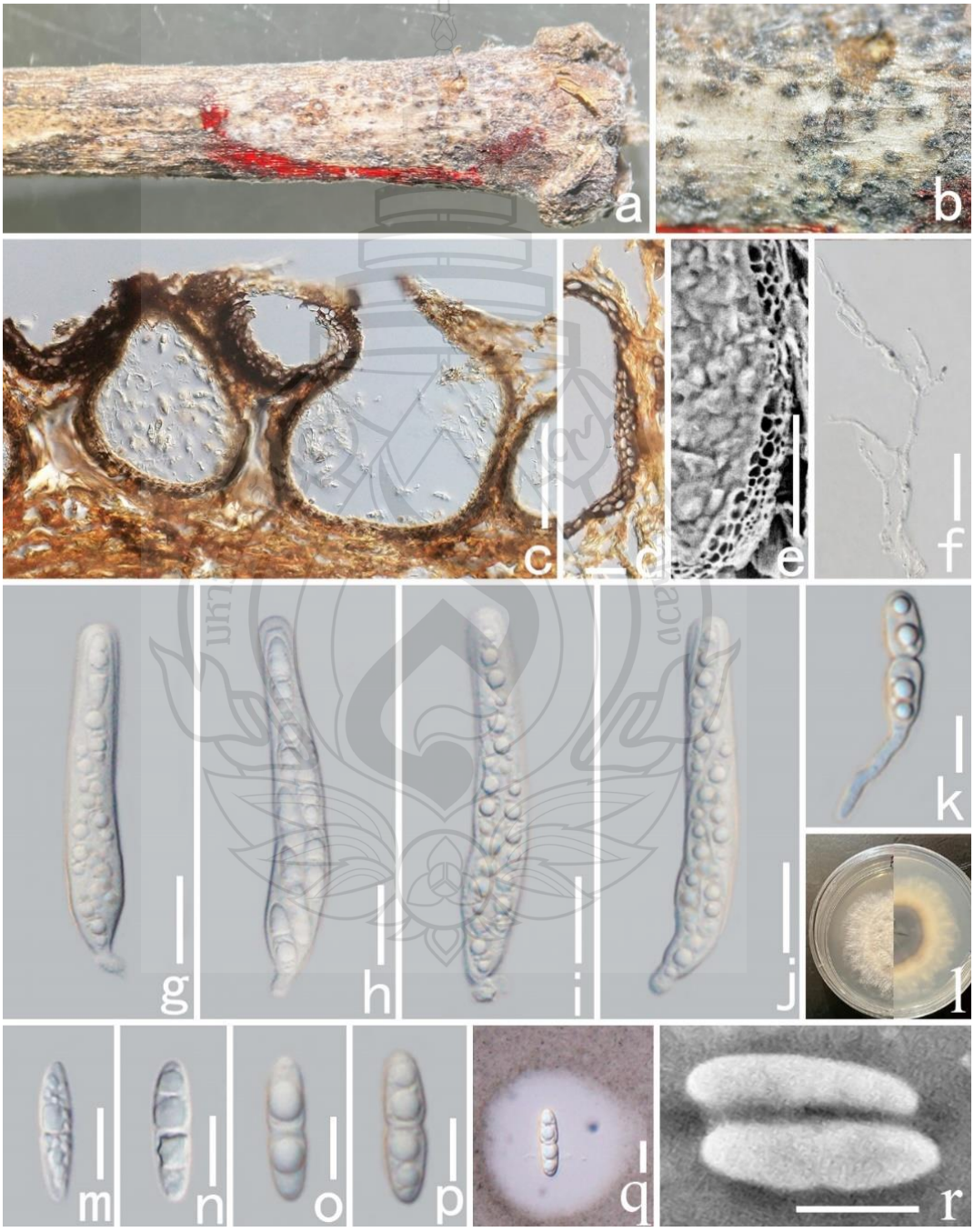


Figure 2.96 *Neomassaria palmae* (ZHKU 24-0551, new host record)

Figure 2.96 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascomata. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium of trabeculate. g–j Asci. k Germinated ascospore. l Culture on PDA from above and below. m–r Ascospores (q: An ascospore stained with Indian ink; r: SEM microphotographs of ascospores). Scale bars: c = 100 μm, d, e = 30 μm, f–j = 20 μm, k, m–r = 10 μm.

Neomassaria puerensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903634; *Facesoffungi number*: FoF 17580; Figure 2.75

Etymology: The epithet of the species refers to the type location "Pu'er", China.

Holotype: MHZU 24-0547

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph:** *Ascomata* 200–300 × 200–300 μm ($\bar{x}$ = 269 × 272 μm, n = 15), subglobose to globose, sparse, immersed, arising protuberant black cristae on superficial, dark brown to black. *Peridium* 35–55 μm wide ($\bar{x}$ = 43 μm, n = 20), multilayered, hyaline to light brown, comprising cells of *textura epidermoidea*. *Hamathecium* of 1–2 μm wide ($\bar{x}$ = 1.5 μm, n = 20), hyaline, anastomosing, trabecular pseudoparaphyses. *Asci* 80–120 × 6.5–8.5 μm ($\bar{x}$ = 98 × 7.5 μm, n = 20), bitunicate, fissitunicate, 8-spored, short stalked and club-like, cylindrical to filiform, straight. *Ascospores* 15–25 × 3–5 μm ($\bar{x}$ = 20 × 4 μm, n = 30), overlapping uniseriate, hyaline, fusoid, 1-septate in the middle, constricted at the septum, guttulate, without a mucilaginous sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 2 cm diam. after one month at 25°C, irregular, slightly raised, radially striated with lobate edge, green. Dark green from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC30 (MHZU 24-0547, holotype), ex-type ZHKUCC 24-0999, other living culture ZHKUCC 24-1000.

GenBank numbers: ZHKUCC 24-0999: ITS = PQ608306, LSU = PQ608139, SSU = PQ607993, *TEF*1-α = PQ628152, *RPB*2 = PV221308; ZHKUCC 24-1000: ITS = PQ608307, LSU = PQ608140, SSU = PQ607994, *TEF*1-α = PQ628153, *RPB*2 = PV221309.

Notes: Phylogeny combined ITS, LSU, SSU, *TEF*1-α, and *RPB*2 sequence data (Figure 2.70) indicates that *Neomassaria puerensis* (ZHKUCC 24-0999, ex-type and ZHKUCC 24-1000) formed a separate lineage near to *N. livustonae* (SNC146, type) with 71% ML and 0.93 BYPP statistical support. Our new collection is morphologically similar to *N. livustonae* in having 1-septate, hyaline, and fusoid ascospores (Zhang et al., 2024). However, *N. puerensis* can be distinguished from *N. livustonae* by ascomata producing protuberant black cristae on substrate and small ascospores (15–25 × 3–5 µm, L/W = 3–8.3 vs. 24–28 × 4–6 µm, L/W = 4–7) (Figure 75). Besides, based on nucleotide comparisons, *N. puerensis* (ZHKUCC 24-0999, ex-type) is different from the *N. livustonae* (SNC146, type) by 15/952 bp (1.6%, without gaps) of the ITS, 38/940 bp (4%, without gaps) of the *TEF*1-α and 12/1026 bp (1.2%, without gaps) of the *RPB*2, while LSU and SSU are similar. Therefore, *N. puerensis* is introduced here as a new species in *Neomassaria*, collected from *Coffea* sp. in China.

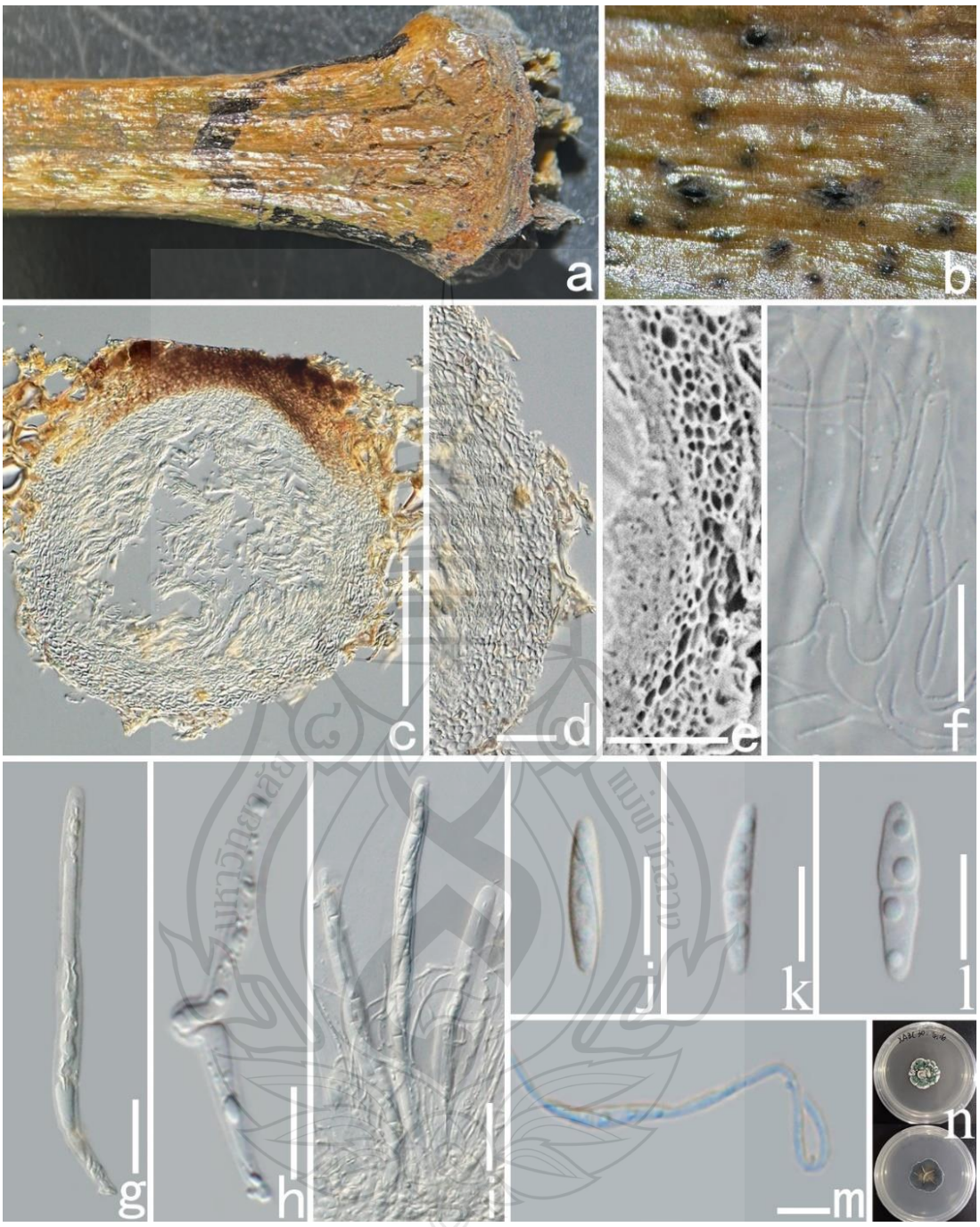


Figure 2.97 *Neomassaria puerensis* (MHZU 24-0547, holotype)

Figure 2.97 a, b Ascomata on a decaying branch of *Coffea arabica*. c Longitudinal section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium of trabeculate. g–i Asci. j–l Ascospores. m Germinated ascospore. n Culture on PDA from above and below. Scale bars: c = 100 µm, d, e = 30 µm, f–i= 20 µm, j–m = 10 µm.

Neomassaria yunnanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903635; *Facesoffungi number*: FoF 14378; Figure 2.76

Etymology: The species epithet refers to the type location "Yunnan", China.

Holotype: MHZU 24-0550

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 180–230 × 240–280 µm ($\bar{x}$ = 210 × 26 µm, n = 15), immersed, solitary or scattered, unilocular, globose to subglobose, ostioles central. *Peridium* 15–30 µm wide ($\bar{x}$ = 20 µm, n = 15), light brown to hyaline, comprising 2–4 layers of cells of *textura angularis*. *Hamathecium* of 1.5–2.5 µm wide ($\bar{x}$ = 1.8 µm, n = 20), hyaline, septate, branched, anastomosing, trabecular pseudoparaphyses. *Asci* 100–120 × 10–15 µm ($\bar{x}$ = 109 × 13 µm, n = 20), 8-spored, bitunicate, fissitunicate, oblong to cylindrical, short pedicellate and club-like, apically with a long ocular chamber. *Ascospores* 17–20 × 5–6 µm ($\bar{x}$ = 19 × 5.4 µm, n = 30), overlapping 1–2-seriate, hyaline, ellipsoid to broadly fusiform, 1-septate in the middle, slightly constricted at the septum, guttulate, surrounded by a thick mucilaginous sheath. **Asexual morph:** Not observed.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp. (1672 m), 12 September 2021, Li Lu, JHMH12 (MHZU 24-0550, holotype), ex-type ZHKUCC 24-1005, other living culture ZHKUCC 24-1006.

GenBank numbers: ZHKUCC 24-1005: ITS = PQ608301, LSU = PQ608134, SSU = PQ607988, *TEF*1-α = PQ628147, *RPB*2 = PV221303; ZHKUCC 24-1006: ITS = PQ608302, LSU = PQ608135, SSU = PQ607989, *TEF*1-α = PQ628148, *RPB*2 = PV221304.

Notes: Phylogenetic analyses of the combined ITS, SSU, LSU, *RPB*2 and *TEF*1-α sequences dataset shows that *N. yunnanensis* separates well with *N. fabacearum* (MFLUCC 16-1875 and MFLU 15-0372, type), with a strong statistical support (97% ML, 1.00 BYPP; Figure 70). Morphologically, *N. yunnanensis* resembles *N. fabacearum* in having ellipsoid to broadly fusiform ascospores but differs by possessing asci with long apical ocular chamber, whereas *N. fabacearum* has a wide ocular chamber (Hyde et al., 2016; Figure 2.76). Based on nucleotide comparisons, *N. yunnanensis* (ZHKUCC 24-1005, ex-type) is different from the *N. fabacearum* (MFLU 15-0372, type) by 90/844 bp (10.6%, without gaps) of the *TEF*1-α, LSU and

SSU are similar. However, *N. fabacearum* do not have ITS and *RPB*2 gene sequence data. Herein, *N. yunnanensis* is introduced as a new species.



Figure 2.98 *Neomassaria yunnanensis* (MHZU 24-0550, holotype)

Figure 2.98 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium of trabeculate. g–j Asci. k–o Ascospores (k: SEM microphotographs of ascospore; o: ascospore surrounded by a hyaline gelatinous sheath in Indian ink). Scale bars: c = 50 μm, d–j = 20 μm, k–o = 10 μm.

Neomassarinaceae Mapook & K.D. Hyde, Fungal Diversity 101: 52 (2020)

Pseudohelminthosporium Phukhams. & K.D. Hyde, Fungal Diversity: 59 (2020)

Notes: *Pseudohelminthosporium* was introduced by Phukhamsakda et al. (2020) with the type species *P. clematidis*, which is a first report of the asexual morph in Neomassarinaceae, based on the multi-gene analysis. *Pseudohelminthosporium* is morphologically similar to *Helminthosporium* in having brown to dark brown phragmosporous conidia (Voglmayr & Jaklitsch, 2017; Phukhamsakda et al., 2020). Based on the asexual morph of the species *P. clematidis*, *Pseudohelminthosporium* is distinguishable by its macronematous conidiophores, solitary and branched at the apex, stripes straight or flexuous, with monotretic or polytretic conidiogenous cells, phragmosporous, broad fusiform or obclavate conidia, distoseptate when young, becoming aseptate at maturity, with hyaline, elongate c ells at the upper end of the conidia and with a large guttulate in each cell (Phukhamsakda et al., 2020). *Pseudohelminthosporium clematidis* is a hyphomycete and reported on decaying wood or herbaceous plant material in terrestrial habitats in Thailand. In this study, we introduced the coelomycetous asexual state and sexual morph of *P. clematidis.* Furthermore, we reject the synonymization of *Pseudohelminthosporium* with *Neopodoconis* proposed by Koukol and Delgado (2021), which was based solely on morphological characteristics. Instead, our comprehensive morphological assessment and robust phylogenetic analysis confirm that *Pseudohelminthosporium* remains within Neomassarinaceae, reinstating the taxonomic identity of *Pseudohelminthosporium* as a distinct genus.

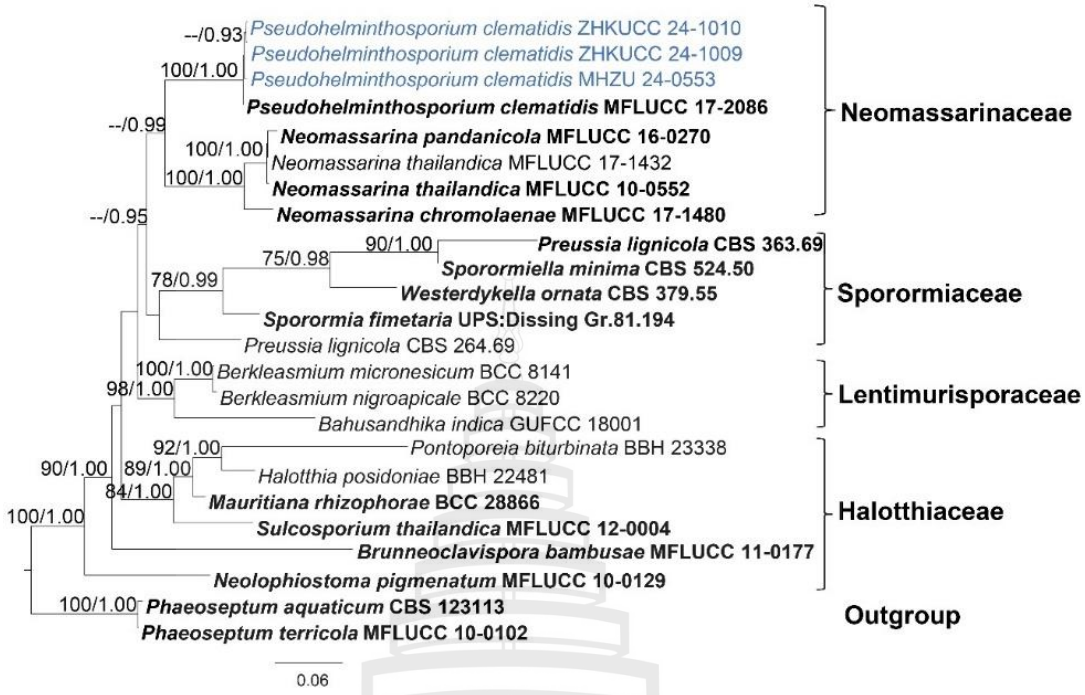


Figure 2.99 Phylogenetic tree of *Pseudohelminthosporium*

Figure 2.99 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Twenty-five strains are included in the combined sequence analysis, which comprises 4,248 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Phaeoseptum aquaticum* (CBS 123113) and *P. terricola* MFLUCC (10-0102).

Pseudohelminthosporium clematidis Phukhams. & K.D. Hyde, Fungal Diversity 102: 59 (2020)

Index Fungorum number: IF 557192; *Facesoffungi number*: FoF 07284, Figure 2.78, Figure 2.79.

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph (Figure 2.78):** *Ascomata* 150–250 × 200–300 µm ($\bar{x}$ = 188 × 241 µm, n = 15), immersed to semi-immersed, solitary, scattered, subglobose, coriaceous, dark brown to pale black. *Peridium* 15–25 µm wide ($\bar{x}$ = 20 µm, n = 20), comprising several layers of thick-walled,

yellowish brown to brown cells of *textura angularis. Hamathecium* of 1.5–2.5 µm wide ($\bar{x}$ = 1.8 µm, n = 20), hypha-like, branched, hyaline, filamentous, pseudoparaphyses. *Asci* 80–100 × 7–10 µm ($\bar{x}$ = 93 × 8 µm, n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, pedicellate. *Ascospores* 10–12 × 4.5–6 µm ($\bar{x}$ = 11.2 × 5 µm, n = 30), uni-seriate, ellipsoid with round ends, 1-septate, hyaline, constricted at the septum, granulate in each cell, surrounded by a thick mucilaginous sheath. **Asexual morph (Coelomycetes, Figure 2.79):** Coelomycetous. *Conidiomata* 70–100 × 80–140 µm ($\bar{x}$ = 90 × 116 µm, n = 15), immersed to semi-immersed, solitary, scattered, globose to subglobose, coriaceous, dark brown in the host surface. *Pycnidial wall* 8–10 µm wide ($\bar{x}$ = 9.5 µm, n = 20), comprising several layers of thick-walled, yellowish brown to hyaline cells of *textura angularis. Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–7.5 × 3–5 µm ($\bar{x}$ = 6 × 3.6 µm, n = X), enteroblastic, phialidic, ampulliform to subcylindrical, hyaline, smooth-walled. *Conidia* 3.5–4.5 × 2–3 µm ($\bar{x}$ = 3.9 × 2.9 µm, n = 30), ellipsoidal, hyaline, thin and smooth-walled, aseptate with guttules.

Culture characteristics: Ascospore germinating on PDA within 12 h. Colonies on PDA after four weeks at 25–27°C, raised in center, circular, white in surface, pale yellow in center, white edge from below (Figure 78-r).

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (1053 m), 30 July 2022, Li Lu, BS1-C26 (MHZU 24-0553); China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (25°14' N, 98.8 E, 737.3 m), 30 July 2022, Li Lu, BS4-C7 (MHZU 24-0552), living culture ZHKUCC 24-1009, other living culture ZHKUCC 24-1010.

GenBank numbers: MHZU 24-0553: ITS = PQ608327, SSU = PQ608014, *TEF*1-α = PQ628172, *RPB*2 = PV357185; ZHKUCC 24-1009: ITS = PQ608325, LSU = PQ608158, SSU = PQ608012, *TEF*1-α = PQ628170, *RPB*2 = PV357183; ZHKUCC 24-1010: ITS = PQ608326, LSU = PQ608159, SSU = PQ608013, *TEF*1-α = PQ628171, *RPB*2 = PV357184.

Known hosts: *Clematis sikkimensis* (Phukhamsakda et al., 2020); *Coffea* sp. (In this study).

Known distribution: Thailand (Phukhamsakda et al., 2020); China (In this study).

Notes: Morphologically, *Pseudohelminthosporium clematidis* was reported as a hyphomycetous asexual morph by Phukhamsakda et al. (2020). However, our isolates (MHZU 24-0552 and MHZU 24-0553) are coelomycetous sexual and asexual morphs (Figure 2.78, 2.79); hence, we cannot identify our isolates by comparing morphological characteristics. In the phylogenetic tree, our isolates formed a close lineage to the type species *P. clematidis* (100% ML/1.00 BYPP, Figure 2.77). Based on pairwise nucleotide comparisons, our isolates (ZHKUCC 24-1009) diverge from *P. clematidis* (MFLUCC 17-2081, ex-type) by 0/499 bp (0%, without gaps) for ITS, 0/800 bp (0%, without gaps) for LSU, 2/1000 bp (0.2%, without gaps) for SSU, 3/868 bp (0.34%, without gaps) for *TEF*1-α, 1/749 bp (0.13%, without gaps) for *RPB*2. Thus, based on phylogenetic analyses, we identified our collection MHZU 24-0552 as a sexual morph of *P. clematidis,* with another collection MHZU 24-0553 as asexual morph (coelomycetes). This is the first report of *P. clematidis* from a coffee host in China.

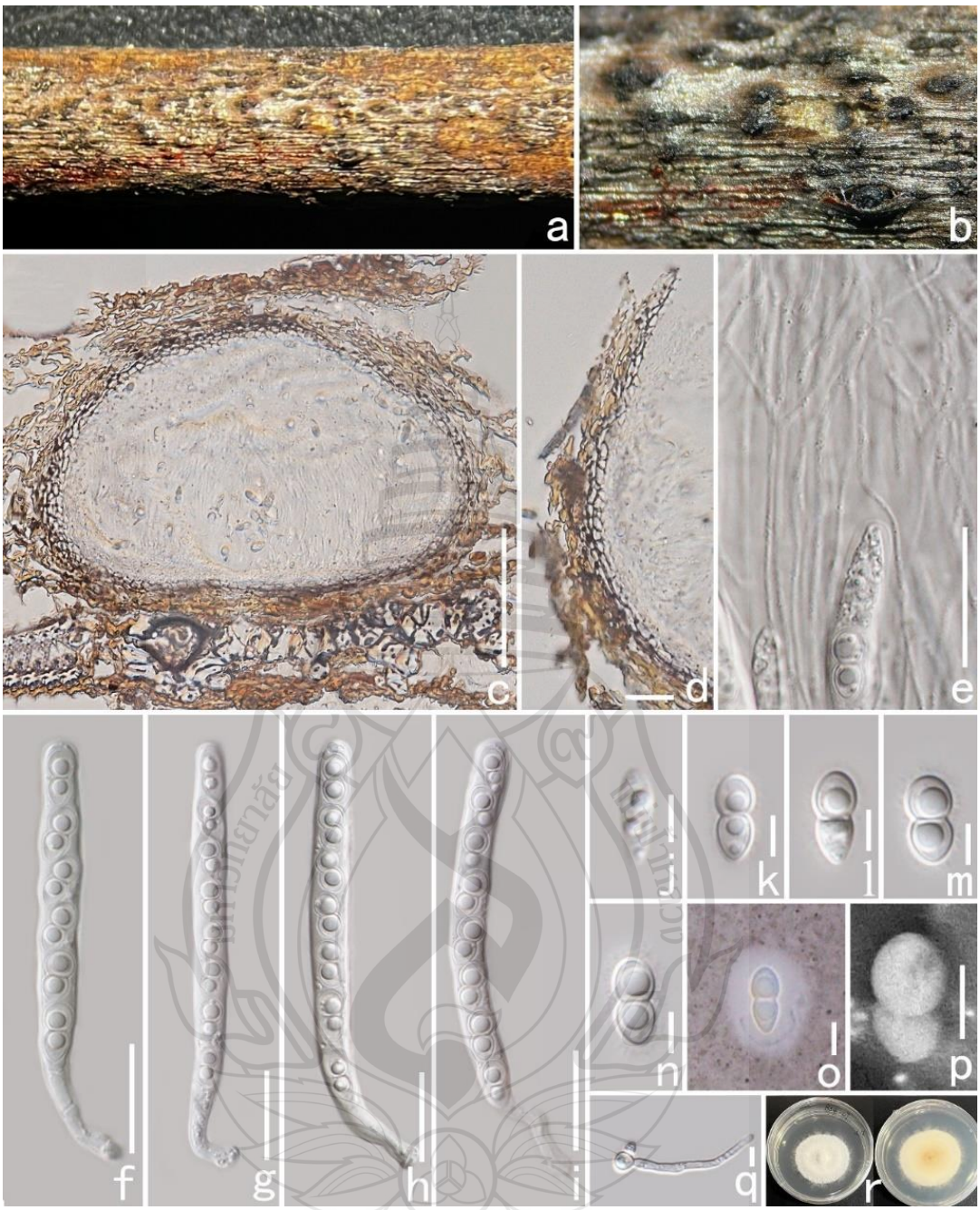


Figure 2.100 *Pseudohelminthosporium clematidis* (MHZU 24-0552, new sexual morph)

Figure 2.100 a, b Ascomata on the host surface. c Vertical section of ascoma. d Peridium. e Hamathecium. f–i Asci. j–p Ascospores (o: Ascospore stained with India ink; p: SEM microphotographs of ascospore). q Germinated ascospore. r Culture on PDA from above and below. Scale bars: c = 100 µm, d–i = 20 µm, k–q = 5 µm.

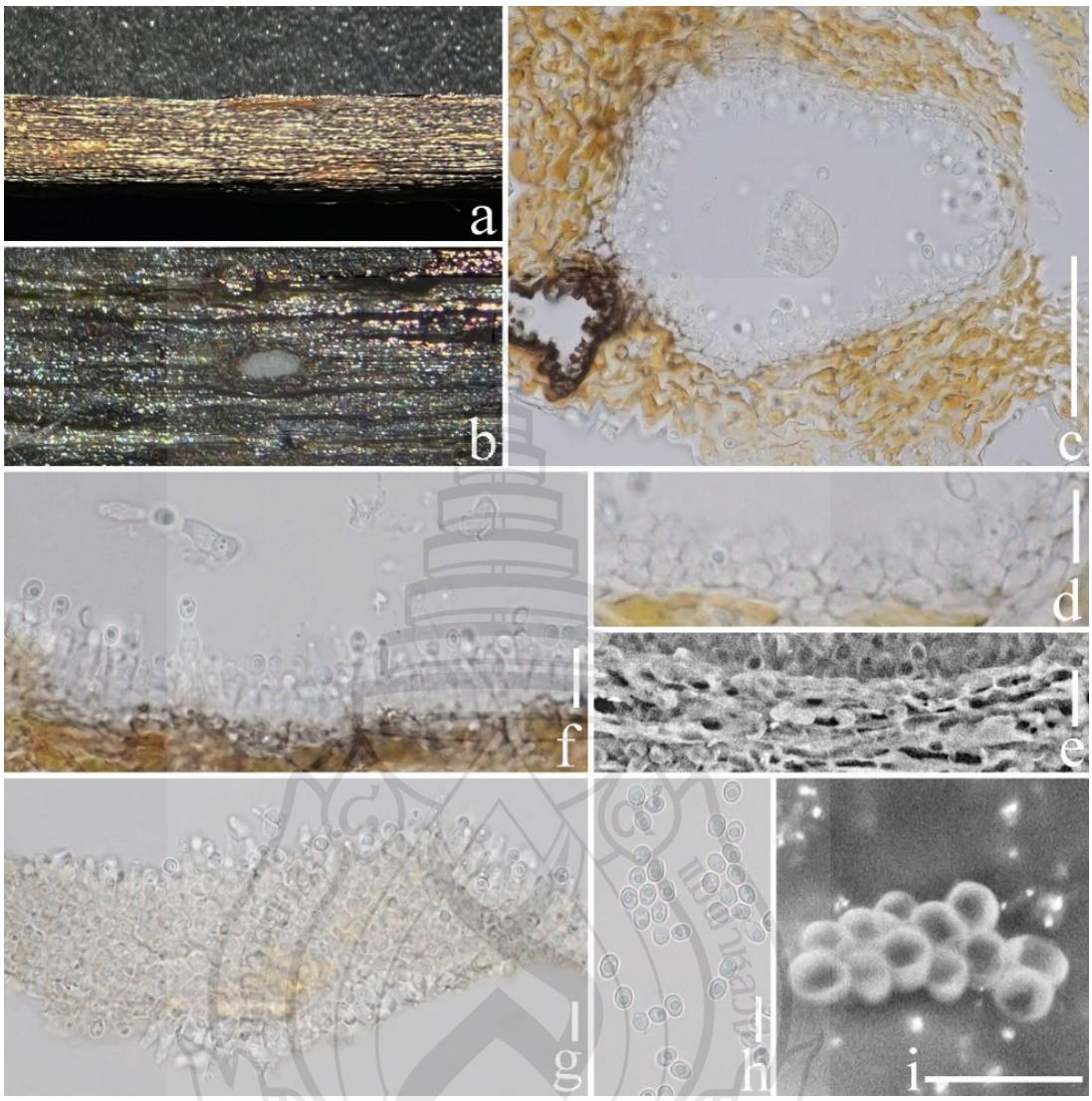


Figure 2.101 *Pseudohelminthosporium clematidis* (MHZU 24-0553, new asexual morph)

Figure 2.101 a, b Conidiomata on the host surface. c Vertical section of conidioma. d, e Pycnidial wall (e: SEM microphotographs of pycnidia wall). f, g Conidiogenous cells with conidia. h, i Conidia (i: SEM microphotographs of conidia). Scale bars: c = 50 µm, d–i = 10 µm.

Neohendersoniaceae Giraldo & Crous, Mycological Progress 16 (4): 343 (2017)

Crassiparies M. Matsum., K. Hiray. & Kaz. Tanaka, Fungal Diversity 78: 63 (2016)

Notes: *Crassiparies* was introduced by Li et al. (2016) with the sexual morph of *C. quadrisporus* as the type species, collected on dead twigs of *Acer* sp. (Sapindaceae) in Japan. Tanaka et al. (2017) revised the descriptions of *Crassiparies* and changed its placement from *incertae sedis* to Neohendersoniaceae based on maximum likelihood (ML) and Bayesian analyses (BYPP). The sexual morph of *Crassiparies* is characterized by scattered, immersed, subglobose ascomata with ostiolar neck, thin ascomatal wall with polygonal to rectangular cells, septate, branched and anastomosed pseudoparaphyses; cylindrical to clavate, pedicellate asci; and broadly fusiform, l-septate ascospores (Li et al., 2016, Tanaka et al., 2017). Asexual morph of *Crassiparies* is characterized by globose to depressed pycnidial conidiomata with cylindrical to papillate ostiolar neck, conidiomata wall composed of rectangular to polygonal cells; cylindrical to lageniform phialidic conidiogenous cells, and cylindrical, aseptate conidia (Tanaka et al., 2017).

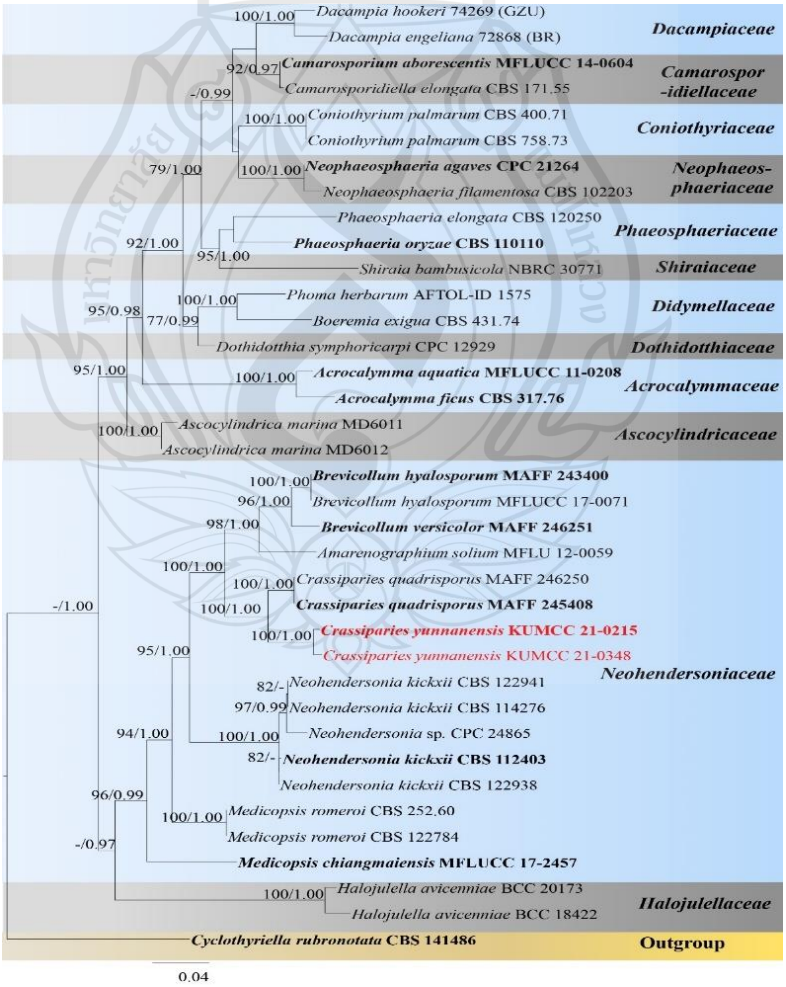


Figure 2.102 Phylogenetic tree of *Crassiparies*

Figure 2.102 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Thirty-seven strains are included in the combined sequence analysis, which comprises 4,280 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Cyclothyriella rubronotata* **(**CBS 141486**)**.

Crassiparies yunnanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 558827; *Facesoffungi number:* FoF 10578; Figure 2.81

Etymology: Refers to the place where the type species was collected.

Holotype: HKAS 121977

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 90–360 × 130–330 µm ($\overline{x}$ = 198 × 242 µm, n = 10), scattered, solitary, semi-immersed to immersed, irregular in shape, some globose to subglobose, uni-loculate, with short central ostiole, oozing out orange secretion on the substrate. *Peridium* 15–35 µm thick, thick-walled, of equal thickness, outer layers hyaline, composed of cells of *textura angularis*. *Hamathecium* 1–2.5 µm wide, composed of numerous, septate, branched, long, hyaline pseudoparaphyses anastomosing at the apex, embedded in a gelatinous matrix. *Asci* 110–300 × 20–30 µm ($\overline{x}$ = 182 × 23 µm, n = 20), 8-spored, fissitunicate, cylindrical to clavate, hyaline, sometimes with long pedicels up to 110 µm. *Ascospores* 20–35 × 8–14 µm ($\overline{x}$ = 28 × 11 µm, n = 30), 1–2 seriate, hyaline, broadly fusiform, smooth-walled, conical at both ends, 1-septate, with upper cell bigger than the lower cell, septum prominent when immature, each cell with a single large guttule when mature. **Asexual morph:** *Mycelium* 1.5–3 µm broad ($\overline{x}$ = 2.2 µm, n = 20), hyaline to pale brown, septate, branched. *Chlamydospores* apical or intercalary, produced after 120 days of growth on PDA at 28°C, 6–14 × 6–16 µm ($\overline{x}$ = 9.8 × 10.8 µm, n = 20), subglobose or elliposidal, thick-walled, colorless when young, light-brown when mature.

Culture characteristics: Ascospores germinated within 12 hours on PDA, colonies grown on PDA at room temperature (20–25°C), reaching about 35 mm diam. after one month. Colonies circular to irregular, dull surface and wrinkled, yellow-green to brown, aerial hyphae at the edge. Dark green on the reverse, producing a yellow-orange pigment on PDA.

Material examined: China, Yunnan Province: Pu'er, on dead twigs of coffee, 23 December 2020, Li Lu, MJ-C7 (HKAS 121977, **holotype**); ex-type KUMCC 21-0215; living culture, isotype KUMCC 21-0348.

GenBank numbers: KUMCC 21-0215: ITS = OK564664, LSU = OK564661, SSU = OK564663, *TEF*1-α = OK562423, *RPB*2 = OK562422; KUMCC 21-0348: ITS = OL679694, LSU = OL679695, SSU = OL679696, *TEF*1-α = OL689026, *RPB*2 = OL689027.

Notes: Based on BLAST search results of ITS, LSU, SSU, *rpb*2 and *tef* sequence data, our collection is closely related to *Crassiparies quadrisporus*, with similarity rates of NR_148185: 95.2%, LC271241: 97.7%, NG_061267: 99.57%, LC271251: 93.3%, LC271247: 93.5%. Phylogenetic analyses show *C. yunnanensis* is well-separated from *C. quadrisporus* with 100% ML, 1.00 BYPP statistical supports (Figure 2.1). *Crassiparies yunnanensis* shares morphological similarities with *C. quadrisporus* but the two species can be distinguished by asci characteristics. *Crassiparies quadrisporus* has only 2–4 ascospores per ascus, while *C. yunnanensis* has 8 ascospores and the asci have a long stipe (Li et al., 2016, Tanaka et al., 2017). Hence, based on both morphology and phylogeny, we introduce our collection as a new species of *Crassiparies*.

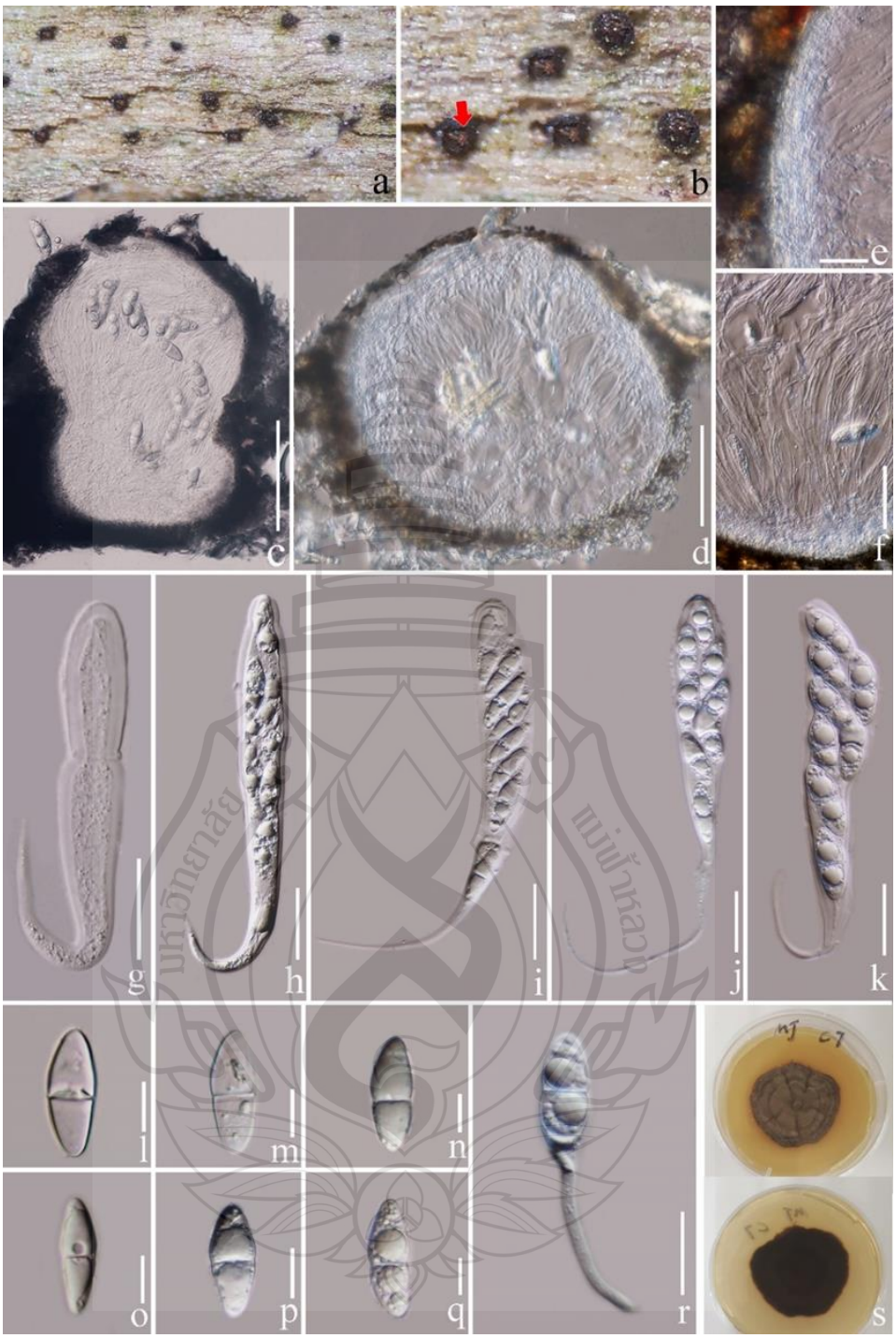


Figure 2.103 *Crassiparies yunnanensis* (HKAS 121977, holotype)

Figure 2.103 a, b. Ascomata on coffee twig surface **(the** arrow indicates orange secretion**).** c, d. Vertical section of ascomata**.** e. Peridium**.** f. Hamathecium**.** g–k**.** Asci**.** l–q. Ascospores**.** r. Germinating ascospore**.** s. Colony on PDA medium**.** Scale bars**:** c = 100 µm, d = 50 µm, e, r = 20 µm, f = 50 µm, g–k = 30 µm, l–q = 10 µm**.**



Figure 2.104 *Crassiparies yunnanensis* (KUMCC 21-0215, ex-type) on PDA

Figure 2.104 a. A germinating ascospore**.** b, c. Growth of asexual morph on plant tissues on PDA**.** d–g **.**Chlamydospores growing from hyphae**.** h. Chlamydospores**.** Scale bars**:** a, d–h = 20 µm.

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

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

Notes: *Nigrograna* was established by De Gruyter et al. (2013) and is typified by *N. mackinnonii.* There are 32 epithets of *Nigrograna* listed in Index Fungorum (2025). Species of *Nigrograna* form different life modes, including endophytes, human pathogens, or saprobes, and can be found in freshwater and terrestrial habitats (Hongsanan et al., 2020; Boonmee et al., 202; Hyde et al., 2023). Furthermore, the species of *Nigrograna* are widely distributed in different countries, i.e., Austria, Canada, China, Ecuador, India, Italy, Norway, Peru, Thailand, Venezuela (Shaw et al., 2015; Kolařík 2018; Lu et al., 2022; Digra & Nonzom, 2023; Bundhun et al., 2023; Mack et al., 2024). In this study, four new species of *Nigrograna* are introduced from coffee in China.

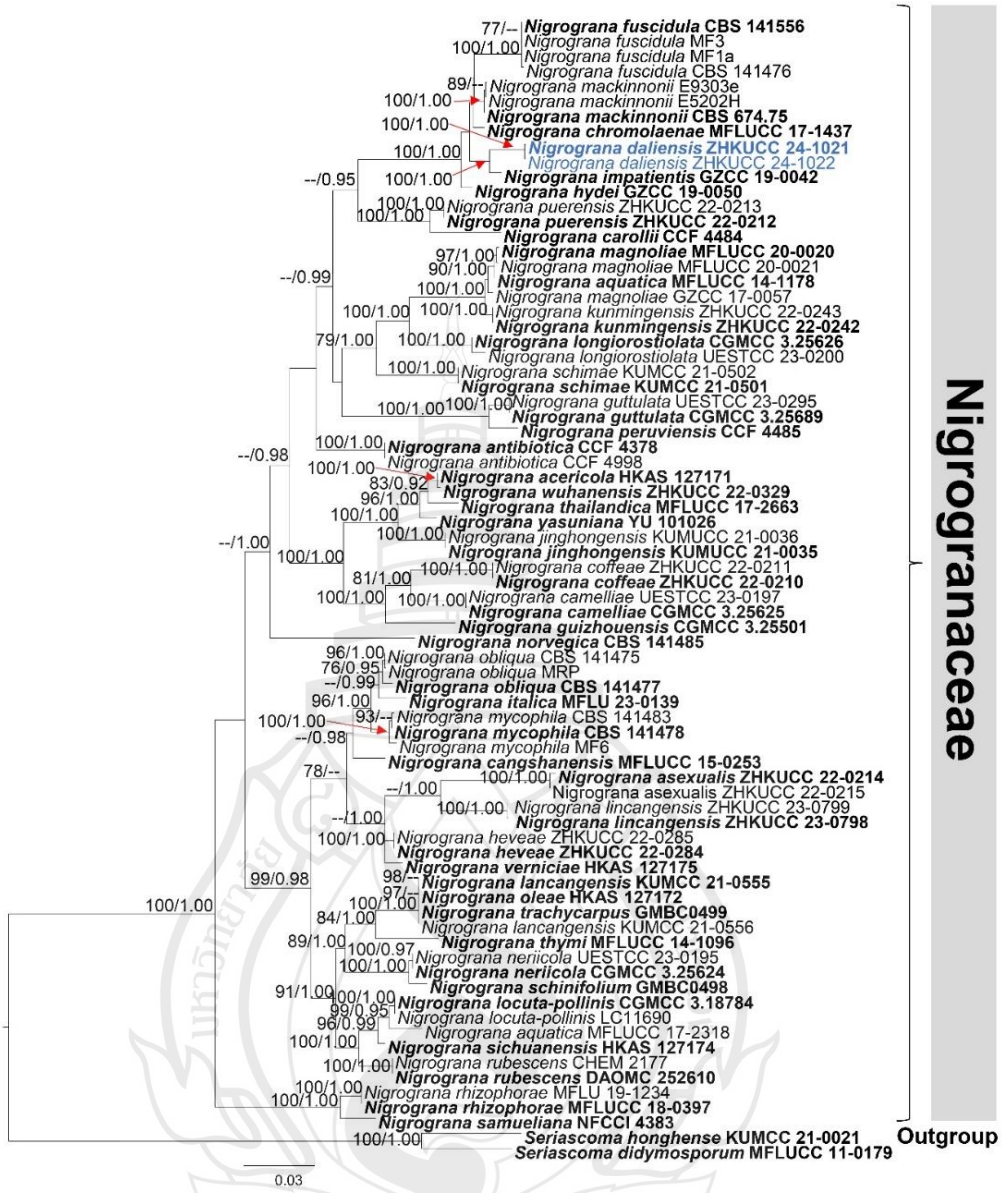


Figure 2.105 Phylogenetic tree of *Nigrograna*

Figure 2.105 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Swenty-six strains are included in the combined sequence analysis, which comprises 4,326 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Seriascoma honghense* (KUMCC 21-0021) and *S. didymosporum* (MFLUCC 11-0179).

Nigrograna asexualis L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559427; *Facesoffungi number*: FoF 12767; Figure 2.4

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

Holotype: ZHKU 22-0123

Saprobic on decaying branch of *Coffea arabica.* **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Pycnidia* 100–230 µm high, 120–180 µm wide ($\overline{x}$ = 156 × 144 µm, n = 10), globose to subglobose, or pyriform, immersed, solitary, unilocular, dark brown, papillate ostiole, appearing as black spots on host surface. *Pycnidial wall* 11–16 µm wide ($\overline{x}$ = 14 µm, n = 15), brown (#937463), the wall with pseudoparenchymatous cells. *Conidiophores* arising from the pycnidial wall, up to 46 µm long and 3–4.4 µm wide ($\overline{x}$ = 3.4 µm, n = 25), filiform, septate, hyaline, simple to sparsely branched, with pegs along one or two sides and solitary phialides terminally. *Phialides* 3–6 × 1–2 µm ($\overline{x}$ = 4.5 × 1.5 µm, n = 15), variable in shape, phialidic, discrete, ampulliform-lageniform-subcylindrical. *Conidia* 5–6.5 × 3–4 µm ($\overline{x}$ = 5.5 × 3.7 µm, n = 30), ellipsoidal, unicellular, aseptate with 1–2 granules, subhyaline, smooth-walled.

Culture characteristics: Conidium germinated on PDA within 24 h. Colonies growing on PDA reaching 5 cm diam. after two months at room temperature (22–26℃). Colony dense, circular, surface sparsely hairy, radially striate, with a fimbriate edge, yellowish (#eabf83) to pale brown (#e1af33) at the center and dark brown (#6e5031) at the margin, reverse dark brown (#6e5031).

Material examined: Pu'er City, Yunnan Province, China, on a decaying branch of *Coffea arabica*, (101°0'59", 22°36'2" N, 1016.43 m), 16 September 2021, LiLu, Puer 1-14 (ZHKU 22-0123, holotype), ZHKUCC 22-0214 = ZHKUCC 22-0215.

GenBank number: ITS: OP450965, LSU: OP450971, *rpb*2: OP432241, SSU: OP450979, *tef*1-α: OP432245 (ZHKUCC 22-0214, ex-type); ITS: OP450966, LSU: OP450972, *rpb*2: OP432242, SSU: OP450980, *tef*1-α: OP432246 (ZHKUCC 22-0215).

Notes: In multi-gene phylogeny, *Nigrograna asexualis* formed a separate (68% ML, 0.97 BIPP) and distinct clade within *Nigrograna* (Figure 2.1). Morphologically, *N. asexualis* conforms with the morphological characteristics of *Nigrograna* by having hyaline or subhyaline, long and branched conidiophores, solitary phialides, and aseptate, ellipsoidal or cylindrical conidia (Jaklitsch & Voglmayr, 2016;

Dayarathne et al., 2020; Wanasinghe et al., 2020). Blast results of the sequences show that ITS is similar to *N. fuscidula* with 89% (MH856004), and SSU is similar to *N. mycophila* with 99.8% (KX650510). *Nigrograna asexualis* is different from *N. fuscidula* and *N. mycophila* by its ellipsoidal conidia, but the similarities of these three species are hyaline, 1-celled, smooth-walled conidia forming on philipides (Jaklitsch & Voglmayr, 2016). The LSU and *rpb*2 sequences of our strain blast results are similar to *N. obliqua*, and the similarities are 98.9% (KX650560) and 87% (KX650579) respectively, but *N. obliqua* lacks the asexual morph (Jaklitsch & Voglmayr, 2016). The *tef*1-α sequence of our strain is 95.8% (MF939615) similar to *N. locuta-pollinis*, which was isolated from hive-stored pollen of *Brassica campestris* L. that lacks morphology (Zhao et al., 2018). Therefore, we introduce *N. asexualis* as a distinct new species from coffee in China.

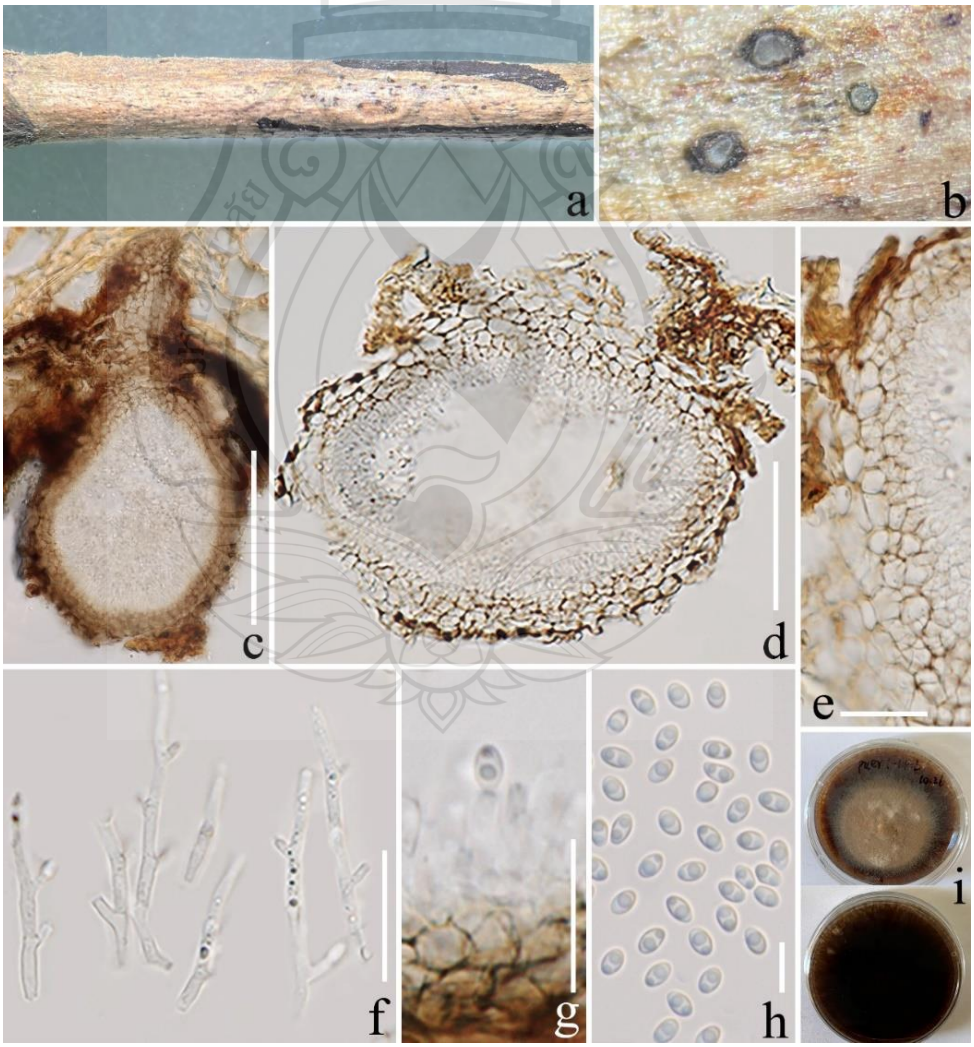


Figure 2.106 *Nigrograna asexualis* (ZHKU 22-0123, holotype)

Figure 2.106 a, b Conidiomata on the host substrate**.** c, d Vertical sections of a conidioma**.** e Peridium**.** f, g Conidiophores with phialides**.** h Conidia. i Culture on PDA from above and reverse**.** Scale bars**:** 100 μm (c), 50 μm (d), 15 μm (e), 30 μm (f), 20 μm (g), 10 μm (h)**.**

Nigrograna coffeae L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559425; *Facesoffungi number*: FoF 12765; Figure 2.2

Etymology: Species epithet refers to the host genus "*Coffea*" where the fungus was isolated.

Holotype: ZHKU 22-0121

Saprobic on decaying branch of *Coffea arabica*. **Sexual morph:** *Ascomata* 90–140 μm high, 140–200 μm wide ($\overline{x}$ = 115 × 168 μm, n = 10), immersed, solitary, black spots on substrate, subglobose to oval, sometimes obpyriform, some with ostiolate. *Peridium* 10–15 μm wide, composed of 3–5 layers, hyaline to brown (#937463) cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide, composed of numerous, hyaline, filamentous, septate, branched, pseudoparaphyses. *Asci* 50–70 × 7–11 μm ($\overline{x}$ = 58 × 9 μm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, short stalked, some with club-shape pedicel, apically rounded, with a small ocular chamber. *Ascospores* 12–16 × 4–5 μm, ($\overline{x}$ = 14.4 × 4.6 μm, n = 30), overlapping uni- to bi-seriately arranged, fusiform, straight or slightly curved, hyaline when immature and become pale brown (#e1af33) to dark-brown (#6e5031) when mature, mostly 1-septate, few 2 or 3-septate, constricted at each septum, with obviously guttulate. **Asexual morph:** Undetermined.

Culture characteristics: Ascospores germinated on PDA within 24 h and germ tubes arising from both ends. Colonies on PDA, reaching 4.5 cm diam. after two months of incubation at room temperature (22–26℃), initially white (#f2f3f4) becoming grey (#bbbeb2) to dark brown (#6e5031) at maturity, dense, circular, slightly raised, smooth surface, radially fimbriate at the edge, reverse dark green (#3a4543) to brown (#937463).

Material examined: Pu'wen Town, Xishuangbanna, Yunnan Province, China, on a decaying branch of *Coffea arabica*, (101°2'44" E, 22°31'18" N, 856.89 m),

15 September 2021, LiLu, JHPW16 (ZHKU 22-0121, holotype), ZHKUCC 22-0210 = ZHKUCC 22-0211.

GenBank number: ITS: OP450967, LSU: OP450973, *rpb*2: OP432243, SSU: OP450981, *tef*1-α: OP432247 (ZHKUCC 22-0210, ex-type); ITS: OP450968, LSU: OP450974, *rpb*2: OP432244, SSU: OP450982, *tef*1-α: OP432248 (ZHKUCC 22-0211).

*Notes***:** Our phylogenetic analyses showed that *Nigrograna coffeae* forms an independent clade (100% ML, 1.00 BIPP, Figure 2.1), and is phylogenetically related to *N. yasuniana* and *N. jinghongensis*. *Nigrograna yasuniana* was reported as endophytes from *Conceveiba guianensis* Aubl. in Ecuador, but there were not enough morphological data, the comparison of base pairs in ITS showed 3.4 % differences (15/433 bp), LSU showed 1.5% differences (12/812bp), SSU only showed 0.3% differences (3/1028 bp), *rpb*2 showed 14% differences (117/829 bp), and *tef*1-α showed 3.2% differences (31/954 bp) (Kolařík et al., 2017). *Nigrograna jinghongensis* was introduced as a saprobic fungus from woody litter in China, and our new isolate shares a similar size (12–16 × 4–5 µm *vs* 12–15 × 4–5.5 µm) and color (hyaline to dark brown *vs* yellowish-brown to brown) of ascospores with *N. jinghongensis* (Boonmee et al., 2021), but there are some significant differences in the size of the ascomata (90–140 µm high, 140–200 µm wide *vs* 300–400 µm high 220–300 µm wide) and the shape of ascospores (fusiform, straight or slightly curved *vs* ellipsoid) (Boonmee et al., 2021). Based on the sequence blast results, ITS, LSU and *rpb*2 gene sequences were similar to *Nigrograna* sp., with 97.5% (MZ270683), 98.4% (MK762716), and 86% (MZ508421) respectively, SSU was similar to *N. mycophila* with 99% (KX650510), and *tef*1-α was similar to *N. yasuniana* with 96.6% (LN626670). Therefore, we introduce our new isolate as a new species *N. coffeae* based on both morphological characteristics and phylogenetic analyses.

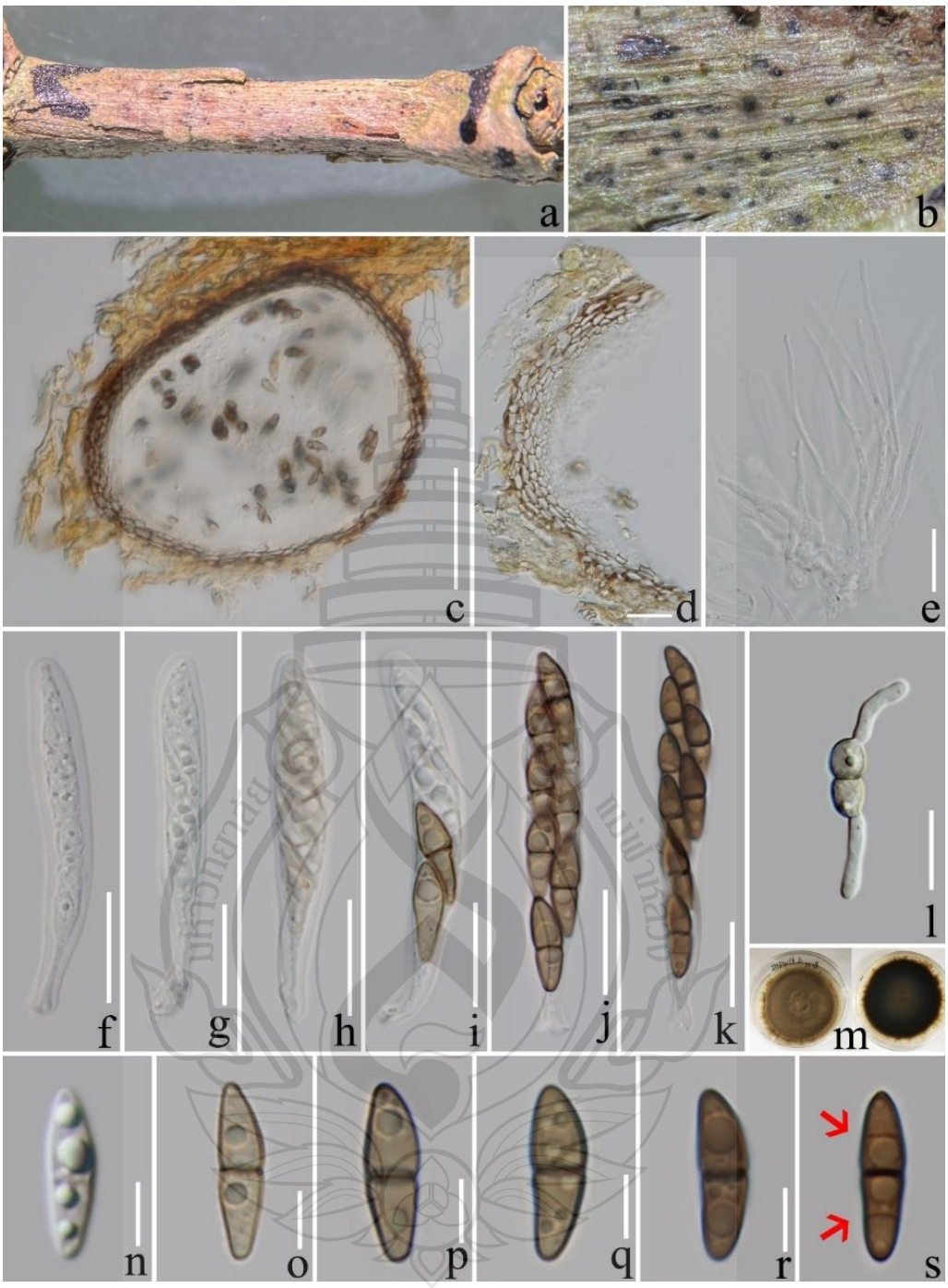


Figure 2.107 *Nigrograna coffeae* (ZHKU 22-0121, holotype)

Figure 2.107 a, b Ascomata on the host substrate. c A vertical section through an ascoma. d Peridium. e Hamathecium. f–k Asci. l Germinated ascospore. m Culture on PDA from above and reverse. n–s Ascospores (arrows indicate the septa). Scale bars: 50 μm (c), 10 μm (d–l), 5 μm (n–s).

Nigrograna daliensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903636; *Facesoffungi number:* FoF 17581; Figure 2.81

Etymology: The species epithet refers to the type location "Dali", China.

Holotype: MHZU 24-0559

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 165–250 × 175–260 µm ($\overline{x}$ = 190 × 196 µm, n = 10), forming black spots on the host surface, immersed, solitary to clustered in groups, subglobose to globose, ostiolate. *Ostioles* central and short, papillate. *Peridium* 15–25 µm wide ($\overline{x}$ = 18 µm, n = 20) µm, thick-walled, consisting of several cell layers of *textura angularis*, hyaline to brown. *Hamathecium* of 1.3–2.5 µm wide ($\overline{x}$ = 1.8 µm, n = 20), numerous, hyaline, septate and branched, filamentous, pseudoparaphyses. *Asci* 45–65 × 7–11 µm ($\overline{x}$ = 54 × 8.5 µm, n = 20) µm, 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a short pedicel, apically rounded. *Ascospores* 10–13.5 × 4–5µm, ($\overline{x}$ = 11.5 × 4 µm, n = 20), overlapping, bi-seriate, fusoid, 1-septate and hyaline to yellow-brown when young, 3-septate and brown when mature, slightly constricted and strongly pigment at septum, apical cell and basal cell conical, guttulate. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on PDA, reaching 4.5 cm diam. after two months of incubation at 25°C, initially white becoming grey, dense, circular, regular at edge, from below dark brown.

Material examined: China, Yunnan Province, Dali City, Zhukula Coffee Plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C1 (MHZU 24-0559, holotype), ex-type ZHKUCC 24-1021, other living culture ZHKUCC 24-1022.

GenBank numbers: ZHKUCC 24-1021: ITS = PQ608312, LSU = PQ608145, SSU = PQ607999, *TEF*1-α = PQ628158, *RPB*2 = PV357179; ZHKUCC 24-1022: ITS = PQ608313, LSU = PQ608146, SSU = PQ608000, *TEF*1-α = PQ628159, *RPB*2 = PV357180.

Notes: In the multi-gene phylogenetic tree, our isolates (ZHKUCC 24-1021, ex-type and ZHKUCC 24-1022) formed a sister lineage to *Nigrograna impatientis* (GZCC 19-0042, ex-type) with 100% ML, 1.00 BYPP bootstrap support (Figure 2.80). The nucleotide pairwise of new collection and *N. impatientis* in ITS showed 2.5 %

differences (12/471 bp, without gaps), LSU and *TEF*1-α almost same. No SSU and *RPB*2 sequences available for *N. impatientis*. In morphology, the ascomata of *N. impatientis* are surrounded by brown to olivaceous, subcircular hyphae; however, this structure is not observed in our new collection (Zhang et al., 2020; Figure 2.81). In addition, the color of ascospore of *N. impatientis* is pale brownish to yellow-brown when young, turning dark to chocolate brown upon maturation, while our collection is 1-septate and hyaline to yellow-brown when young, brown when mature (Zhang et al., 2020; Figure 2.81). Hence, we introduce *Nigrograna daliensis* as a new species based on morphology coupled with molecular data.

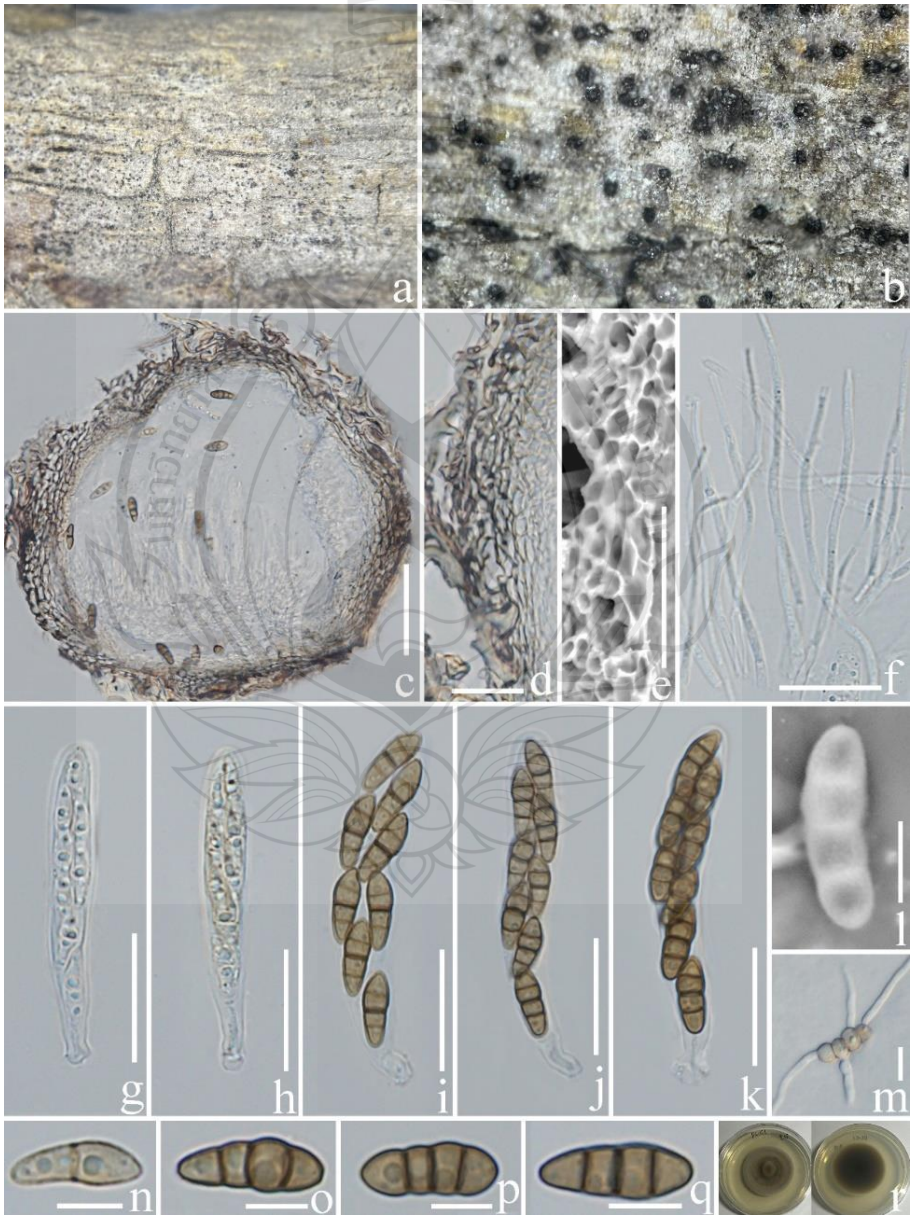


Figure 2.108 *Nigrograna daliensis* (MHZU 24-0559, holotype)

Figure 2.108 a, b Ascomata on the host substrate. c Vertical section of ascoma. d Peridium (e: SEM microphotographs of peridium). f Hamathecium. g–k Asci. l SEM microphotographs of ascospore. m Germinated ascospore. n–q Ascospores. r Culture on PDA from above and below. Scale bars: c = 50 µm, d–k = 20 µm, l–q = 5 µm.

Nigrograna puerensis L. Lu & Tibpromma, sp. nov.

Index Fungorum number: IF 559426; *Facesoffungi number*: FoF 12766; Figure 2.3

Etymology: The specific epithet "*puerensis*" refers to the location Pu'er City, where the type species was collected.

Holotype: ZHKU 22-0122

Saprobic on decaying branch of *Coffea arabica*. **Sexual morph:** *Ascomata* 90–180 µm high, 90–150 µm wide ($\overline{x}$ = 138 × 115 µm, n = 10), immersed, with only ostiolar necks visible on the host surface or erumpent, solitary, subglobose to ellipsoid, dark brown (#6e5031). *Peridium* 10–15 µm wide ($\overline{x}$ = 13 µm, n = 15), outer layer consists of 2–3 layers of *textura prismatica*, brown (#937463) and thick-walled cells, inner layer hyaline with thin-walled cells. *Hamathecium* composed of numerous, 1.5–2 µm wide ($\overline{x}$ = 1.8 µm, n = 20), filamentous, hyaline, septate, pseudoparaphyse. *Asci* 50–80 × 8–11 µm ($\overline{x}$ = 66 × 9.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded, with poorly developed ocular chamber. *Ascospores* 15–18 × 4–5 µm, ($\overline{x}$ = 16 × 4.5 µm, n = 30), uni- to bi-seriately arranged, fusoid, apical cell and basal cell acute, and apical cell slightly wider than basal cell, straight or slightly curved, 1-septate, constricted at septum, guttulate, hyaline to yellow-brownish (#daceb8) when young, brownish (#937463) when mature. **Asexual morph:** Undetermined.

Culture characteristics: On PDA, colonies reached up to 4 cm diam. after two months at room temperature (22–26°C). Colony dense, circular, slightly raised at the center, surface with white aerial mycelium, fluffy, with a serrate edge, grayish (#c9bfb3) to dark brown (#6e5031) from center to edge, reverse dark green (#3a4543) to dark brown (#6e5031).

Material examined: Pu'er City, Yunnan Province, China, on a decaying branch of *Coffea arabica*, (101°0'59", 22°36'2" N, 1016.43 m), 16 September 2021, LiLu, Puer 1-4 (ZHKU 22-0122, holotype), ZHKUCC 22-0212 = ZHKUCC 22-0213.

GenBank number: ITS: OP450969, LSU: OP450975, SSU: OP450983, *tef*1-α: OP432249 (ZHKUCC 22-0212, ex-type); ITS: OP450970, LSU: OP450976, SSU: OP450984, *tef*1-α: OP432250 (ZHKUCC 22-0213).

Notes: *Nigrograna puerensis* clusters with *N. carollii* with significant statistical support from ML 100% and BIPP 1.00. In morphology, our new strains best fit *Nigrograna* by having immersed ascomata, clavate and short pedicellate asci, and pale to brown, fusoid to narrowly ellipsoid, and septate ascospores (Jaklitsch & Voglmayr, et al., 2016; Zhang et al., 2020). Blast search results of ITS, LSU and *tef*1-α sequence data revealed that our taxon (ZHKUCC 22-0212) is similar to *N. mackinnonii* (96% MZ270697, 99% KJ605422, and 95% LT797087 respectively), while the similarity of SSU sequence to *N. carollii* is high as 99%. Based on nucleotide comparisons, our isolate (ZHKUCC 22-0212) differs from *N. carollii* (CCF 4484) by 9/490 bp (1.8%) in ITS, 2/222 bp (1%) in LSU, 2/1306 bp (0.2%) in SSU, and 10/530 bp (2%) in *tef*1-α. Unfortunately, for *N. carollii*, sufficient morphological data was not available to compare with our novel taxon which was isolated as an endophyte on living sapwood of wild *Hevea brasiliensis* Müll. Arg., and *N. mackinnonii* which was isolated as a human pathogen (de Gruyter et al., 2012; Kolařík et al., 2017). In addition, the colony morphology of *N. carollii* on PDA is described as colonies plane, effuse, and light gray (Kolařík et al., 2017), while *N. puerensis* colony surface is seen as white aerial mycelium, fluffy, with a serrate edge, and grayish to dark brown from center to edge. Therefore, based on morphological and phylogenetic analyses, we introduce *N. puerensis* as a distinct new species.

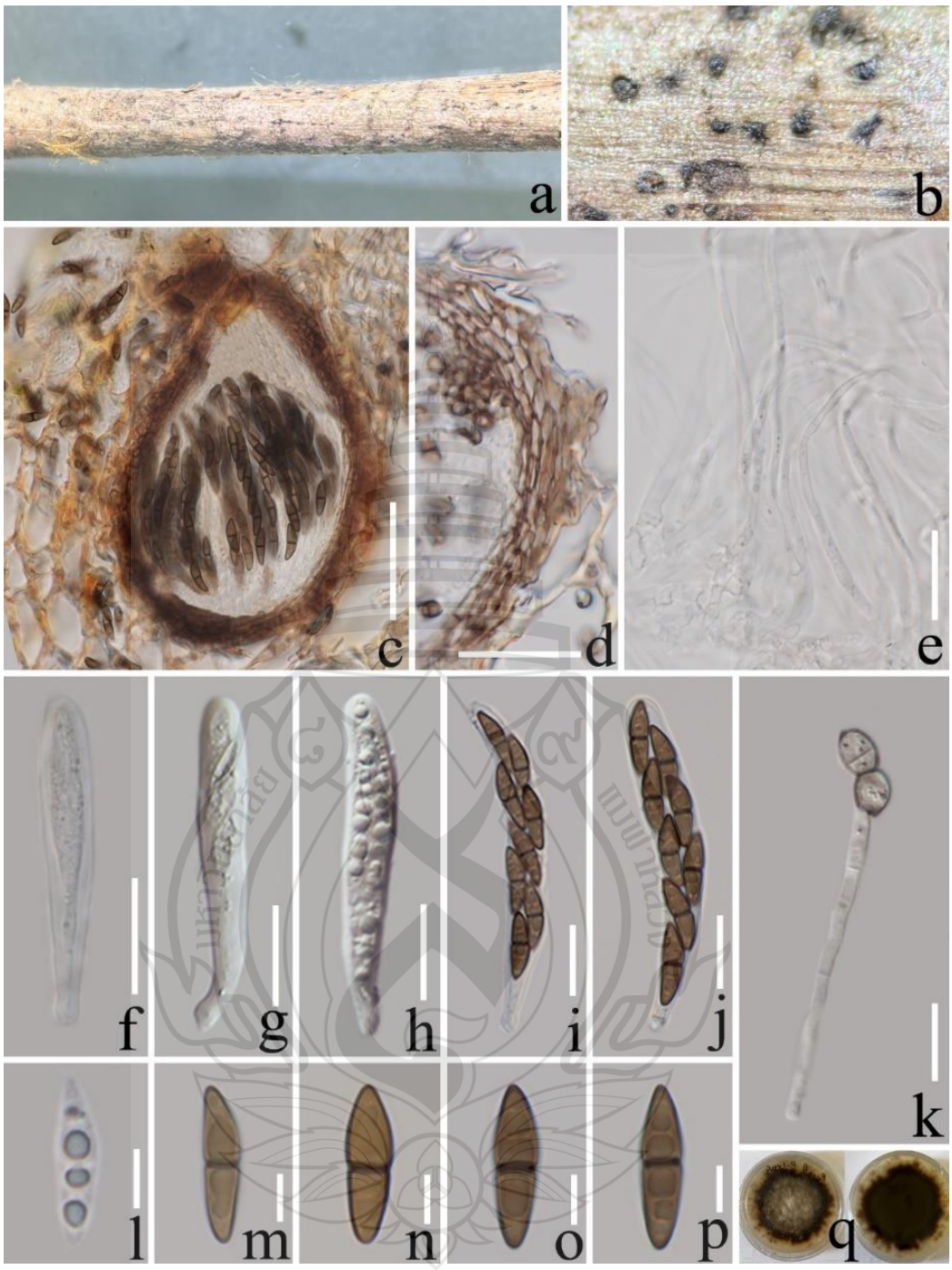


Figure 2.109 *Nigrograna puerensis* (ZHKU 22-0122, holotype)

Figure 2.109 a, b Ascomata observed on host substrate. c A vertical section through an ascoma. d Peridium. e Hamathecium. f–j Asci. k Germinated ascospore. l–p Ascospores. q Culture on PDA from above and reverse. Scale bars: 50 μm (c), 30 μm (d), 15 μm (e–k), 5 μm (l–p).

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

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

Notes: *Brunneofusispora* was established by Phookamsak et al. (2019) and is typified with *B. sinensis*. Hongsanan et al. (2020) discussed the morphological differences between *Brunneofusispora* and other genera in Occultibambusaceae, which can be differentiated by uni-loculate ascomata with a long prominent neck. Wanasinghe et al. (2020) observed the coelomycetous asexual morph of *B. sinensis* and amended the generic and species description to accommodate the asexual morph. There are six species (*B. baoshanensis*, *B. clematidis*, *B. hyalina*, *B. inclinatiostiola*, *B. sennae-torae*, and *B. sinensis*) accepted in *Brunneofusispora* (Index Fungorum, 2025), identified as saprobes on *Clematis subumbellata*, *Coffea* sp., *Magnolia denudat*a, *Senna tora* and *Trachycarpus fortunei*, collected from terrestrial and freshwater habitats distributed in Australia, China, and Thailand (Phookamsak et al., 2019; Phukhamsakda et al., 2020; Wanasinghe et al., 2020; Calabon et al., 2021; Yu et al., 2021; Liu et al., 2024). In this study, we introduce two new species (*B. coffeae* and *B. chiangraiensis*) and one new collection (*B. baoshanensis*) from coffee hosts in China and Thailand.

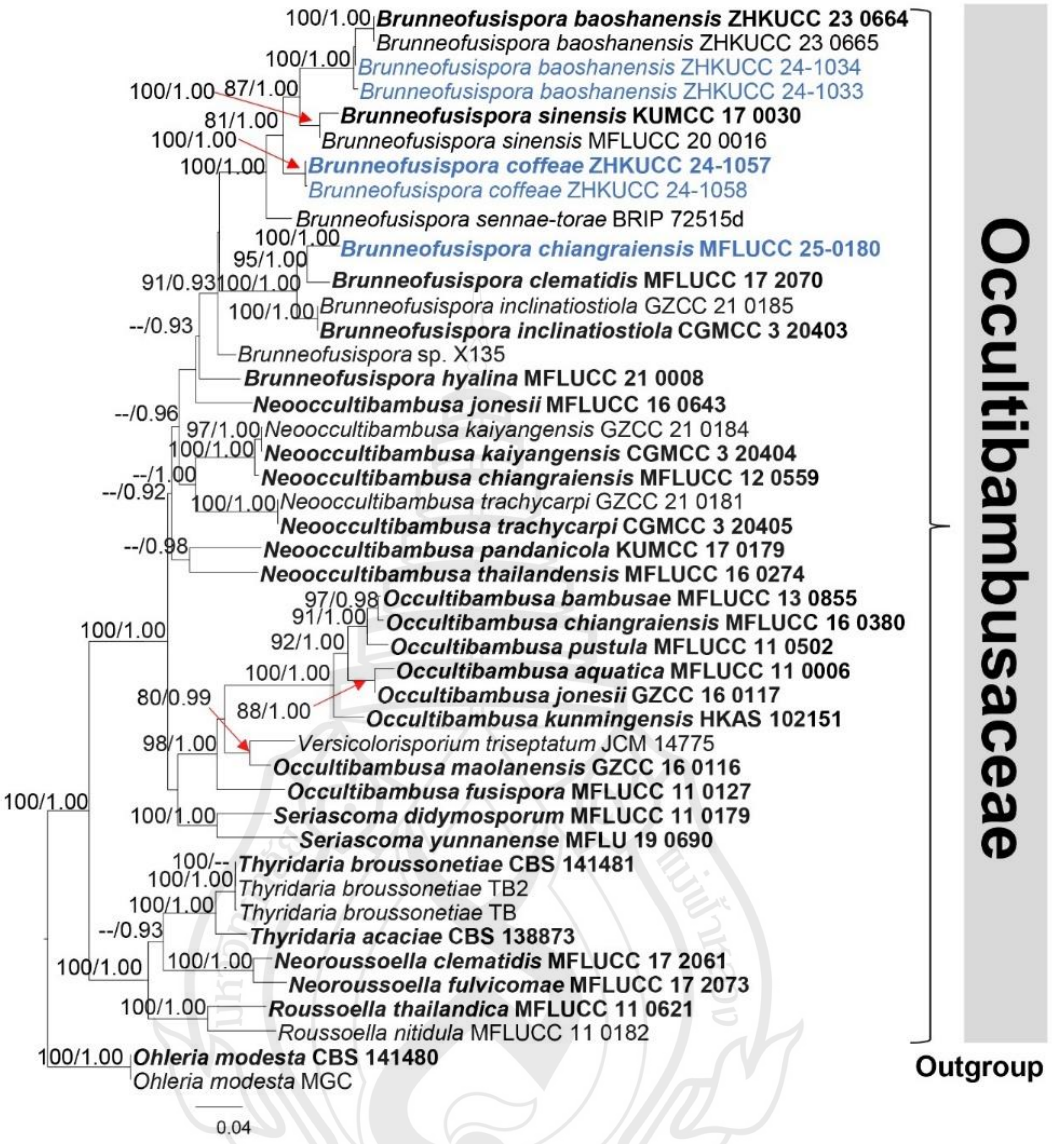


Figure 2.110 Phylogenetic tree of *Brunneofusispora*

Figure 2.110 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Forty-four strains are included in the combined sequence analysis, which comprises 6,421 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Ohleria modesta* (CBS 141480 and MGC).

Brunneofusispora baoshanensis X.F. Liu, Tibpromma & K.D. Hyde

Index Fungorum number: IF 901183; Facesoffungi number: FoF 14924; Figure 2.83

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 150–300 × 150–260 µm ($\bar{x}$ = 236 × 210 µm, n = 10), solitary, gregarious, uniloculate, immersed to semi-immersed, visible as erumpent long neck on host surface, shiny, globose to subglobose, glabrous, coriaceous, brown to dark brown, rough-walled. *Peridium* 20–50 µm wide, composed of 4–6 layers of brown to dark brown cells of *textura angularis*, the inner layer hyaline to pale brown and heavily pigmented at the outer layer. *Hamathecium* of 1.8–3.6 µm wide, medium dense, filamentous, branched, septate pseudoparaphyses, embedded in a gelatinous matrix, longer than asci. *Asci* 60–99 × 11–18 µm ($\bar{x}$ = 81.20 × 14.51 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, short pedicel, rounded at the apex. *Ascospores* 18–26 × 6–8 µm ($\bar{x}$ = 22.27 × 7.26 µm, n = 60), uni to biseriate, broad fusiform to ellipsoid, mostly inequilateral, ends acute, initially hyaline, pale brown at maturity, septate, constricted at the septum, slightly enlarged towards the median septum, with guttules, smooth-walled. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h; colonies on PDA after two months attaining a diam. of 35 mm at 25℃, fluffy, brown with grayish-white margins, with greyish white aerial mycelia on the surface, dense, circular to irregular; from below black, with edge greyish white.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*. (22.6 N, 100.96 E, 1073 m), 2 April 2024, Li Lu, XAZC-2-8 (MHZU 24-0565), living culture ZHKUCC 24-1033, other living culture ZHKUCC 24-1034.

GenBank numbers: ZHKUCC 24-1033: ITS = PQ608277, LSU = PQ608110, SSU = PQ607968, *TEF*1-α = PQ628124, *RPB*2 = PV186836; ZHKUCC 24-1034: ITS = PQ608278, LSU = PQ608111, SSU = PQ607969, *TEF*1-α = PQ628125, *RPB*2 = PV186837.

Known host: Coffea sp. (Liu et al., 2024), *Coffea arabica* (This study).

Known distribution: China (Liu et al., 2024; This study)

Notes: In our phylogenetic analyses, our new collection formed a sister lineage to *Brunneofusispora baoshanensis* (ZHKUCC 23-0664 and ZHKUCC 23-0665,

ex-type) with 100% ML and 1.00 BYPP bootstrap support (Figure 2.82). Morphologically, it is the same as *B. baoshanensis* (ZHKU 23-0077, holotype) (Liu et al., 2024; Figure 2.83). The holotype of this species was collected from Yunnan Province, Baoshan City, while our new collection was obtained from Pu'er City in Yunnan Province, but both specimens were collected from coffee plants.

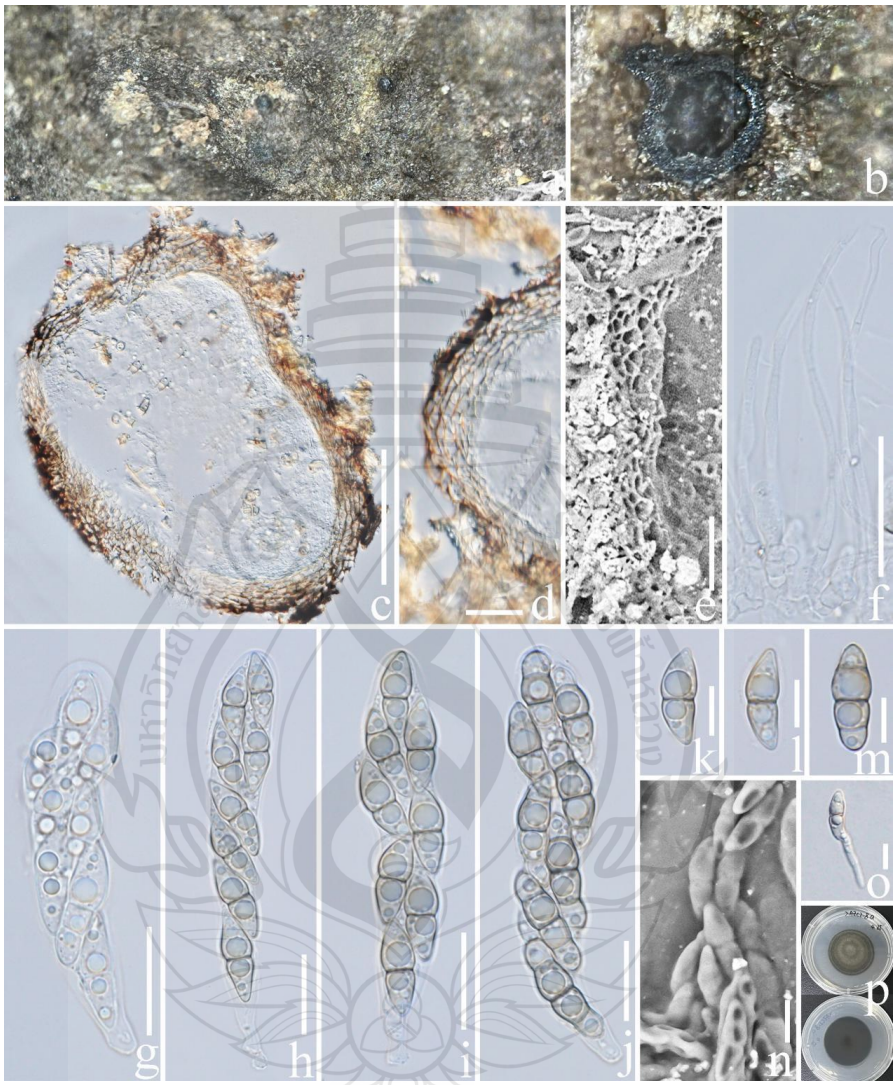


Figure 2.111 *Brunneofusispora baoshanensis* (MHZU 24-0565, new collection)

Figure 2.111 a, b Ascomata on the host substrate. c Vertical section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium. g–j Asci. k–m. Ascospores (n: SEM microphotographs of ascospores). o Germinated ascospore. p Culture on PDA from above and below. Scale bars: c = 100 µm, d = 50 µm, f–j = 20 µm, k–o = 10 µm.

Brunneofusispora coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903605; *Facesoffungi number*: FoF 17582; Figure 2.84

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0581

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: Not observed. **Asexual morph:** Coelomycetous. *Conidiomata* 100–250 × 100–150 µm, semi-immersed to immersed, solitary or gregarious, globose to subglobose, uni or multi-locule, brown, shiny, without hairs, smooth-walled, ostiolate. *Conidiomatal wall* 12–25 µm wide, outer layer composed of multi-layered, brown to light brown cells of *textura angularis*, lined with a hyaline layer bearing conidiogenous cells, or reduced to conidiogenous cells. *Conidiophores* often reduced to conidiogenous cells, sparsely septate at the base and unbranched. *Conidiogenous cells* 5–10 × 1.5–2.5 µm ($\bar{x}$ = 7.29 × 2.12 µm, n = 60), holoblastic, phialidic, ampulliform to cylindrical, unbranched, hyaline, and smooth-walled. *Conidia* 3–5 × 1–3 µm ($\bar{x}$ = 3.66 × 2.18 µm, n = 60), oval or subglobose, slightly curved, smooth-walled, 1–2 (–3)-granulate, hyaline, aseptate, without a sheath.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*. (22.6 N, 100.96 E, 1073 m), 2 April 2024, Li Lu, XAZC-2-9 (MHZU 24-0581, holotype), ex-type ZHKUCC 24-1057, other living culture ZHKUCC 24-1058.

GenBank numbers: ZHKUCC 24-1057: ITS = PQ608279, LSU = PQ608112, SSU = PQ607970, *TEF*1-α = PQ628126, *RPB*2 = PV186838; ZHKUCC 24-1058: ITS = PQ608280, LSU = PQ608113, SSU = PQ607971, *TEF*1-α = PQ628127, *RPB*2 = PV186839.

Notes: In the phylogenetic tree, *Brunneofusispora coffeae* formed a distinct lineage within *Brunneofusispora*, sister to *B. sinensis* and *B. sennae-torae*, with 81% ML and 1.00 BYPP bootstrap support (Figure 2.82). The nucleotide comparison between *Brunneofusispora coffeae* (ZHKUCC 24-1057, ex-type) and *B. sinensis* (KUMCC 17-0030, type) revealed sequence differences of 3.92% (21/536 bp, without gaps) in ITS, 1.15% (9/782 bp, without gaps) in LSU, 5.99% (38/634 bp, without gaps) in SSU, and 3.60% (34/945 bp, without gaps) in *TEF*1-α. Additionally, it also differed from *B. sennae-torae* (BRIP 72515d) by 4.83% (27/559 bp, without gaps) in ITS and 0.33% (3/899 bp, without gaps) in LSU. Morphologically, *B. coffeae* differs from *B. sinensis* by slender

conidiogenous cells (5–10 × 1.5–2.5 µm, L/W = 2–6.6 vs. 6–7.5 × 2.5–3 µm, L/W = 2–3) and granulate conidia (Wanasinghe et al., 2020; Figure 2.84). The morphology of *B. sennae-torae* was not provided (Tan et al., 2021). Based on the phylogenetic analyses and morphological characteristics, *Brunneofusispora coffeae* is described as a new species, and this is the second time the asexual morph has been reported from a *Brunneofusispora* species.

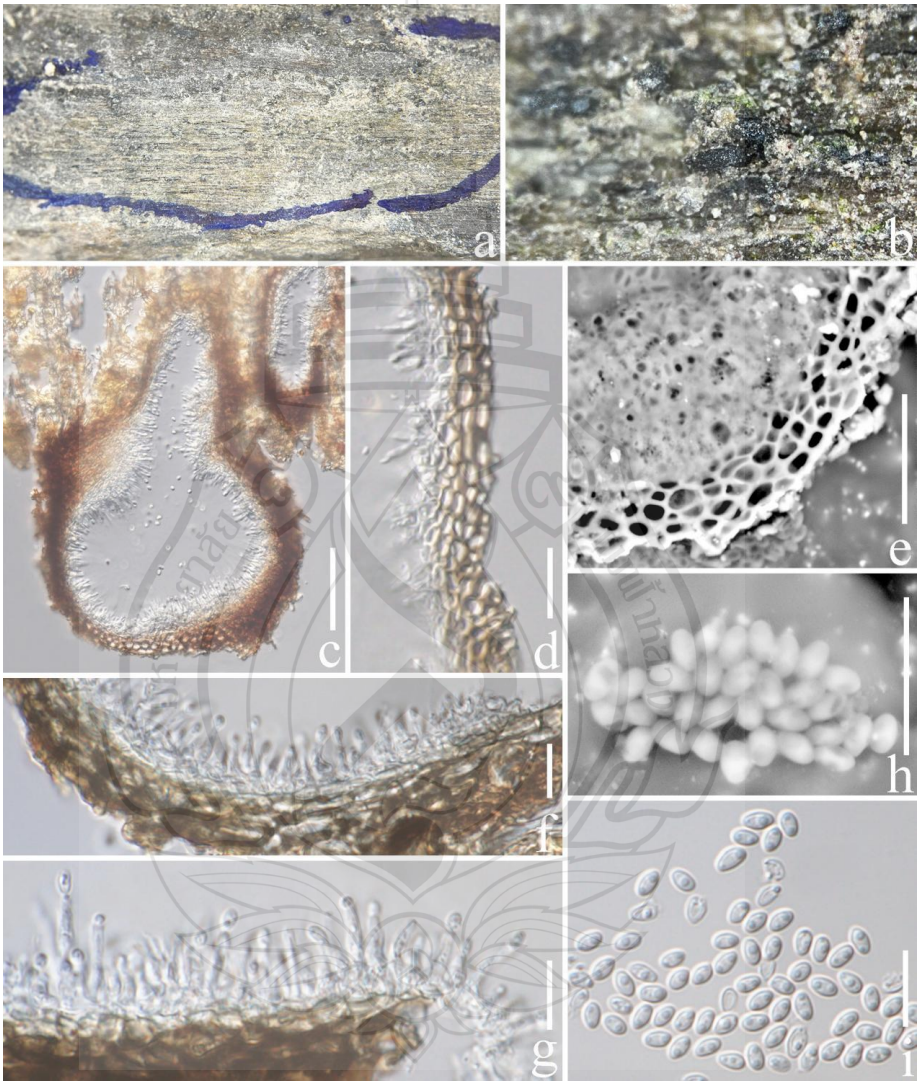


Figure 2.112 *Brunneofusispora coffeae* (MHZU 24-0581, holotype)

Figure 2.112 a, b Conidiomata on the host substrate. c Vertical section of conidioma. d, e Section of conidioma wall (e: SEM microphotographs of conidioma wall). f, g Conidiogenous cells. h, i Conidia (h: SEM microphotographs of conidia). Scale bars: c = 100 µm, d = 50 µm, f–j = 20 µm, k–o = 10 µm.

Brunneofusispora chiangraiensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903604; *Facesoffungi number*: FoF 17583; Figure 2.85

Etymology: The species epithet refers to the type location "Chiang Rai", Thailand.

Holotype: MFLU 25-0093

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 200–300 × 200–270 µm ($\bar{x}$ = 249 × 231 µm, n = 10), solitary, gregarious, uniloculate, immersed to semi-immersed, visible as erumpent long necks on host surface, shiny, globose to subglobose, glabrous, coriaceous, brown to dark brown, rough-walled, covered by undulate or straight setae at the top. *Setae* 70–150 µm long, arising from the apical collar, conspicuously rough, dark brown, septate, unbranched, erect, conical at the tips. *Peridium* 15–25 µm wide, composed of 5–8 layers of brown to dark brown cells of *textura angularis*, the inner layer hyaline to pale brown, and heavily pigmented at the outer layer. *Hamathecium* comprising 2.2–4.7 µm wide, medium dense, filamentous, branched, cellular, septate pseudoparaphyses, embedded in a gelatinous matrix, longer than asci. *Asci* 65–95 × 15–24 µm ($\bar{x}$ = 79.69 × 18.81 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 20–27 × 5–9 µm ($\bar{x}$ = 25.26 × 7.31 µm, n = 60), uni to biseriate, broad fusiform to ellipsoid, mostly inequilateral, ends acute, initially hyaline, pale brown at maturity, 1-septate, constricted at the septum, with guttules, smooth-walled, surrounded by a thick mucilaginous sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h; colonies on PDA after two months attaining a diam of 35 mm at 25℃, fluffy, black, irregular margin, with greyish white aerial mycelia on the surface, dense, circular to irregular; from below black.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 20 September 2023, Li Lu, LC1-10 (MFLU 25-0093, holotype), ex-type MFLUCC 25-0180.

GenBank numbers: MFLUCC 25-0180: ITS = PQ608281, LSU = PQ608114, SSU = PQ607972, *TEF*1-α = PQ628128.

Notes: In the phylogenetic tree, *Brunneofusispora chiangraiensis* formed a distinct lineage within *Brunneofusispora*, sister to *B. clematidis* (MFLUCC 17-2070, ex-type) and *B. inclinatiostiola* (GZCC 21-0185 and CGMCC 3.20403, ex-type) with 95% ML and 1.00 BYPP bootstrap support (Figure 2.82). However, the nucleotide comparison between *B. chiangraiensis* (MFLUCC 25-0180, ex-type) and *B. clematidis* (MFLUCC 17-2070, type) showed that there are 3.75% (22/587 bp, without gaps) in ITS, 2.11% (18/854 bp, without gaps) in LSU, 2.93% (20/682 bp, without gaps) in SSU, 3.51% (33/941 bp, without gaps) in *RPB2*, and 5.37% (31/577 bp, without gaps) in *TEF*1-α. Differs with *B. inclinatiostiola* (CGMCC 3.20403, type) by 7.44% (34/457 bp, without gaps) in ITS, 1.43% (12/839 bp, without gaps) in LSU, 1.59% (8/502 bp, without gaps) in SSU, 3.32% (29/874 bp, without gaps) in *RPB2*, and 4.14% (40/967 bp, without gaps) in *TEF1-α*. Morphologically, *Brunneofusispora chiangraiensis* can easily be distinguished from other species by ascomata covered by undulate or slightly setae at the apex (Figure 2.85). Based on the phylogenetic analyses and morphological characteristics, *B. chiangraiensis* is introduced as a new species.

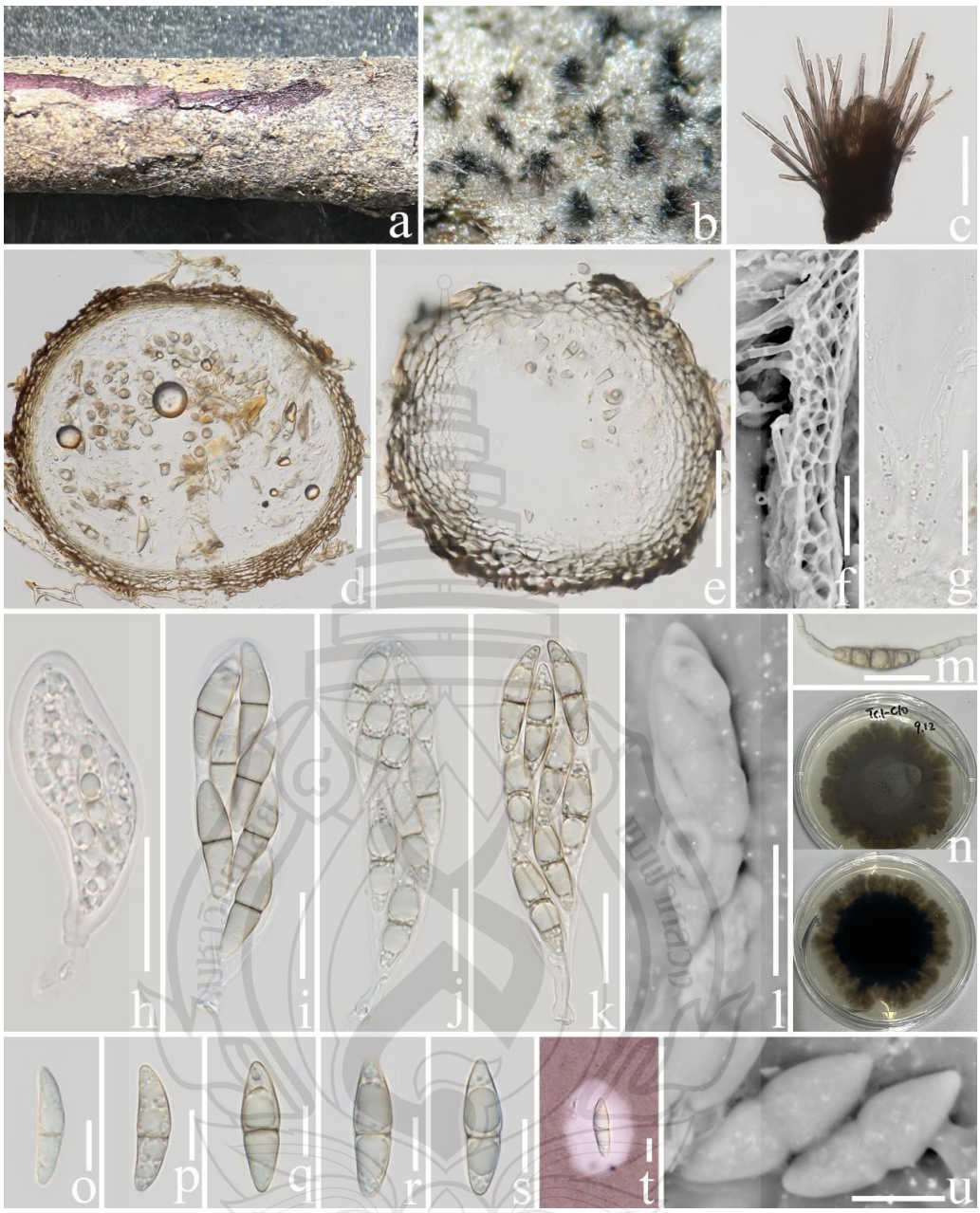


Figure 2.113 *Brunneofusispora chiangraiensis* (MFLU 25-0093, holotype)

Figure 2.113 a, b Ascomata on the host substrate. c Setae. d, e Vertical sections of ascomata. f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–l Asci (l: SEM microphotographs of ascus). m Germinating ascospore. n Culture on PDA from above and below. o–u. Ascospores (t: Ascospore stained with India Ink, u: SEM microphotographs of ascospores). Scale bars: c–e = 50 µm, f–m, u = 20 µm, n–t = 10 µm.

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

Notes: Neooccultibambusa was introduced in *Occultibambusaceae,* based on phenotypic characteristics and phylogenetic analyses, with *N. chiangraiensis* Doilom & K.D. Hyde as the type species (Doilom et al., 2017). In this study, a new species of *Neooccultibambusa* is introduced from an Arabica coffee plant in Yunnan Province, China, which is the first report of *Neooccultibambusa* from a coffee host.

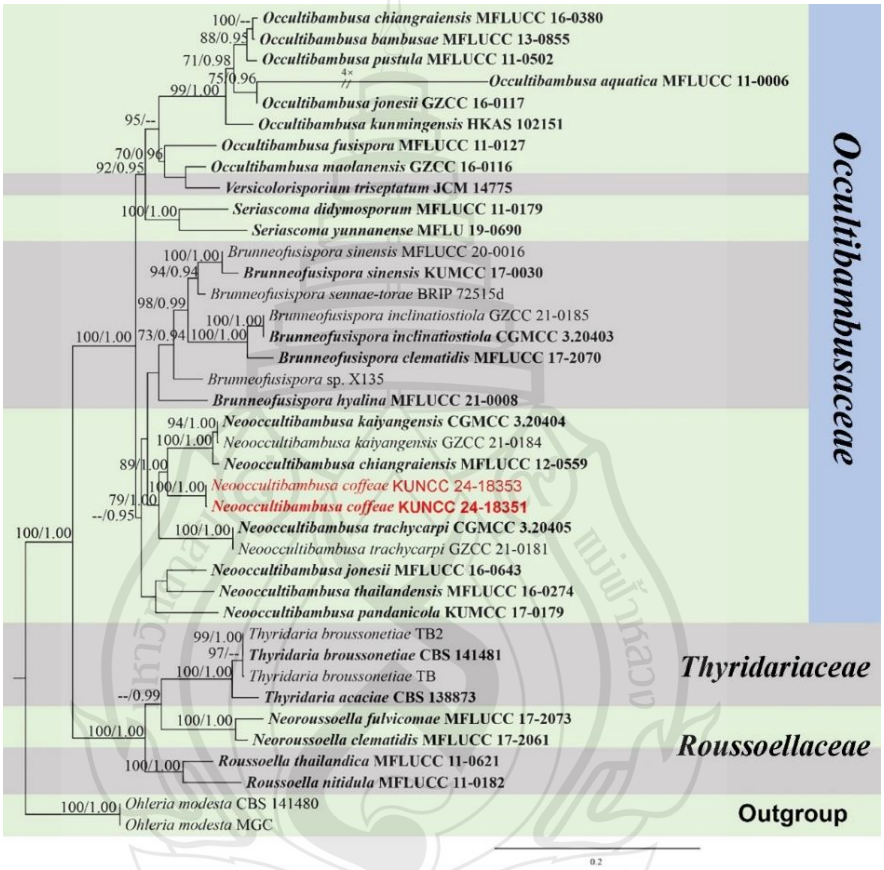


Figure 2.114 Phylogenetic tree of *Neooccultibambusa*

Figure 2.114 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Thirty-nine strains are included in the combined sequence analysis, which comprises 4,387 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Ohleria modesta* (CBS 141480 and MGC).

Neooccultibambusa coffeae L. Lu & Tibpromma, sp. nov. Figure 2.16.

Index Fungorum number: IF 901005; *Facesofungi number:* FoF 14731.

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137604.

Description: *Saprobic* on decaying branch of *C. arabica*. Teleomorph: *Ascomata* 140–180 × 200–250 µm ($\overline{x}$ = 156 × 218 µm, n = 10), superficial to semi-immersed, solitary to gregarious, small, black spots on host surface, unilocular, globose or subglobose, some with ostiolate. *Peridium* 10–20 µm wide ($\overline{x}$ = 15 µm, n = 20), outer walls comprising 2–4 layers of *textura angularis* cells, brown to dark brown, inner walls thin, hyaline and density. *Hamathecium* 2–4 µm wide ($\overline{x}$ = 3.2 µm, n = 20), hyphae-like, hyaline, filiform, branched, pseudoparaphyses numerous. *Asci* 100–200 × 20–30 µm ($\overline{x}$ = 156 × 24 µm, n = 20), 8-spored, bitunicate, cylindrical-clavate, straight, with a short furcate, apically rounded, with an ocular chamber. *Ascospores* 30–40 × 8–12 µm ($\overline{x}$ = 36.6 × 10.3 µm, n = 50), overlapping biseriate, hyaline when young, greyish-green when mature, fusoid or elliptical, 1–3-septate, guttulate, smooth-walled, mucilaginous sheath present. Anamorph: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h, colonies reached 4 cm in diameter after two months at 25℃, mycelia superficial, filamentous, with filiform margin, flat, smooth, from above, brown at the centre, dark brown at the edge, from below, dark brown.

Materials examined: China, Yunnan Province, Xishuangbanna, Pu'wen Town**,** on a decaying branch of *Coffea arabica* (*Rubiaceae*) **(**22°31'18" N, 101°2'44" E, 850 m alt.**)**, 15 September 2021, LiLu, JHPW 13 (HKAS 137604, holotype), isotype MHZU 23-0056, ex-type living culture KUNCC 24-18351, ex-isotype living culture ZHKUCC 23-0622; China, Yunnan Province, Pu'er, on a decaying branch of *C. arabica*, (22°36'2" N, 101°0'59" E, 1015 m alt.), 16 September 2021, LiLu, Pu'er 1-5 (HKAS 137603, paratype), isoparatype MHZU 23-0057, ex-paratype living culture KUNCC 24-18353, ex-isoparatype living culture ZHKUCC 23-0624.

GenBank numbers: KUNCC 24-18351: ITS = OR428394, LSU = OR428416, SSU = OR428374, *RPB*2 = OR515518, *TEF*1-α = OR509748; KUNCC 24-18353: ITS = OR428393, LSU = OR428415, SSU = OR428373, *RPB*2 = OR515517,

*TEF*1-α = OR509747.

Notes: In the concatenated phylogenetic analysis, *Neooccultibambusa coffeae* forms a distinct lineage within *Neooccultibambusa*, closely related to *N. chiangraiensis* and *N. kaiyangensis* (Figure 2.17). Morphologically, the new species resembles *N. chiangraiensis* and *N. kaiyangensis* in shape, but differs in the colour of ascospores. The ascospores of *N. coffeae* are greyish-green when mature, while the ascospores of *N. chiangraiensis* and *N. kaiyangensis* are pale brown (Figure 2.16; Doilom et al., 2017; Yu et al., 2021). Based on nucleotide comparisons, *N. coffeae* (ZHKUCC 23-0622) is different from *N. chiangraiensis* (MFLUCC 12-0559) by 50/494 bp (10%, without gaps) of the ITS, 22/872 bp (2.5%, without gaps) of the LSU, 16/943 bp (1.6%, without gaps) of the SSU and 32/613 bp (5%, without gaps) of the *TEF*1-α; In comparison, it is different from *N. kaiyangensis* (CGMCC 3.20404) in 42/467 bp (9%, without gaps) of the ITS, 20/836 bp (2%, without gaps) of the LSU, 16/1009 bp (1.5%, without gaps) of the SSU, 42/963 bp (4%, without gaps) of the *TEF*1-α and 88/886 bp (10%, without gaps) of the *RPB*2. In the BLASTn NCBI GenBank database search of ITS, LSU, SSU, *RPB*2 and *TEF*1-α sequences, ITS results are similar to *Brunneofusispora hyalina* M.S. Calabon & K.D. Hyde, (MFLU 21-0016) with 90% similarity, LSU is similar to *N. trachycarpi* X.D. Yu, S.N. Zhang & Jian K. Liu, (CGMCC 3.20405) with 98% similarity, SSU is similar to *Roussoella* sp. (GMB1323) with 93% similarity, *RPB*2 and *TEF*1-α results are similar to *N. kaiyangensis* (MFLUCC 17-2128) with 90% and 96% similarity, respectively. In addition, the PHI test results (Figure 2.22h) revealed no significant recombination relationships between *N. coffeae* and its phylogenetically related taxa. The morphological differences and phylogenetic analyses support the introduction of *N. coffeae* as a new species.

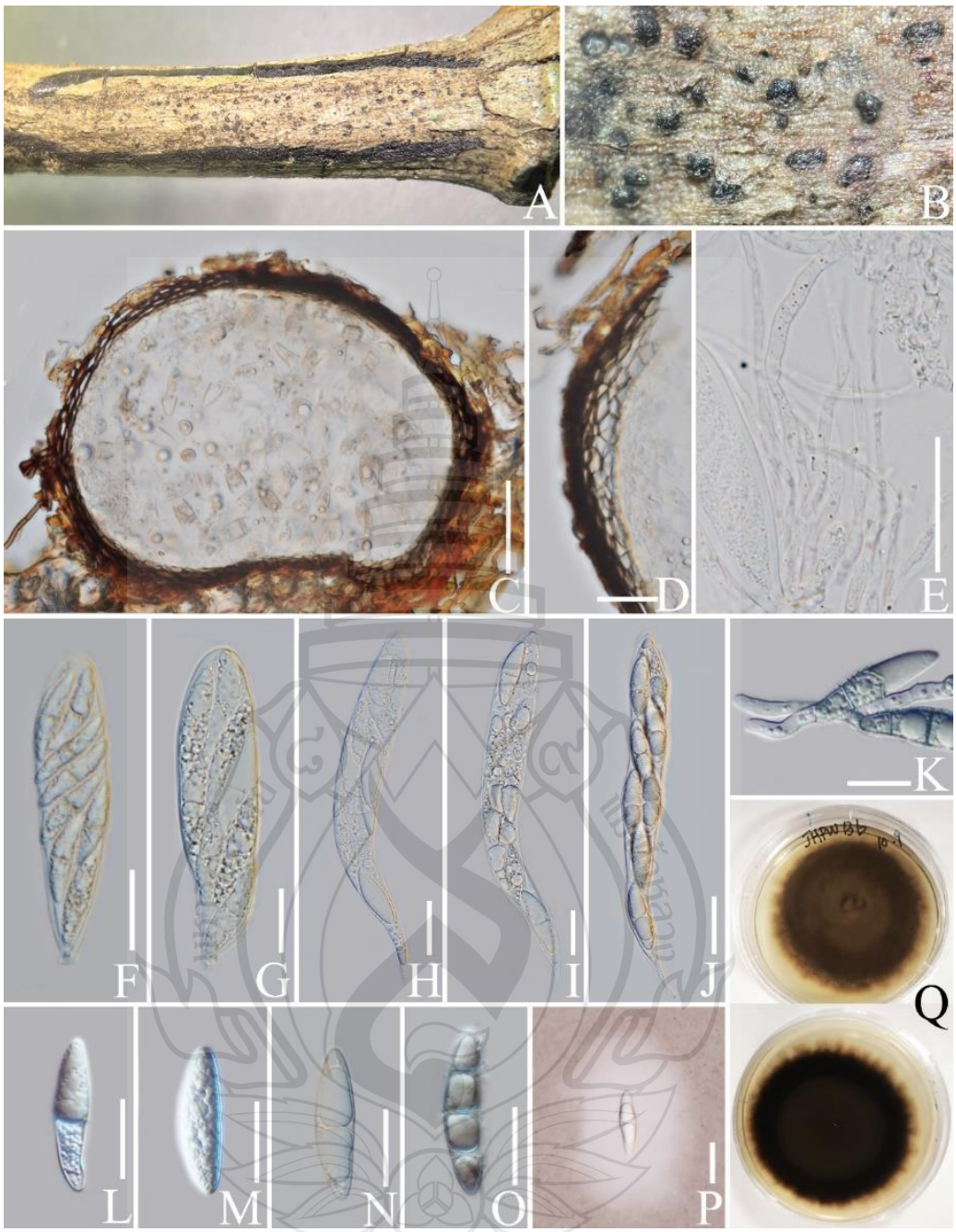


Figure 2.115 *Neooccultibambusa coffeae* (HKAS 137604, holotype)

Figure 2.115 A, B Ascomata on a decaying branch of *C. arabica*; C Longitudinal section of an ascoma; D Peridium wall; E Pseudoparaphyses; F–J Asci; L–O Ascospores; P An ascospore stained with Indian ink; K Germinated ascospores; Q Culture on PDA from obverse and reverse. Scale bars: C = 50 μm, D, E, K–P = 20 μm, F–J = 30 μm.

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

Paradictyoarthrinium Matsush., Matsushima Mycological Memoirs 9: 18 (1996).

Notes: The monotypic genus *Paradictyoarthrinium* was introduced by Matsushima (1996) with *P. diffractum* as the type species. *Paradictyoarthrinium* species are easily distinguished by their unique morphology, such as gregarious, black, powdery colonies and macronematous conidiophores with asymmetrically and unevenly dictyoseptate, muriform, subglobose to ellipsoidal, dark brown conidia (Liu et al., 2015, 2018). There are five accepted species in this genus, *viz*. *P. aquatica*, *P. diffractum*, *P. hydei*, *P. salsipaludicola* and *P. tectonicola* (Index Fungorum, 2025). Members of *Paradictyoarthrinium* were isolated from different hosts and are distributed in China, India, Thailand and South Africa, and can be found in terrestrial and aquatic habitats as saprobes (Matsushima, 1996; Prabhugaonkar & Bhat, 2011; Liu et al., 2015, 2018; Doilom et al., 2017; Htet et al., 2023; Xu et al., 2023). This study introduces a new host record of *Paradictyoarthrinium* from coffee in Thailand.

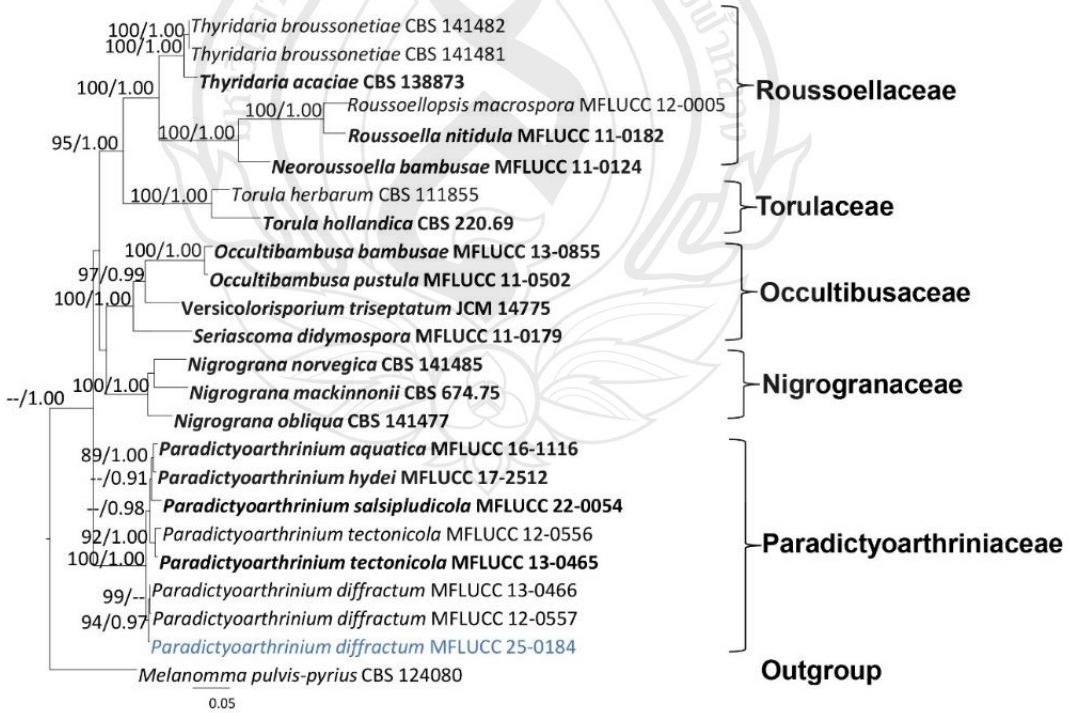


Figure 2.116 Phylogenetic tree of *Paradictyoarthrinium*

Figure 2.116 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *RPB2* sequence data. Twenty-four strains are included in the combined sequence analysis, which comprises 3,107 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Melanomma pulvis-pyrius* (CBS 124080).

Paradictyoarthrinium diffractum Matsush., Matsushima Mycological Memoirs 9: 18 (1996)

Index Fungorum: IF 415849; *Facesoffungi number*: FoF 01854; Figure 2.87

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph:** Hyphomycetous. *Colonies* on natural substrate, superficial, gregarious, scattered, dark green to black, powdery. *Conidiophores* up to 50 µm long, macronematous, erect to slightly curved, constricted at the septa, smooth-walled, branched, arising from hyphae. *Conidiogenous cells* 4–6 × 3–5 ($\overline{x}$ = 5.3 × 4 µm n = 20), blastic, integrated, terminal, determinate, globose to subglobose, or cylindrical, hyaline to light green. *Conidia* 10–17 × 8–12 ($\overline{x}$ = 13.8 × 11 µm n = 20), muriform, initially globose to subglobose, becoming ellipsoidal to irregular in shape, peacock green to brown, solitary or developing in branched chains, with 1–2 short chains, verrucose, very variable in size and shape, rounded to truncate at the base.

Culture characteristics: Conidia germinating on PDA within 12 h, reaching 30–40 mm in two weeks at 25°C. Colonies on PDA circular, with entire margin, umbonate, surface rough, wrinkled, sparse aerial hyphae, from above dark gray; from below dark brown.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea* sp. (19.80.5, 99.54.54, 990 m), 1 November 2023, Li Lu, LC3-2-9 (MFLU 25-0097), living culture MFLUCC 25-0184.

GenBank numbers: MFLUCC 25-0184: ITS = PQ608318, LSU = PQ608151, SSU = PQ608005.

Known hosts: Dead plant (Matsushima, 1996), dead decaying spathe of *Cocos nucifera* (Prabhugaonkar & Bhat, 2011), dead stumps of *Tectona grandis* (Doilom et al., 2017), decaying petioles of *Trachycarpus fortune* (Zhang et al., 2024),

Coffea sp. (This study).

Known distribution: China (Zhang et al., 2024), South Africa (Matsushima, 1996), India (Prabhugaonkar & Bhat, 2011), Thailand (Doilom et al., 2017; This study).

Notes: Paradictyoarthrinium diffractum was introduced as a hyphomycete found on dead plant material from a rivulet in South Africa (Matsushima, 1996). The DNA sequence of *P. diffractum* was provided by Liu et al. (2015). The multi-locus phylogenetic analysis results showed our new strains form a sister lineage to *P. diffractum* (MFLUCC 13-0466 and MFLUCC 12-0557; Figure 2.86) with 94% ML and 0.97 BYPP statistical bootstrap support. Besides, the morphology of our collection is similar to *P. diffractum* in having superficial, gregarious and powdery colonies on natural substrate, brown and muriform conidia (Doilom et al., 2017; Figure 2.87). We, therefore, introduce our collection as *P. diffractum* which is a new host record form *Coffea* sp. in Thailand.

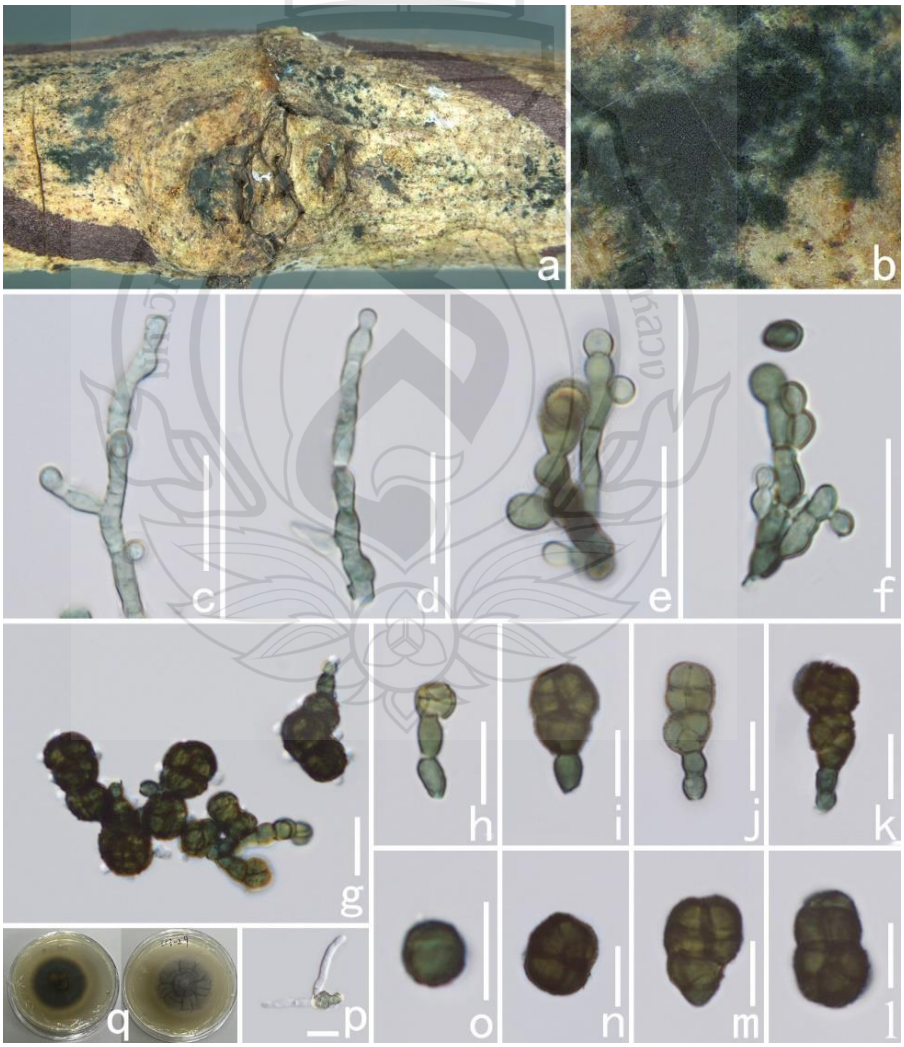


Figure 2.117 *Paradictyoarthrinium diffractum* (MFLU 25-0097, new host record)

Figure 2.117 a, b Colonies on a decaying branch of *Coffea* sp. c–f Conidiophores and conidiogenous cells. g–k Developmental stage of conidia. l–o Conidia. p Germinated conidium. q Culture on PDA from above and below. Scale bars: c–g = 15 µm, h–p = 10 µm.

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

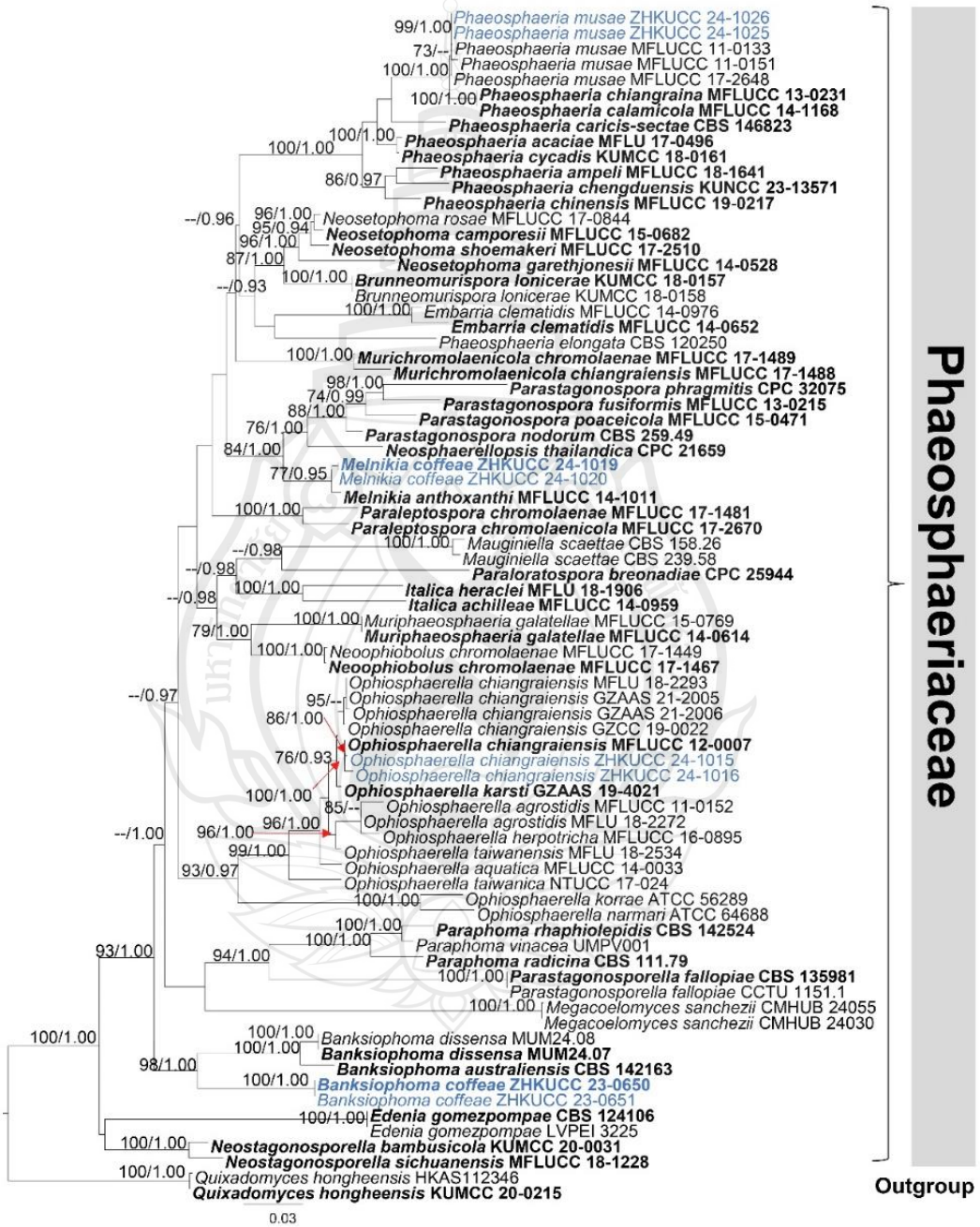


Figure 2.118 Phylogenetic tree of Phaeosphaeriaceae

Figure 2.118 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Swenty-seven strains are included in the combined sequence analysis, which comprises 3961 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Quixadomyces hongheensis* (HKAS112346 and KUMCC 20-0215).

Banksiophoma Crous, in Crous et al., Persoonia 38: 255 (2017)

Notes: *Banksiophoma* was introduced by Crous et al. (2017) to accommodate *B. australiensis*, which was isolated from leaves of *Banksia coccinea* in Australia. The second species, *B. dissensa* was introduced and isolated from a black discolouration on a deteriorated funerary art piece from Portugal, and they also amended the descriptions for *Banksiophoma* (Paiva et al., 2024). So far, *Banksiophoma* has been reported as a coelomycetous and hyphomycetous genus (Paiva et al., 2024). It is characterized by pycnidial, globose, brown conidiomata with ostiole, hyaline, subcylindrical to ampulliform conidiophores, and ellipsoid to globose or subglobose conidia, hyaline, aseptate, in chains, and globose to subglobose chlamydospores or microsclerotia (Crous et al., 2017; Paiva et al., 2024). Herein, a new *Banksiophoma* species is introduced from a coffee host from China, and this is the first sexual morph record of *Banksiophoma.*

Banksiophoma coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903602; *Facesoffungi number*: FoF 17584; Figure 2.89

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 23-0070

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 170–260 × 220–275 μm ($\bar{x}$ = 205 × 243 μm, n = 20), immersed, visible as black raised region on the host surface, glabrous, scattered, solitary, subglobose to globose, with central periphysate ostiole. *Peridium* 25–35 μm wide ($\bar{x}$ = 30, n = 20), thick-walled, composed of several layers, yellowish to brown cells of *textura globulosa* to *textura angularis*. *Hamathecium* of 2–3 μm wide ($\bar{x}$ = 2.5, n = 20), branched, septate,

filamentous, pseudoparaphyses. *Asci* 65–105 × 7–11 µm ($\bar{x}$ = 95 × 14 µm, n = 20), 8-spored, bitunicate, cylindrical to cylindric-clavate, apically rounded, short pedicellate and club-like. *Ascospores* 12.5–20 × 7.5–10 µm ($\bar{x}$ = 16 × 8.8 µm, n = 20), uni-seriate to bi-seriate, hyaline to brown, muriform, ellipsoidal, 1 transverse septum when young, 3–5 transverse septa when mature, 2–4 longitudinal septate, slightly constricted at the transverse septa, guttulate. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm after one month at 25°C, colonies circular, regular margin, from above: white to cream to gray, from observe: white to brown to dark brown.

Material examined: China, Yunnan Province, Dali City, Zhukula coffee plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C12 (MHZU 23-0070, holotype), ex-type ZHKUCC 23-0650, other living culture ZHKUCC 23-0651.

GenBank numbers: ZHKUCC 23-0650: ITS = PQ608274, LSU = PQ608107, SSU = PQ607965, *TEF*1-α = PQ628121, *RPB*2 = PV186833; ZHKUCC 23-0651: ITS = PQ608275, LSU = PQ608108, SSU = PQ607966, *TEF*1-α = PQ628122, *RPB*2 = PV186834.

Notes: Phylogenetically, our isolates (ZHKUCC 23-0650, ex-type and ZHKUCC 23-0651) clustered with *Banksiophoma australiensis* (CBS 142163, ex-type) with 98% ML, 1.00 BYPP statistical support (Figure 2.88). Our new strain (ZHKUCC 23-0650, ex-type) differs from *B. australiensis* (CBS 142163, ex-type) 83/541 bp (15.3%, without gaps) differences in ITS, and 9/834 bp (1.07%, without gaps) differences in LSU based on pairwise nucleotide comparison; in contrast, SSU, *TEF*1-α and *RPB*2 sequence data of *B. australiensis* (CBS 142163) are unavailable. Morphologically, only the asexual morph of *B. australiensis* has been reported (Crous et al., 2017); therefore, a morphological comparison is not possible (Figure 2.89). However, the phylogenetic tree and nucleotide comparison can distinguish the two species well. Thus, we introduced *Banksiophoma coffeae* as a novel species.

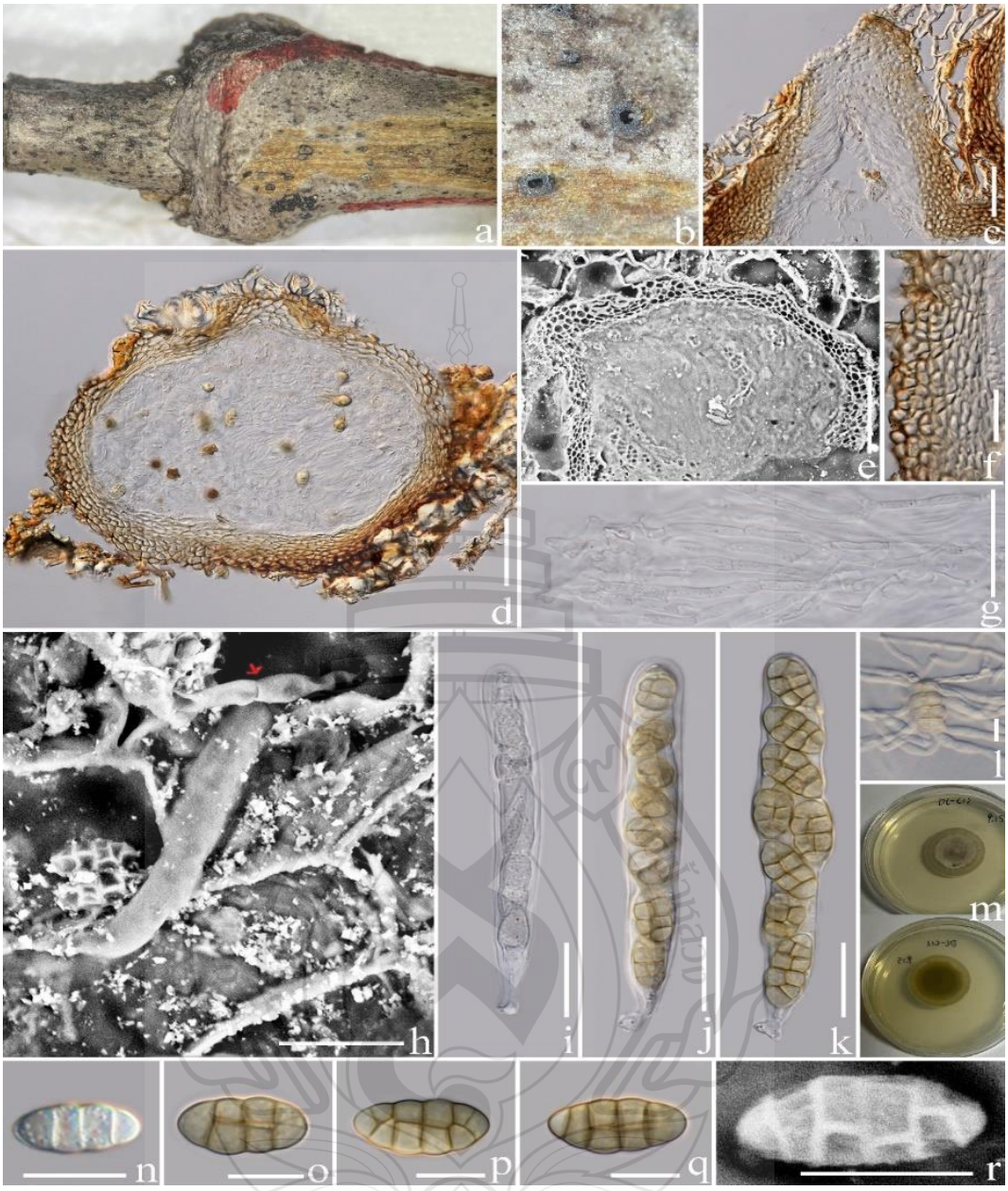


Figure 2.119 *Banksiophoma coffeae* (MHZU 23-0070, holotype)

Figure 2.119 a, b Appearance of ascomata on substrate. c Ostiole. d Vertical section of ascoma. e, f Peridium (e: SEM microphotographs of peridium). g Hamathecium. h–k Asci (h: SEM microphotographs of asci, the arrow indicates the septate of hamathecium). l Germinated ascospore. m Culture on PDA from above and below. n–r Ascospores (r: SEM microphotographs of ascospore). Scale bars: c–e = 50 µm, f–k = 20 µm, l, n–r = 10 µm.

Melnikia Wijayaw., Goonas., Bhat & K.D. Hyde, in Wijayawardene et al., Fungal Diversity: 10.1007/s13225-016-0360-2, (2016)

Notes: Melnikia was introduced by Wijayawardene et al. (2016), with *M. anthoxanthi* as the type species, which is isolated from *Anthoxanthum* sp. in Italy. *Melnikia* is characterized by pycnidial, globose, unilocular conidiomata with a central ostiole, enteroblastic, phialidic, ampulliform to lageniform, hyaline to pale brown conidiogenous cells, and ellipsoidal or sigmoid, 2–3 septate conidia. In this study, the second species of *Melnikia* will be introduced based on both morphological and phylogenetic analyses.

Melnikia coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903623; *Facesoffungi number*: FoF 17585; Figure 2.90

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0558

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 55–100 × 60–90 µm ($\overline{x}$ = 70 × 75 µm, n = 10), pycnidial, scattered, solitary, immersed to semi-immersed, black spots on the host surface, unilocular, globose, pale brown to brown. *Pycnidial wall* 8–14 µm wide, composed of 3-4 layers of brown to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5.5 × 3–5 µm ($\overline{x}$ = 4.13 × 4.11 µm, n = 10), enteroblastic, phialidic, ampulliform or lageniform, discrete, unbranched, hyaline, aseptate, smooth-walled, with distinct periclinal thickening. *Conidia* 8.5–13.5 × 2.5–3.5 µm ($\overline{x}$ = 11 × 3 µm, n = 30), subcylindrical to fusiform, hyaline, thin- and smooth-walled, aseptate and hyaline when young, 1-septate and pale brown at maturity, rounded at both ends. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 10 h. Colonies on PDA after four weeks at 25–27°C. Colonies circular, irregular margin, cottony, white from the above and pale brown to white from below.

Material examined: China, Yunnan Province, Dali City, Zhukula coffee plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C43 (MHZU 24-0558, holotype), ex-type ZHKUCC 24-1019, other living culture ZHKUCC 24-1020.

GenBank numbers: ZHKUCC 24-1019: ITS = PQ608299, LSU = PQ608132, SSU = PQ607986, *TEF*1-α = PQ628145; ZHKUCC 24-1020: ITS =

PQ608300, LSU = PQ608133, SSU = PQ607987, *TEF*1-α = PQ628146.

Notes: In the phylogenetic tree, the isolates ZHKUCC 24-1019 and ZHKUCC 24-1020 clustered with *Melnikia anthoxanthi* (MFLUCC 14-1011, ex-type) with 77% ML, 0.95 BYPP (Figure 2.88). Morphologically, our new collection differs from *M. anthoxanthi* in having larger conidiogenous cells (3–5.5 × 3–5 µm, L/W = 0.6–1.8 vs. 2–3×1–2 µm, L/W = 2–3), and smaller conidia (8.5–13.5 × 2.5–3.5 µm, L/W = 2.4–5.4 vs. 11–18 × 3–6 µm, L/W = 1.8–6). Additionally, the conidia of our new collection was observed as 1-septate, however, in *M. anthoxanthi* they are 2–3-septate (Wijayawardene et al., 2016; Figure 2.90). Hence, based on the phylogeny coupled with morphology, we introduced *M. coffeae* as a novel species in *Melnikia*. This is the first report of a *Melnikia* species from a coffee host.

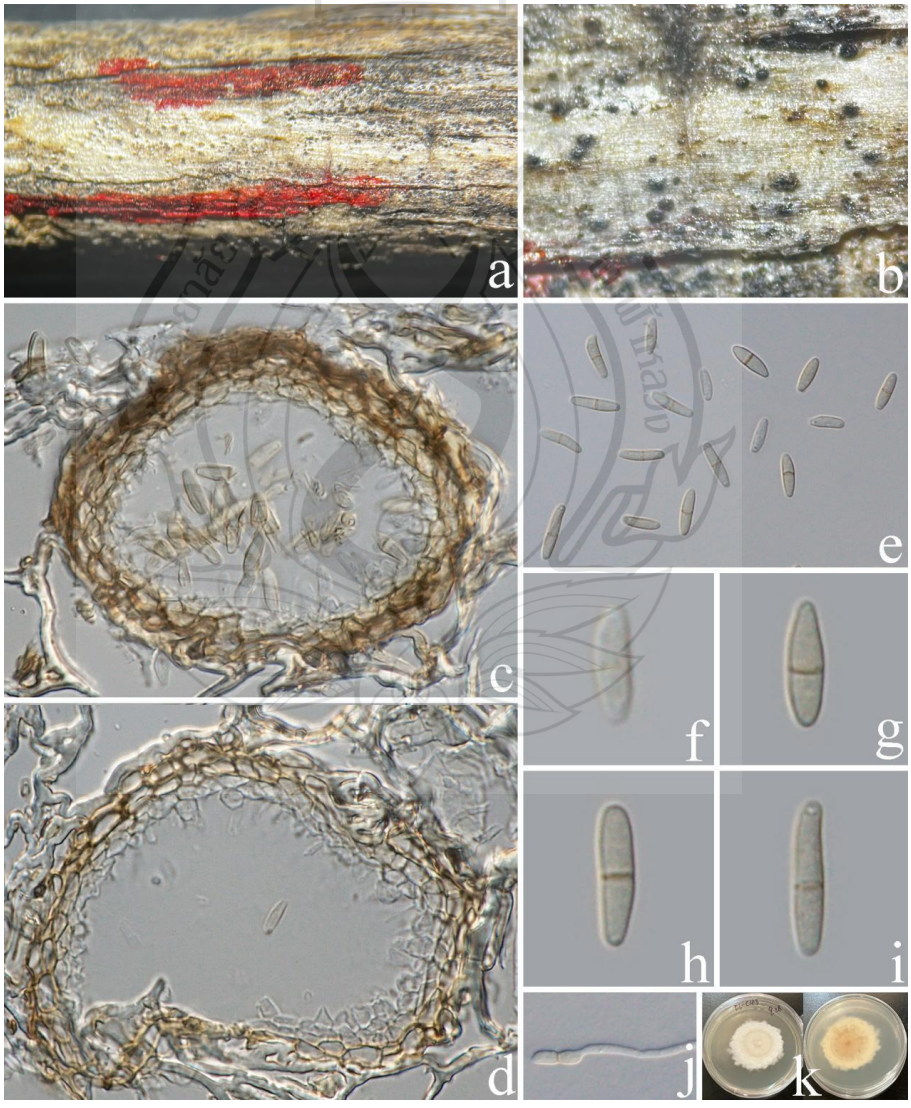


Figure 2.120 *Melnikia coffeae* (MHZU 24-0558, holotype)

Figure 2.120 a, b Conidiomata on the host surface. c Vertical section of conidioma. d Section of conidioma with conidiogenous cells, pycnidial wall. e–i Conidia. j Germinated conidium. k Culture on PDA from above and below. Scale bars: c–e = 20 µm, f–j = 5 µm.

Ophiosphaerella Speg., Anal. Mus. nac. B. Aires, Ser. 3 12: 401 (1909)

Notes: Ophiosphaerella was established by Spegazzini (1909) and typified by *O. graminicola*. A total of 17 species are listed under this genus in Index Fungorum (2025). The members of *Ophiosphaerella* are characterized by papillate ascomata, cylindrical asci, and pale brown, filamentous, and multi-septate ascospores (Tennakoon et al., 2020). *Ophiosphaerella* species have been reported as pathogens or saprobes and often occurred on Poaceae and Cyperaceae plants (Câmara et al., 2000). This study introduces a new host record, *Ophiosphaerella chiangraiensis,* from coffee in China.

Ophiosphaerella chiangraiensis Phookamsak & K.D. Hyde, Fungal Diversity 104: 29 (2020) (LC2-C11)

Index Fungorum number: IF 556471; *Facesoffungi number*: FoF 06128; Figure 2.91

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 165–270 × 130–280 µm ($\overline{x}$ = 235 × 215 µm, n = 20), black, immersed to semi-immersed, scattered, solitary, globose to subglobose, with a central ostiole. *Peridium* 15–30 µm wide ($\overline{x}$ = 20 µm), composed of several cells layers, paler to brown from inner layers to outer layers, arranged in *textura angularis*. *Hamathecium* of 1.7–3 µm wide ($\overline{x}$ = 2.3 µm), numerous, filamentous, septate pseudoparaphyses, anastomosing above the asci, embedded in a hyaline gelatinous matrix. *Asci* 90–155 × 6.5–9.5 µm ($\overline{x}$ = 120 × 8.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, apically rounded, with ocular chamber, short pedicellate with a club-like, truncate or furcate pedicel. *Ascospores* 115–140 × 2.5–3 µm ($\overline{x}$ = 127.5 × 2.7 µm, n = 20), overlapping, filiform, tapering at each both ends, hyaline to pale yellowish, curved, multi-septate, smooth-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, colonies circular, dense, with regular edge, from above, white to cream; from below, cream to pale yellowish.

Material examined: China, Yunnan Province, Lincang City, on a decaying branch of *Coffea* sp. (960 m), 28 July 2022, Li Lu, LC2-C11 (MHZU 24-0556), living culture ZHKUCC 24-1015, other living culture ZHKUCC 24-1016.

GenBank numbers: ZHKUCC 24-1015: ITS = PQ608314, LSU = PQ608147, SSU = PQ608001, *TEF*1-α = PQ628160, *RPB*2 = PV357181; ZHKUCC 24-1016: ITS = PQ608315, LSU = PQ608148, SSU = PQ608002, *TEF*1-α = PQ628161, *RPB*2 = PV357182.

Known hosts: Dead culm of grass (Yuan et al., 2020), dead culm of unidentified herbaceous plant (Zhang et al., 2023), *Coffea* sp. (This study).

Known distribution: Thailand (Yuan et al., 2020), China (Zhang et al., 2023; This study).

Notes: In our phylogenetic tree, our isolates clustered with *Ophiosphaerella chiangraiensis* (MFLUCC 12-0007) with 100 ML, 1.00 BYPP support (Figure 2.88). In addition, the morphological features of our collection largely overlap with *O. chiangraiensis* in its filiform and multi-septate ascospores (Yuan et al., 2020; Zhang et al., 2023; Figure 2.91). Hence, our collection is identified as *O. chiangraiensis* based on phylogeny and morphological evidence, and this is first time this species was isolated from a coffee host.

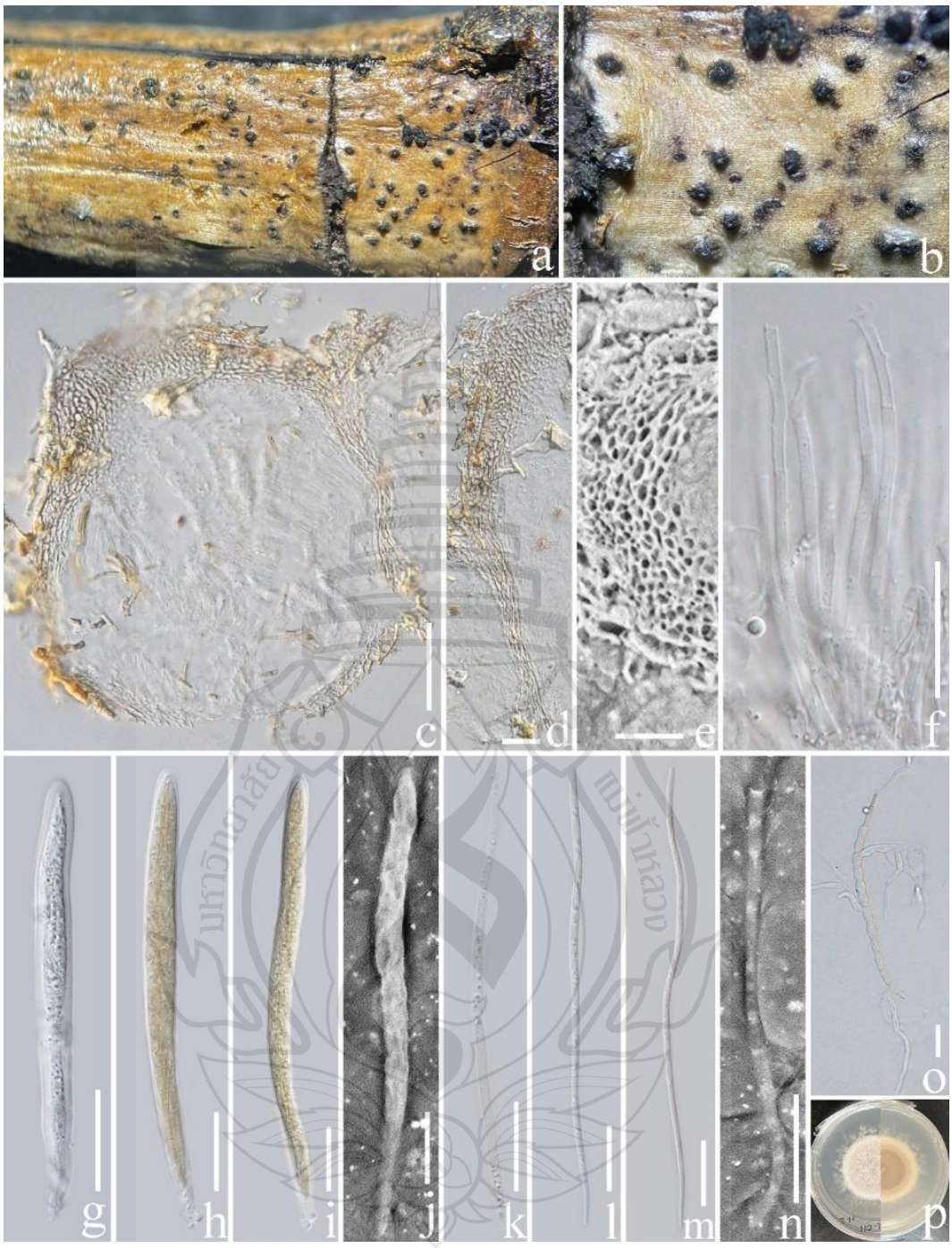


Figure 2.121 *Ophiosphaerella chiangraiensis* (MHZU 24-0556, new host record)

Figure 2.121 a, b Appearance of ascomata on the substrate. c Vertical section of ascoma. d Peridium. e SEM of peridium. f Hamathecium. g–i Asci. j SEM of ascus. k–m Ascospores. n SEM of ascospore. o Germinated ascospore. p Culture on PDA. Scale bars: c = 50 μm, d–o = 20 μm.

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

Notes: Phaeosphaeria was established by Miyake (1909) with *P. oryzae* as the type species. A total of 228 species are listed under this genus in Index Fungorum (2025). The sexual morph of *Phaeosphaeria* is characterized by globose to subglobose, glabrous ascomata with central ostioles; fissitunicate, broadly cylindrical asci with an ocular chamber; and phragmosporous, narrowly fusiform septate ascospores with or without a mucilaginous sheaths (Câmara et al., 2002; Phookamsak et al., 2014). The asexual morph of *Phaeosphaeria* is characterized by pycnidial, subglobose to globose, brown conidiomata; holoblastic, phialidic, ampulliform to doliiform conidiogenous cells; and phragmosporous, oblong to cylindrical, septate conidia (Abdullah et al., 2005; Hyde et al., 2011; Zhang et al., 2012; Phookamsak et al., 2014). Furthermore, the members of *Phaeosphaeria* occurred on monocotyledons or dicotyledons as saprobes or pathogens in temperate or tropical countries (Zhang et al., 2012; Phookamsak et al., 2014; Tennakoon et al., 2019). This study introduces a new host record of *Phaeosphaeria musae* from coffee in China.

Phaeosphaeria musae Sawada, Special Publication College of Agriculture, National Taiwan University 8: 66 (1959)

Index Fungorum number: IF 336200; *Facesoffungi number*: FoF 00262; Figure 2.92

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 80–150 × 80–165 µm ($\overline{x}$ = 115 × 145 µm, n = 20), visible as black spots on substrate, immersed, solitary, scattered, subglobose to globose, brown to dark brown. *Peridium* 13–20 µm wide ($\overline{x}$ = 16 µm, n = 20), composed of several layers of hyaline to brown cells of *textura angularis*. *Hamathecium* of 2–6 µm wide ($\overline{x}$ = 3.5 µm, n = 20), numerous, hyaline, filiform, septate, branched, cellular pseudoparaphyses, embedded in gelatinous matrix, anastomosing at the apex. *Asci* 60–75 × 9.5–13.5 µm ($\overline{x}$ = 67.5 × 11.5 µm, n = 25), 2–8-spored, bitunicate, fissitunicate, cylindrical to clavate, apically rounded with an ocular chamber, short pedicellate, some with a club-shaped pedicle. *Ascospores* 24–29 × 4.5–5.5 µm ($\overline{x}$ = 26.5 × 5 µm, n = 30), overlapping, 1–3-seriate, yellowish-brown, fusiform with narrowly rounded ends, 3–5-septate, slightly constricted at the septum, some enlarged in second cell from apex, guttulate, surrounded by an inconspicuous mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm after one month at 25°C. Colonies from above: dense, circular, velvety to hairy; from below white to yellowish from margin to center.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April. 2024, Li Lu, DH2-3 (ZHKU 24-0561), living culture ZHKUCC 24-1025, other living culture ZHKUCC 24-1026.

GenBank numbers: ZHKUCC 24-1025: ITS = PQ608319, LSU = PQ608152, SSU = PQ608006, *TEF*1-α = PQ628164; ZHKUCC 24-1026: ITS = PQ608320, LSU = PQ608153, SSU = PQ608007, *TEF*1-α = PQ628165.

Known hosts: Musa cavendishii (Sawada, 1959), pathogen on Asparagaceae (*Cordyline* sp.) and Marantaceae (*Calathea* sp.) (Phookamsak et al., 2014), dead leaf of palms (Liu et al., 2015), dead leaf of *Roystonea regia* (Arecaceae) (Tennakoon et al., 2019), *Coffea arabica* (This study).

Known distribution: China (Sawada, 1959; Tennakoon et al., 2019; This study), Thailand (Phookamsak et al., 2014; Liu et al., 2015).

Notes: In the phylogenetic tree, our isolates are nested with *Phaeosphaeria musae* (CBS 120026, MFLUCC 17-2648, MFLUCC 11-0151 and MFLUCC 11-0133) with 99% ML and 1.00 BYPP bootstrap support (Figure 2.88). *Phaeosphaeria musae* was introduced by Miyake (1909) based on its asexual morph. Subsequently, Phookamsak et al. (2014), Liu et al. (2015), and Tennakoon et al. (2019) reported its sexual morph and the morphological characteristics of our new collection resemble it. The ascospores of Phookamsak et al. (2014) and Tennakoon et al. (2019) have 3-septa, Liu et al. (2015) have 5-cells, and our isolates have 3–5-septa and 4–6-cells (Figure 2.92). This variation could be possibly due to the environment or host change leading to slight differences. However, the phylogenetic evidence strongly supports that our new collection as *P. musae*. Thus, herein we provide the first record of *P. musae* from a coffee host.

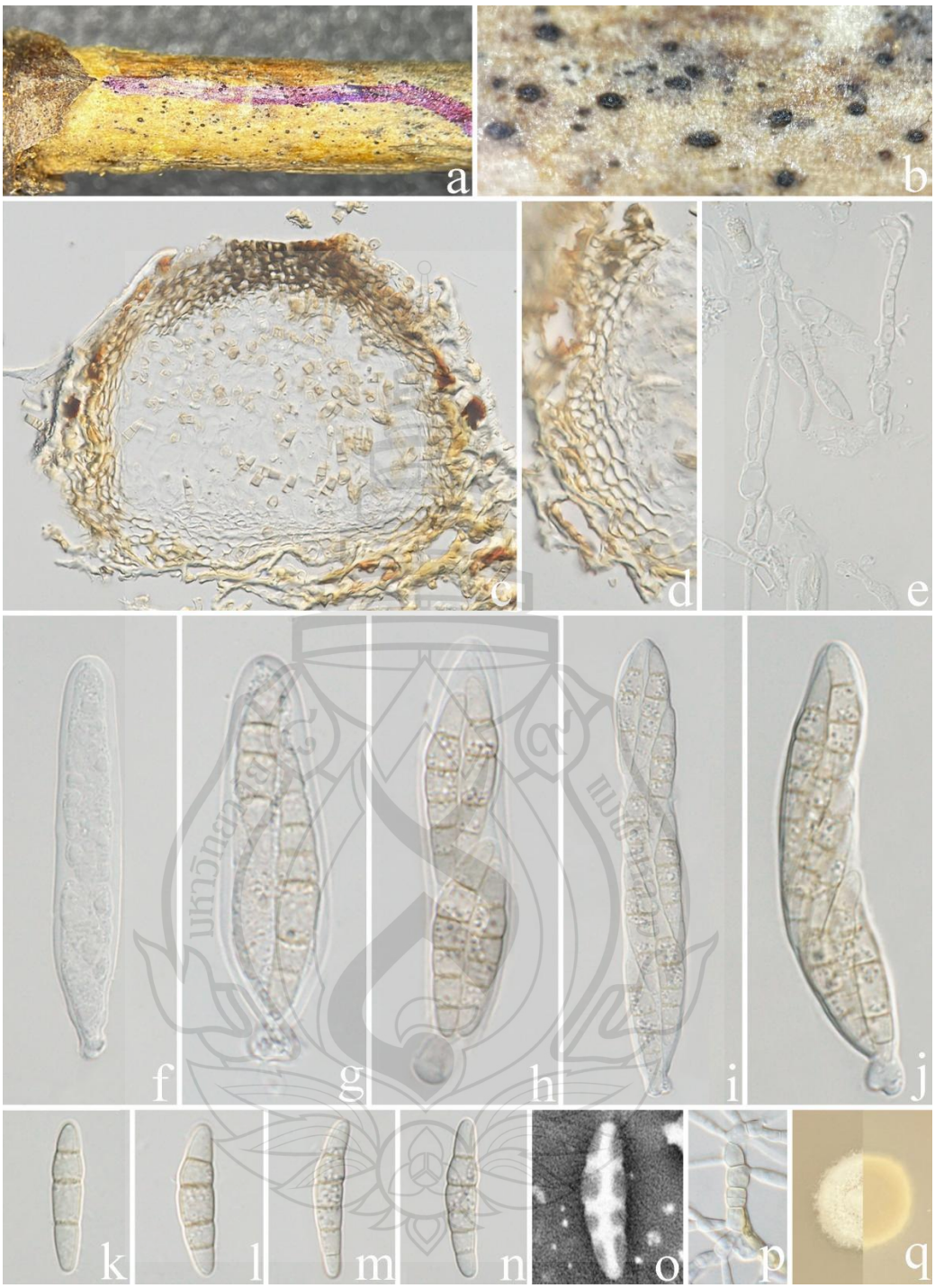


Figure 2.122 *Phaeosphaeria musae* (ZHKU 24-0561, new host record)

Figure 2.122 a, b Appearance of ascomata on substrate. c Vertical section of ascoma. d Peridium. e Hamathecium. f–j Asci. k–o Ascospores. (o: SEM microphotographs of ascospore). p Germinated ascospore. q Culture on PDA from above and below. Scale bars: c = 50 μm, d–j = 20 μm, k–p = 10 μm.

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

Pararoussoella Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 89: 169 (2018)

Notes: *Pararoussoella* was proposed by Wanasinghe et al. (2018) with the type species *P. rosarum* Wanas., E.B.G. Jones & K.D. Hyde. The genus was introduced for the species that are distantly related to the type species of *Roussoella* Sacc., *R. nitidula* Sacc. & Paol. (Phukhamsakda et al., 2020). *Pararoussoella* comprises only five species and is reported as anamorph and teleomorph (Crous et al., 2019, 2020). *Pararoussoella coffeae* is introduced herein as a new species with anamorph; it was isolated from an Arabica coffee plant in Yunnan Province, China and this is the first report of *Pararoussoella* from a coffee host.

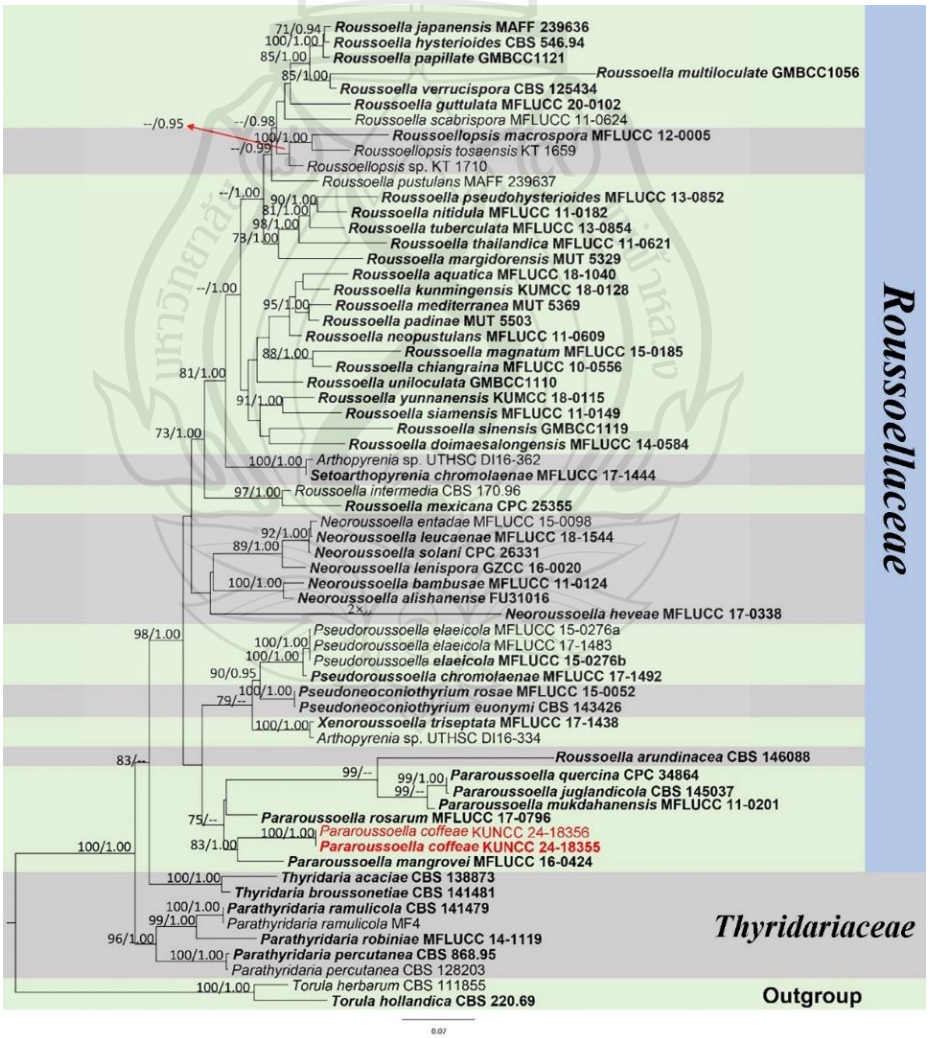


Figure 2.123 Phylogenetic tree of *Pararoussoella*

Figure 2.123 Phylogram generated from the best scoring RAxML tree. based on a combined ITS LSU, SSU, *RPB*2 and *TEF*1-α sequence dataset. *Torula herbarum* (Pers.) Link, (CBS 111855) and *T. hollandica* Crous, (CBS 220.69) are selected as the outgroup taxa. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given above the nodes. All type strains are in bold and newly-generated sequences are in red.

Pararoussoella coffeae L. Lu & Tibpromma, sp. nov. Figure 2.18.

Index Fungorum number: IF 901006*; Facesofungi number:* FoF 14732.

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Diagnosis: Differs from other *Pararoussoella* species by the subcylindrical to ellipsoid or, sometimes, ovoid conidia.

Holotype: HKAS 137609.

Description: *Saprobic* on decaying branch of *C. arabica*. Teleomorph: Not observed. Anamorph: *Conidiomata* 60–120 µm high × 100–160 µm diam. ($\overline{x}$ = 92 × 121 µm, n = 15), pycnidial, immersed, globose to subglobose, brown, with central ostioles. *Conidiomatal wall* 15–25 µm wide ($\overline{x}$ = 19 µm, n = 20), hyaline to light brown, thick, 4–6 layers, outer layer composed of brown cells of *textura angularis*, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* inconspicuous or micronematous, often reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, oval to obpyriform or doliiform, phialidic with periclinal thickening at apex, 3–5 × 2–5 µm ($\overline{x}$ = 4 × 3.5 µm, n = 30). *Conidia* 3.5–5 × 2–3 µm ($\overline{x}$ = 4.4 × 2.4 µm, n = 30), aseptate, solitary, guttulate, subcylindrical to ellipsoid or, sometimes, ovoid, smooth, apex bluntly rounded, base truncate, hyaline when young, becoming light brown when mature.

Culture characteristics: Conidia germinating on PDA within 24 h, colonies reached 2.5–3 cm in diameter after one month at 25°C, filamentous, with entire margin, flat to raised, with many white aerial mycelia, from above, white at the centre, yellowish at the edge, from below, yellowish.

Materials examined: China, Yunnan Province, Lincang, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (24°17' N, 99°99' E, 960 m alt.), 28 July 2022, LiLu, LC1-C3 (HKAS 137609, holotype), isotype MHZU 23-0061, ex-type living

culture KUNCC 24-18355 = KUNCC 24-18356, ex-isotype living culture ZHKUCC 23-0632 = ZHKUCC 23-0633.

GenBank numbers: KUNCC 24-18355: ITS = OR428401, LSU = OR428423, SSU = OR428381, *RPB*2 = OR515521, *TEF*1-α = OR509755; KUNCC 24-18356: ITS = OR428402, LSU = OR428424, SSU = OR428382, *RPB*2 = OR515522, *TEF*1-α = OR509756.

Notes: In the concatenated phylogenetic analysis, *Pararoussoella coffeae* forms a sister branch basal to *P. mangrovei* (Phukhams. & K.D. Hyde) Phukhams. & K.D. Hyde (Figure 2.19). Since *P. mangrovei* has only been reported as teleomorph, we performed nucleotide comparisons; *P. coffeae* (ZHKUCC 23-0632) is different from *P. mangrovei* (MFLUCC 16-0424) by 20/434 bp (4.6%, without gaps) of the ITS, 14/805 bp (1.7%, without gaps) of the LSU, 99/796 bp (12%, without gaps) of the *RPB*2 and 28/718 bp (3.8%, without gaps) of the *TEF*1-α. Based on morphology, our novel taxon in *Pararoussoella* is similar to the species *P. juglandicola* Crous & R.K. Schumach. in aseptate and brown conidia, but differs in the shape of conidia. The conidia of our new species are subcylindrical to ellipsoid, sometimes ovoid, while the conidia of *P. juglandicola* are subcylindrical; besides, the characteristics of guttulate in our species are more distinct than *P. juglandicola* (Figure 2.18; Crous et al., 2019). Therefore, the morphological differences and phylogenetic analyses support the introduction of *P. coffeae* as a new species.

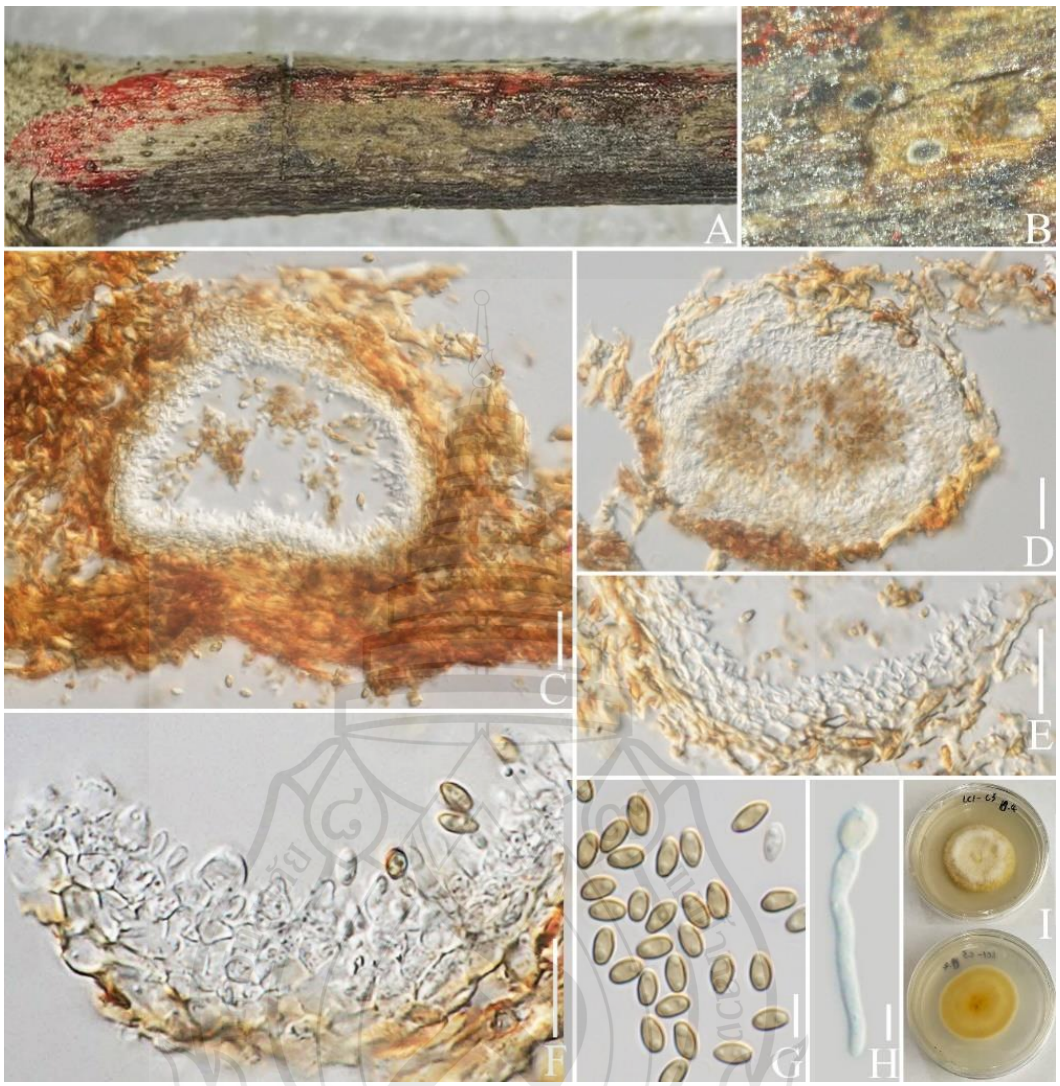


Figure 2.124 *Pararoussoella coffeae* (HKAS 137609, holotype)

Figure 2.124 A, B Appearance of conidiomata on a decaying branch of *C. arabica*; C, D Longitudinal section of a conidioma; E Conidiomata wall; F Conidiogenous cells and conidia; G Conidia; H Germinated conidium; I Culture on PDA from the obverse and reverse. Scale bars: C–F = 20 μm, G, H = 5 μm.

Similroussoella L. Lu, K.D. Hyde & Tibpromma, *gen. nov.*

Index Fungorum number: IF 903646; Facesoffungi number: FoF 17586

Etymology: The genus name refers to the characteristics similar to the type genus *Roussoella*.

Type species: *Similroussoella jinghongensis*

Saprobic on a dead or decaying plants. **Sexual morph:** *Ascomata* solitary, immersed, uni-loculate, black, subglobose to oblate spheroid, with an ostiole. *Ostioles* central, papillate, opening by a pore, with periphyses. *Peridium* comprising several layers of hyaline to brown cells of *textura angularis*, some fusing with the substrate. *Hamathecium* of dense, cellular, septate, slight constricted at the septa, and branched, pseudoparaphyses. *Asci* 8-spored, bitunicate, cylindrical, short pedicellate and club-shaped, apically rounded poor-developed ocular chamber. *Ascospores* uniseriate, sometimes partially overlapping, oval to ellipsoid, few fusiform, with apical ends, yellowish to brown, uni-septate, constricted at septum, with guttules in each cell, verruculose, longitudinally striate. **Asexual morph**: Not observed.

Notes: *Similroussoella* formed an independent branch in Roussoellaceae within 100% ML, 1.00 BYPP statistical support (Figure 2.93), close to *Setoarthopyrenia chromolaenae* (MFLUCC 17-1444, ex-type) and *Arthopyrenia* sp. (UTHSC: DI16-362). *Setoarthopyrenia* is characterized by a protruding ostiolar neck, with numerous external brown to dark brown setae of the ascomata, and hyaline, ellipsoid to obovoid, 1-septate ascospores, without a gelatinous sheath (Mapook et al., 2020). In contrast, *Similroussoella* differs in having immersed, subglobose to oblate spheroid ascomata, without setae, and yellowish to brown, oval to ellipsoid, or fusiform ascospores (Ren et al., 2024; Figure 2.94). However, we could not compare the morphological characteristics with *Arthopyrenia*, as the morphology of *Arthopyrenia* sp. (UTHSC: DI16-362) has not been reported (Mapook et al., 2020). Morphologically, *Similroussoella* is also similar to the type genus *Roussoella* by fusiform to ellipsoidal ascospores, brown and two-celled (Dai et al., 2022). Therefore, *Similroussoella* is provided to accommodate *S. jinghongensis*, based on morphology and phylogeny.

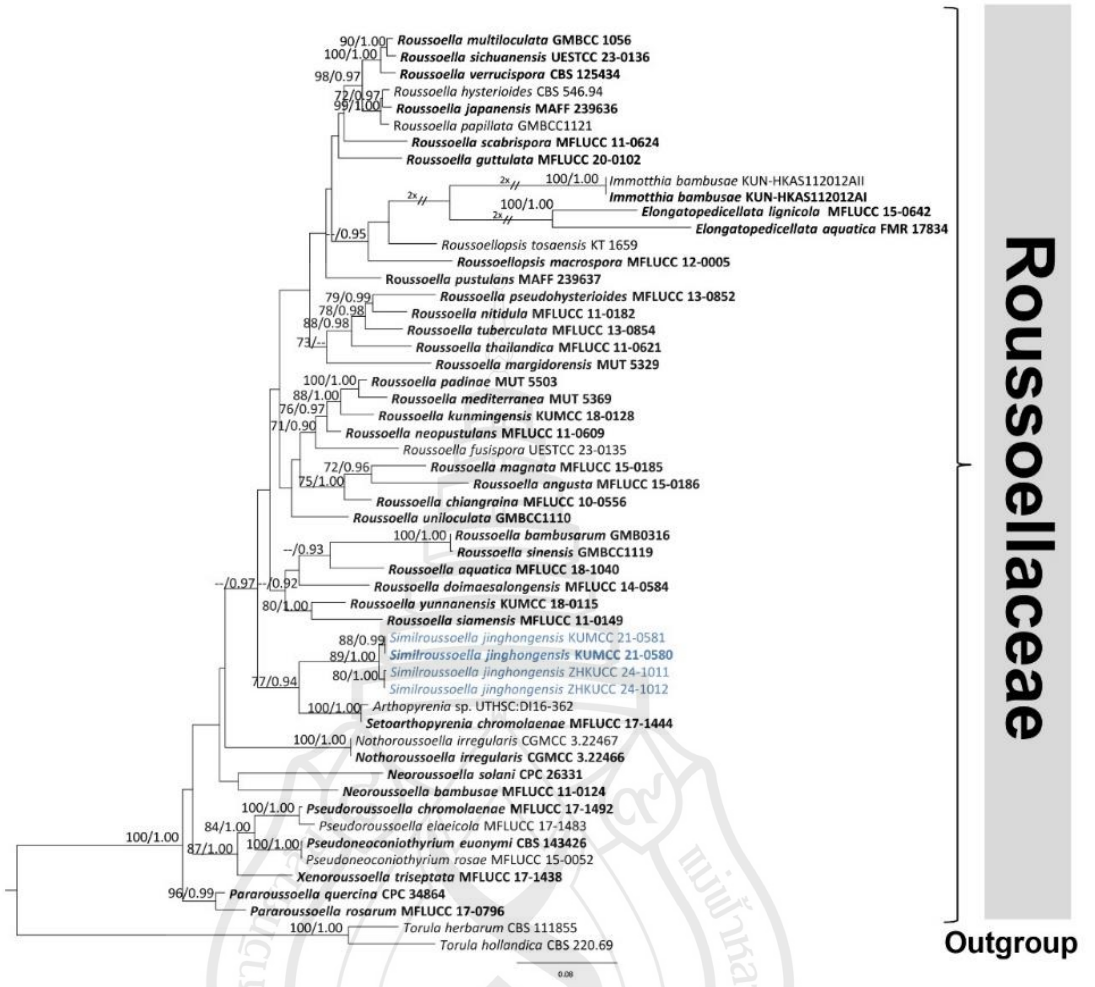


Figure 2.125 Phylogenetic tree of *Similroussoella*

Figure 2.125 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, and *TEF*1-α sequence data. Fifty-four strains are included in the combined sequence analysis, which comprises 3,349 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Torula herbarum* (CBS 111855) *and Torula hollandica* (CBS 220.69).

Similroussoella jinghongensis L. Lu, K.D. Hyde & Tibpromma (G.C. Ren & K.D. Hyde), *comb. nov.*

Basionym: *Setoarthopyrenia jinghongensis* G.C. Ren & K.D. Hyde, Mycosphere 15 (1): 1046 (2024)

Index Fungorum number: IF 903647; *Facesoffungi number*: FoF 17587; Figure 2.94.

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 100–230 × 150–370 μm ($\overline{x}$ = 166 × 240 μm, n = 15), solitary, raised, immersed, uni-loculate, black, subglobose to oblate spheroid, with short ostiole. *Ostioles* central, papillate, opening by a pore, with periphyses. *Peridium* 15–25 μm wide ($\overline{x}$ = 19 μm, n = 20), comprising several layers of hyaline to brown cells of *textura angularis* to *textura prismatica*, some fusing with the substrate. *Hamathecium* of 2–5 μm wide ($\overline{x}$ = 3.4 μm, n = 30), dense, septate, branched, cellular pseudoparaphyses, slightly constricted at the septa. *Asci* 80–130 × 8–12 μm ($\overline{x}$ = 102 × 9.5 μm, n = 30), 8-spored, bitunicate, cylindrical, short pedicellate and club-shaped, apically rounded with poorly-developed ocular chamber. *Ascospores* 15–20 × 6.5–8.5 μm ($\overline{x}$ = 16.8 × 7.6 μm, n = 30), uniseriate, sometimes partially overlapping, oval to ellipsoid, some fusiform, with apical ends, yellowish to brown, 1-septate, constricted at septum, with guttules in each cell, normally both cells the same size, verruculose, longitudinally striate. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in two weeks at 25°C, circular, slightly raised, with filiform margin, radially furrowed at the center, fluffy, from above gray, from below, dark brown to black, wrinkled.

Material examined: China, Yunnan Province, Nujiang City, on a decaying branch of *Coffea* sp. (25.80 N, 98.85 E, 1005 m), 22 April 2023, Li Lu, C-27 (MHZU 24-0554), living culture ZHKUCC 24-1011, other living culture ZHKUCC 24-1012.

GenBank numbers: ZHKUCC 24-1011: ITS = PQ608260, LSU = PQ608093, *RPB*2 = PV186829, *TEF*1-α = PQ602134; ITS = PQ608261, LSU = PQ608094, *RPB*2 = PV186830, *TEF*1-α = PQ602135.

Known hosts: Dead twigs of *Ehretia acuminata* (Ren et al., 2024), *Coffea* sp. (This study).

Known distribution: China (Ren et al., 2024; This study).

Notes: Based on distinct morphology and phylogenetic position, *Similroussoella jinghongensis* was previously placed in *Setoarthopyrenia* by Ren et al. (2024). In our phylogenetic tree of combined ITS, LSU, *RPB*2, and *TEF*1-α, *Setoarthopyrenia jinghongensis* and our new collection forms an independent lineage under the type species *Setoarthopyrenia chromolaenae* (MFLUCC 17-1444, ex-type). *Setoarthopyrenia jinghongensis* is characterized by oval or obpyriform ascomata, without setae, clavate or cylindrical asci, and uniseriate, ellipsoid, brown to dark brown ascospores (Ren et al., 2024; Figure 2.94), while *Setoarthopyrenia chromolaenae* has globose ascomata with brown to dark brown setae, cylindric-clavate asci, and biseriate, hyaline, ellipsoid to obovoid ascospores (Mapook et al., 2020). Base pair comparison between *Setoarthopyrenia jinghongensis* (KUMCC 21-0580, ex-type) and *Setoarthopyrenia chromolaenae* (MFLUCC 17-1444, ex-type) showed 8.2% (39/475 bp, without gaps) in ITS, 1.3% (10/797 bp, without gaps) in LSU and 3.9% (35/890 bp, without gaps) in *TEF*1-α. Based on the large difference in both morphology and phylogeny between *Setoarthopyrenia chromolaenae* and *Setoarthopyrenia jinghongensis*. *Setoarthopyrenia jinghongensis* was transferred to the new genus *Similroussoella*, named as *Similroussoella jinghongensis*. In addition, we hereby introduce our collection as a new host record of *Similroussoella jinghongensis*, supported by both morphological comparison and phylogenetic analyses. Our species also revealed that *Similroussoella jinghongensis* possesses longitudinally striated ascospores (Figure 2.94); this feature was not observed in the type species (Ren et al., 2024).

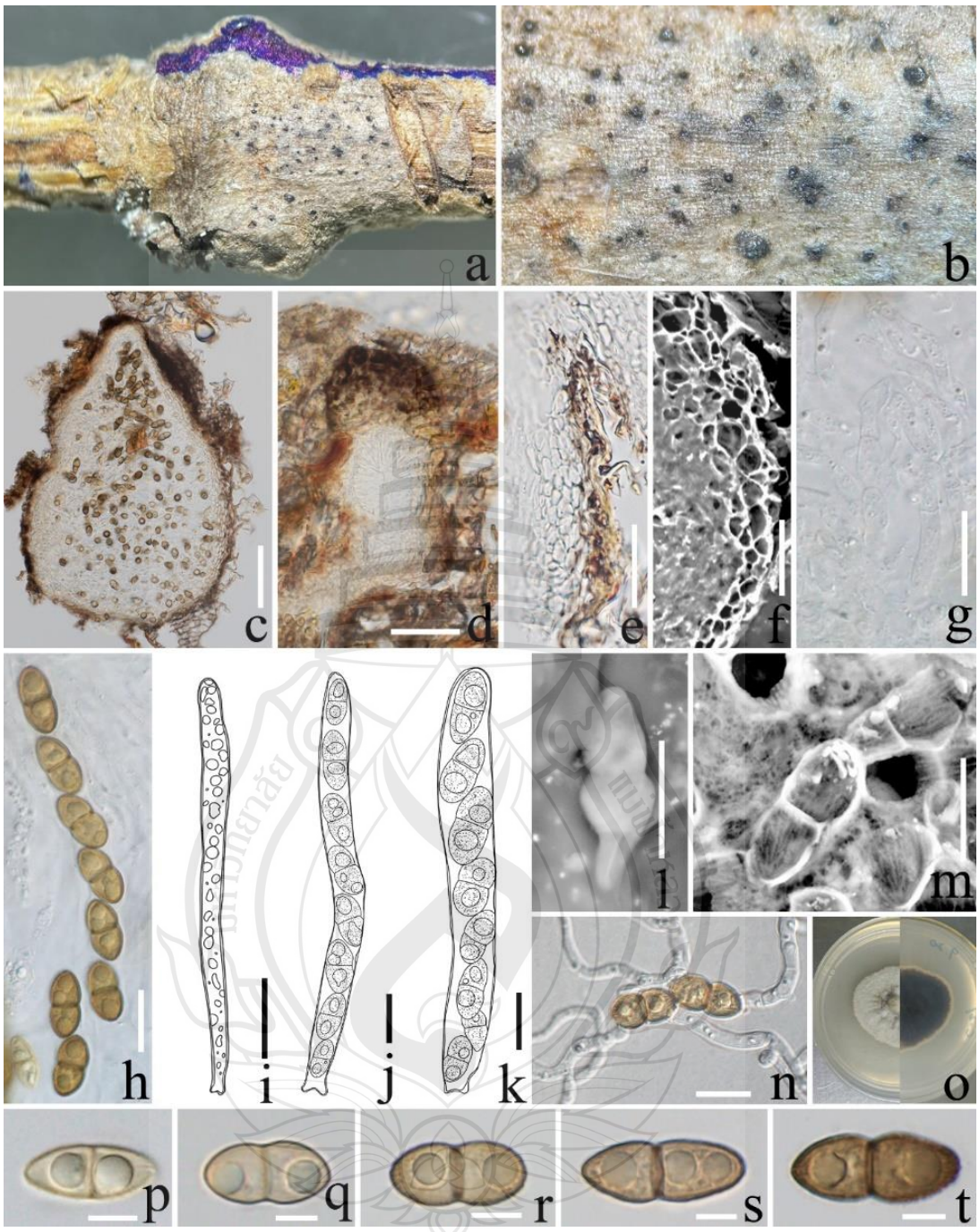


Figure 2.126 *Similrousoella jinghongensis* (MHZU 24-0554, new host record)

Figure 2.126 a, b Ascomata on host surface. c Longitudinal section of ascoma. d Ostiole. e, f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–k Asci. l, m SEM microphotographs of ascospores. p–t Ascospore. n Germinated ascospores. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, d–j = 15 µm, k–m = 10 µm, o–s = 5 µm.

Sulcatisporaceae Kaz. Tanaka & K. Hiray., Studies in Mycology 82: 119 (2015)

Loculosulcatispora G.C. Ren & K.D. Hyde, Phytotaxa 475 (2): 70 (2020)

Notes: Loculosulcatispora introduced by Ren et al. (2020) and typified by *L. thailandica*, has four reported species, *viz. L. thailandica* (Ren et al., 2020), *L. hongheensis* (Wanasinghe et al., 2022), *L. juglandis* (Wang et al., 2023a) and *L. paeoniae* (Li et al., 2023). Members of this genus are reported to be saprobes on different plants and are distributed in China and Thailand (Ren et al., 2020; Wanasinghe et al., 2022; Li et al., 2023; Wang et al., 2023a). The sexual morph of *Loculosulcatispora* is characterized by scattered ascomata, globose to subglobose, with a central ostiole, clavate asci, with a short pedicel, with or without an ocular chamber, and hyaline, fusiform, 1-septate ascospores, with acute ends, surrounded by a mucilaginous sheath (Wanasinghe et al., 2022), and asexual morph is characterized by solitary or scattered, conical, ostiolate, multilocular conidiomata, ostioles single or multiple, arising from the stratum, holoblastic, determinate, hyaline, doliiform to cylindrical, aseptate, unbranched conidiogenous cells, and hyaline, oblong, 1-celled conidia (Ren et al., 2020). This study introduces a new host and new country record of *Loculosulcatispora thailandica* from coffee in China.

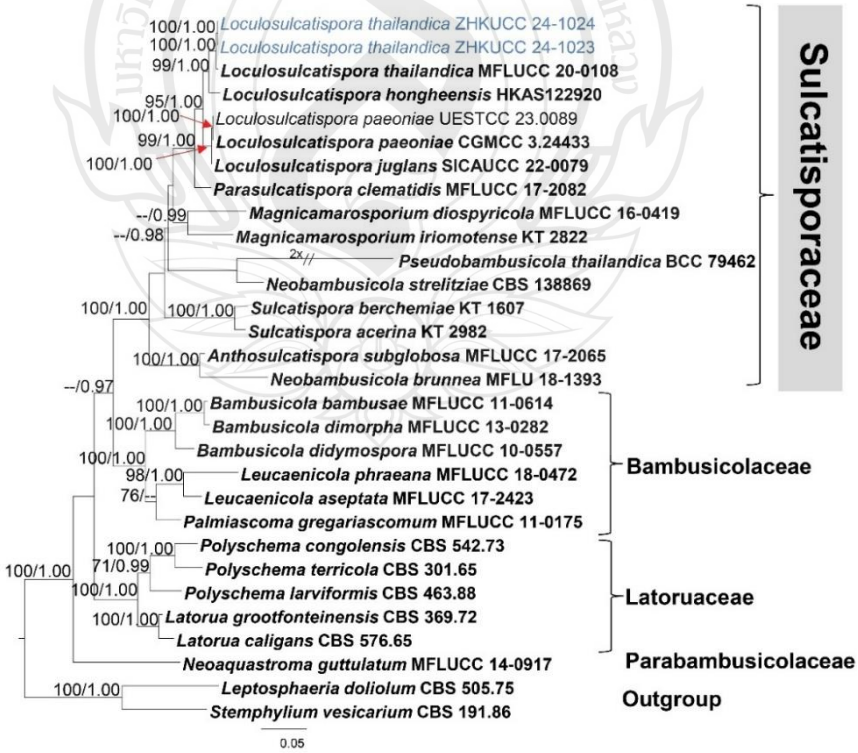


Figure 2.127 Phylogenetic tree of *Loculosulcatispora*

Figure 2.127 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Thirty strains are included in the combined sequence analysis, which comprises 4,622 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Stemphylium vesicarium* (CBS 191.86) and *Leptosphaeria doliolum* (CBS 505.75).

Loculosulcatispora thailandica G.C. Ren & K.D. Hyde, Phytotaxa 475 (2): 73 (2020)

Index Fungorum number: IF 557590; *Facesoffungi number:* FoF 07977; Figure 2.96

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Coelomycetous. *Conidiomata* 180–260 × 300–360 µm ($\bar{x}$ = 200 × 320, n = 5), subglobose or conical, black, scattered, semi-immersed, 2–8-loculate, ostiolate; each locule 50–80 × 40–80 µm ($\bar{x}$ = 68 × 63, n = 10), subglobose to ellipsoidal. *Ostioles* single or multiple, black, papillate, central. *Conidiomatal wall* 10–20 µm wide, 2–4 layered, outer layer comprising brown cells of *textura angularis*, inner wall thin, comprising hyaline cells of *textura angularis*. *Hamathecium* of 1–2 µm wide, sparse, aseptate, hyaline, unbranched paraphyses, arising around inner wall of locules. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous* cells 4–12 × 1.5–3.5 µm ($\bar{x}$ = 7.9 × 2, n = 30), enteroblastic, phialidic, discrete, determinate, doliiform to cylindrical, hyaline, smooth-walled, arising from stratum. *Conidia* 6–8.5 × 2.5–3.5 µm ($\bar{x}$ = 7.3 × 3.2, n = 30), unicellular, oblong, hyaline, smooth-walled, guttulate. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm in one month at 25°C. Colony dense, circular, with umbonate edge, raised in the middle, floccose, white granular and circular crack on the surface, from below atrovirens, darkening towards center and white at edge.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH 1-10 (MHZU 24-0560), living culture ZHKUCC 24-1023, other living culture ZHKUCC 24-1024.

GenBank numbers: ZHKUCC 24-1023: ITS = PQ608296, LSU = PQ608129, SSU = PQ607983, *TEF*1-α = PQ628143, *RPB*2 = PV221300; ZHKUCC 24-1024: ITS = PQ608297, LSU = PQ608130, SSU = PQ607984, *TEF*1-α = PQ628144, *RPB*2 = PV221301.

Known hosts: On decaying woody litter (Ren et al., 2020), *Coffea arabica* (This study).

Known distribution: Thailand (Ren et al., 2020), China (This study).

Notes: Loculosulcatispora thailandica was introduced by Ren et al. (2020) from decaying woody litter in Thailand. Based on phylogenetic analyses of a concatenated ITS, LSU, SSU, *TEF*1-α, and *RPB*2 sequence data, our new collection clustered with *L. thailandica* (MFLUCC 20-0108, ex-type) with 100% ML and 1.00 BYPP statistical support (Figure 2.95). Morphologically, our species also shares similar characteristics to *L. thailandica* by having multi loculate conidiomata, conical or subglobose, aseptate and unbranched paraphyses, doliiform to cylindrical conidiogenous cells with oblong, hyaline and 1-celled conidia (Ren et al., 2020; Figure 2.96). Thus, we identified our new collection as *L. thailandica*, which was collected from *Coffea* sp. for the first time.

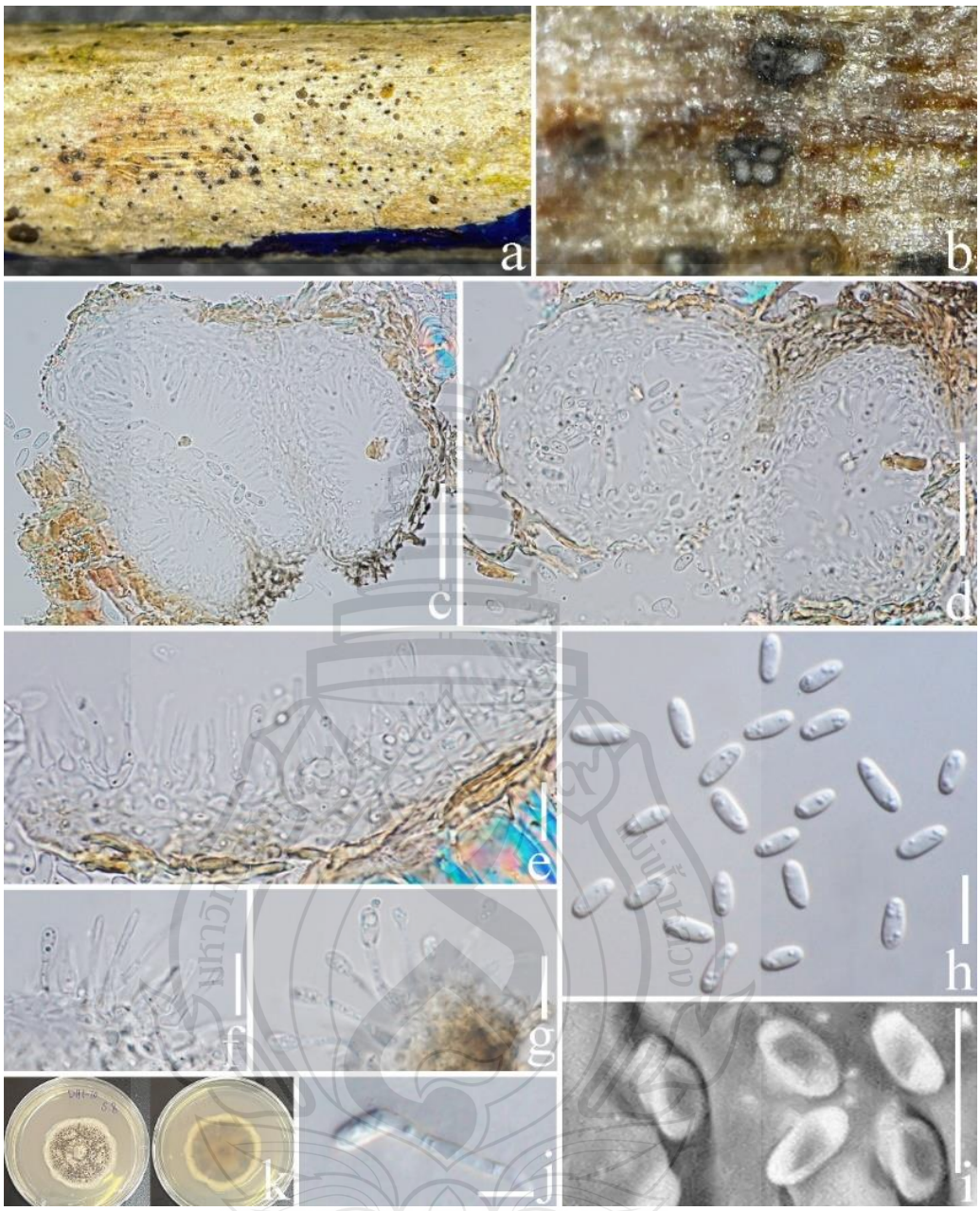


Figure 2.128 *Loculosulcatispora thailandica* (MHZU 24-0560, new host and country record)

Figure 2.128 a, b Appearance of conidiomata on *Coffea* sp. c, d Vertical sections of conidiomata and conidiomata wall. e–g Paraphyses and conidiogenous cells with conidia. h, i Conidia (i: SEM microphotographs of conidia). j Germinated conidium. k Culture on PDA from above and below. Scale bars: c, d = 30 µm, e–j = 10 µm.

Thyridariaceae Q. Tian & K.D. Hyde, Fungal Diversity 63 (1): 254 (2013)

Cycasicola Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 89: 161 (2018)

Notes: Cycasicola, typified by *C. goaensis* Wanas., E.B.G. Jones & K.D. Hyde, was introduced by Wanasinghe et al. (2018), based on multi-gene phylogenetic analyses. This genus consists of only two species: *C. goaensis* and *C. leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde; both have been reported as saprobic with an anamorph from *Cycas* sp. in India and *Leucaena* sp. in Thailand, respectively (Wanasinghe et al., 2018; Jayasiri et al., 2019). In this study, we provide an updated tree for the family and introduce a new species, *C. coffeae*, from an Arabica coffee plant. This is the first report of *Cycasicola* from a coffee host.

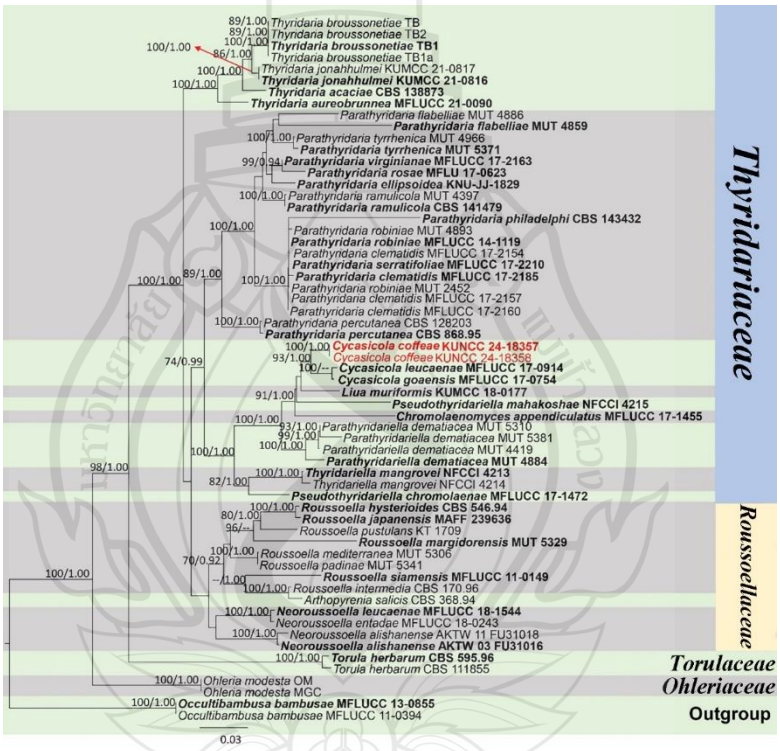


Figure 2.129 Phylogenetic tree of *Cycasicola*

Figure 2.129 Phylogram generated from the best scoring RAxML tree, based on a combined ITS LSU, SSU and *TEF*1-α sequence dataset. *Occultibambusa bambusae* D.Q. Dai & K.D. Hyde, (MFLUCC 13-0855 and MFLUCC 11-0394) are selected as the outgroup taxa. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given above the nodes. All type strains are in bold and newly-generated sequences are in red.

Cycasicola coffeae L. Lu & Tibpromma, sp. nov. Figure 2.20.

Index Fungorum number: IF 901007; *Facesofungi number:* FoF 14733.

Etymology: The species epithet "*coffeae*" refers to the host plant genus "*Coffea*" from which the fungus was isolated.

Holotype: HKAS 137613.

Saprobic on decaying branch of *C. arabica*. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 100–180 µm high × 120–200 µm diam. ($\overline{x}$ = 132 × 160 µm, n = 20), pycnidial, solitary, gregarious or confluent, immersed, unilocular, globose to subglobose or irregular, brown, with central ostiolar. *Conidiomatal wall* 15–20 µm wide ($\overline{x}$ =17.5 µm, n = 30), composed of 2–3 brown cells in the outer layers and two hyaline cells in the inner layer, with *textura angularis* cells. *Conidiophores* inconspicuous or micronematous, often reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 3–5 µm ($\overline{x}$ = 5 × 4 µm, n = 30), phialidic, hyaline, cylindrical to ampulliform, smooth-walled. *Conidia* 4–7 × 2–3 µm ($\overline{x}$ = 5.5 × 2.7 µm, n = 30), hyaline to brownish-orange, ellipsoid to cylindrical or some ovoid, continuous, straight or slightly curved, obtuse at apex and base, aseptate, guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h, colonies reached 3.5 cm in diameter after one month at 25°C, circular, radially striated, with a filiform edge, flat, smooth, colonies from above brown at the centre, hyaline to grey at the middle, dark green at the edge, from below, dark green to black.

Materials examined: China, Yunnan Province, Dali, on a decaying branch of *Coffea arabica* (*Rubiaceae*) (26°09' N, 101°91' E, 1415 m alt.), 25 July 2022, LiLu, DL-C4 (HKAS 137613, holotype), isotype MHZU 23-0065, ex-type living culture KUNCC 24-18357 = KUNCC 24-18358, ex-isotype living culture ZHKUCC 23-0640 = ZHKUCC 23-0641.

GenBank numbers: KUNCC24-18357: ITS = OR428409, LSU = OR428431, SSU = OR428387, *TEF*1-α = OR509761; KUNCC24-18358: ITS = OR428410, LSU = OR428432, SSU = OR428388, *TEF*1-α = OR509762.

Notes: In the concatenated phylogenetic analysis, *Cycasicola coffeae* forms a distinct allied basal lineage with *C. goaensis* and *C. leucaenae* (Figure 2.21). Based on morphology, the conidia of our fungus are very similar to those of *C. goaensis* (type species). However, the conidia of *C. coffeae* (4–7 × 2–3 µm) are larger than *C. goaensis*

(3.5–5 × 2.2–2.6 µm) (Figure 2.20; Wanasinghe et al., 2018). Based on nucleotide comparisons, *C. coffeae* (ZHKUCC 23-0640) is different from *C. goaensis* (MFLUCC 17-0754) by 31/485 bp (6.5%, without gaps) of the ITS, 4/850 bp (0.5%, without gaps) of the LSU, 2/1036 bp (0.2%, without gaps) of the SSU and 25/925 bp (2.7%, without gaps) of the *TEF*1-α. Therefore, the morphological differences and phylogenetic analyses support the introduction of *C. coffeae* as a new species.

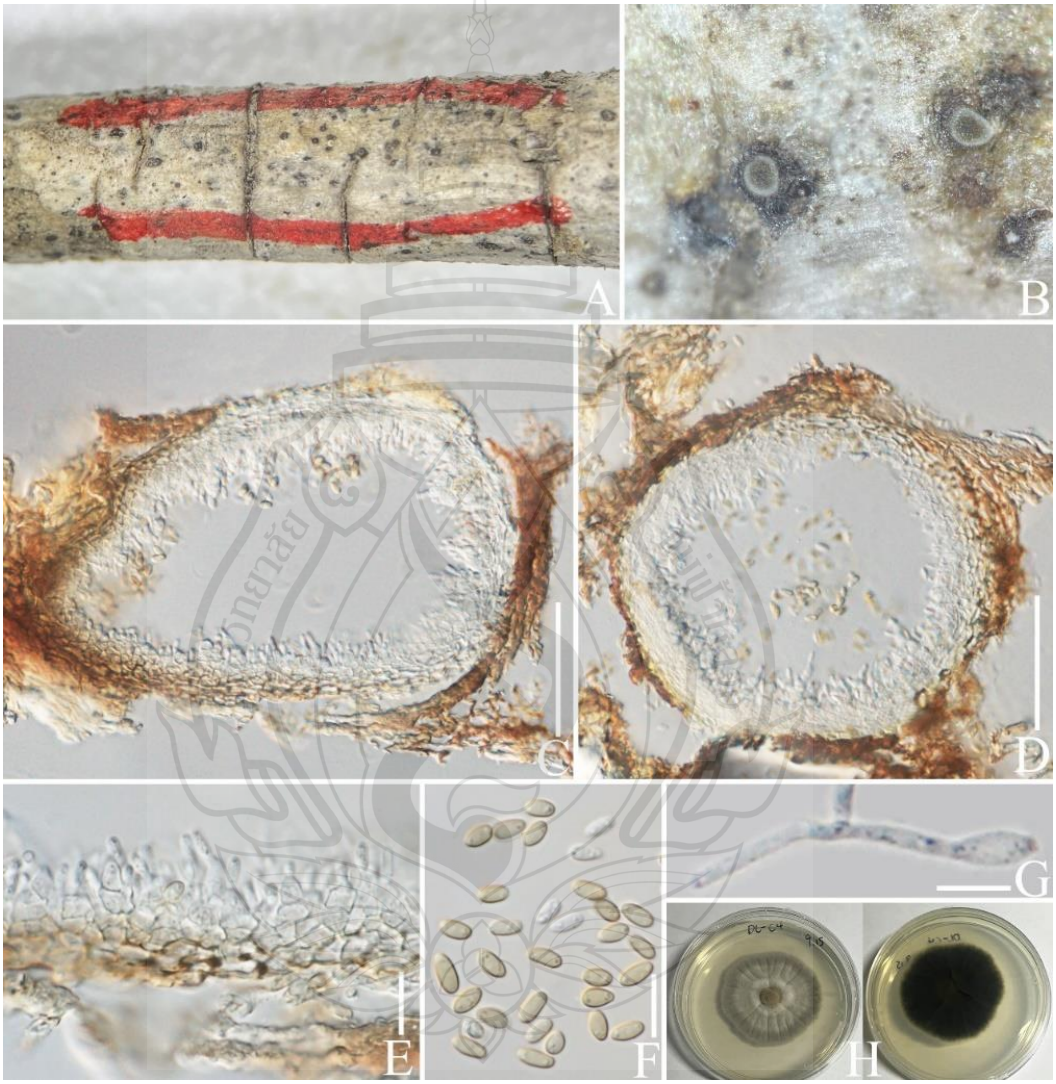


Figure 2.130 *Cycasicola coffeae* (HKAS 137613, holotype)

Figure 2.130 A, B Conidiomata on a decaying branch of *C. arabica*; C, D Longitudinal section of a conidioma; E Conidioma wall and conidiogenous cells; F Conidia; G Germinated conidium; H Culture on PDA from the obverse and reverse. Scale bars: C, D = 50 µm, E–G = 10 µm.

Liua Phookamsak & K.D. Hyde, Fungal Diversity 95: 71 (2019)

Notes: The monotypic genus *Liua* was introduced by Hyde et al. (2019) to accommodate *L. muriformis*, as it has distinct asexual morphological characteristics in Thyridariaceae. The type species is collected from *Lonicera maackii* from China as a saprobe (Hyde et al., 2019). The asexual morph of *Liua* is characterized by coelomycetous pycnidial, globose to subglobose, unilocular, conidiomata, with central ostioles with pore-like opening, pseudoparenchymatous conidiomata walls with cell arranged in a *textura angularis* to *textura prismatica*, conidiophores reduced to conidiogenous cells, ampulliform to cylindrical conidiogenous cells and phragmosporous to muriform, dark brown, oblong to ellipsoidal, or obovoid conidia (Hyde et al., 2019). This study introduces a new host record of *Liua muriformis* from coffee in China.

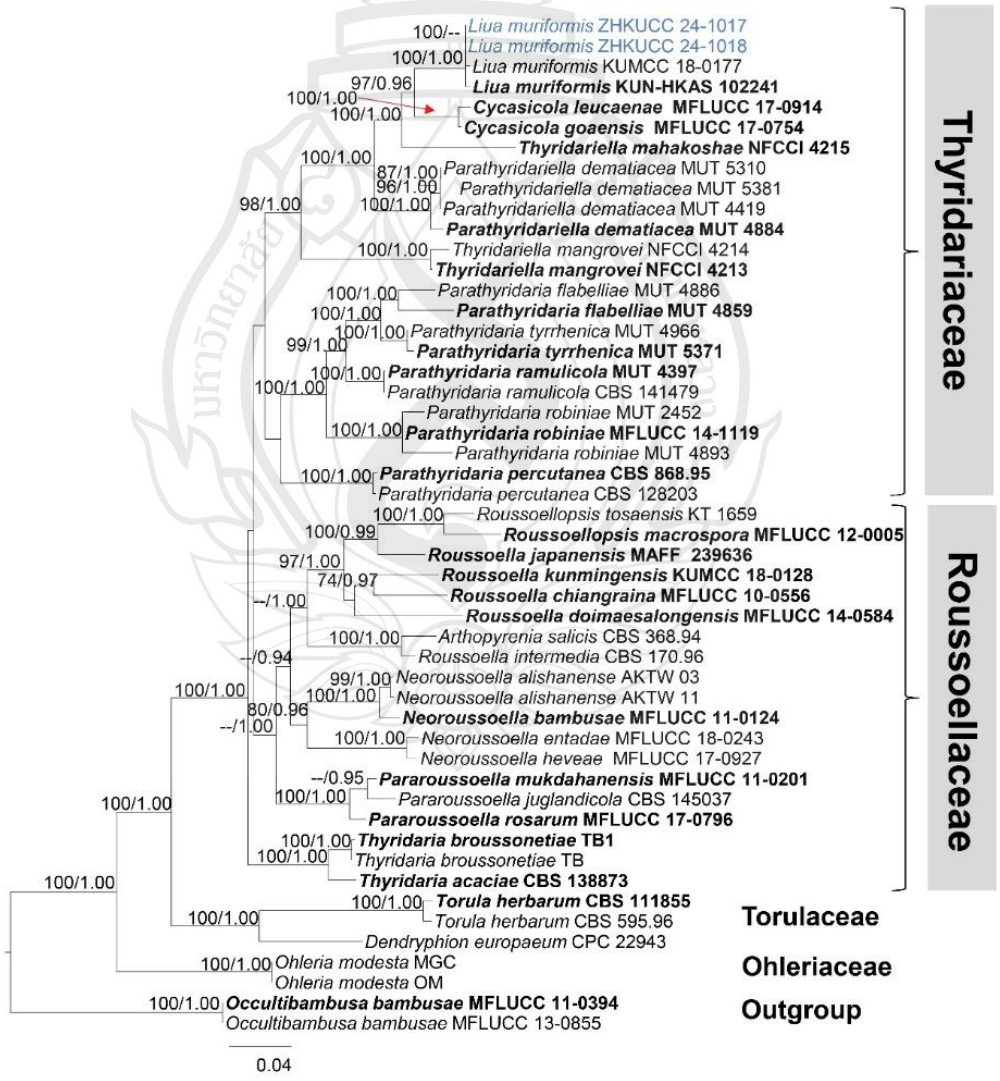


Figure 2.131 Phylogenetic tree of *Liua*

Figure 2.131 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Fifty strains are included in the combined sequence analysis, which comprises 4,296 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Occultibambusa bambusae* (MFLUCC 11-0394 and MFLUCC 13-0855).

Liua muriformis Phookamsak, H.B. Jiang & K.D. Hyde, Fungal Diversity 95: 74 (2019)

Index Fungorum number: IF 556176; *Facesoffungi number:* FoF 05710; Figure 2.98

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Coelomycetous. *Conidiomata* 100–150 × 100–180 µm ($\overline{x}$ = 123 × 143 µm, n = 15), pycnidial, solitary or scattered, immersed, slightly raised, visible as small black dot on host surface, uni-loculate, globose to subglobose, glabrous, dark brown to black, ostioles central, apapillate. *Conidiomatal wall* 10–15 µm wide ($\overline{x}$ = 13 µm, n = 20), thin-walled, of equal thickness, composed of 3–5 cell layers, of flattened, yellowish to brown, pseudoparenchymatous cells, arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 4–7 µm ($\overline{x}$ = 7.7 × 5 µm, n = 25), holoblastic, phialidic, discrete, determinate, ampulliform, unbranched, aseptate, hyaline, smooth, arising from the inner cavity of the conidioma wall. *Conidia* 10–15 × 7–9 µm ($\overline{x}$ = 13 × 8 µm, n = 25), phragmosporous to muriform, hyaline to dark brown, oblong to ellipsoidal, or obovoid, 1–3-transversely septate, with 0–3-longitudinal septa, slightly constricted at the septa, some constricted at middle cell, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm in one month at 25°C. Colony dense, circular, with edge entire, raised, surface rough, velvety; from above, pale yellowish to greyish green; from below, dark brown to black.

Material examined: China, Yunnan Province, Dali City, Zhukula coffee plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C49 (MHZU 24-0557), living culture ZHKUCC 24-1017, other living culture ZHKUCC 24-1018.

GenBank numbers: ZHKUCC 24-1017: ITS = PQ608294, LSU = PQ608127, SSU = PQ607981, *TEF*1-α = PQ628141, *RPB*2 = PV221298; ZHKUCC 24-1018: ITS = PQ608295, LSU = PQ608128, SSU = PQ607982, *TEF*1-α = PQ628142, *RPB*2 = PV221299.

Known hosts: On dead hanging branches of *Lonicera maackii* (Hyde et al., 2019), *Coffea arabica* (This study).

Known distribution: China (Hyde et al., 2019, This study).

Notes: Phylogenetic analyses of a concatenated ITS, LSU, SSU, *TEF*1-α, and *RPB*2 sequence dataset reveal that our isolates cluster with *Liua muriformis* (KUMCC 18-0177, ex-type) with statistical support of 100% ML and 1.00 BYPP (Figure 2.97). Morphologically, our species also share similar characters with *L. muriformis* in having pycnidial conidiomata, ampulliform conidiogenous cells, and phragmosporous to muriform, dark brown conidia (Hyde et al., 2019; Figure 2.98). We, therefore, identified our collection as *L. muriformis* which is a new host record from *Coffea arabica* in China.

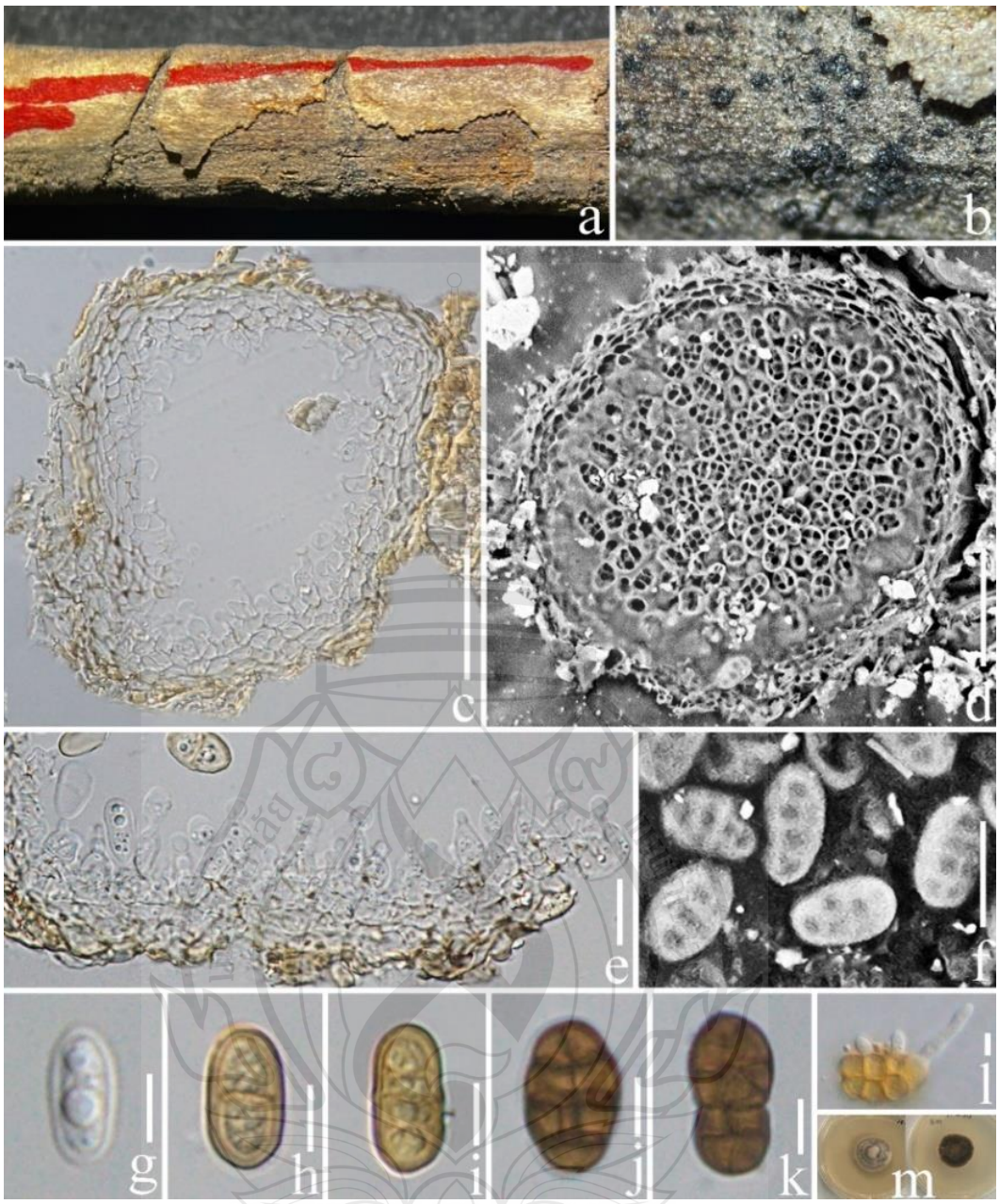


Figure 2.132 *Liua muriformis* (MHZU 24-0557, new host record)

Figure 2.132 a, b Appearance of conidiomata on *Coffea* sp. c, d Vertical section of conidiomata and conidiomata wall (d: SEM microphotographs of conidioma). e Conidiogenous cells with conidia. f–k Conidia (f: SEM microphotographs of conidia). l Germinated conidium. m Culture on PDA from above and below. Scale bars: c, d = 30 µm, e, f = 15 µm, g–l = 5 µm.

Torulaceae Corda, Deutschlands Flora, Abt. III. Die Pilze Deutschlands 2: 71 (1829)

Notes: Torula was proposed by Persoon (1794) to accommodate *T. herbarum* as the type. Later, Crous et al. (2015) accepted *Torula* in Torulaceae (Pleosporales) based on phylogenetic analysis. *Torula* is an asexual and hyphomycetous genus that commonly inhabits terrestrial and aquatic habitats in temperate to tropical regions and reported as saprobes (Su et al., 2018; de Silva et al., 2022; Tian et al., 2023). The genus is characterized by terminal or lateral, monoblastic or polyblastic conidiogenous cells and dark brown, cylindrical to subcylindrical, solitary to catenate, acrogenous, simple, phragmosporous, septate conidia (Crane & Miller, 2016; Li et al., 2017a; Hyde et al., 2020b; de Silva et al., 2022). *Torula* has an ancient origin and consists of 542 species epithets in Index Fungorum (2024), but only a few species have molecular data. *Torula* species can be distinguished by their conidial size, number of septa, and chains (Crous et al., 2015; Dong et al., 2023; Tian et al., 2023).

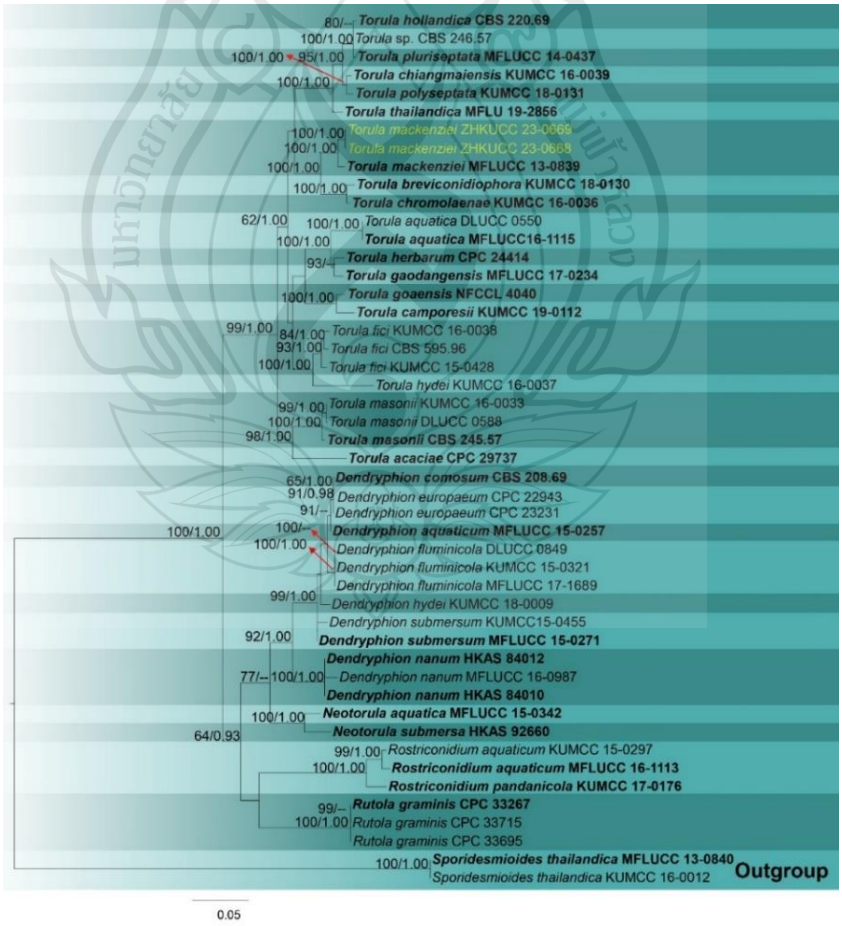


Figure 2.133 Phylogenetic tree of *Torula*

Figure 2.133 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Forty-eight strains are included in the combined sequence analysis, which comprises 4,603 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in green. The tree is rooted with *Sporidesmioides thailandica* (MFLUCC 13-0840 and KUMCC 16-0012).

Torula mackenziei J.F. Li, Phookamsak & K.D. Hyde, Mycological Progress 16 (4): 455 (2017)

Index Fungorum number: IF 819537; *Facesoffungi number*: FoF 02714; Figure 2.31

Saprobic on dead twig of *Coffea arabica*. Sexual morph: Undetermined. Asexual morph: *Colonies* on the host substrate, sporadic, black, powdery. *Mycelium* immersed through the substrate, composed of septate, branched, smooth, hyaline to light brown hyphae. *Conidiophores* 5–7 µm long × 3–5 µm wide ($\overline{x}$ = 6.4 × 4 µm, n = 10), macronematous, mononematous, solitary, erect, branched, light brown, thick-walled, without apical branches, ellipsoid to subglobose, arising from hypha, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 4–5.5 µm long × 3.5–6 µm wide ($\overline{x}$ = 4.8 × 4.8 µm, n = 10), polyblastic, terminal, dark brown to black, paler at apex, smooth to minutely verruculose, thick-walled, globose to ellipsoid. *Conidia* 10–19 µm long × 5–8 µm wide ($\overline{x}$ = 15 × 6.5 µm, n = 20) acrogenous, catenated, phragmosporous, light brown to dark brown, smooth to minutely verruculose, 1–3-septate, slightly constricted at some septa, rounded at both ends, often paler at apex, composed of moniliform cells, mainly subcylindrical.

Culture characteristics: Conidia germinating on PDA within 12 hours. Colonies on PDA reaching 20 mm within 4 weeks at 25°C. Culture from above, cream, circular, margin entire, flat, slightly effuse in middle, cottony; reverse yellowish.

Material examined: China, Yunnan Province, Dali City, on a dead twig of *Coffea arabica* (*Rubiaceae*), 25 July 2022, Li Lu, DL-C3 (MHZU 23-0079), living cultures ZHKUCC 23-0668 = ZHKUCC 23-0669.

GenBank numbers: ZHKUCC 23-0668: ITS: OR826583, LSU: OR836015, SSU: OR836021, *rpb*2: OR832765, *tef*1-*α*: OR832757; ZHKUCC 23-0669: ITS: OR826584, LSU: OR836016, SSU: OR836022, *rpb*2: OR832766, *tef*1-α: OR832758.

Known distribution (based on molecular data): China (Yunnan, Sichuan) (this study, Tian et al., 2023), Thailand (Li et al., 2017a).

Known hosts (based on molecular data): *Coffea arabica* (*Rubiaceae*) (this study), dead branches of unknown hosts (Tian et al., 2023), dead branch of *Bidens pilosa* (Li et al., 2017a).

Note: Phylogenetic analyses of the combined ITS, LSU, SSU, *rpb*2 and *tef*1-α sequence dataset revealed that our strains (ZHKUCC 23-0668 and ZHKUCC 23-0669) grouped with *T. mackenziei* (MFLUCC 13-0839) with 100% ML and 1.00 BYPP bootstrap support (Figure 2.30). The nucleotide base comparison of ITS, LSU, SSU, *rpb*2 and *tef*1-α regions shows that our strain (ZHKUCC 23-0668) differs from the type strain of *T. mackenziei* (MFLUCC 13–0839) by 7/497 bp (1.4%), 0/880 bp (0%), 1/849 bp (0.1%), 24/895 bp (2.6%) and 2/904 bp (0.2%) respectively. *Torula mackenziei* was introduced by Li et al. (2017a) based on morphology and phylogeny. The fungus has been reported on dead branches of *Bidens pilosa* in Thailand and dead branches of unidentified hosts in China. Our collection (MHZU 23-0079) was found on the twigs of *Coffea arabica* in China. The morphology of our isolates is similar to *T. mackenziei* (holotype). However, our collection has longer conidiophores and wider conidia than in the original description (conidiophores: 5–7 µm × 3–5 µm *vs*. s 3–4.3 µm × 3.4–3.7 µm; conidia: 10–19 µm long × 5–8 µm *vs*. a 9.4–18.5 µm long × (3.8–)4.4–4.7 µm) (Li et al., 2017a). Thus, following Chethana et al. (2021a) and conclusions based on morphology and phylogeny we identify our new collection is *T. mackenziei* and it is a new host record from *Coffee*.



Figure 2.134 *Torula mackenziei* (MHZU 23-0079, new host record)

Figure 2.134 a, b Colonies on a dead branch of *Coffea arabica*. c, d Hyphae, conidiophores, and conidiogenous cells. e Conidia in catenated chain. f A germinated conidium. g Culture on PDA from above and reverse. h Budding on conidia. i–m Immature and mature stages of conidia. Scale bars: c = 30 µm, d–m = 10 µm.

Dendryphion Wallr., Flora Cryptogamica Germaniae 2: 300 (1833)

Notes: Dendryphion was introduced by Wallroth (1833) and typified by hyphomycetous species, *D. comosum*. Crous et al. (2014a) introduced *D. europaeum* based on morphological characteristics and molecular data, subsequently, Crous et al. (2015) accommodated the species in Torulaceae and further accepted *Dendryphion* in

Torulaceae. *Dendryphion* is the most species-rich genus in Torulaceae, with 85 epithets recorded in Index Fungorum (2025). Members of this genus are commonly known to be saprobic on dead stems of herbaceous plants and decaying wood (Su et al., 2016; Li et al., 2020). *Dendryphion* is characterized by hairy and effuse colonies, branched in the upper part, polytretic conidiogenous cells with pores encircled by dark scars, and chains of brown, septate (didymo- or cheiro) conidia (Crous et al., 2014b). This study introduces a new host record, *Dendryphion verrucosum*, from a coffee host in China.

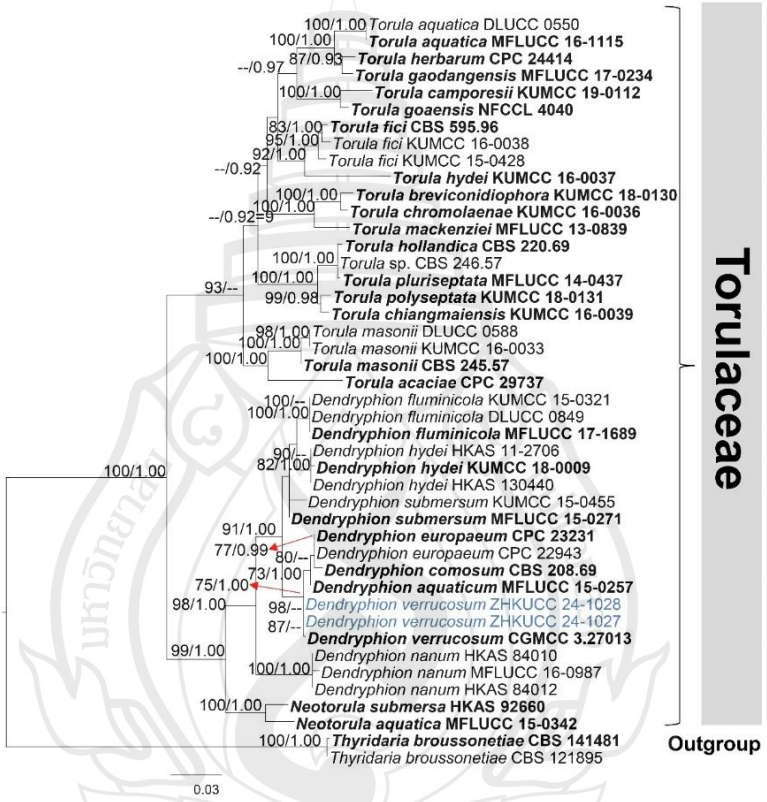


Figure 2.135 Phylogenetic tree of *Dendryphion*

Figure 2.135 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Fouty-four strains are included in the combined sequence analysis, which comprises 4,037 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Thyridaria broussonetiae* (CBS 141481 and CBS 121895).

Dendryphion verrucosum S. Luan, H.W. Shen & Z.L. Luo, Phytotaxa 676 (1): 69 (2024)

Index Fungorum number: IF902832; *Facesoffungi number:* FoF 17588; Figure 2.100

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on the substratum, superficial, effuse, gregarious, hairy, brown to black. *Mycelium* immersed, hyaline to pale brown hyphae. *Conidiophores* 80–150 × 5–7 µm ($\overline{x}$ = 118.8 × 6 µm, n = 15), macronematous, mononematous, septate, smooth, brown, thick-walled, branching from base or penicillate at the tip of primary branches, flexuous. *Conidiogenous cells* 8–15 × 4–6 µm ($\overline{x}$ = 11 × 5 µm, n = 20) holoblastic, terminal, integrated, cylindrical, hyaline to pale brown. *Conidia* (12–)17–35(–40) × 6–10 µm ($\overline{x}$ = 26 µm × 8.2 µm, n = 30), simple or branched chains, yellowish to pale brown, septate (didymo- or cheiro), verrucose, monilioid, subcylindrical, 1–5-septate, constricted at the septa. Conidial secession schizolytic.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, flossy, velvety, slightly raised, circular, with filiform margin, with aerial mycelium, white from above, yellowish from below, light brown in the middle.

Material examined: China, Yunnan Province, Dali City, Zhukula Coffee Plantation, on a decaying branch of *Coffea arabica*, 25 July 2022, Li Lu, DL-C40 (MHZU 24-0562), living culture ZHKUCC 24-1027, other living culture ZHKUCC 24-1028.

GenBank numbers: ZHKUCC 24-1027: ITS = PQ608286, LSU = PQ608119, SSU = PQ607977, *TEF*1-α = PQ628133, *RPB*2 = PV221294; ZHKUCC 24-1028: ITS = PQ608287, LSU = PQ608120, SSU = PQ607978, *TEF*1-α = PQ628134, *RPB*2 = PV221295.

Known hosts: On submerged decaying unidentified wood (Wang et al., 2024b), *Coffea arabica* (This study).

Known distribution: China (Wang et al., 2024b, This study).

Notes: Based on the phylogenetic analyses of combined multi-genes, our isolates form a sister lineage to *Dendryphion verrucosum* (CGMCC 3.27013, ex-type) with 98% ML and 1.00 BYPP statistical support (Figure 2.99). *Dendryphion verrucosum* was introduced and collected from freshwater habitat by Wang et al. (2024). In morphology, the new collection is similar to the genetic descriptions of *D. verrucosum* by erect, brown and septate conidiophores, and pale brown, monilioid conidia (Wang et al., 2024b, Figure 2.100). However, our collection is unique in having conidiophores branching from the base, while the holotype is simply branched in the upper part. Based on the base pair comparison of ITS, LSU, SSU, *RPB*2, and *TEF*1-α, they are almost the same. We, therefore, identified our collection as *D. verrucosum*, which is the first time it has been reported from the coffee host in China.

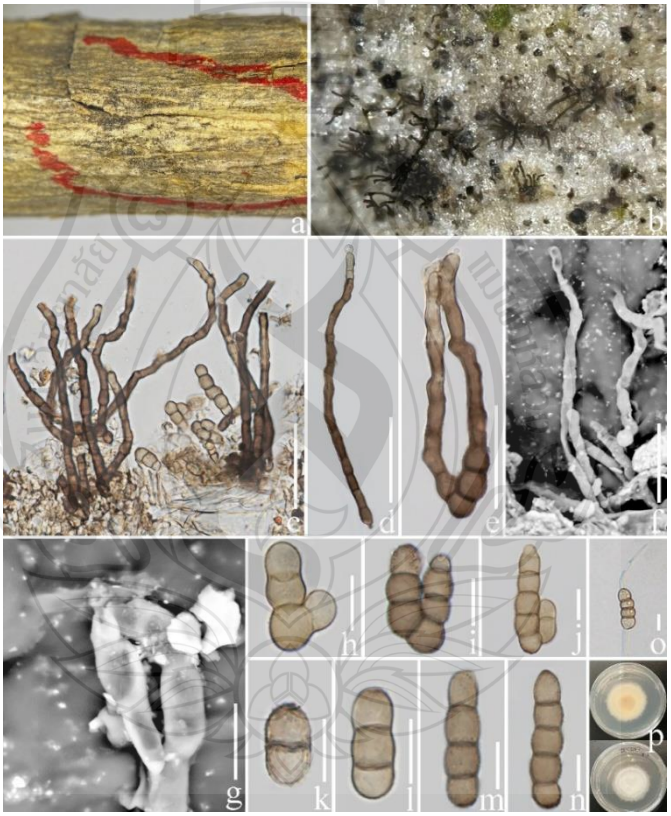


Figure 2.136 *Dendryphion verrucosum* (MHZU 24-0562, new host record)

Figure 2.136 a, b Colonies on a decaying branch of *Coffea* sp. c–f Conidiophores with conidiogenous cells (f: SEM microphotographs of conidiophores with conidia). g–n Conidia (g: SEM microphotographs of monilioid conidia). o Germinated conidium. p Culture on PDA from above and below. Scale bars: c, d = 50 µm, e, f = 30 µm, g–o= 10 µm.

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

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

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

Notes: Tubeufia was introduced by Penzig (1897) and typified by *T. javanica*. *Tubeufia* is a widespread genus distributed from temperate to tropical regions. *Tubeufia* comprises 86 species, including our three new species in this study (Ma et al., 2024). Morphologically, several species with dictyospores are added to *Tubeufia* (e.g. *T. chlamydospora* and *T. dictyospora*), which showed that the conidia of *Tubeufia* are not only helicoid (Lu et al., 2018; Ma et al., 2024), but also are muriform, dorsiventrally curved, coiled, ovate, or ellipsoid conidia bearing one or more small, globose secondary conidia (Ma et al., 2024). In this study, three new species of *Tubeufia* are introduced from a coffee host based on both morphological and phylogenetic analyses.

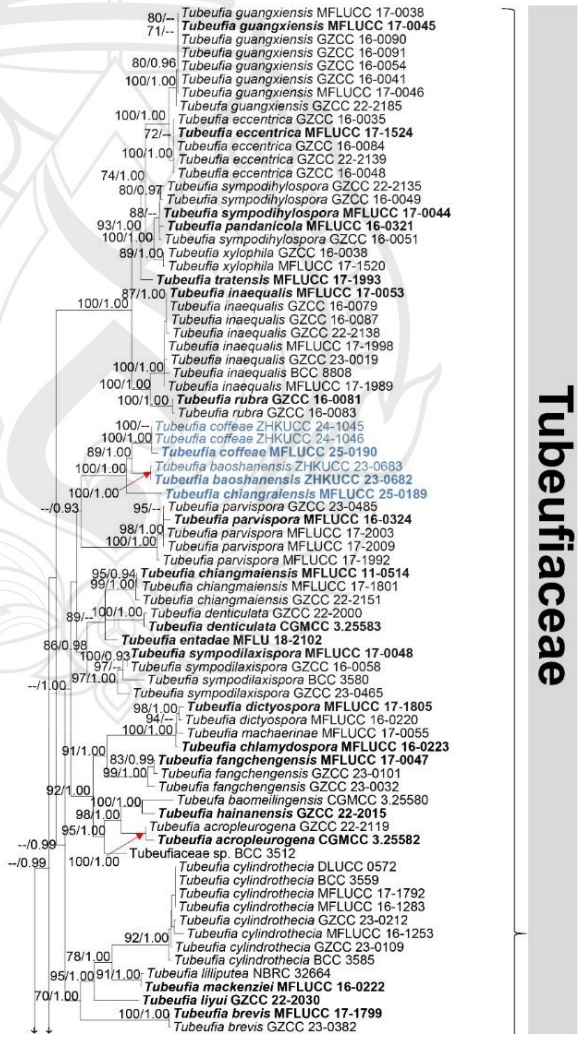


Figure 2.137 Phylogenetic tree of *Tubeufia*

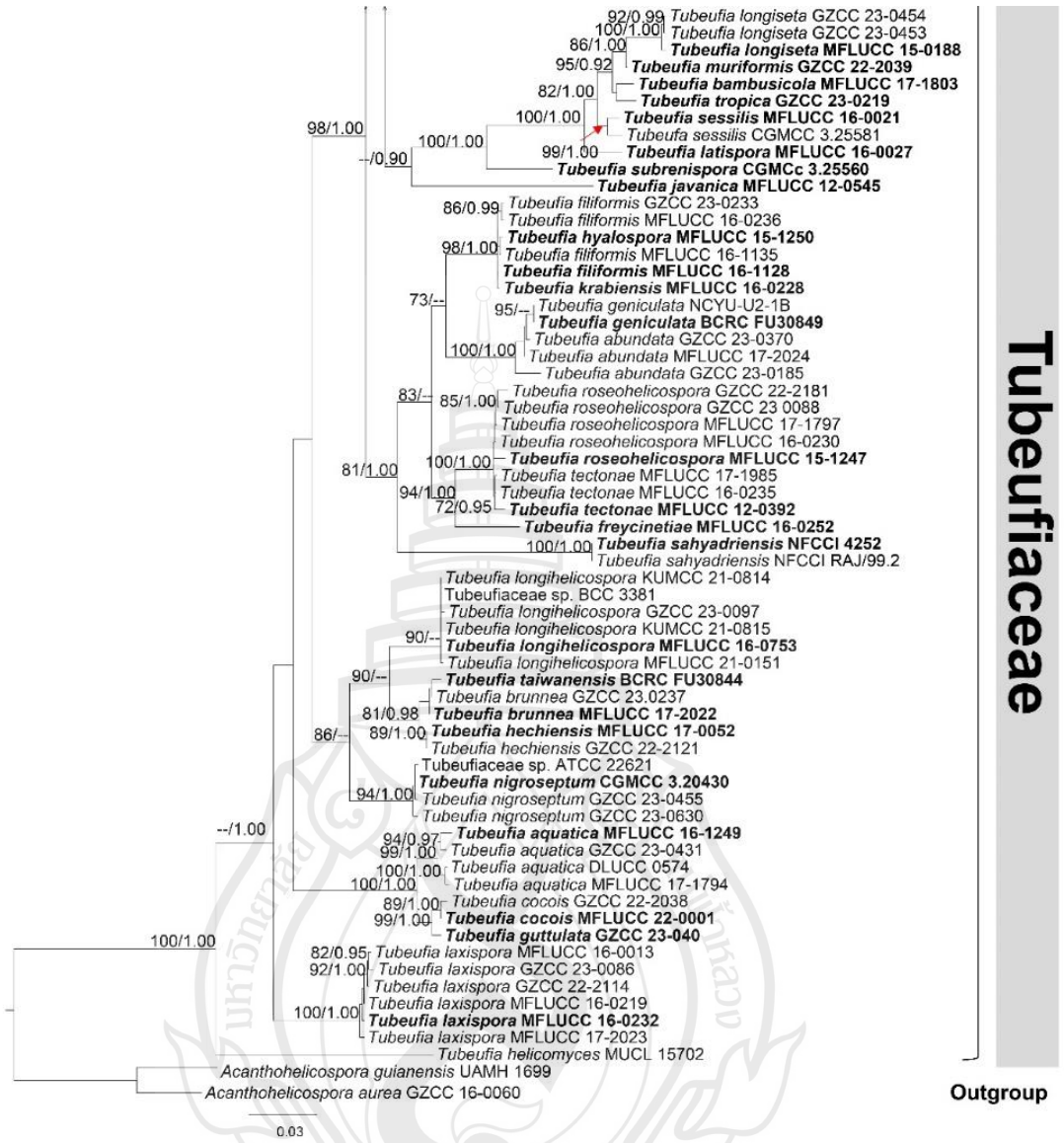


Figure 2.137 (continued)

Figure 2.137 Phylogram generated from maximum likelihood analysis based on a combined dataset of LSU, ITS, *RPB*2, and *TEF*1-α sequence data. One hundred forty-one strains are included in the combined sequence analysis, which comprises 3,391 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Acanthohelicospora aurea* (GZCC 16-0060) and *A*. *guianensis* (UAMH 1699).

Tubeufia baoshanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903652; *Facesoffungi number*: FoF 17589; Figure 2.102

Etymology: The species epithet refers to the type location "Baoshan", China.

Holotype: MHZU 23-0086

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 125–210 long, 155–250 µm diam. ($\bar{x}$ = 164 × 185 µm, n = 10), globose to subglobose, superficial, dark brown to black. *Peridium* 17.5–25 µm wide ($\bar{x}$ = 20, n = 15), thick-walled, composed of several pale brown outer layer cells of *textura angularis*, with hyaline to pale brown internal cells of *textura subprismatica. Hamathecium* of 1.6–3.2 µm wide ($\bar{x}$ = 2.2, n = 18), hypha-like, branched, septate, filamentous, pseudoparaphyses. *Asci* 75–100 × 10–17 µm ($\bar{x}$ = 84 × 13 µm, n = 15), 8-spored, bitunicate, cylindrical, rounded at the apex, with an ocular chamber, thick-walled. *Ascospores* 40–43 × 4–6 µm, ($\bar{x}$ = 36.5 × 5 µm, n = 20), fusiform, tapering towards rounded ends, up to 9-septate, hyaline, slightly curved, verrucose, guttulate. **Asexual morph**: Not observed.

Culture characteristics: Ascospore germinating on PDA within 24 h. Colonies growing on PDA, reaching 50 mm after one month at 25°C, colonies from above: circular, margin entire, flat, brown appearance; from below: grey to pale brown.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (25°14' N, 98.8 E, 737.3 m), 30 July 2022, Li Lu, BS4-C1 (MHZU 23-0086, holotype), ex-type ZHKUCC 23-0682, other living culture ZHKUCC 23-0683.

GenBank numbers: ZHKUCC 23-0682: ITS = PQ608348, LSU = PQ608180, *RPB2* = PV367523, *TEF*1-α= PQ628189; ZHKUCC 23-0683: ITS = PQ608349, LSU = PQ608181, *RPB2* = PV367524, *TEF*1-α= PQ628190.

Notes: The multi-gene phylogenetic result shows that *Tubeufia baoshanensis* (ZHKUCC 23-0682 and ZHKUCC 23-0683) is a distinct species and is sister to *T. coffeae* (MFLUCC 25-0190, ex-type) (Figure 101). Nucleotide comparisons between *T. baoshanensis* (ZHKUCC 23-0682, ex-type) and *T. coffeae* (MFLUCC 25-0190, ex-type) are shown in Table 4. *Tubeufia baoshanensis* can be distinguished from *T. coffeae* by having multi-septate ascospores, while it is similar to *T. bambusicola* by its

8-spored, bitunicate, cylindrical asci, and fusiform, septate, slightly curved ascospores. However, it can be differentiated by the size of asci and ascospores (Lu et al., 2018; Figure 2.102). The asci and ascospores of *T. baoshanensis* are smaller than *T. bambusicola* (75–100 × 10–17 µm, L/W = 4.4–10 vs. 110–145 × 13–18 µm, L/W = 6.1–11.1) and (40–43 × 4–6 µm, L/W = 6.6–10.7 vs. 50–73 × 5–7 µm, L/W = 7.1–14.6), respectively.

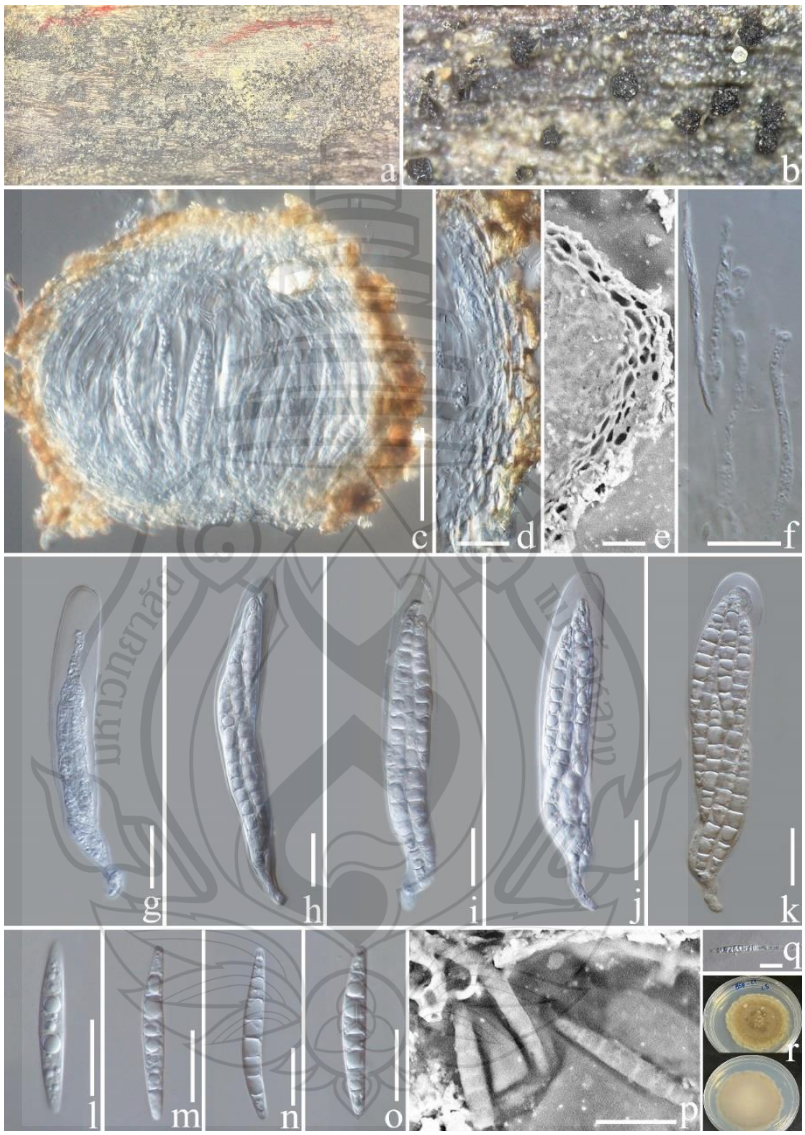


Figure 2.138 *Tubeufia baoshanensis* (MHZU 23-0086, holotype)

Figure 2.138 a, b Appearance of ascomata on substrate. c Vertical section of ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium. g–k Asci. l–p Ascospores (p: SEM microphotographs of ascospore). q Germinated ascospore. r Culture on PDA from above and below. Scale bars: c = 50 µm, d–q = 15 µm.

Tubeufia chiangraiensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903653; *Facesoffungi number*: FoF 04792; Figure 2.103

Etymology: The species epithet refers to the location "Chiang Rai", Thailand.

Holotype: MFLU 25-0102

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 120–190 long, 170–200 µm diam. ($\overline{x}$ = 174.5 × 190 µm, n = 10), ellipsoidal, subglobose, superficial, with a central ostiole, dark brown to black. *Ostioles* single, central. *Peridium* 13.5–23 µm wide ($\overline{x}$ = 18, n = 18), thick-walled, composed of several brown outer layer cells of *textura angularis*, with hyaline to pale brown internal cells of *textura subprismatica*. *Hamathecium* of 1.5–2.5 µm wide ($\overline{x}$ = 2, n = 15), hypha-like, branched, septate, filamentous, pseudoparaphyses. *Asci* 65–95 × 11–15 µm ($\overline{x}$ = 86 × 12.5 µm, n = 15), 8-spored, bitunicate, cylindrical, rounded at the apex, with an ocular chamber, thick-walled, sessile. *Ascospores* 31–40.5 × 5–7 µm, ($\overline{x}$ = 35.5 × 6 µm, n = 20), fusiform, elongate, tapering towards rounded ends, up to 7-septate, slightly curved, verrucose, guttulate, hyaline. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm after one month at 25°C, colonies from above: circular, margin entire, umbonate, grey to dark brown appearance; from below: grey to pale brown.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea* sp., 1 November 2023, Li Lu, LC3-2-10 (MFLU 25-0102, holotype), ex-type MFLUCC 25-0189.

GenBank numbers: MFLUCC 25-0189: ITS = PQ608350, LSU = PQ608182, *RPB2* = PV367525, *TEF*1-α= PQ628191.

Notes: Tubeufia chiangraiensis is introduced here as a novel species based on its distinct morphological characteristics and phylogenetic placement. The phylogenetic analysis recognizes *T. chiangraiensis* belonging to *Tubeufia*, where it is sister to *T. coffeae* and *T. baoshanensis* with 100% ML/1.00 BYPP support (Figure 2.101). Nucleotide comparisons between *T. chiangraiensis* (MFLUCC 25-0189, ex-type), *T. baoshanensis* (ZHKUCC 23-0682, ex-type), and *T. coffeae* (MFLUCC 25-0190, ex-type) are shown in Table 4. *Tubeufia chiangraiensis* (MFLU 25-0102,

holotype) differs from *T. coffeae* (MFLU 25-0103, holotype) and *T. baoshanensis* (MHZU 23-0086, holotype) in the sizes of ascospores. The ascospores of *Tubeufia chiangraiensis* (31–40.5 × 5–7 µm, L/W = 4.4–10.1) are smaller than *T. coffeae* (42–59 × 6–7.5 µm, L/W = 5.6–9.8) and *T. baoshanensis* (40–43 × 4–6 µm, L/W = 6.6–10.7) (Figure 2.102, 2.103, 2.104). Therefore, we introduce it as a novel species.

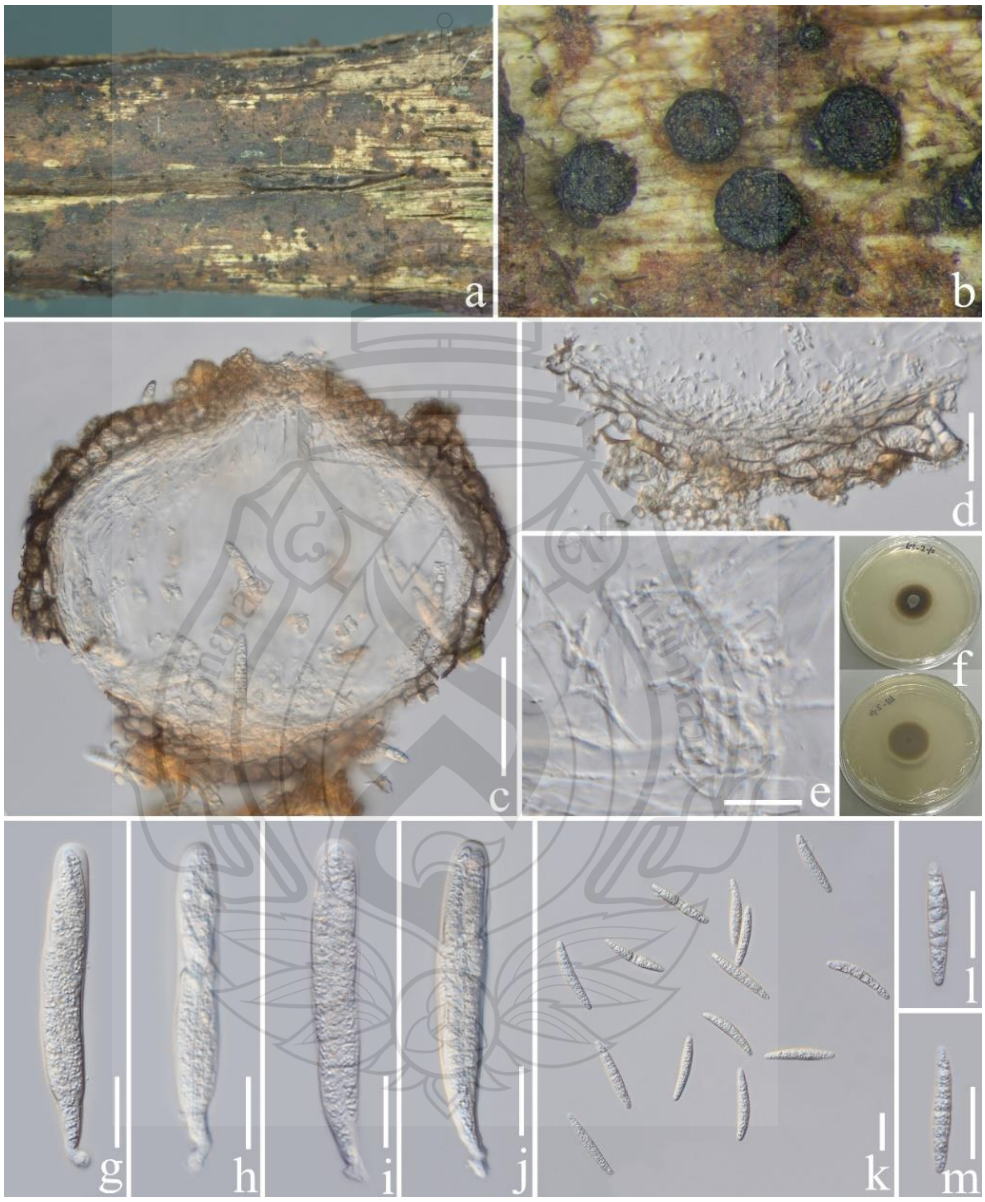


Figure 2.139 *Tubeufia chiangraiensis* (MFLU 25-0102, holotype)

Figure 2.139 a, b Appearance of ascomata on substrate. c Vertical section of ascoma. d Peridium. e Hamathecium. g–j Asci. k–m Ascospores. f Culture on PDA from above and below. Scale bars: c = 50 µm, d, e, g–m = 20 µm.

Tubeufia coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903654; *Facesoffungi number*: FoF 17590; Figure 2.104, Figure 2.105

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MFLU 25-0103

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph (Figure 2.104)**: *Ascomata* 138–197 long, 144–219 µm diam. ($\overline{x}$ = 164 × 181 µm, n = 10), globose to subglobose, superficial, with a central ostiole, brown to dark brown. *Ostioles* single, central. *Peridium* 15–42 µm wide ($\overline{x}$ = 23.5, n = 18), thick-walled, composed of several brown outer layer cells of *textura angularis*, with hyaline to pale brown internal cells of *textura angularis*. *Hamathecium* of 2–3.5 µm wide ($\overline{x}$ = 2.9, n = 11), hypha-like, branched, septate, filamentous, pseudoparaphyses. *Asci* 79–106 × 14–20 µm ($\overline{x}$ = 87 × 17 µm, n = 15), 8-spored, bitunicate, cylindrical, rounded at the apex, with an ocular chamber, thick-walled, sessile. *Ascospores* 42–59 × 6–7.5 µm, ($\overline{x}$ = 51 × 6.5 µm, n = 30), broadly fusiform, cylindrical, tapering towards rounded ends, aseptate, verrucose, guttulate, hyaline. **Asexual morph (Figure 2.105)**: *Colonies* on natural substratum effuse, translucent or pale yellowish, chalky white when dry. *Mycelium* partly immersed in woody substratum and partly superficial, hyaline, smooth, thin-walled hyphae. *Conidiophores* yellowish to light brown, arising singly as lateral branches from procumbent hyphae, up to 40 µm long, 3–5 mm wide, simple or branched, thin and smooth-walled, straight or flexuous. *Conidiogenous cells* 8–12 × 3–5 µm ($\overline{x}$ = 9.8 × 4.2 µm, n = 20), monoblastic or polyblastic, sympodial with cylindrical denticles, hyaline, septate. *Conidia* 30–50 × 4–7 mm ($\overline{x}$ = 38 × 5.4 µm, n = 30), solitary, borne acrogenously on denticles, hyaline or pale yellowish, predominantly fusoid to sickle-shaped, sometimes sigmoid, rarely straight, thin-walled, smooth, up to 9-septate when mature, not constricted at the septa, densely guttulate, some conically rounded at both ends, basal cell obconical, pedicellate.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm after one month at 25°C, colonies from above: circular, margin undulate, flat, brown to dark brown appearance; from below: pale brown to dark brown (Figure 2.104). Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm after one month at 25°C, colonies from

above: circular, entire margin, flat, light brown appearance; from below: yellowish to light brown (Figure 2.105).

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 20 September 2023, Li Lu, LC2-4 (MFLU 25-0103, holotype), ex-type MFLUCC 25-0190; China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH5-2 (MHZU 24-0573, paratype), ex-paratype ZHKUCC 24-1045, other living culture ZHKUCC 24-1046

GenBank numbers: MFLUCC 25-0190: ITS = PQ608353, LSU = PQ608185, *RPB*2 = PV367528, *TEF*1-α = PQ628194; ZHKUCC 24-1045: ITS = PQ608351, LSU = PQ608183, *RPB*2 = PV367526, *TEF*1-α= PQ628192; ZHKUCC 24-1046: ITS = PQ608352, LSU = PQ608184, *RPB*2 = PV367527, *TEF*1-α= PQ628193.

Notes: Our new species, *Tubeufia coffeae* is phylogenetically closely related to *T. baoshanensis* (ZHKUCC 23-0682, ex-type and ZHKUCC 23-0683) with 100% ML, 1.00 BYPP support (Figure 2.101). A comparison of ITS, LSU, *TEF*1-α, and *RPB*2 sequence data between *T. coffeae* (MFLUCC 25-0190, ex-type) and *T. baoshanensis* (ZHKUCC 23-0682, ex-type) is shown in Table 4. Morphologically, *T. coffeae* (MFLU 25-0103, holotype) can be distinguished from *T. baoshanensis* (MHZU 23-0086, holotype) by its longer ascospores (42–59 × 6–7.5 µm, L/W = 5.6–9.8 vs. 41.5–43 × 4–6 µm, L/W = 6.9–10.7) (Figure 104). Another collection (MHZU 24-0573) represented the asexual morph of *T. baoshanensis*, the fusoid conidia is similar to the asexual morph of *T. asiana* (Tsui et al., 2007; Figure 2.105). Therefore, based on the findings from both molecular and morphological evidence, we establish *T. coffeae* as a new species with sexual and asexual morphs. Interestingly, *T. coffeae* was recorded from both China and Thailand in coffee host (Figure 2.104, 2.105).

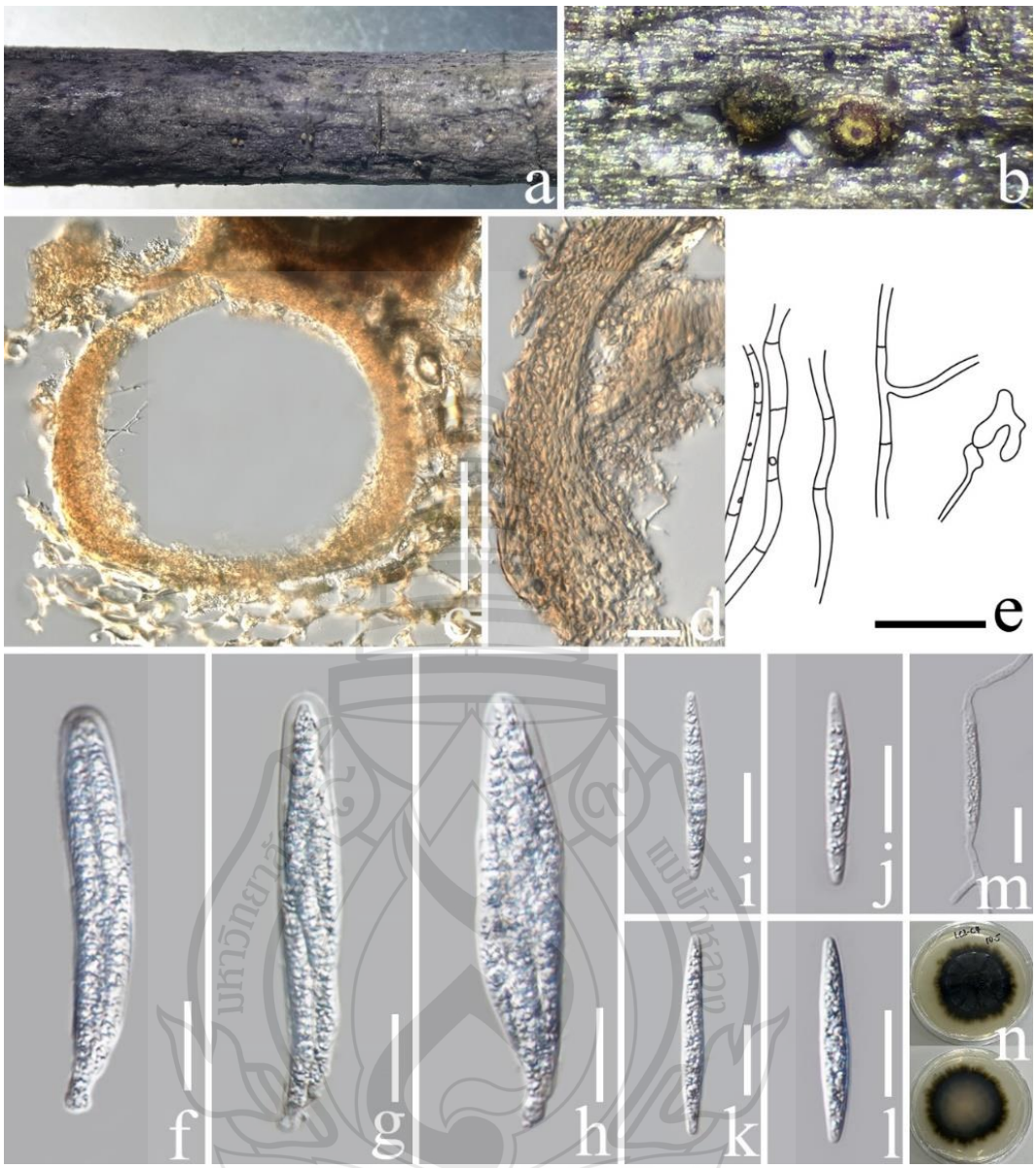


Figure 2.140 *Tubeufia coffeae* (MFLU 25-0103, holotype)

Figure 2.140 a, b Appearance of ascomata on substrate. c Vertical section of ascoma. d Peridium. e Hamathecium. f–h Asci. i–l Ascospores. m Germinated ascospore. n Culture on PDA from above and below. Scale bars: c = 50 µm, d–m = 20 µm.

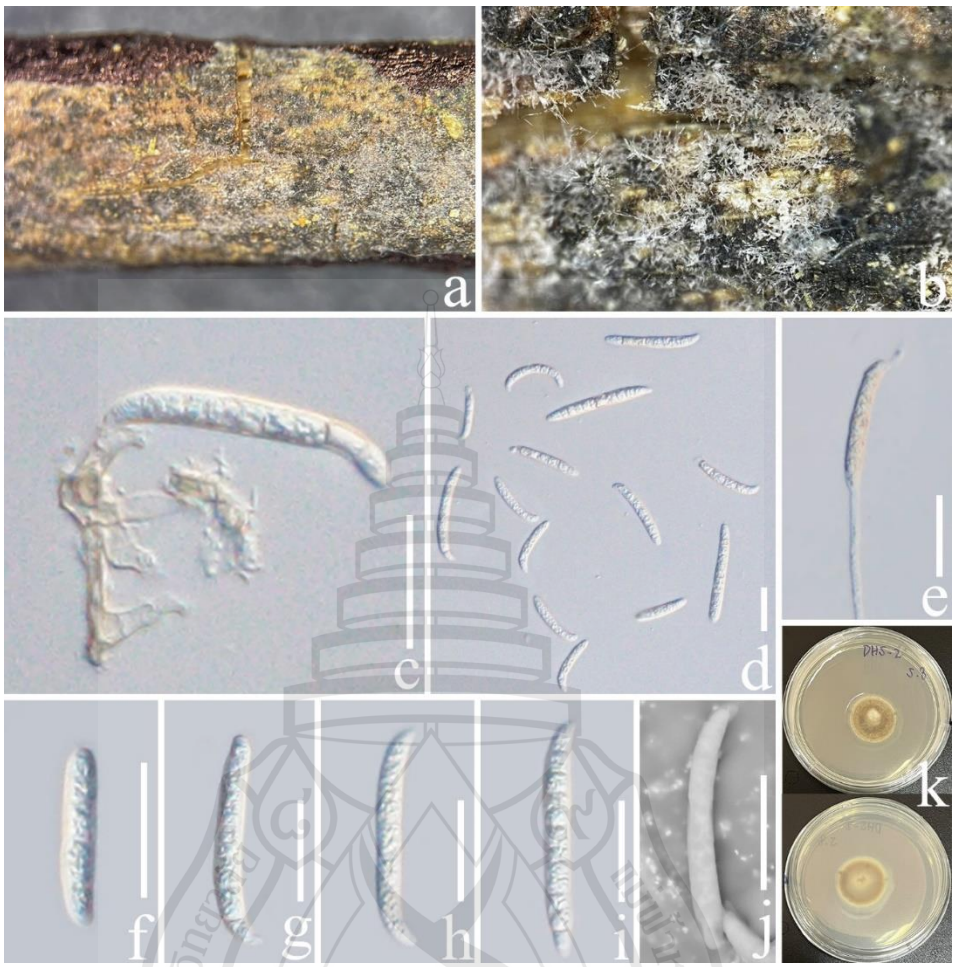


Figure 2.141 *Tubeufia coffeae* (ZHKU 24-0573, paratype)

Figure 2.141 a, b Colony on substrate. c Conidiophores and conidiogenous cell with conidia. d, f–j Conidia (j: SEM microphotographs of the conidium). e Germinated conidium. k Culture on PDA from above and below. Scale bars: c–j = 20 μm.

Table 2.4 Nucleotide differences in the ITS, LSU, *RPB*2, and *TEF*1-α (not trimmed sequence) of *Tubeufia* species. All sequences are shown without gaps

Species	ITS (%)	LSU (%)	*RPB*2 (%)	*TEF*1-α (%)
T. baoshanensis ZHKUCC 23-0682 vs. *T. chiangraiensis* MFLUCC 25-0189	15/539 (2.7%)	5/863 (0.5%)	35/1103 (3.1%)	30/956 (3%)
T. chiangraiensis MFLUCC 25-0189 vs. *T. coffeae* MFLUCC 25-0190	19/506 (3.1%)	11/921(1.2%)	36/1168 (3%)	29/958 (3%)
T. coffeae MFLUCC 25-0190 vs. *T. baoshanensis* ZHKUCC 23-0682	16/498 (3.2%)	2/863 (0.2%)	34/1167 (2.9%)	18/956 (1.9%)

2.3.2.2 Lecanoromycetes

Ostropales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis 8 (2): 68 (1932)

Stictidaceae Fr., Summa vegetabilium Scandinaviae 2: 345, 372 (1849)

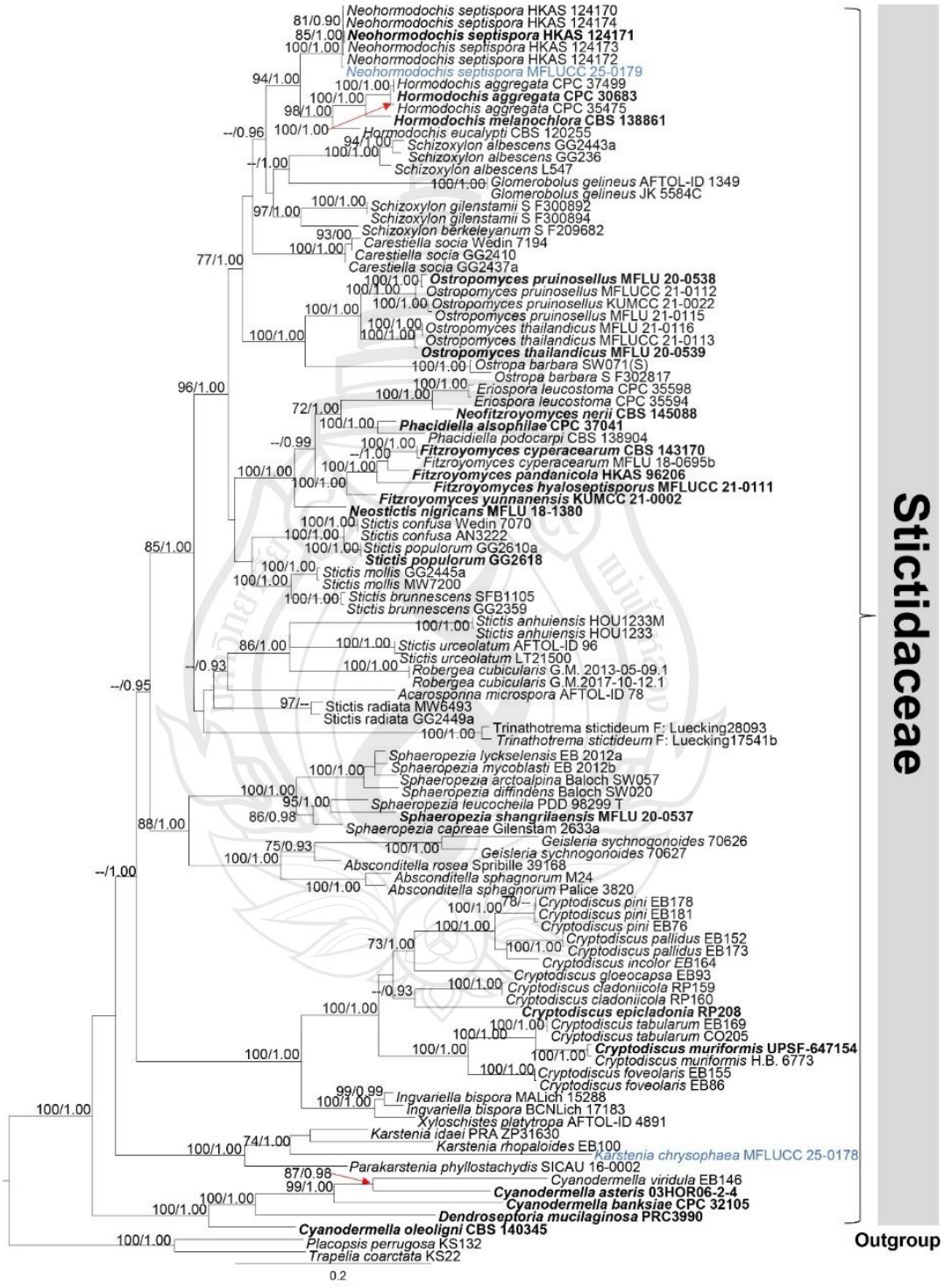


Figure 2.142 Phylogenetic tree of Stictidaceae

Figure 2.142 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, mtSSU and *RPB2* sequence data. One hundred and three strains are included in the combined sequence analysis, which comprises 2,991 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Placopsis perrugosa* (KS132) and *Trapelia coarctata* (KS22).

Karstenia Fr. ex P. Karst., Acta Soc. Fauna Fl. Fenn. 2 (6): 166 (1885)

Notes: The non-lichenized genus *Karstenia* was proposed by Karsten (1885) and typified by *K. sorbina*. It is a poorly known genus that has been confused in the past with the genus *Ramonia*. Cannon et al. (2024) transferred several *Ramonia* species to *Karstenia*. However, due to the limited availability of molecular data and the antiquity of many species, the synonymy of these two genera remains unconfirmed. A total of 17 epithets are listed in Index Fungorum (2025). Members of *Karstenia* species are all saprotrophs, primarily associated with wood and bark (Cannon et al., 2024). *Karstenia* is characterized by absent thallus, urceolate to lenticular apothecia and the disc pinkish or grey-white, exciple well-developed, clavate asci with 8-spored, hyaline ascospores, with transversely multiseptate or muriform (Sherwood, 1977, 1980; Cannon et al., 2024). In this study, we provide a new host and new country records, as well as new sequence data, this will facilitate the future identification of species within this genus.

Karstenia chrysophaea (Pers.) Coppins, Aptroot & P.F. Cannon, Revisions of British and Irish Lichens 38: 52 (2024)

Index Fungorum number: IF 900671; *Facesoffungi number*: FoF 17591; Figure 2.107

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Apothecia* 200–250 × 400–450 µm ($\bar{x}$ = 220 × 439 µm, n = 15), immersed, urceolate to lenticular, raising the substrate into small pustules, initially with a narrow pore but finally rupturing the exciple to form a margin of irregular teeth, not becoming erumpent, the disc grey-white. *Exciple* 30–50 µm wide ($\bar{x}$ = 43 µm, n = 30), well-developed, usually colourless, not containing copious crystals, composed of several layers of

textura angularis cells. *Hamathecium* of 1.5–2.5 µm wide ($\overline{x}$ = 2 µm, n = 30), hyaline, aseptate, filiform and numerous, paraphyses. *Asci* 70–110 × 8–18 µm ($\overline{x}$ = 94 × 14 µm, n = 30), 8-spored, bitunicate, cylindrical to clavate, short-stalked or absent, uniformly thin-walled, without an apical apparatus. *Ascospores* 40–80 × 3–4 µm ($\overline{x}$ = 60 × 3.7 µm, n = 30), fusiform, overlapping or crowded, hyaline, smooth-walled, both ends rounded, aseptate when young, transversely multiseptated when mature, (6–)11–16 transversely septate. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 5 cm diam. after one month at 25°C, circular, filiform margin, flat, radially furrowed at the center, flocculent and snow white in the middle, brownish on the edge. Orange to light brown at the from below, wrinkled.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 Nov. 2023, Li Lu, LC3-1-4 (MFLU 25-0091), living culture MFLUCC 25-0178.

GenBank numbers: MFLUCC 25-0178: ITS = PQ608244, mtSSU = PQ607919, *RPB2* = PV186819.

Known hosts: Quercus, *Fraxinus*, *Ulmus* and wood inside hollow *Ilex* (Cannon et al., 2024), *Coffea* sp. (This study).

Known distributions: The United Kingdom and Ireland (Cannon et al., 2024), Thailand (This study).

Notes: Multi-gene phylogenetic analyses showed that our isolates (MFLUCC 25-0178) formed a sister lineage to *Karstenia rhopaloides* with 74% ML and 1.00 BYPP statistical support (Figure 2.106). Morphologically, our collections is different from *K. rhopaloides* in having long ascospore (40–80 × 3–4 µm, L/W = 10–26.6 vs. 24–43 × 4.5–7 µm, L/W = 3.4–9.5; (6–)11–16 septate vs. 7–9-septate) (Cannon et al., 2024; Figure 2.107). In addition, we compared the morphology of our new collection with other *Karstenia* species lacking sequence data; we found that our strain is basically the same as the neotypes descriptions of *K. chrysophaea* (Vêzda, 1966; Cannon et al., 2024). *Karstenia chrysophaea* was previously introduced as *Ramonia chrysophaea* (Vêzda, 1966), then Cannon et al. (2024) formally synonymized the two species only based on the morphology descriptions. Therefore, we introduced our isolates as *K. chrysophaea* with the completed photoplates and molecular data. This is

the first time a *Karstenia* species is reported from a coffee host worldwide.

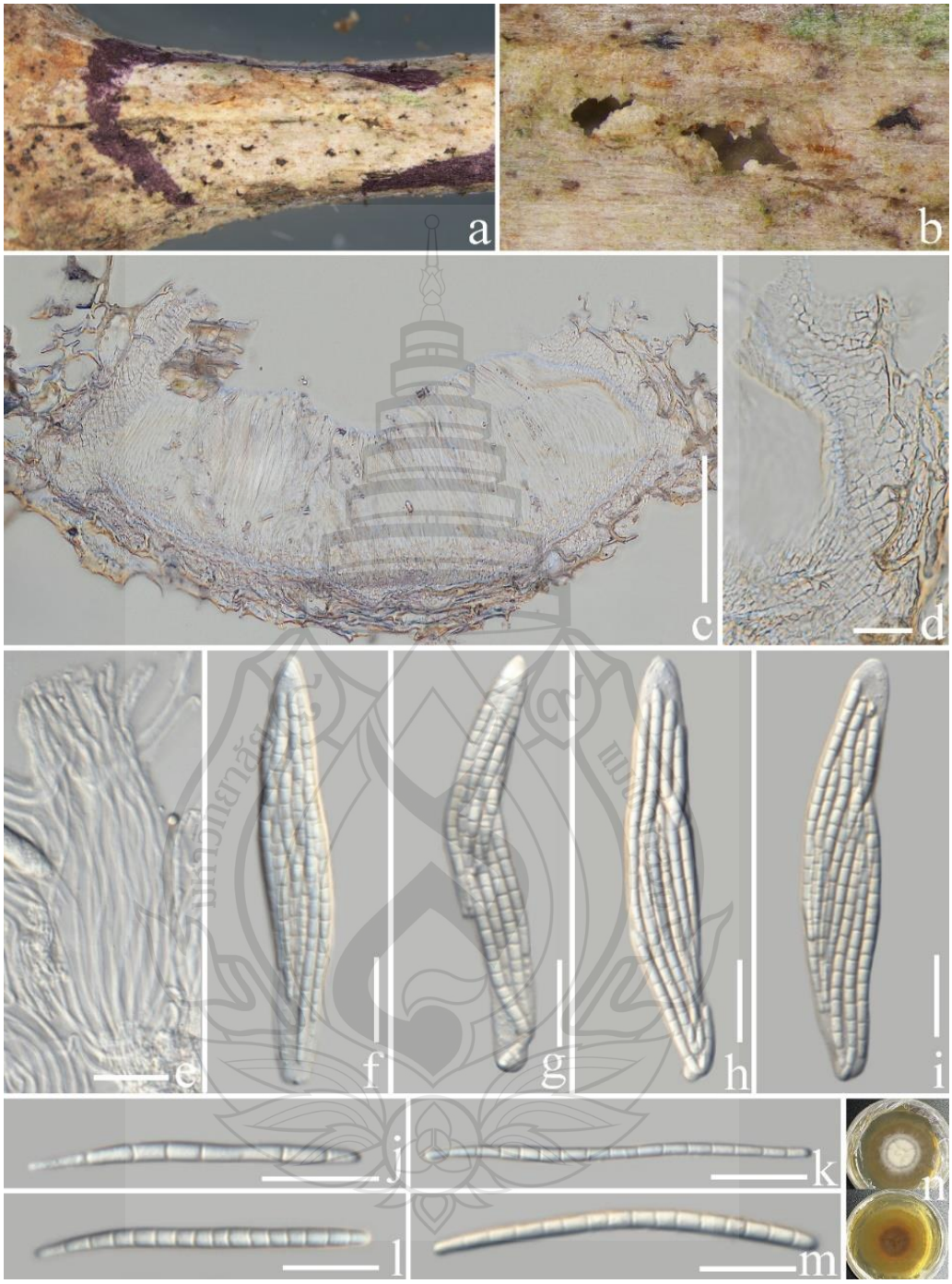


Figure 2.143 *Karstenia chrysophaea* (MFLU 25-0091, new host and country record)

Figure 2.143 a, b Apothecia on a decaying branch of *Coffea arabica*. c Section of an apothecium. d Exciple. e Hamathecium. f–i Asci. j–m Ascospores. n Culture on PDA from above and below. Scale bars: c = 100 μm, d–m = 20 μm.

Neohormodochis D.P. Wei & K.D. Hyde, Phytotaxa 573 (2): 252 (2022)

Notes: Based on the morphological characterization and phylogenetic analysis, *Neohormodochis* was introduced by Wei et al. (2022b) as a monotypic genus within Stictidaceae with the type species *N. septispora*, which was identified as saprobic from terrestrial habitats. *Neohormodochis* is nested with *Hormodochis* in phylogeny, while *Neohormodochis* species are distinguished from *Hormodochis* by producing white-pruinose conidiomata, crystalline conidiomatal wall and hyaline, holoblastic conidiogenous cells with upper cells becoming fertile and budding new conidia rather than arthroconidia (Wei et al., 2022). No further species have been introduced to this genus, which remains monotypic. In this study, we provide a new host and a new country record collected from a coffee host in Thailand.

Neohormodochis septispora D.P. Wei & K.D. Hyde, Phytotaxa 573 (2): 254 (2022)

Index Fungorum number: IF 559772; *Facesoffungi number*: FoF 12298; Figure 2.108

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Coelomycetous. *Conidiomata* 160–260 × 140–240 μm ($\overline{x}$ = 194 × 170, n = 15), solitary or aggregated, perithecial, immersed, conical to subglobose. *Ostioles* white-pruinose, circular, apical. *Conidiomatal wall* 15–20 μm wide ($\overline{x}$ = 18, n = 30), consisting of hyaline, intricate hyphae, being encompassed by a layer of irregularly-shaped crystals. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–8 × 0.8–2 μm ($\overline{x}$ = 6 × 1.5, n = 25), holoblastic, arising from stromatic cells, hyaline, cylindrical, thin-walled, the first conidium becoming conidiogenous by apical wall-building to form connected chain. *Conidia* 6–10 × 2–3 μm ($\overline{x}$ = 7.5 × 2.5, n = 40), hyaline, oblong to ellipsoidal, one-celled, arranged in branched chain, smooth-walled. **Sexual morph**: Not observed.

Culture characteristic: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 25 mm in one month at 25°C, dense, circular and entire margin, radially furrowed at the center, velvety, from above white to yellowish, from below yellowish.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-6 (MFLU 25-0092), living culture MFLUCC 25-0179.

GenBank numbers: MFLUCC 25-0179: ITS = PQ608245, LSU = PQ608078, mtSSU = PQ607920, *RPB*2 = PV186820.

Known hosts: on an unidentified dead twig (Wei et al., 2022), *Coffea arabica* (This study).

Known distribution: China (Wei et al., 2022), Thailand (This study).

Notes: Neohormodochis septispora was isolated as saprobes on an unidentified dead twig in China (Wei et al., 2022). In our phylogenetic analysis, our strains cluster with *N. septispora* with 100% ML and 1.00 BYPP statistical support (Figure 2.106). In a BLASTn search, the ITS, LSU, mtSSU, and *RPB*2 sequence (MFLUCC 25-0179) of our isolate showed 99.5% similarity to *N. septispora* (HKAS 124171, type). In addition, the asexual morphology of our new collection is the same as *N. septispora* by having immersed conidiomata with white-pruinose, crystalline substances present and cylindrical conidiogenous cells with ellipsoidal conidia (Wei et al., 2022). However, the conidia of our collection are slightly different from *N. septispora*, our new collection are usually unicellular, whereas *N. septispora* are two-celled, occasionally aseptate (Figure 2.108), we suspect that this difference may be due to the conidia in our new collection not being fully developed (Wei et al., 2022). We, therefore, identified our collection as *N. septispora,* which is a new host record and new country record from a coffee host in Thailand.

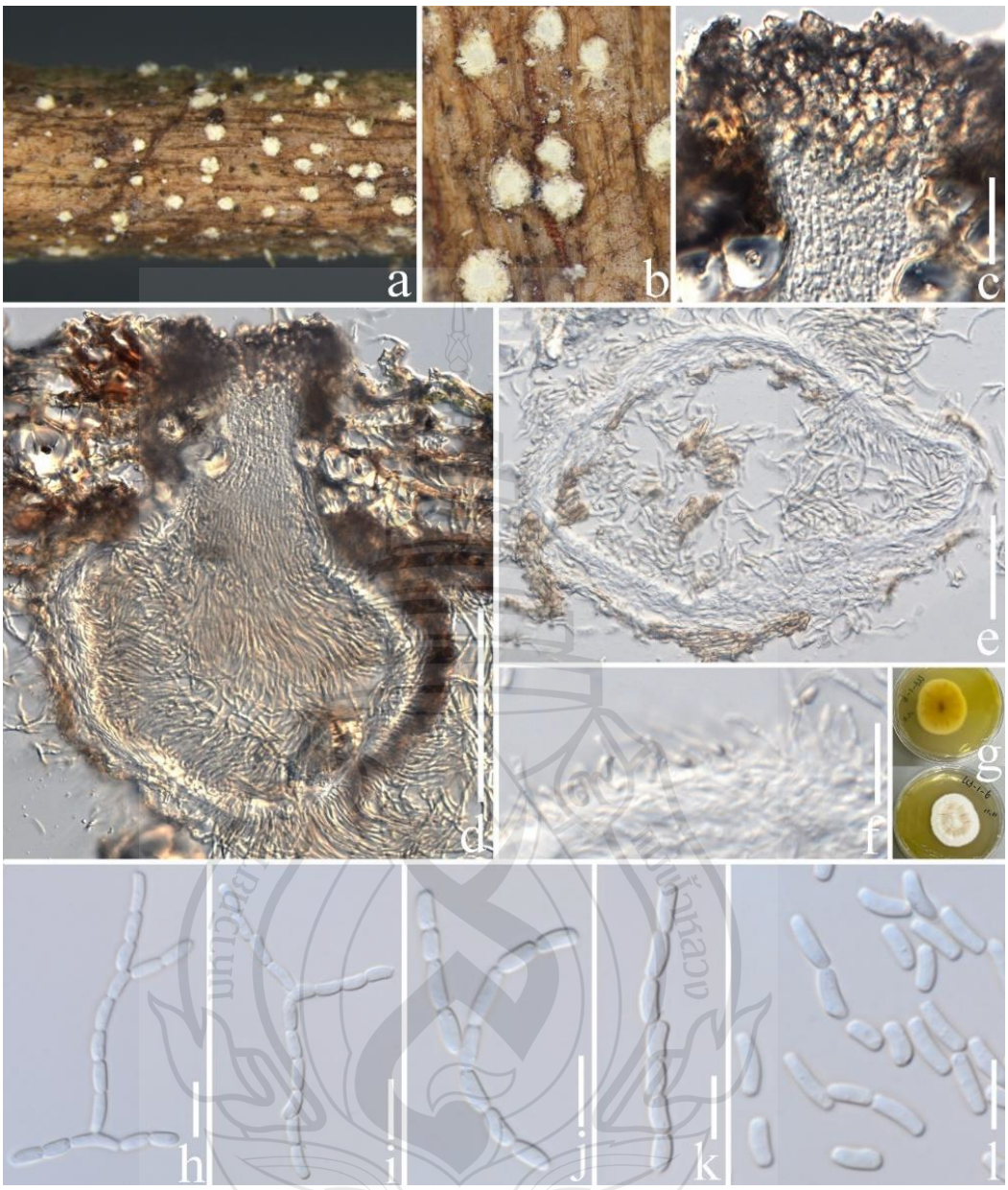


Figure 2.144 *Neohormodochis septispora* (MFLU 25-0092, new host and country record)

Figure 2.144 a, b Conidiomata on a decaying branch of *Coffea arabica*. c Crystals. d, e Vertical section through a conidioma. f Conidiogenous cells. g Culture on PDA from above and below. h–l Conidial chains and conidia. Scale bars: d, e = 100 μm, c, f = 20 μm, h–l = 10 μm.

Fitzroyomyces Crous et al., Persoonia 39: 389 (2017)

Notes: Fitzroyomyces was introduced by Crous et al. (2017) with *Fitzroyomyces cyperi* as the type species, which was recorded in its asexual state from leaves of Cyperaceae in Australia. The taxon has similar morphological characteristics to *Septoria* but clustered within Stictidaceae in phylogenetic analyses (Quaedvlieg et al., 2013, Verkley et al., 2013, Crous et al., 2017). *Fitzroyomyces* species are saprobic, and the asexual morph characteristics are conidiomata with central ostiole, exuding a creamy conidial mass that comprises hyaline, cylindrical, septate and flexuous conidia (Crous et al., 2017). The sexual morph of *F. cyperacearum* was recorded from dead stems of *Clematis subumbellata* and *Epilobium angustifolium* in Thailand and the U.K. (Ekanayaka et al., 2019; Phukhamsakda et al., 2020). The sexual morph is characterized by cupulate apothecia immersed in the substrate, whitish to cream disc, numerous, long filiform, and aseptate paraphyses, long and hyaline asci, with filiform, multiseptate and hyaline ascospores. Wei et al. (2021) introduced *F. hyaloseptisporus* and synonymized *Stictis pandanicola* under *Fitzroyomyces* based on morphological and phylogenetic analyses. *Fitzroyomyces* comprises three species, *F. cyperacearum*, *F. pandanicola* (=*Stictis pandanicola*) and *F. hyaloseptisporus* (Crous et al., 2017; Tibpromma et al., 2018; Wei et al., 2021).

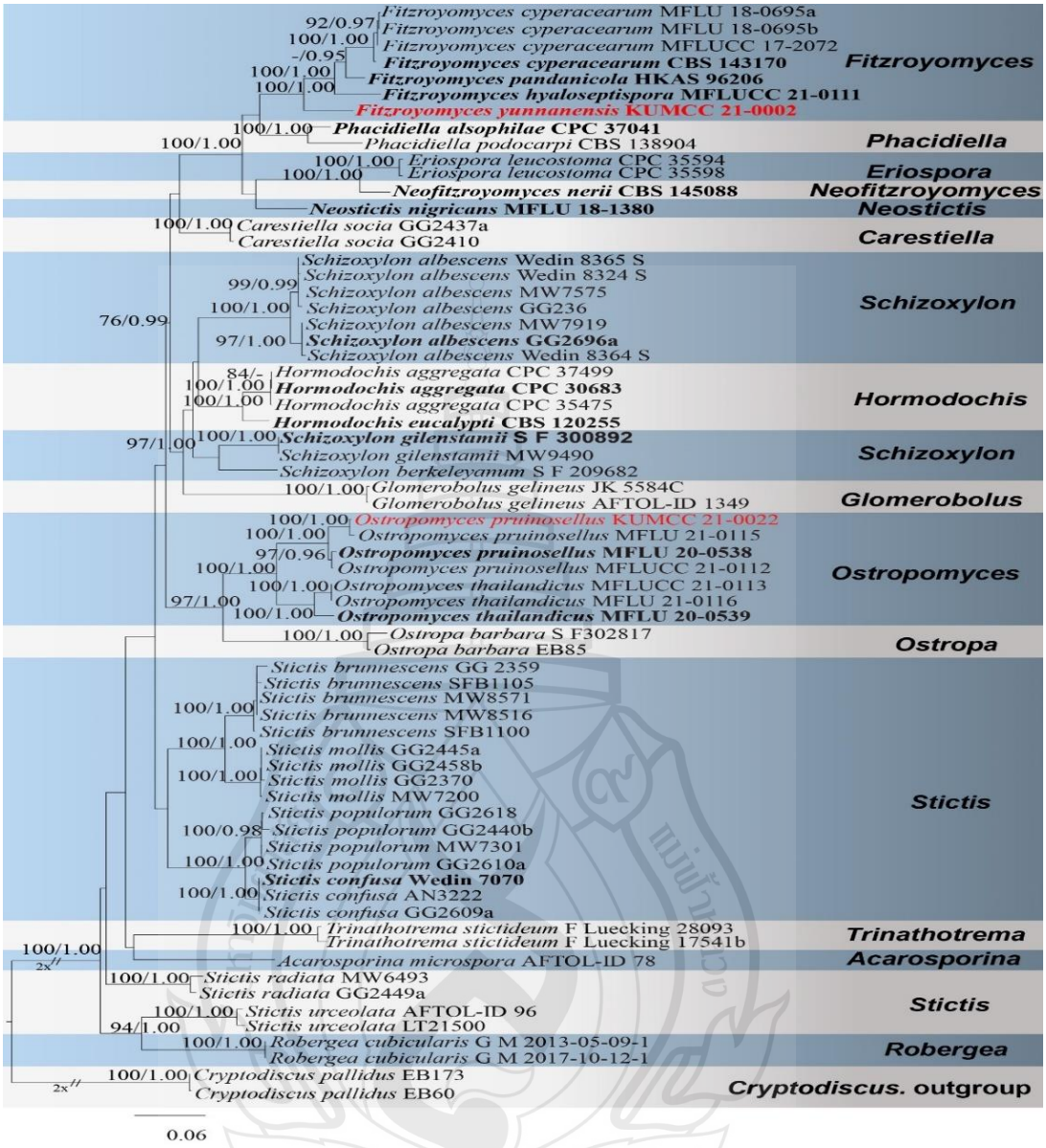


Figure 2.145 Phylogenetic tree of *Fitzroyomyces*

Figure 2.145 Phylogram generated from maximum likelihood analysis based on a combined dataset of mtSSU, LSU, and ITS sequence data. Sixty-seven strains are included in the combined sequence analysis, which comprises 3,091 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Cryptodiscus pallidus* (EB60) and *C. pallidus* (EB173).

Fitzroyomyces yunnanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 558662; *Facesoffungi number:* FoF 09896; Figure 2.2

Etymology: The species epithet refers to the type location "Yunnan", China.

Holotype: HKAS 113186

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Apothecia* 550–1000 × 230–370 µm ($\overline{x}$ = 800 × 270 µm, n = 10), immersed at first, opening by entire pore at maturity, subglobose. *Disc* deeply cupulate, pale creamy, with white-pruinose margin. *Exciple* 25–50 µm wide ($\overline{x}$ = 38 µm, n = 10), thick-walled, comprising hyaline cells of *textura intricata*, inner layer composed of hyaline cells of *textura angularis*. *Hamathecium* comprising asci and paraphyses. *Paraphyses* hyaline, 1–2 µm wide ($\overline{x}$ = 1.8 µm), numerous, long filiform, unbranched, aseptate. *Asci* 100–140 × 5–10 µm ($\overline{x}$ = 112 × 8 µm, n = 10), unitunicate, 6–8-spored, cylindrical to ovoid, broadest at middle, rounded apex and short stalked. *Ascospores* 80–120 × 2–3 µm ($\overline{x}$ = 88 × 2.7 µm, n = 10), overlapping uni- to bi-seriate, fusiform, 12–18-septate, hyaline, not easily breaking into different sizes, smooth-walled, guttulate, without a mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Colonies on PDA reaching 35 mm diam, after 4 weeks at room temperature (20–25°C). Culture from above, convex with surface, dry, rough, white to pale brown, circular, towards the edge with irregular white aerial mycelia, spreading, slightly covered; reverse brown to yellowish, with radiating white mycelia.

Material examined: China, Yunnan Province: Xishuangbanna, on dead wood of coffee, 24 November 2020, Saowaluck Tibpromma, XSBN-C5 (HKAS 113186, holotype); ex-type living culture KUMCC 21-0002.

GenBank numbers: KUMCC 21-0002: ITS = MZ781316, LSU = MZ781317, mtSSU = MZ781329.

Notes: ITS blast result showed that *Fitzroyomyces yunnanensis* is 89% similar to *F. cyperacearum* (MK499349). The results of LSU blast showed that our strain is 96% similar to *Stictis* sp. (MH260319), while mtSSU results showed it to be 90% similar to *Carestiella socia* (AY661678). Based on phylogenetic analyses, the new strain clustered with *Fitzroyomyces* and formed a well-separated clade with 100%

ML, 1.00 BYPP boostrap support with the extant species of *Fitzroyomyces*. *Fitzroyomyces yunnanensis* differs from extant species of *Fitzroyomyces* in its larger apothecia, with a clear border between outer and inner layers in the exciple, and shorter asci and ascospores. This is the first *Fitzroyomyces* species reported from coffee.

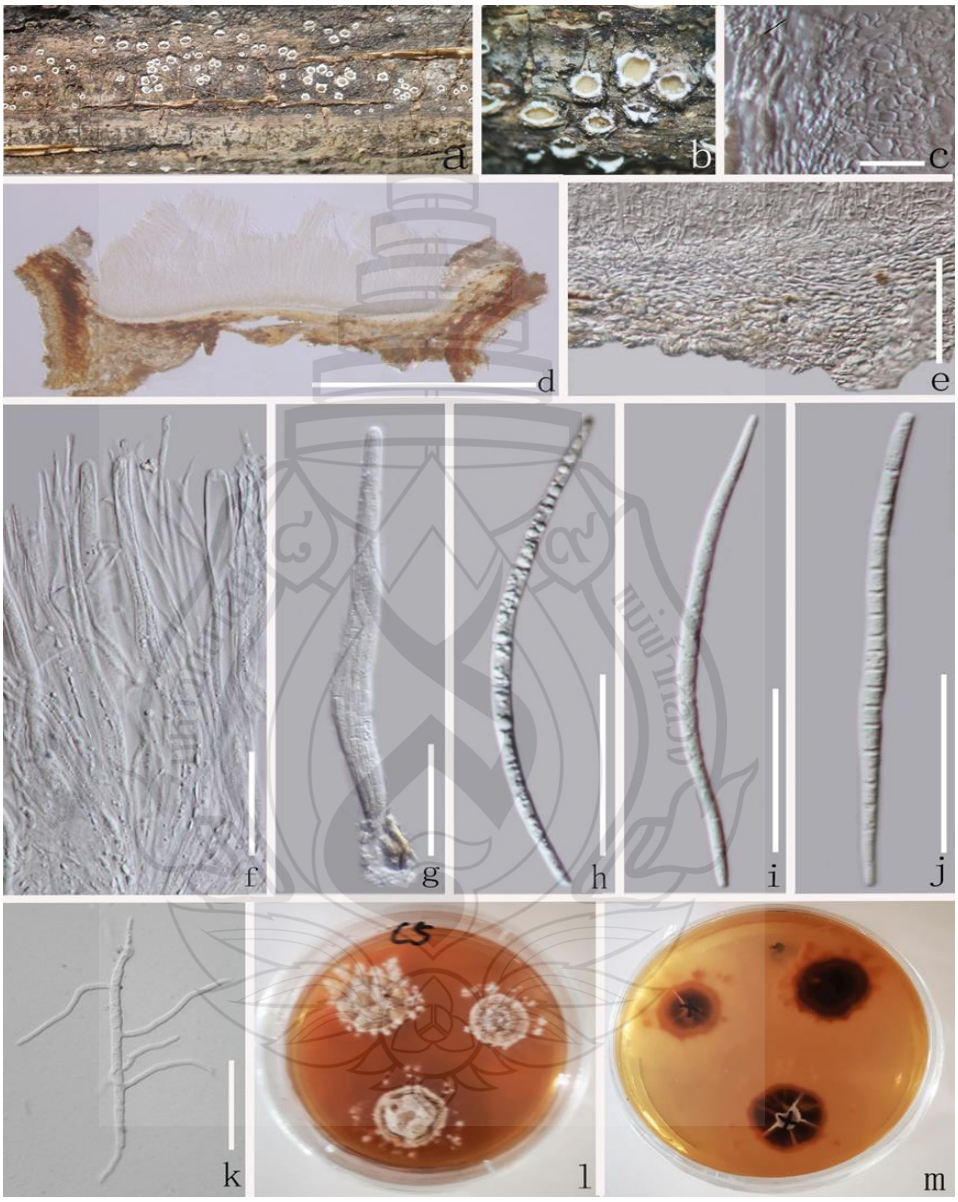


Figure 2.146 *Fitzroyomyces yunnanensis* (HKAS 113186, holotype)

Figure 2.146 a, b. Ascomata on coffee wood. c, e. Exciple. d. Vertical section of apothecium. f. Paraphyses. g. Ascus. h–j. Ascospores. k. Germinating ascospore. l, m. Colonies on PDA media. Scale bars: c = 10 µm, d = 500 µm, e–k = 30 µm.

Ostropomyces Thiyagaraja, Lücking, Ertz & K.D. Hyde, 2021

Notes: Ostropomyces was introduced by Thiyagaraja et al. (2021), and the genus has two saprobic members, with *O. pruinosellus* as the type species. The sexual morph of this genus is characterized by immersed fruiting bodies with long-cylindrical, 4-spored asci and filiform, multi-septate ascospores. The asexual morph is characterized by erumpent pycnidia with ostioles, and filiform conidia which are hyaline, and guttulate at maturity.

Ostropomyces pruinosellus Thiyagaraja, Lücking, Ertz & K.D. Hyde, in Thiyagaraja *et al.,* Journal of Fungi 7(2):105 (2021).

Index Fungorum number: IF 556556; *Facesoffungi number*: FoF 09512; Figure 2.110

Saprobic on a decaying branch of *Coffea* sp. *Pycnidia* with a pruinose appearance on the surface, irregular shape, solitary. **Sexual morph**: Not observed. **Asexual morph**: *Pycnidia* (excluding neck) 100–300 µm wide, 80–250 µm high ($\overline{x}$ = 206 × 127 µm, n = 10), immersed, globose to oval, single or clustered under the substrate, with short ostiole. *Pycnidial wall* 5–35 µm wide ($\overline{x}$ = 21 µm, n = 20), transverse section shows two layers; outer layer hyaline, thin-walled, densely packed, and inner layer of *textura angularis*, hyaline, loosely packed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 µm wide ($\overline{x}$ = 5.5 µm, n = 10), hyaline, lining the inside wall. *Conidia* 5–10 × 2–4 µm ($\overline{x}$ = 7.5 × 2.7 µm, n = 30), allantoid to filiform, aseptate, hyaline, catenate, guttulate at maturity, conidia connect to form a large branch.

Culture characteristics: Colonies on PDA reaching 15 mm diam after 4 weeks at room temperature (20–25°C). Culture from above, white, circular, with clusters of bumps that secrete brown liquid, towards the edge with irregular white aerial mycelia. Reverse side changes from dark brown in the middle to lighter on both sides.

Material examined: China, Yunnan Province: Pu'er, on dead wood of coffee, 23 December 2020, Li Lu, MJ-C5 (HKAS 113187); living culture KUMCC 21-0022.

GenBank numbers: KUMCC 21-0022: ITS = MZ781300, LSU = MZ781304, mtSSU = MZ781306.

Known hosts: Unidentified dicotyledonous plant (Thiyagaraja et al., 2021), *Coffea* sp. (this study).

Known distribution: Thailand (Thiyagaraja et al., 2021), China (This study).

Notes: Based on ITS and LSU blast results, our isolate is 95% similar to *Ostropomyces. pruinosellus* (NR_172006), and 98% similar to *O. pruinosellus* (NG_074507). The new strain formed a group together with *O. pruinosellus* in the combined mtSSU, LSU and ITS phylogenetic analyses with 100% ML, 1.00 BYPP boostrap support and shares similar morphological characteristics (asexual morph) with *O. thailandicus.* Our new collection differs from *O. thailandicus* in its allantoid to filiform conidia, and large branched conidial chains, whereas *O. thailandicus* has filiform conidia with unbranched chains, but similar in having catenate conidia and pruinose on the surface. Comparison of mtSSU, LSU and ITS regions of our new isolate with *O. pruinosellus* (MFLU 20-0538) reveals 0/6/13 (-/0.69%/2.4%) base pair differences, with *O. pruinosellus* (MFLU 21-0115) 4/0/3 (0.55%/0/0.57%) base pair differences and with *O. pruinosellus* (MFLUCC 21-0112) 10/4/13 (1.36%/0.47%/2.4%) base pair differences. Therefore, we identify our strain as *O. pruinosellus* based on guidelines of Jeewon and Hyde (2016). *Ostropomyces pruinosellus* has been reported as sexual morph from unidentified dicotyledonous plant from Thailand (Thiyagaraja et al., 2021, Wei et al., 2021). Thus, this is first report of the asexual morph of *O. pruinosellus* with a new host record from coffee and new geographical record from China.

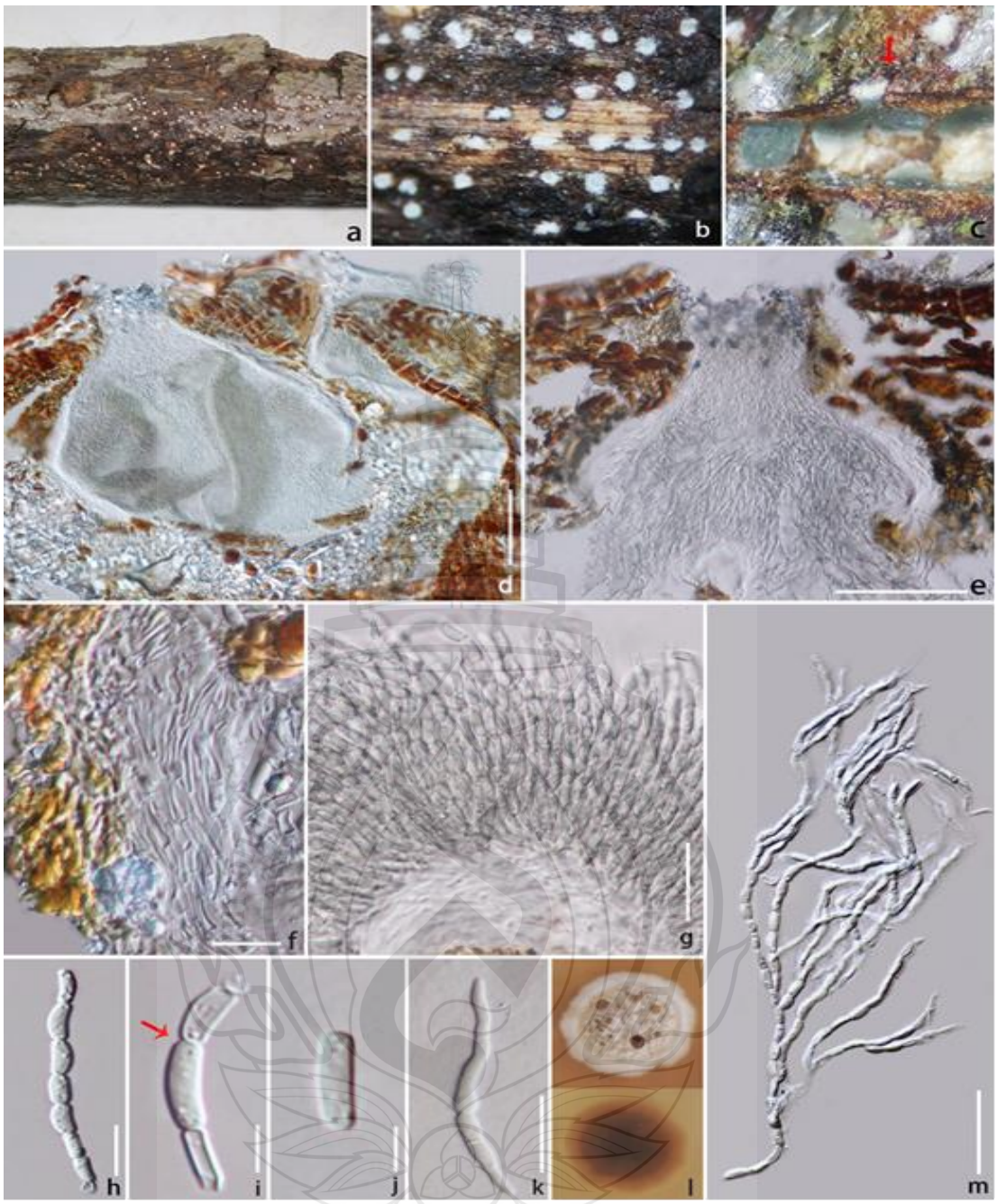


Figure 2.147 *Ostropomyces pruinosellus* (HKAS 113187, new record)

Figure 2.147 a, b. Pycnidia on coffee wood. c–e. Vertical section through pycnidia (arrow showing short ostiole). f. Pycnidial wall. g. Conidiophores and conidiogenous cells. h–j. Conidia (arrow showing septation). k. Germinating conidium. l. Colony on PDA medium. m. Conidia forming a large branch. Scale bars: d, e = 100 µm, f, h, i = 10 µm, g, k = 20 µm, j = 5 µm, m = 30 µm.

2.3.2.3 Sordariomycetes

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycological Research 108 (12): 378 (2004)

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

Lomaantha Subram., J. Indian bot. Soc. 33: 31 (1954).

Notes: Lomaantha was introduced by Subramanian (1954) and typified by *L. pooga*, which was collected from dead stems of *Areca catechu* in India. Reddy et al. (1978) introduced the second species, *L. santalii,* from India on stems of *Santalum album*. Ma et al. (2011) described *L. phragmitis*, which is the first new *Lomaantha* species from China. Delgado et al. (2024) expanded and emended six species from *Ellisembia, Helminthosporium* and *Pyrigemmula*. Subsequently, Crous et al. (2024) described one new species, *L. quercina*, which was isolated from twigs of *Quercus suber*. To date, 10 species are listed within *Lomaantha* (Index Fungorum, 2025). *Lomaantha* is mainly characterized by having erect and septate conidiophores, integrated, terminal, monoblastic, determinate conidiogenous cells, acrogenous, solitary, obclavate, smooth, distoseptate conidia with apical or subapical appendages and the sexual morph is unknown (Subramanian, 1954; Reddy et al., 1978; Wu & Zhuang, 2005; Ma, 2011). In this study, one new host record reported from a coffee host is introduced.

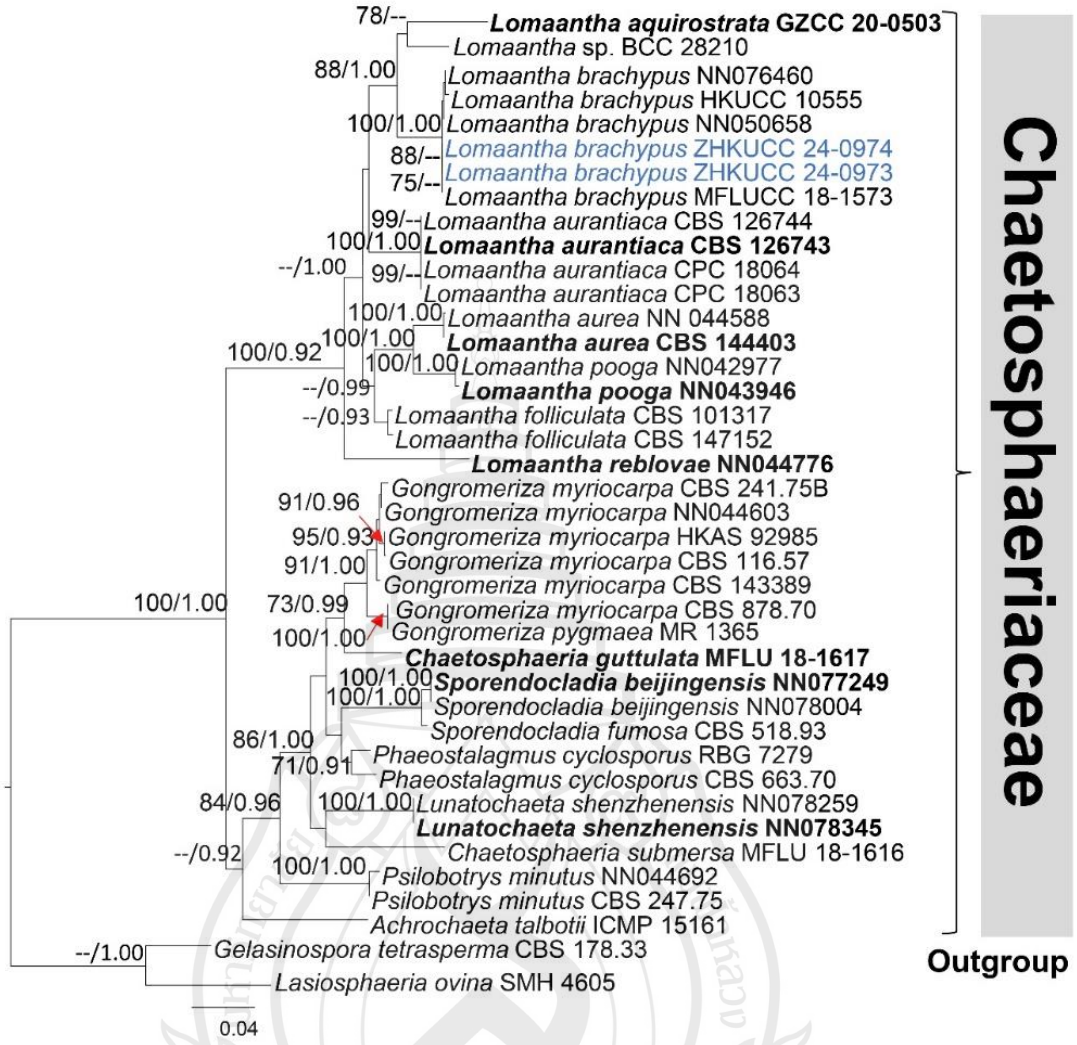


Figure 2.148 Phylogenetic tree of *Lomaantha*

Figure 2.148 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS and LSU sequence data. Forty strains are included in the combined sequence analysis, which comprises 1,377 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Gelasinospora tetrasperma* (CBS 178.33) and *Lasiosphaeria ovina* (SMH 4605).

Lomaantha brachypus (Ellis & Everh.) G. Delgado, Koukol & Maciá-Vicente, in Delgado, Koukol, Maciá-Vicente, Colbert & Piepenbring, Mycol. Progr. 23(no. 32): 17 (2024).

Index Fungorum number: IF 851181; *Facesoffungi number*: FoF 17592; Figure 2.110

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. Colonies on natural substrate effuse, hairy, black. *Mycelium* mostly immersed in the substratum, composed of brown, septate, smooth, branched hyphae. *Conidiophores* 40–100 × 5–9 µm ($\overline{x}$ = 66.6 × 7.2 µm, n = 25), macronematous, mononematous, single or aggregated in groups, simple, cylindrical, unbranched, erect, straight or flexuous, smooth, 3–10-septate, brown to dark brown or dark reddish brown, rarely with 1 percurrent extension, sometimes with 1–2-enteroblastic regenerative extensions unrelated to conidiation, base often blackish brown and bulbous. *Conidiogenous cells* 20–27 × 5–7 µm ($\overline{x}$ = 23.15 × 6.05 µm, n = 25), monoblastic, integrated, terminal, cylindrical, determinate, smooth, brown, attenuated to a truncate apex, 3–4 µm wide, rarely percurrent and lageniform or doliiform, with terminal pore. *Conidia* 35–55 × 11–17 µm ($\overline{x}$ = 42 × 13.55 µm, n = 30), acrogenous, obclavate, rostrate, smooth, sub-hyaline to pale olivaceous when young, pale brown to brown when mature, apical cells extending into pale brown to hyaline, basal cell conical-truncate, darker than other cells, (–2)4–5(–6)-distoseptate, not constricted at the septa, with a central darkened pore at the septa when mature, apical cell extended into a hyaline to subhyaline, with one filiform appendage arising from the apical portion of the conidia, 30–45 µm long, unbranched, hyaline.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 25 mm after one month at 25°C, colonies from above: circular, margin irregular, flat, gray to brown; from below: light brown to dark brown; the pink pigments produced in the cultures.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH3-8 (MHZU 24-0534), living culture ZHKUCC 24-0973, other living culture ZHKUCC 24-0974.

GenBank numbers: ZHKUCC 24-0973: ITS = PQ608213, LSU = PQ608042, SSU = PQ607923; ZHKUCC 24-0974: ITS = PQ608214, LSU = PQ608043, SSU = PQ607924.

Known hosts: *Areca catechu* (Matsushima, 1980), *Canarium tonkinense* (Shi & Zhang, 2007), *Coffea* sp. (this study), *Freycinetia banksii* (McKenzie, 1995), *Ocotea usambarensis* (Kirk, 1985), *Pandanus furcatus* (McKenzie, 1995), *Phoenix canariensis* (Kobayashi, 2007), *Populus balsamifera* (Farr & Rossman, 2021), *Populus* sp. (Farr & Rossman, 2021), *Populus tremuloides* (Farr & Rossman, 2021), *Sabal* sp. (Delgado, 2008), *Ripogonum scandens* (Farr & Rossman, 2021), *Ulmus* sp. (Farr & Rossman, 2021), *Vitis coignetiae* (Shirouzu & Harada, 2004).

Known distribution: Canada (Farr & Rossman, 2021), China (Matsushima, 1980; McKenzie, 1995; Shi & Zhang, 2007; This study), Japan (Shirouzu & Harada, 2004; Kobayashi, 2007), Kenya (Kirk, 1985), New Zealand (McKenzie, 1995; Farr & Rossman, 2021), USA (Delgado, 2008; Farr & Rossman, 2021).

Notes: Lomaantha brachypus was established by Delgado et al. (2024), previously basionymized with *Helminthosporium brachypus* by Millspaugh and Nuttall (1896), but Delgado et al. (2024) transferred it to *Lomaantha* based on morphology and phylogeny. In the phylogenetic tree, our two isolates (ZHKUCC 24-0973 and ZHKUCC 24-0974) developed as sister lineage with *L. brachypus* (CBS 147395, CBS 147396, HKUCC 10555, MFLUCC 18-1573, NN 050658 and NN 076460; Figure 2.109), which is collected from *Coffea* sp. from Yunnan Province, China. Morphologically, the two collections also fit well with the generic description of *L. brachypus* in having brown to dark brown, single or aggregated in groups, unbranched, erect, conidiophores, and acrogenous, fusiform to obclavate conidia, basal cell conical-truncate, with a filiform appendage (Delgado et al., 2024; Figure 2.110). Based on the phylogeny and morphological evidence, our collection is identified as *L. brachypus* and this is first time isolated this species from a coffee host.

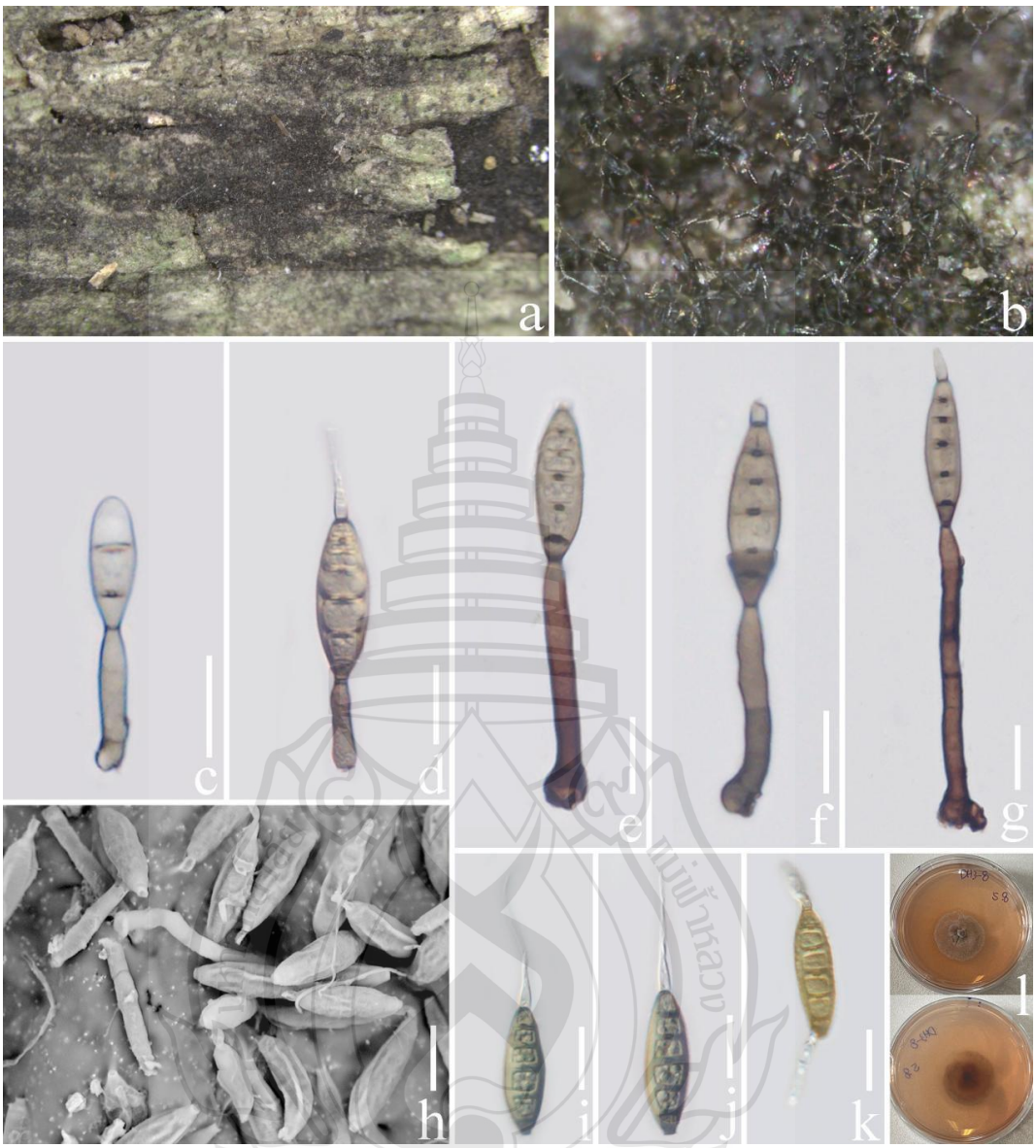


Figure 2.149 *Lomaantha brachypus* (MHZU 24-0534, new host record)

Figure 2.149 a, b Colony on host substrate. c–g Conidiophores with conidia. h SEM microphotographs of conidia. i, j Conidia. k Germinated conidium. l Culture on PDA from above and below. Scale bars: c–k = 20 µm.

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

Notes: Menisporopsis is a fungal genus of Chaetosphaeriales in Sordariomycetes, which was introduced by Hughes (1952) with the type species *M. theobromae*. Seventeen species are reported in *Menisporopsis* (Index Fungorum, 2025). In natural environments, most *Menisporopsis* species occurred as saprobes on decaying leaves and submerged wood in pantropical regions (Tsui et al., 1999; Seifert et al., 2011) and are frequently collected from aquatic and marine habitats (Chen et al., 2022). However, between species, they are distinguished primarily by conidial morphology and dimensions (Ellis, 1971; Kirk & Sutton, 1985; Castañeda-Ruiz et al., 1997; Siboe et al., 1999; Tsui et al., 1999; Seifert et al., 2011; Tibpromma et al., 2018; Wu et al., 2022). Our phylogenetic analysis corroborates the findings of Wu et al. (2022), demonstrating that *Menisporopsis* forms two distinct clades, further confirming the polyphyletic nature of the genus. *Menisporopsis* is characterized by pigmented, synnematous conidiophores growing around a central, simple, dark brown seta. The conidiogenous cells are phialidic, producing lunate to falcate, 0 to 1-septate conidia with one to several setulae inserted at the ends or irregularly (Hughes, 1952; Pirozynski & Hodges, 1973; Varghese & Rao, 1978; Rao & de Hoog, 1986; Tibpromma et al., 2018). In this study, a new host record from coffee in China and Thailand is introduced, along with descriptions of its sexual and asexual morph characteristics.

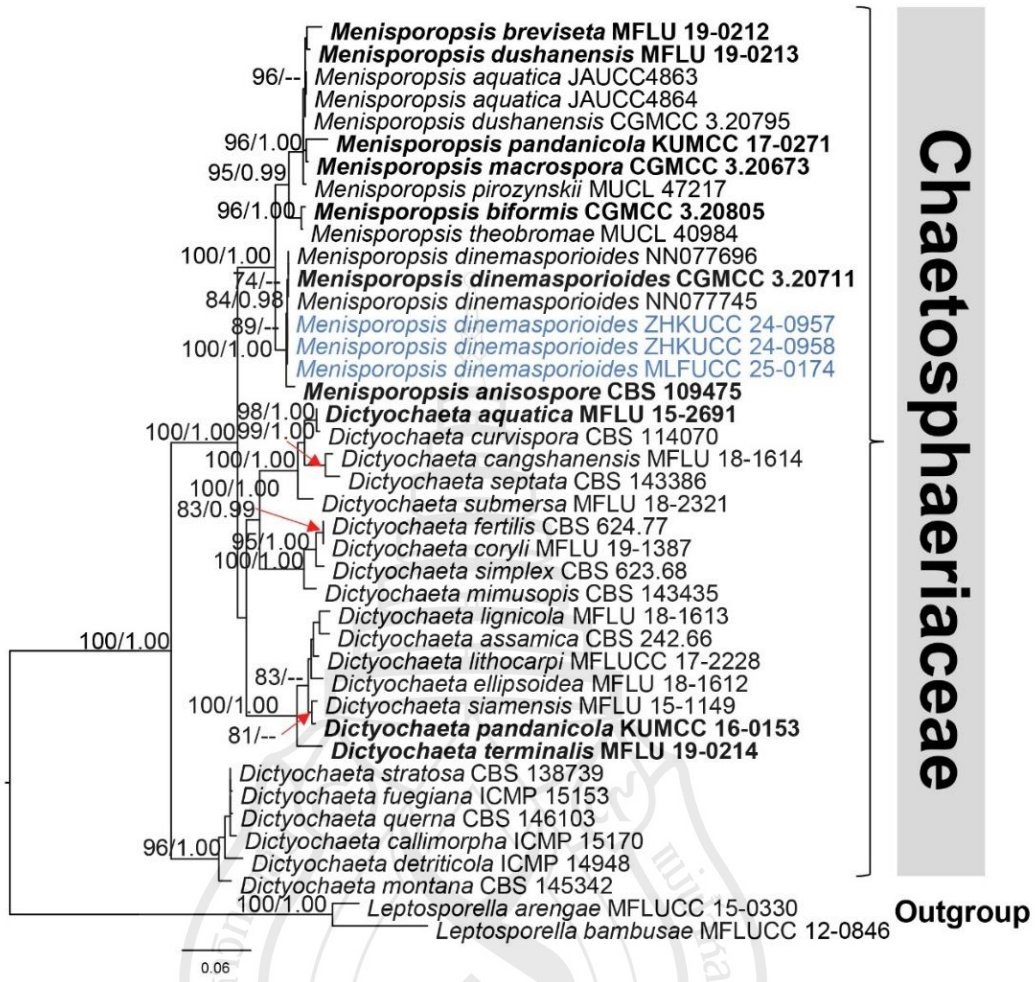


Figure 2.150 Phylogenetic tree of *Menisporopsis*

Figure 2.150 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS and LSU sequence data. Forty-one strains are included in the combined sequence analysis, which comprises 1,405 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Leptosporella arengae* (MFLUCC 15-0330) and *L. bambusae* (MFLUCC 12-0846).

Menisporopsis dinemasporioides W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 380 (2022)

Index Fungorum number: IF 841628; *Facesoffungi number*: FoF 17593; Figure 2.112, 2.113, 2.114

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph** (**Figure 2.112**): *Ascomata* 150–250 × 220–250 µm ($\overline{x}$ = 190 × 230 µm, n = 15), semi-immersed to immersed, solitary, subglobose to obpyriform, or irregular, dark brown to black, with a central ostiole. *Peridium* 15–25 µm wide ($\overline{x}$ = 21 µm, n = 30), pseudoparenchymatous, outer layers thick-walled, dark brown, composed of cells of *textura angularis*, inner layers thin-walled, hyaline, composed of cells of *textura prismatica*. *Hamathecium* of 2–4 µm wide ($\overline{x}$= 3 µm, n = 30), hyaline, branched, aseptate, paraphyses. *Asci* 80–110 × 10–15 µm ($\overline{x}$ = 90.5 × 11 µm, n = 30), unitunicate, 8-spored, thin-walled, cylindrical, with a short furcate pedicel, apically rounded, J-, apical ring. *Ascospores* 12–15 × 6–7 µm ($\overline{x}$ = 14 × 6.2 µm, n = 30), uni- or partially overlapping, oval to ellipsoidal with granular contents, hyaline, smooth-walled, aseptate, surrounded by a thick mucilaginous sheath when im-mature, mature ascospores with inconspicuous sheath. **Asexual morph** (**Figure 2.114**): Hyphomycetous. *Colonies* effuse, thick, conspicuous, superficial, aggregated. *Mycelium* immersed or superficial, composed of pale brown, septate hyphae. *Synnemata* solitary, erect, straight or flexuous, cup-shaped, with a basal stroma and a cup-shaped sporulating part with excipulum-like structure and 1 setae arising centrally, upper part is transparent and the lower part is brown. *Setae* 200–300 × 5–8 µm ($\overline{x}$ = 270 × 7 µm, n = 10), 1–2 in each conidiomata, cylindrical, erect, straight, unbranched, dark brown, becoming paler toward the apex, septate, smooth, apex rounded. *Conidiophores* 150–200 × 50–120 µm ($\overline{x}$ = 170 × 82 µm, n = 15), closely compacted into synnemata; synnemata dark brown to black, lower part blackish, upper part loosely packaged with excipulum-like structure; conidiophores cylindrical, erect, straight of flexuous, unbranched or branched, hyaline to pale brown, septate, smooth- and thin-walled, terminating in a conidiogenous cell. *Conidiogenous cells* 15–20 × 3–5 µm ($\overline{x}$ = 19 × 3.6 µm, n = 20), monophialidic, integrated, terminal, cylindrical, lageniform, erect, straight, thin-walled, periclinal thickening obvious, collarette inconspicuous. *Conidia* 24–27 × 5–6 µm ($\overline{x}$ = 25 × 5.5 µm, n = 30), aggregated in white slimy heads around the conidiogenous cells, hyaline, aseptate, smooth- and thin-walled, falcate, fusiform, curved, both ends rounded, appendiculate with one setula of 8–

12 µm long at each end, some with guttules.

Culture characteristic: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25°C, slightly raised, irregular and entire margin, surface rough and with aerial mycelium, from above yellowish, from below light brown. Sporulated in cultures (PDA media) after one month at 25°C. *Conidiophores* arise directly from aerial hyphae, septate and branched, sub-hyaline, cells with guttules, 2–5 µm wide, macronematous or semi-macronematous, and mononematous. *Conidiogenous cells* integrated, terminal, phialidic, solitary, hyaline, thin-walled, with rounded apex. *Conidia* 10–18 × 3–5 µm ($\bar{x}$ = 14 × 3.2 µm, n = 30), hyaline, smooth-walled, oblong, falcate or fusiform, aseptate, appendiculate with one or without setula when young, appendiculate with one setula up 7 µm long at each end when mature (Figure 2.113).

Material examined: China, Yunnan Province, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH 1-8 (MHZU 24-0526), living culture ZHKUCC 24-0957, other living culture ZHKUCC 24-0958; Thailand, Chiang Rai Province, on a decaying branch of *Coffea* sp. (990 m), 1 November 2023, Li Lu, LC3-2-6 (MFLU 25-0087), living culture MFLUCC 25-0174.

GenBank numbers: ZHKUCC 24-0957: ITS = PQ608211, LSU = PQ608040; ZHKUCC 24-0958: ITS = PQ608212, LSU = PQ608041; MFLUCC 25-0174: ITS = PQ608210, LSU = PQ608039.

Known hosts: on dead leaves of unidentified tree (Wu et al., 2022); *Coffea* sp. (This study).

Known distribution: China (Wu et al., 2022; This study); Thailand (This study).

Notes: Menisporopsis dinemasporioides was isolated as a saprobe on dead leaves of an unidentified tree in China, with only the asexual morph (Wu et al., 2022). In a BLASTn search, the ITS and LSU sequences (ZHKUCC 24-0957) of our collection showed 99.5% similarity to *M. dinemasporioides* (NN077696). In our phylogenetic analysis, our strains also clustered with *M. dinemasporioides* (NN077696, NN077745 and CGMCC 3.20711, type) with 100% ML and 0.99 BYPP statistical support (Figure 2.111). In addition, the asexual morphology of our collection (MFLU 25-0087) is the same as *M. dinemasporioides* by having similar synnemata, falcate or fusiform conidia, and appendiculate with one setula at both ends (Wu et al., 2022; Figure 2.114). We, therefore, identified our collection as *M. dinemasporioides*. In addition, we also

provide the sexual morph of *M. dinemasporioides* (Figure 2.112, 2.113), and this is the first sexual morph report for *Menisporopsis*.

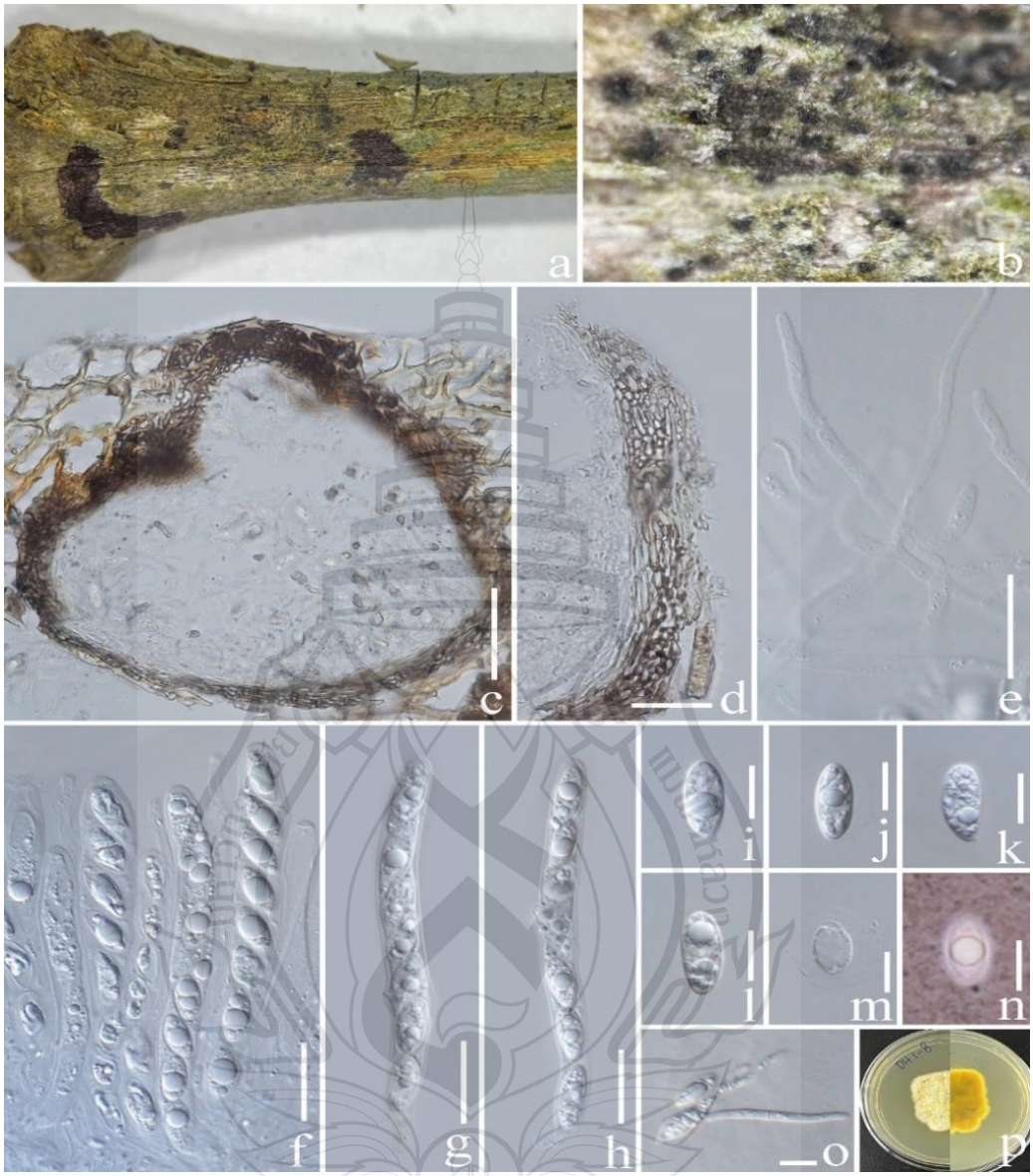


Figure 2.151 *Menisporopsis dinemasporioides* (MHZU 24-0526, new host record)

Figure 2.151 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. D Peridium. E Hamathecium. F–h Asci. I–n Ascospores (m: Immature ascospore with an obvious sheath; n: mature ascospore stained with India ink). o Germinated ascospores. p Culture on PDA from above and below. Scale bars: c = 50 µm, d–h = 20 µm, i–o= 10 µm.

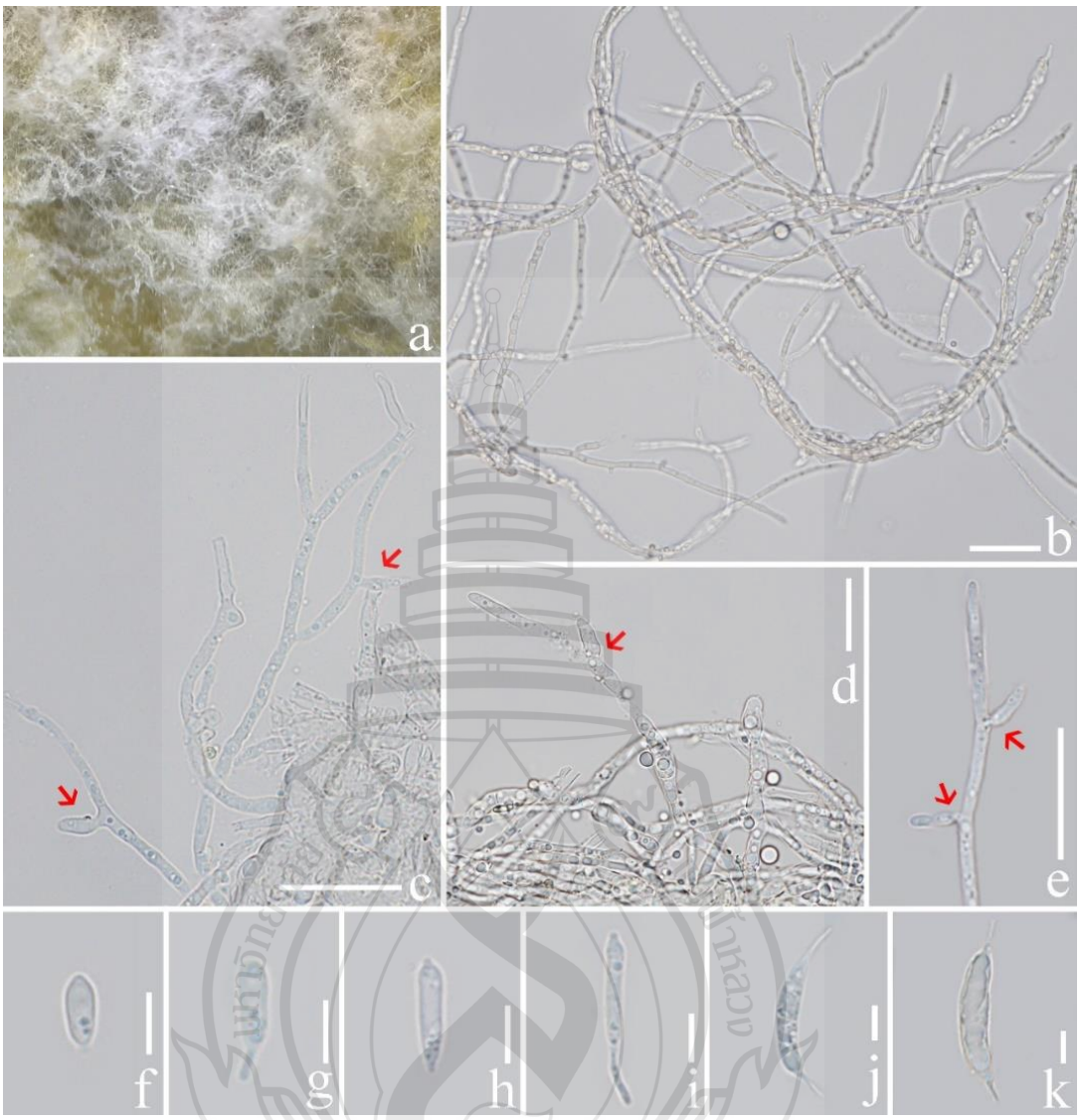


Figure 2.152 Asexual morphology of *Menisporopsis dinemasporioides* (ZHKUCC 24-0957) on PDA

Figure 2.152 a Hypha grown on PDA. b Conidiophores (arrows indicate the growing conidia). c–e Conidiogenous cells with conidia (arrows indicate the growing conidia). f–k Immature to mature conidia. Scale bars: b = 30 µm, c–e = 20 µm, f–k = 5 µm.

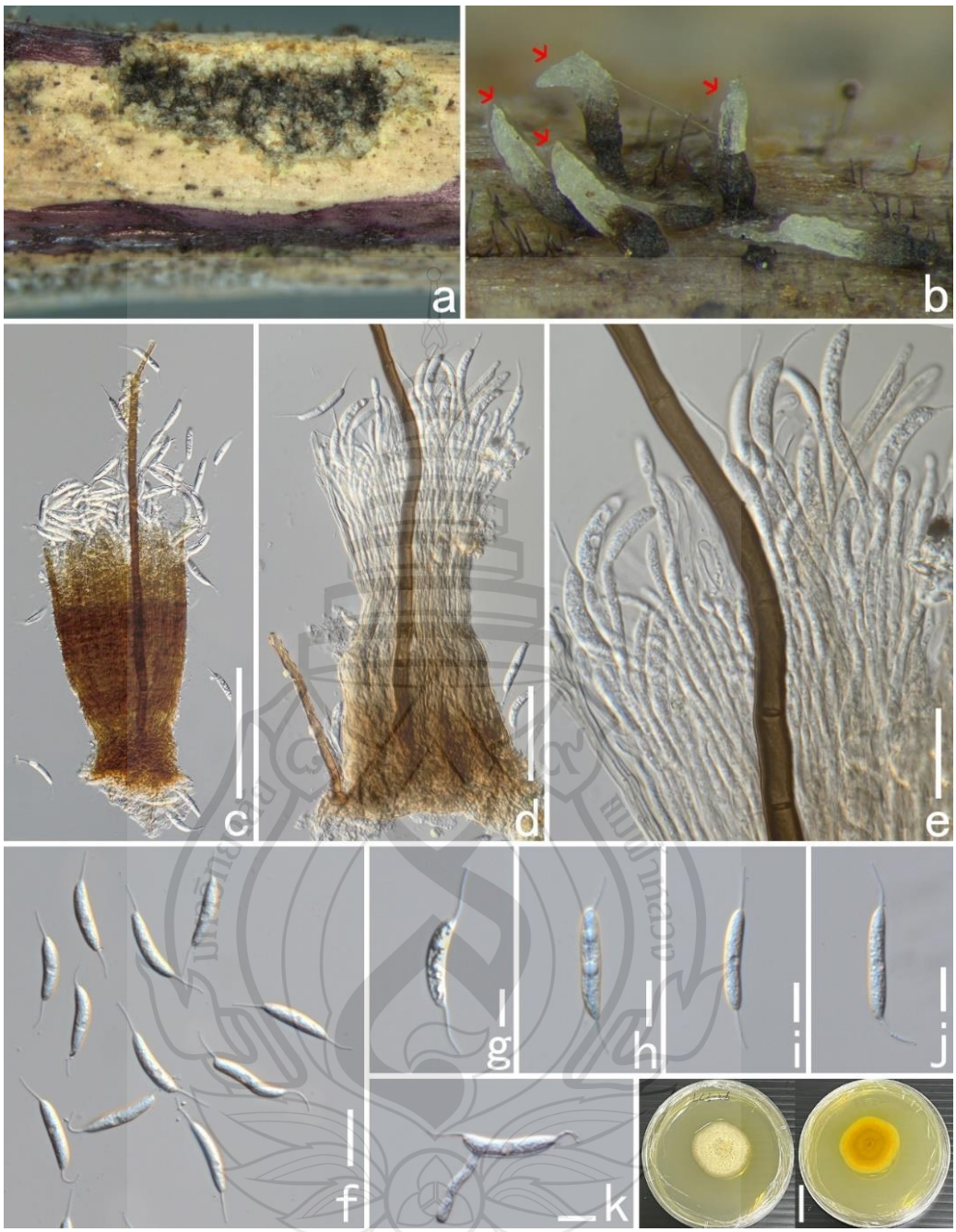


Figure 2.153 *Menisporopsis dinemasporioides* (MFLU 25-0087, new county record)

Figure 2.153 a, b Colonies on dead branch of *Coffea* sp. (arrows indicate the conidia aggregated in white slimy heads around the conidiogenous cells). c–e Synnematous conidiomata with setae, conidiophores, conidiogenous cells with conidia. f–j Conidia. k A germinating conidium. l Culture on PDA from above and below. Scale bars: c = 100 µm, d = 50 µm, e, f = 20 µm, g–k = 10 µm.

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

Coniochaetaceae Malloch & Cain, Canadian Journal of Botany 49 (6): 878 (1971)

Coniochaeta (Sacc.) Cooke, Grevillea 16 (77): 16 (1887)

Notes: The subgenus *Coniochaeta* was first introduced by Saccardo and Traverso (1882) for those species of *Rosellinia* with small, gregarious, and hairy perithecia. It was raised to genus by Cooke (1887). The previously given name *Coniochaeta* has been retained for *Lecythophora*, following the "one fungus, one name" nomenclature change in January 2013 (Kabtani et al., 2022). *Coniochaeta* is pleomorphic ascomycetous fungi belonging to the family Coniochaetaceae (Weber et al., 2002) and with *Coniochaeta ligniaria* as the type species (Garci´a et al., 2006; Silva et al., 2023). *Coniochaeta* comprises more than 100 species, and they are ubiquitously distributed in the environment. They have been isolated from several natural substrates, including soil, wood, plants, freshwater, and food (Kamiya et al., 1995; Guarro et al., 1997; Yuan et al., 1997; Gao et al., 2022). This genus is an important group among ascomycetes with rich species diversity and high economic value. Some species can produce a variety of secondary metabolites, such as *C. ellipsoidea*, which produces compounds with strong antibacterial and antifungal activities (Wang et al., 1995; Segeth et al., 2003). However, other species of this genus are destructive and can parasitize plants, animals, and humans, causing diseases. For example, *C. prunicola* is a pathogenic fungus of almond and peach trees, which causes serious economic loss to agricultural production (Damm et al., 2010; Gao et al., 2022). *Coniochaeta* is characterized by having superficial or semi-immersed ascomata; cylindrical or clavate asci; one-celled, narrowly ellipsoid to fusoid, brown to dark brown, olive greenish to dark olivaceous, or black ascospores (García et al., 2006; Silva et al., 2023). The asexual morph of *Coniochaeta* is characterized by having colonies varying from nearly white to yellowish or orange, salmon-coloured, pink, or isabelline in colour (Weber, 2002), hyaline hyphae, and mostly intercalary phialides with very short lateral necks, periclinal wall thickening, and flaring collarettes (Weber, 2002; Silva et al., 2023). In this study, a new host record from coffee is introduced.

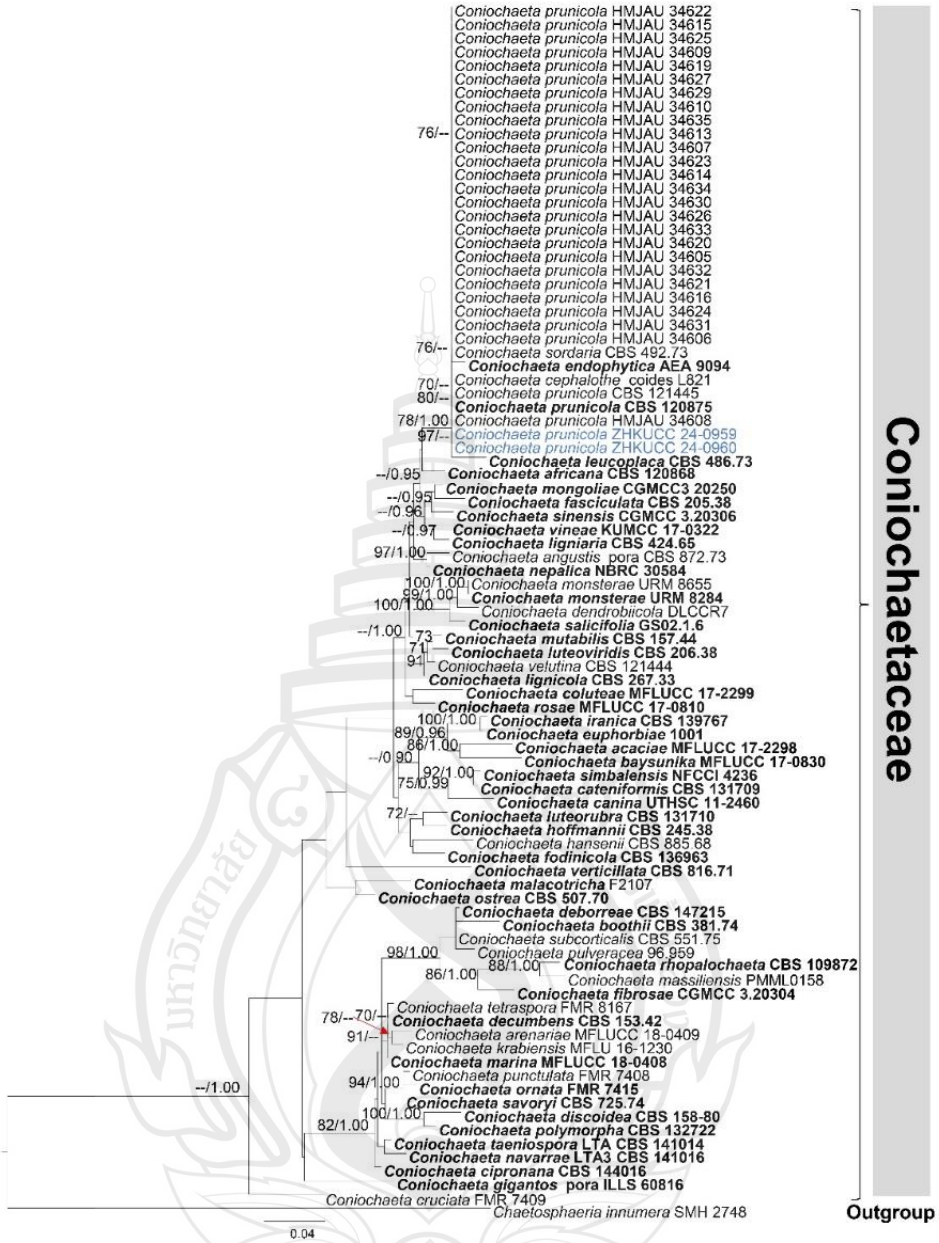


Figure 2.154 Phylogenetic tree of *Coniochaeta*

Figure 2.154 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS and LSU sequence data. Eighty-nine strains are included in the combined sequence analysis, which comprises 1,420 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Chaetosphaeria innumera* (SMH 2748).

Coniochaeta prunicola Damm & Crous, Persoonia 24: 73 (2010)

Index Fungorum number: IF 516629; *Facesoffungi number*: FoF 17594; Figure 2.116

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 200–250 × 200–250 µm ($\overline{x}$ = 220 × 210 µm, n = 15), superficial, solitary or clustered, subglobose to globose, or pyriform, black, with a central ostiole. *Setae* dark brown, straight, short, cylindrical, tapering to a round tip, smooth-walled or granulate. *Peridium* 20–40 µm wide ($\overline{x}$ = 35 µm, n = 30), pseudoparenchymatous, outer layers thick-walled, dark brown to black, composed of cells of *textura angularis*, inner layers thin-walled, hyaline, composed of cells of *textura prismatica. Hamathecium* of 2–3.5 µm wide ($\overline{x}$ = 2.5 µm, n = 30), hyaline, septate, paraphyses. *Asci* 65–75 × 7–10 µm ($\overline{x}$ = 72 × 8.4 µm, n = 30), unitunicate, 6–8-spored, thin-walled, cylindrical, with a short furcate pedicel, apically rounded, J-, apical ring. *Ascospores* 8–10 × 6–8 µm ($\overline{x}$ = 9.3 × 7 µm, n = 30), uni- or overlapping seriate, 1-celled, hyaline to brown, smooth-walled, at first 'saucer-shaped' (broadly-ellipsoidal in top view and reniform from the side) with granular contents; broadly almond-shaped when mature, with inconspicuous longitudinal germ slit. **Asexual morph**: See Ivanová et al. (2012).

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm in one month at 25°C, flat, circular and entire margin, surface rough and with aerial mycelium, from above and below, white.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS2-C6 (MHZU 24-0527), living culture ZHKUCC 24-0959, other living culture ZHKUCC 24-0960.

GenBank numbers: ZHKUCC 24-0959: ITS = PQ608215, LSU = PQ608044; ZHKUCC 24-0960: ITS = PQ608216, LSU = PQ608045.

Known hosts: Cerasus argenteus, Acer, cerasus flos, Camphora, Quercus mongolica, Locusta nigra; Flens salix, Siccus salix, Prunus armeniaca, Prunus salicina, Prunus cerasus, Persica vulgaris, Laurocerasus officinalis, Umbilicaria mammulata, Juniperus virginiana (Damm et al., 2010; Ivanová et al., 2012; Ivanová 2013; Arnold 2021; Gao et al., 2022); *Coffea* sp. (This study).

Known distribution: China, Europe, South Africa, Slovakia (Damm et al., 2010; Ivanová et al., 2012; Ivanová 2013; Arnold 2021; Gao et al., 2022; This study).

Notes: Coniochaeta prunicola was isolated as endophytic, pathogenic, and saprobic on different hosts worldwide (Damm et al., 2010; Ivanová et al., 2012; Ivanová 2013; Arnold 2021; Gao et al., 2022). In a BLASTn search, the ITS and LSU sequence of our collection showed 100% similarity to *C. prunicola* (Strain, 1359). In our phylogenetic analysis, our strains grouped with *C. prunicola* with 97% ML statistical support (Figure 2.115). In addition, the morphology of our collection is almost of same as *C. prunicola* (HMJAU 34612) in morphological characters by having cylindrical asci and one-celled, ellipsoidal ascospores, brown when mature (Gao et al., 2022; Figure 2.116). We, therefore, identified our collection as *C. prunicola* which is a new host record form *Coffea* sp. in China.

Furthermore, *Coniochaeta cephalothecoides* (L821), *C. endophytica* (AEA 9094, ex-type), *C. leucoplaca* (CBS 486.73), *C. prunicola* (CBS 120875, ex-type), and *C. sordaria* (CBS 492.73) consistently clustered within the same branch in our phylogenetic analysis, which is consistent with the findings reported by Silva et al. (2023). We hypothesize that these species may represent a single taxonomic entity as their morphology is also similar; however, further analysis involving more isolates is required to confirm this possibility.

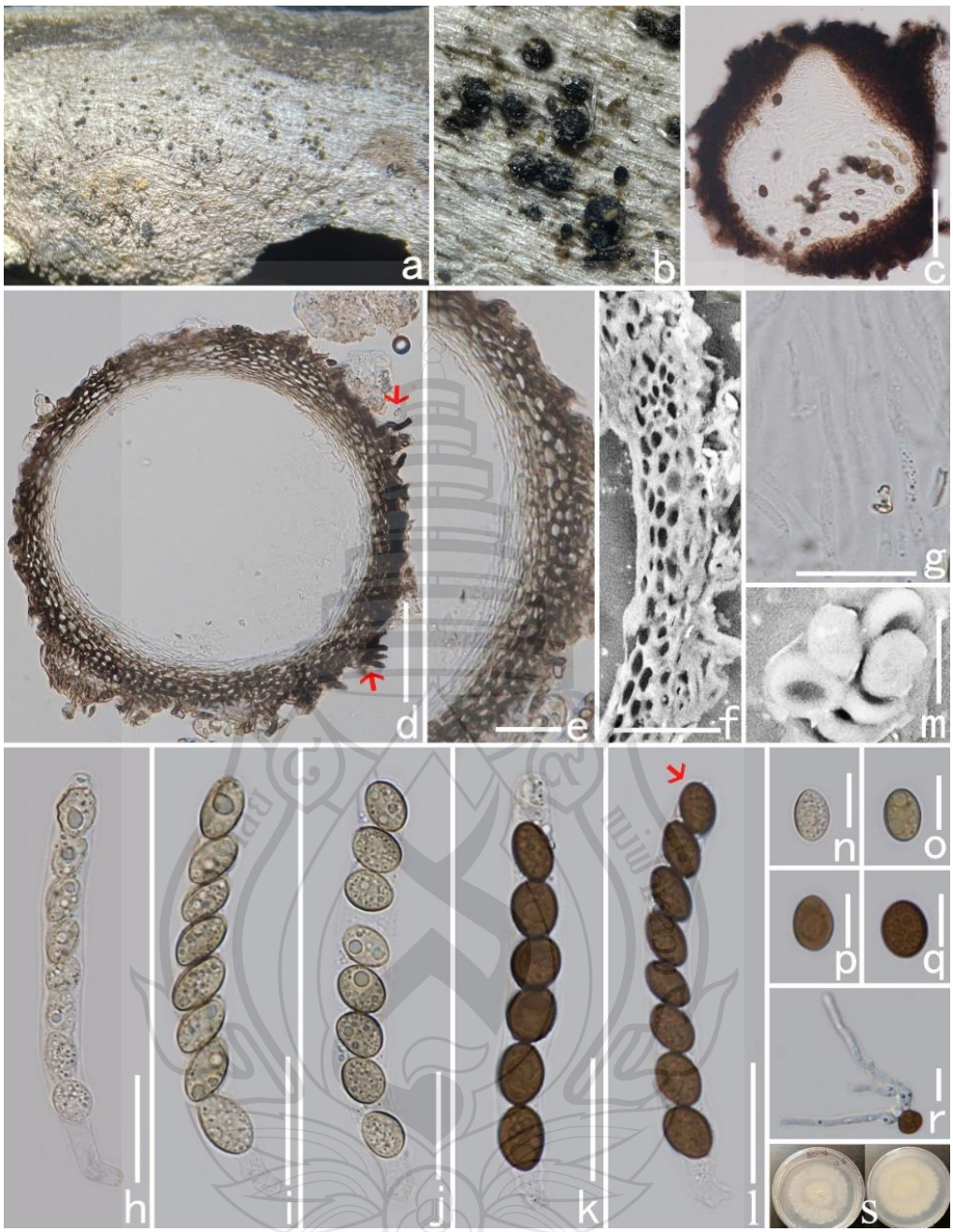


Figure 2.155 *Coniochaeta prunicola* (MHZU 24-0527, new host record)

Figure 2.155 a, b Ascomata on a decaying branch of *Coffea* sp. c, d Longitudinal section of ascomata (red arrows indicate setae). e, f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–l Asci (red arrow indicates germ slit). m–q Ascospores (m: SEM microphotographs of ascospores). r Germinated ascospore. s Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–l = 20 µm, m–r= 10 µm.

Conlariales K.D. Hyde & Hongsanan - Fungal Diversity 107:71–105. (2021)

Conlariaceae H. Zhang, K.D. Hyde & Maharachch - Fungal Diversity 85: 75–110. (2017)

Conlarium F. Liu & L. Cai - Mycologia 104(5): 1180 (2012)

Notes: *Conlarium* was introduced to accommodate a holomorphic type species *C. dupliciascosporum* (Liu et al., 2012). However, the species in *Conlarium* are mainly known by the asexual morph in the subsequent study, with *C. dupliciascosporum* remaining the only species described as holomorphic within the genus (Liu et al., 2012; Zhang et al., 2017; Phookamsak et al., 2019; Xie et al., 2019; Dong et al., 2021; Dubey & Manikpuri, 2021; Zhang et al., 2021; Hyde et al., 2023; Yang et al., 2023; Hyde et al., 2024b). The sexual morph of *Conlarium* is characterized by partially immersed to superficial ascomata with a long neck, branched and septate paraphyses, conspicuous apical ring of asci and biseriate, hyaline, fusiform, 0–5-septate ascospores with or without globose or papillary appendages at one or both ends (Liu et al., 2012). The asexual morph of *Conlarium* is characterized by muriform, irregularly globose or subglobose conidia (Liu et al., 2012; Xie et al., 2019; Hyde et al., 2020b, 2023, 2024b; Zhang et al., 2021; Yang et al., 2023). This genus comprises 13 species, with six documented in freshwater habitats and seven in terrestrial habitats (Liu et al., 2012; Zhang et al., 2017; Phookamsak et al., 2019; Xie et al., 2019; Dong et al., 2021; Dubey & Manikpuri, 2021; Zhang et al., 2021; Hyde et al., 2023, 2024a; Yang et al., 2023; Index Fungorum, 2025). In this study, a new host and a country record from coffee is introduced

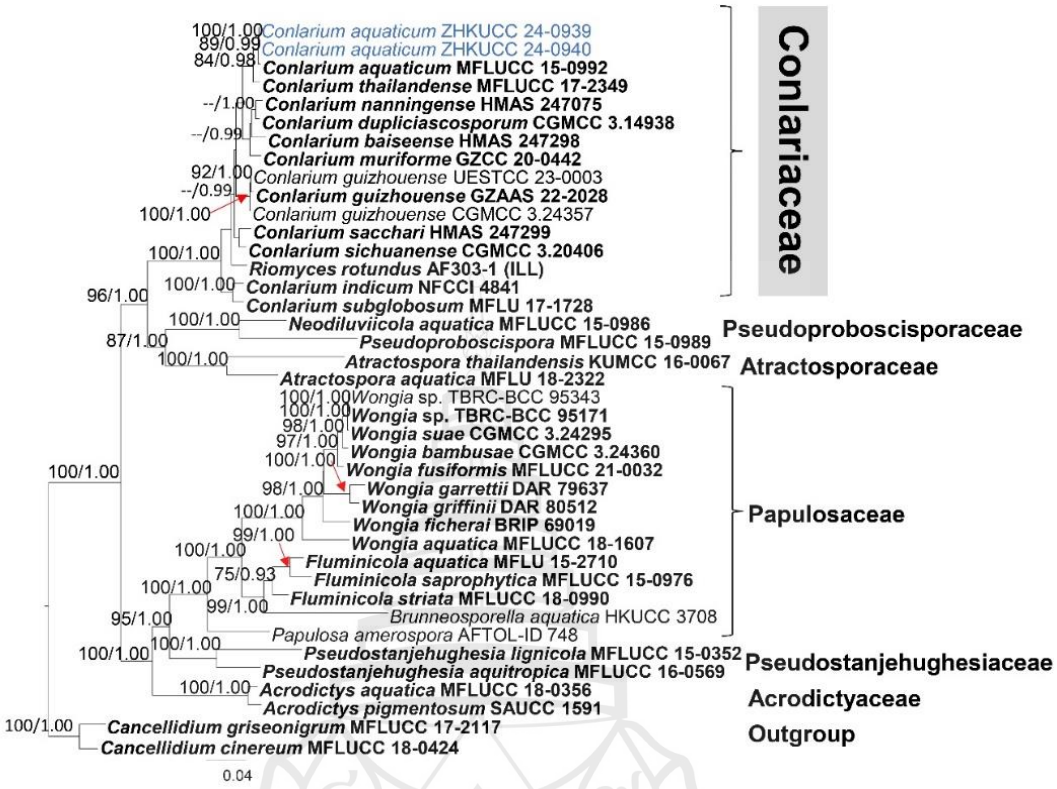


Figure 2.156 Phylogenetic tree of *Conlarium*

Figure 2.156 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Forty strains are included in the combined sequence analysis, which comprises 4,103 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Cancellidium cinereum* (MFLUCC 18-0424) and *C. griseonigrum* (MFLUCC 17-2117).

Conlarium aquaticum W. Dong, H. Zhang & K.D. Hyde, Fungal Diversity 85, 75–110. (2017)

Index Fungorum number: IF 553759; *Facesoffungi number*: FoF 03337; Figure 118

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* sporodochial, broadly punctiform, gregarious or scattered, raised, dark brown to black, velvety. *Mycelium* mostly

immersed on natural substratum, branched, septate, thin-walled, smooth, pale brown to brown hyphae. *Conidiophores* absent or reduced to conidiogenous cells. *Conidiogenous cells* up to 35 µm long, monoblastic, holoblastic, integrated, determinate, cylindrical, hyaline to pale brown, smooth-walled. *Conidia* 30–70 × 25–50 µm ($\overline{x}$ = 45 × 33.5 µm, n = 30), acrogenous, solitary, dry, subglobose, ellipsoidal, oblong, or irregular, brown, clathrate, muriform, 5–8-transversely septate, 6–9-longitudinal septate, slightly constricted at the septa, smooth, and thin-walled. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, grey to dark brown from above, black from below, umbonate, rough, wrinkled, dry, edge undulate.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH1-5 (MHZU 24-0516), living culture ZHKUCC 24-0939, other living culture ZHKUCC 24-0940.

GenBank numbers: ZHKUCC 24-0939: ITS = PQ608217, LSU = PQ608046, SSU = PQ607925, *RPB*2 = PV186803, *TEF*1-α = PQ602099; ZHKUCC 24-0940: ITS = PQ608218, LSU = PQ608047, SSU = PQ607926, *RPB*2 = PV186804, *TEF*1-α = PQ602100.

Known hosts: decaying, submerged wood in freshwater (Zhang et al., 2017); *Coffea* sp. (This study).

Known distribution: Thailand (Zhang et al., 2017); China (this study).

Notes: Conlarium aquaticum was introduced by Zhang et al. (2017) and collected from submerged wood of an unidentified host in freshwater in Thailand. In the phylogenetic tree, our two strains (ZHKUCC 24-0939 and ZHKUCC 24-0940) developed a sister lineage to *C. aquaticum* (MFLUCC 15-0992, ex-type) with 89% ML and 0.99 BYPP bootstrap support (Figure 2.117); they are collected from *Coffea* sp. from China. Based on nucleotide comparisons, our isolates (ZHKUCC 24-0939) were nearly the same as *C. aquaticum* (MFLUCC 15-0992, ex-type) by 3/516 bp (0.6%, without gaps) in ITS, 5/925 bp (0.5%, without gaps) in *TEF*1-α and the same in LSU and SSU. Morphologically, our collection fits well with the *C. aquaticum* (Zhang et al., 2017; Figure 2.118). Combining both phylogeny and morphological evidence, our isolates are identified as *C. aquaticum*, and this is the first report of *C. aquaticum* from a coffee host.

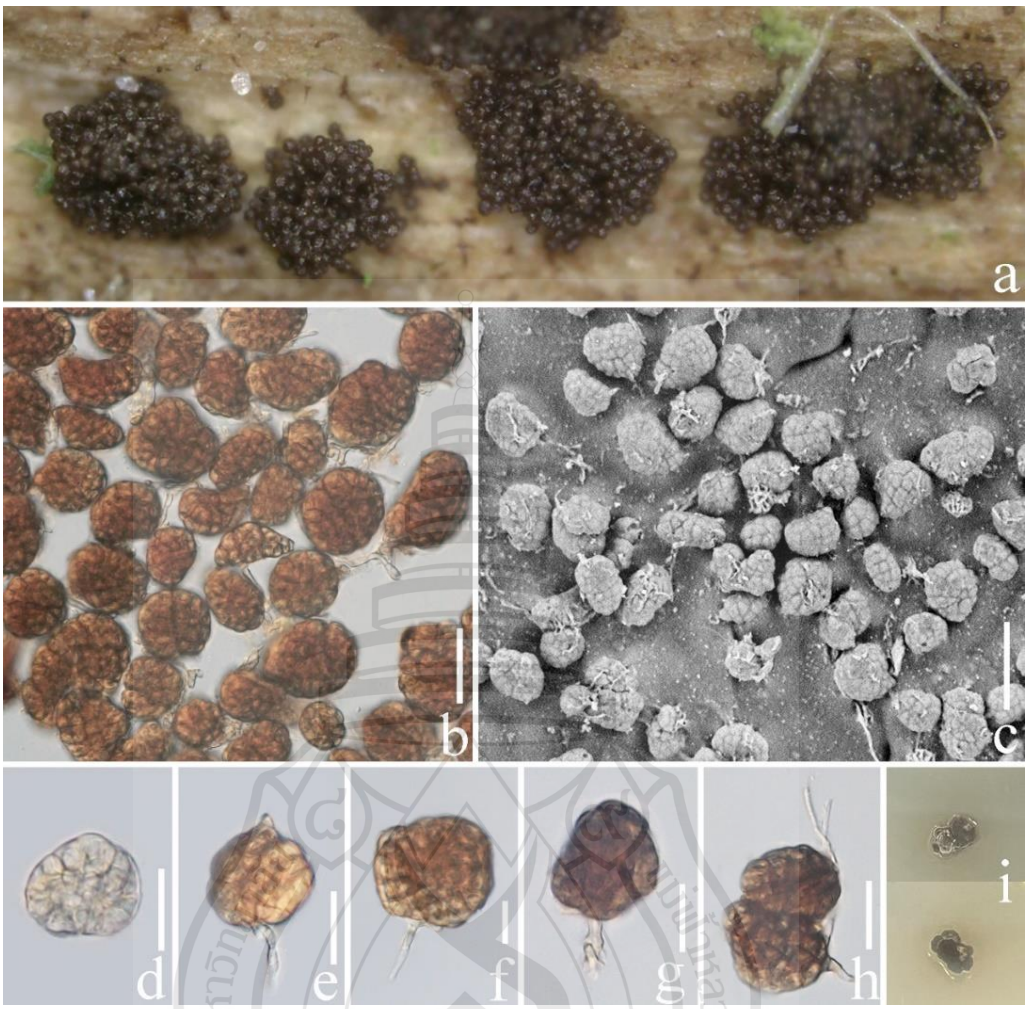


Figure 2.157 *Conlarium aquaticum* (MHZU 24-0516, new host and country record)

Figure 2.157 a Colonies on substrate. b–h Conidia (c: SEM microphotographs of conidia). i Culture on PDA from above and below. Scale bars: b, c = 50 μm, d–h = 20 μm.

Coronophorales Nannf.

Nitschkiaceae (Fitzp.) Nannf.

Fracchiaea Sacc.

Notes: Fracchiaea was introduced by Saccardo (1873) with the type species *F. heterogenea*, based on several collections of material made on branches of *Acer*, *Aesculus*, *Buxus*, *Lonicera,* and *Rhamnus* in Italy (Saccardo, 1873). Later, a few species previously placed in *Sphaeria* were transferred to *Fracchiaea*, and a number of new species were described (Fitzpatrick, 1924). There are 37 epithets in Index Fungorum (2025), however, many species are lack molecular data, until now only *F. broomeana*,

F. heveae, *F. lunata* and *F. myricoides* were sequenced (Huhndorf et al., 2004; Mugambi & Huhndorf, 2010; Bundhun et al., 2021; Senwanna et al., 2021; Huang et al., 2021). This study introduces a new host and country record from coffee plants.

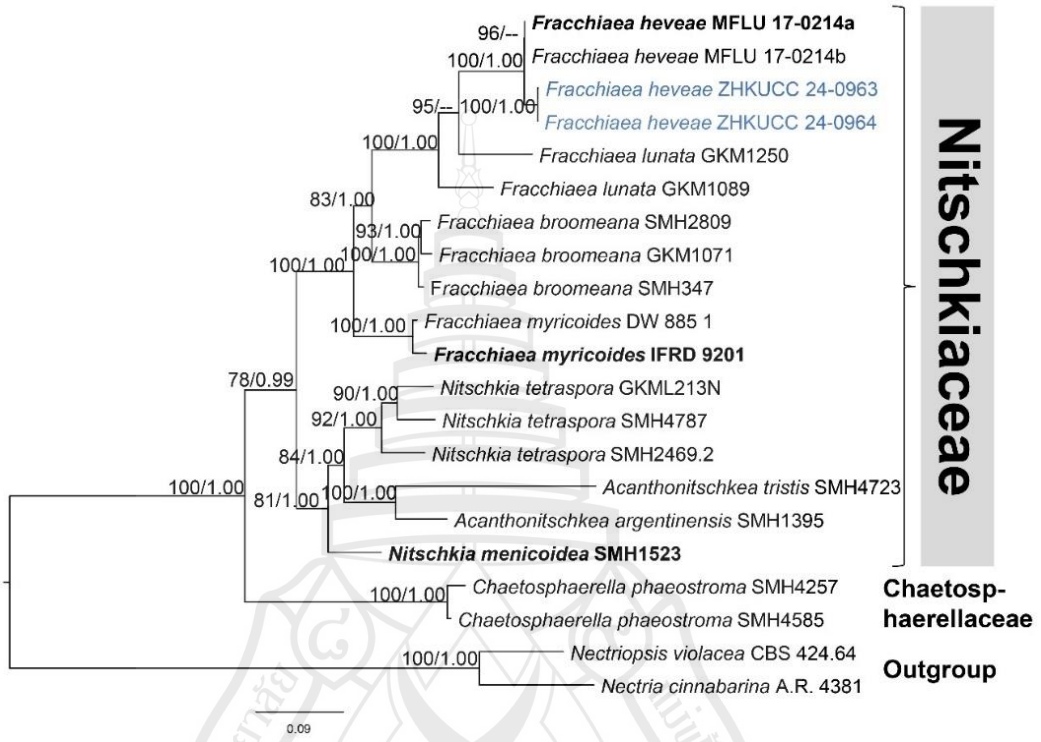


Figure 2.158 Phylogenetic tree of *Fracchiaea*

Figure 2.158 Phylogram generated from maximum likelihood analysis based on a combined dataset of LSU, *RPB*2, and *TEF*1-α sequence data. Twenty-one strains are included in the combined sequence analysis, which comprises 2,547 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Nectria cinnabarina* (A.R. 4381) and *Nectriopsis violacea* (CBS 424.64).

Fracchiaea heveae Senwanna, Cheew. & K.D. Hyde, Mycosphere 12 (1): 1415 (2021)

Index Fungorum number: IF 559364; *Facesoffungi number*: FoF 17595; Figure 2.120

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 300–450 × 350– 450 µm ($\overline{x}$ = 375 × 403 µm, n = 15), superficial or erumpent through the bark of the host, solitary or clustered, globose, black, coriaceous, with pointed spines. Ostioles hardly prominent, with hyaline periphysate. *Peridium* 35–75 µm wide ($\overline{x}$ = 59 µm, n = 30), outer layers thick-walled, dark brown to black, inner layers thin-walled, hyaline, composed of cells of *textura angularis*. *Paraphyses* absent. *Asci* 100–130 × 15–25 µm ($\overline{x}$ = 113 × 18 µm, n = 30), numerous ascospores, unitunicate, thin-walled, clavate to cylindrical, some with a short furcate pedicel, apically rounded, without apical ring. *Ascospores* 13–20 × 2.5–3.5 µm ($\overline{x}$ = 16 × 2.9 µm, n = 30), crowded, hyaline, lunate or cylindrical, with acute ends, curved, aseptate, smooth-walled, with small guttules. **Asexual morph**: Not observed.

Material examined: China, Yunnan Province, Xishuangbanna, on a decaying branch of *Coffea* sp., 25 November 2020, Tibpromma S., XSBN-C16 (MHZU 24-0529), living culture ZHKUCC 24-0963, other living culture ZHKUCC 24-0964.

GenBank numbers: ZHKUCC 24-0963: ITS = PQ608219, LSU = PQ608048, *RPB*2 = PV186805, *TEF*1-α = PQ602101; ZHKUCC 24-0964: ITS = PQ608220, LSU = PQ608049, *RPB*2 = PV186806, *TEF*1-α = PQ602102.

Known hosts: Hevea brasiliensis (Senwanna et al., 2021); *Coffea* sp. (This study).

Known distribution: Thailand (Senwanna et al., 2021); China (This study).

Notes: Fracchiaea heveae was isolated as saprobic on branches of *Hevea brasiliensis* in Thailand (Senwanna et al., 2021). In a BLASTn search, the ITS and LSU sequences of our collection showed 99% similarity to *F. heveae* (MFLU 17-0214). In the present phylogenetic analysis, our strains cluster with *F. heveae* with 100% ML and 1.00 BYPP statistical support (Figure 119. In addition, the morphology of our collection is the same as *F. heveae* in morphological characteristics (Senwanna et al., 2021; Figure 2.120). We, therefore, identified our collection as *F. heveae,* which is a new host record and new country record form *Coffea* sp. in China.

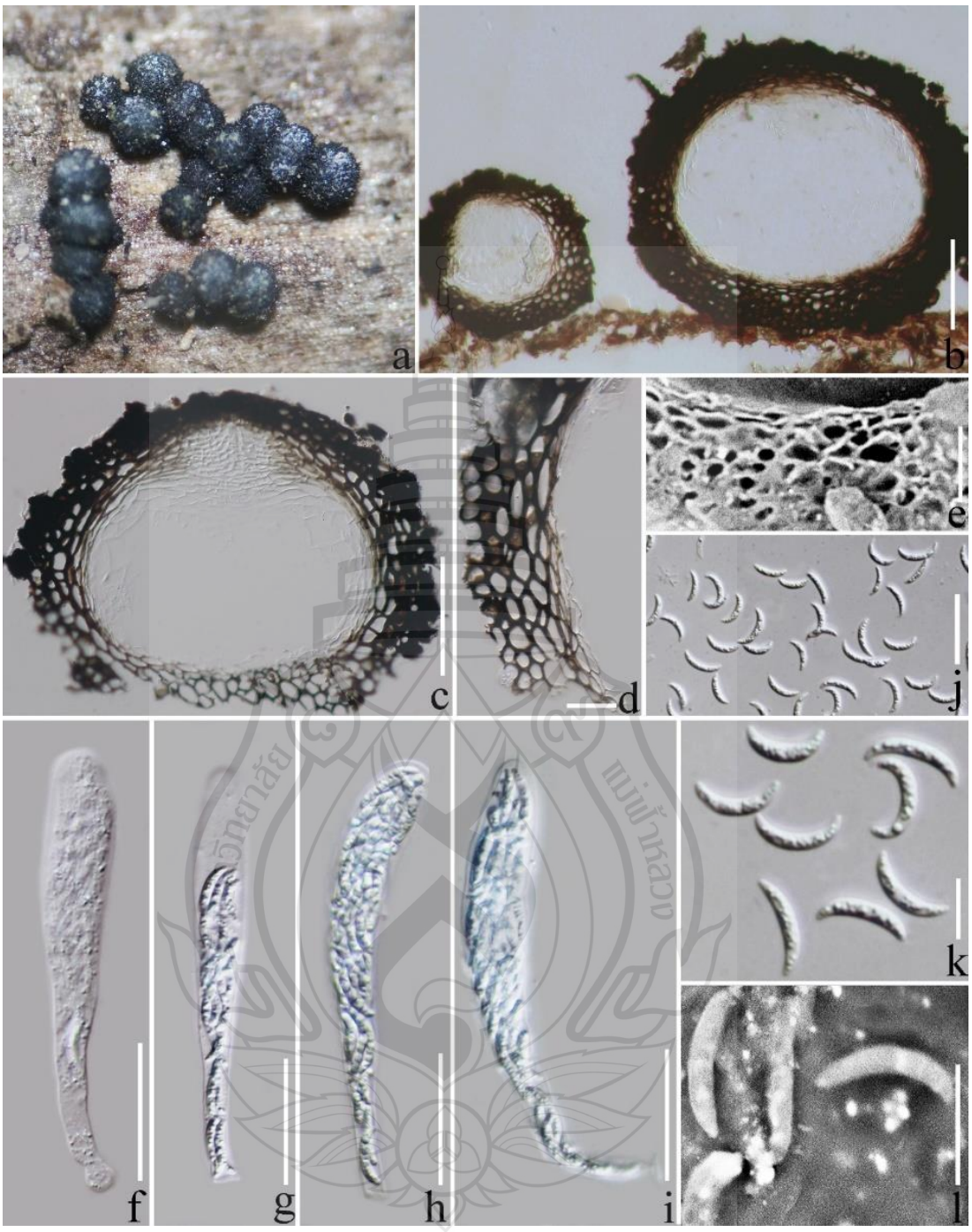


Figure 2.159 *Fracchiaea heveae* (MHZU 24-0529, new host and country record)

Figure 2.159 a Ascomata on a decaying branch of *Coffea* sp. b, c Longitudinal section of ascomata. d, e Peridium (e: SEM microphotographs of peridium). f–i Asci. j–l Ascospores (l: SEM microphotographs of ascospores). Scale bars: b, c = 100 μm, d–j = 30 μm, k, l = 10 μm.

Scortechiniaceae Huhndorf, A.N. Mill. & F.A. Fernández, Mycological Research 108 (12): 1387 (2004)

Neocryptosphaerella S.K. Huang & K.D. Hyde, Mycosphere 12 (1): 935 (2021)

Notes: Neocryptosphaerella was established by Huang et al. (2021) to accommodate *N. celata* (type) and *N. globosa*. The two species had initially been described as *Cryptosphaerella celata* and *C. globosa*, respectively, but they do not group with other *Cryptosphaerella* species in phylogenetic analyses (Mugambi & Huhndorf, 2010). In addition, Huang et al. (2021) found that the morphology of *C. celata* and *C. globosa* can be distinguished from the type of *Cryptosphaerella* by having ascomata lacking ostioles, Quellkörper and polysporous asci with allantoid to cylindrical ascospores, and they moved *C. celata* and *C. globosa* to a new genus *Neocryptosphaerella* in Scortechiniaceae, and the genus *Cryptosphaerella* was excluded from Scortechiniaceae to Sordariomycetes genera *incertae sedis* (Mugambi & Huhndorf, 2010; Huang et al., 2021). Presently, there are only two species deposited in *Neocryptosphaerella* (Index Fungorum, 2025). This study introduces two new *Neocryptosphaerella* species from coffee in Yunnan Province, China.

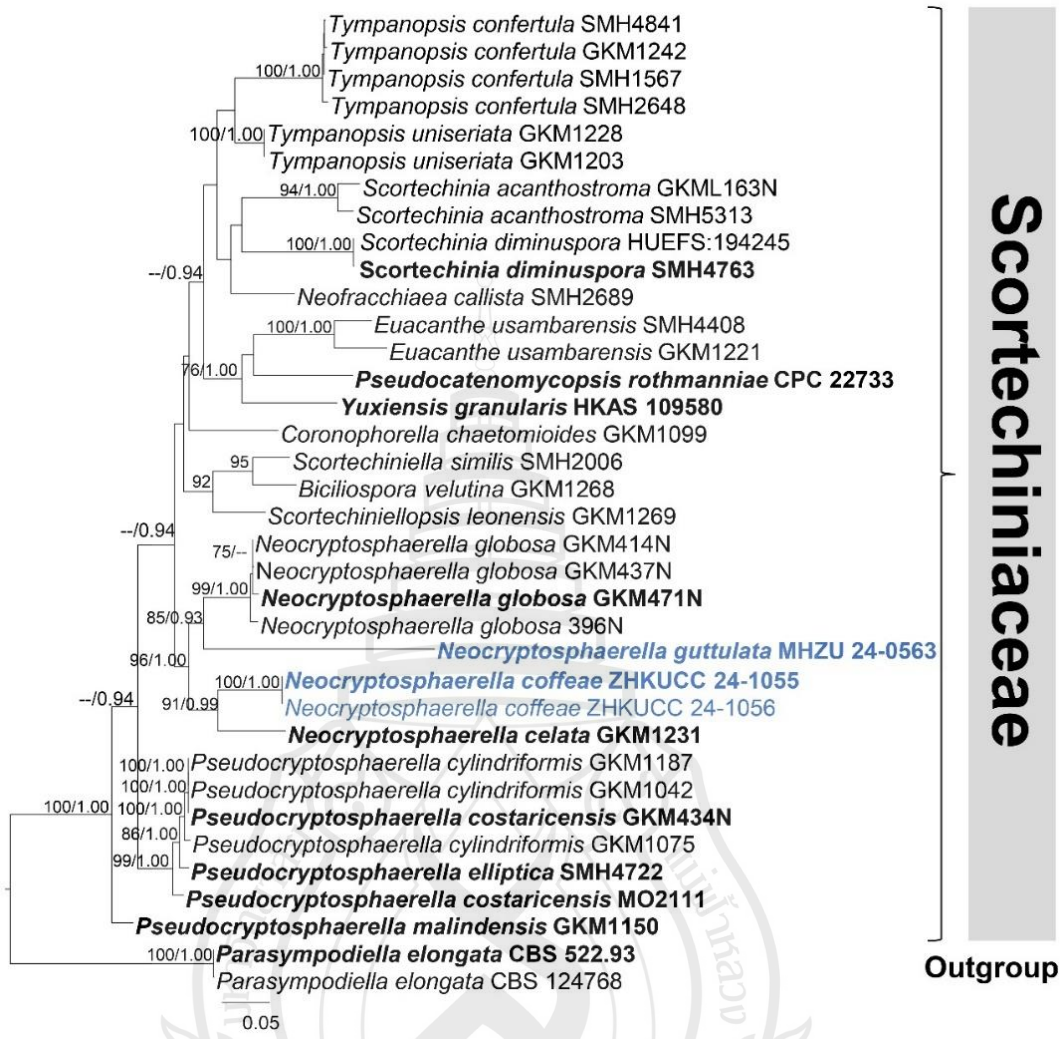


Figure 2.160 Phylogenetic tree of *Neocryptosphaerella*

Figure 2.160 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, and *TEF*1-α sequence data. Thirty-six strains are included in the combined sequence analysis, which comprises 3,437 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Parasympodiella elongata* (CBS 522.93) and *P. elongata* (CBS 124768).

Neocryptosphaerella coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903630*; Facesoffungi number:* FoF 17596*;* Figure 2.122

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0580

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 180–240 × 300–340 µm ($\bar{x}$ = 207 × 323 µm, n = 15), solitary or scattered, semi-immersed to superficial, black, subglobose, turbinate, the apex collapsing when dry, tuberculate, sitting in a subiculum, lacking ostioles, with a central, conical Quellkörper. *Peridium* 30–60 µm wide ($\bar{x}$ = 48 µm, n = 20), thick-walled, heavily pigmented at outermost layer, with dark brown cells, middle layer comprising brown cells of *textura globulosa* to *textura angularis*, innermost layer composed of hyaline, thin-walled cells of *textura prismatica* towards the locule; Munk pores visible. *Paraphyses* absent. *Asci* 80–110 × 7.5–10 µm ($\bar{x}$ = 92 × 8.7 µm, n = 20), 8-spored, unitunicate, clavate, with long pedicel, apex rounded, without apical ring, evanescent. *Ascospores* 9–14 × 3–3.5 µm ($\bar{x}$ = 11 × 3.3 µm, n = 30), bi-seriate or overlapping, hyaline, allantoid to cylindrical, slightly curved, aseptate, smooth-walled, granules almost invisible. **Asexual morph**: Not observed.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* (22.66 N, 100.96 E, 1073 m), 2 February 2024, Li Lu, XAZC-2-2 (MHZU 24-0580, holotype), ex-type ZHKUCC 24-1055, other living culture ZHKUCC 24-1056.

GenBank numbers: ZHKUCC 24-1055: ITS = PQ608221, LSU = PQ608051, *TEF*1-α = PQ602104; ZHKUCC 24-1056: ITS = PQ608222, LSU = PQ608052, *TEF*1-α = PQ602105.

Notes: Based on the phylogenetic analyses of combined ITS, LSU, *TEF*1-α, and *RPB*2 sequence, *Neocryptosphaerella coffeae* forms a sister lineage to *N. celata* (GKM1231, type) (Figure 2.121). The base pair comparison of *N. coffeae* (ZHKUCC 24-1055, ex-type) and *N. celata* (GKM1231, type) shows 25/904 bp (2.7%, without gaps) differences in LSU and 62/700 bp (8.8%, without gaps) differences in *TEF*1-α. Morphologically, *N. coffeae* is similar to *N. celata* in having ascomata with Quellkörpers and Munk pores present in ascomal wall cells, and clavate asci with allantoid to cylindrical ascospores, however, *N. coffeae* is different with *N. celata* by 8-

spored asci and ascospores granules being almost invisible, *N. celata* has polysporous asci and two distinct guttules in the ascospores (Mugambi & Huhndorf, 2010; Huang et al., 2021; Figure 2.122). We, therefore, identified our collection as a new species in *Neocryptosphaerella* (*N. coffeae*).

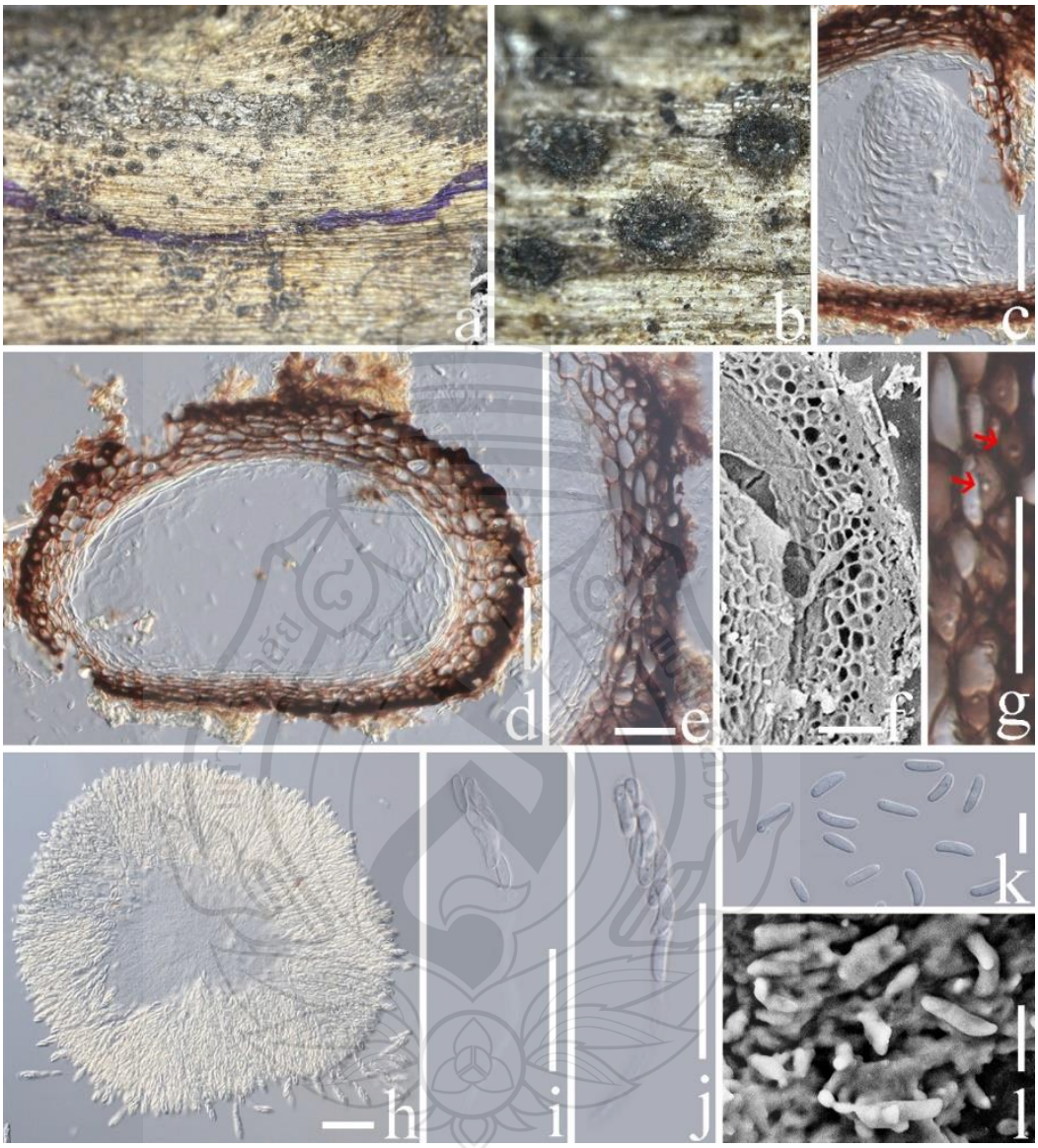


Figure 2.161 *Neocryptosphaerella coffeae* (MHZU 24-0580, holotype)

Figure 2.161 a, b Ascomata on a decaying branch of *Coffea arabica.* c Quellkörper. d Longitudinal section of ascoma. e, f Peridium (f: SEM microphotographs of wall). g Munk pores (arrow). h–j Asci. k, l Conidia (l: SEM microphotographs of conidia). Scale bars: c, d, h = 50 µm, e–g, i, j = 30 µm, k, l = 10 µm.

Neocryptosphaerella guttulata L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903631*; Facesoffungi number:* FoF 17597*;* Figure 2.123

Etymology: The specific epithet refers to the distinctly guttulate ascospores.

Holotype: MHZU 24-0563

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph:** *Ascomata* 200–300 × 300–600 µm ($\bar{x}$ = 237 × 419 µm, n = 15), solitary or scattered, semi-immersed to immersed, black, subglobose or irregular, tuberculate, sitting in a subiculum, lacking ostioles. *Peridium* 40–70 µm wide ($\bar{x}$ = 55 µm, n = 20), thick-walled, outer layer comprising brown to black cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis* to *textura prismatica*; Munk pores visible. *Paraphyses* absent. *Asci* 100–180 × 15–25 µm ($\bar{x}$ = 148 × 20 µm, n = 20), spore-bearing part 50–80 µm, polysporous, arising from a hyaline placenta-like tissue, unitunicate, clavate, long pedicel, apex rounded, without apical ring, evanescent. *Ascospores* 8.5–13 × 3–4 µm ($\bar{x}$ = 11.5 × 3.5 µm, n = 30), overlapping, hyaline, allantoid to oblong, some oval, slightly curved, aseptate, smooth-walled, with distinct guttules. **Asexual morph**: Not observed.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* (22.66 N, 100.96 E, 1073 m), 2 February 2024, Li Lu, XAZC-2-13 (MHZU 24-0563, holotype).

GenBank numbers: MHZU 24-0563: LSU = PQ608050, *TEF*1-α = PQ602103, *RPB*2 = PV186807.

Notes: Based on the multi-gene phylogenetic analyses, *Neocryptosphaerella guttulata* forms a separate lineage to *N. globosa* (396N, GKM414N, GKM437N, and GKM471N, type) with 85% ML, 0.93 BYPP statistical support (Figure 2.121). Morphologically, *N. guttulata* aligns with the general descriptions of *N. globosa*, such as polysporous asci, without apical ring (Mugambi & Huhndorf, 2010; Huang et al., 2021), however, *N. guttulata* can be distinguished by the shape of ascospores, which are allantoid to oblong, occasionally oval, and distinctly guttulate (Figure 2.123). We, therefore, identified our collection as a new species in *Neocryptosphaerella* (*N. guttulata*).

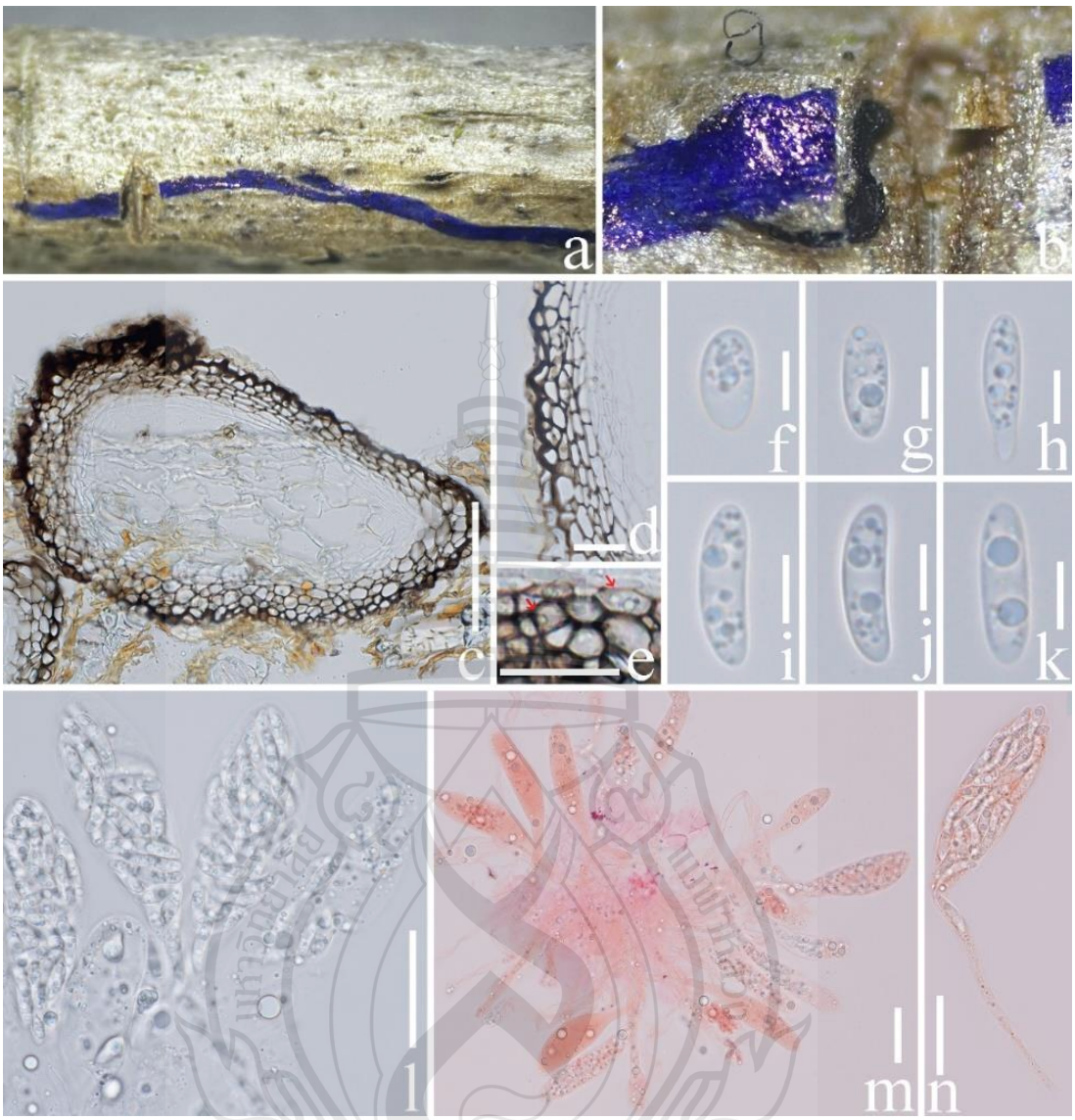


Figure 2.162 *Neocryptosphaerella guttulata* (MHZU 24-0563, holotype)

Figure 2.162 a, b Ascomata on a decaying branch of *Coffea arabica.* c Longitudinal section of ascoma. d Peridium. e Munk pores (arrow). f–k Conidia. l–n Asci (m, n stained with Congo red reagent). Scale bars: c = 100 µm, d, e, l–n = 30 µm, f–k = 5 µm.

Delonicicolales R.H. Perera, Maharachch. & K.D. Hyde

Leptosilliaceae Voglmayr & Jaklitsch, Persoonia 42: 240 (2019)

Leptosillia Höhn., Mitt. bot. Inst. tech. Hochsch. Wien 5: 111 (1928)

Notes: Leptosillia was introduced by Höhnel (1928) with *L. notha* as the type species; 12 epithets are listed in Index Fungorum (2025). *Leptosillia* species can be endophytes isolated from phloem, sapwood of various living, broad-leaf trees, and woody hosts (Voglmayr et al., 2019) or can be saprobic, isolated from dead leaves (Senanayake et al., 2020). The sexual morph of *Leptosillia* is characterized by superficial to semi-immersed ascomata, a peridium of *textura angularis* or *textura prismatica*, clavate to cylindrical or curved to sinuous asci, and falcate, lunate, sinuous, allantoid, sigmoid to hook-shaped, bi to uni-seriate or fasciculately arranged ascospores (Voglmayr et al., 2019). The asexual morph of *Leptosillia* is characterized by having pycnidial, superficial to partly immersed conidiomata, cylindrical to lageniform conidiogenous cells with enteroblastic-phialidic or holoblastic sympodial conidiogenesis and allantoid, falcate, or filiform conidia (Voglmayr et al., 2019). This study introduces a new *Leptosillia* species from a coffee host in China.

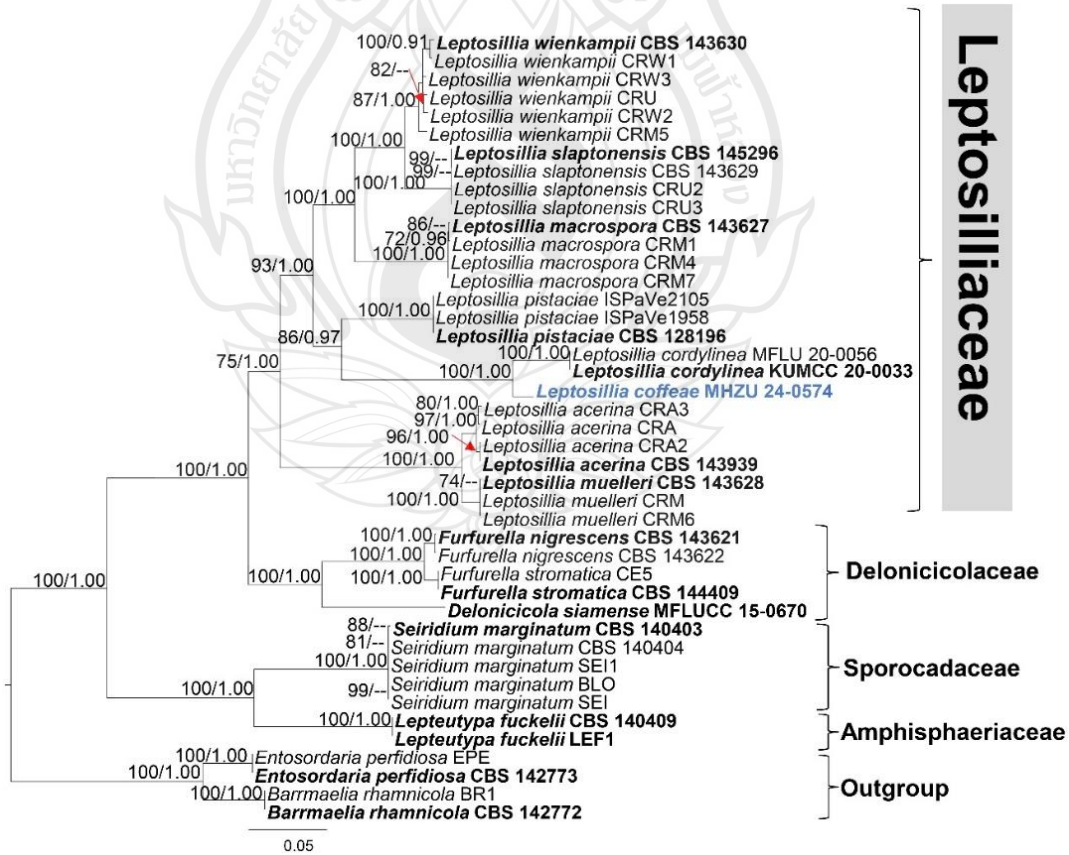


Figure 2.163 Phylogenetic tree of *Leptosillia*

Figure 2.163 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, *TUB*2, and *TEF*1-α sequence data. Forty-three strains are included in the combined sequence analysis, which comprises 4,652 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Barrmaelia rhamnicola* (CBS 142772 and BR1) and *Entosordaria perfidiosa* (EPE and CBS 142772).

Leptosillia coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903616; *Facesoffungi number*: FoF 17598; Figure 2.125

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0574

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 120–180 × 100–240 µm, ($\bar{x}$ = 148 × 170 µm, n = 15), subglobose to globose, immersed, as black spots on the host surface, slightly raised, solitary or aggregated, uniloculate, without papilla and ostiole. *Peridium* 15–25 µm wide ($\bar{x}$ = 20.5 µm, n = 20), thick-walled, composed of several brown outer layer cells of *textura angularis*, with hyaline inner cells of *textura angularis*. *Hamathecium* of 1.5–2.5 µm wide ($\bar{x}$ = 2, n = 20), hyaline, unbranched, granulate, aseptate, filamentous, paraphyses. *Asci* 40–65 × 6–7.5 µm ($\bar{x}$ = 55 × 6.5 µm, n = 20), 8-spored, cylindrical to clavate, apically rounded, pedicellate. *Ascospores* 8.5–12 × 2.5–4 µm, ($\bar{x}$ = 10.3 × 3.2 µm, n = 30), 1–2-seriate, overlapping, hyaline, inequilateral or cylindrical, aseptate, one-celled, with guttules, thick-walled. **Asexual morph**: Not observed.

Material examined: China, Yunnan Province, Jinghong City, on a decaying branch of *Coffea* sp., 15 September 2021, Li Lu, JHPW5 (MHZU 24-0574, holotype).

GenBank numbers: MHZU 24-0574: ITS = PQ608364, LSU = PQ608190, *RPB*2 = PV367533, *TEF*1-α = PQ628195.

Notes: Based on phylogenetic analyses of combined ITS, LSU, *TEF*1-α, *TUB*2, and *RPB*2, the new strain (MHZU 24-0574) clustered within *Leptosillia* and formed a separate lineage with *L. cordylinea* (KUMCC 20-0033 and MFLU 20-0056, type) (Figure 2.124). *Leptosillia cordylinea* was discovered as an asexual morph from

Cordyline fruticosa in Guangdong Province, China (Senanayake et al., 2020). While our isolates (*Leptosillia coffeae*) have sexual morph, thus, the morphological differences between *L. cordylinea* and *L. coffeae* cannot be compared (Figure 2.125). The base pair comparison of *L. coffeae* (MHZU 24-0574, holotype) and *L. cordylinea* (MFLU 20-0056, type) shows 29/619 bp differences in ITS (4.6%, without gaps), 54/897 bp differences in LSU (6%, gaps 6 bp), 7/1,129 bp differences in *RPB*2 (0.6%, gaps 6 bp), 110/1,003 bp differences in LSU (10.9%, gaps 3 bp). Therefore, we introduce *L. coffeae* as a new species based on morphology and multigene phylogenetic analysis. This is the first time this genus is isolated from *Coffea* sp.

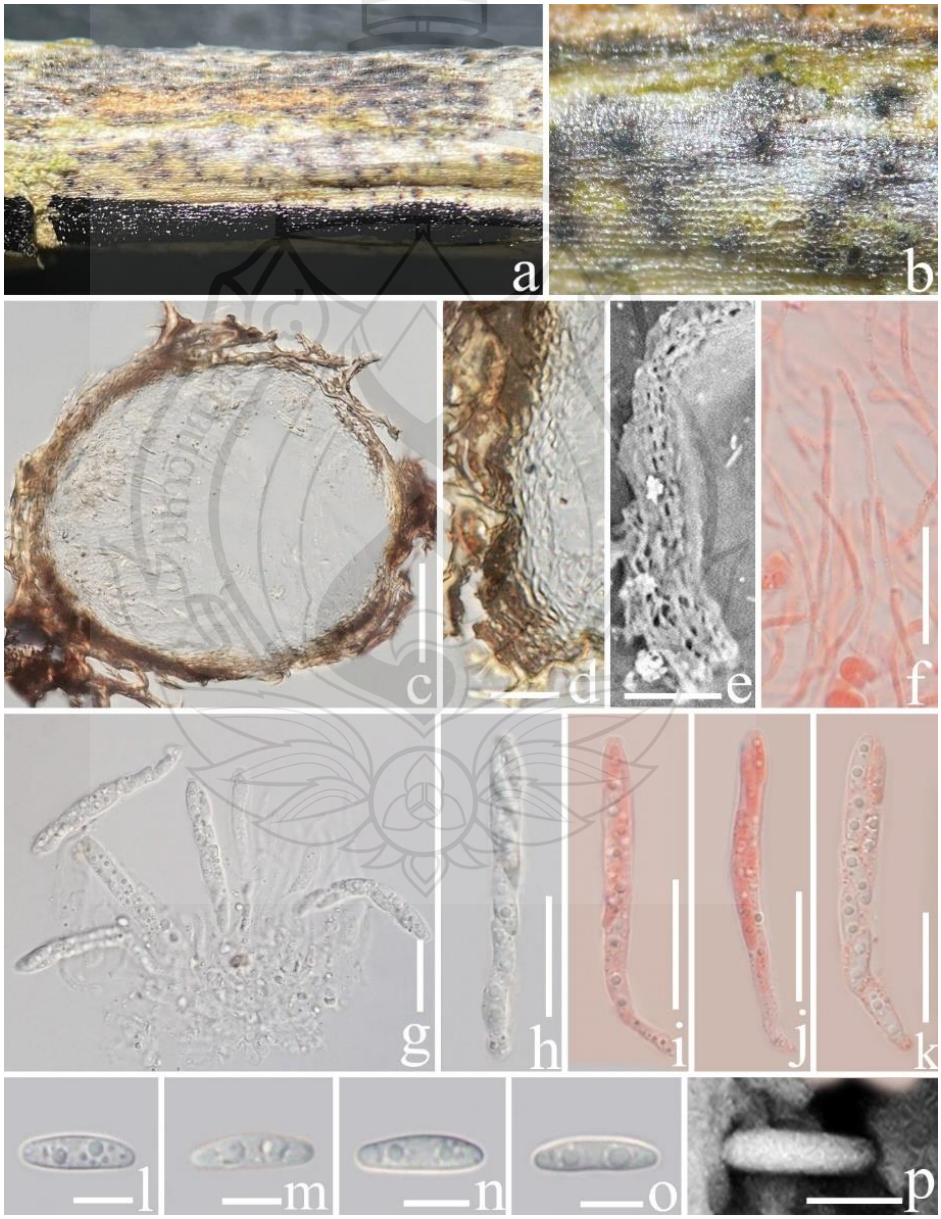


Figure 2.164 *Leptosillia coffeae* (MHZU 24-0574, holotype)

Figure 2.164 a, b Appearance of ascomata on substrate. c Vertical section through ascoma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium (stained with Congo red reagent). g–k Asci (i–k strained with Congo red reagent). l–p Ascospores (p: SEM microphotographs of ascospore). Scale bars: c = 50 µm, d–k = 20 µm, l–p = 5 µm.

Diaporthales Nannf.

Cytosporaceae H. Zhang, K.D. Hyde & Maharachch - Fungal Diversity 85: 75–110. (2017)

Cytospora Ehrenb.,Sylv.Mycol.Berol.(Berlin):28.1818

Notes: *Cytospora* was introduced by Ehrenberg (1818), with *C. chrysosperma* designated as the type species. The taxonomy and correspondence between the sexual and asexual morphs of *Cytospora* remain ambiguous (Jia et al., 2024). Following the "one fungus, one name" principle (Wingfield et al., 2012), *Cytospora* was proposed by Fan et al. (2015a, 2015b) and Rossman et al. (2015) as the correct name, with priority over *Leucostoma*, *Leucocytospora*, *Valsa*, *Valsella*, and *Valseutypella*. Most *Cytospora* species are important pathogens causing canker and dieback disease in a wide range of plants (Adams et al., 2005, 2006; Hyde et al., 2016; Norphanphoun et al., 2017; Fan et al., 2020). A total of 770 species are listed in *Cytospora* (Index Fungorum, 2025). This study introduces a new *Cytospora* species from a coffee host in China.

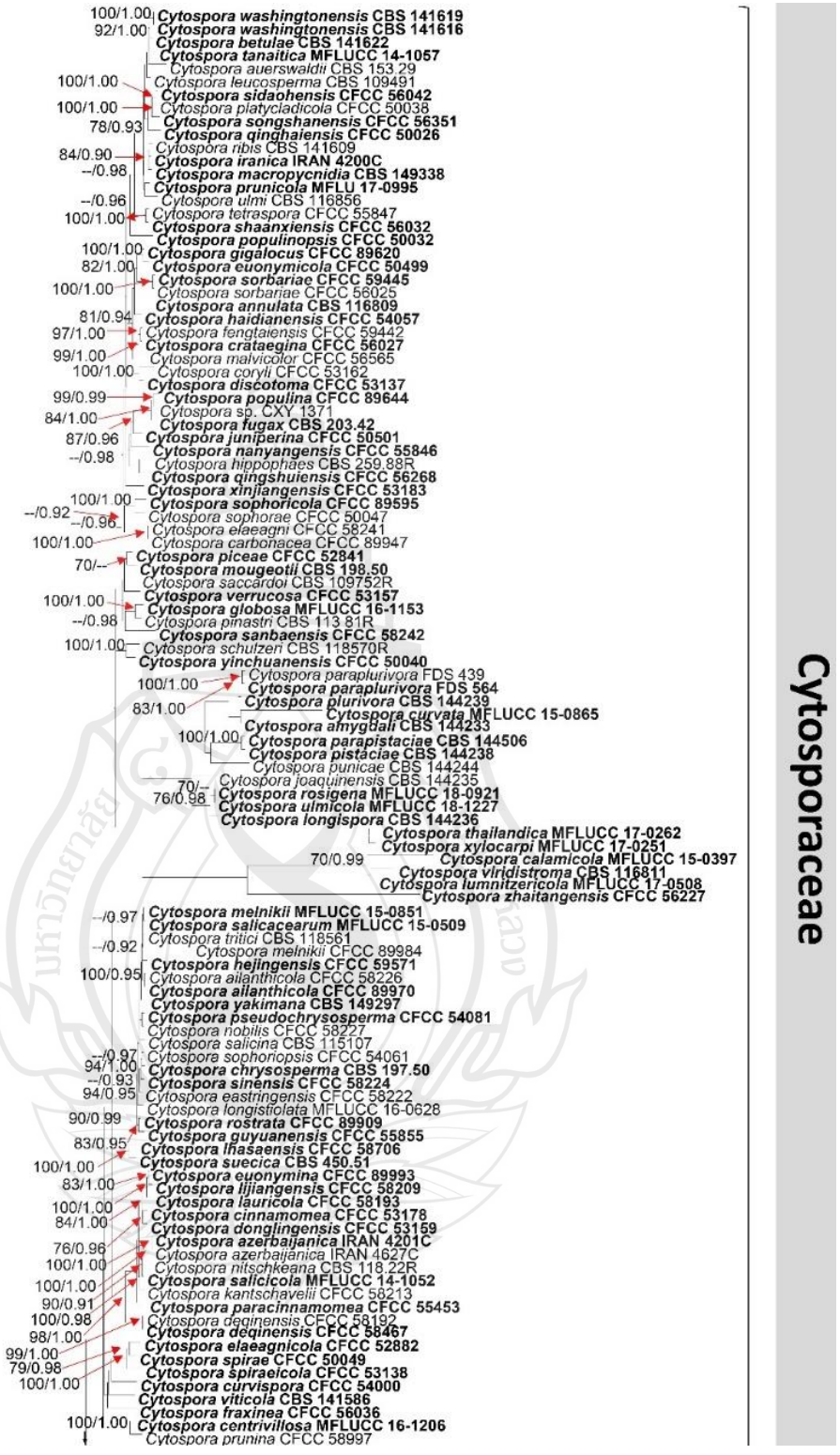


Figure 2.165 Phylogenetic tree of *Cytospora*

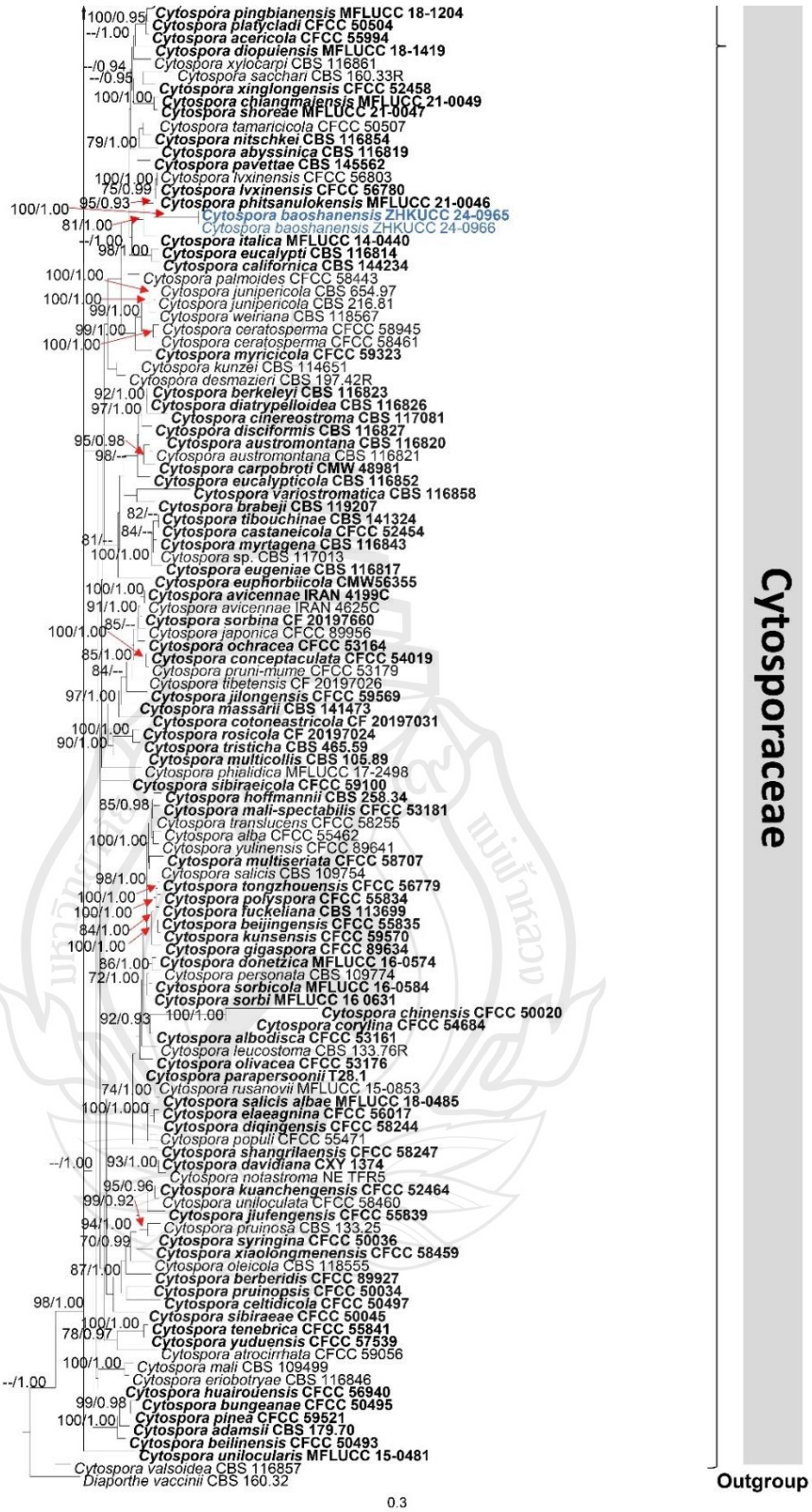


Figure 2.165 (continued)

Figure 2.165 Phylogram generated from maximum likelihood analysis based on a combined dataset of ACT1, LSU, *RPB*2, *TEF*1-α, and *TUB*2 sequence data. Two hundred twenty-six strains are included in the combined sequence analysis, which comprises 2,459 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Diaporthe vaccinii* (CBS 160.32).

Cytospora baoshanensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903608; *Facesoffungi number*: FoF 17599; Figure 2.127

Etymology: The species epithet refers to the type location "Baoshan", China.

Holotype: MHZU 24-0530

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata pycnidial* 150–300 × 150–320 μm ($\bar{x}$ = 200 × 230 μm, n=20), rosette, labyrinthine cytosporoid, solitary to aggregated, forming aggregated black convex papillae at the area of dehiscence, area below disc a lighter entostroma, immersed, luteous to charcoal. *Conceptacle* absent. *Ectostromatic disc* grey to brown, circular to ovoid, producing 1–4-ostioles per disc when mature. *Ostioles* in the centre of the disc, numerous, dark brown to charcoal, conspicuous, circular to ovoid, at the same level as the disc surface. *Locules* subdivided frequently by invaginations with independent walls, 2–6 loculate, circular to ovoid. *Peridium* 10–16 μm wide ($\bar{x}$ = 13 μm, n=20), comprising small, thick-walled, brown cells of *textura angularis*. *Conidiophores* 10–23 × 1.5–2.5 μm ($\bar{x}$ = 16.8 × 1.9 μm, n=20), hyaline, thin-walled, filamentous, borne on hymenial layer inner cavity, branched irregularly at the base and above. *Conidiogenous cells* enteroblastic, polyphialidic, subcylindrical to cylindrical, integrated or discrete, determinate, tapering towards the apices. *Conidia* 4–6 × 1–1.8 μm ($\bar{x}$ = 5 × 1.5 μm, n=20), hyaline, elongate allantoid, aseptate, smooth, and thin-walled.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, circular, slightly raised, fluffy surface with entire edge and white colony, from below whitish cream.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS3-C1 (MHZU 24-0530, holotype), ex-type ZHKUCC 24-0965, other living culture ZHKUCC 24-0966.

GenBank numbers: ZHKUCC 24-0965: ACT = PQ572168, ITS = PQ608223, LSU = PQ608053, *RPB*2 = PV186808, *TUB*2 = PQ572183, *TEF*1-α = PQ602106; ZHKUCC 24-0966: ACT = PQ572169, ITS = PQ608224, LSU = PQ608054, *RPB*2 = PV186809, *TUB*2 = PQ572184, *TEF*1-α = PQ602107.

Notes: Phylogenetically, *Cytospora baoshanensis* forms a distinct lineage to *C. phitsanulokensis* (MFLUCC 21-0046, ex-type) with 95% ML and 0.93 BYPP statistical support (Figure 2.126). Morphologically, *Cytospora baoshanensis* has a conspicuous dark brown to charcoal ostiole, and *C. phitsanulokensis* shows an inconspicuous ostioles (Monkai et al., 2021). In addition, *Cytospora baoshanensis* is distinguished from *C. phitsanulokensis* by its branched conidiophores (Monkai et al., 2021; Figure 2.127). Based on phylogenetic and morphological evidence, we describe a new species, *Cytospora baoshanensis*, found on *Coffea* sp. from China.

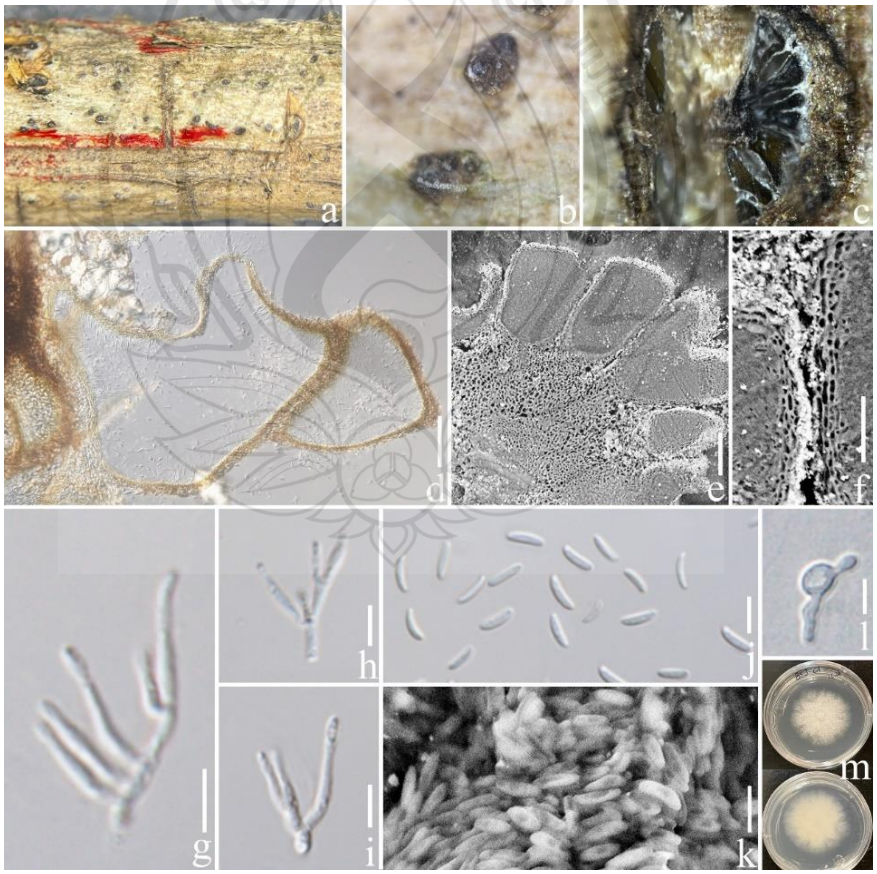


Figure 2.166 *Cytospora baoshanensis* (MHZU 24-0530, holotype)

Figure 2.166 a, b Conidiomata on substrate. c–e Vertical cross-sections of conidiomata (e: SEM microphotographs of section of conidiomata). f SEM microphotographs of peridium. g–i Conidiophore and conidiogenous cells. j, k Conidia (k: SEM microphotographs of conidia). l Germinated conidium. m Culture on PDA from above and below. Scale bars: d, e = 50 μm, f = 20 μm, g–l = 5 μm.

Erythrogloeaceae Senan., Maharachch. & K.D. Hyde, Studies in Mycology 86: 258 (2017)

Dendrostoma X.L. Fan & C.M. Tian, Persoonia 40: 124 (2018)

Notes: Dendrostoma was proposed by Fan et al. (2018) to accommodate three species and placed in Erythrogloeaceae, Diaporthales (Hyde et al., 2020). *Dendrostoma mali* as the type species and reported from *Malus spectabilis*, together with two other species, *D. osmanthi* and *D. quercinum* (Fan et al., 2018). Species of *Dendrostoma* are all known and described from symptomatic tissues, while the pathogenicity has not been confirmed (Chen et al., 2022). *Dendrostoma* is the only genus of *Erythrogloeaceae* for which both sexual and asexual morphs are reported. The sexual morphs of *Dendrostoma* are characterized by having erumpent pseudostromata, usually an orange ectostromatic disc, semi-immersed to superficial, causing a pustulate bark surface, deliquescent paraphyses, fusoid, 8-spored, asci, with an apical ring, becoming detached from the perithecial wall, and hyaline, bicellular, fusoid to cylindrical, multiguttulate, septate, 2–3-seriate ascospores, which are constricted at the septum. The asexual morph is characterized by acervular conidiomata, with subcylindrical to ampulliform conidiogenous cells and hyaline to olivaceous, aseptate conidia (Fan et al., 2018; Jiang et al., 2019; Chen et al., 2022). A total of 25 species are listed in Index Fungorum (2025). This study introduces a new *Dendrostoma* species, it is the first *Dendrostoma* species collected from a coffee host from China.

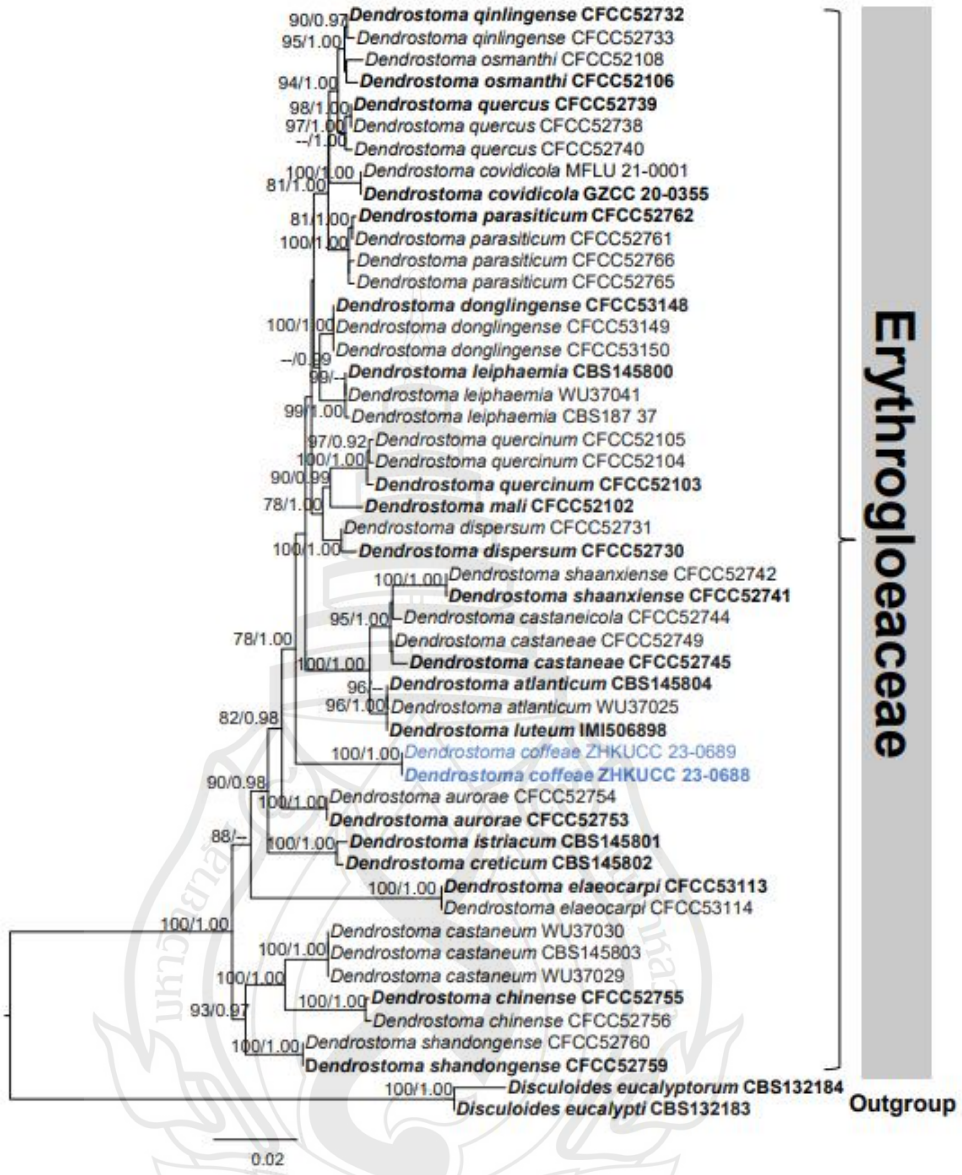


Figure 2.167 Phylogenetic tree of *Dendrostoma*

Figure 2.167 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, and *TEF*1-αsequence data. Fifty strains are included in the combined sequence analysis, which comprises 2,563 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Disculoides eucalyptorum* (CBS132184) and *Disculoides eucalypti* (CBS132183).

Dendrostoma coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903610; *Facesoffungi number*: FoF 17600; Figure 2.129

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 23-0089

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Stromata* erumpent, distinct, up to 200–300 μm high, 350–650 μm diam., immersed to semi-immersed, black, causing a pustulate bark surface. *Conidiomata* 200–300 × 100–300 μm ($\overline{x}$ = 237 × 189 μm, n = 15), loculate, 1–3 locules gregariously immersed in the stromata, pycnidial, conical or irregular, surrounded by bark flaps. *Conidiomata wall* 15–25 μm wide ($\overline{x}$ = 20 μm, n = 20), comprising several layers of hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 2–4 μm ($\overline{x}$ = 7.5 × 2.8 μm, n = 20), enteroblastic, lining the inner walls of the cavity, hyaline, subcylindrical to ampulliform. *Conidia* 5–8 × 2–3 μm ($\overline{x}$ = 6.5 × 2.3 μm, n = 20), hyaline, ellipsoid or fusiform, both ends apex acutely rounded or truncate, straight, aseptate, multiguttulate, smooth and thin-walled.

Culture characteristics: Conidia germinating on PDA within 24 h, germ tubes produced from the apical cell of conidia. Colonies growing on PDA, reaching 20–30 mm in two months at 25°C, surface rough, flat, circular and entire margin, wrinkled, from above, olive yellow, from below, dark brown.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC20 (MHZU 23-0089, holotype), ex-type ZHKUCC 23-0688, other living culture ZHKUCC 23-0689.

GenBank numbers: ZHKUCC 23-0688: ITS = PQ608225, LSU = PQ608055, *RPB*2 = PV186810, *TEF*1-α = PQ602108; ZHKUCC 23-0689: ITS = PQ608226, LSU = PQ608056, *RPB*2 = PV186811, *TEF*1-α = PQ602109.

Notes: Based on the phylogenetic analysis of combined LSU, ITS, *TEF*1-α, and *RPB*2 sequence data, the new strains of *Dendrostoma coffeae* (ZHKUCC 23-0688 and ZHKUCC 23-0689) form an independent lineage within *Dendrostoma* with 78% ML and 1.00 BYPP statistical support (Figure 2.128). *Dendrostoma coffeae* represents the first report from *Coffea arabica*. Morphologically, Jiang et al. (2019) summarized

the asexual characteristics of *Dendrostoma*; *D. coffeae* can be distinguished from other asexual species by black stromata, loculate, and small conidiomata (Jiang et al., 2019; Figure 2.129). Therefore, we introduce *D. coffeae* as a new species with morphological characteristics and phylogenetic analyses.

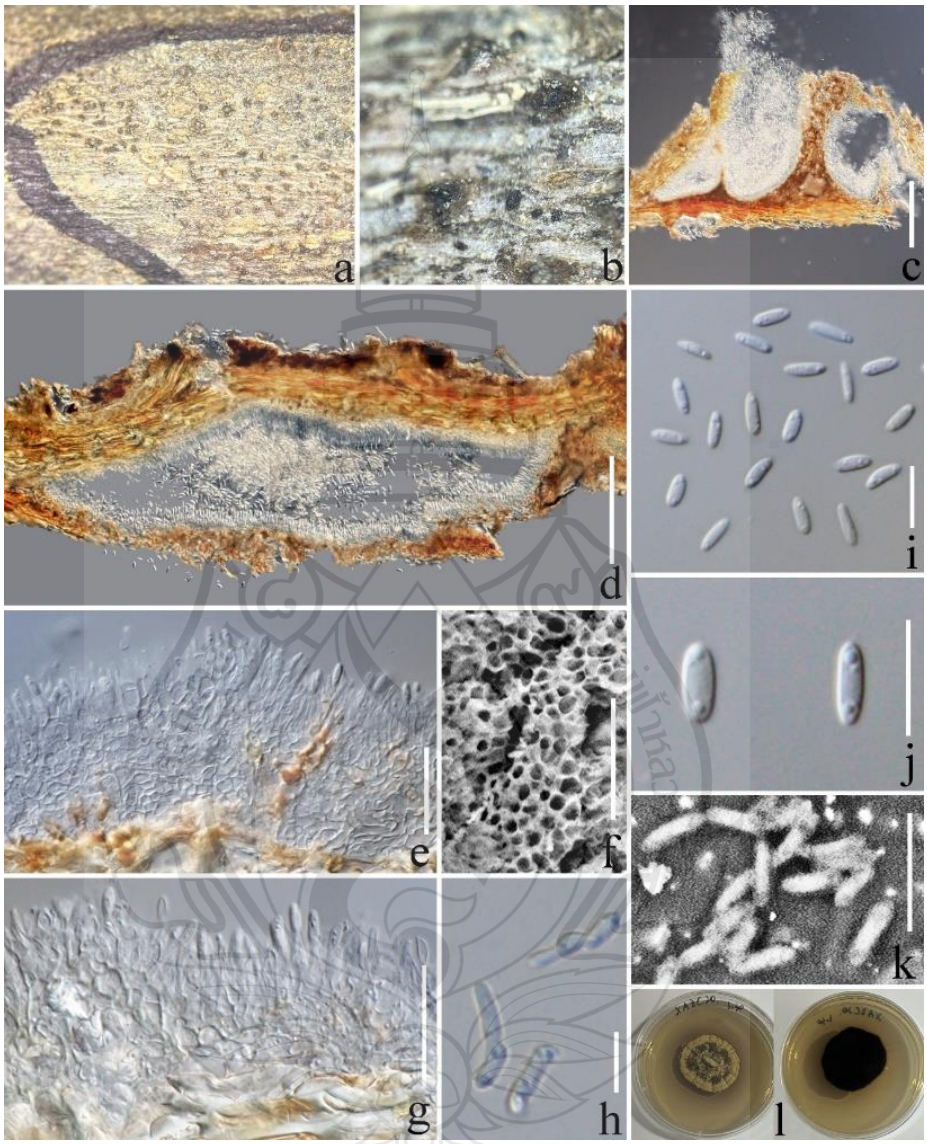


Figure 2.168 *Dendrostoma coffeae* (MHZU 23-0089, holotype)

Figure 2.168 a, b Conidiomata on host surface. c, d Longitudinal sections through conidiomata. e–g Conidiomata wall and conidiogenous cells with conidia (f: SEM microphotographs of conidiomata wall). h Germinated conidia. i–k Conidia (k: SEM microphotographs of conidia). l Culture on PDA from above and below. Scale bars: c, d = 100 µm, e–g = 20 µm, h–k = 10 µm.

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 99: 482 (2019)

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

Distoseptispora K.D. Hyde, McKenzie, Maharachch. Fungal Diversity 80:375–409 (2016)

Notes: *Distoseptispora* was introduced by Su et al. (2016) to accommodate species segregated from *Sporidesmium*, with *D. fluminicola* as the type species. *Distoseptispora* species are characterized by relatively short conidiophores and long, cylindrical, darker conidia with slightly paler, rounded apices (Su et al., 2016; Luo et al., 2019). Phylogenetic analyses support the separation of *Distoseptispora* and *Sporidesmium*, placing *Distoseptispora* in Distoseptisporaceae and *Sporidesmium* in Sporidesmiaceae, respectively (Monkai et al., 2020; Hyde et al., 2020). Therefore, many *Distoseptispora* species were previously identified as *Sporidesmium* (Tsui et al., 2000; Luo et al., 2004). Yang et al. (2021) reported *D. hyalina* as the first sexual morph of the genus, characterized by perithecial, subglobose to ellipsoidal, ostiolate, dark brown ascomata and hyaline, 0–3-septate ascospores with a mucilaginous sheath. Asexual morphs in the genus are typically hyphomycetous, characterized by macronematous, unbranched conidiophores, and cylindrical or clavate conidiogenous cells producing acrogenous, cylindrical, or obclavate conidia. There are 84 species listed under *Distoseptispora* (Index Fungorum, 2025), with species commonly found in freshwater habitats in China and Thailand (Su et al., 2016; Luo et al., 2018, 2019; Yang et al., 2018; Hyde et al., 2019, 2020; Shen et al., 2021; Yang et al., 2021; Ma et al., 2022; Zhai et al., 2022; Liu et al., 2023). This study introduces a new host record from coffee.

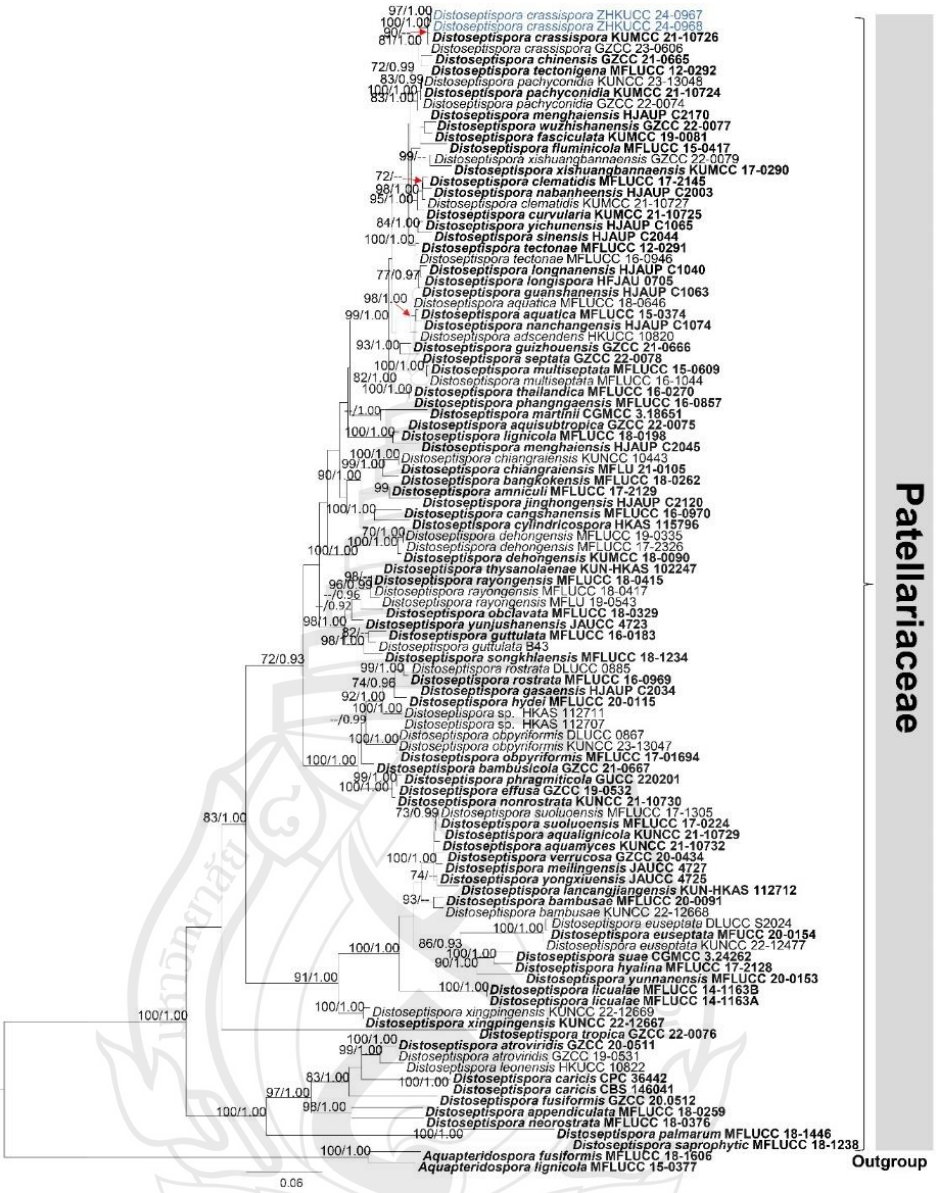


Figure 2.169 Phylogenetic tree of *Distoseptispora*

Figure 2.169 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, and *TEF*1-α sequence data. One hundred and five strains are included in the combined sequence analysis, which comprises 3,067 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Aquapteridospora fusiformis* (MFLUCC 18–1606) and *A. lignicola* (MFLUCC 15–0377).

Distoseptispora crassispora R. Zhu & H. Zhang. Journal of Fungi, 8(10), 1063. (2022)

Index Fungorum number: IF 559920; *Facesoffungi number*: FoF 12577; Figure 2.131

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on the substratum superficial, effuse, scattered, erect, hairy, dark olive. *Mycelium* mostly immersed, composed of branched, septate, smooth, dark-brown to olive hyphae. *Conidiophores* 12–40 × 5–8 μm ($\overline{x}$ = 28 × 6.8 μm, n = 20), macronematous, mononematous, unbranched, septate, cylindrical, straight or flexuous, 1–3-septate, smooth, brown, robust at the base. *Conidiogenous cells* 5–10 × 4–7 μm ($\overline{x}$ = 7 × 5 μm, n = 20), monoblastic, integrated, determinate, terminal, cylindrical, brown, smooth-walled. *Conidia* 60–350 μm long ($\overline{x}$ = 281 μm, n=30) (rostrum included), 8–13 μm at the widest part ($\overline{x}$ = 11.6 μm, n=30), 4–7.5 μm wide at the apex ($\overline{x}$ = 5.6 m, n =30), acrogenous, obclavate, rarely oblong, rostrate, mostly curved, 8–32 distoseptate, partially perforated septum, truncate at the base, rounded at the apex, smooth and thick-walled, olive with a brown tinge.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, circular, aerial mycelium dense, slate-gray, from below dark-brown, with entire, dark margin.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April. 2024, Li Lu, DH3-11 (MHZU 24-0531), living culture ZHKUCC 24-0967, other living culture ZHKUCC 24-0968.

GenBank numbers: ZHKUCC 24-0967: ITS = PQ608227, LSU = PQ608057, *TEF*1-α = PQ602110; ZHKUCC 24-0968: ITS = PQ608228, LSU = PQ608058, *TEF*1-α = PQ602111.

Known hosts: Decaying, submerged wood in freshwater (Zhang et al., 2022), *Coffea* sp. (This study).

Known distribution: China (Zhang et al., 2022; This study).

Notes: Distoseptispora crassispora was introduced by Zhang et al. (2022) and collected from decaying wood submerged in unidentified hosts in freshwater in China. In the phylogenetic tree, our isolates developed a sister lineage to *D. crassispora* with 100% ML and 1.00 BYPP bootstrap support (Figure 2.130), which was collected

from *Coffea* sp. from China. Based on nucleotide comparisons, our isolates (ZHKUCC 24-0967) are nearly the same as *D. crassispora* (KUNCC 12–10726, ex-type) by 2/547 bp (0.4%, without gaps) in ITS, 5/948 bp (0.5%, without gaps) in TEF1-α, and identical in LSU. Morphologically, our collection fits well with the *D. crassispora* description (Zhang et al., 2022; Figure 2.131). Combining both phylogeny and morphological evidence, our collection was identified as *D. crassispora*, and this is the first time this species was found from the coffee host.

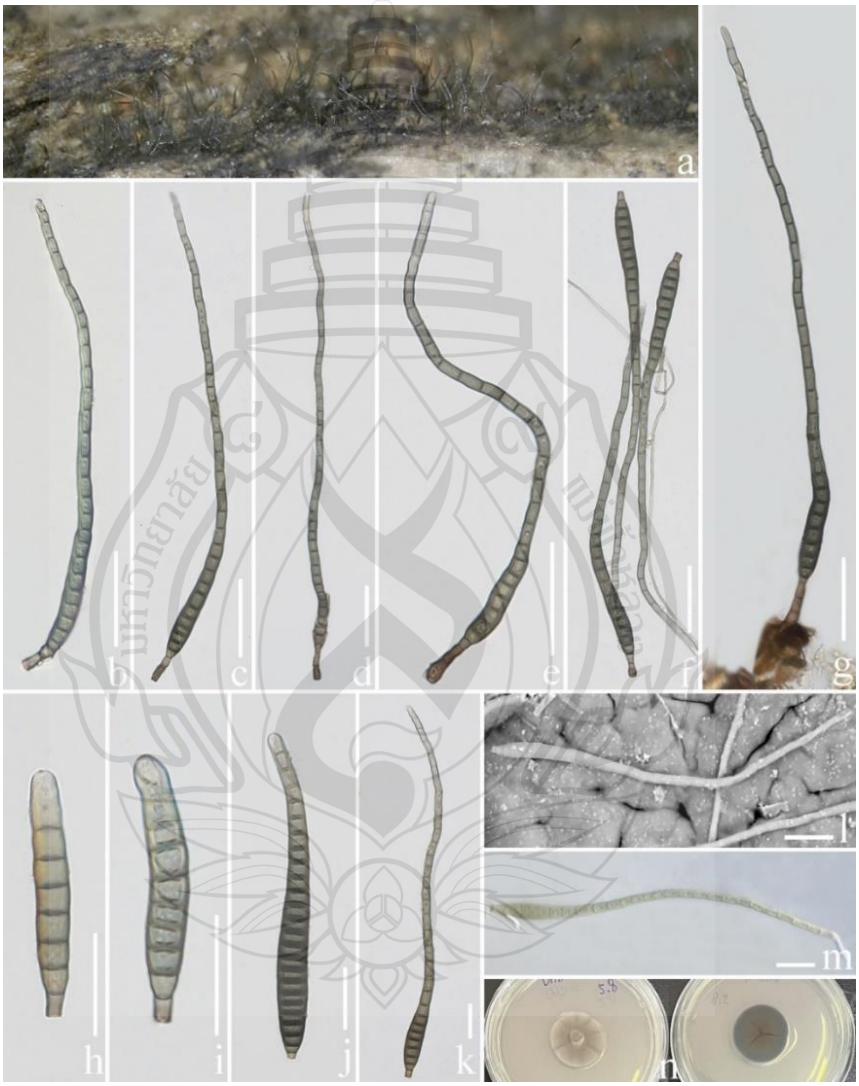


Figure 2.170 *Distoseptispora crassispora* (MHZU 24-0531, new host record)

Figure 2.170 a Colonies on substrate. b–g Conidiophore or conidiogenous cells with conidia. h–l Conidia (l: SEM microphotographs of conidia). m Germinated conidium. n Culture on PDA from above and below. Scale bars: b–g = 50 μm, h–m = 30 μm.

Glomerellales Chadef. ex Réblová, W. Gams & Seifert, Studies in Mycology 68: 170 (2011)

Plectosphaerellaceae W. Gams, Summerbell & Zare, Nova Hedwigia 85 (3-4): 476 (2007)

Acrostalagmus Corda, Icon. fung. (Prague) 2: 15 (1838).

Notes: Acrostalagmus was introduced by Corda (1838) and typified by *A. luteoalbus*, which is described as having mononematous or synnematous conidiophores, enteroblastic, monophialidic conidiogenous cells, and hyaline or bright orange to reddish, oval, ellipsoidal to oblong-ellipsoidal conidia, held together by slime (Corda, 1838; Giraldo & Crous, 2019; Zare et al., 2004). Zare et al. (2004) refuted the previously established asexual-sexual link for *Acrostalagmus* through an integrative approach combining morphological characteristics, substrate associations, and phylogenetic analyses, therefore, the sexual morph of *Acrostalagmus* remains undetermined (Hyde et al., 2020). *Acrostalagmus* is a widespread genus, with 55 epithets recorded in Index Fungorum (2025); most species have been moved to another genus and only contains 13 species (Hyde et al., 2024a). In addition, *Acrostalagmus* species is known for the ability to produce numerous bioactive natural products, making it valuable in drug development (Shi et al., 2023). This study introduces a new host record of *Acrostalagmus annulatus* collected from a coffee host in Thailand.

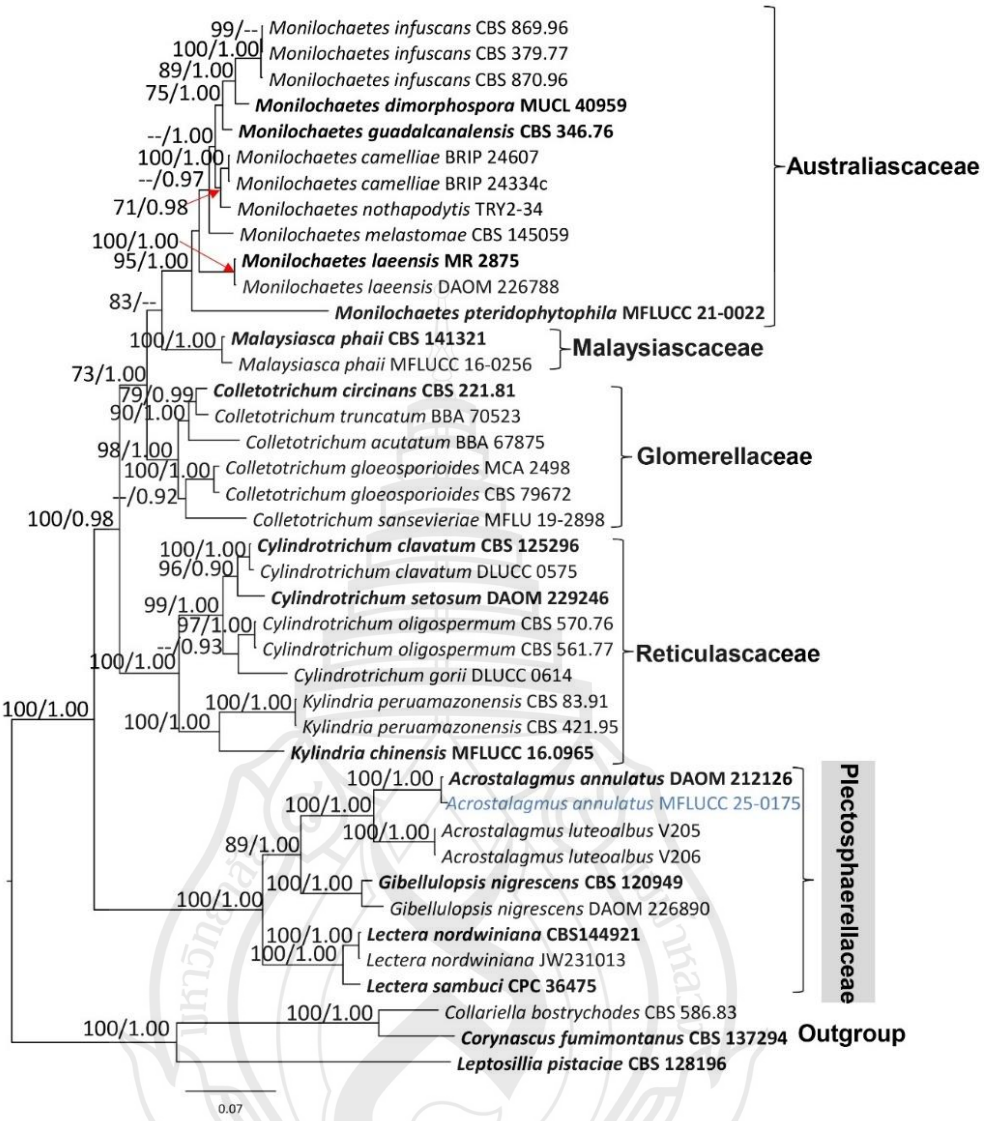


Figure 2.171 Phylogenetic tree of *Acrostalagmus*

Figure 2.171 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU and *RPB*2 sequence data. Forty-one strains are included in the combined sequence analysis, which comprises 3,681 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Collariella bostrychodes* (CBS 586.83), *Corynascus fumimontanus* (CBS 137294) and *Leptosillia pistaciae* (CBS 128196).

Acrostalagmus annulatus (Berk. & M.A. Curtis) Seifert, in Réblová, Gams & Seifert, Stud. Mycol. 68: 186 (2011).

Index Fungorum number: IF 518663; *Facesoffungi number*: FoF 14302; Figure 2.133

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous, forming rounded reddish brown slimy heads, globose. *Synnemata* 300–700 × 30–60 μm ($\bar{x}$ = 454 × 47 μm, n = 150), scattered, gregarious or caespitose, cylindrical capitate, clavate or cylindrical, straight or slightly bent, unbranched, often proliferating percurrently, smooth or villose at the base, with stipes white to pale orange-brown, and capitula orange-brown. *Hyphae* of stipe smooth-walled, hyaline. *Conidiophores* 2–3.5 μm wide ($\bar{x}$ = 2.7 μm, n = 30), axis erect, repeatedly branched, pale reddish brown at the base and hyaline at the apex, full-grown conidiophore stipes at the base. *Phialides* phialidic, terminal, lateral, solitary or rarely in whorls, cylindrical or subulate, straight or sinuous, orange in mass, with a conspicuous flared collarette and periclinal thickening at the conidiogenous locus. *Conidial mass* globose, hemisphaerical, initially yellow, becoming orange, then dark red to red-brown when mature. *Conidia* 3.7–5.8 × 2.5–3.4 μm ($\bar{x}$ = 4.76 × 2.74 μm, n = 30), hyaline, ellipsoidal to oblong-ellipsoidal, single-celled, arranged in slimy heads.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 45 mm after one month at 25°C, colonies from above: circular to irregular, margin filamentous, flat, dark gray to yellow; from below: yellow to light brown.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 20 September 2023, Li Lu, LC1-9 (MFLU 25-0088), living culture MFLUCC 25-0175.

GenBank numbers: MFLUCC 25-0175: ITS = PQ608229, LSU = PQ608063, SSU = PQ607931, *RPB*2 = PV186812.

Known hosts: Decaying fruits of unidentified species (Hyde et al., 2019), *Ananas comosus* (Giraldo & Crous, 2019; Farr & Rossman, 2021), *Brassica* sp. (Seifert, 1985), *Coffea arabica* (This study), *Glycine max* and *G. soja* (Giraldo & Crous, 2019; Farr & Rossman, 2021), *Luffa acutangula* and decayed fruits of unidentified plants (Giraldo & Crous, 2019), and dead stem as well as soil and roots (Giraldo & Crous, 2019).

Known distribution: Brazil (Farr & Rossman, 2021), Cuba (Giraldo & Crous, 2019; Farr & Rossman, 2021), Japan (Farr & Rossman, 2021), Mexico (Giraldo & Crous, 2019; Farr & Rossman, 2021), Sierra Leone (Giraldo & Crous, 2019; Farr & Rossman, 2021), Thailand (Hyde et al., 2019; This study) and Venezuela (Giraldo & Crous, 2019; Hyde et al., 2019; Farr & Rossman, 2021).

Notes: Acrostalagmus annulatus was previously synonymized with *Stilbella annulata* by Seifert (1985), then Seifert et al. (2011) transferred it back to *Acrostalagmus*. In the phylogenetic tree, our isolate (MFLUCC 25-0175) developed as sister lineage to *A. annulatus* (DAOM 212126) with 100% ML and 1.00 BYPP bootstrap support (Figure 2.132), which was collected from *Coffea arabica* in China. Morphologically, our collection also fits well with the description of *A. annulatus* (CBS 185.70) by erect, roughened, verticillate conidiophores, phialidic conidiogenous cells and oblong-ellipsoidal conidia accumulating in slime (Giraldo & Crous, 2019; Figure 2.133). Combining both phylogeny and morphological evidence, our species was identified as *A. annulatus* and this is first time isolated this species from coffee host from Thailand.

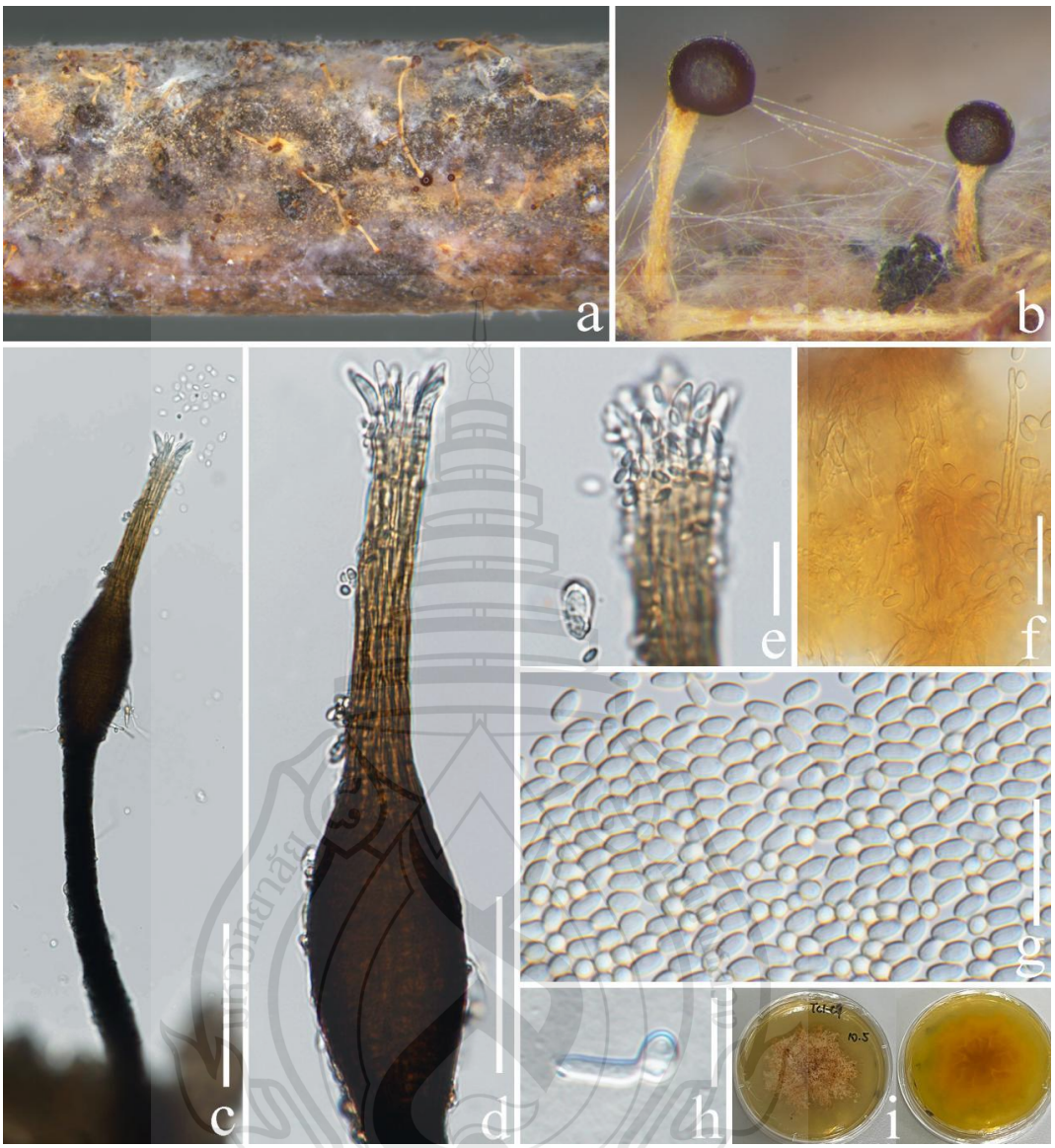


Figure 2.172 *Acrostalagmus annulatus* (MFLU 25-0088, new host record)

Figure 2.172 a, b Colony on substrate. c, d Synnemata. e, f Conidiogenous cells and conidia. g Conidia. h Germinated conidium. i Culture on PDA from above and below. Scale bars: c = 100 µm, d = 50 µm, e–g = 20 µm, h = 10 µm.

Hypocreales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 343 (1897)

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

Stephanonectria Schroers & Samuels, Sydowia 51: 116 (1999)

Notes: Stephanonectria was described for the type species *S. keithii* by Schroers (1999). *Stephanonectria keithii* was originally described as *Nectria keithii*, then Schroers (1999) transferred and renamed it as *S. keithii* due to its crown-like structure around the ostiole. Later, several studies confirmed *S. keithii* is a member of Bionectriaceae by phylogenetic analyses (Castlebury et al., 2004; Supaphon et al., 2017; Zeng & Zhuang, 2018). *Stephanonectria* has always been regarded as a monotypic genus until the new species *S. chromolaenae* and *S. ellipsoidea*, were introduced by Perera et al. (2023) and He et al. (2023), respectively. *Stephanonectria* species were isolated as saprobes from different dead woody substrata and soil distributed worldwide (Schroers et al., 1999; Perera et al., 2023; He et al., 2023). The sexual morph of *Stephanonectria* is characterized by gregarious to crowded ascomata, superficial, minutely papillate, ostiolate, ostioles surrounded by a crown-like structure, 8-spored, clavate asci, containing uniseriate to biseriate ascospores, that are hyaline, ellipsoidal, 1-septate, covered with short striae (Schroers, 1999). The asexual morph is characterized by myrothecium-like conidiomata, sporodochial, fat to cup-shaped sporodochia with dense and parallel conidiophores, phialidic conidiogenous cells with aseptate, ellipsoidal, symmetrical or asymmetrical, hyaline conidia, or white to pale orange en masse, arranged in chains (Schroers, 1999). This study introduces a new host record collected from coffee in China.

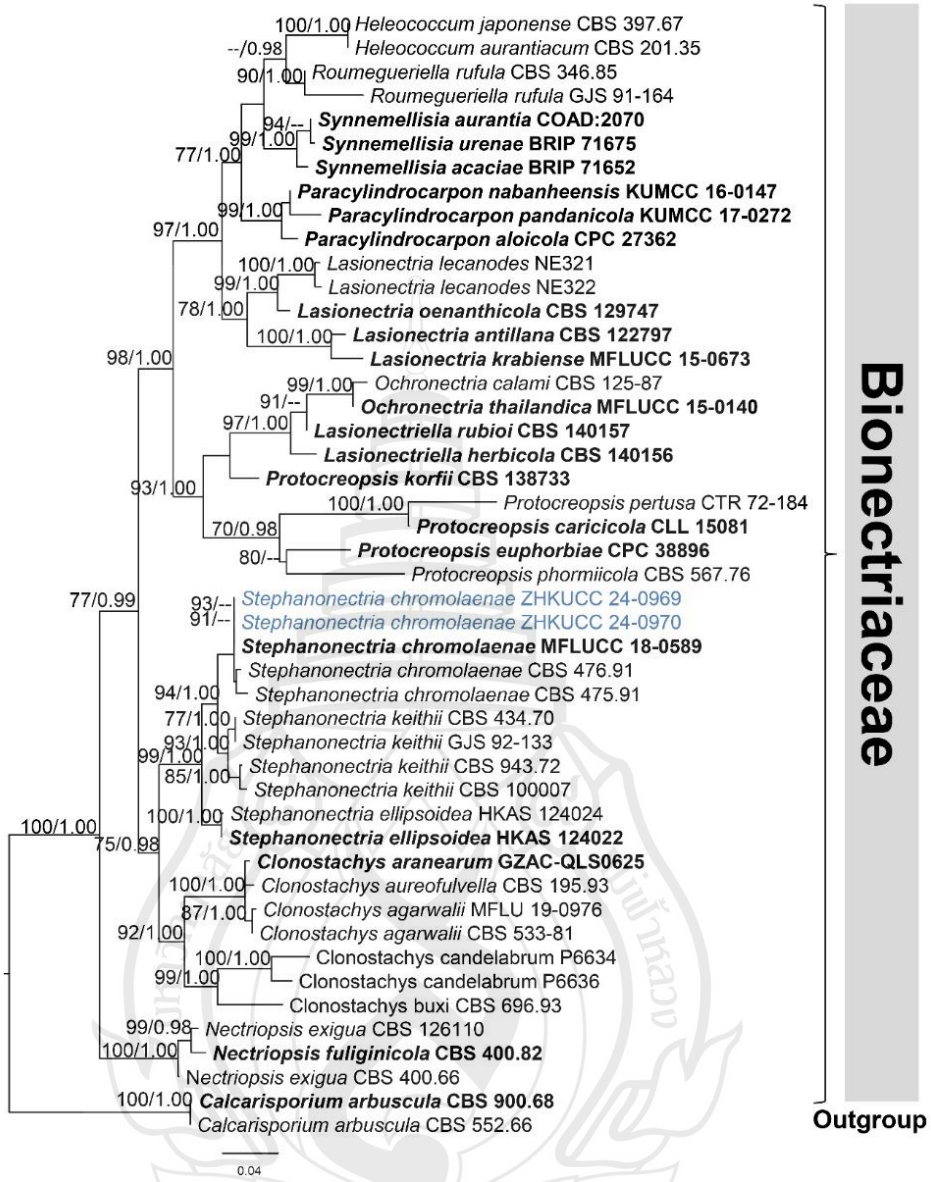


Figure 2.173 Phylogenetic tree of *Stephanonectria*

Figure 2.173 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS and LSU sequence data. Forty-seven strains are included in the combined sequence analysis, which comprises 1,314 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Calcarisporium arbuscula* (CBS:900.68 and CBS:552.66).

Stephanonectria chromolaenae R.H. Perera & K.D. Hyde, Fungal Diversity 118: 134 (2023)

Index Fungorum number: IF 559630, *Facesoffungi number:* FoF 10907; Figure 2.135

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: Hyphomycetous, sporodochial. *Sporodochia* flat to cup-shaped, composed of dense, parallel conidiophores, hymenium consisting of densely arranged phialides. *Conidiophores* up to 90 µm long, monomorphic, penicillate, branched, septate, hyaline, smooth-walled, with 1–4 phialides on each supporting cell. *Conidiogenous cells* 10–15 µm × 2–3 µm ($\overline{x}$ = 12 × 2.7 µm, n = 25), phialidic, cylindrical to clavate, integrated or discrete, determinate, smooth-walled, with a minute collarette. *Conidia* 5–6.5 × 2.5–3.5 µm ($\overline{x}$ = 5.6 × 2.9 µm, n = 25), aseptate, ellipsoidal or ovoid, symmetrical or asymmetrical, bi-guttulate, hyaline, smooth-walled. *Conidial masses* white, arranged in disconnected linear or somewhat imbricate chains. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm in one month at 25°C, circular with filiform margin, fat, surface transparent to somewhat cottony at the center, aerial mycelium sparse, from below transparent to yellowish, wrinkled.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp., 30 July 2022, Li Lu, BS3-C8 (MHZU 24-0532), living culture ZHKUCC 24-0969, other living culture ZHKUCC 24-0970.

GenBank numbers: ZHKUCC 24-0969: ITS = PQ608236, LSU = PQ608070; ZHKUCC 24-0970: ITS = PQ608237, LSU = PQ608071.

Known hosts: Brassica sp., *Chromolaena odorata* (Asteraceae), dried fruit from a deciduous forest plant and soil (Schroers et al., 1999; Perera et al., 2023; He et al., 2023; Zhao et al., 2023), *Coffea* sp. (This study).

Known distribution: China, England, France, Japan, New Zealand, Netherlands, Turkey, and Thailand (Schroers et al., 1999; Perera et al., 2023; He et al., 2023; Zhao et al., 2023; This study).

Notes: Stephanonectria chromolaenae was introduced by Perera et al. (2023) from the dead stem of *Chromolaena odorata* from Thailand. Then another new record was isolated from soil in Turkey (Zhao et al., 2023). In a BLASTn search, the ITS and LSU

sequences of our collection showed 100% similarity to *S. chromolaenae* (MFLUCC 18-0589, ex-type). In our phylogenetic analysis, our isolates formed a fully supported lineage to *S. chromolaenae* with 91% ML statistical support (Figure 2.134). Besides, the morphology of our collection is basically the same as *S. chromolaenae* in morphological characters in Perera et al. (2023) (Figure 2.135). We, therefore, identified our collection as *S. chromolaenae*, which is a new host record form *Coffea* sp. in China.

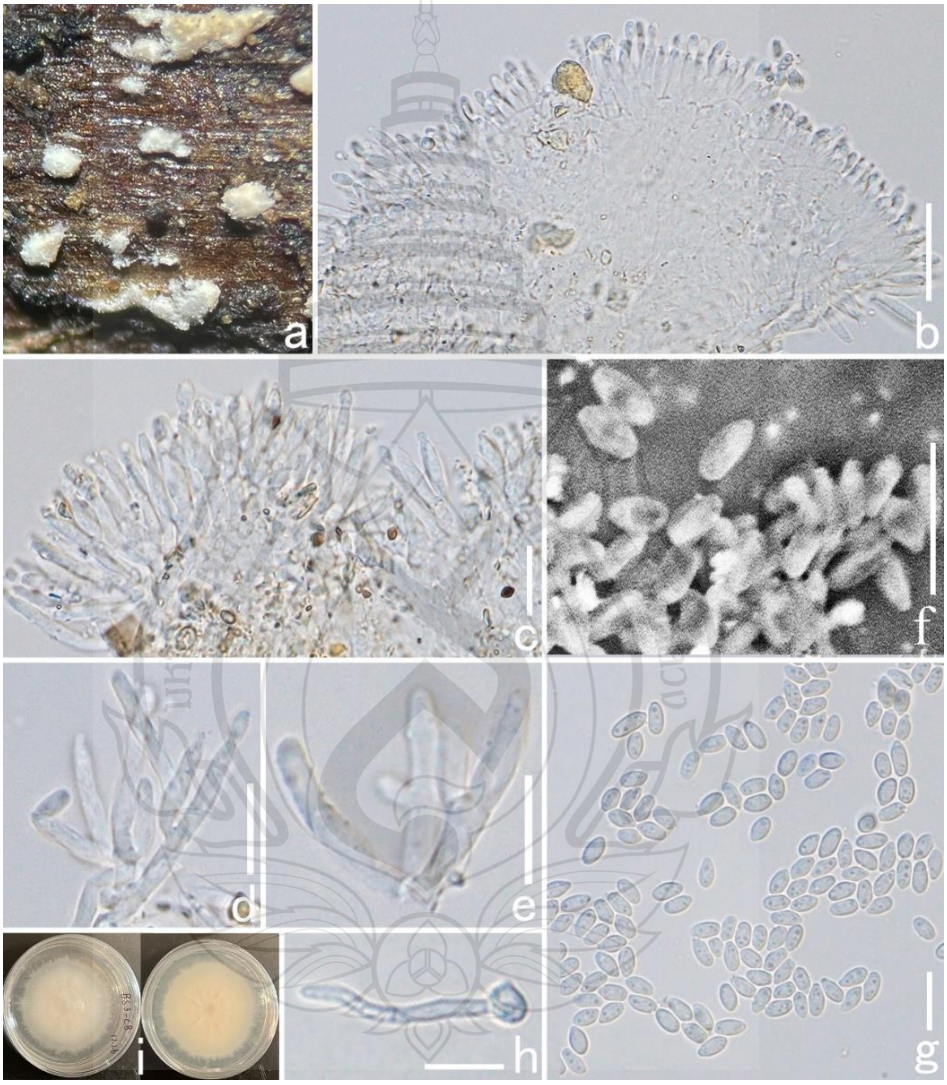


Figure 2.174 *Stephanonectria chromolaenae* (MHZU 24-0532, new host record)

Figure 2.174 a Appearance of sporodochia on *Coffea* sp. b Vertical section of sporodochium. c–e Conidiophores, phialides and conidia. f, g Conidia (f: SEM microphotographs of the conidia). h Germinated conidium. i Culture on PDA from above and below. Scale bars: b = 20 μm, c–h = 10 μm.

Nectriaceae Tul. & C. Tul. [as 'Nectriei'], Select. fung. carpol. (Paris) 3: 3 (1865).

Sarcopodium Ehrenb., Sylv. mycol. berol. (Berlin): 23 (1818).

Notes: *Sarcopodium* was introduced by Ehrenberg (1818) and typified by *S. circinatum*, which is described as having perithecia superficial, solitary or in groups, red to reddish brown, subglobose to broadly obpyriform, not collapsing when dry, with hooked or straight, septate hairs on surface; clavate to fusiform asci containing eight ellipsoidal to fusiform, striate, 1-septate ascospores; verticillate or penicillate, branched, hyaline and smooth conidiophores; and cylindrical to ellipsoidal, straight, aseptate conidia with guttules, often aggregated in slimy masses (Ehrenberg, 1818; Sutton, 1981; Rossman et al., 1999; Lombard et al., 2015). *Sarcopodium* is a widespread genus distributed from tropical and subtropical areas (Zeng & Zhuang, 2021), with 35 epithets recorded in Index Fungorum (2025) belonging to 20 species (Hyde et al., 2024a). Members of the *Sarcopodium* are facultative and mainly occur on twigs and bark of dead trees and herbaceous stems, decaying fruits, stromata of pyrenomycetes, and even in deep-sea sediments (Rossman et al., 1999; Liu & Paterson, 2011; Matsuo et al., 2018; Zeng & Zhuang, 2021). A few *Sarcopodium* species are plant pathogens, causing stem galls and cankers (Alfieri & Samuels, 1979; Alfieri et al., 1979; Watanabe, 1993), whereas some species produce secondary metabolites that showed cytotoxic activity against human cell lines (Matsuo et al., 2018). This study introduces a new species, *Sarcopodium coffeae*, from a coffee host in China.

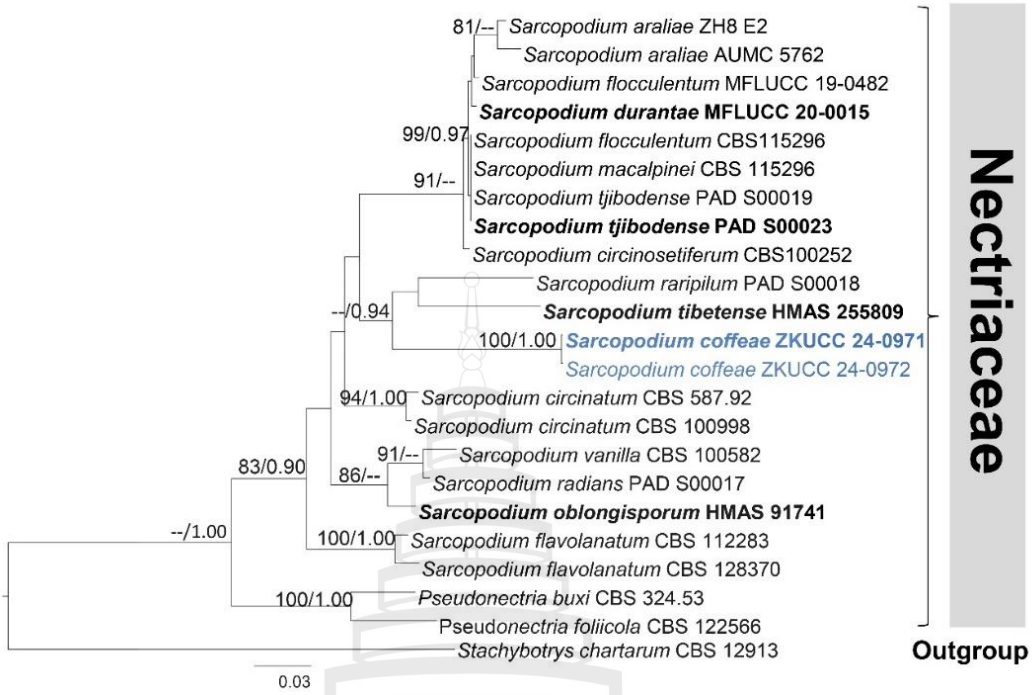


Figure 2.175 Phylogenetic tree of *Sarcopodium*

Figure 2.175 Phylogram generated from maximum likelihood analysis based on a combined dataset of ACT, ITS, LSU and *TUB*2 sequence data. Twenty-three strains are included in the combined sequence analysis, which comprises 2,247 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Stachybotrys chartarum* (CBS 12913).

Sarcopodium coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903645; *Facesoffungi number*: FoF 17601; Figure 2.137

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MHZU 24-0533

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 150–250 × 200–300 µm ($\bar{x}$ = 184 × 240 µm, n = 30), semi-immersed, solitary or gregarious, globose to subglobose, uni or multi-

loculate, brown to dark brown, shiny, without hairs. *Conidiomatal wall* 14–27 µm wide ($\bar{x}$ = 20.8 µm, n = 30), composed of 3–5 layers, with *textura angularis* to *textura globulosa* cells, hyaline to brown. *Conidiophores* penicillate, aseptate, terminal, 1 whorls with 1–5 phialides. *Phialides* 6–11 × 2–4 µm ($\bar{x}$ = 8.12 × 2.89 µm, n = 30), enteroblastic, phialidic, ampulliform to cylindrical, tapering towards apex, slender, integrated or discrete, determinate, hyaline, compactly arranged, aseptate, and smooth-walled, with minute collarette near apex. *Conidia* 4–7 × 2–5 µm ($\bar{x}$ = 5.71 × 3.51 µm; n = 30), solitary, oval or ellipsoid, straight, smooth-walled, granulate, hyaline, aseptate.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 55 mm after one month at 25°C, colonies from above: fluffy, white to pale yellow, with aerial mycelia on the surface, dense, circular; from below pale yellow.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH5-3 (MHZU 24-0533, holotype), ex-type ZHKUCC 24-0971, other living culture ZHKUCC 24-0972.

GenBank numbers: ZHKUCC 24-0971: ACT = PQ572170, ITS = PQ608234, LSU = PQ608068, *TUB*2 = PQ572189; ZHKUCC 24-0972: ACT = PQ572171, ITS = PQ608235, LSU = PQ608069, *TUB*2 = PQ572190.

Notes: In the multigene phylogenetic analyses, *Sarcopodium coffeae* formed a distinct lineage and sister to *S. tjibodense* with 0.94 BYPP bootstrap support (Figure 2.136). However, the nucleotide comparison between *S. coffeae* (ZHKUCC 24-0971, ex-type) and *S. tibetense* (HMAS 255809, holotype) showed that there are 1.69% (15/889 bp, without gaps) differences in LSU, 6.54% (38/581 bp, without gaps) in ITS, 25.97% (67/258 bp, without gaps) in *ACT*, and 16.28% (92/565 bp, without gaps) in *TUB*2. Morphologically, *S. coffeae* is similar to *S. tibetense* in having hyaline, ellipsoidal, and aseptate conidia. Differs from *S. tibetense* by ampulliform to cylindrical phialides, it is also shorter than *S. tibetense* (6–11 × 2–4 µm, L/W = 1.5–5.5 vs. 40–65 × 1.5–3, L/W = 13.3–43.3) (Zeng et al., 2021; Figure 2.137). Based on the phylogenetic analyses and morphological characteristics, *Sarcopodium coffeae* is described as a new species in this study.

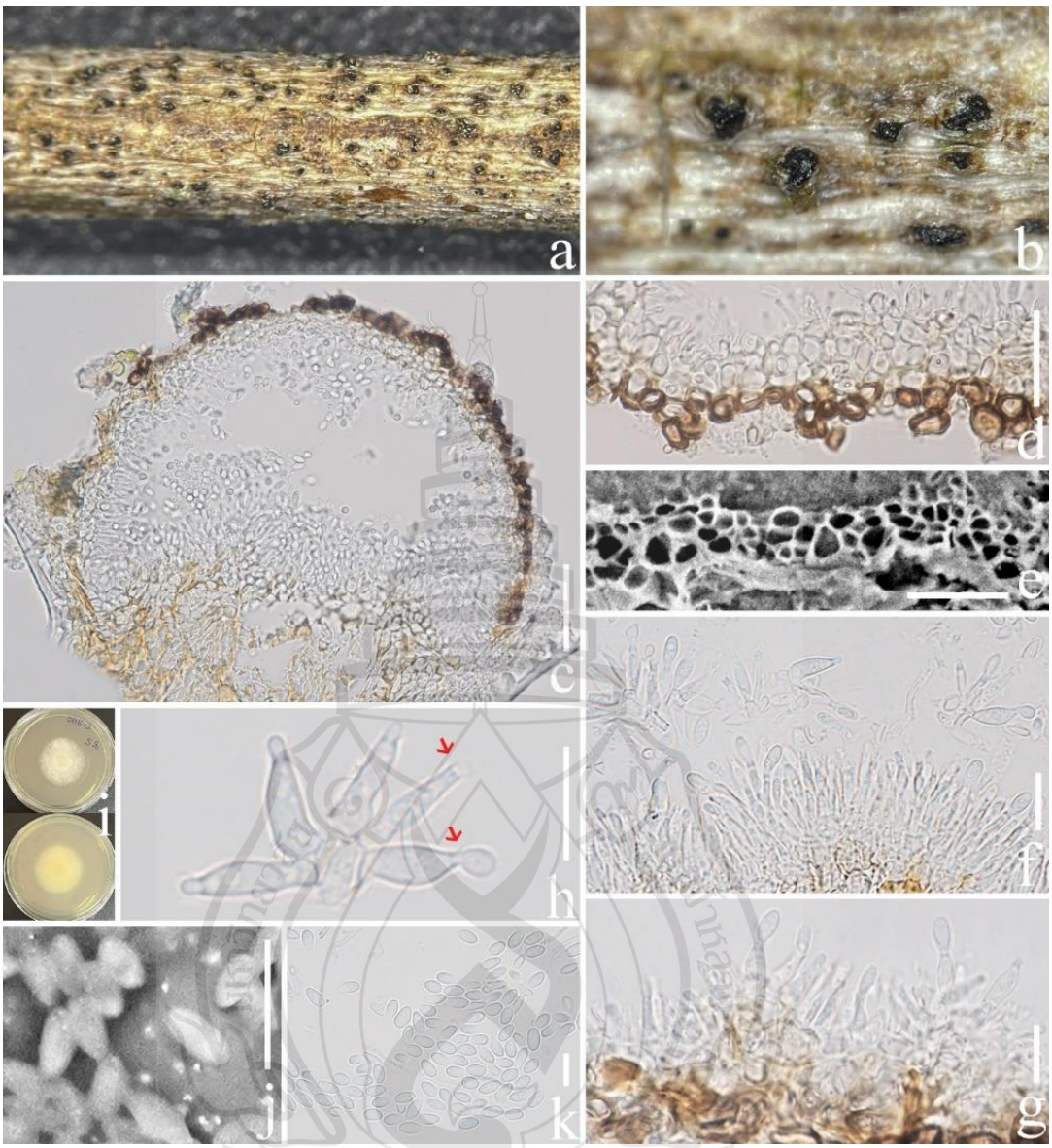


Figure 2.176 *Sarcopodium coffeae* (MHZU 24-0533, holotype)

Figure 2.176 a, b Conidiomata the host substrate. c Vertical section through a conidioma. d, e Section of a conidioma wall (e: SEM microphotographs of peridium). f–h Conidiogenous cells and conidia (arrows indicate phialidic). i Culture on PDA from above and below. j, k Conidia (j: SEM microphotographs of conidia). Scale bars: c = 50 µm, d, e = 20 µm, f–h, j, k = 10 µm.

Stachybotryaceae L. Lombard & Crous, Persoonia 32: 283 (2014)

Myrothecium Tode, Fungi Mecklenburgenses Selecti 1: 25 (1790)

Notes: The asexual genus *Myrothecium* was introduced by Tode (1790), with *M. inundatum* as the type species. Previously, the genus was placed in Hypocreales order *incertae sedis* (Castlebury et al., 2004; Lumbsch & Huhndorf, 2010; Summerbell et al., 2011; Wijayawardene et al., 2012). Crous et al. (2014) transferred it to Stachybotryaceae, and the phylogenic placement was confirmed by Maharachchikumbura et al. (2015). Species of this genus are saprobes in the soil and plant pathogens worldwide, and can be found on different decaying plants, soil, rotting leaves, dung and algae (Tulloch, 1972; Matsushima, 1989; Jiang et al., 2014; Liu et al., 2015; Wu et al., 2015; Tibpromma et al., 2017; Dai et al., 2017). There are 89 epithets of this genus that have been recorded in Index Fungorum (2025). Some *Myrothecium* species are well-known for their cellulolytic activity (Okunowo et al., 2010), and some are also known to produce a cocktail of secondary metabolites that have strong antifungal and antibiotic activity (Ruma et al., 2015; Lombard et al., 2016). In this study, two new *Myrothecium* species from coffee will be introduced.

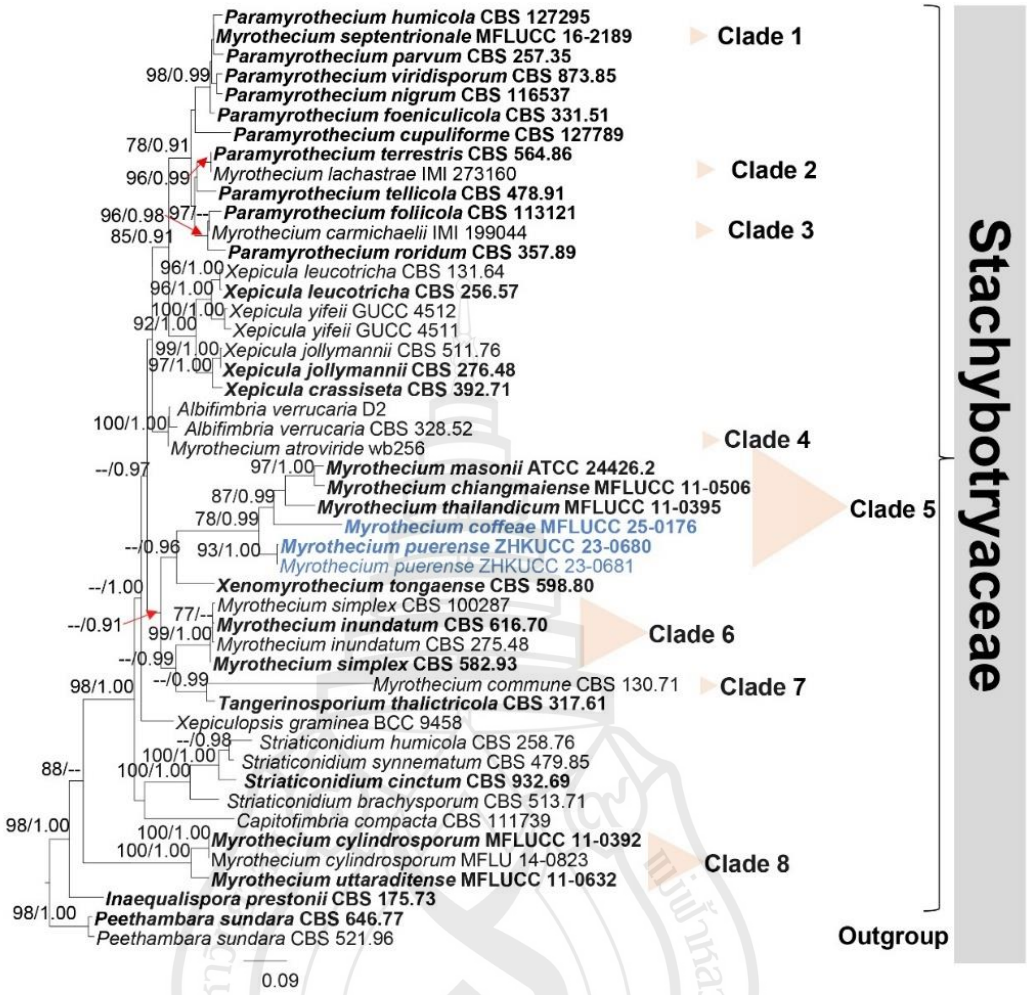


Figure 2.177 Phylogenetic tree of *Myrothecium*

Figure 2.177 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, *TEF*1-α, *TUB*2, and *cmd*A sequence data. Forty-eight strains are included in the combined sequence analysis, which comprises 3,806 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Peethambara sundara* (CBS 646.77) and *Peethambara sundara* (CBS 521.96).

Myrothecium coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903625; *Facesoffungi number*: FoF 17602; Figure 2.139

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MFLU 25-0089

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Hyphomycetous. *Synnemata* 400–600 × 60–80 µm, long stalked, solitary, smooth, olive-brown, cylindrical to cylindrical-capitate, unbranched, apically crowned by a slimy, glistening, greenish brown to black mass of conidia, mucous cap, 100–150 wide. *Stipe* mostly of parallel, rough, septate hyphae. *Conidiophores* macronematous, cylindrical, hyaline to light green, septate, unbranched, straight, rough or smooth-walled, single conidiophores 40–80 × 3–4 µm ($\bar{x}$ = 63 × 3.2 µm, n = 20). *Conidiogenous cells* 10–15 × 2–3 µm ($\bar{x}$ = 12 × 2.6 µm, n = 20), phialidic, integrated or discrete, cylindrical, hyaline to light green, rough or smooth-walled, straight. *Conidia* 7–8 × 2–3.5 µm ($\bar{x}$ = 7.6 × 2.8 µm, n = 20), cylindrical or ellipsoid, narrow at the apex, truncate at the base, straight, aseptate, hyaline to light brown, smooth-walled, with guttules. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours. Colonies on PDA reaching 1 cm diam. after one month at 25°C, irregular edge, entire margin, umbonate, flocculent and white in the middle, orange on the edge, wrinkled. Orange to light brown from below, wrinkled.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-7 (MFLU 25-0089, holotype), ex-type MFLUCC 25-0176.

GenBank numbers: MFLUCC 25-0176: ITS = PQ608232, LSU = PQ608066, SSU = PQ607932, *RPB*2 = PV186815, *TEF*1-α = PQ602118, *TUB*2 = PQ572187.

Notes: Phylogenetic analyses showed that *Myrothecium coffeae* (MFLUCC 25-0176) formed a sister to *M. chiangmaiense*, *M. masonii*, and *M. thailandicum* with 87% ML and 0.99 BYPP statistical support (Figure 2.138). Morphologically, *M. coffeae* is similar to *M. chiangmaiense*, *M. masonii,* and *M. thailandicum* in having phialidic conidiogenous cells and cylindrical or ellipsoid conidia (Tulloch, 1972; Dai et al., 2017).

However, *M. coffeae* is distinguished from these three species by long stalked synnemata with greenish brown to black conidia mass and light brown conidia when mature (Tulloch, 1972; Dai et al., 2017; Figure 2.139). Synnemata of *M. chiangmaiense* are creamish white (Dai et al., 2017), *M. masonii* are white to cinnamon (Tulloch, 1972), and *M. thailandicum* synnemata are white (Dai et al., 2017). Conidia of the three species are hyaline. Thus, we identified our strain as a distinct new species, *M. coffeae*.

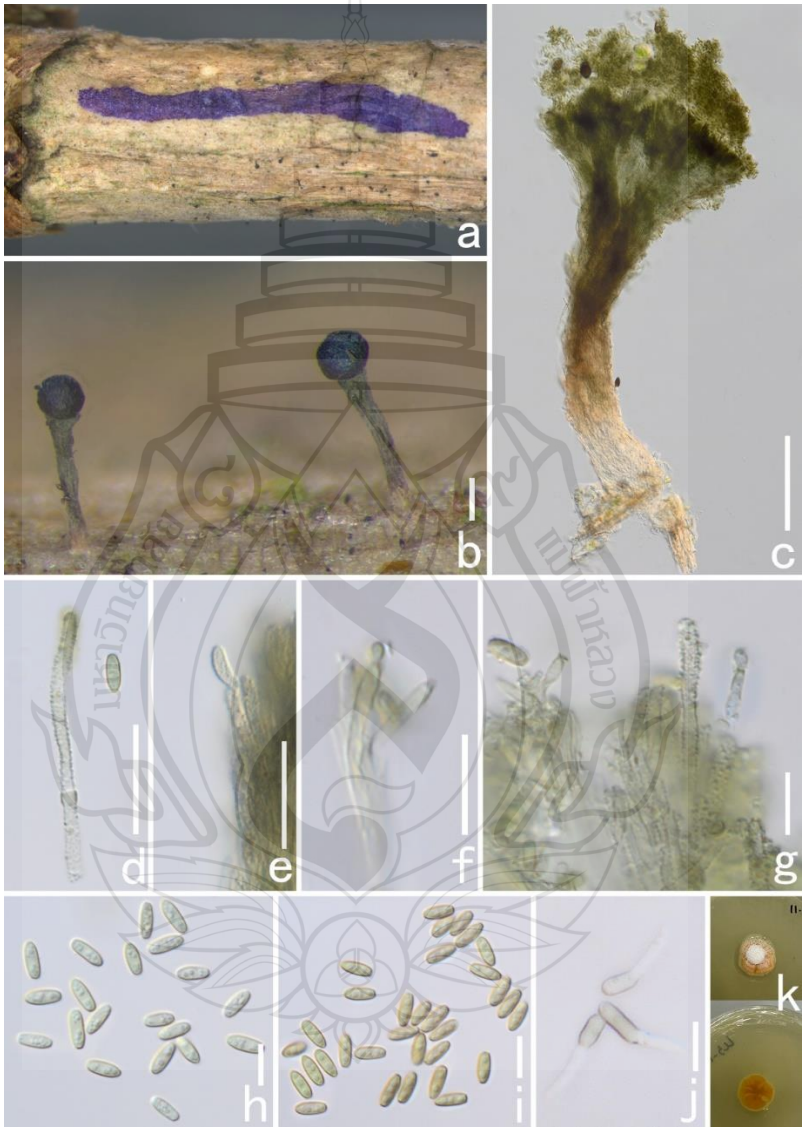


Figure 2.178 *Myrothecium coffeae* (MFLU 25-0089, holotype)

Figure 2.178 a, b Synnemata on a decaying branch of *Coffea arabica*. c, d Conidiophores. e–g Conidiogenous cells. h, i Conidia. j Germinated conidia. k Culture on PDA from above and below. Scale bars: b, c = 100 µm, d = 20 µm, e–j = 10 µm.

Myrothecium puerense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903626; *Facesoffungi number*: FoF 17603; Figure 2.140

Etymology: The species epithet refers to the type location "Pu'er", China.

Saprobic on a decaying branch of *Coffea* sp. **Asexual morph**: *Mycelium* immersed in the substrate, composed of septate, branched hyphae. *Sporodochia* 300–500 µm wide, comprising white mycelium, circular to irregular, dark green to black with a white margin, without setae. *Conidiophores* macronematous, cylindrical, hyaline, septate, branching irregularly penicillate, straight, smooth, single conidiophores 12–15 × 2–3 µm ($\bar{x}$ = 14 × 2.5 µm, n = 20). *Conidiogenous cells* 4–5 × 2–3 µm ($\bar{x}$ = 4.8 × 2.3 µm, n = 20), phialidic, integrated or discrete, cylindrical, hyaline, smooth, straight. *Conidia* 8–10 × 2–3 µm ($\bar{x}$ = 8.5 × 2.6 µm, n = 20) µm, cylindrical to long ellipsoid, truncate at the base, aseptate, hyaline to grey, straight, smooth-walled, without guttules. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours. Colonies on PDA reaching 8 cm diam. after one month at 25°C, circular, white to yellowish, flat, filiform margin, with fluffy aerial mycelium, brown from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp., 16 September 2021, Li Lu, puer 4-2 (MHZU 23-0085, holotype), ex-type ZHKUCC 23-0680, other living culture ZHKUCC 23-0681.

GenBank numbers: ZHKUCC 23-0680: ITS = PQ608230, LSU = PQ608064, *RPB*2 = PV186813, *TEF*1-α = PQ602116, *TUB*2 = PQ572185, *cmd*A = PQ572172; ZHKUCC 23-0681: ITS = PQ608231, LSU = PQ608065, *RPB*2 = PV186814, *TEF*1-α = PQ602117, *TUB*2 = PQ572186, *cmd*A = PQ572173.

Notes: Myrothecium puerense resembles *M. uttaraditense* in its dark sporodochia with white mycelium and cylindrical to ellipsoid conidia. However, hyaline to grey conidia, and lack of guttules in *M. puerense* differ from the pale brown, distinctly guttulate conidia in *M. uttaraditense* (Dai et al., 2017; Figure 2.138). However, *M. puerense* phylogenetically separates from the above species and formed an independent branch close to *M. coffeae* with 78% ML and 0.99 BYPP statistical support (Figure 2.140). The difference between *M. puerense* and *M. coffeae* are conidia without guttules and the different color of the conidia (hyaline to grey vs. hyaline to

light brown). Therefore, *M. puerense* is introduced here as a new species isolated from *Coffea* sp. in China.

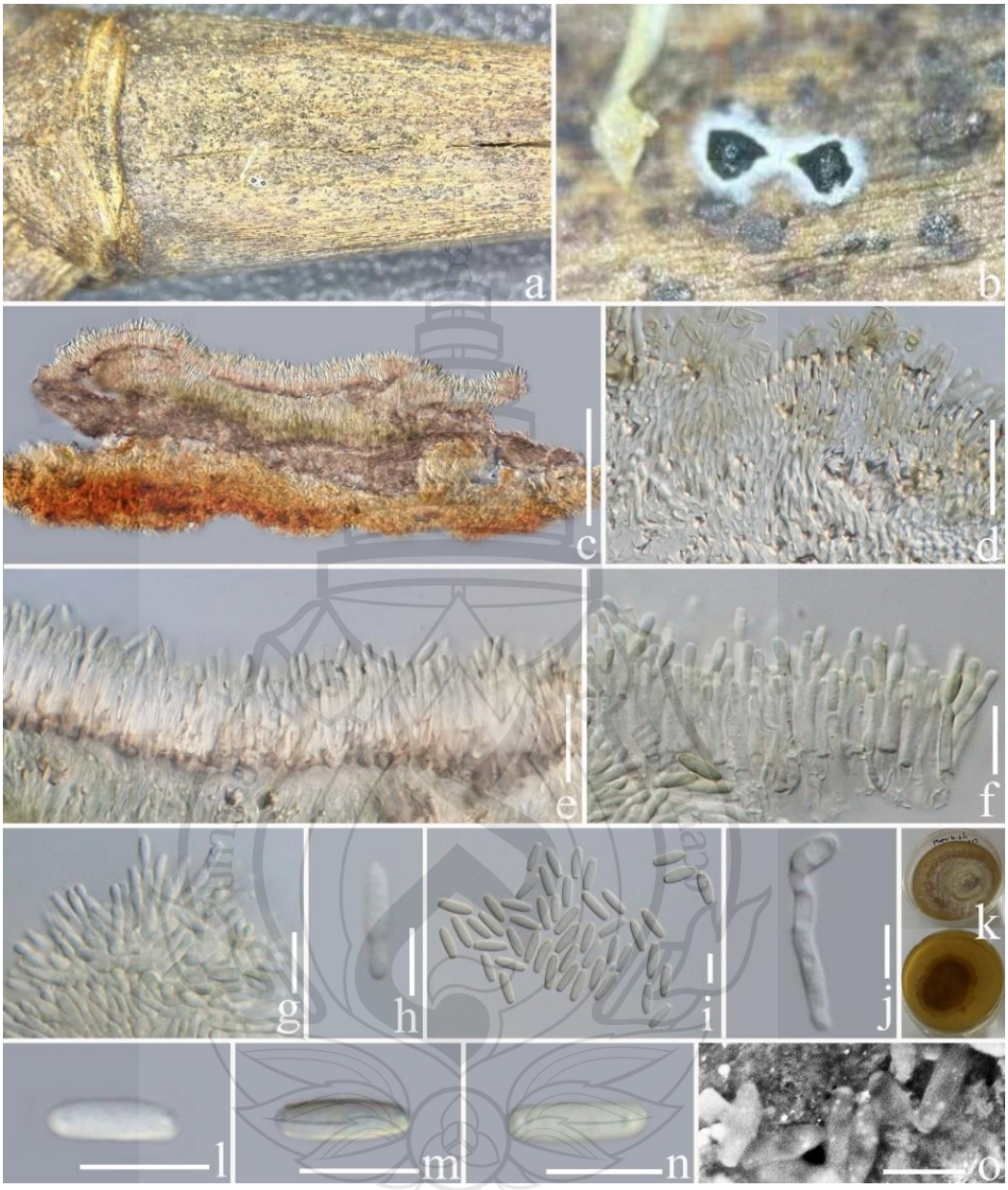


Figure 2.179 *Myrothecium puerense* (MHZU 23-0085, holotype)

Figure 2.179 a, b Sporodochia on a decaying branch of *Coffea* sp. c A vertical section of a sporodochium. d–g Conidiophores and conidia. h Conidiogenous cells. i, l–o Conidia. (o: SEM microphotographs of conidia). j Germinated conidium. k Culture on PDA from above and below. Scale bars: c = 100 µm, d, e = 20 µm, f, g = 10 µm, h–j, l–o = 5 µm.

Peethambara Subram. & Bhat, Revue de Mycologie (Paris) 42: 52 (1978)

Notes: The sexual genus *Peethambara* was established to accommodate the sexual morph of the asexual species *Putagraivam sundaram* (Subramanian & Bhat, 1978), which was later synonymized under *Didymostilbe* as *Di. sundara* by Seifert (1985). Preliminary molecular data suggest that *Peethambara* belongs in the Bionectriaceae allied with other asexual genera characterized by synnema and green multi-septate conidia (Subram et al., 1978). This genus is now placed in Stachybotryaceae as the sexual and asexual morphs are now regarded as equal with the abolishment of dual nomenclature of fungi (Lombard et al., 2016). The second species, *Pe. spirostriata* (= *Nectria spirostriata*) was later introduced by Rossman et al. (1999) and linked to the asexual morph *Di. echinofibrosa* (= *Virgatospora echinofibrosa*) based on its phenotypic similarity to *Pe. Sundara.* However, *Pe. spirostriata* has already been moved to *Nectria*. *Peethambara* is a monotypic genus (Index Fungorum, 2025) and was described as having a nectria-type centrum with a distinct ascomatal wall of two regions, one of which consists of extremely thick-walled, sclerenchyma-like cells (Subramanian & Bhat, 1978). *Peethambara* is characterized by yellow, globose perithecial ascomata having a synnematous asexual morph producing thick-walled, 1-septate conidia in green slimy masses (Subramanian & Bhat, 1978; Seifert, 1985; Rossman et al., 1999). Its ecological role is uncertain, and it is presumed to be saprobic based on the substrates from which it has been isolated from woody hosts (Subramanian & Bhat, 1978; Seifert 1985; Rossman et al., 1999). This study introduces a new species from a coffee host in Thailand.

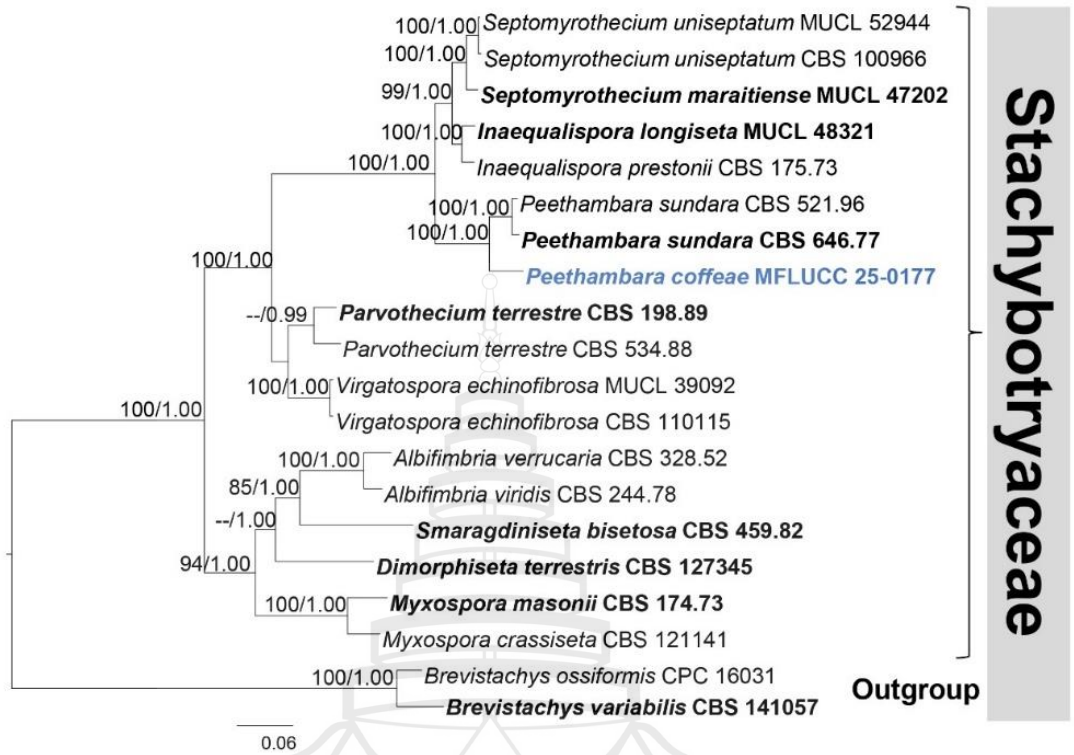


Figure 2.180 Phylogenetic tree of *Peethambara*

Figure 2.180 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, *TEF*1-α, and *TUB* sequence data. Twenty-seven strains are included in the combined sequence analysis, which comprises 3,377 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Brevistachys ossiformis* (CPC 16031) and *B. variabilis* (CBS 141057).

Peethambara coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903638; *Facesoffungi number*: FoF 17604; Figure 2.142

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MFLU 25-0090

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Hyphomycetous. *Synnemata* 300–700 × 20–50 µm ($\bar{x}$ = 507 × 29 µm, n = 15), solitary

to gregarious, cylindrical to cylindrical-capitate, unbranched, fairly slender, hyaline to yellow-brown, smooth-walled. *Hyphae* of stipe 2–4 µm wide in the base, 1.5–2.5 µm wide in stipe; marginal hyphae are finely echinulate. *Phialides* 20–30 µm long, 3–5 µm wide (x = 26 × 3.5 µm, n = 15), enteroblastic, phialidic, cylindrical to clavate, integrated or discrete, branched, usually terminal, sometimes lateral and terminal, usually with a prominent apical cupulate collarette, periclinal thickening usually evident. *Conidial mass* hyaline to light-orange, hemisphaerical to globose, 80–150 µm diam. *Conidia* 15–25 × 5–8 µm (x = 20 × 6 µm, n = 25), 1-septate when mature, guttulate, ellipsoidal, fusoid, with indistinct nipple-like apex. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours and germ tubes produced from both ends of the conidia. Colonies on PDA reaching 9 cm diam. after one month at 25°C, circular, white, flat, filiform margin, with fluffy aerial mycelium in the surface. Yellowish from below.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 20 September 2023, Li Lu, LC2-20 (MFLU 25-0090, holotype), ex-type MFLUCC 25-0177.

GenBank numbers: MFLUCC 25-0177: ITS = PQ608233, LSU = PQ608067, *RPB*2 = PV186816, *TEF*1-α = PQ602119, *TUB*2 = PQ572188.

Notes: Based on phylogenetic analysis, *Peethambara coffeae* formed an independent branch under *Pe. sundara* with 100% ML and 100 BYPP statistical support (Figure 2.141). In morphology, the conidia of *Pe. coffeae* lack of nipple-like apex (Figure 2.142), it can be distinguished from *Pe. sundara* (Seifert, 1985). In pairwise nucleotide comparisons of type species of *Pe. sundara* (CBS 646.77, ex-type) and *Pe. coffeae* (MFLUCC 25-0177, ex-type), there are 4.1% nucleotide differences in ITS (23/557 bp, without gaps), 1% nucleotide differences in LSU (9/876 bp, without gaps), 9% nucleotide differences in *RPB*2 (69/720 bp, without gaps), and 9% nucleotide differences in *RPB*2 (33/360 bp, without gaps). Therefore, *Peethambara coffeae* is introduced here as a new species isolated from *Coffea arabica* in Thailand.

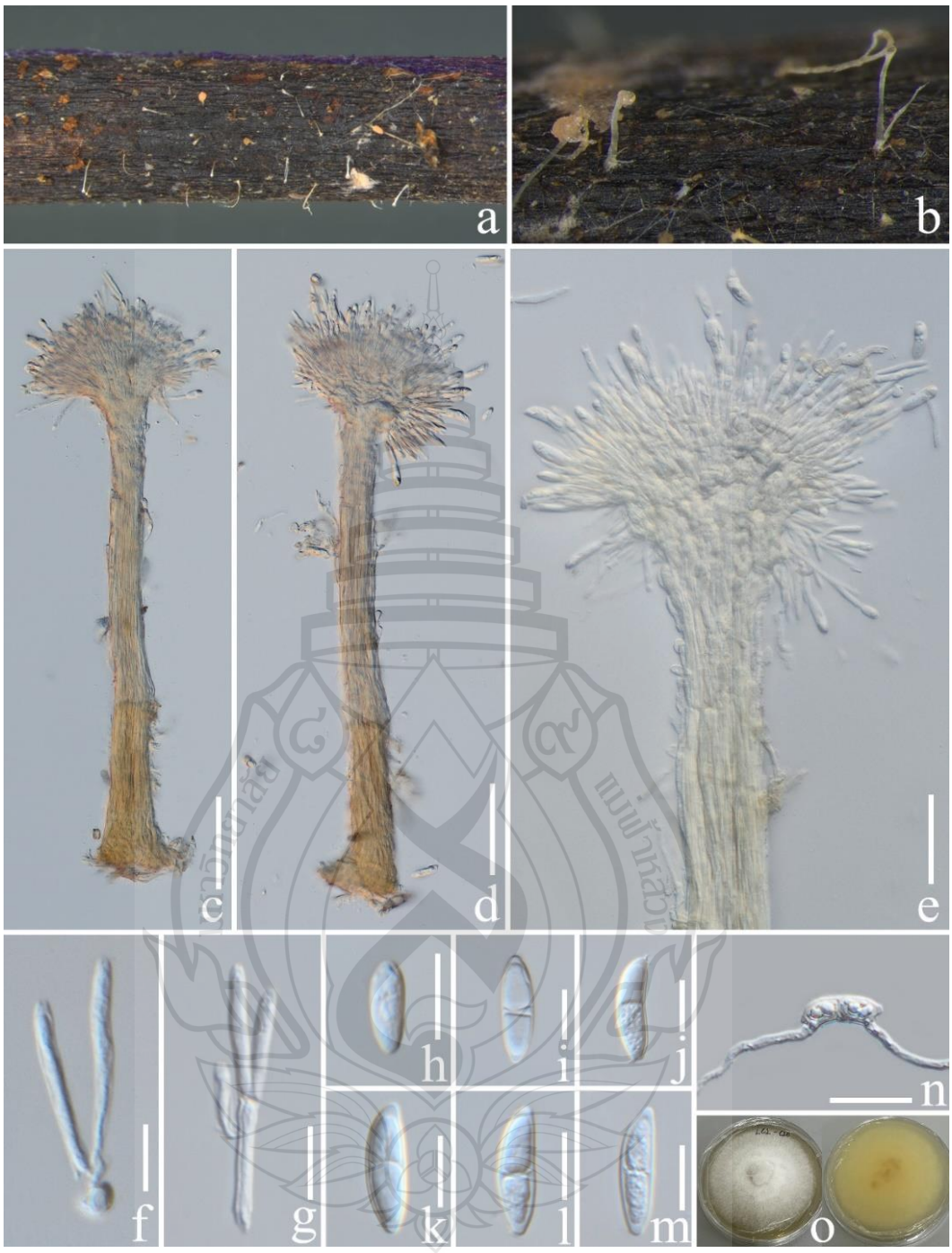


Figure 2.181 *Peethambara coffeae* (MFLU 25-0090, holotype)

Figure 2.181 a, b Synnemata on a decaying branch of *Coffea arabica*. c, d Synnemata in water. e Marginal hyphae and conidia produced by phialides. f, g Phialides. h–m Conidia. n Germinated conidium. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, e = 30 µm, f, n = 20 µm, g–m = 10 µm.

Pleurotheciales Réblová & Seifert, Persoonia 37: 63 (2015)

Pleurotheciaceae Réblová & Seifert, Persoonia 37: 63 (2015)

Pleurotheciella Réblová, Seifert & J. Fourn., Mycologia 104 (6): 1304 (2012)

Notes: Based on morphological and molecular data, *Pleurotheciella* was introduced to accommodate the holomorphic species *P. rivularia* (type) and an asexual fungus *P. centenaria* (Réblová et al., 2012). The genus is characterized by chaetosphaeria-like ascomata and blastic conidia produced sympodially on a rachis or on denticles (dactylaria-like asexual morphs) (Réblová et al., 2012; Luo et al., 2018; Shi et al., 2021). So far, 20 species are included in the genus and most are known from freshwater habitats (Réblová et al., 2012; Luo et al., 2018; Shi et al., 2021; Liu et al., 2024; Index Fungorum, 2025), few are reported from terrestrial habitats (Boonmee et al., 2021; Visagie et al., 2024). This study introduces a new species, *Pleurotheciella coffeae*. This is the first time *Pleurotheciella* species are reported from coffee hosts in Thailand.

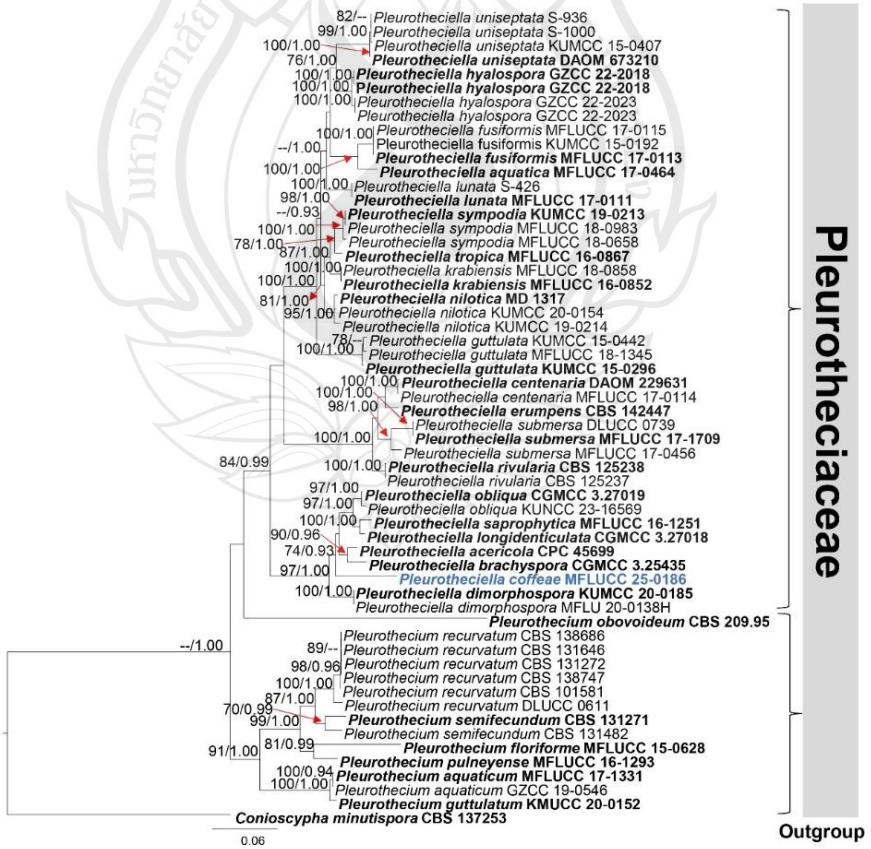


Figure 2.182 Phylogenetic tree of *Pleurotheciella*

Figure 2.182 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, and *RPB*2 sequence data. Fifty-eight strains are included in the combined sequence analysis, which comprises 3,534 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Conioscypha minutispora* (CBS137253).

Pleurotheciella coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903640; Facesoffungi number: FoF 17605; Figure 2.144

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MFLU 25-0099

Saprobic on a decaying branch of *Coffea arabica*. **Asexual morph**: Hyphomycetous. *Colonies* effuse, superficial, clustered, hairy, grayish to brown with visible whitish conidia. *Mycelium* mostly immersed. *Conidiophores* 60–160 × 3.5–5 µm ($\overline{x}$ = 105 × 3.7 µm, n = 15), macronematous, mononematous, straight or slightly flexuous, cylindrical, multi-septate, smooth-walled, olive green to pale brown, becoming subhyaline towards the apex, unbranched. *Conidiogenous cells* 10–12 × 2.5–3 µm ($\overline{x}$ = 11 × 2.7 µm, n = 15), polyblastic, terminal, integrated, cylindrical to tapered, sympodial, with denticles, pale brown near base, subhyaline towards apex. *Conidia* 9–13 × 4–6 µm ($\overline{x}$ = 11.5 × 5 µm, n = 30), oval to ellipsoidal, straight, rounded at the apex, tapering towards the base, 1-septate, slightly constricted at the septa, hyaline, with conspicuous guttules, often with 1–2 guttules in each cell, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 hours. Colonies on PDA reaching 1.5 cm diam. after one month at 25°C, radially striated with lobate edge, entire margin, umbonate, density, from above gray-green, dark green from below.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 20 September 2023, Li Lu, LC2-10 (MFLU 25-0099, holotype), ex-type MFLUCC 25-0186.

GenBank numbers: MFLUCC 25-0186: ITS = PQ608332, LSU = PQ608163, SSU = PQ608019, *RPB*2 = PV357189.

Notes: Multi-gene phylogenetic analyses showed that our isolates (MFLUCC 25-0186, ex-type) formed an independent lineage between *Pleurotheciella saprophytica* (MFLUCC 16-1251, ex-type) and *P. dimorphospora* (KUMCC 20-0185, ex-type) with 74% ML and 0.93 BYPP statistical support (Figure 2.143). Morphologically, our collection can be recognized from *P. saprophytica* by having oval to ellipsoidal conidia with conspicuous guttules (Luo et al., 2018), while those of our species formed effuse, superficial, clustered and hairy colonies on the substrate (Figure 2.144), which was different from *P. dimorphospora* (Boonmee et al., 2021). Combining phylogenetic trees and morphological features showed that they are distinct species. Therefore, we introduced our isolates as a new species in the genus *Pleurotheciella*, named *P. coffeae.*

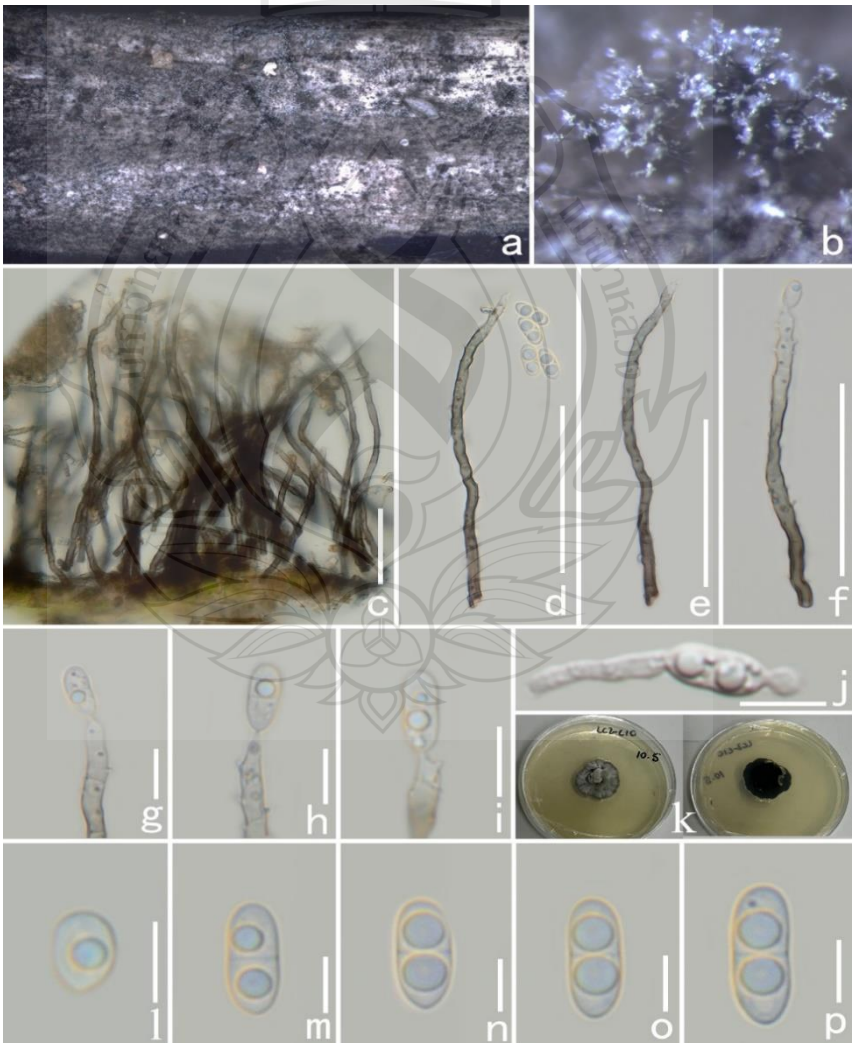


Figure 2.183 *Pleurotheciella coffeae* (MFLU 25-0099, holotype)

Figure 2.183 a, b Colonies on a decaying branch of *Coffea arabica*. c–f Conidiophores. g–i Conidiogenous cells with conidia. j Germinated conidium. k Culture on PDA from above and below. l–p Conidia. Scale bars: c–f = 50 µm, g–j = 10 µm, l–p = 5 µm.

Pseudodactylariales Crous, Persoonia 39: 421 (2017)

Pseudodactylariaceae Crous, Persoonia 39: 421 (2017)

Pseudodactylaria Crous, Persoonia 39: 421 (2017)

Notes: Pseudodactylaria was introduced by Crous et al. (2017) to accommodate a new species *P. xanthorrhoeae* (type species) and a new combination *P. hyalotunicata*. There are 11 species listed in the genus (Index Fungorum, 2025); they are saprobic on dead wood collected from aquatic and terrestrial habitats (Bao et al., 2021, Yang et al., 2023). *Pseudodactylaria* is characterized by white erect conidiophores and fusoid-ellipsoid conidia that are surrounded by a thin mucilaginous sheath (Crous et al., 2017). In this study, *Pseudodactylaria coffeae* is introduced as a new species, representing the first sexual morph of *Pseudodactylaria*. In addition, this is the first record of a *Pseudodactylaria* species reported from a coffee host in Thailand.

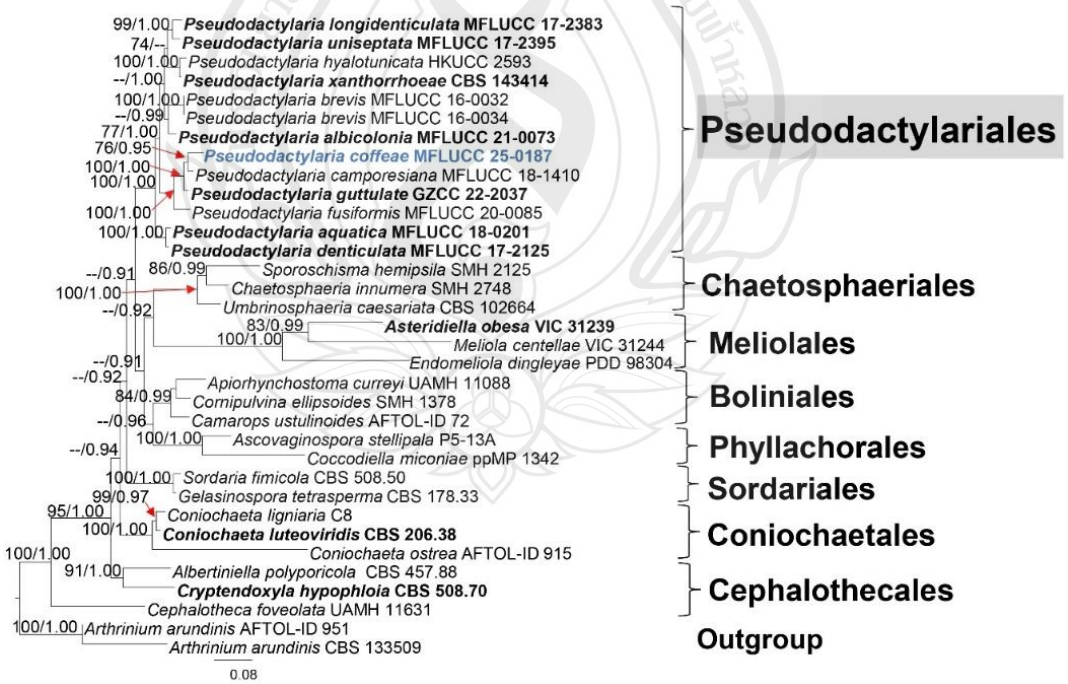


Figure 2.184 Phylogenetic tree of *Pseudodactylaria*

Figure 2.184 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB*2, and *TEF*1-α sequence data. Thirty-four strains are included in the combined sequence analysis, which comprises 4,256 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Arthrinium arundinis* (CBS 133509 and AFTOL-ID 951).

Pseudodactylaria coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903643; *Facesoffungi number*: FoF 17606; Figure 2.146

Etymology: The species epithet refers to the host genus "*Coffea*".

Holotype: MFLU 25-0100

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 120–200 × 150–220 µm ($\overline{x}$ = 155 × 167 µm, n = 15), superficial, solitary or clustered, globose to subglobose, black, carbonaceous, with a central ostiole. *Peridium* 15–30 µm wide ($\overline{x}$ = 24 µm, n = 30), consisting of two layers, outer layers thick-walled, dark brown, composed of cells of *textura angularis*, inner layers thin-walled, hyaline. *Hamathecium* of 1.5–2 µm wide ($\overline{x}$ = 1.8 µm, n = 30), hyaline, branched and aseptate, paraphyses. *Asci* 60–85 × 8–12 µm ($\overline{x}$ = 71 × 10 µm, n = 30), unitunicate, 8-spored, thin-walled, clavate to cylindrical, short stalked, with J-, apical ring. *Ascospores* 10–15 × 5–6 µm ($\overline{x}$= 13 × 5.3 µm, n = 30), uni- or overlapping seriate, hyaline, smooth-walled, aseptate, occasionally 1-septate, oval to ellipsoidal, guttulate, rough-walled, sheath absent. **Asexual morph**: Not observed.

Culture characteristic: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 30 mm in one month at 25 °C, flat, circular and entire margin, surface smooth and glistening, from above hyaline to yellowish, from below yellowish.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea* sp. (990 m), 1 November 2023, Li Lu, LC3-2-3 (MFLU 25-0100, holotype), ex-type MFLUCC 25-0187.

GenBank numbers: MFLUCC 25-0187: ITS = PQ608333, LSU = PQ608164, SSU = PQ608020, *TEF*1-α = PQ628176, *RPB*2 = PV357190.

Notes: In the multi-gene phylogenetic analyses, *Pseudodactylaria coffeae* shares a sister relationship to *P. camporesiana* with 76% ML, 0.95 BYPP statistical bootstrap support (Figure 2.145). Only the asexual form is known for *P. camporesiana* , while *P. coffeae* has only been observed in its sexual form (Figure 2.146), making morphological comparisons impossible (Hyde et al., 2020). In pairwise nucleotide comparisons of the type species of *P. camporesiana* (MFLUCC 18-1410) and *P. coffeae* (MFLUCC 25-0187), there are 3.4% nucleotide differences in ITS (18/520 bp, without gaps), LSU and SSU are identical, and *P. camporesiana* without *TEF*1-α and *RPB*2 genes. In addition, we compared nuclear base pair differences among several closely related species within this genus (e.g., *P. albicolonia, P. brevis*, *P. denticulata*, and *P. aquatica*), and the ITS region shows significant divergence, whereas the LSU and SSU regions exhibit low variability or are nearly identical. Lu et al. (2022) introduced the new species *P. fusiformis* based on a large difference of ITS from the close species *P. camporesiana*. Consequently, we propose that the ITS region can serve as a key genetic marker for species delimitation within this genus. We, therefore, identified *P. coffeae* as a new species, which is the first sexual report of *Pseudodactylaria*.

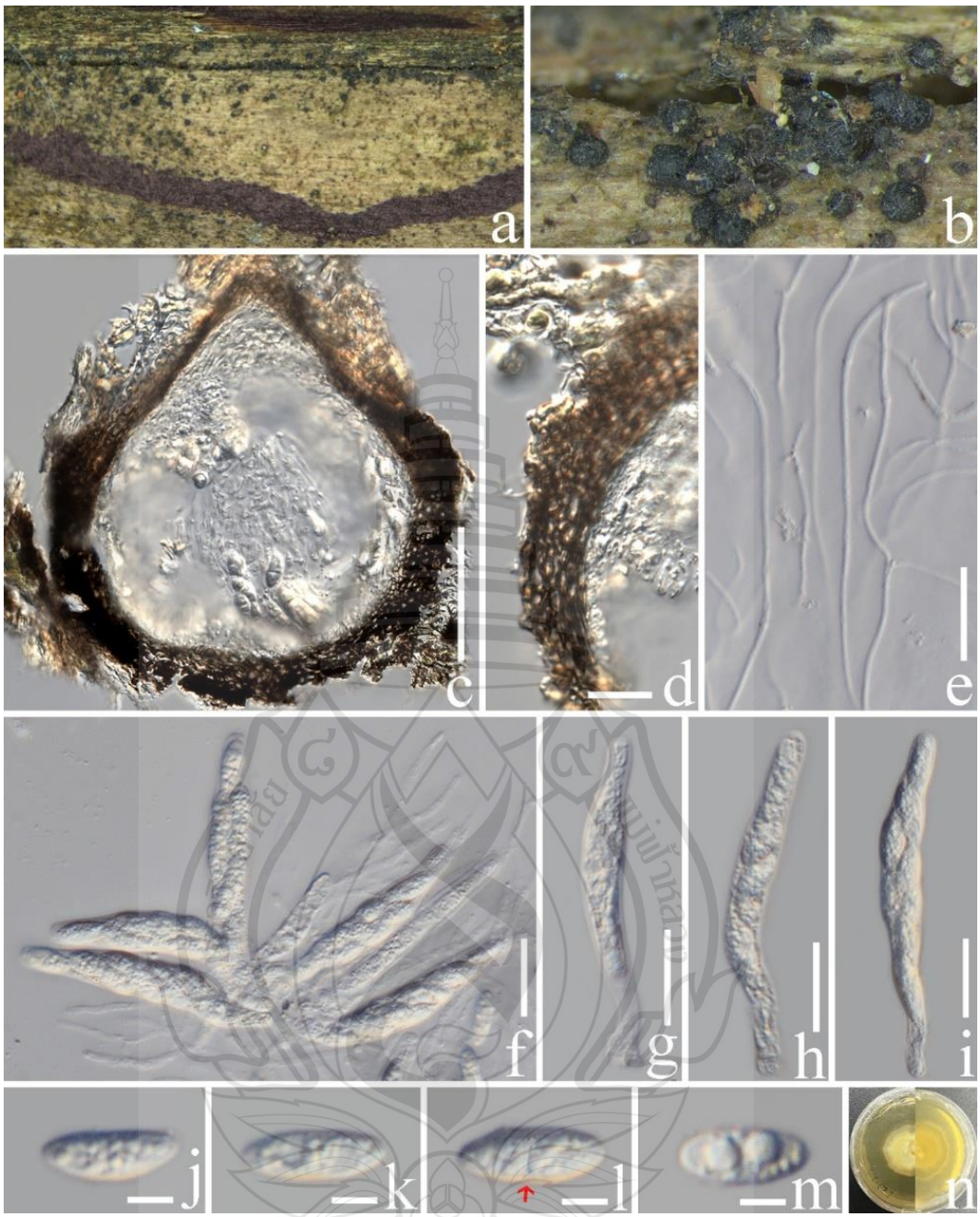


Figure 2.185 *Pseudodactylaria coffeae* (MFLU 25-0100, holotype)

Figure 2.185 a, b Ascomata on a decaying branch of *Coffea* sp. c Longitudinal section of ascoma. d Peridium. e Trabeculate paraphyses. f–i Asci. j–m Ascospores (arrow indicate septa). n Culture on PDA from above and below. Scale bars: c = 50 µm, d–i = 20 µm, j–m = 5 µm.

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 182 (1986)

Helminthosphaeriaceae Samuels, Cand. & Magni, Mycologia 89: 144 (1997)

Hilberina Huhndorf & A.N. Mill., Mycological Research 108 (1): 31 (2004)

Notes: Lasiosphaeria species can be arranged into four groups based on ascospore morphology, *Hilberina* was proposed to accommodate one of *Lasiosphaeria* group by Miller and Huhndorf (2004) based on nuclear LSU sequences, with *H. caudata* as the type species. *Hilberina* species can be distinguished by the presence of setose ascomatal vestitures and cylindrical ascospores that taper to a distinct point at one end (Miller & Huhndorf, 2004; Miller et al., 2014). To date, 20 species records of *Hilberina* are in Index Fungorum (2025). However, molecular data are available for only six species (*Hilberina caudata*, *H. hongheensis, H. sphagnorum*, *H. punctata*, *H. robusta,* and *H. munkii*) (Yang et al., 2023). This study introduces a new host and new country record of *H. hongheensis* from coffee in Thailand.

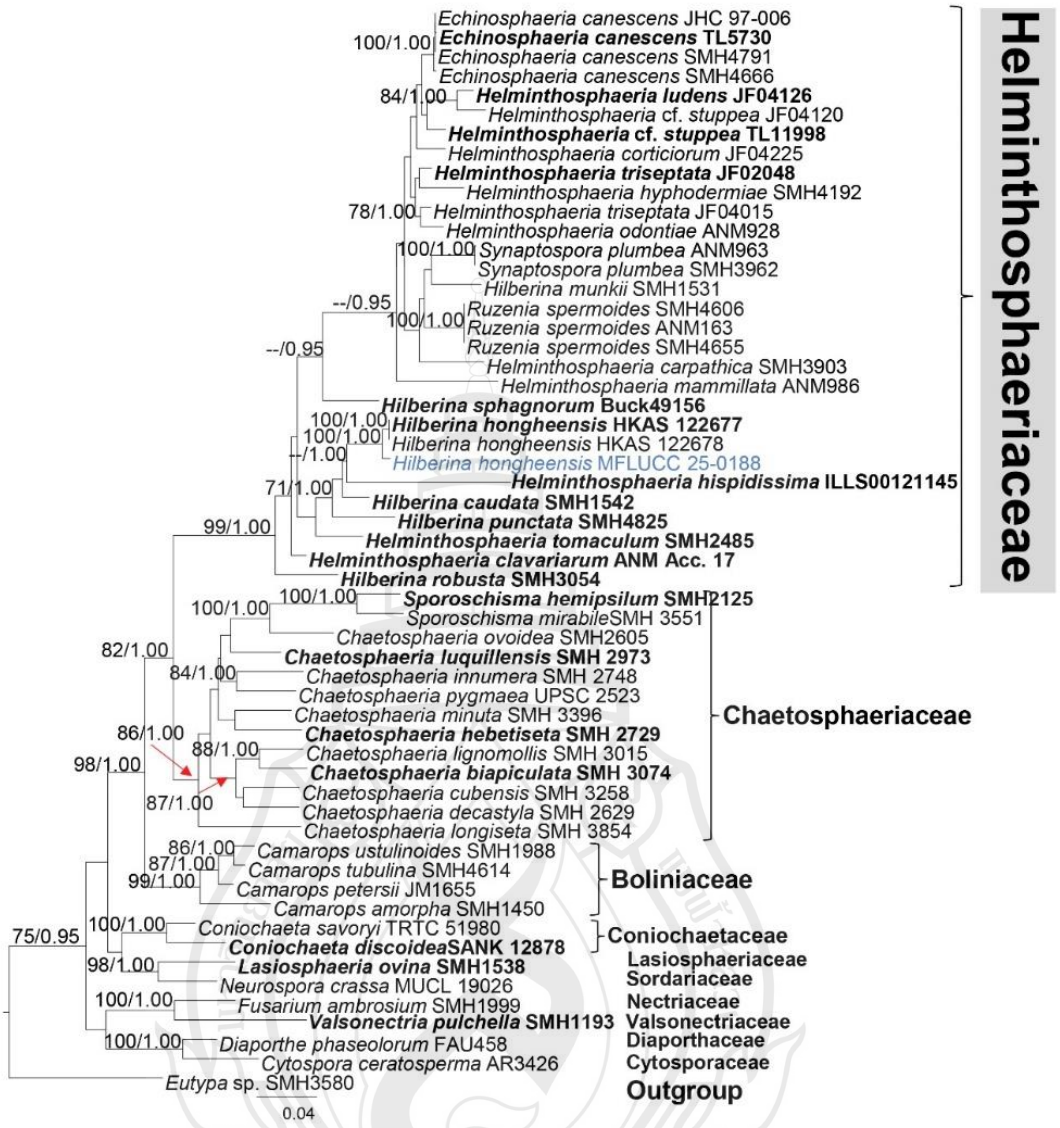


Figure 2.186 Phylogenetic tree of *Hilberina*

Figure 2.186 Phylogram generated from maximum likelihood analysis based on a combined dataset of LSU and *TUB*2 sequence data. Fifty-six strains are included in the combined sequence analysis, which comprises 1,457 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Eutypa* sp. (SMH3580).

Hilberina hongheensis E.F. Yang & Tibpromma, J. Fungi 9 (6, no.680): 16 (2023)

Index Fungorum number: IF 571289; *Facesoffungi number*: FoF 17607; Figure 2.148

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 160–250 × 180–280 µm ($\bar{x}$ = 200 × 220 µm, n = 15), superficial, subglobose, scattered or solitary, carbonaceous, black, setiferous on the surface of the substrate, with long black papilla visible at the surface, with a poorly developed ostiole. *Setae* 20–100 µm long, pale brown, sub-hyaline at the tip, septate, straight to slightly flexuous, smooth, with a narrow acute apex. *Ascomata wall* 30–45 µm wide ($\bar{x}$ = 35 µm, n = 30), multilayered, thick-walled, comprising hyaline cells of *textura angularis* inwardly, outer layers appearing dark brown cells of *textura angularis*. *Hamathecium* of 3–7 µm wide ($\bar{x}$ = 5 µm, n = 30), hyaline, septate, filamentous, branched and septate, constricted at the septa, paraphysate. *Asci* 80–110 × 10–12 µm ($\bar{x}$ = 93 × 11 µm, n = 30), unitunicate, 4–8-spored, clavate, hyaline, slightly shining, short pedicellate, with J-, apical ring. *Ascospores* 12–18 × 7–9 µm ($\bar{x}$ = 15 × 7.9 µm, n = 30), uniseriately overlapping, oval to ellipsoid, hyaline, thin and smooth-walled, without a gelatinous sheath and appendages. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 3 cm diam. after one month at 25°C, filamentous, with lobate margin, umbonate, density, brownish from above. Dark brown from below.

Material examined: Thailand, Chiang Rai Province, on a decaying branch of *Coffea arabica*, 01 November 2023, Li Lu, LC3-1-14 (MFLU 25-0101, holotype), ex-type MFLUCC 25-0188.

GenBank numbers: MFLUCC 25-0188: ITS = PV053822, LSU = PQ608165.

Known hosts: On dead branch of *Mangifera indica* (Yang et al., 2023); *Coffea arabica* (This study).

Known distribution: China (Yang et al., 2023); Thailand (This study).

Notes: Hilberina hongheensis was introduced by Yang et al. (2023) with sexual morph. The phylogenetic analyses showed that our isolate (MFLUCC 25-0188) formed a sister lineage to *H. hongheensis* (HKAS 122677, type and HKAS 122678)

with 100% ML and 1.00 BYPP statistical support (Figure 2.147). Based on nucleotide comparisons, our isolate (MFLUCC 25-0188, ex-type) is similar to *H. hongheensis* (HKAS 122677, holotype) by 3/537 bp (0.5%, without gaps) in ITS and 5/868 bp (0.5%, without gaps) in LSU. Morphologically, our species is similar to *H. hongheensis* in having ascomata with setae and oval ascospores (Yang et al., 2023). However, our species exhibits 4–8-spored asci, whereas *H. hongheensis* has only 4-spored asci; this finding further complements the morphological characteristics of *H. hongheensis* (Yang et al., 2023; Figure 2.148). Therefore, we identified our collection as *H. hongheensis*.

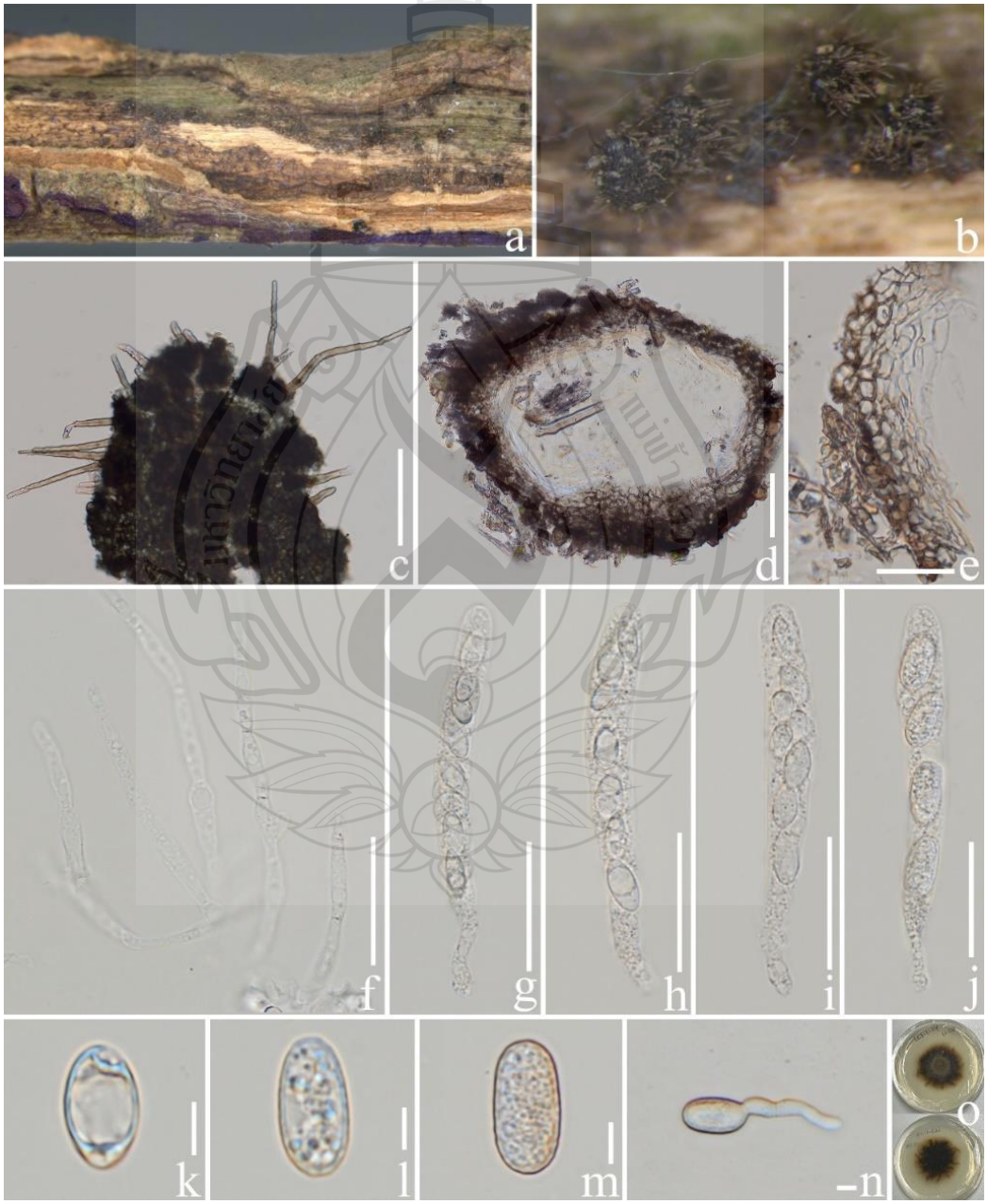


Figure 2.187 *Hilberina hongheensis* (MFLU 25-0101, new host and country record)

Figure 2.187 a, b Ascomata on a decaying branch of *Coffea arabica*. c Apical section of ascoma with setae. d Vertical section of ascoma. e Ascomata wall. f Paraphyses. g–j Asci. k–m Ascospores. n Germinated ascospore. o Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–j = 30 µm, k–n = 5 µm.

Podosporaceae X. Wei Wang & Houbraken, Studies in Mycology 93: 223 (2019)

Triangularia Boedijn, Ann. Mycol. 32 (3-4): 302 (1934)

Notes: Triangularia was transferred from *Trigonia* and typified by *T. bambusae* (Boedijn, 1934). This genus was accepted in Podosporaceae by Wang et al. (2019) based on phylogenetic studies. Most *Triangularia* species have been reclassified from *Apiosordaria*, *Cercospora*, *Sordaria*, and *Zopfiella*, therefore, the phylogenetic relationships within this genus remain ambiguous (Wang et al., 2019; Marin-Felix et al., 2020). Recently, Huang et al. (2021) transferred seven species to *Triangularia* based on morphological and phylogenetic studies, they also demonstrated species of *Apiosordaria* and *Triangularia* are also scattered in Naviculisporaceae and Neoschizotheciaceae. There are 37 epithets in Index Fungorum (2025), and most members of this genus are isolated from soil, animal dung, sand, and decaying plants and found in terrestrial habitats (Wang et al., 2019; Huang et al., 2021). This study introduces a new host record from a coffee host in China.

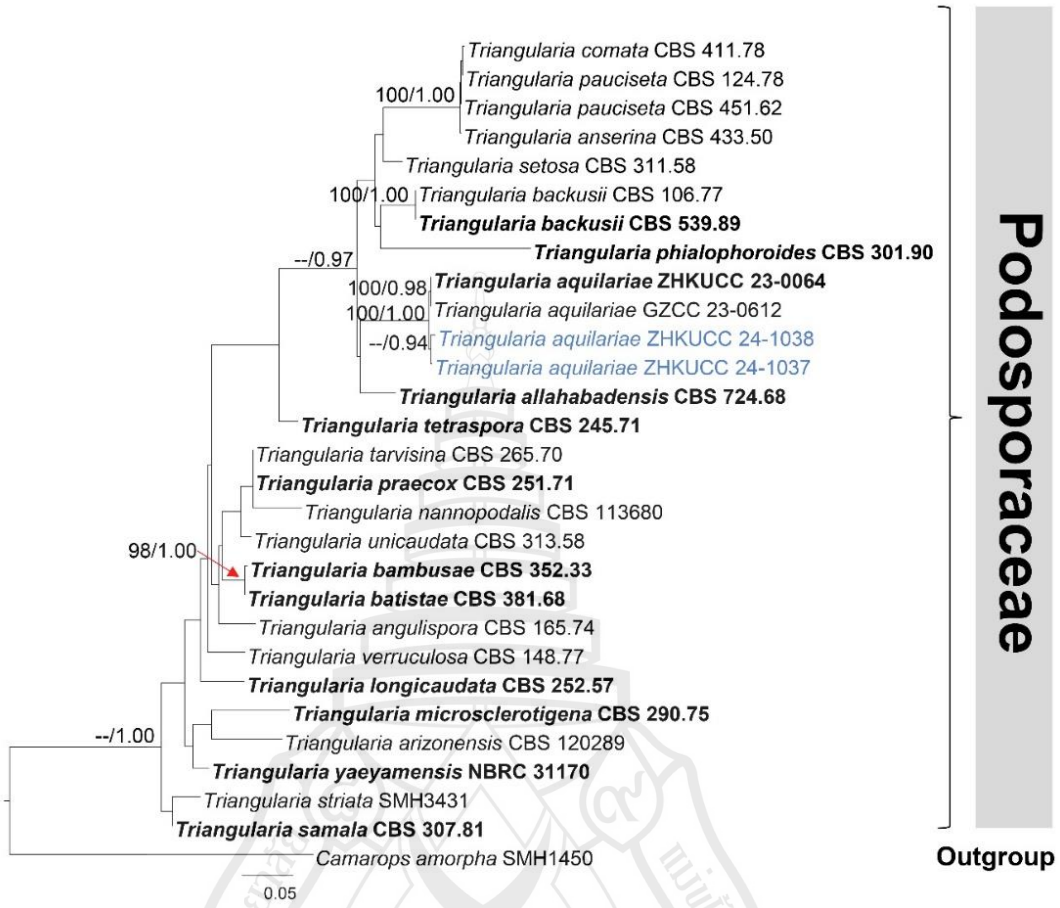


Figure 2.188 Phylogenetic tree of *Triangularia*

Figure 2.188 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB2*, and *TUB2* sequence data. Twenty-nine strains are included in the combined sequence analysis, which comprises 2,894 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Camarops amorpha* (SMH1450).

Triangularia aquilariae T. Y. Du, Tibpromma & Karun. JSE. (2024)

Index Fungorum number: IF 854005; *Facesoffungi number:* FoF 15269; Figure 2.150

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Ascomata* 200–350 × 300–400 µm ($\overline{x}$ = 280 × 331 µm, n = 15), semi-immersed, solitary or loosely aggregated, subglobose to obpyriform, glabrous, black. *Peridium* 30–40 µm wide ($\overline{x}$ = 34 µm, n = 30), membranaceous, outer layer composed of dark brown cells, inner layer composed of three to five layers of elongated to flattened, hyaline cells of *textura angularis* to *textura prismatica. Hamathecium* of 2.5–7.5 µm wide ($\overline{x}$= 4.2 µm, n = 30), hyaline, filiform, some broad, septate, branched, paraphyses, slightly constricted at the septa. *Asci* 200–280 × 10–18 µm ($\overline{x}$ = 230 × 13.5 µm, n = 30), 8-spored, unitunicate, thin-walled, biseriate to triseriate, elongated clavate or fusiform, long pedicellate and club-like, evanescent, or persistent until ascospores mature. *Ascospores* gelatinous bipolar appendages present at maturity, two-celled, upper cell 15–22 × 6.5–10 µm ($\overline{x}$ = 18 × 8.4 µm, n = 30), hyaline to dark brown, ellipsoid, truncate at the base, conical at the apex, with an apical germ pore; lower cell (primary appendage or pedicel) 25–40 µm long × 4.5–7 µm wide ($\overline{x}$ = 29 × 5.4 µm, n = 30), elongated and narrow, slightly sigmoid, hyaline to pale brown, with gelatinous secondary appendages, guttulate, smooth-walled, without ornamentations. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm in one month at 25°C, circular, filamentous, flat, fluffy with abundant aerial hyphae, white from above, yellowish from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* (100°96 E, 22°66 N, 1073 m), 2 April 2024, Li Lu, XAZC-2-11 (MHZU 24-0569), living culture ZHKUCC 24-1037, other living culture ZHKUCC 24-1038.

GenBank numbers: ZHKUCC 24-1037: ITS = PQ608334, LSU = PQ608166, *TUB*2 = PQ572192, *RPB*2 = PV357191; ZHKUCC 24-1038: ITS = PQ608335, LSU = PQ608167, *TUB*2 = PQ572193, *RPB*2 = PV357192.

Known hosts: On dead branch of *Aquilaria sinensis* (Du et al., 2024); *Coffea arabica* (This study).

Known distribution: China (Du et al., 2024; This study).

Notes: In the present phylogenetic analyses, our new collection clustered together with *Triangularia aquilariae* with 100% ML and 1.00 BYPP statistical support (Figure 2.149). *Triangularia aquilariae* was collected from *Aquilaria sinensis* (Thymelaeaceae) as a saprobe in Yunnan, China (Du et al., 2024). In morphology, our strains are identical to the holotype description of *T. aquilariae* (Figure 2.150; Du et al., 2024). We, therefore, identified our collection as *T. aquilariae* which is a new host record form *Coffea arabica* in China.

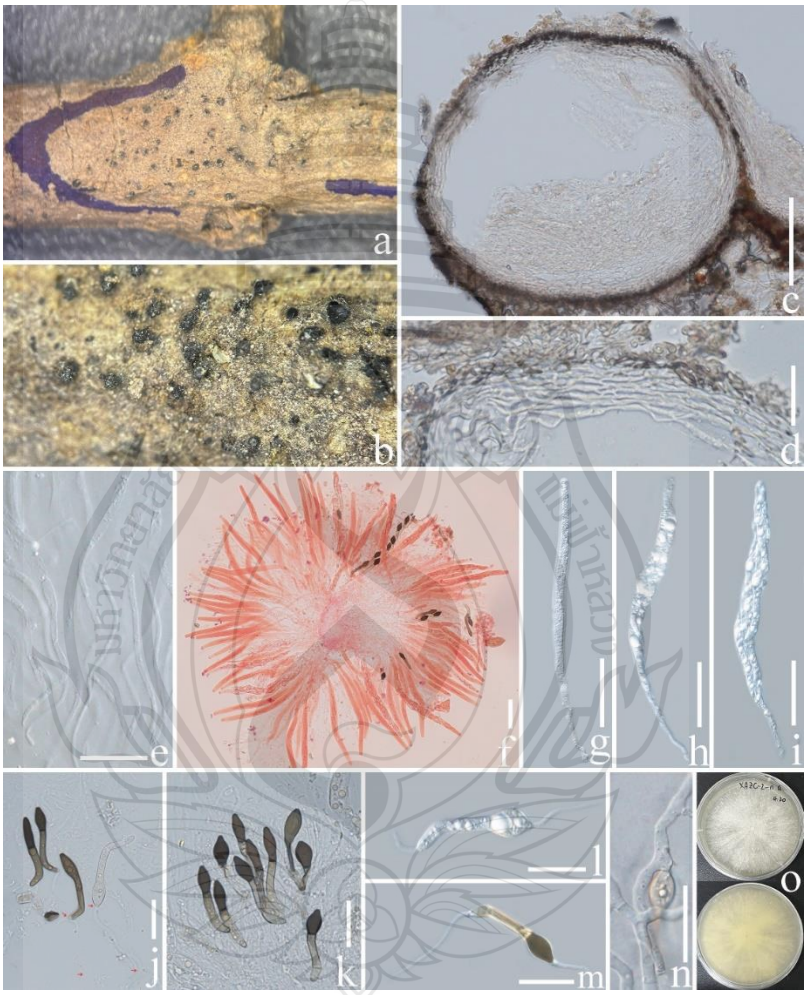


Figure 2.189 *Triangularia aquilariae* (MHZU 24-0569, new host record)

Figure 2.189 a, b Ascomata on a decaying branch of *Coffea arabica*. c Vertical section through ascoma. d Peridium. e Hamathecium. f–i Asci (f: Asci stained with Congo red reagent). j–m Ascospores. n Germinated ascospore. o Culture on PDA from above and below. Scale bars: c = 100 µm, d, e, j–n = 30 µm, f–i= 50 µm.

Sporidesmiales Crous, Persoonia 40: 377 (2018)

Sporidesmiaceae Fr., Summa vegetabilium Scandinaviae 2: 504 (1849)

Sporidesmium Link, Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin 3 (1): 41 (1809)

Notes: Sporidesmium was introduced by Link (1809) with *S. atrum* as the type, then redescribed by Ellis (1958) with a broad generic concept. Since morphological characters are very generic, *Sporidesmium* have segregated in different genera, namely *Ellisembia*, *Imimyces*, *Linkosia*, *Penzigomyces*, *Polydesmus*, *Repetophragma*, *Sporidesmiella* and *Stanjehughesia* (Subramanian, 1992; Hernandez-Gutierrez & Sutton, 1997). To date, 504 epithets of *Sporidesmium* are recorded in Index Fungorum (2025). However, many previously described species were revised and transferred to over 30 genera (Iturriaga et al., 2008; Hyde et al., 2020). Many *Sporidesmium* species are lost specimens and lack of molecular data, as they were published since in 1800s or early 1900s (Dong et al., 2021). Several studies shown the generic boundary based on morphological characteristics is problematic, phylogenetic analysis of combined ITS, LSU, SSU, *RPB*2 and *TEF*1-α sequence data has been carried out to further re-examine the classification of the *Sporidesmium* taxon, and it has been found that *Sporidesmium* is polyphyletic and they are also distributed in different families and orders of Dothideomycetes and Sordariomycetes (Su et al., 2016; Yang et al., 2018; Liu et al., 2019; Hyde et al., 2020; Bao et al., 2021).

Sporidesmium is a typical example to show the polyphyletic nature of freshwater hyphomycetes (Bao et al., 2021). Before 2017, the genus was only reported as an asexual morph and commonly found in freshwater in China and Thailand (Cai et al., 2003; Luo et al., 2004; Su et al., 2016; Yang et al., 2018; Luo et al., 2019). *Sporidesmium* asexual morph of characteristics by hyphomycetous, black and erumpent colonies on the substrate, brown, cylindrical, straight or curved and septate conidiophores, monoblastic, terminal and brown conidiogenous cells, and solitary, acrogenous, pale brown to brown, obclavate, or cylindrical with tapering ends conidia, with hyaline apex and truncate base, euseptate or distoseptate, truncate at the base, some with basal scar (Su et al., 2016). The first sexual morph of *S. thailandense* was introduced based on molecular data (Zhang et al., 2017), later Luo et al. (2019) reported the second sexual morph *S. lignicola*. The morphological characteristics of sexual

morphs, such as immersed ascomata with neck erumpent through host substrate, cylindrical asci with a distinct, refractive, wedge-shaped, and apical ring, and fusiform, hyaline ascospores (Zhang et al., 2017; Luo et al., 2019; Dong et al., 2021). In this study, four new species and two new records are introduced in *Sporidesmium*, based on both morphological and phylogenetic analyses.

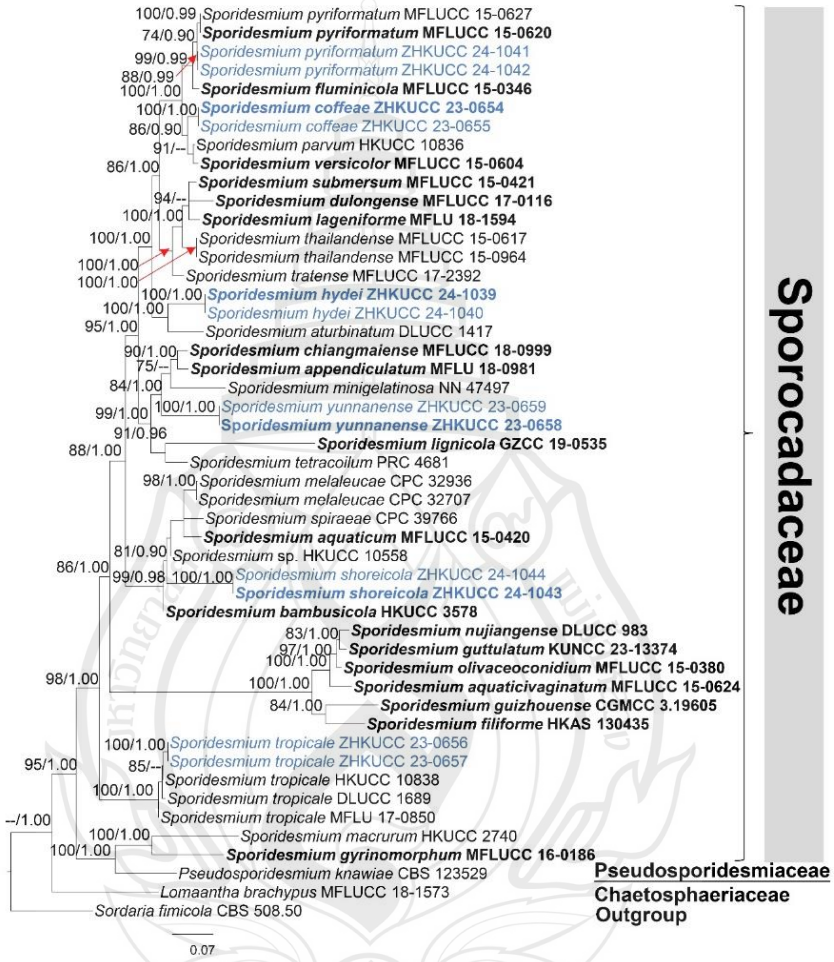


Figure 2.190 Phylogenetic tree of *Sporidesmium*

Figure 2.190 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, SSU, *RPB2* and *TUB2* sequence data. Forty-nine strains are included in the combined sequence analysis, which comprises 4,172 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Sordaria fimicola* (CBS 508.50).

Sporidesmium coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903648; *Facesoffungi number*: FoF 17608; Figure 2.152

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 23-0072

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on superficial substratum, solitary or clustered, hairy, effuse and brown to dark brown. *Mycelium* partly immersed, composed of septate, branched, hyaline to pale brown hyphae. *Conidiophores* 80–160 × 4–6 μm ($\bar{x}$ = 131 × 5.3 μm, n = 15), macronematous, mononematous, fasciculate, erect, cylindrical, straight or flexuous, up to 10-septate, with dark bands and constricted at the septa, unbranched, brown or olivaceous, surface smooth, some have verrucose. *Conidiogenous cells* 10–20 × 4–6 μm ($\bar{x}$ = 16 × 5.2 μm, n = 15), holoblastic, monoblastic, integrated, determinate, terminal, cylindrical or subcylindrical, pale brown to brown. *Conidia* 25–35 × 8–10 μm ($\bar{x}$ = 29 × 8.9 μm, n = 15), acrogenous, solitary, dry, pyriform, rostrate, straight or slightly curved, dark moderate orange to brown, truncate at the base, tapering towards and sub-hyaline at the apex, with sub-hyaline and roundish cells at apex, thin-walled, 3–4-septate, guttulate, without appendages, sheath absent.

Culture characteristics: Conidia germinating on PDA within 24 h, germ tubes produced from the apical cell of conidia. Colonies growing on PDA, reaching 20–30 mm in two months at 25°C, surface rough, raised, dry, circular and entire margin, from above, white and rough mycelia in the center, the edge is smooth and looks like fleshy pinks colloidal substance, from below, egg yellow in the center, white at the edge.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 17 November 2020, Li Lu, QX-C9 (MHZU 23-0072, holotype), ex-type ZHKUCC 23-0654, other living culture ZHKUCC 23-0655.

GenBank numbers: ZHKUCC 23-0654: ITS = PQ608338, LSU = PQ608170, SSU = PQ608021, *RPB*2 = PV357195, *TEF*1-α = PQ628179; ZHKUCC 23-0655: ITS = PQ608339, LSU = PQ608171, SSU = PQ608022, *RPB*2 = PV357196, *TEF*1-α = PQ628180.

Notes: Phylogenetic analysis of combined SSU, LSU, ITS, *TEF*1-α and *RPB*2 sequence data, supports the placement of *Sporidesmium coffeae* within *Sporidesmium* and reveals a close relationship to *S. parvum* (HKUCC 10836) and *S. versicolor* (MFLUCC 15-0604, ex-type) (Figure 2.151). In the BLASTn search of sequences, ITS, LSU and SSU sequences shown 94% (OP377871), 98% (OP377956) and 99% (OP378050) similarity with *Sporidesmium* sp. (KUNCC 23-12871), respectively. The *TEF*1-α and *RPB*2 sequences shown 96% (MF135663) and 91% (MF135650) similarity with *S. pyriformatum* (MFLUCC 15-0627), respectively. Morphologically, the conidial shape (pyriform) and color (brown) of *S. coffeae* resembles those of *S. parvum, S. pyriformatum* and *S. versicolor* (Hyde et al., 2016; Su et al., 2016; Yang et al., 2023). However, *S. coffeae* conidia are different from them by having 3–4-septate conidia, with subhyaline and roundish cells at the apex (Figure 2.152). Therefore, we introduce *S. coffeae* as new species in *Sporidesmium* with morphological and molecular data derived.



Figure 2.191 *Sporidesmium coffeae* (MHZU 23-0072, holotype)

Figure 2.191 a Colonies on host surface. b–e Conidiophores and conidia. f Germinated conidium. g Culture on PDA from above and below. h–l Conidia (l: SEM microphotographs of conidia). Scale bars: b, c = 50 μm, d, e = 30 μm, f, h–l = 10 μm.

Sporidesmium hydei L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903649; *Facesoffungi number*: FoF 17609; Figure 153

Etymology: The species epithet “hydei” is named in honour of Prof. Kevin D. Hyde for his contributions to mycology.

Holotype: MHZU 24-0570

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* effuse, gregarious, hairy, brown to black. *Mycelium* partly immersed in the substratum, partly superficial, septate, branched, brown, with smooth hyphae. *Conidiophores* 40–120 × 3–5 μm ($\bar{x}$ = 80 × 4 μm, n = 15), macronematous, mononematous, solitary or clustered, fasciculate, erect, cylindrical, straight or flexuous, with dark bands at the septa, up to 6-septate, brown, smooth-walled. *Conidiogenous cells* 10–16 × 4–6 μm ($\bar{x}$ = 14 × 5.5 μm, n = 15), holoblastic, monoblastic, integrated, terminal, subcylindrical, light brown, some swollen, smooth-walled. *Conidia* 17–28 × 7–9 μm ($\bar{x}$ = 24 × 8 μm, n = 30), acrogenous, solitary, clavate to pyriform or bell inverted shape, thin-walled, rostrate, tapering to the apex, straight, 2–4-septate, constricted at the septa, one or two upper cells subhyaline, lower cells brown to dark brown, guttulate.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 10 mm after one month at 25°C, surface rough, convex, circular, with entire or irregular margin, from above gray, from below dark olivaceous, outside white.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 15 April 2022, Li Lu, DH1-1 (MHZU 24-0570, holotype), ex-type ZHKUCC 24-1039, other living culture ZHKUCC 24-1040.

GenBank numbers: ZHKUCC 24-1039: ITS = PQ608342, LSU = PQ608174, *RPB*2 = PV367517, *TEF*1-α = PQ628183; ZHKUCC 24-1040: ITS = PQ608343, LSU = PQ608175, *RPB*2 = PV367518, *TEF*1-α = PQ628184.

Notes: In the phylogenetic analyses, *Sporidesmium hydei* forms a separate lineage with *S. aturbinatum* (DLUCC 1417, type) with 100% ML and 1.00 BYPP bootstrap support (Figure 2.151). In morphology, *S. hydei* differs from *S. aturbinatum* in having clavate to pyriform conidia, with 2–4 septa. In addition, the conidia of our

species are longer than *S. aturbinatum* (Ellis, 1958; Bao et al., 2021; Figure 2.153). Thus, based on morphology and phylogenetic support, *S. hydei* is introduced as a new species.

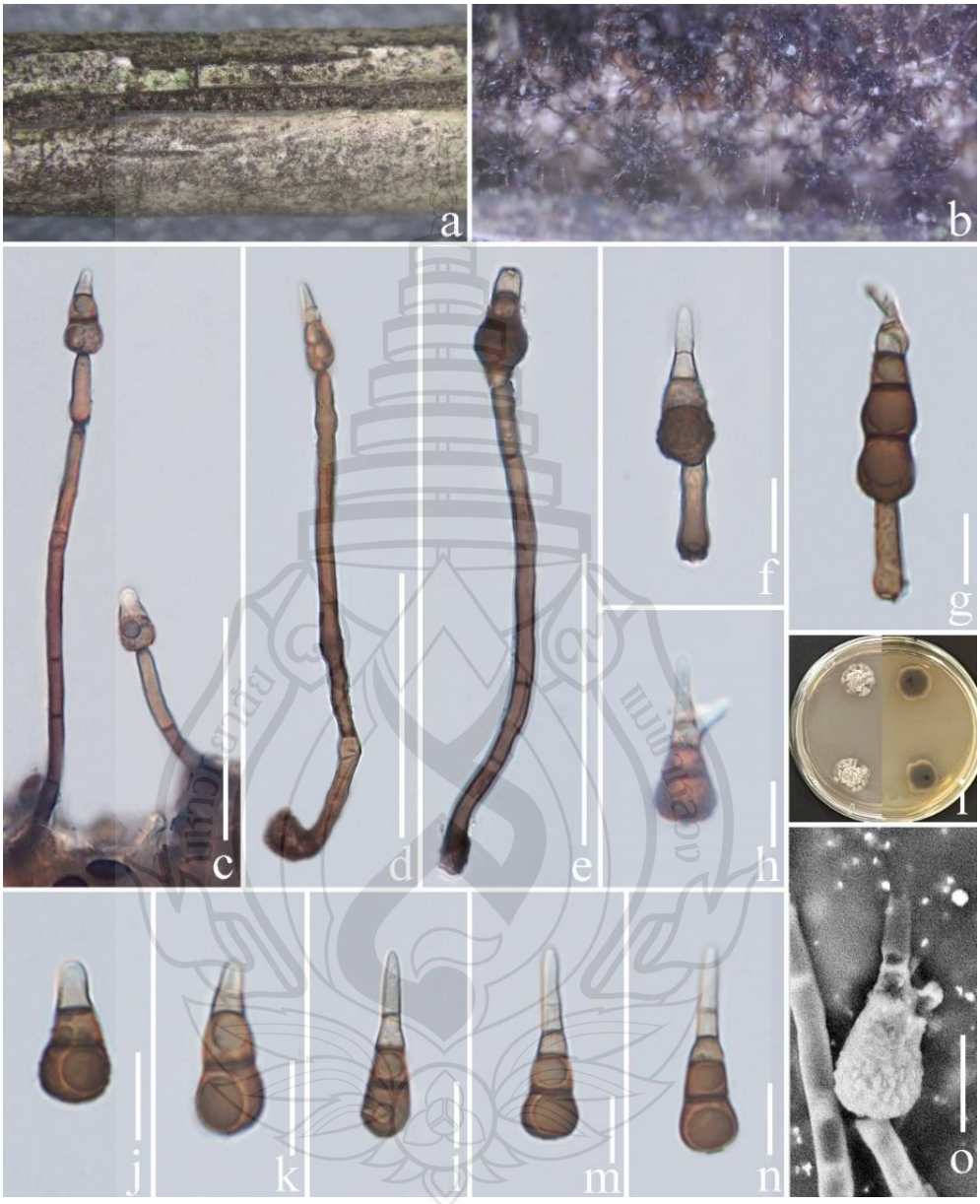


Figure 2.192 *Sporidesmium hydei* (MHZU 24-0570, holotype)

Figure 2.192 a, b Colonies on host surface. c–g Conidiophores and conidiogenous cells with conidia. h Germinated conidium. i Culture on PDA from above and below. j–o Conidia (o: SEM microphotographs of conidia showing rough surface). Scale bars: c–e = 50 µm, f–h, j–o = 10 µm.

Sporidesmium pyriformatum J. Yang & K.D. Hyde, Fungal Diversity 80: 216 (2016)

Index Fungorum number: IF 552227; *Facesoffungi number*: FoF 02245; Figure 2.154

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* superficial, effuse, gregarious, hairy, brown to black. *Mycelium* immersed in the substratum, partly superficial, septate, branched, hyaline to pale brown. *Conidiophores* 90–200 × 4–6 μm ($\bar{x}$ = 146 × 5 μm, n = 15), macronematous, mononematous, solitary or caespitose, cylindrical, straight or slightly flexuous, smooth, 4–8-septate, brown, paler towards the apex. *Conidiogenous cells* 12–25 × 4–6 μm ($\bar{x}$ = 19 × 5 μm, n = 15), holoblastic, integrated, lageniform, terminal, brown, darkened and truncate at the apex. *Conidia* 25–35 × 12–15 μm ($\bar{x}$ = 30 × 13 μm, n = 30), acrogenous, solitary, pyriform or obclavate, 2–5-septate, brown, with pale brown to subhyaline apical cell, round or conical at apex, darkened at the septa, guttulate.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA slowly, reaching 15 mm after two months at 25°C, surface rough, dense, flat, circular, with entire margin, from above white, from below white to yellowish.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 15 April 2024, Li Lu, DH1-4 (MHZU 24-0571), living culture ZHKUCC 24-1041, other living culture ZHKUCC 24-1042.

GenBank numbers: ZHKUCC 24-1041: ITS = PQ608336, LSU = PQ608168, *RPB2* = PV357193, *TEF*1-α = PQ628177; ZHKUCC 24-1042: ITS = PQ608337, LSU = PQ608169, *RPB2* = PV357194, *TEF*1-α = PQ628178.

Known hosts: on submerged wood (Hyde et al., 2016); *Coffea* sp. (This study).

Known distribution: Thailand (Hyde et al., 2016); China (This study).

Notes: Sporidesmium pyriformatum was isolated from submerged wood in Thailand by Hyde et al. (2016). In the combined phylogenetic analysis, our strain is phylogenetically most closely related to *S. pyriformatum* (MFLUCC 15-0620, ex-type) (Figure 2.151). Our isolate resembles *S. pyriformatum* in the shape and size of the

conidia. However, our collection (MHZU 24-0571) has dark brown conidia than the strain MFLU 15-1155 of *S. pyriformatum* (Hyde et al., 2016; Figure 2.154). This is the first record of *S. pyriformatum* isolated from coffee from China.

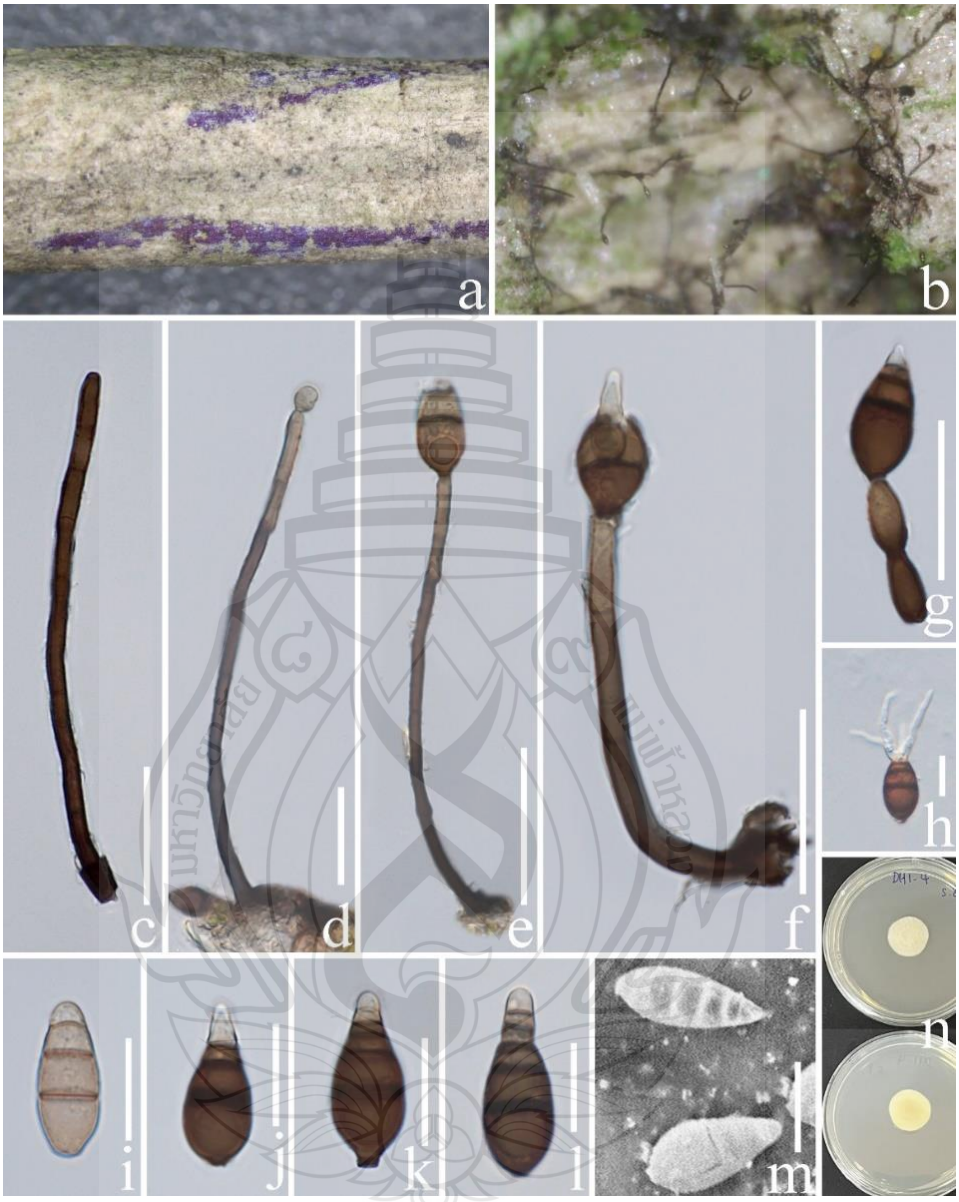


Figure 2.193 *Sporidesmium pyriformatum* (MHZU 24-0571, new host and country record)

Figure 2.193 a, b Colonies on host surface. c–g Conidiophores and conidiogenous cells with conidia. h Germinated conidium. i–m Conidia (m: SEM microphotographs of conidia). n Culture on PDA from above and below. Scale bars: c–g = 30 µm, h–m = 15 µm.

Sporidesmium shoreicola L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903650; *Facesoffungi number*: FoF 17610; Figure 2.155

Etymology: The species epithet refers to the short conidiophores.

Holotype: MHZU 24-0572

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* superficial, fluffy, effuse, gregarious, hairy, light brown and glistening. *Mycelium* immersed in the substratum, partly superficial, septate, branched, hyaline. *Conidiophores* 25–45 × 4–6 µm ($\bar{x}$ = 36 × 5 µm, n = 15), macronematous, mononematous, fasciculate, erect, cylindrical, straight or flexuous, solitary or sometimes in a small group, with dark bands at the septa, unbranched, brown, 4–6-septate, single or in groups. *Conidiogenous cells* 10–15 × 4–6 µm ($\bar{x}$ = 12 × 4.9 µm, n = 15), holoblastic, monoblastic, determinate, integrated, terminal, subcylindrical light brown, smooth. *Conidia* 50–140 × 4–7 µm ($\bar{x}$ = 92 × 5.9 µm, n = 30), acrogenous, solitary, thin and smooth-walled, light brown, filiform to pyriform or obclavate, rostrate, with a long and slender apex, straight or slightly curved, tapering to the apex, subhyaline to yellowish, 6–14-septate, with the proximal part usually verrucose, without a sheath.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 20 mm after one month at 25°C, wrinkled, flat, circular, with entire margin, from above white, and with hyalin aerial mycelium, from below yellowish.

Material examined: China, Yunnan Province, Dehong City, on a decaying branch of *Coffea* sp., 16 April 2024, Li Lu, DH3-2 (MHZU 24-0572, Holotype), ex-type ZHKUCC 24-1043, other living culture ZHKUCC 24-1044.

GenBank numbers: ZHKUCC 24-1043: ITS = PQ608344, LSU = PQ608176, SSU = PQ608025, *RPB*2 = PV367519, *TEF*1-α = PQ628185; ZHKUCC 24-1044: ITS = PQ608345, LSU = PQ608177, SSU = PQ608026, *RPB*2 = PV367520, *TEF*1-α = PQ628186.

Notes: In the phylogenetic analyses, *Sporidesmium shoreicola* is placed as an independent taxon in *Sporidesmium* with 81% ML and 0.90 BYPP statistical bootstrap support (Figure 2.151). *Sporidesmium shoreicola* shows the basic

characteristics of the genus *Sporidesmium* (hyphomycetes), by having fusiform, obclavate, obpyriform conidia (Ellis, 1958, 1971; Su et al., 2016). However, *Sporidesmium shoreicola* can be distinguished from other *Sporidesmium* species by short, unbranched and brown conidiophores, and light brown conidia, without a sheath (Su et al., 2016; Yang et al., 2018; Liu et al., 2019; Hyde et al., 2020; Bao et al., 2021; Figure 2.155). Therefore, we introduce *S. shoreicola* as a new species.



Figure 2.194 *Sporidesmium shoreicola* (MHZU 24-0572, holotype)

Figure 2.194 a, b Colonies on host surface. c, d Conidiophores and conidiogenous cells with conidia. e–k Conidia (k: SEM microphotographs of conidia). l Germinated conidium. m Culture on PDA from above and below. Scale bars: c, d = 50 µm, e–l = 20 µm.

Sporidesmium tropicale M.B. Ellis, Mycol. Pap. 70: 58 (1958)

Index Fungorum: IF 306326*, Facesoffungi number:* FoF 03363; Figure 2.156

Saprobic on a decaying branch of *Coffea arabica.* **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on superficial substratum, solitary or clustered, hairy, effuse and brown to black. *Mycelium* partly immersed, composed of septate, branched, brown hyphae. *Conidiophores* 200–300 × 6–8 µm ($\bar{x}$ = 227 × 7 µm, n = 15), macronematous, mononematous, unbranched, cylindrical, erect, straight or slightly flexuous, single, 6–16-septate, pale brown to dark brown, paler towards apex, smooth and thick-walled, single or in groups. *Conidiogenous cells* 15–25 × 5–7 µm ($\bar{x}$ = 20 × 6 µm, n = 15), monoblastic, holoblastic, terminal, integrated, percurrently proliferating, light brown, cylindrical, with rounded apex. *Conidia* 90–200 × 10–16 µm ($\bar{x}$ = 143 × 14 µm, n = 25), acrogenous, solitary, dry, pyriform, rostrate, obclavate and with verrucose, with a long and slender apex, straight or slightly curved, tapering to the apex, truncate at the base, dark brown, hyaline to pale brown at the apex, 10–18-septate, rough and thick-walled.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 30–40 mm in one months at 25°C, surface rough, with dense mycelia, flat, filiform, from above dark green, and with hyalin aerial mycelium, from below dark green to black, rugose.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica* (22°40'28", 100°56'9", 1090.5 m), 16 September 2021, Li Lu, puer 3-6 (MHZU 23-0073), living culture ZHKUCC 23-0656, other living culture ZHKUCC 23-0657.

GenBank numbers: ZHKUCC 23-0656: ITS = PQ608346, LSU = PQ608178, SSU = PQ608027, *RPB*2 = PV367521, *TEF*1-α = PQ628187; ZHKUCC 23-0657: ITS = PQ608347, LSU = PQ608179, SSU = PQ608028, *RPB*2 = PV367522, *TEF*1-α = PQ628188.

Known hosts: Psidium guajava (Eills, 1971), decaying wood in stream water (Yang et al., 2018), submerged decaying wood (Bao et al., 2021), *Hevea brasiliensis* (Senwanna et al., 2022), *Coffea arabica* (This study).

Known distribution: Bolivia, China, India, Ghana, Jamaica, Malaya, Nigeria, Sierra Leone, Sri Lanka, Thailand and USA (Ellis, 1958, 1971; Wu & Zhuang, 2005;

Yang et al., 2018; Bao et al., 2021; This study).

Notes: Sporidesmium tropicale was described by Ellis (1971) and reported from worldwide (Ellis, 1958, 1971; Wu & Zhuang, 2005; Yang et al., 2018; Bao et al., 2021). In the phylogenetic analyses (Figure 2.151), our new collection grouped with three strains of *S. tropicale* (DLUCC 1689, HKUCC 10838 and MFLU 17-0850) with statistical bootstrap support (85% ML). Besides, the morphological characteristics of this collection is the same as *S. tropicale* in Bao et al. (2021) (Figure 2.156). This is the first report of *S. tropicale* from coffee.



Figure 2.195 *Sporidesmium tropicale* (MHZU 23-0073, new host record)

Figure 2.195 a, b Colonies on host surface. c–f Conidiophores and conidiogenous cells with conidia. g–k Conidia (k: SEM microphotographs of conidium). l Germinated conidium. m, n Culture on PDA from above and below. Scale bars: c–f = 50 μm, g–l = 30 μm.

Sporidesmium yunnanense L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903651; *Facesoffungi number*: FoF 17611; Figure 2.157

Etymology: The species epithet refers to the location "Yunnan" from which the fungus was isolated.

Holotype: MHZU 23-0074

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* superficial, effuse, gregarious, hairy, brown to black. *Mycelium* partly immersed in the substratum, partly superficial, septate, branched, hyaline, with smooth hyphae. *Conidiophores* 30–80 × 5–6 μm ($\bar{x}$ = 54 × 5.3 μm, n = 15), macronematous, mononematous, fasciculate, erect, cylindrical, straight or flexuous, solitary or sometimes in a small group, with dark bands at the septa, 2–4-septate, unbranched, brown, smooth-walled. *Conidiogenous cells* 10–20 × 4–6 μm ($\bar{x}$ = 14 × 4.7 μm, n = 15), holoblastic, monoblastic, determinate, integrated, terminal, subcylindrical or ovoid, brown, some narrowly, single or in groups, smooth-walled. *Conidia* 50–100 × 7–10 μm ($\bar{x}$ = 75 × 8.5 μm, n = 20), acrogenous, solitary, thin-walled, smooth, clavate to fusiform, straight or slightly curved, subhyaline when young, pale olivaceous or yellowish when mature, with a truncate, cuneiform base, tapering towards apex, hyaline in apical cells, 0–10-distoseptate, sometimes constrict at penultimate cell, guttulate, apex with a hyaline, filamentous appendage, up to 50 μm long, without a sheath.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 40 mm after two months at 25°C, surface rough, wrinkled, flat, circular, with entire margin, from above orange, and with hyalin aerial mycelium, from below deep orange.

Material examined: China, Yunnan Province, Lincang City, on a decaying branch of *Coffea* sp. (960 m), 28 July 2022, Li Lu, LC2-C7 (MHZU 23-0074, holotype), ex-type ZHKUCC 23-0658, other living culture ZHKUCC 23-0659.

GenBank numbers: ZHKUCC 23-0658: ITS = PQ608340, LSU = PQ608172, SSU = PQ608023, *RPB*2 = PV367515, *TEF*1-α = PQ628181; ZHKUCC 23-0659: ITS = PQ608341, LSU = PQ608173, SSU = PQ608024, *RPB*2 = PV367516, *TEF*1-α = PQ628182.

Notes: In the phylogenetic analyses, *Sporidesmium yunnanense* is placed as an independent taxon in *Sporidesmium* with 84% ML and 1.00 BYPP strong bootstrap support (Figure 2.151). *Sporidesmium yunnanense* resembles *S. chiangmaiense* in having hyaline and filamentous appendage at the apex (Dong et al., 2021). However, its distinctive in the genus *Sporidesmium* in having constrict at penultimate cell and pale olivaceous or yellowish conidia (Bao et al., 2021; Dong et al., 2021; Figure 2.157). Comparison of ITS and LSU regions with *S. chiangmaiense* (MFLUCC 18-0999, ex-type), revealed 67 bp/490 bp (13%, without gaps) and 23 bp/838 bp (2.7%, without gaps) differences, respectively. Therefore, we introduce *S. yunnanense* as a new species.

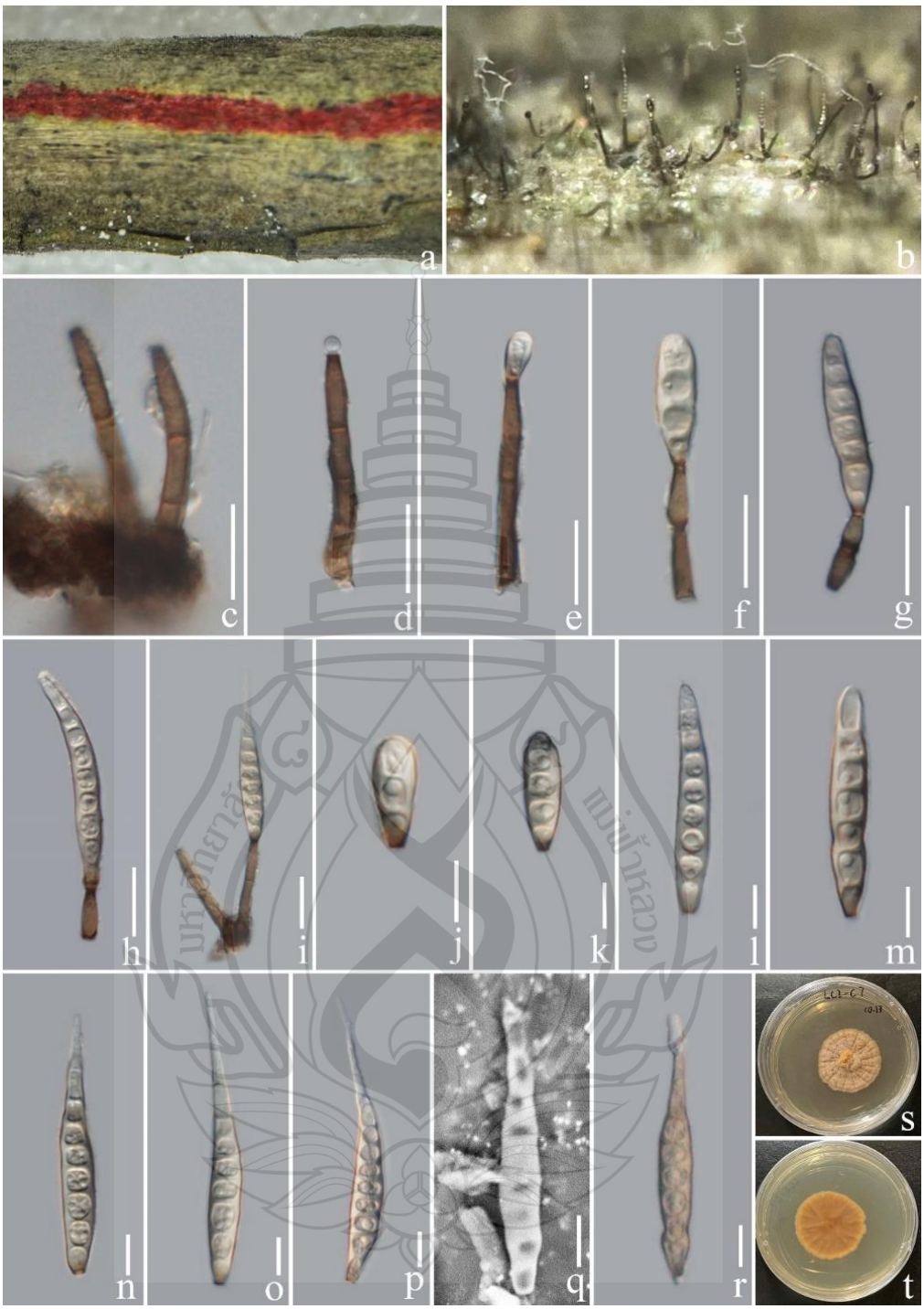


Figure 2.196 *Sporidesmium yunnanense* (MHZU 23-0074, holotype)

Figure 2.196 a, b Colonies on host surface. c–i Conidiophores and conidiogenous cells with conidia. j–q Conidia (q: SEM microphotographs of the conidia). r Germinated conidium. s, t Culture on PDA from above and below. Scale bars: c–i = 20 µm, j–q = 10 µm.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis Ser. IV. 8 (2): 66 (1932)

Coniocessiaceae Asgari & Zare, Mycological Progress 10 (2): 195 (2011)

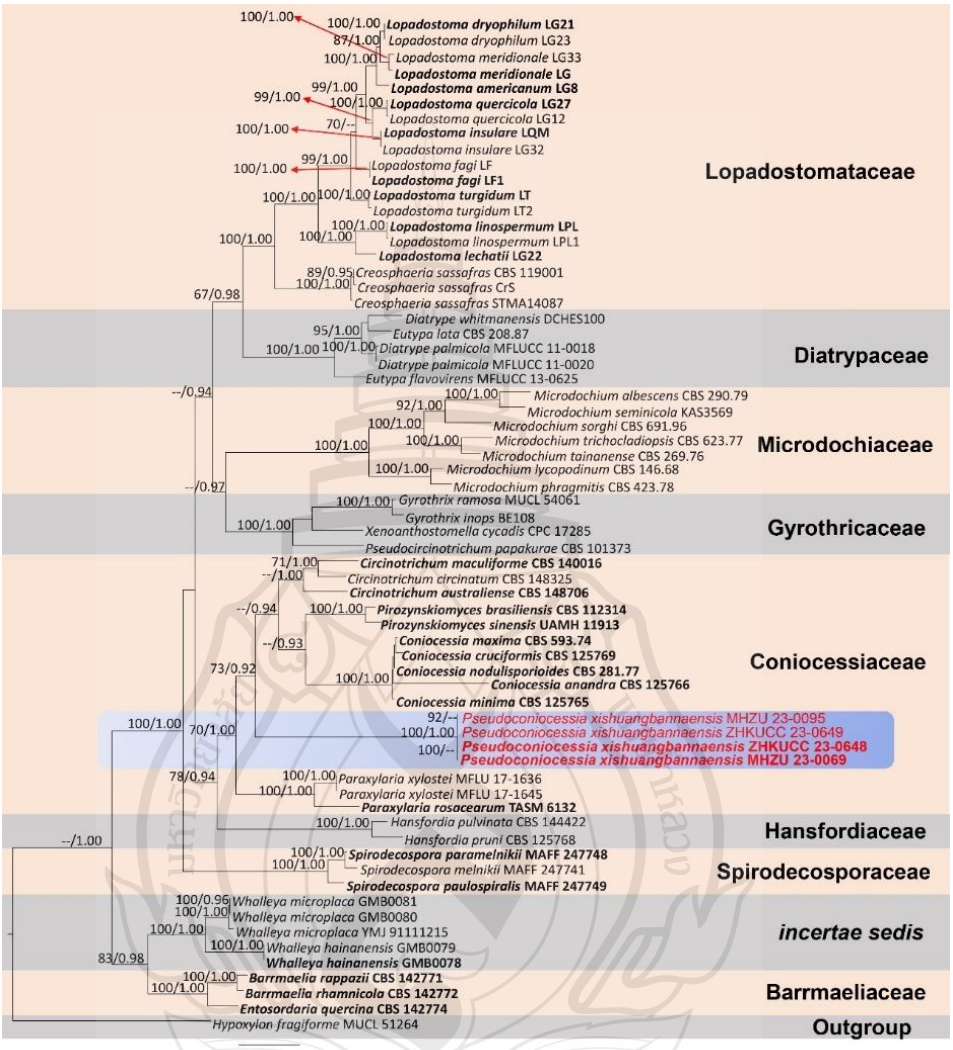


Figure 2.197 Phylogenetic tree of *Pseudoconiocessia*

Figure 2.197 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU and *RPB*2 sequence data. Sixty-six strains are included in the combined sequence analysis, which comprises 2,551 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in red. The tree is rooted with *Hypoxylon fragiforme* (MUCL 51264).

Pseudoconiocessia L. Lu & Tibpromma, *gen. nov.*

Index Fungorum number: IF 901343; *Facesoffungi number*: FoF 15057

Etymology: Named after its morphological similarity to *Coniocessia*.

Type species: *Pseudoconiocessia xishuangbannaensis*

Saprobic on dead or decaying plants. **Sexual morph:** *Ascomata* carbonaceous, some erumpent above the host surface, solitary or scattered, semi-immersed to immersed beneath the clypeus, visible as black patches, sub-globose to globose in shape, uni-loculate, cone-shaped, with ostiole at central, shiny black, periphasate ostiolar canal. *Peridium* brown to blackish brown, composed of cells of *textura angularis*. *Hamathecium* numerous, asepate, branched, flexuous, paraphyses. *Asci* 4–8-spored, unitunicate, cylindrical, hyaline, with furcate pedicel, with apical ring, J+ in Melzer's reagent. *Ascospores* uniseriate, yellowish to brown, fusiform or ellipsoid, straight, guttulate, conical at the lower end, aseptate, germ slit present when mature, without a sheath. **Asexual morph:** Not observed.

Notes: Based on phylogenetic analyses, our strains clustered within Coniocessiaceae and formed an independent lineage well separated from *Coniocessia* and *Paraxylaria* with 73% ML, 0.92 PP statistical support (Figure 2.1). However, *Pseudoconiocessia* can be distinguished from *Coniocessia* and *Paraxylaria* by aseptate hamathecium, 4–8-spored asci with flat apical ring, and fusiform ascospores, conical at lower end (Asgari & Zare, 2011; Wanasinghe et al., 2018; Samarakoon et al., 2022). *Coniocessia* consists of five species that are reported as epiphytic fungi with sexual morphs, some with nodulisporium-like anamorphs, while *Coniocessia* is different from *Pseudoconiocessia* by having 4-spored asci without apical structures, and with a distinct germ-slit extending over the whole length of the ascospores (Asgari & Zare, 2011), whereas *Paraxylaria* contains only two species and they were discovered as saprobic fungi with sexual morphs; it can be distinguished from *Pseudoconiocessia* by ascospores that lack germ slits (Wanasinghe et al., 2018; Samarakoon et al., 2022). Additionally, our new taxon shares similar morphology to the generic concept of Coniocessiaceae in having immersed ascomata with ostiole, and unitunicate asci with brown and ellipsoidal or fusiform ascospores (Asgari & Zare, 2011; Wanasinghe et al., 2018; Samarakoon et al., 2022). Therefore, *Pseudoconiocessia* is introduced here as a new genus in Coniocessiaceae, with *P. xishuangbannaensis* as the type species, isolated

from decaying twigs of Liberian coffee plants in China.

Pseudoconiocessia xishuangbannaensis L. Lu & Tibpromma, *sp. nov.*

Index Fungorum number: IF 901344; *Facesoffungi number*: FoF 15058; Figure 2.45

Etymology: The specific epithet refers to the location, Xishuangbanna, from where the holotype was collected.

Holotype: MHZU 23-0069

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph:** *Ascomata* 130–300 µm, 150–300 µm ($\overline{x}$ = 200 × 230 µm, n = 10), carbonaceous, some erumpent above the host surface, solitary or scattered, semi-immersed to immersed beneath the clypeus, visible as black patches, sub-globose to globose in shape, uni-loculate, cone-shaped, with short ostiole at central, shiny black, periphasate ostiolar canal. *Peridium* 10–20 µm ($\overline{x}$ = 15 µm, n = 20), hard in upper regions, outer layer blackish brown and thick-walled, inner layer hyaline and thin-walled, both composed of cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide ($\overline{x}$ = 2 µm, n = 20), composed of numerous, asepate, branched, flexuous, long, hyaline, paraphyses. *Asci* 50–75 × 4–5 µm ($\overline{x}$ = 66 × 4.5 µm, n = 20), 4–8-spored, unitunicate, cylindrical, hyaline, with a short furcate pedicel, with a thin flat apical ring, J+ in Melzer's reagent. *Ascospores* 7–9 × 2.5–3.5 µm ($\overline{x}$ = 7.8 × 3 µm, n = 30), uniseriate, yellowish to brown, fusiform or ellipsoid, straight, guttulate, sometimes conical at the lower end, aseptate, germ slit present when mature, without a sheath. **Asexual morph:** Not observed.

Culture characteristics: Ascospores germinated within 12 hours on PDA. Colonies grow on PDA at room temperature (20–25°C), reaching around 35 mm diam after one month. Colonies on PDA circular, white, surface smooth with aerial mycelium, entire margin. Yellowish on the reverse. No pigment produced in PDA media.

Material examined: Xishuangbanna, Yunnan Province, China, on decaying twigs of Liberian coffee (Rubiaceae), 24 November 2020, Li Lu, XTBG-C5 (MHZU 23-0069, holotype); ex-type ZHKUCC 23-0648; ibid., 12 July 2022, Li Lu, XSBN-C7 (ZHKU 23-0095, paratype); ex-paratype ZHKUCC 23-0649.

GenBank numbers: MHZU 23-0069: ITS = OR762241, LSU = OR762245, *TUB*2 = OR742341; MHZU 23-0095: ITS = OR762243, LSU = OR762247.

Notes: The phylogenetic analyses showed that *Pseudoconiocessia xishuangbannaensis* forms a monophyletic branch with 73% ML, and 0.92 PP statistical support (Figure 2.1). In morphology, *P. xishuangbannaensis* is similar to *Coniocessia* and *Paraxylaria*, but is distinguished from the two genera by aseptate hamathecium, 4–8-spored asci with a flat apical ring, and fusiform ascospores, conical at lower end (Asgari & Zare, 2011, Samarakoon et al., 2022, Figure 2.2). Herein we introduce *P. xishuangbannaensis* as a new species based on both morphological comparison and phylogenetic analyses. Based on the BLASTn results of ITS sequences of our strain (ZHKUCC 23-0648, ex-type) is 96.9% similar with Xylariomycetidae sp. (JQ761899), LSU and *RPB*2 results are similar to *Lopadostoma polynesium* (LAG) with 95% (KC774600) and 88% (KC774553), respectively. *Lopadostoma polynesium* was introduced in Lopadostomataceae by Rappaz (1995), but the species had initially been described as *Sphaeria polynesia* by Berkeley (1874). In our phylogenetic analysis, *L. polynesium* was placed outside Lopadostomaceae and appears as a sister group with our new species in Coniocessiaceae (Supplementary Figure 2.1) and our results showed the same placement of *L. polynesium,* which was also observed by Dhanushka et al. (2018). Based on nucleotide comparisons, *P. xishuangbannaensis* (ZHKUCC 23-0648) differs from *L. polynesium* (LAG) by 96/564 bp (17%, 39 gaps) in ITS, 60/957 bp (6%, without gaps) in LSU and 119/1085 bp (10%, without gaps) in *RPB*2. In morphology, *P. xishuangbannaensis* is similar to *L. polynesium* by having cylindrical asci and apical ring J+ in Melzer's reagent, with uniseriate and ellipsoid ascospores (Rappaz, 1995; Jaklitsch et al., 2014), while *P. xishuangbannaensis* has a flat apical ring in the asci that differs from apical rings in the plug and pendant of *L. polynesium* (Rappaz, 1995). However, the morphology of *L. polynesium* fits well with *Lopadostoma* by having cylindrical asci, brown and ellipsoid ascospores with rounded or sometimes weakly pointed ends (Rappaz, 1995), and also similar to the new genus *Pseudoconiocessia* by having brown and ellipsoid ascospores. While *L. polynesium* also showed a big difference with the type species *L. turgidum* (LT) (ITS-LSU 95/1916 bp, 5%) (Jaklitsch et al., 2014). Besides, Jaklitsch et al. (2014) revised the phylogeny and taxonomy of *Lopadostoma* based on both morphology and molecular phylogeny using LSU, ITS, and *RPB*2 sequences, and they also showed *L. polynesium* is phylogenetically distinct from *Lopadostoma*. Thus, it is advised that *L. polynesium* needs more fresh collections

to resolve the taxonomic problems and also to provide a better understanding of their phylogeny and evolution.

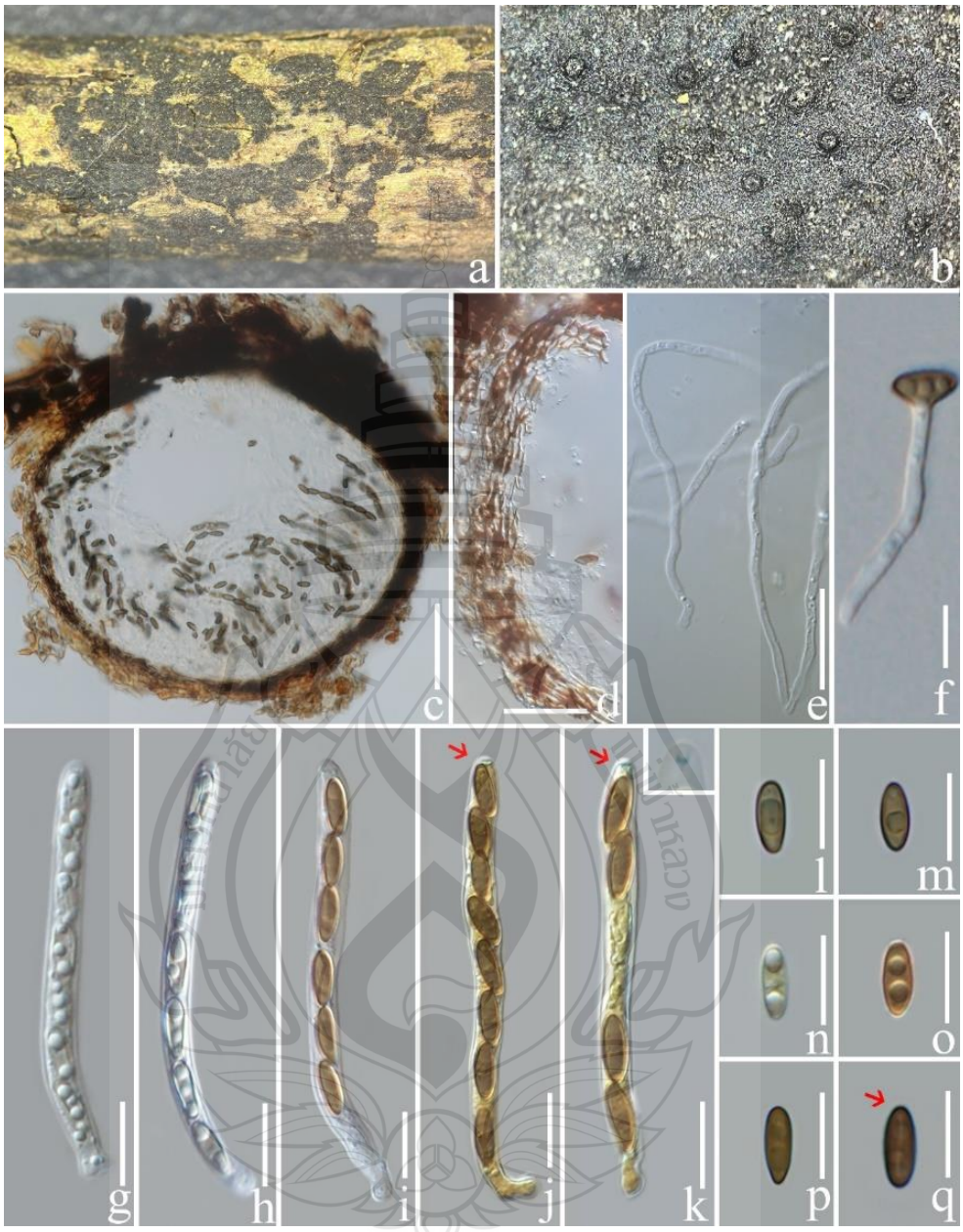


Figure 2.198 *Pseudoconiocessia xishuangbannaensis* (MHZU 23-0069, holotype)

Figure 2.198 a, b. Ascomata on Liberian coffee twig surface**.** c. A vertical section of an ascoma**.** d. Peridium of an ascoma**.** e. Hamathecium**.** f. A germinating ascospore**.** g–k. Asci (arrows indicate the thin apical ring J+ in Melzer's reagent)**.** l–q. Ascospores (arrows indicate the germ slit)**.** Scale bars**:** c = 50 µm, d, e = 20 µm, f–q = 10 µm.

Diatrypaceae Nitschke, Pyrenomycetes Germanici 1: 62 (1867)

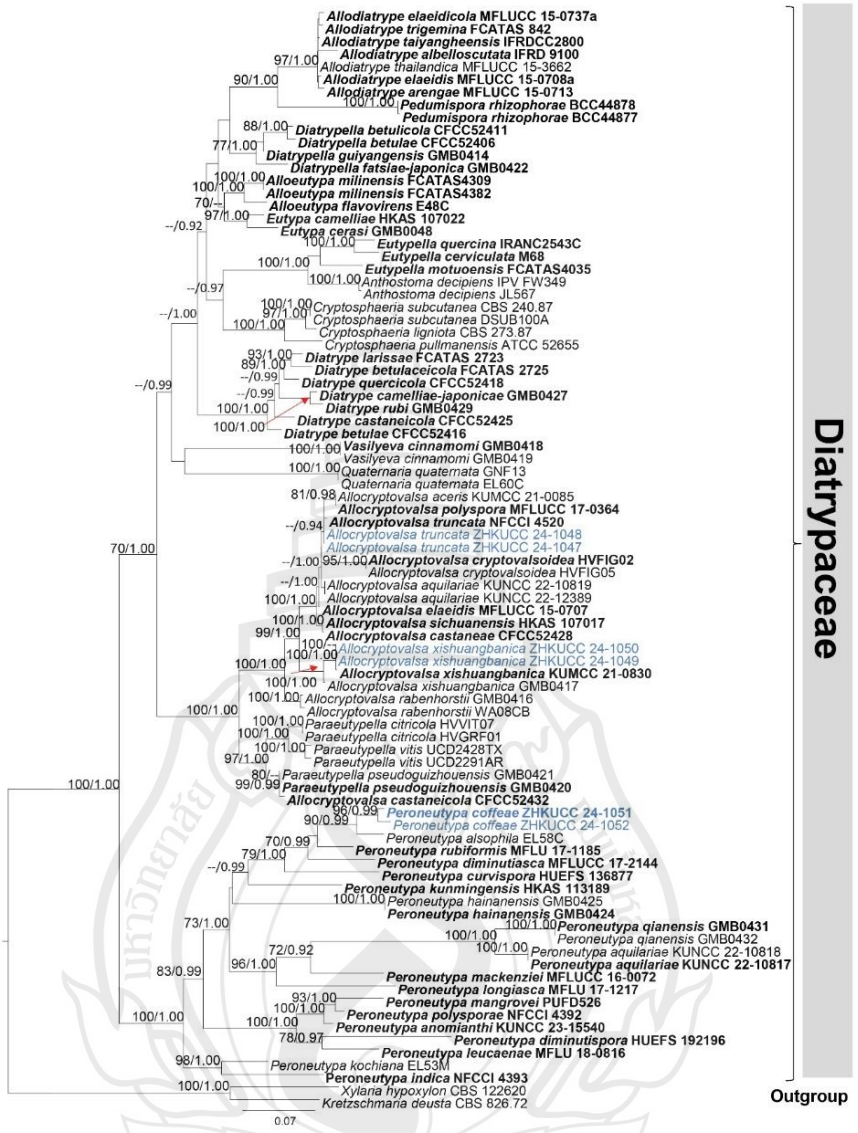


Figure 2.199 Phylogenetic tree of Diatrypaceae

Figure 2.199 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS and TUB2 sequence data. Eighty-seven strains are included in the combined sequence analysis, which comprises 1,780 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with Xylaria hypoxylon (CBS 122620) and Kretzschmaria deusta (CBS 826.72).

Allocryptovalsa Senwanna, Phookamsak & K.D. Hyde, Mycosphere 8(10): 1839 (2017)

Notes: *Allocryptovalsa* was introduced by Senwanna et al. (2017) and is typified by *A. polyspora*. Based on the phylogenetic analysis by de Almeida et al. (2016) and morphological evidence from Trouillas et al. (2011), *Eutypella cryptovalsoidea* and *Cryptovalsa rabenhorstii* were combined into *Allocryptovalsa* following in-depth phylogenetic and morphological analysis by Senwanna et al. (2017). *Allocryptovalsa* is characterized by immersed perithecia, ostioles with periphyses, polysporous asci and oblong to allantoid ascospores. The asexual morph exhibits hyaline and elongate allantoid conidia (Senwanna et al., 2017; Zhu et al., 2021; Chethana et al., 2023). *Allocryptovalsa* is a saprobic genus reported to inhabit various plants, primarily found in America, Australia, China, India, and Thailand (Trouillas et al., 2011; Senwanna et al., 2017; Konta et al., 2020; Zhu et al., 2021). There are 11 species listed in Index Fungorum (2025) under this genus. In this study, two new records (*A. xishuangbanica* and *A. truncata*) are introduced from coffee plants from China.

Allocryptovalsa xishuangbanica Maharachch. & Wanas., Life 12 (5, no. 635): 9 (2022)

Index Fungorum number: IF 843438; *Facesoffungi number*: FoF 17612; Figure 2.159

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Stromata* solitary to gregarious, with 2–4 locules, immersed to semi-immersed, erumpent through the surface of the bark. *Perithecia* 300–400 × 150–300 µm ($\overline{x}$ = 342 × 107 µm, n = 15), flask-shaped, perithecial necks erumpent in groups, dark brown, with individual ostioles. *Ostiole* central, numerous, gregarious, umbilicate, dark brown, periphysate. *Peridium* 20–30 µm wide ($\overline{x}$ = 25.4 µm, n = 20), outer layer comprising dark brown, thick-walled cells of *textura angularis*, inner layer composed of light brown to hyaline, thin-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* of 3–9 µm wide ($\overline{x}$ = 5.7 µm, n = 30), sparsely, filiform, septate, unbranched, hyaline, swollen, paraphyses. *Asci* 65–100 × 6–10 µm ($\overline{x}$ = 84.8 × 7.4 µm, n = 30), 8-spored, unitunicate, clavate, apically rounded, narrowing towards lower region, with long and fragile pedicels, without apical ring, with long stalks. *Ascospores* 7.5–10 × 2–3 µm ($\overline{x}$ = 8.7 × 2.6 µm, n = 30), elongate-allantoid, thin-walled, yellowish to pale brown at maturity,

slightly curved, aseptate, with two small guttules. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, circular, flat or effuse, slightly raised, fluffy, white to cream-colored from above, cream-colored from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 2 February 2024, Li Lu, XAZC-2-1 (MHZU 24-0577), living culture ZHKUCC 24-1049, other living culture ZHKUCC 24-1050.

GenBank numbers: ZHKUCC 24-1049: ITS = PQ608356, *TUB*2 = PQ572196; ZHKUCC 24-1050: ITS = PQ608357, *TUB*2 = PQ572197.

Known hosts: on a dead twig of an unidentified deciduous host (Maharachchikumbura et al., 2022), on branches of *Bombax ceiba* Linnaeus (Li et al., 2023), *Coffea arabica* (This study).

Known distribution: China (Maharachchikumbura et al., 2022; Li et al., 2023; This study).

Notes: Allocryptovalsa xishuangbanica was established as a distinct species within the genus *Allocryptovalsa*, as it possesses 8-spored asci, in contrast to the polysporous asci found in other species of the genus (Maharachchikumbura et al., 2022). The phylogeny suggests that our new collection shares a closely related phylogenetic affinity with *A. xishuangbanica* (KUMCC 21-0830, ex-type) (Figure 2.158). Further, the morphology is identical with the holotype description of *A. xishuangbanica* (Maharachchikumbura et al., 2022; Figure 2.159). Therefore, our new collection is identified as *A. xishuangbanica* and this is the first report of *A. xishuangbanica* from coffee.

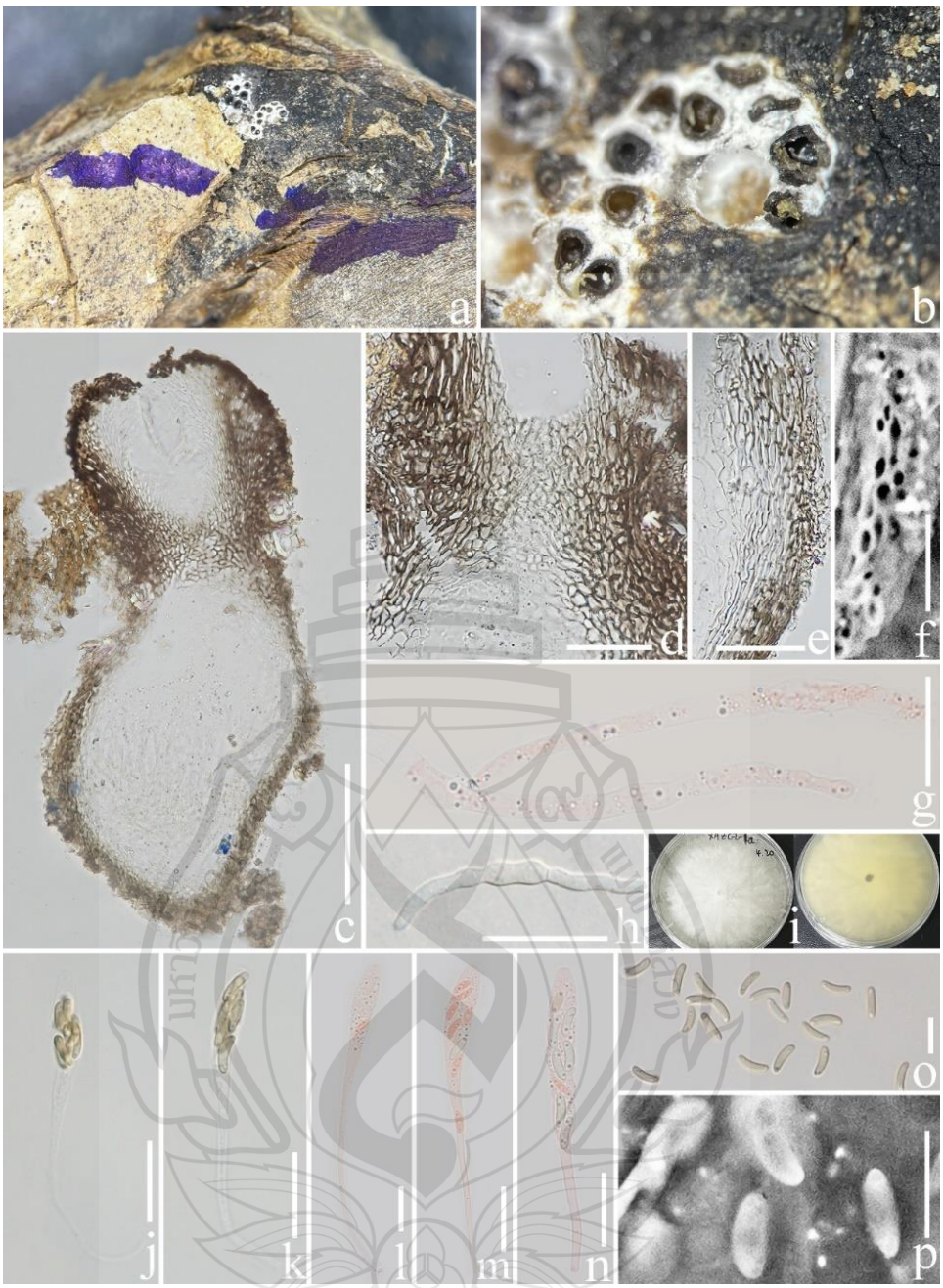


Figure 2.200 *Allocryptovalsa xishuangbanica* (MHZU 24-0577, new host record)

Figure 2.200 a Appearance of ascostromata on substrate. b Cross section through stroma. c Vertical section of stroma. d Ostiole with short periphyses. e, f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h Germinated ascospore. i Culture on PDA from above and below. j–n Asci (l–n: asci stained with Congo red reagent). o, p Ascospores (p: SEM microphotographs of ascospores). Scale bars: c = 100 µm, d–f = 30 µm, g, h, j–n = 20 µm, o, p = 10 µm.

Allocryptovalsa truncata M. Niranjan & V.V. Sarma, Mycosphere 11 (1): 572 (2020)

Index Fungorum number: IF 556619; *Facesoffungi number*: FoF 06262; Figure 2.160

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Stromata* superficial, in irregular clusters, beneath the periderm, outer black thin layer, inner white powdery coat around each ascoma. *Ascomata* 240–450 × 300–500 µm ($\overline{x}$ = 340 × 410 µm, n = 15), solitary or scattered, immersed, perithecial, coriaceous, subglobose, aggregated, raised individually, ostiolate, periphysate. *Peridium* 25–45 µm wide ($\overline{x}$ = 32.5 µm, n = 20), thick-walled, composed of dark brown to hyaline cells of *textura angularis*. *Hamathecium* of 3–10 µm wide ($\overline{x}$ = 6 µm, n = 30), septate and unbranched, hyaline, sparsely present, some with swollen, paraphyses. *Asci* 120–170 × 17–20 µm ($\overline{x}$ = 138.7 × 18.5 µm, n = 20), unitunicate, polysporous, clavate, with J-, apical ring, with a long pedicel, apices truncate, broader in the upper region, narrowing towards lower region. *Ascospores* 8–12 × 2.5–3.2 µm ($\overline{x}$ = 10 × 2.9 µm, n = 30), overlapping, hyaline to yellow-brown, allantoid, slightly curved, aseptate, smooth-walled, granulate almost invisible. **Asexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, white colony, flat, filamentous, from below center brown and white towards edges.

Material examined: China, Yunnan Province, Baoshan City, on a decaying branch of *Coffea* sp. (25°14' N, 98.8 E, 737.3 m), 30 July 2022, Li Lu, BS4-C6 (MHZU 24-0576), living culture ZHKUCC 24-1047, other living culture ZHKUCC 24-1048.

GenBank numbers: ZHKUCC 24-1047: ITS = PQ608354, *TUB*2 = PQ572194; ZHKUCC 24-1048: ITS = PQ608355, *TUB*2 = PQ572195.

Known hosts: decaying twigs (Hyde et al., 2020), *Coffea* sp. (This study).

Known distribution: India (Hyde et al., 2020), China (This study).

Notes: Allocryptovalsa truncata was described as a novel taxon distinguished by its unique feature of ascal apices (Hyde et al., 2020). In the phylogenetic tree, our two isolates (ZHKUCC 24-1047 and ZHKUCC 24-1048) developed a sister lineage to *A. truncata* (NFCCI-4520, ex-type) (Figure 2.158), and our isolates isolated from *Coffea* sp. from China. Morphologically, our new collection

fits well with *A. truncata* (Hyde et al., 2020; Figure 2.160). Based on a combination of phylogenetic and morphological evidence, our new collection is identified as *A. truncata*, it's the first report of this species on a coffee host in China.

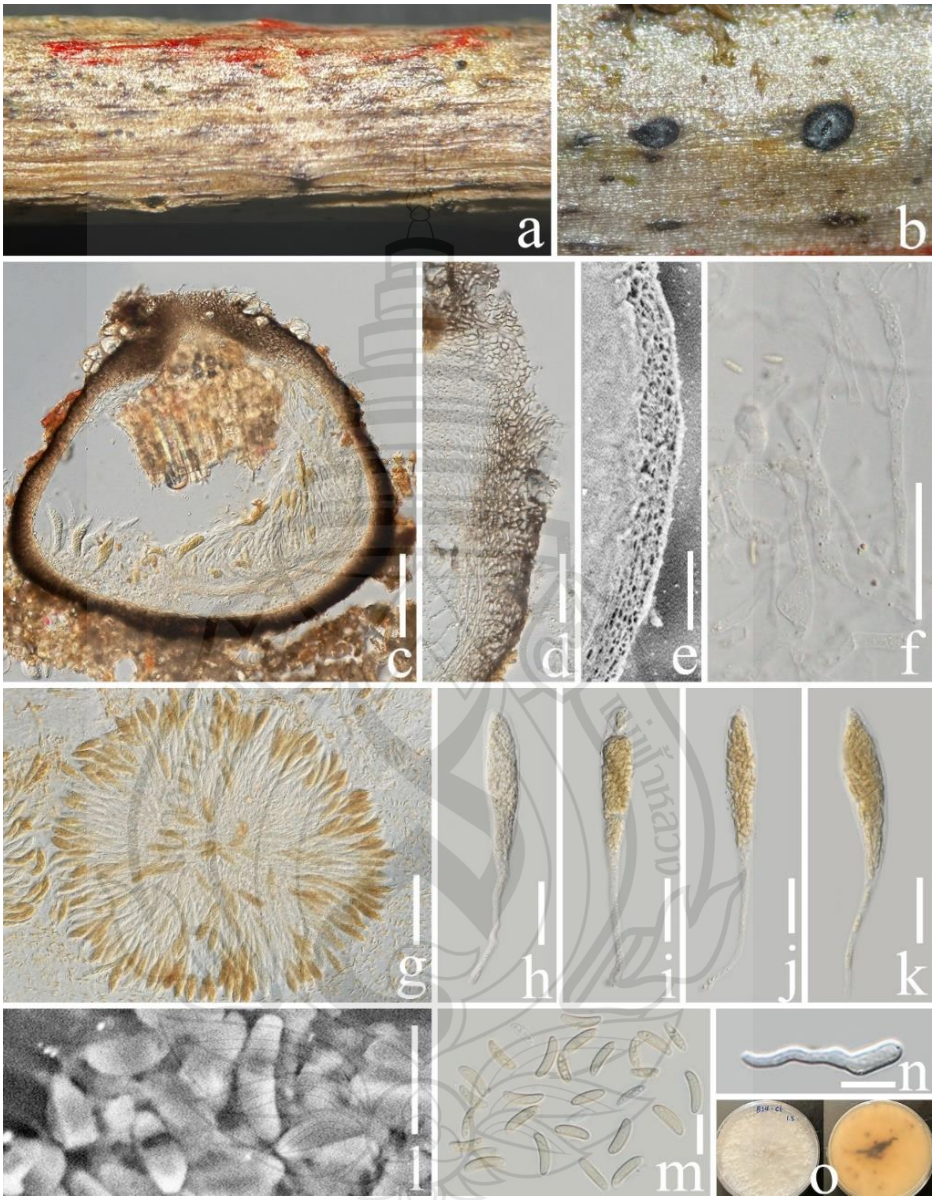


Figure 2.201 *Allocryptovalsa truncata* (MHZU 24-0576, new host and country record)

Figure 2.201 a, b Appearance of stromata on substrate. c Vertical section of stroma. d, e Peridium (e: SEM microphotographs of peridium). f Hamathecium. g–k Asci. l, m Conidia (l: SEM microphotographs of conidia). n Germinated ascospore. o Culture on PDA from above and below. Scale bars: c, g = 100 μm, d–f, h–k = 30 μm, l–n = 10 μm.

Peroneutypa Berl., Icon. fung. (Abellini) 3(3-4): 80 (1902)

Notes: *Peroneutypa* was initially introduced to accommodate *P. bellula*, *P. corniculata*, and *P. heteracantha* without assigning a type species (Berlese, 1902). Rappaz (1987) designated *P. bellula* as the type species and synonymized *Peroneutypa* with *Eutypella*. Nonetheless, *Peroneutypa* was reinstated to include eight species based on phylogenetic analyses by Acero et al. (2004) and morphological evidence by Carmarán et al., (2006). *Peroneutypa* is characterized by poorly developed, valsoid ascostromata, featuring packed, long prominent necks, sessile to long pedicels, small clavate asci with truncate apices, and allantoid, hyaline or yellowish ascospores (Carmarán et al., 2006, 2014; Senwanna et al., 2017; Shang et al., 2017; Du et al., 2022). Members of *Peroneutypa* are distributed globally, exhibiting different life modes such as saprobic or pathogenic in terrestrial, marine, and arboreal habitats (Du et al., 2022). As of now, 30 species are accepted in *Peroneutypa* (Hyde et al., 2024a). A new *Peroneutypa* species will be introduced from coffee host from China in this study.

Peroneutypa coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903639; *Facesoffungi number*: FoF 17613; Figure 2.161

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0578

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Stromata* solitary to gregarious, with 2–4 locules, immersed, becoming raised to erumpent by a small ostiolar canal, dark brown to black, glabrous, circular. *Ascomata* 180–400 × 160–360 µm ($\bar{x}$ = 242 × 246 µm, n = 15), perithecial, immersed in a stroma, dark brown to black, subglobose to ellipsoid, glabrous, with individual ostioles. *Ostiole* central, cylindrical, sulcate, with periphyses. *Peridium* 25–45 µm wide ($\bar{x}$ = 29.6 µm, n = 20) wide, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of light brown to hyaline, thin-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* of 3–8 µm wide ($\bar{x}$ = 5 µm, n = 30), sparsely, cylindrical, septate, constricted at the septa, hyaline, swollen, paraphyses. *Asci* 25–40 × 4–5.5 µm ($\bar{x}$ = 32.4 × 4.4 µm, n = 30), 8-spored, unitunicate, clavate, apically rounded to truncate, with J+, apical ring, with long and fragile pedicels. *Ascospores* 4–5 × 1.5–2 µm

($\bar{x}$ = 4.7 × 1.7 µm, n = 30), bi-seriate or overlapping, reniform to allantoid, some curved, aseptate, hyaline to yellowish, smooth-walled, with two small guttules. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA, reaching 60 mm after one month at 25°C, circular, flattened, cottony and fluffy, white to gray from above, yellowish to dark brown from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 2 February 2024, Li Lu, XAZC-2-3 (MHZU 24-0578, holotype), ex-type ZHKUCC 24-1051, other living culture ZHKUCC 24-1052.

GenBank numbers: ZHKUCC 24-1051: ITS = PQ608360, *TUB*2 = PQ572200; ZHKUCC 24-1052: ITS = PQ608361, *TUB*2 = PQ572201.

Notes: Two new strains (ZHKUCC 24-1051 and ZHKUCC 24-1052) form an independent lineage that is closely related to *Peroneutypa alsophila* (CBS 250.87, Lectotype), supported by 90% ML and 0.99 BYPP in our phylogenetic analysis of combined ITS and *TUB*2 sequence data (Figure 2.158). The morphology of *P. alsophila* (CBS 250.87) only have urn-shaped asci, with truncate apex and are wider in the middle where ascospores tend to be clustered (Carmarán et al., 2006), it is similar with our new collection (Figure 2.161). The base pair differences in ITS between the new strain (ZHKUCC 24-1051, ex-type) and *P. alsophila* (CBS 250.87) is 3.3% (17/512, without gaps); *P. Alsophila* lacks *TUB*2 genes. Therefore, we introduce *Peroneutypa coffeae* as a new species, based on morphology and phylogenetic analysis.

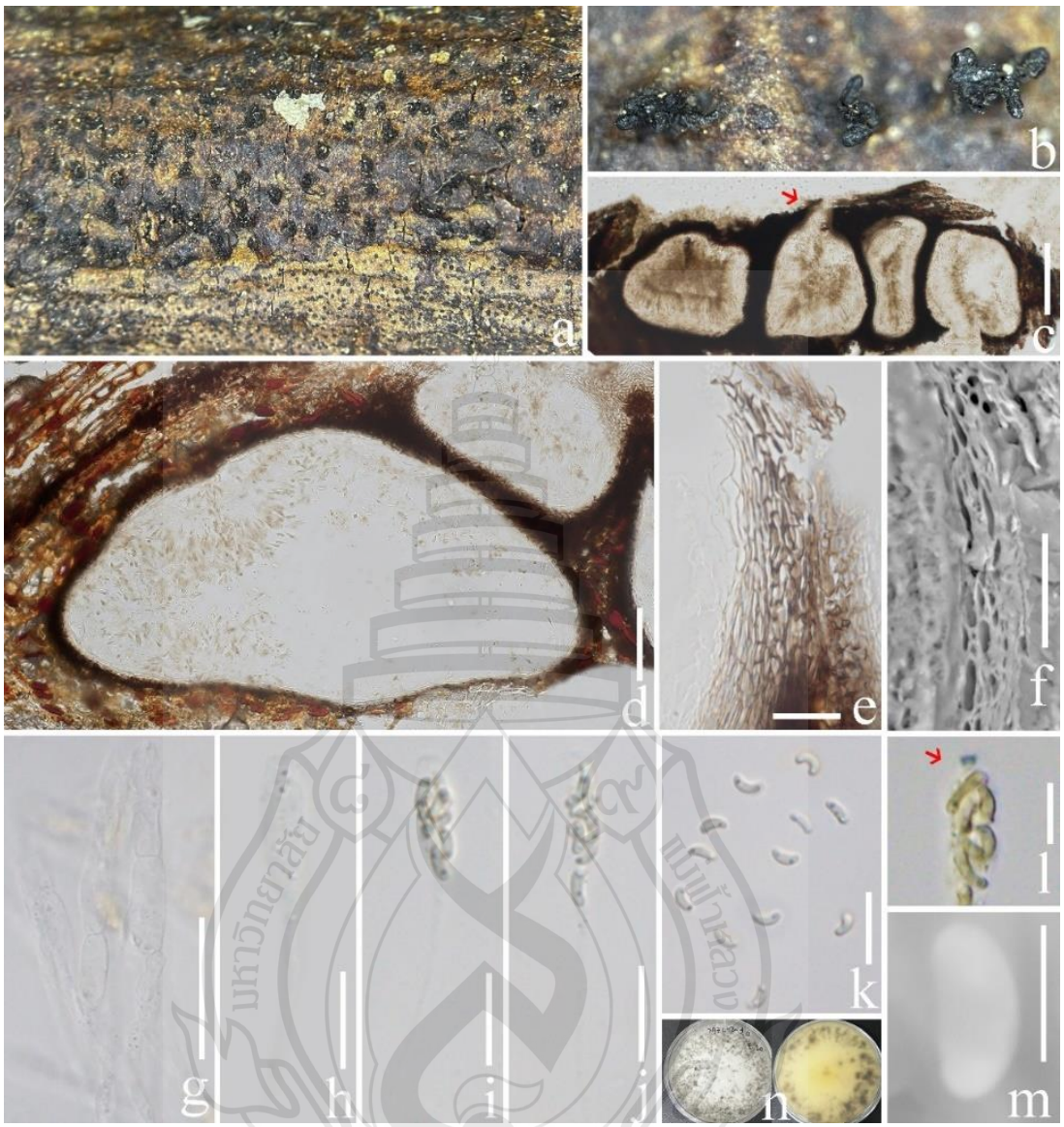


Figure 2.202 *Peroneutypa coffeae* (MHZU 24-0578, holotype)

Figure 2.202 a, b Appearance of stromata on substrate. c, d Vertical section of stromata (arrow indicates ostiole). e, f Peridium (f: SEM microphotographs of peridium). g Hamathecium. h–j Asci. k Conidia. l Ascus stained with Melzer's reagent, arrow indicates J+ apical ring. m SEM microphotographs of conidium). n Culture on PDA from above and below. Scale bars: c = 100 µm, d = 50 µm, e–g = 20 µm, h–l = 10 µm, m = 3 µm.

Hypoxylaceae DC. Fl. franc¸., Edn 3 (Paris) 2: 280 (1805)

Hypomontagnella Sir, L. Wendt & C. Lamb. Mycological Progress: 1–15 (2018)

Notes: Based on the analysis of combined ITS, LSU, *RPB*2 and *TUB*2 sequence data, Lambert et al. (2019) introduced *Hypomontagnella* to accommodate several species previously described as *Hypoxylon* species. *Hypomontagnella* with *H. monticulosa* as type species. *Hypomontagnella* appears highly similar to the genera *Annulohypoxylon*, *Jackrogersella*, and *Hypoxylon*, but *Hypomontagnella* differs from *Annulohypoxylon* and *Jackrogersella* by smooth perispores or with transversally striate ornamentations, and differs from *Hypoxylon* species in having woody to carbonaceous stromata, lacking colored granules, papillate ostioles usually with a black annulate disc, and without apparent KOH-extractable pigments in mature stromata (Lambert et al., 2019). *Hypomontagnella* has six epithets listed in Index Fungorum (2025). *Hypomontagnella* is characterized by waxy to carbonaceous stromata, lacking colored granules below the stromatal surface, mature stromata without KOH-extractable pigments, ostioles conical-papillate usually encircled by a superficial or slightly concave black annulate disc, the anamorph more usually with virgariella-like branching patterns (Lambert et al., 2019). In this study, a new species *Hypomontagnella coffeae* is introduced from coffee host from China.

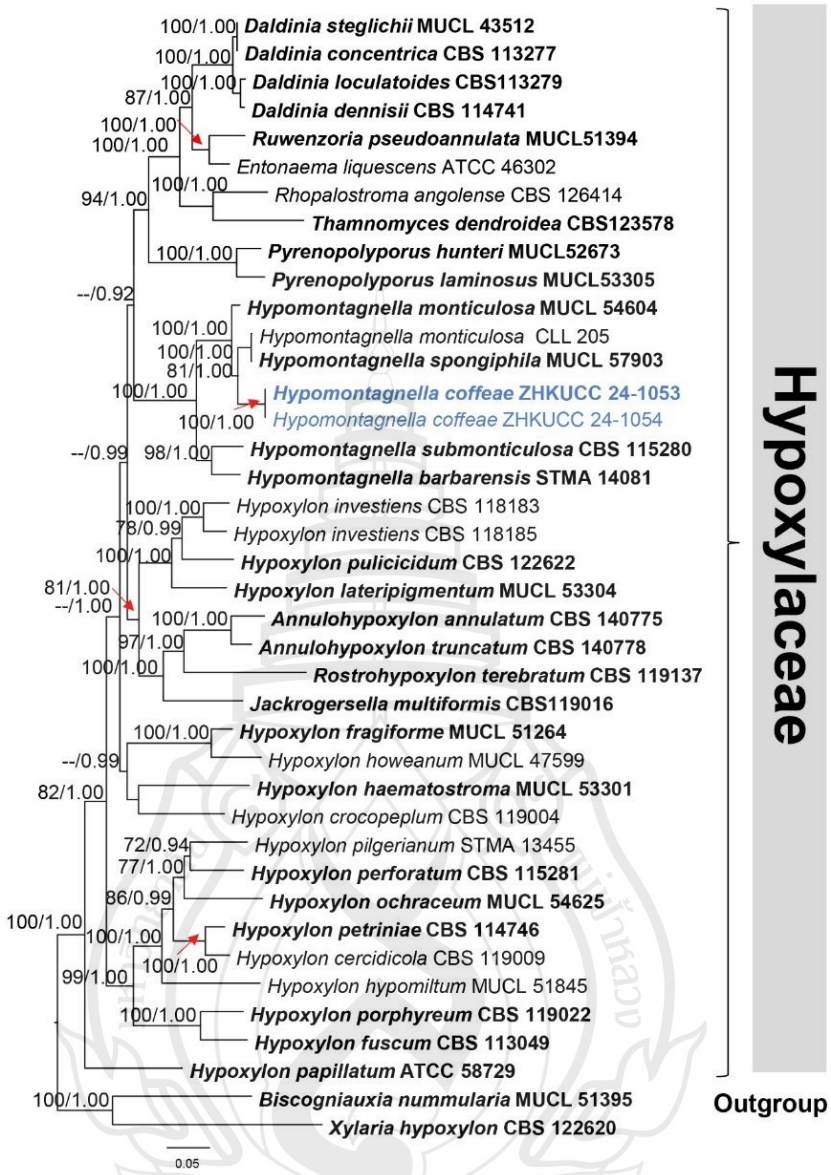


Figure 2.203 Phylogenetic tree of *Hypomontagnella*

Figure 2.203 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2 and *TUB*2 sequence data. Forty strains are included in the combined sequence analysis, which comprises 4,203 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Xylaria hypoxylon* (CBS 122620) and *Biscogniauxia nummularia* (MUCL 51395).

Hypomontagnella coffeae L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903614; *Facesoffungi number*: FoF 17614; Figure 2.163

Etymology: The species epithet refers to the host genus "*Coffea*" from which the fungus was isolated.

Holotype: MHZU 24-0579

Saprobic on a decaying branch of *Coffea arabica*. **Sexual morph**: *Stromata* effused-pulvinate, with conspicuous perithecial mounds, surface black, blackish woody to carbonaceous tissue immediately beneath surface and between perithecia. *Perithecia* 350–500 × 250–400 μm ($\overline{x}$ = 526 × 310 μm, n = 15), spherical to obovoid, ostioles central, minutely conical papillate. *Peridium* 18–30 μm wide ($\overline{x}$ = 22.4 μm, n = 20), carbonaceous texture, composed of two layers, inner layer hyaline, arranged in a *textura angularis* cells, outer layer brown, thick-walled, composed of *textura prismatica* cells. *Hamathecium* of 3.5–6 μm wide ($\overline{x}$ = 4.4 μm, n = 20), hypha-like, granulate, aseptate, prominent, paraphyses. *Asci* 85–115 × 5–6.5 μm ($\overline{x}$ = 97 × 5.8 μm, n = 20), 8-spored, cylindrical, unitunicate, with amyloid, discoid apical apparatus, with J+, wedge-shaped apical ring bluing in Melzer's reagent. *Ascospores* 5–10 × 3–4.5 μm ($\overline{x}$ = 7.6 × 3.6 μm, n = 30), uniseriate, hyaline to brown, ellipsoid-inequilateral, unicellular, guttulate, with broadly to less frequently narrowly rounded ends, with straight germ slit spore-length on convex side, dehiscent perispore in 10% KOH. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA, colonies grow on PDA, rough, soft, cotton, circular, flat, entire edge, white from above, cream to yellowish from below.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea arabica*, 18 March 2023, Li Lu, XAZC2 (MHZU 24-0579, holotype), ex-type ZHKUCC 24-1053, other living culture ZHKUCC 24-1054.

GenBank numbers: ZHKUCC 24-1053: ITS = PQ608362, LSU = PQ608188, *RPB2* = PV367531; ZHKUCC 24-1054: ITS = PQ608363, LSU = PQ608189, *RPB2* = PV367532.

Notes: Based on phylogenetic analyses, our isolates clustered with *Hypomontagnella monticulosa* (MUCL 54604 (type) and CLL 205) and *Hypomontagnella spongiphila* (MUCL 57903, type) (Figure 2.162). *Hypomontagnella coffeae* and

H. monticulosa are different by having without the KOH-extractable pigments vinaceous purple in young stromata (Lambert et al., 2019; Figure 2.163). While *Hypomontagnella spongiphila* was proposed as a new marine-derived lineage, the sexual and asexual morph characteristics were not given (Wibberg et al., 2021). Moreover, base pair comparison of *H. coffeae* (ZHKUCC 24-1053, ex-type) and *H. monticulosa* (MUCL 54604, type) shows 8/567 bp differences in ITS (1.4%, gap 1 bp), 18/882 bp differences in LSU (2%, gaps 3 bp), 18/1003 bp differences in *RPB*2 (1.8%), compared with *H. spongiphila* (MUCL 57903, type) shows 10/532 bp differences in ITS (1.9%, gaps 2 bp), 23/887 bp differences in LSU (2.6%, gaps 7 bp), 25/1151 bp differences in *RPB*2 (2.2%, gaps 2 bp). Therefore, we introduce *H. coffeae* as a new species based on morphology and multigene phylogenetic analysis.

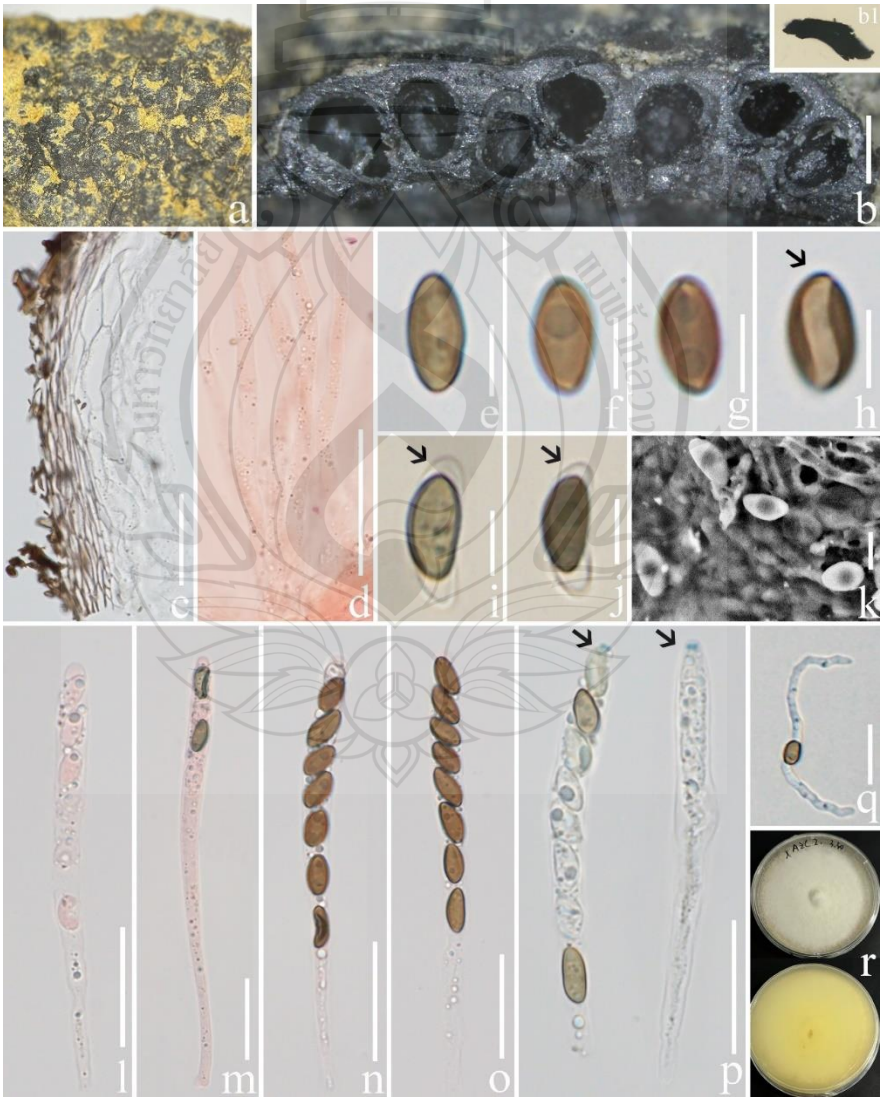


Figure 2.204 *Hypomontagnella coffeae* (MHZU 24-0579, holotype)

Figure 2.204 a Stromata on host surface. b Stromata in vertical section showing the perithecia and the sub-perithecial tissue (b1: Young stromata in KOH solution without pigments). c Peridium. d Hamathecium stained with Congo red reagent. e–h Ascospores in water (arrow indicates germ slit). i, j Arrow indicates ascospores with dehiscent perispore stained with 10% KOH. k SEM microphotographs of ascospores. l–p Asci (l, m: Asci stained with Congo red reagent, p: Asci stained with Melzer's reagent, arrow indicates J+ apical ring). q Germinated ascospore. r Culture on PDA from above and below. Scale bars: b = 300 μm, c, d = 30 μm, e–k= 5 μm, l–q = 20 μm.

Xylariaceae Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei - Valsei - Sphaeriei 2: 3 (1863)

Muscodor Worapong, Strobel & W.M. Hess, Mycotaxon 79: 71 (2001)

Notes: *Muscodor* was introduced by Worapong et al. (2001) based on their characteristic volatile organic compounds and inconclusive hyphal characters. The evolutionary position of the genus *Muscodor* was considered questionable due to the absence of taxon sampling and reference data (Stadler et al., 2013). Lumbsch and Huhndorf (2010) did not accept the genus, but Seifert and Gams (2011), Maharachchikumbura et al. (2016), and Daranagama et al. (2018) accepted the genus and placed it in Xylariales genera *incertae sedis*, in the concept of this genus with other generic concepts of Xylariaceae. Wendt et al. (2018) proposed to reject the genus from the family due to poor taxonomic standards. Based on a polyphasic taxonomic approach, including a multi-locus genealogy, as well as volatile metabolite profiles and dual culture experiments, Samarakoon et al. (2020) include *Muscodor* in *Induratia*, and erected nine new species and several new combinations of *Induratia*. However, Cedeño-Sanchez et al. (2023) re-identified the type species of *Induratia* (*I. apiospora*, ex-holotype) through detailed morphological and molecular phylogenetic analyses. Their study revealed a close relationship between *I. apiospora* and Barrmaeliaceae, and they formally reintroduced *Muscodor* as an independent genus within Xylariaceae. *Muscodor* has 26 epithets listed in Index Fungorum (2025), with *M. albus* as the type species. In this study, a new species, *M. puerensis* is introduced from a coffee host from China.

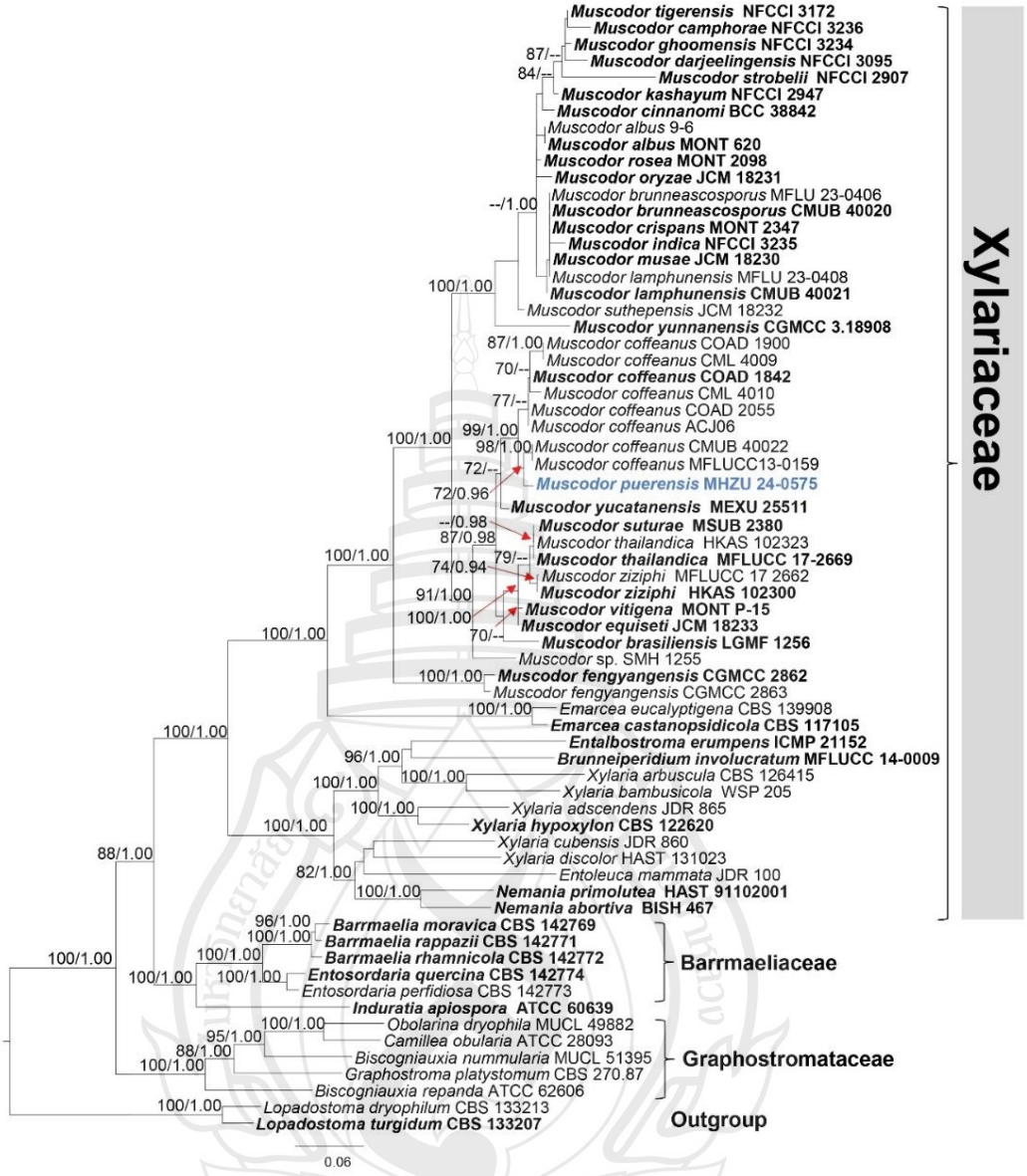


Figure 2.205 Phylogenetic tree of *Muscodor*

Figure 2.205 Phylogram generated from maximum likelihood analysis based on a combined dataset of ITS, LSU, *RPB*2, and *TUB*2 sequence data. Sixty-eight strains are included in the combined sequence analysis, which comprises 4,283 characters with gaps. The tree topology of the ML analysis was similar to the BYPP. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. All type strains are in black bold, and newly generated sequences are in blue. The tree is rooted with *Lopadostoma turgidum* (CBS 133207) and *L. dryophilum* (CBS 133213).

Muscodor puerensis L. Lu, K.D. Hyde & Tibpromma, *sp. nov.*

Index Fungorum number: IF 903624; *Facesoffungi number*: FoF 17615; Figure 2.165

Etymology: The species epithet refers to the type location "Pu'er", China.

Holotype: MHZU 24-0575

Saprobic on a decaying branch of *Coffea* sp. **Sexual morph**: *Ascomata* 180–320 × 200–380 µm ($\overline{x}$ = 263 × 280 µm, n = 15), immersed, visible as blackened, solitary or rarely gregarious, globose to subglobose, attached to substrate with a broad base. *Peridium* 25–35 µm wide ($\overline{x}$ = 28, n = 20), thick-walled, composed of several layers, inner layer hyaline, middle layer pale-brown to brown of *textura angularis*, out layer brown. *Hamathecium* of 3.5–6.5 µm wide ($\overline{x}$ = 5, n = 20), hypha-like, unbranched, septate, prominent, swollen, paraphyses. *Asci* 90–160 × 5.5–8.5 µm ($\overline{x}$ = 123 × 7 µm, n = 30), 8-spored, unitunicate, cylindrical, hyaline, short pedicellate, apically rounded, with J+ apical ring bluing in Melzer's reagent. *Ascospores* 10–15 × 3.5–6.5 µm ($\overline{x}$ = 13.4 × 5.2 µm, n = 30), uniseriate, ellipsoidal, hyaline, constricted apiosporous; apical cell long, conical shape, guttulate with remnants at the top, with the hat-like sheaths at the bases; base cell short, guttulate at the base. **Asexual morph**: Not observed.

Material examined: China, Yunnan Province, Pu'er City, on a decaying branch of *Coffea* sp., 16 September 2021, Li Lu, puer 1-2 (MHZU 24-0575, holotype).

GenBank numbers: MHZU 24-0575: ITS = PQ608358, LSU = PQ608186, *RPB2* = PV367529, *TUB2* = PQ572198.

Notes: Based on phylogenetic analyses of combined ITS, LSU, *RPB2*, and *TUB2*, the new collection MHZU 24-0575 formed a sister lineage to *Muscodor coffeanus* (MFLUCC 13-0159), with 72% ML and 0.96 BYPP statistical support (Figure 2.164). *Muscodor coffeanus* (COAD 1842, ex-type) was introduced as an endophyte based on molecular phylogenetic studies and hyphal characteristics, which isolated from the stems of *Coffea arabica* from Brazil (Hongsanan et al., 2015). Later, many endophyte strains of *M. coffeanus* were re-isolated by da Silva et al. (2021) and Gomes et al. (2023) from Brazil and revealed it can produce volatile organic compounds with antimicrobial activity, which inhibit or lower the growth rate of some *Aspergillus* species. The first saprobes of *M. coffeanus* (MFLUCC 13-0159) were introduced by Li, Kang et al. (2022) with its sexual morph, isolated from a deadwood of an unidentified

plant from Thailand. Morphologically, our collection resembles the new record *Muscodor coffeanus* (MFLUCC 13-0159) in having cylindrical asci with hyaline, ellipsoidal ascospores. However, it can be distinguished by its apiosporous ascospores with hat-like sheaths on the apical cell, whereas the ascospores of *M. coffeanus* (MFLUCC 13-0159) are bicellular with a median septum and contain hat-like sheaths at both ends (Li, Kang et al., 2022; Figure 2.165).

In addition, base pair comparison between our strain (MHZU 24-0575, holotype) and other closest strains (MFLUCC 13-0159, CML 4009 and COAD 1842, ex-type) showed little difference of ITS and LSU, with the main difference concentrated on the *RPB2* and *TUB2* sequence (Table 2.5). Based on morphological and phylogenetic evidence, our new collection is introduced as a new species, *M. puerensis*, which was collected from a coffee host in China. Besides, we also hypothesize that *M. coffeanus* (MFLUCC 13-0159) may represent an independent species, as it forms a distinct phylogenetic lineage separate from other strains of *M. coffeanus*, with notable differences observed in the *TUB2* gene (Table 2.5). Further confirmation may require additional saprobic records.

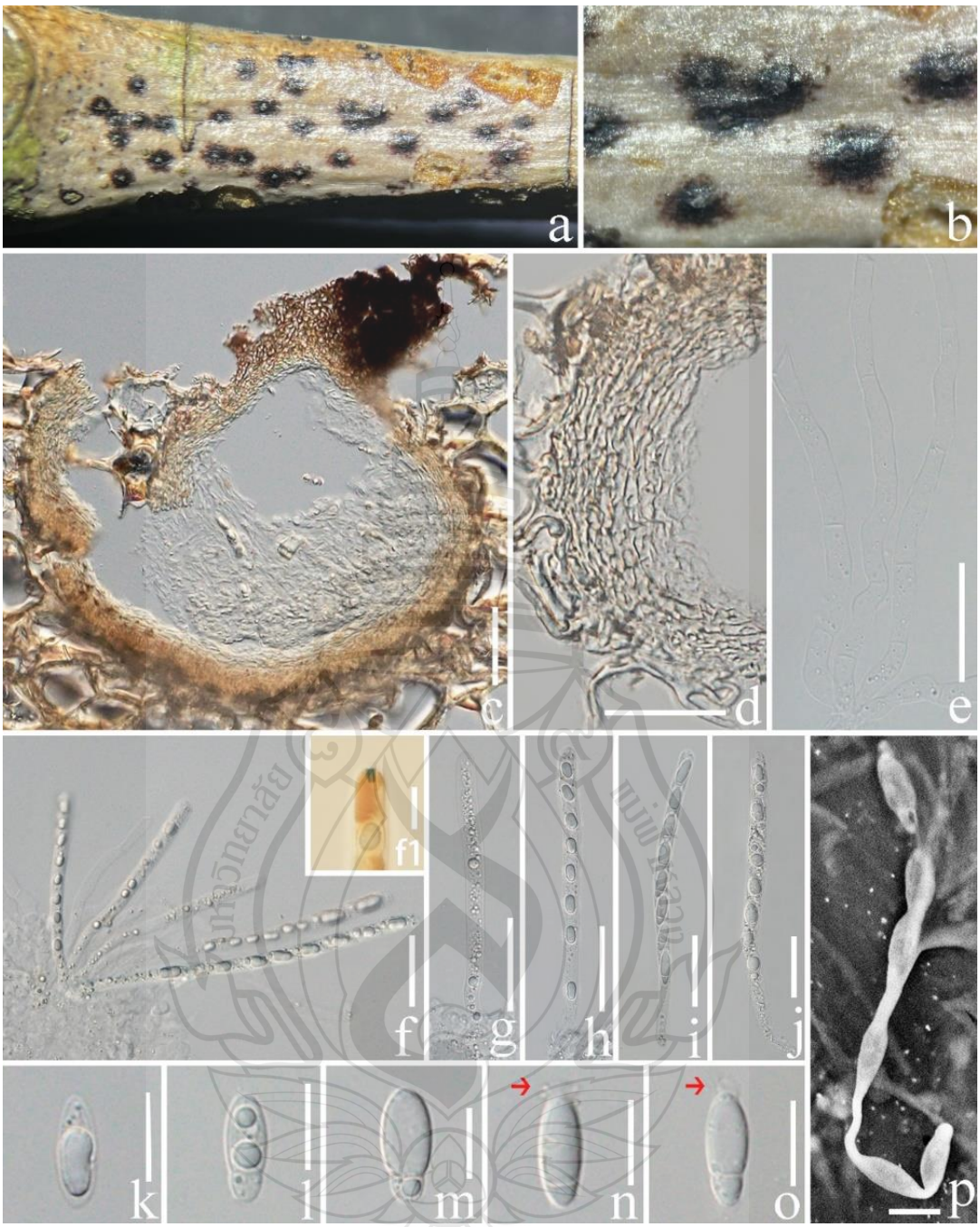


Figure 2.206 *Muscodor puerensis* (MHZU 24-0575, holotype)

Figure 2.206 a, b Appearance of ascomata on substrate. c Vertical sections of ascoma. d Peridium. e Hamathecium. f–j, p Asci (p: SEM microphotographs of ascus; f1: Asci stained with Melzer's reagent with bluing apical ring). k–o Ascospores (arrows indicate hat-like sheaths). c = 50 µm, d–j = 30 µm, f1, k–p = 10 µm.

Table 2.5 Nucleotide differences in the ITS, LSU, *RPB*2, and *TUB*2 (not trimmed sequence) of *Muscodor coffeanus* and *M. puerensis*. All sequences are without gaps, and "/" indicates a sequence is unavailable

Species	ITS (%)	LSU (%)	*RPB*2 (%)	*TUB*2 (%)
M. puerensis MHZU 24-0575 (type) vs. *M. coffeanus* COAD 1842 (type)	3/563 (0.3%)	NA	5/866 (0.6%)	NA
M. puerensis MHZU 24-0575 vs. *M. coffeanus* MFLUCC 13-0159	3/501 (0.6%)	2/1125(0.2%)	11/1059 (1%)	21/398 (5.3%)
M. puerensis MHZU 24-0575 vs. *M. coffeanus* CML 4009	4/429 (0.9%)	NA	4/865 (0.4%)	74/693 (10%)
M. coffeanus MFLUCC 13-0159 vs. *M. coffeanus* COAD 1842	3/499 (0.6%)	NA	10/850 (1.1%)	NA
M. coffeanus MFLUCC 13-0159 vs. *M. coffeanus* CML 4009	5/429 (1%)	NA	10/849 (1.1%)	24/347 (6.9%)
M. coffeanus COAD 1842 vs. *M. coffeanus* CML 4009	2/563 (0.2%)	NA	0/865(0%)	NA

2.4 Discussion

The discovery of new fungal species has accelerated with advancements in molecular techniques, underscoring the extensive fungal diversity on Earth (Lu et al., 2022a, 2024; Hyde et al., 2024c). In this study, we collected 360 collections of coffee-associated saprobes from eight locations in China and Thailand and conducted a comprehensive diversity analysis. Among these, 100 collections were identified based on multi-gene phylogenetic analysis and morphological examination. Notably, our study has introduced five novel genera, 51 new species, 39 new records, and four new collections, two new combinations, and we present new molecular data for Karstenia chrysophaea, defining its taxonomic position on the phylogenetic tree for the first time, all of which are significant contributions to the field

2.4.1 Morphological Diversity

Our research has revealed that certain species exhibit varying morphological characteristics associated with the coffee host. This comprehensive approach directly addresses the concerns raised by Koukol and Delgado (2021), who argued that establishing new species solely based on phylogenetic branching data without

comprehensive phenotypic analysis is inadequate and lacks scientific rigor. For example, *Pseudohelminthosporium clematidis* was introduced by Phukhamsakda et al. (2020) to represent the first asexual morph (hyphomycetes) in Neomassarinaceae; however, Koukol and Delgado (2021) synonymized it with the morphologically similar genus *Neopodoconis*, disregarding the significance of molecular data. In our study, we describe the sexual and asexual morphs of *Pseudohelminthosporium clematidis* and present a well-supported phylogenetic analysis that confirms its taxonomic placement within *Neomassarinaceae*, as proposed by Phukhamsakda et al. (2020). Our findings not only demonstrate the occurrence of ascomycetous, coelomycetous, and hyphomycetous morphs within the same species but also validate the classification of *Pseudohelminthosporium clematidis*, providing a solid foundation for future research in this area.

2.4.2 Taxonomy

Fungi play a crucial role in maintaining global coffee productivity; however, their taxonomic diversity in tropical and subtropical regions remains largely unexplored (Ochoa-Henriquez et al., 2024). Based on our research and previous studies, few reports of new families or orders at higher taxonomic levels were identified on coffee plants (Ochoa-Henriquez et al., 2024; Lu et al., 2024, 2025). Several hypotheses are proposed here to explain this phenomenon. Firstly, the concentration of fungal diversity research may be a contributing factor. Studies on coffee-associated fungi have predominantly focused on economically important pathogenic fungi (such as Hemileia vastatrix, which causes coffee leaf rust) or endophytic fungi (Lu et al., 2022b). Despite their negative impact on coffee plants, these fungi play crucial ecological roles. For instance, endophytic fungi can enhance the plant's tolerance to environmental stress. These fungi are primarily classified within existing families and orders, and their ecological adaptations and biological characteristics have been extensively studied. Consequently, researchers often explore the ecological roles of these fungi within established classifications rather than investigating the potential existence of new families or higher taxa.

Secondly, habitat and host specificity may influence the formation of new higher-level taxa. Coffee primarily grows in tropical and subtropical regions (Asegid, 2020), and many fungi may have adapted to specific ecological environments and host

plant characteristics (Leger et al., 1997; Jain et al., 2019), resulting in similar morphological and ecological adaptations. Therefore, identifying new fungi tends to be concentrated at the species or genus level rather than at the family or order level. In other words, the ecological niche of coffee hosts and their specific relationships with fungi may limit the diversity of fungi at higher taxonomic ranks.

Thirdly, the limitations of taxonomic methods and molecular data may also have contributed to this phenomenon. However, the identification of new families or orders at higher taxonomic levels requires significant morphological differences and phylogenetic support (Liu et al., 2016; Jayawardena et al., 2021). However, many coffee-associated fungi exhibit convergent ecological adaptations and lack significant morphological or genetic differentiation, challenging their classification as new families or orders. Thus, while there has been continuous expansion in species and genus diversity, little advancement has been made at higher taxonomic levels. This phenomenon suggests that the coffee ecosystem may harbor previously underexplored fungal communities, potentially holding the key to understanding and improving coffee productivity. Therefore, the need for future research to further investigate the diversity of fungi associated with coffee is not just a suggestion but a compelling call to action.

Lastly, coffee trees are evergreen shrubs or small trees that grow in tropical to sub-tropical areas, it is predominantly cultivated for commercial purposes. Human intervention in these cultivation practices further limits the occurrence and diversity of coffee-associated fungi (Naik et al., 2021; https://www.britannica.com/topic/coffee-production). Research on coffee has primarily focused on screening for high-yield and disease-resistant varieties (Melese et al., 2021; Naik et al., 2021), leaving the study of fungi associated with coffee trees relatively underdeveloped (Lu et al., 2022b).

2.4.3 Lifestyles

A total of 360 collections, belonging to 137 genera, were obtained in this study from dead or decaying coffee plants as saprobes. According to previous studies, 158 collections representing 71 genera were exclusively reported as saprobes, followed by 148 collections from 44 genera that were previously reported as both saprobes and endophytes or pathogens. Additionally, 32 collections from 13 genera were reported as both saprobes and endophytes. The lowest number of collections (22 collections) belonged to genera reported as both saprobes and pathogens, comprising nine genera

(Figure 2.3). Our study also reconfirmed the proposal of Liao et al. (2025) that many saprobes have an endophytic phase and that endophytes can switch between lifestyles (saprobes and pathogens), adapting to various ecological niches.

Saprobes, the largest group of fungi, grow on dead organic matter, including dead insects and animals (Hou et al., 2012). They play an important role in the decomposition of organic matter and nutrient cycling by excreting various hydrolases (Hou et al., 2012; Liao et al., 2025). Most of the genera identified in this study have been previously reported only for saprobes, including those with higher isolation frequencies, such as *Brunneofusispora, Longiostiolum, Montagnula, Neomassaria, Neooccultibambusa, Sporidesmium,* and *Tubeufia*, which were collected from various cities within the coffee host region of this study. *Montagnula* and *Neomassaria* are known to be dominant saprobes in woody substrates in terrestrial habitats (Lu et al., 2025), while *Tubeufia* and *Sporidesmium* are frequently found in humid environments (predominantly aquatic habitats) (Bao et al., 2021; Ma et al., 2024), while their ability to colonize coffee plant suggests that they might be a key role in the nutrient cycling process within coffee ecosystems. However, further research is needed to determine whether these fungi exhibit host specificity or host preference toward coffee plants. Comparative analyses with fungal communities from other hosts could provide insights into their ecological preferences and potential interactions within different ecosystems.

In this study, we introduce several saprobes which recognized as pathogens on other hosts, such as *Coniochaeta prunicola*, *Dothiorella acericola*, *Lasiodiplodia pseudotheobromae*, *Neofusicoccum podocarpi*, and *Phaeosphaeria musae*. This dual ecological role raises important questions about the factors influencing their transition from saprobes to pathogens lifestyles and their potential ecological and economic impacts. Among them, *N. podocarpi* has previously only been reported as a pathogen on *Podocarpus henkelii* (Zhang et al., 2021), and *L. pseudotheobromae* was only reported as a pathogen associated with coffee dieback disease (Freitas-Lopes et al., 2020). The other three species (*C. prunicola*, *D. acericola*, and *P. musae*) were reported as both saprobes and pathogens on other hosts.

The ability of these fungi to switch between saprobes and pathogens lifestyles highlights their ecological flexibility. This suggests that environmental conditions, host availability, and genetic adaptability play crucial roles in determining their ecological

niche (Cooney & Klein, 2008). The presence of these species in a saprobes state does not preclude their potential to cause disease under favorable conditions, such as when susceptible hosts are introduced or when environmental stressors weaken host defenses. Understanding these triggers is critical for predicting and mitigating disease outbreaks. Then, the genetic and metabolic mechanisms underlying the dual lifestyles of these fungi warrant further investigation. Some species may possess virulence factors that are conditionally expressed, allowing them to exploit both dead organic matter and living hosts (Casadevall & Pirofski, 2007). Therefore, the identification of saprobes introduced in this study with known pathogenic potential underscores the complexity of fungal ecology. Furthermore, Bhunjun et al. (2024) propose that all fungi have endophyte ancestors. The presence of appressoria in some genera with different lifestyles is a key factor in the phenomenon of lifestyle switching. The lifestyles of pathogens and saprobes observed in these fungi may result from the inactivity of appressoria in healthy plants, which become activated under specific conditions, triggering a transition to either pathogenic or saprobic behavior. This suggests that these fungi have achieved significant ecological plasticity, enabling optimal growth and reproduction across a variety of hosts and expanding their biogeographic distribution. In the future, by exploring the factors that influence their behavior, we can better predict and mitigate their impacts on agriculture, human health, and the environment.

2.4.4 Where did the Fungi on Coffee come from?

Over 1,000 years ago, Ethiopia, a land steeped in history, was the revered birthplace of coffee, a discovery that predates all others (Amamo, 2014). The first successful cultivation of coffee in China occurred in Taiwan Province, China, in 1884, with the inaugural coffee tree (Arabica coffee) planted in Zhukula Village, Dali City, Yunnan Province, China, in 1892 (Zhang et al., 2014). The journey of coffee cultivation in Thailand began in 1969 in Doi Chang Village, Chiang Rai Province (Kunta, 2020).

The microbiome of coffee plants, a complex and wondrous system, is influenced by a myriad of factors. The journey begins with seedlings that have been colonized by seed endophytes, some of which adhere to the seed parchment and others to the germination substrate (Vaughan et al., 2015). As these seedlings transition to the field, they are exposed to the elements, acquiring microbes from the air, soil, and water. The modes of microbial immigration and emigration, such as splash dispersal and human

vectoring, are intricately impacted by crop density and specific cultural practices that vary based on cultivar and growing region. Pruning, a common practice, can vector microbes between plants, provide new entry points for colonization, and facilitate new vegetative growth for colonization (Céu Silva et al., 2006; Illy & Viani, 2005; Gaitán et al., 2015). Furthermore, the world of coffee is rich and diverse, with different plant varieties shaping unique microbial communities. Each cultivar, with its distinct characteristics, influences the susceptibility to microbial colonization (Vaughan et al., 2015). Some of the fungi isolated from coffee may be endophytes that naturally colonize the coffee seeds, while others may colonize the coffee plants during their growth or through other means. The isolated saprobes, a testament to the diversity of the coffee world, may have originated from these endophytes, which altered their lifestyles in response to specific environmental or physiological stresses while continuing to fulfill their ecological roles (Liao et al., 2025).

2.4.5 Host Jumping

Some coffee plantations strategically incorporate mixed cropping systems, such as those with rubber trees, not only for ecological reasons but also to unlock additional economic benefits (Zaro et al., 2020). This approach significantly increases the potential for fungal host jump between crops. There is evidence that fungi on coffee may have been colonized from other hosts through host jumping. Some of the coffee saprobes introduced here or previously have also been reported on rubber trees (*Hevea brasiliensis*), such as *Fracchiaea heveae*, *Melomastia puerensis, Montagnula thailandica*, and *Sporidesmium tropicale* (Senwanna et al., 2021; Senwanna et al., 2022; Xu et al., 2024). Among them, our collection of *Melomastia puerensis* and the collection reported on rubber were both reported from Pu'er City, Yunnan Province, China; *Fracchiaea heveae*, *Montagnula thailandica*, and *Sporidesmium tropicale* was found in Thailand (Senwanna et al., 2021; Senwanna et al., 2022), however, these three records were report from coffee in China (Lu et al., 2022d; This study); In addition, we observed that coffee-associated fungi may also be related to other native and introduced plants. For example, *Muyocopron lithocarpi* has been reported as a saprobe in Thailand on *Chromolaena odorata, Lithocarpus lucidus*, and *Peltophorum* sp. (Mapook et al., 2016a, Jayasiri et al., 2019), as well as in China on *Cercis chinensis* and *Paeonia suffruticosa* (Jayasiri et al., 2019; Li et al., 2023a).

The occurrence of these species on multiple hosts not only indicates insights into host jumping, a process in which a fungus migrates and establishes itself on different host plants, but also showcases the remarkable adaptability of these saprobes. In this case, environmental factors, resource overlap, or physiological changes in the plants could facilitate the transition of these saprobes between coffee trees and other hosts, demonstrating the species' adaptability to diverse plant substrates. However, this phenomenon requires further validation with more species. Future research should focus on exploring the fungal communities in the coffee-rubber agroforestry system to determine whether host jumps occur between the two plant species. Special attention should be given to understanding the ecological and genetic mechanisms driving such transitions, particularly examining the shift from pathogens to saprobes. This will provide deeper insights into the dynamics of fungal adaptation and its implications for sustainable agricultural practices.

CHAPTER 3

ENDOPHYTIC FUNGI ASSOCIATED WITH COFFEE LEAVES IN CHINA EXHIBITED IN VITRO ANTAGONISM AGAINST FUNGAL AND BACTERIAL PATHOGENS

3.1 Introduction

Coffee is one of the most important crops around the world that grow in tropical and subtropical areas, and it is the second-largest export commodity after crude oil (Ghosh et al., 2014; Asegid, 2020). Coffee is susceptible to diseases and pests, but most coffee diseases are caused by pathogenic fungi, which can infect various tissues of coffee before and after coffee harvest and affect the yield and quality of the fruit (Ribeyre & Avelino, 2012; Lemessa et al., 2015). Cerda et al. (2017) showed that pests and diseases cause up to 38% of coffee yield losses. In order to reduce the impact of diseases on coffee, cultural control, chemical control, and biological control strate-gies have been developed (Rutherford et al., 2006; Muller et al., 2009). Cultural control can avoid and reduce some plant dis-eases and generally requires workers to implement it manually, which is time-consuming and labor-intensive (Muller et al., 2009). Chemicals can control diseases and increase yields, such as the use of the fungicides cyproconazole and thiamethoxam in the soil to control rust disease (Capucho et al., 2013), but the chemical methods can result in environmental and food contamination, which forces society to use nonchemical methods for plant disease control (Ghini et al., 2011). Carl von Tubeuf was the first person to use biological control to manage plant diseases in 1914 (Baker, 1987; Cook, 1998; Khalil et al., 2021a, 2021b). The biological control of plant diseases occurs with several distinct mechanisms, including competition for nutrients between a pathogen and a harmless species, parasitism, and production of antibiotics (Faull, 1988; Van Driesche et al., 2012). Biological controls have the advantages of being environmentally compatible, can exhibit broad or narrow targets depending on the organism, can be site-specific, less prone to re-sistance, safe, and inexpensive compared with chemical pesticides. Due to these ad-vantages,

biocontrol has become a popular method of plant disease management (Hokkanen et al., 2003; De Silva et al., 2019; Elnahal et al., 2022). Currently, some fungi and bacteria as biocontrol agents are available as commer-cial products (De Silva et al., 2019). A total of 101 microbial biological control agents were registered for disease control in Australia, Brazil, Canada, Europe, Japan, New Zealand, and the United States in 2017 (Köhl et al., 2019).

Endophytes are microorganisms such as actinomycetes, bacteria, or fungi that live in plant tissues and do not cause the host to produce any disease symptoms (Nair, 2014; Fan et al., 2020; Hyde et al., 2008). They is generally considered reciprocal and neutral, but can cause disease or become saprophytic when senescence occurs in the host, its vitality decreases, and other fac-tors are weakened (Terhonen et al., 2019; Langer et al., 2021). The host strongly restricts the growth of endophytes, but it can overcome the host's defense by secreting biologically active metabolites or chang-ing the balance of plant hormones in the host (Navarro-Meléndez et al., 2014; Fadiji et al., 2020). Endophytes spend all or part of their life cycle in the healthy tissues of plants (Pecundo et al., 2021; Kumar et al., 2021). The bioactive compounds syn-thesized by endophytes enhance the resistance of plants to pathogenic microorganisms and pests, protect the host from environmental stresses such as high temperature and drought, and help the host to more easily access nutrients to promote the growth nec-essary for a stable symbiosis (Azeem et al., 2021). These bioactive metabolites produced by en-dophytes can be used directly or indirectly as potential biological fertilizers to promote plant growth and biocontrol agents to control pathogenic-causing diseases (Saad et al., 2019; Ma et al., 2021; Monkai et al., 2021; Saengket et al., 2020). Fadiji and Babalola (Fadiji et al., 2020) summarized the applications of endophytes into four catego-ries. These are: (i) plant growth promotion, including nutrient uptake, photostimula-tion, and phosphate solubilization; (ii) plant health and protection (antimicrobial ac-tivities and pathogen displacement); (iii) pollution control and phytoremediation; and (iv) medical and industrial applications (anticancer and antiviral). Since endophytes can produce large amounts of biologically active substances, the use of endophytes to control plant diseases and to increase crop yields has become the focus of the agricul-tural industry (Abo Nouh, 2019; Ortega et al., 2020; Muñoz-Guerrero et al., 2021).

Endophytic fungi are one of the groups of microorganisms that colonize plant tissues and interact with plants, which can be used for biological control and resistance induction, and these fungi are one of the most interesting groups with high utilization value and high diversity (Fontana et al., 2021). Endophytic fungi are known to produce important sec-ondary metabolites such as anticancer, antifungal, antidiabetic, and immunosuppres-sant compounds, which can be used as a source of some important secondary metabo-lites (Priti et al., 2009; Schulz et al., 2002). Numerous attempts have been made to control wilt diseases through bio-control agents using endophytic fungi, and this way holds great promise for improving crop productivity while serving as an alternative to chemical fungicides and synthetic fertilizers (Wang et al., 2016; Wu et al., 2016; Saravanakumar et al., 2016; Raza et al., 2017). A huge number of studies have shown that fungal endophytes have potential research values (e.g., endophytic fungi secrete hormones such as indoleacetic acid and gibberellins that aid in plant developmental processes and improve plant growth and crop productivity) (Fu et al., 2015; Teale et al., 2006). The endophytic fungus *Penicillium indica* can regulate the production of phytohormones and contributes to root growth in crops such as barley and tobacco (Johnson et al., 2014; Prasad et al., 2020). The endophytic fungus *Acremonium alternatum* controls the damage caused by the moth *Plutella xylostella* in beans and induces resistance against *Leveillula taurica* (the powdery mildew pathogen) in tomatoes (Ek-Ramos et al., 2013). Ek-Ramos et al. (2013) showed that the cotton fungal endophyte *Phomopsis* sp. reduces caterpillar herbivory activity in cotton plants. The endophytic fungi *Aspergillus terreus* and *Penicillium citrinum* reduce the pathogenic *Sclerotium rolfsii* and induce increases in the biomass yield of sunflower plants (Potshangbam et al., 2017). Many studies have revealed that endophytic fungi, such as *Ampelomyces quisqualis*, *Aureobasidium pullulans*, *Beauveria bassiana*, *Botryosphaeria* sp., *Candida oleophila*, *Coniothyrium minitans*, *Gliocladium catenulatum*, *Metarhizium anisopliae*, *Paecilomyces lilacinus*, *Pestalotiopsis microspora*, *Phlebiopsis gigantea*, *Purpureocillium lilacinum*, *Trichoderma asperellum*, *T. atroviride*, *T. gamsii*, *T. polysporum,* and *Verticillium lecanii,* can be used as biocontrol agents in commercial products (Strobel, 2002; Phongpaichit et al., 2006; Vinale et al., 2008; Tranier et al., 2014; Herrera et al., 2016; Larran et al., 2016). Therefore, endophytic fungi represent an effective agent in managing diseases and

promoting plant growth; they also provide great opportunities for researching new products.

Studies of endophytic fungi in coffee were pioneered by Rayner in 1948 (Rayner, 1948). Since 1948, many studies have been published on coffee endophytes but no research has been carried out on the antagonistic effects of coffee endophytes as evaluated by a dual-culture assay. *Beauveria bassiana* can be established in coffee seedlings through different inoculation methods and the plants can resist coffee berry borers (Posada et al., 2007). Fernandes et al. (2009) showed that the fungal endophytes isolated from the healthy leaves of *Coffea arabica* could produce bacteriostatic, antifungal, and antitumor bioactive substances. *Trichoderma* sp. isolated from healthy coffee roots by Mulaw et al. (2013) was demonstrated to have an antagonistic effect on the fungus *Fusarium* sp., which causes vascular wilt diseases. Monteiro et al. (2017) isolated endophytes from *Coffea arabica*, and the results showed that *Acremonium*, *Muscodor*, and *Simplicillium* have antibacterial activities against *Aspergillus ochraceus*, while six different endophytic fungal strains can inhibit the growth of *Fusarium verticillioides*. The endophyte *Simplicillium coffeanum* isolated from coffee branches by Gomes et al. (2018) has antimicrobial activities against *Aspergillus niger*, *A. ochraceus*, *A. sydowii*, and *A. tubingensis*. *Trichoderma harzianum* (CRF1) and *T. viride* (CRF-2), isolated from coffee rhizosphere soil by Ranjini et al. (2019), can control *Myrothecium roridum* in vivo, a fungus that causes stem necrosis and leaf spot of coffee seedlings.

Both bacteria and fungi cause diseases in coffee. *Alternaria alternata* was identified in Brazil in 1999 as the causative agent of necrotic spots on coffee leaves (Amorim et al., 2002). This pathogen is more serious when present in other fruits and vegetables, and the current control methods include fungicides, synthetic chemical fungicides, and biological control (Troncoso-Rojas et al., 2014). *Penicillium digitatum* is a destructive postharvest pathogen causing green mold in fruit, especially citrus fruits (Julca et al., 2016). Fungicides are still the main control agent of postharvest green mold, and it is necessary to develop novel and safer strategies for effectively controlling plant diseases (Cheng et al., 2020). Bacterial halo blight disease caused by *Pseudomonas syringae* has affected coffee plantations in Brazil and Ethiopia. Due to only a few efficient commercial products being available on the market to control this

disease and the low efficiency of the chemical control on field conditions, biological control and disease-resistant variety development should be the most promising management methods (Destéfano et al., 2010; Botrel et al., 2018; Rodrigues et al., 2021). *Salmonella enterica* subsp. *enterica* is a common pathogen of animals, humans, or plants (Wiedemann et al., 2015). *Salmonella* can adhere to plant surfaces before actively infecting the interior of different plants, leading to the colonization of plant organs (Gu et al., 2011; Klerks et al., 2017) and suppression of the plant immune system (Schikora et al., 2012). In addition, *Salmonella* originating from plants reduces its virulence toward animals (Schikora et al., 2011). Therefore, plants act as an alternative host for *Salmonella* pathogens and have a role in transmitting back to animals. Moreover, *Salmonella* can adapt to survive in different environments outside the host organism, such as low pH or high temperatures (Semenov et al., 2007).

The microfungal diversity of the Greater Mekong Subregion (GMS) has been relatively well-studied, but their secondary metabolites have not been well-studied (Chaiwan et al., 2021). Since endophytic fungi have become the source of new antibacterial and antifungal agents, with some examples producing valuable secondary metabolites, this study was planned to identify and examine the antagonistic abilities against two fungal and two bacterial pathogens of endophytic fungi, which were isolated from healthy coffee leaves from four coffee-growing areas in Pu'er city, Yunnan province, China.

3.2 Materials and Methods

3.2.1 Sampling Location and Leaf Collection

Pu'er city has the largest coffee planting area, with the highest yield, and the best-quality coffee production in Yunnan province, China. This study was con-ducted on mature and healthy leaf samples collected from four coffee-planting areas in Pu'er city, Yunnan province, China (Figures 3.1, 3.2). All sites were >30 km and <210 km apart. More than 50 healthy leaves were collected from each coffee plant host, placed in clean plastic bags, kept in iceboxes, brought to the laboratory, and refriger-ated at 4°C until further processing.



Figure 3.1 Coffee trees

Figure 3.1 (a) Aerial view of a coffee plantation in Pu'er city; (b) Arabica coffee trees; (c) Catimor coffee trees; (d) Yellow Bourbon coffee trees.

Host (Varieties)	Coffee Plantation Site in Pu'er City	Location (Latitude; Longitude; Altitude)	Abbreviation	Collection Date
Coffea arabica (Catimor)	Xiao Ao Zi coffee plantation (小凹子咖啡庄园)	22.6618° N; 100.9584° E; 1066 m	XCE	21 December 2020
	Qi Xiang coffee plantation (奇象咖啡庄园)	22.7040° N; 101.3462° E; 900 m	QCE	22 December 2020
	Mo Jiang Jing Gong coffee plantation (墨江晶工咖啡庄园)	23.2543° N; 101.7390° E; 1100 m	ME	23 December 2020
Coffea arabica (Aika)	Xiang Yuan Shu He coffee plantation (香橼树河咖啡庄园)	22.7541° N; 101.2869° E; 1006 m	AKE	22 December 2020
Coffea arabica (P4)			P4E	22 December 2020
Coffea arabica (PT)			PTE	22 December 2020
Coffea arabica (T5175)			T5E	22 December 2020
Coffea arabica (T8667)			T8E	22 December 2020
Coffea arabica (Yellow Bourbon)	Xiao Ao Zi coffee plantation (小凹子咖啡庄园)	22.6618° N; 100.9584° E; 1066 m	XYE	21 December 2020

Figure 3.2 Information on the host species and sample collection sites

3.2.2 Coffee Leaves Processing and Fungal Endophytes Isolation

The isolation process of endophytic fungi refers to the slightly modified method of Tibpromma et al. (2018) and Du et al. (2022). Sterile water, 70% alcohol, 1% sodium hy-pochlorite, a sterile scalpel, sterile tissue paper, sterile fine-tip forceps, and potato dex-trose agar (PDA) plates (supplemented with amoxicillin) were prepared. Ten healthy leaves were randomly selected for each host and each leaf was washed under running tap water and then air-dried. Working under an aseptic laminar hood, a hole puncher was used to randomly punch the leaves to obtain 5 mm size pieces (10 pieces/leaf) and these were washed in sterile water for one minute, dried on sterile tissue paper, soaked in 70% alcohol for 30 s, transferred to 1% sodium hypochlorite and soaked for one mi-nute, then soaked in 70% alcohol for 30 s, and finally transferred to sterile water for one minute to remove chemicals. Afterwards, they were dried on sterile tissue paper; then, five pieces were placed on 90 mm-diameter PDA plates. A total of 30 leaf pieces were placed on six PDA plates for each host and each location. All PDA plates were incubated at 28 °C and observation of the culture plates was performed every day to check emerging hypha from the edge of the leaves. After colonies had grown, a small piece of mycelium with agar was cut and transferred to new PDA plates to obtain a pure culture (Santamaría & Bayman, 2005; Van et al., 2015). There was a total of 270 coffee leaf pieces, including Arabica coffee (150 pieces × 5 plants × 1 place), Catimor (90 pieces × 1 plant × 3 places), and Yellow Bourbon (30 pieces × 1 plant × 1 places). A total of 235 pure cultures were iso-lated in this study (Table 3.1).

Table 3.1 Information on the host species and sample collection sites

Class	Genus	AKE	ME	P4E	PTE	QCE	T5E	T8E	XCE	XYE	Total
Dothideomycetes	*Cladosporium*	-	1	-	-	-	-	-	1	-	2
	Phyllosticta	2	2	1	1	2	2	-	1	5	16
	Pyrenochaetopsis	-	-	-	-	-	1	-	-	-	1
	Shiraia	-	-	-	-	1	-	-	-	-	1
Sordariomycetes	*Annulohypoxylon*	1	-	1	1	-	-	1	-	-	4
	Arthrinium	-	-	-	-	-	-	-	2	3	5
	Biscogniauxia	1	-	-	1	-	-	-	-	-	2
	Cladorrhinum	1	-	1	1	-	-	2	-	-	5
	Colletotrichum	8	15	7	5	20	6	8	17	14	100
	Daldinia	5	1	4	3	4	3	4	-	1	25
	Diaporthe	-	2	1	-	-	-	-	-	-	3
	Fusarium	-	-	-	-	1	-	-	-	-	1
	Hypoxylon	-	-	-	1	-	-	2	1	1	5
	Kretzschmaria	-	-	-	1	-	-	-	-	-	1
	Naviculispora	-	-	-	-	-	1	-	-	-	1
	Nemania	-	-	-	-	-	-	-	-	2	2
	Neurospora	-	-	1	-	-	-	-	-	-	1
	Nigrospora	-	-	1	-	-	3	1	2	-	7
	Nodulisporium	-	-	-	-	-	-	2	-	-	2
	Pestalotiopsis	-	-	-	-	-	1	-	-	-	1
	Xylaria	6	-	5	4	1	3	6	1	3	29
-	Unknown	2	-	1	5	2	4	6	1	-	21
Total	**21**	**26**	**21**	**23**	**23**	**31**	**24**	**32**	**26**	**29**	**235**

3.2.3 DNA Extraction, PCR Amplification, and ITS Gene Sequencing

The Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, Beijing, China) was used for DNA extraction from pure cultures grown on PDA for 7–10 days. The extraction process followed the protocol of the manufacturer. Internal transcribed spacer (ITS) regions 1 and 2 of the nuclear ribosomal DNA operon, including the 5.8S region, were amplified by the primers ITS5 and ITS4 (White et al., 1990). The methods of Lu et al. (2021) were followed for the polymerase chain reaction (PCR). Amplification reactions were performed in a 25 μL reaction volume which contained 2 μL DNA, 1 μL of each re-verse and forward primers and 8.5 μL ddH2O, 12.5 μL 2 × FastTaq Premix (mixture of FastTaq TM DNA Polymerase, buffer, dNTP Mixture, and stabilizer) (Beijing Qingke Biological Technology Co., Ltd., Beijing, China). The

amplified PCR products were sent to Bioer Technology Co., Ltd., Hangzhou, and Beijing Kinco Biotechnology Co., Ltd. Kunming Branch, China for sequencing.

3.2.4 Molecular Identification and Phylogenetic Analyses

A total of 235 sequences were obtained, and the newly generated sequences were merged forward and reversed by Geneious 9.1.2 (https://www.geneious.com/, accessed on 30 June 2022). The BLAST search of the sequences was carried out and the top five high-similarity results were recorded. Among our isolates, resistant genera based on published papers and less frequently isolated genera were selected (61 isolates) for the dual-culture assay. The closest match of sequences for the 61 isolates that were used for dual-culture assay were retrieved from GenBank. Multiple alignments were prepared using the online tool MAFFT version 7 (https://mafft.cbrc.jp/alignment/server/, accessed on 1 June 2022) (Katoh et al., 2013), manually edited in BioEdit v. 7.0.5.2 (Hall, 1999), and then their format converted from FASTA to PHYLIP by ALTER online tool (https://www.sing-group.org/ALTER/, accessed on 1 April 2022) (Glez-Peña et al., 2010). Phylogenetic analyses of the aligned sequences were conducted using the maximum likelihood method (Dissanayake et al., 2020). Maximum likelihood trees were generated via RAxML-HPC version 8 on XSEDE (8.2.12) (Stamatakis et al., 2006; Stamatakis, 2014) in the CIPRES Science Gateway platform (Miller et al., 2010) using the GTR+I+G model of evolution. The resulting trees were visualized with FigTree version 1.4.0 and annotated in Microsoft 365 PowerPoint. Sixty-one generated sequences were deposited in GenBank and accession numbers were obtained.

3.2.5 Diversity Analysis

The doughnut chart in Excel 365 was used to show the family, order, and class distribution of endophytic fungi. The colonization rate (CR) and the isolation frequency (IF) of the calculated endophytic fungi: CR = NS/NL × 100%, IF = NS/NT × 100%, NS = number of strains isolated from the location, NL = number of leaf pieces prepared from the location, NT = all number of isolates from all location. Then, the taxonomic diversity based on the species/genera (S/G) ratio was calculated to evaluate the endophyte diversity of each host. In addition, the relative abundances of the species were calculated and the similarity between the fungal communities was estimated using Sorensen's index (Brower et al., 1984). The species diversity of different hosts in each

sampling site was calculated by the Shannon diversity (H'), Margalef diversity (d), and the Pielou even-ness indices (J'), H' = -∑ (Pi ln (Pi)), Pi = ni/N, ni = number of individuals of the species i, and N = total number of individuals of all species; d = S-1/Log N, where S is the num-ber of species and N is the total number of specimens in the sample; J' = H'/Log (S), where H' is the value obtained by the Shannon index and S is species richness (Oliveira et al., 2014; Kumar et al., 2022).

3.2.6 Tests for Antagonism: Endophytic Fungi vs. Pathogenic Fungi/Bacteria

Endophytes were selected for dual-culture testing in vitro based on the information reported in the literature (Grabka et al., 2022; Lacava et al., 2022) and the less frequent strains from our results. The living cultures of the 61 endophytic fungi were deposited in the Kunming Institute of Botany Culture Collection (KUMCC). The 61 endophytic fungi were tested for du-al-culture assays in 9 cm Petri dishes with two fungal and bacterial pathogens (i.e., *Alternaria alternata*, *Penicillium digitatum*, *Pseudomonas syringae*, and Salmonella enterica subsp. *enterica*) (Table 3.2) from China General Microbiological Culture Collection Center (CGMCC). *Alternaria alternata* was identified in Brazil in 1999 as the causative agent of necrotic spots on coffee leaves (Amorim et al., 2002). This pathogen is more serious when present in other fruits and vegetables, and also caused brown spot of coffee leaves in Yunnan Province, China (Zhang et al., 2024); *Penicillium digitatum* is a destructive postharvest pathogen causing green mold in coffee fruit, fungicides are still the main control agent of postharvest green mold, and it is necessary to develop novel and safer strategies for effectively controlling plant diseases; Bacterial halo blight disease caused by *Pseudomonas syringae* has affected coffee plantations in Brazil and Ethiopia, due to only a few efficient commercial products being available on the market to control this disease and the low efficiency of the chemical control on field conditions, biological control and disease-resistant variety development should be the most promising management methods (Destéfano et al., 2010; Rodrigues et al., 2021); While, *Salmonella enterica* subsp. *enterica*, a known foodborne pathogen, has been detected in cold brew coffee (Klerks et al., 2007; Parra 2024), it also can adhere to plant surfaces before actively infecting the interior of different plants, leading to the colonization of plant organs. Therefore, these pathogens were selected for our experiments because they are cause different diseases on numerous hosts (including coffee host) (Table 3.2)

and have been used in biological control tests. The PDA was supplemented with amoxicillin antibiotic and nutrient agar (NA) was prepared without amoxicillin antibiotic. The steps used are given in Figure 3.3.

Table 3.2 Information of the pathogens obtained from CGMCC

Pathogen Group	Species Name	Strain Number	Major Disease
Bacteria	*Pseudomonas syringae*	CGMCC 1.3333	Canker, halo blight of bean (Rodrigues et al., 2021)
	Salmonella enterica subsp. *enterica*	CGMCC 1.10603	Food-borne illness (Klerks et al., 2007)
Fungi	*Alternaria alternata*	CGMCC 3.15535	Black spots (Amorim et al., 2002)
	Penicillium digitatum	CGMCC 3.15410	Fruit post-harvest diseases (Julca et al., 2016)

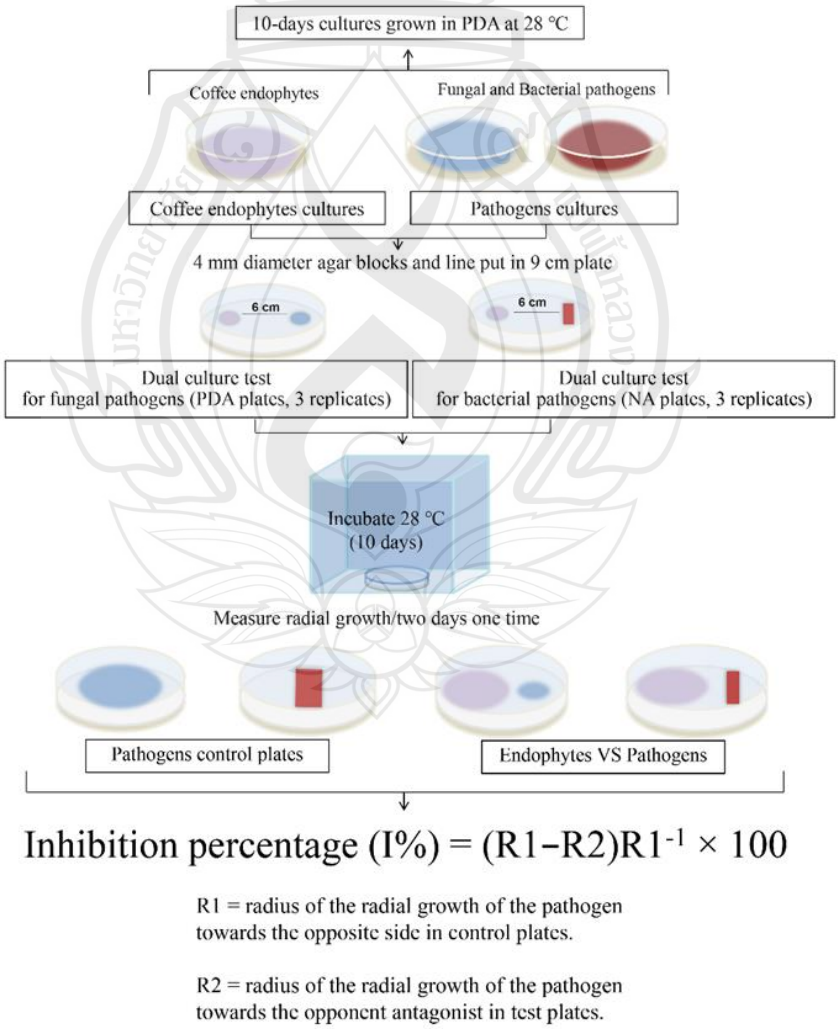


Figure 3.3 Dual-culture assay steps and the percentage inhibition formula

3.3 Results

3.3.1 Isolation and Identification of Endophytic Fungi

A total of 235 fungal endophytes were isolated from 270 coffee leaf pieces obtained from four coffee plantations in Yunnan Province, China. All endophytes were used for the molecular identification, based on the blast result of ITS sequences, and the closest species information was obtained. Overall, 235 endophytes belong to Ascomycota (100%) and are distributed among two classes, 10 orders, and 17 families (Figure 3.4). At the class level, 91% are members of the Sordariomycetes, while 9% are members of the Dothideomycetes. At the order level, the Glomerellales (42.6%) is the largest group, while the Amphisphaeriales (0.4%) and the Hypocreales (0.4%) are re-ported as the least important. At the family level, the Glomerellaceae (42.6%) is the most common family, while the Cucurbitariaceae (0.4%), Naviculisporaceae (0.4%), Nectriaceae (0.4%), Podosporaceae (0.4%), Pestalotiopsidaceae (0.4%), Sordariaceae (0.4%), and Shiraiaceae (0.4%) are the less important families.

Table 3.1 shows that 235 species are distributed in 21 genera. Colletotrichum is the most common genus, composed of 100 isolates, and found in each location and on each host. This is followed by Xylaria (composed of 29 isolates) and Daldinia (composed of 25 isolates.) Seven genera (Fusarium, Kretzschmaria, Naviculispora, Neurospora, Pestalo-tiopsis, Pyrenochaetopsis, and Shiraia) have a low frequency of occurrence; all of these are represented by one isolate and are distributed in two coffee plantations. In addition, 21 genus names could not be determined from only the blast results of ITS, which in-dicated these as unidentified fungal endophytes, unidentified fungal species, or an undetermined species in the Sordariomycetes.

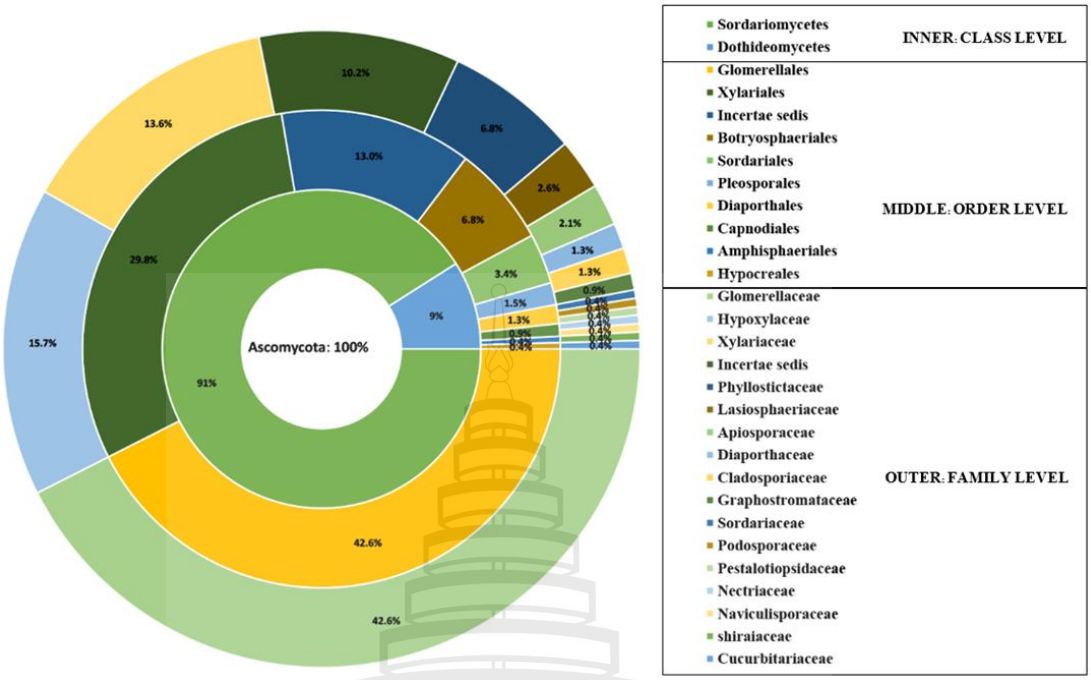


Figure 3.4 Taxonomic distribution of the fungal taxa (n = 235) from the coffee

3.3.2 Phylogenetic Analyses

Phylogenetic analyses were carried out on the 61 endophytes that were used for the dual-culture testing. Our ITS sequences were combined with the sequences of close relatives in GenBank to construct an ITS phylogenetic tree that was composed of 167 sequences. The ML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 13283.937651. The alignment has 684 dis-tinct alignment patterns, with 32.41% completely undetermined characters and gaps. Parameters for the GTR+I+G model: estimated base frequencies A = 0.246497, C = 0.253353, G = 0.238501, T = 0.261649; substitution rates AC = 0.867207, AG = 1.955827, AT = 1.257643, CG = 0.680575, CT = 2.861925, GT = 1.000000; and gamma distribution shape parameter α = 0.259865. The RAxML analysis resulted in a tree which is shown in Figure 34.

The phylogenetic tree includes two classes, seven orders, and nine families. Five orders (Amphisphaeriales, Diaporthales, Glomerellales, Sordariales and Xylariales) and seven families (Apiosporaceae, Diaporthaceae, Glomerellaceae, Graphostroma-taceae, Hypoxylaceae, Lasiosphaeriaceae and Xylariaceae) belong to the class Sordar-iomycetes. Another two orders (Botryosphaeriales and Capnodiales) and two families

(Cladosporiaceae and Phyllostictaceae) belong to the class Dothideomycetes (Figure 3.5).

Since the blast result of XCE-26 has a high similarity with both Podospora intestinacea (MN341351, 99.40%) and Cercophora thailandica (NR_164483, 99.12%), we were not able to determine the genus name and it was treated as Lasiosphaeriaceae sp.

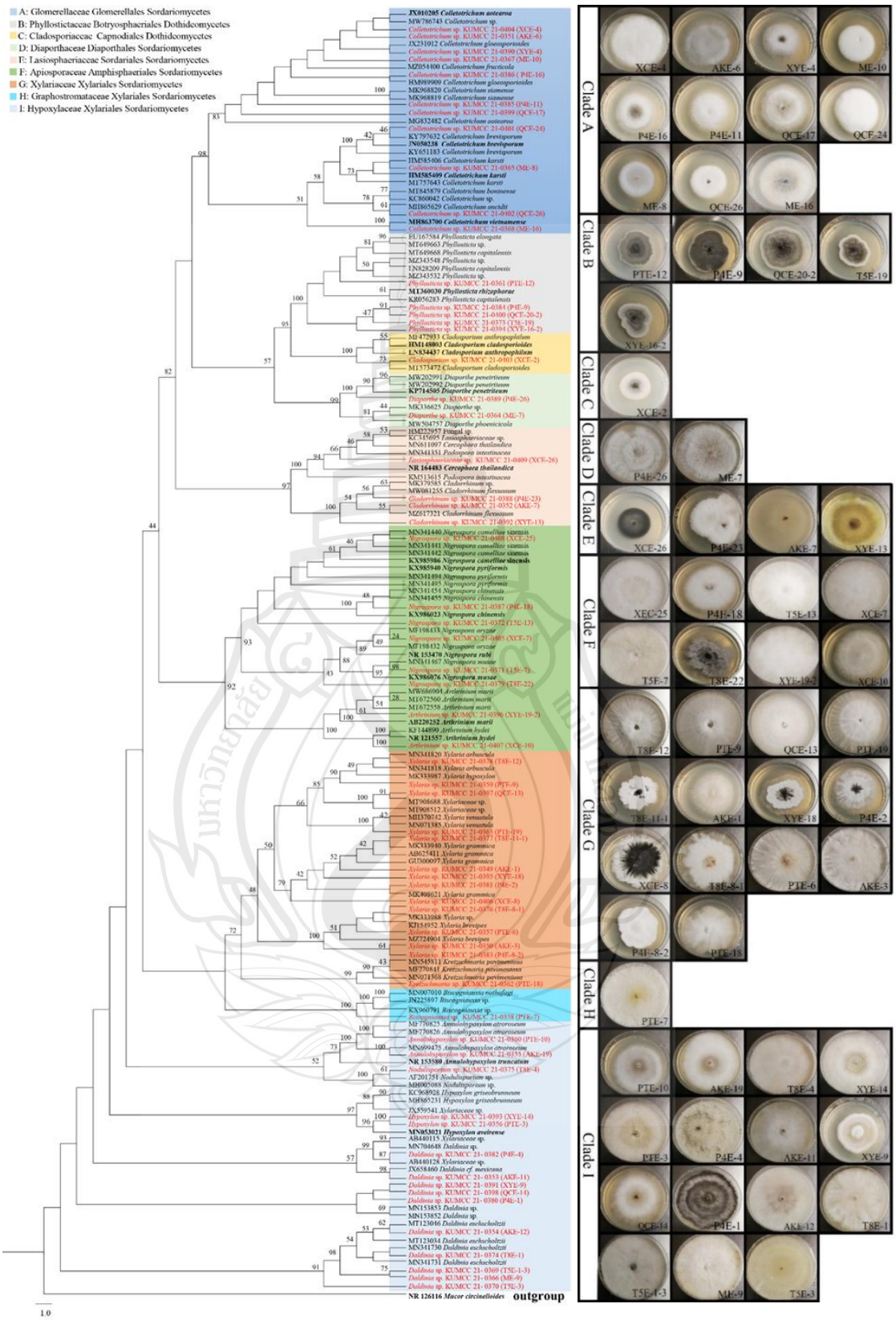


Figure 3.5 A maximum likelihood analysis showing the phylogenetic relationships of coffee fungal endophytes

Figure 3.5 The tree has a total of 167 fungal sequences, of which 61 fungal sequences came from the present study and 106 reference sequences of close relatives came from the GenBank. *Mucor circinelloides* (NR126116; Mucoraceae; Mucorale; Mucoromycetes) was used as the outgroup taxon. The bootstrap support values (≥50%) are indicated at the nodes. The bold font indicates the type species from the GenBank and data presented in the red font are the isolate code and culture number of the fungal endophytes obtained from the coffee leaves. Fungal isolates are further highlighted in different colors according to the family classification. Images on the right side of the phylogeny tree are the morphotypes of each clade.

3.3.3 Diversity of Coffee Fungal Endophytes

In Table 3.3, the highest colonization rate (CR) and the isolation frequency (IF) were reported from Coffea arabica (T8667) from the Xiang Yuan Shu He coffee plantation (CR = 106.67%, IF = 13.62%), while Catimor (ME) from the Mo Jiang Jing Gong coffee plan-tation reported the lowest (CR = 70.00%, IF = 8.94%). By analyzing the taxonomic di-versity through the computation of the (S/G) ratio, and the relative abundance of the species through the calculation of Margalef diversity (d), Shannon diversity (H'), and the Pielou evenness indices (J'), we found that Coffea arabica (P4) from the Xiang Yuan Shu He coffee plantation showed the highest species richness (d = 5.7407, H' = 2.8944, J' = 0.9830), followed by Coffea arabica (T5175) from the same coffee plantation (d = 4.7199, H' = 2.6582, J' = 0.9587). The number of species and the genera of these two hosts are P4 (18 species, nine genera, S/G = 2.00) and T5175 (15 species, eight genera, S/G = 1.88). Furthermore, the best S/G ratio was reported from Coffea arabica (PT) from the Xiang Yuan Shu He coffee plantation, which was reported as 14 species belonging to nine genera, S/G = 1.56.

Table 3.3 Records and diversity of fungal endophytes associated with coffee hosts from different population sites

Isolate Name	Leaf Pieces	R	S	G	S/G Ratio	d	H'	J'	CR (%)	IF (%)
AKE	30	26	12	7	1.71	3.9901	2.4382	0.9506	86.67%	11.06%
ME	30	21	11	5	2.20	3.2846	2.2524	0.9393	70.00%	8.94%
P4E	30	23	18	9	2.00	5.7407	2.8944	0.9830	76.67%	9.79%
PTE	30	23	14	9	1.56	4.4650	2.5218	0.9312	76.67%	9.79%
QCE	30	31	16	6	2.67	4.3681	2.5246	0.9106	103.33%	13.19%
T5E	30	24	15	8	1.88	4.7199	2.6582	0.9587	80.00%	10.21%
T8E	30	32	15	9	1.67	4.3281	2.6205	0.9452	106.67%	13.62%
XCE	30	26	13	7	1.86	3.9901	2.2125	0.8384	86.67%	11.06%
XYE	30	29	13	7	1.86	3.5637	2.3303	0.9085	96.67%	12.34%

Note R = individuals/records, S = number of species, G = number of genera, d = Margalef diversity, H' = Shannon diversity index, J' = Pielou evenness index, CR = colonization rate, IF = isolation fre-quency.

3.3.4 Dual-Culture Assay

To evaluate the antagonistic abilities of coffee endophytes, 61 coffee endophytes along with four pathogens were selected for a dual-culture assay in our study. The results are shown in Table 3.4. We had some dual-culture plates grown for 10 days with an inhibition rate greater or equal to 60%. For bacterial pathogens, only two endophytes exhibited significant values of growth inhibition against *Pseudomonas syringae* (1.3333) and *Salmonella enterica* subsp. *enterica* (1.10603) (Figure 3.6). In contrast, the effect of fungal pathogens (Figure 3.7) was appreciably greater than that of bacteria. For example, 13 endophytes exhibited significant values of growth inhibition against *Alternaria alternata* (3.15535) and 10 endophytes exhibited significant values of growth inhibition against *Penicillium digitatum* (3.15410).

Table 3.4 Results of the dual-culture assay of 61 selected endophytes against the four pathogens. The type of fungal interaction for each isolate against each pathogen and the percentage of growth inhibition (I%) ± standard deviation (SD) is indicated

Isolate Code	Species Name	Strain Number	GenBank Accession Number (ITS)	Percent Inhibition (PI) of 10 Days ± SD			
				Penicillium digitatum **CGMCC 3.15410**	***Alternaria alternata*** **CGMCC 3.15535**	***Pseudomonas syringae*** **CGMCC 1.3333**	***Salmonella enterica*** **subsp. *Enterica* CGMCC 1.10603**
AKE-1	*Xylaria* sp.	KUMCC 21-0349	ON100618	52.00 ± 3.56	43.98 ± 5.57	28.89 ± 9.88	41.67 ± 8.68
AKE-3	*Xylaria* sp.	KUMCC 21-0350	ON100619	52.00 ± 14.22	44.44 ± 5.14	0.00 ± 0.00	39.58 ± 8.68
AKE-6	*Colletotrichum* sp.	KUMCC 21-0351	ON100620	59.11 ± 1.58	44.44 ± 1.29	24.44 ± 2.47	43.75 ± 26.04
AKE-7	*Cladorrhinum* sp.	KUMCC 21-0352	ON100621	52.00 ± 15.41	43.52 ± 0.43	22.22 ± 9.88	52.08 ± 8.68
AKE-11	*Daldinia* sp.	KUMCC 21-0353	ON100622	67.56 ± 5.14	60.00 ± 2.04	31.11 ± 9.88	39.58 ± 8.68
AKE-12	*Daldinia* sp.	KUMCC 21-0354	ON100623	64.00 ± 4.74	60.19 ± 0.43	53.33 ± 29.63	54.17 ± 8.68
AKE-19	*Annulohypoxylon* sp.	KUMCC 21-0355	ON100624	53.33 ± 1.19	43.98 ± 3.00	20.00 ± 29.63	43.75 ± 26.04
ME-7	*Diaporthe* sp.	KUMCC 21-0364	ON100633	64.89 ± 7.51	63.43 ± 0.43	37.78 ± 9.88	40.63 ± 8.68
ME-8	*Colletotrichum* sp.	KUMCC 21-0365	ON100634	50.22 ± 0.40	45.83 ± 1.29	28.89 ± 39.51	41.67 ± 8.68
ME-9	*Daldinia* sp.	KUMCC 21-0366	ON100635	74.67 ± 8.30	71.30 ± 0.43	60.00 ± 7.41	50.00 ± 6.51
ME-10	*Colletotrichum* sp.	KUMCC 21-0367	ON100636	51.56 ± 5.14	46.30 ± 3.00	31.11 ± 2.47	41.67 ± 8.68
ME-16	*Colletotrichum* sp.	KUMCC 21-0368	ON100637	57.78 ± 0.40	44.44 ± 1.29	26.67 ± 29.63	29.17 ± 8.68
PTE-3	*Hypoxylon* sp.	KUMCC 21-0356	ON100625	58.67 ± 3.56	56.94 ± 5.14	4.44 ± 9.88	39.58 ± 8.68
PTE-6	*Xylaria* sp.	KUMCC 21-0357	ON100626	50.22 ± 0.40	37.50 ± 9.00	0.00 ± 0.00	45.83 ± 34.72
PTE-7	*Biscogniauxia* sp.	KUMCC 21-0358	ON100627	67.56 ± 0.40	61.11 ± 1.29	53.33 ± 0.00	60.42 ±8.68
PTE-9	*Xylaria* sp.	KUMCC 21-0359	ON100628	50.22 ± 0.40	43.06 ± 1.29	35.56 ± 9.88	25.00 ± 26.04
PTE-10	*Annulohypoxylon* sp.	KUMCC 21-0360	ON100629	57.78 ± 2.77	58.33 ± 0.00	31.11 ± 17.28	39.58 ± 34.72
PTE-12	*Phyllosticta* sp.	KUMCC 21-0361	ON100630	46.67 ± 18.96	44.44 ± 1.29	28.89 ± 17.28	37.50 ± 6.51
PTE-18	*Kretzschmaria* sp.	KUMCC 21-0362	ON100631	47.56 ± 0.40	37.96 ± 3.00	0.00 ± 0.00	39.58 ± 8.68
PTE-19	*Xylaria* sp.	KUMCC 21-0363	ON100632	47.56 ± 0.40	41.20 ± 5.57	0.00 ± 0.00	39.58 ± 8.68

Table 3.4 (continued)

Isolate Code	Species Name	Strain Number	GenBank Accession Number (ITS)	Percent Inhibition (PI) of 10 Days ± SD			
				Penicillium digitatum **CGMCC 3.15410**	***Alternaria alternata*** **CGMCC 3.15535**	***Pseudomonas syringae*** **CGMCC 1.3333**	***Salmonella enterica*** **subsp. *Enterica* CGMCC 1.10603**
P4E-1	*Daldinia* sp.	KUMCC 21-0380	ON072525	64.89 ± 6.32	54.63 ± 1.71	46.67 ± 29.63	41.67 ± 8.68
P4E-2	*Xylaria* sp.	KUMCC 21-0381	ON072526	46.67 ± 1.19	29.63 ± 3.00	33.33 ± 0.00	37.50 ± 0.00
P4E-4	*Daldinia* sp.	KUMCC 21-0382	ON072527	47.56 ± 0.40	53.70 ± 3.00	4.44 ± 39.51	47.92 ± 8.68
P4E-8-2	*Xylaria* sp.	KUMCC 21-0383	ON072528	49.78 ± 0.40	30.56 ± 1.29	8.89 ± 69.14	39.58 ± 8.68
P4E-9	*Phyllosticta* sp.	KUMCC 21-0384	ON072529	44.89 ± 2.77	30.56 ± 1.29	33.33 ± 0.00	41.67 ± 8.68
P4E-11	*Colletotrichum* sp.	KUMCC 21-0385	ON072530	47.56 ± 2.77	26.39 ± 1.29	22.22 ± 39.51	37.50 ± 0.00
P4E-16	*Colletotrichum* sp.	KUMCC 21-0386	ON072531	40.89 ± 0.40	32.87 ± 3.00	33.33 ± 29.63	39.58 ± 8.68
P4E-18	*Nigrospora* sp.	KUMCC 21-0387	ON072532	43.56 ± 0.40	29.17 ± 1.29	28.89 ± 69.14	45.83 ± 8.68
P4E-23	*Cladorrhinum* sp.	KUMCC 21-0388	ON072533	43.56 ± 0.40	28.24 ± 3.00	31.11 ± 32.10	43.75 ± 0.00
P4E-26	*Diaporthe* sp.	KUMCC 21-0389	ON072534	46.22 ± 0.40	34.72 ± 1.29	31.11 ± 9.88	41.67 ±8.68
QCE-13	*Xylaria* sp.	KUMCC 21-0397	ON072542	37.33 ± 1.19	24.07 ± 3.00	2.22 ± 9.88	25.00 ± 26.04
QCE-14	*Daldinia* sp.	KUMCC 21-0398	ON072543	44.89 ± 0.40	53.70 ± 1.71	24.44 ± 9.88	41.67 ± 8.68
QCE-17	*Colletotrichum* sp.	KUMCC 21-0399	ON072544	44.89 ± 1.58	34.26 ± 3.00	6.67 ± 29.63	45.83 ± 34.72
QCE-20-2	*Phyllosticta* sp.	KUMCC 21-0400	ON072545	44.44 ± 1.58	30.56 ± 1.29	0.00 ± 0.00	41.67 ± 8.68
QCE-24	*Colletotrichum* sp.	KUMCC 21-0401	ON072546	55.56 ± 2.77	44.44 ± 1.29	22.22 ± 69.14	47.92 ± 8.68
QCE-26	*Colletotrichum* sp.	KUMCC 21-0402	ON072547	46.67 ± 1.19	34.72 ± 1.29	0.00 ± 0.00	39.58 ± 8.68
T5E-1-3	*Daldinia* sp.	KUMCC 21-0369	ON100638	70.67 ± 4.74	63.43 ± 3.00	55.56 ± 9.88	60.42 ± 8.68
T5E-3	*Daldinia* sp.	KUMCC 21-0370	ON100639	68.00 ± 1.19	68.52 ± 0.43	21.11 ± 17.28	39.58 ± 8.68
T5E-7	*Nigrospora* sp.	KUMCC 21-0371	ON100640	72.00 ± 1.19	65.74 ± 3.00	13.33 ± 29.63	41.67 ± 6.51
T5E-13	*Nigrospora* sp.	KUMCC 21-0372	ON100641	65.78 ± 2.77	48.61 ± 1.29	27.78 ± 17.28	52.08 ± 8.68
T5E-19	*Phyllosticta* sp.	KUMCC 21-0373	ON100642	51.56 ± 2.77	36.11 ± 5.14	24.44 ± 9.88	35.42 ± 8.68
T8E-1	*Daldinia* sp.	KUMCC 21-0374	ON100643	52.89 ± 11.06	55.56 ± 5.14	46.67 ± 29.63	5.00 ± 0.00

Table 3.4 (continued)

Isolate Code	Species Name	Strain Number	GenBank Accession Number (ITS)	Percent Inhibition (PI) of 10 Days ± SD			
				Penicillium digitatum **CGMCC 3.15410**	***Alternaria alternata*** **CGMCC 3.15535**	***Pseudomonas syringae*** **CGMCC 1.3333**	***Salmonella enterica*** **subsp. *Enterica* CGMCC 1.10603**
T8E-4	*Nodulisporium* sp.	KUMCC 21-0375	ON100644	58.22 ± 2.77	45.37 ± 3.00	35.56 ± 9.88	43.75 ± 26.4
T8E-8-1	*Xylaria* sp.	KUMCC 21-0376	ON100645	45.78 ± 2.77	43.98 ± 3.00	13.33 ± 29.63	41.67 ± 8.68
T8E-11-1	*Xylaria* sp.	KUMCC 21-0377	ON100646	43.56 ± 2.77	45.37 ± 0.43	35.56 ± 9.88	35.42 ± 8.68
T8E-12	*Xylaria* sp.	KUMCC 21-0378	ON100647	44.44 ± 5.14	43.06 ± 1.29	28.89 ± 39.51	41.67 ± 15.19
T8E-22	*Nigrospora* sp.	KUMCC 21-0379	ON100648	53.33 ± 1.19	43.98 ± 0.43	2.22 ± 9.88	43.75 ± 26.04
XCE-2	*Cladosporium* sp.	KUMCC 21-0403	ON072548	42.67 ± 1.19	32.41 ± 0.43	8.89 ± 39.51	39.58 ± 8.68
XCE-4	*Colletotrichum* sp.	KUMCC 21-0404	ON072549	47.56 ± 2.77	37.50 ± 1.29	4.44 ± 9.88	37.50 ± 26.04
XCE-7	*Nigrospora* sp.	KUMCC 21-0405	ON072550	68.00 ± 1.19	71.76 ± 0.43	61.11± 32.10	56.25 ± 0.00
XCE-8	*Xylaria* sp.	KUMCC 21-0406	ON072551	46.67 ± 1.19	30.56 ± 1.29	40.00 ± 29.63	29.17 ± 8.68
XCE-10	*Arthrinium* sp.	KUMCC 21-0407	ON072552	64.90 ± 2.77	57.87 ± 3.00	28.89 ± 39.51	35.42 ± 15.19
XCE-25	*Nigrospora* sp.	KUMCC 21-0408	ON072553	67.56 ± 6.32	62.50 ± 1.29	15.56 ± 9.88	45.83 ± 34.82
XCE-26	Lasiosphaeriaceae sp.	KUMCC 21-0409	ON072554	48.44 ± 0.40	34.26 ± 3.00	26.67 ± 0.00	33.33 ± 8.68
XYE-4	*Colletotrichum* sp.	KUMCC 21-0390	ON072535	42.22 ± 1.58	32.87 ± 1.71	15.56 ± 39.51	41.67 ± 8.68
XYE-9	*Daldinia* sp.	KUMCC 21-0391	ON072536	47.56 ± 0.40	31.48 ± 0.43	22.22 ± 9.88	41.67 ± 8.68
XYE-13	*Cladorrhinum* sp.	KUMCC 21-0392	ON072537	44.44 ± 0.40	29.17 ± 1.29	46.67 ± 29.63	56.25 ± 0.00
XYE-14	*Hypoxylon* sp.	KUMCC 21-0393	ON072538	44.44 ± 2.77	34.72 ± 1.29	33.33 ± 0.00	35.42 ± 8.68
XYE-16-2	*Phyllosticta* sp.	KUMCC 21-0394	ON072539	46.22 ± 0.40	31.02 ± 5.57	2.22 ± 9.88	39.58 ± 8.68
XYE-18	*Xylaria* sp.	KUMCC 21-0395	ON072540	38.22 ± 5.14	31.94 ± 1.29	33.33 ± 0.00	39.58 ± 8.68
XYE-19-2	*Arthrinium* sp.	KUMCC 21-0396	ON072541	44.44 ± 2.77	34.72 ± 1.29	15.56 ± 9.88	27.08 ± 8.68

Effect of Coffee Endophytes on the Growth of *Pseudomonas syringae* (1.3333):

Nigrospora sp. XCE-7 (Figure 3.6b) was able to inhibit the growth of *Pse. syringae* with an inhibition rate of 61.11%, and *Daldinia* sp. ME-9 (Figure 3.6c) showed an inhibition rate of 60.00%. The *Pse*. *syringae* control plate is shown in Figure 3.5a.

Effect of Coffee Endophytes on the Growth of *Salmonella enterica* subsp. *enterica* (1.10603):

Biscogniauxia sp. PTE-7 (Figure 3.6e) and *Daldinia* sp. T5E-1-3 (Figure 3.6f) showed the same inhibition rate of 60.42% against the growth of *S. enterica* subsp. *enterica*. PTE-7 produced a yellow mycelium after it was in contact with bacterial pathogens. The *S. enterica* subsp. *enterica* control plate is shown in Figure 3.5d.

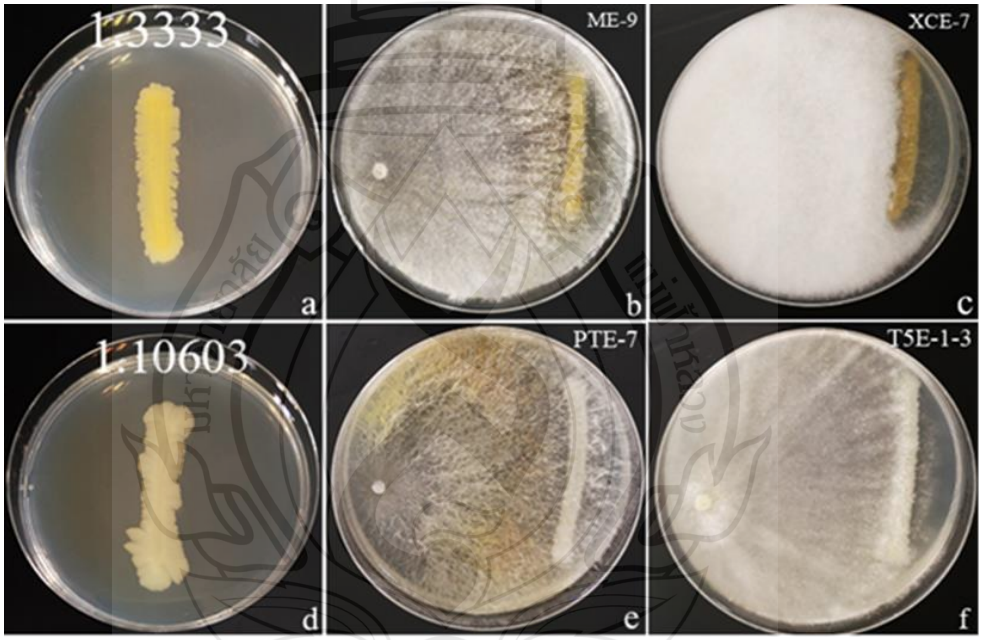


Figure 3.6 Illustration of an antagonist test by the dual-culture technique with two bacterial pathogens and an inhibition rate greater than or equal to 60%

Figure 3.6 The two pathogens were cocultivated with the coffee fungal endophytes on NA plates and incu-bated for 10 days at 28°C. (a) *Pseudomonas syringae* control plate; (b,c) Coffee endophytes control *Pse. Syringae*; (d) S*almonella enterica* subsp. *enterica* control plate; (e,f) Coffee endophytes control *S. enterica* subsp. *enterica*.

Effect of Coffee Endophytes on the Growth of *Alternaria alternata* (3.15535):

Nigrospora sp. XCE-7 (Figure 3.7j) inhibited the growth of *A. alternata* with an interaction characterized by a clear zone around the pathogen and an inhibition rate of 71.76%. It was followed by *Daldinia* sp. ME-9 (Figure 3.7f) with an inhibition rate of 71.30%. Those demonstrating inhibition rates greater than or equal to 60 were *Daldinia* sp. T5E-3 (Figure 6h, 68.52%), *Nigrospora* sp. T5E-7 (Figure 3.7i, 65.74%), *Daldinia* sp. T5E-1-3 (Figure 3.7g, 63.43%), *Diaporthe* sp. ME-7 (Figure 3.7e, 63.43%), *Nigrospora* sp. XCE-25 (Figure 3.7k, 62.50%), *Biscogniauxia* sp. PTE-7 (Figure 3.7d, 61.11%), *Daldinia* sp. AKE-12 (Figure 3.7c, 60.19%), and *Daldinia* sp. AKE-11 (Figure 3.7b, 60.00%). The *A. alternata* control plate is shown in Figure 3.7a.

Effect of Coffee Endophytes on the Growth of *Penicillium digitatum* (3.15410):

Daldinia sp. ME-9 (Figure 3.7q) inhibited the growth of *Pen. digitatum* with an inhibition rate of 74.67%, and this was followed by *Nigrospora* sp. T5E-7 (Figure 3.7t) with an inhibition rate of 72.00%. Inhibition rates greater than or equal to 60 were found in *Daldinia* sp. T5E-1-3 (Figure 3.7r, 70.67%), *Daldinia* sp. T5E-3 (Figure 3.7s, 68.00%), *Nigrospora* sp. XCE-7 (Figure 3.7w, 68.00%), *Daldinia* sp. AKE-11 (Figure 6m, 67.56%), *Biscogniauxia* sp. PTE-7 (Figure 6o, 67.56%), *Nigrospora* sp. XCE-25 (Figure3.7y, 67.56%), *Nigrospora* sp. T5E-13 (Figure 3.7u, 65.78%), *Arthrinium* sp. XCE-10 (Figure 3.7x, 64.90%), *Diaporthe* sp. ME-7 (Figure 3.7p, 64.89%), *Daldinia* sp. P4E-1 (Figure 3.7v, 64.89%), and *Daldinia* sp. AKE-12 (Figure 3.7n, 64.00%). Among these, XCE-7 and T5E-13 inhibited the growth of *Pen. digitatum* by displaying a small zone around the pathogen. The *Pen. digitatum* control plate is shown in Figure 3.7l.

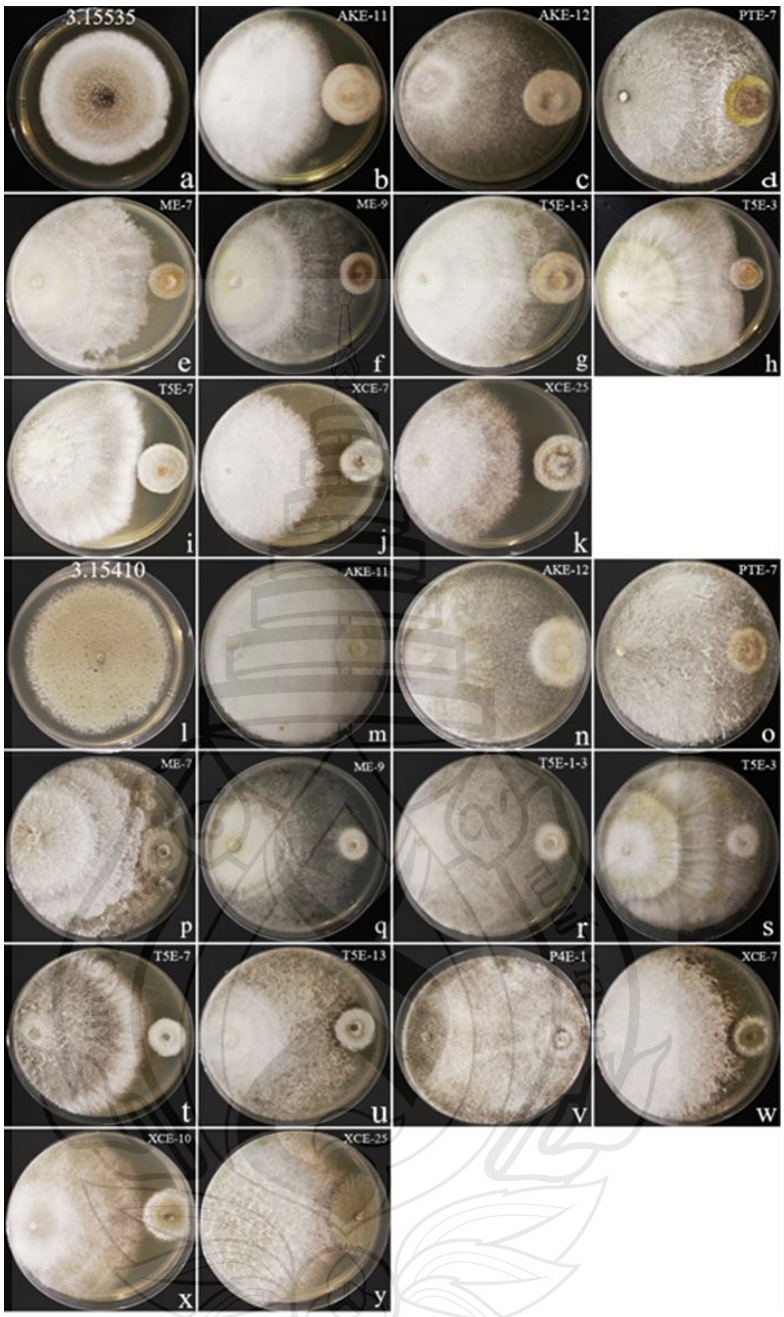


Figure 3.7 Illustration of an antagonist test by the dual-culture technique with two fungal pathogens and an inhibition rate greater than or equal to 60%

Figure 3.7 The two pathogens were cocultivated with the coffee fungal endophytes on PDA plates and incubated for ten days at 28°C. (a) *Alternaria alternata* control plate; (b–k) Coffee endophytes control *A. alternata*; (l) *Penicillium digitatum* control plate; (m–y) Coffee endophytes control *Pen. digitatum*.

Overall, this dual-culture assay demonstrated that most coffee endophytes inhibit the growth of pathogens by competition for nutrients and space, while only two endophytes displayed the mechanism of antibiosis to inhibit the growth of pathogens by producing metabolites (antibiotics and enzymes). One of the *Nigrospora* sp. (XCE-7) isolates produced a clear zone of inhibition for *Pseudomonas syringae*, *Alternaria alternata*, and *Penicillium digitatum*, while *Nigrospora* sp. (T5E-13) had a zone of inhibition only for *Pen. digitatum*. In this study, *Arthrinium* sp., *Biscogniauxia* sp., *Daldinia* sp., *Diaporthe* sp. and *Nigrospora* sp. produced different levels of inhibitory effects on the growth of pathogens. *Arthrinium* sp. (XCE-10) inhibited only the growth of one fungal pathogen (*Pen. digitatum*), but *Diaporthe* sp. (ME-7) inhibited the growth of two fungal pathogens (*Alternaria alternata* and *Pen. digitatum*). *Biscogniauxia* sp. (PTE-7), *Daldinia* sp. (AKE-11, AKE-12, ME-9, P4E-1, T5E-1-3, and T5E-3), and *Nigrospora* sp. (T5E-13, T5E-7, XCE-7, and XCE-25) inhibited the growth of fungal pathogens as well as bacterial pathogens.

3.4 Discussion

The results of our study agree with the results of previous studies (Oliveira et al., 2014; Saucedo-García et al., 2014), which showed that *Colletotrichum* and *Xylaria* are the dominant endophytes in coffee leaves. However, the species richness and diversity of endophytes as determined in the present study are different and higher than those reported by Santamariá and Bay-manet (2005) in Puerto Rico, Saucedo-García et al. (2014) in Mexico, Oliveira et al. (2014) in Brazil for coffee leaf endophytes. Species of *Colletotrichum* are common saprobes, pathogens, and endophytes on a range of economically important plant hosts in tropi-cal regions (Thurston, 1998; Cao et al., 2019), and species of *Xylaria* are recognized as saprotrophic fungi and as endophytic fungi of many plants (Davis et al., 2003). Other unique and less frequently encountered species were reported, most likely due to different climates, altitude, humidity, and sampling period. Herein, nine genera are reported for the first time to be isolated as coffee endophytes. These are *Annulohypoxylon*, *Biscogniauxia*, *Kretzschmaria*, *Naviculispora*, *Neurospora*, and *Pyrenochaetopsis*, and they were isolated from *Coffea*

arabica in the Xiang Yuan Shu He coffee plantation. *Fusarium* sp. and *Shiraia* sp. were isolated from Catimor in the Qi Xiang coffee plantation, and Nemania sp. was isolated from Yellow Bourbon in the Xiao Ao Zi coffee plantation. In this study, only the PDA medium was used, and it is possible that some species were not capable of growing on PDA.

Arthrinium is known for its antifungal capacity (Larrondo et al., 1995). The species *A. aureum* and *A. phaeospermum* have the potential to inhibit the growth of *Fusarium oxysporum* and *F. niveum* and thus can be applied in biological controls (Calvo et al., 2005). Our isolate *Arthrinium* sp. (XCE-10) showed an inhibition rate of 64.89% against the growth of *Penicillium digitatum*.

Biscogniauxia sp. (O-811) isolated from the fresh fruiting bodies of wild mushrooms acts against the rice blast disease *Magnaporthe oryzae* by producing an inhibitory compound (Moriguchi et al., 2019), while our endophytic strain *Biscogniauxia* sp. (PTE-7) can inhibit the growth of the fungal pathogens *Alternaria alternata* and *Penicillium digitatum* while also inhibiting the bacterial pathogen *Salmonella enterica* subsp. *enterica* with inhibition rates of 61.11%, 67.56%, and 60.42%, respectively.

Daldinia cf. *concentrica* prevented the development of molds on organic dried fruits and eliminated *Aspergillus niger* infection in peanuts by emitting volatile organic compounds (Liarzi et al., 2016). The endophytic fungus *Daldinia eschscholtzii* BPEF73 of black pepper showed nematocidal activity by producing metabolites (Sreeja et al., 2016). Six *Daldinia* isolates (T5E-1-3, T5E-3, AKE-11, P4E-1, AKE-12, and ME-9) in our study showed good antagonistic abilities against all four pathogens tested. The isolate ME-9 inhibited *Penicillium digitatum* with the highest inhibition rate of 74.67%.

Studies have shown that some endophytic species belonging to the genus *Diaporthe* can produce metabolites that protect the host from infection or act as a biological control for disease. For example, the endophytic fungus *Diaporthe phaseolorum* isolated from tomatoes can produce 16 different compounds, and it has an inhibitory effect on the growth of *Xanthomonas vesicatoria,* which causes bacterial spot disease in tomatoes (Rashid et al., 2021). Dhakshinamoorthy et al. (2021) showed that the endophytic fungus *Diaporthe caatingaensis* from *Buchanania axillaris* leaves can produce the bioactive metabolite Camptothecin (CPT). While our endophyte

Diaporthe sp. ME-7 has inhibitory effects on the growth of the fungal pathogens *Alternaria alternata* (63.43%) and *Penicillium digitatum* (64.89%), it did not show any apparent inhibitory effects on bacterial pathogens.

Nigrospora oryzae was isolated as an endophytic fungus from the leaves of *Coccinia grandis* and its secondary metabolites can be used as drugs to control diabetes. They also exhibit strong antifungal activities against the plant pathogen *Cladosporium cladosporioides* (Thanabalasingam et al., 2015). Our four *Nigrospora* isolates T5E-13, T5E-7, XCE-7, and XCE-25 showed antagonistic abilities for all three pathogens. The best isolate among all of these was XCE-7 which showed the highest inhibition rate of 71.76% against *Alternaria alternata*.

Our study is the first report on coffee-leaf-endophytic fungal diversity in China. We also tested the antagonistic abilities of endophytic fungi present in coffee leaves against major bacterial and fungal pathogens. Two isolates (*Nigrospora* sp. XCE-7 and *Daldinia* sp. ME-9) showed antagonism against the growth of *Alternaria alternata*, with an inhibition rate of over 70%. Three isolates (*Daldinia* sp. ME-9, *Nigrospora* sp. T5E-7, and *Daldinia* sp. T5E1-3) displayed antagonism against the growth of *Penicillium digitatum*, with an inhibition rate of over 70%. It is necessary to carry out further research on secondary metabolites and identification of the four coffee endophytes ME-9, T5E-1-3, T5E-7, and XCE-7 to the species level.

CHAPTER 4

FIRST REPORT OF A NEW SPECIES, *TRICHOMERIUM PUERENSE*, CAUSING SOOTY MOLD ON *COFFEA ARABICA* IN CHINA

4.1 Introduction

Sooty mould disease is an important disease in various plants (including coffee) and is prevalent in tropical and subtropical regions around the world, that form dark, superficial mycelial layers on the surfaces of leaves, stems, and fruits. These black fungal mats hinder photosynthesis and overall plant growth by blocking sunlight (Chomnunti et al., 2014). Sooty mold development is often associated with the presence of sap-feeding insects, which excrete honeydew—a sugar-rich substrate that facilitates fungal colonization (Auclair, 1963; Hughes, 1976; Nelson, 2008; Chomnunti et al., 2014). Fungi responsible for sooty mould disease have diverse life styles, they can be parasites or saprotrophs. Parasitic fungi absorb nutrients from mesophyll cells through haustorium, while saprophytic fungi colonize the leaves of plants and use honeydew secreted by insects or the secretions of plants as a source of nutrition (Liu et al., 2024).

Coffee is susceptible to diseases and pests, but most coffee diseases are caused by pathogenic fungi, which can infect various tissues of coffee before and after coffee harvest and affect the yield and quality of the fruit (Ribeyre & Avelino, 2012; Lemessa et al., 2015). There are some sooty molds fungi has been reported from coffee, even the impact of sooty mold on coffee plants is currently minimal, continued monitoring is crucial for assessing future risks (Choi et al., 2015; Park et al., 2015).

In this study, sooty mold symptoms were noticed on coffee leaves in the largest coffee-growing region in Yunnan Province, China. The presence of this mold can potentially hinder coffee photosynthesis and growth. The fungus responsible was identified as *Trichomerium puerense* based on morphological characteristics and molecular phylogenetic analysis of ITS, LSU, and SSU sequences. Artificial inoculation of PDA plugs with mycelium to coffee plants validated its pathogenicity.

This is the first global report of *T. puerense* causing sooty mold on coffee plants.

4.2 Materials and Methods

4.2.1 Sample Collection, Morphological Observations And Isolation

A field survey was conducted over approximately 20 hectares (300 mu) of coffee plantations in Yunnan Province, China (22°66'N; 100°96'E; 1073 m), and fresh symptomatic leaves with sooty mold disease were collected and observed. Samples will kept in clean plastic bags, brought to the laboratory, and refriger-ated at 4°C until further processing. The vertical sections of fruiting body structures were prepared for microscope studies and photomicrography. Micro-morphological structures were observed with a Leica DM2500 compound microscope and photographed with an OLYMPUS DP74-CU camera fitted onto the microscope. The measurements were processed in Tarosoft (R) Image Frame Work v. 0.9.7, and photographic plates were made in Adobe Photoshop CC (2018). Senanayake et al. (2020) was followed to carry out single spore isolation and to get a pure culture on potato dextrose agar (PDA), malt extract agar (MEA), and oatmeal agar (OA). Herbarium specimens were deposited in the Mycological Herbarium of Zhongkai University of Agriculture and Engineering (MHZU) while living cultures were deposited in the culture collection of Zhongkai University of Agriculture and Engineering (ZHKUCC). MycoBank (MB) number was obtained as explained in Jayasiri et al. (2015).

4.2.2 DNA Extraction, PCR Amplification, and Sequencing

Actively growing mycelia of two-week-old cultures growing on PDA were scraped by a sterile scalpel from a PDA plate and put into a 1.5 ml centrifuge tube for DNA extraction. The extraction process followed the protocol of the manufacturer. Polymerase chain reaction (PCR) was used to amplify ITS, LSU, and SSU genes, using the primer pairs ITS5/ITS4 (White et al., 1990), LR0R/LR5 and NS1/NS4 (Vilgalys & Hester, 1990). The methods of Lu et al. (2021) were followed for the polymerase chain reaction (PCR). The amplified PCR products were sent to Bioer Technology Co., Ltd., Hangzhou, and Beijing Kinco Biotechnology Co., Ltd. Kunming Branch, China for sequencing.

4.2.3 Molecular Identification and Phylogenetic Analyses

Original sequences generated in this study were combined by the Genious program (9.1.2) and initial identification was performed using a standard BLASTn search. The closely related sequences were downloaded from the GenBank nucleotide database based on recently published papers (Samarakoon et al., 2022) and blast searchers. Sequence alignments for each locus were performed using the online multiple alignment program MAFFT v.7 (http://mafft.cbrc.jp/alignment/server) (Katoh & Standley, 2013), auto-adjusted by trimAl tool (Capella-Gutiérrez, 2009) and refined manually alignment by BioEdit v.7.0.5.2 (Hall, 1999), the ALTER (http://www.sing-group.org/ALTER/) website was used to convert the aligned fasta file to the phylip format and nexus format file for Maximum Likelihood analyses (ML) and Bayesian Inference analysis (BI), respectively (Glez-Peña et al., 2010). Phylogenetic analyses of the aligned sequences referred to Dissanayake et al. (2020) and conducted on the CIPRES Science Gateway platform: https://www.phylo.org/portal2/home.action, using the tool RAxML-HPC v.8 on XSEDE (8.2.12) and MrBayes on XSEDE (3.2.7a) for ML analyses and BI analyses, respectively. The phylogenetic trees were visualized with FigTree v. 1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/) and annotated in Microsoft (365) PowerPoint.

4.2.4 Pathogenicity test For *Trichomerium puerense* Isolates

To fulfill Koch's postulates (Xu et al., 2019), ten healthy arabica coffee plants were selected. Five plants were inoculated with two 3-mm fungus plugs per leaf sheath, and the other five plants were inoculated with PDA agar plugs (control group). All plants were sealed in transparent plastic bags and incubated in a greenhouse at 26 ± 2°C for 28 days, with daily moisturizing using a 5% bee honey solution (with relative humidity maintained at 70%).

4.3 Results

4.3.1 Phylogenic Analyses

The ML analysis of the combined ITS-LSU-SSU dataset yielded a best-scoring tree with a final ML optimization likelihood value of -8610.137577. The alignment has 511

distinct alignment patterns, with 24.61% completely undetermined characters and gaps. Bayesian inference (BI) analyses resulted in almost identical tree topologies with the ML analysis. Only the ML tree is provided in Figure 4.1 with the likelihood bootstrap values (ML ≥ 70%, left) and Bayesian posterior probabilities (PP ≥ 0.90, right) labelled along the branches. Based on the phylogenetic tree, we proposed a new species, *Trichomerium puerense*, which formed a separate lineage within *Trichomerium* with 100% ML, 1.00 PP statistical supports (Figure 4.1), *Phaeosaccardinula dendrocalami* (IFRDCC 2663 and FRDCC 2649) were selected as the outgroup taxa.

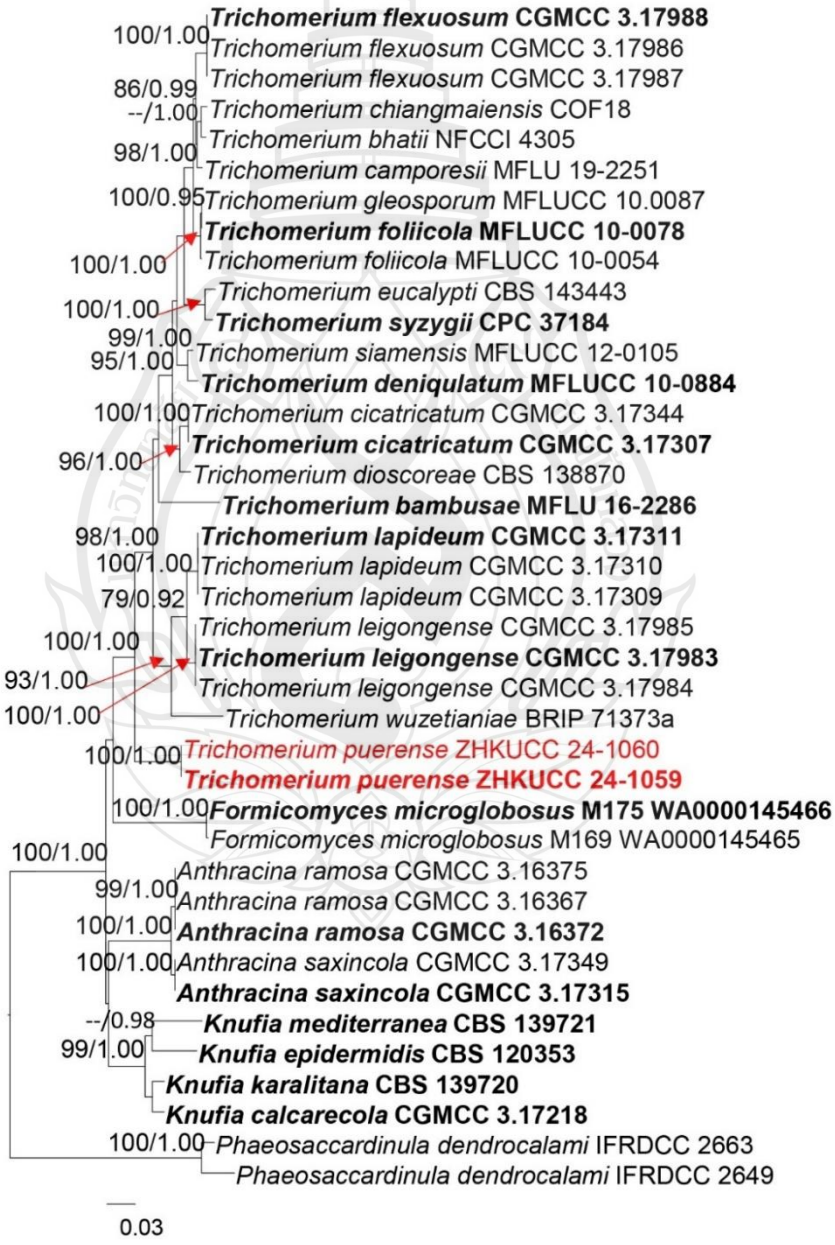


Figure 4.1 Phylogenetic tree of *Trichomerium*

Figure 4.1 RAxML tree based on a combined dataset of ITS, LSU, and *RPB*2 gene sequences. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given above the nodes. Strains of the newly described species are in red, while all the type strains are in bold.

4.3.2 Taxonomy

Trichomerium puerense L. Lu, K.D. Hyde & Tibpromma, sp. nov.

MycoBank number: MB 857498.

Etymology: The epithet refers to the location “Pu’er” from where the holotype was collected.

Holotype: MHZU 24-0582

It forms black sheets which are superficial and thin, cover the leaves, and are composed of cylindrical hyphae. Superficial hyphae 4–6 μm wide also form, are septate, constricted at the septum, unbranched, brown, dense, with cylindrical hyphal cells, and produce guttules. *Ascostromata* are 100–150 × 120–150 μm, superficial, solitary, globose to subglobose, and brown to black. *Setae* are 40–80 × 4–7 μm, straight or flexuous, brown, and septate. *Peridia* are 15–20 μm wide, thick-walled, hyaline to brown, and comprised of *textura angularis* cells. *Asci* are 45–70 × 20–28 μm (n = 30), 8-spored, bitunicate, ellipsoid to clavate, or cylindrical, with a short pedicle and an ocular chamber. *Ascospores* are 20–25 × 7–10 μm (n = 10), fusoid to ellipsoid, hyaline, 1–3-septate, constricted at the septum, with narrow ends, somewhat tapering towards the base when mature, smooth-walled, and produce guttules.

Material examined:China, Yunnan Province, Pu'er City, on fresh leaves of *Coffea arabica*, 6 April 2024, LiLu, sm4 (MHZU 24-0582, holotype); ex-type ZHKUCC 24-1059, other living culture ZHKUCC 24-1060.

GenBank numbers: ZHKUCC 24-1059: ITS = PV056513, LSU = PV056517, SSU = PV056515; ZHKUCC 24-1060: ITS = PV056514, LSU = PV056518, SSU = PV056516.



Figure 4.2 *Trichomerium puerense* (Holotype: MHZU 24-0582)

Figure 4.2 a–d: Sooty molds on fresh coffee stems, leaves and fruits; e: Ascostroma with setae; f, g: Sections through ascomata; h: Setae; i, j: Asci; k–p: Ascospores; q: Germinated ascospore; r: Culture on PDA at two months from the surface and reverse; s, t: Pathogen infection status at 28 days post-inoculation (s: control plants; t: test plants). Scale bars: f: 50 µm; g–j: 20 µm; k–q: 10 µm.

4.3.3 Pathogen Test Results

The results of pathogenicity assay showed that four weeks after inoculation, black sooty mold spread on the leaves that were inoculated with the fungus plugs (Figure 4.2s), while no symptoms were observed on the control leaves (Figure 4.2t).

4.4 Discussion

This study represents the first report of *Trichomerium puerense* associated with coffee sooty mold in China. The identification of this fungal species on *Coffea* plants highlights a previously undocumented component of the sooty mold complex in coffee ecosystems. As sooty mold fungi can negatively affect photosynthesis by covering leaf surfaces with dark mycelial mats, their presence—though not always directly pathogenic—can significantly impair plant vigor and crop yield under favorable conditions. The association of *T. puerense* with coffee suggests a potential ecological linkage between sap-feeding insects, honeydew deposition, and fungal colonization, warranting further investigation into its epidemiology and ecological roles.

Moreover, this finding lays the groundwork for future research on host–fungus–insect interactions, as well as the environmental factors that influence the spread and severity of sooty mold infections in coffee plantations. Understanding the biology, life cycle, and dispersal mechanisms of *T. puerense* may provide insights into integrated disease management strategies, including vector control and cultural practices that reduce honeydew accumulation. Ultimately, this discovery supports the development of targeted and sustainable management approaches for mitigating the impact of sooty mold on coffee production, contributing to improved crop health and economic stability for coffee growers in the region.

CHAPTER 5

CHECKLIST OF COFFEE FUNGI

5.1 Method

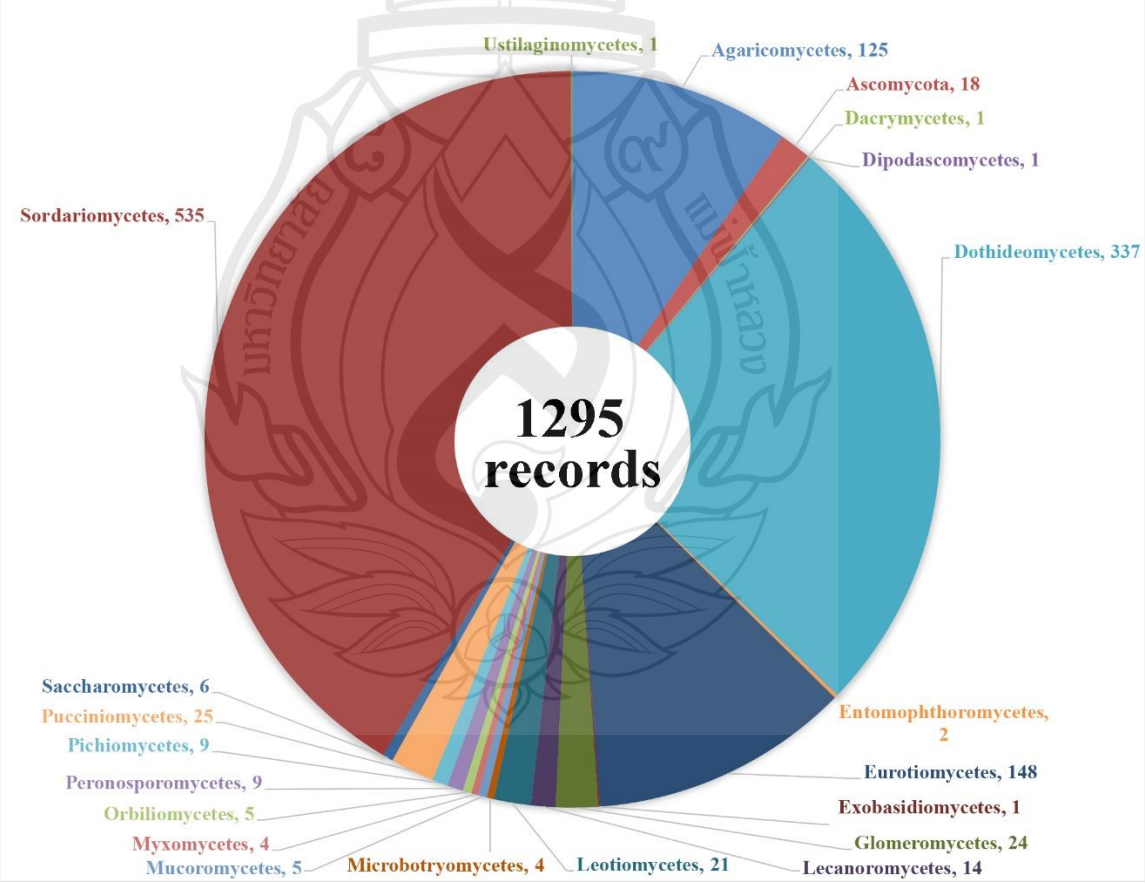
To comprehensively review the diversity of fungi associated with coffee trees globally, we conducted a literature survey using academic databases, including the esteemed Google Scholar and the USDA Fungal Databases (https://fungi.ars.usda.gov/). Keywords such as “coffee” and “fungi” were employed to identify relevant studies. The data we extracted on fungal species, geographic locations and host plants.

5.2 Results with Discussion

We have provided a checklist for all reported fungi species and included details regarding their taxonomic positions, host, and known distributions (Table 4.1). Totally, there are 1295 fungi records associated with coffee documented based on morphology and/or molecular data (Figure 5.1). These species are distributed among 21 classes, 90 orders, 181 families, and 370 genera, including our newly described taxa. Most records are classified into four main classes: Sordariomycetes (535, 41%), Dothideomycetes (337, 26%), Eurotiomycetes (148, 11%), and Agaricomycetes (125, 10%). Figures 5.2–5.5 illustrate the distribution at the order, family, and genus levels. The fungi reported are distributed across more than 80 countries and 46 coffee varieties, reflecting both the global cultivation of coffee and the broad adaptability of fungi to diverse environmental and host conditions. The inclusion of both morphologically and molecularly identified taxa enhances the reliability of the data and emphasizes the importance of integrative approaches in fungal taxonomy. These findings suggest that coffee plants harbor a rich and largely untapped fungal community, which may include both beneficial endophytes and potential pathogens. Continued exploration of this diversity is crucial, not only for

understanding plant–microbe interactions but also for uncovering novel fungal taxa and bioactive compounds of potential agricultural or pharmaceutical value.

According to the checklist, among 1295 fungal records, the most fungal records (682 records, 53%) were obtained from Arabica (*Coffea arabica*) coffees, however, C. arabica-associated fungi have been introduced more frequently when compared with other coffee species. This is because C. arabica is the most widely cultivated and economically significant coffee species worldwide (Vegro et al., 2020). The high concentration of fungal isolates from this species is likely due to it's broad geographic distribution and intensive cultivation, driven by global demand and economic value. As a result, fungal diversity studies have primarily focused on the dominant species, potentially leading to an underrepresentation of fungal taxa associated with less commonly cultivated *Coffea* species.



Note The numbers represent fungal records

Figure 5.1 Distribution of 1295 coffee fungi at the class level

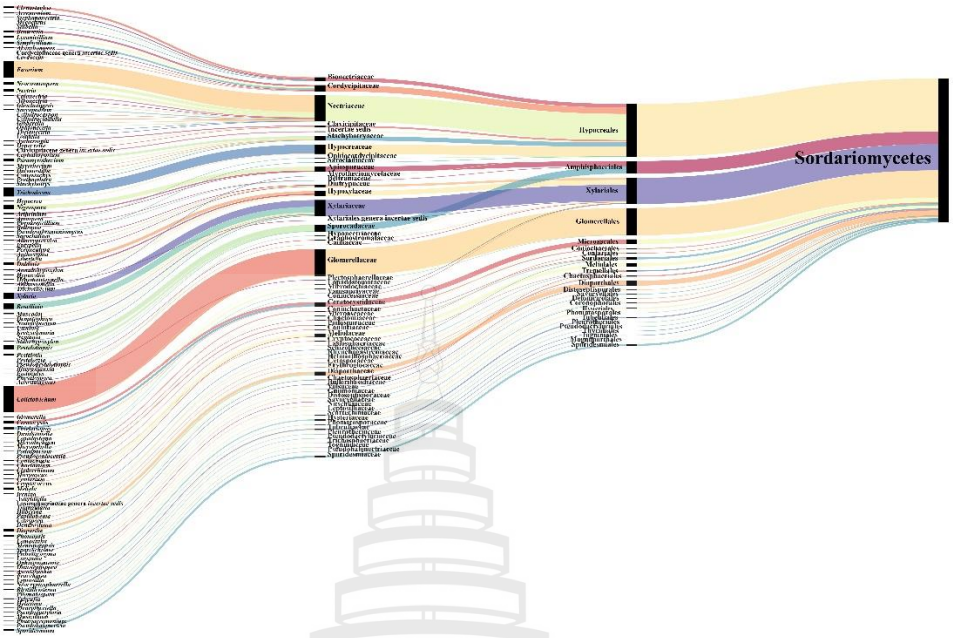


Figure 5.2 Distribution of orders, families and genera of sordariomycetes

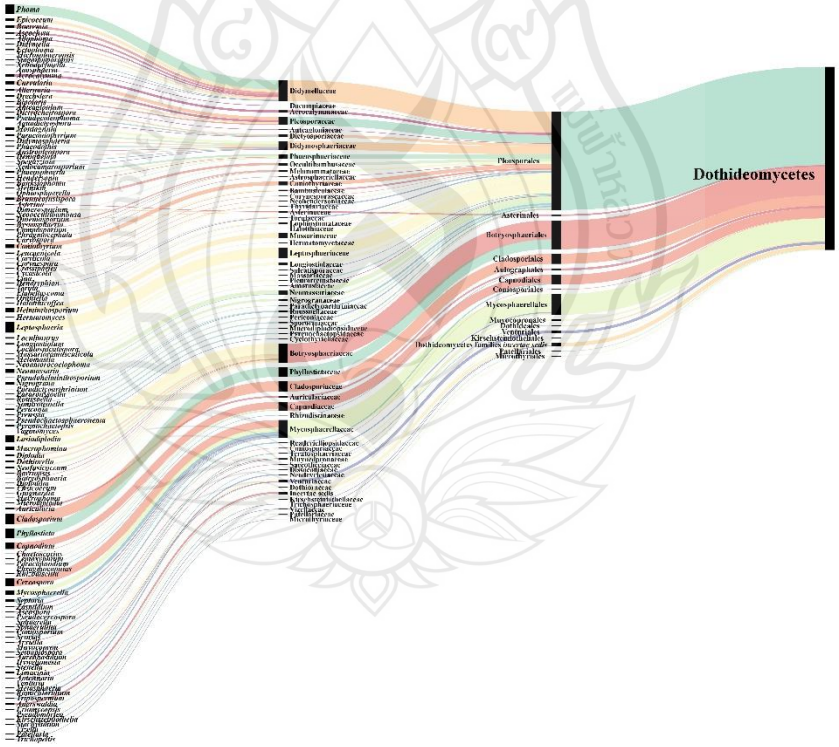


Figure 5.3 Distribution of orders, families and genera of dothideomycetes

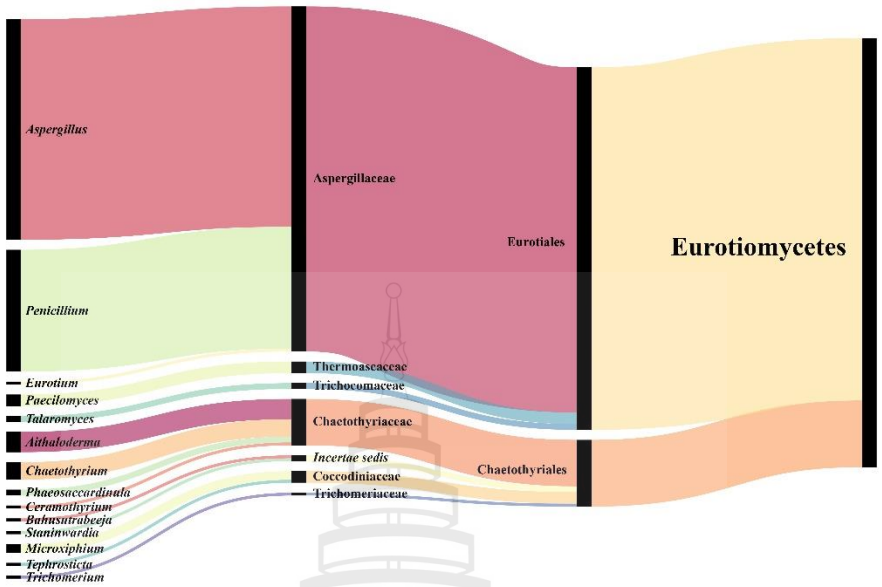


Figure 5.4 Distribution of orders, families and genera of eurotiomycetes

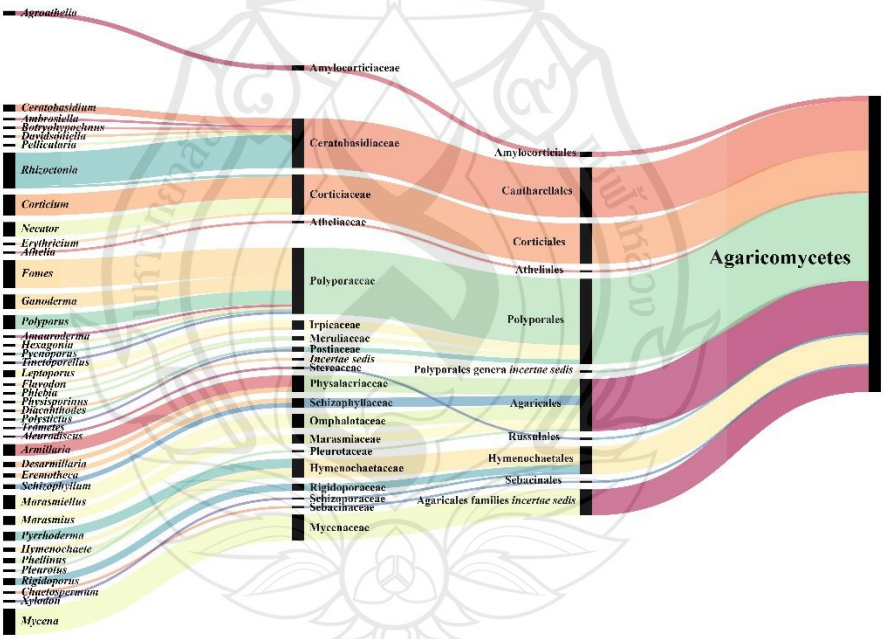


Figure 5.5 Distribution of orders, families and genera of agaricomycetes

Table 5.1 Checklist of fungi associated with coffee

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
Agaricomycetes	Agaricales	Marasmiaceae	*Marasmius*	*Marasmius crinis–equi-* (*Marasmius equicrinis*)	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Marasmius crinis–equi- (*Marasmius equicrinis*)	*Coffea arabica*	Plant	Trinidad and Tobago	USDA
				Marasmius crinis–equi- (*Marasmius equicrinis*)	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Marasmius sp.	*Coffea* sp.	Plant	Malay Peninsula	USDA
		Omphalotaceae	*Marasmiellus*	*Marasmiellus scandens*	*Coffea arabica*	Plant	Fiji, Malaysia	USDA
				Marasmiellus scandens	*Coffea liberica*	Plant	Malaysia	USDA
				Marasmiellus scandens	*Coffea robusta*	Plant	Brunei Darussalam, Malaysia	USDA
				Marasmiellus scandens- (*Marasmius scandens*)	*Coffea arabica*	Plant	Fiji	USDA
				Marasmiellus scandens- (*Marasmius scandens*)	*Coffea canephora var. typica*	NA	Guinea	USDA
				Marasmiellus scandens- (*Marasmius scandens*)	*Coffea liberica*	Plant	Sierra Leone	USDA
		Physalacriaceae	*Armillaria*	*Armillaria mellea*	*Coffea arabica*	Plant	Congo, Guatemala, Kenya, Mexico, Peru, Tanzania, Uganda, Zimbabwe	USDA
				Armillaria mellea	*Coffea canephora var. robusta*	Plant	Congo, West Africa	USDA
				Armillaria mellea	*Coffea* sp.	Plant	Ghana, Papua New Guinea	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Armillaria mellea-(*Armillariella mellea*)	*Coffea arabica*	Plant	Malawi	Saucedo-García et al. (2014)
				Armillaria sp.	*Coffea arabica*	NA	Kenya	USDA
			Desarmillaria	*Desarmillaria tabescens*-(*Clitocybe tabescens*)	*Coffea canephora*	Roots	Madagascar	USDA
				Desarmillaria tabescens-(*Clitocybe tabescens*)	*Coffea canephora var. robusta*	Roots	Madagascar	USDA
		Pleurotaceae	*Pleurotus*	*Pleurotus* sp.	*Coffea* sp.	NA	Philippines	USDA
		Schizophyllaceae	*Eremotheca*	*Eremotheca coffeana*	*Coffea arabica*	Plant	Brazil	USDA
				Eremotheca guianensis-(*Microthyriella guianensis*)	*Coffea liberica*	NA	French Guiana	USDA
			Schizophyllum	*Schizophyllum commune*-(*Schizophyllum alneum*)	*Coffea arabica*	Plant	Brazil	USDA
				Schizophyllum sp.	*Coffea arabica*	Leaves	Brazil	Oliveira et al. (2014)
	Agaricales families incertae sedis	Mycenaceae	*Mycena*	*Mycena citricolor*	*Coffea abeokutae*	Leaves, Twigs	Puerto Rico	USDA
				Mycena citricolor	*Coffea arabica*	Leaves, Twigs	Brazil, Colombia, Cuba, Haiti, Mexico, Panama, Puerto Rico, Venezuela, West Indies	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Mycena citricolor	*Coffea canephora*	Leaves, Twigs	Puerto Rico	USDA
				Mycena citricolor	*Coffea canephora var. laurentii*	Leaves, Twigs	Puerto Rico	USDA
				Mycena citricolor	*Coffea canephora var. robusta*	Leaves, Twigs	Trinidad, Tobago	USDA
				Mycena citricolor	*Coffea liberica*	Leaves, Twigs	Puerto Rico	USDA
				Mycena citricolor	*Coffea* sp.	NA	Puerto Rico	USDA
				Mycena citricolor-(*Omphalia flavida*)	*Coffea arabica*	Plant	El Salvador, Jamaica, Mexico, Trinidad and Tobago	USDA
				Mycena citricolor-(*Stilbella flavidum*)	*Coffea arabica*	Leaves	Colombia, Dominican Republic, Mexico, Venezuela	USDA
				Mycena citricolor-(*Stilbum flavidum*)	*Coffea arabica*	Plant	Mexico	USDA
				Mycena citricolor-(*Stilbum flavidum*)	*Coffea* sp.	NA	Venezuela	USDA
				Agroathelia rolfsii-(*Sclerotium rolfsii*)	*Coffea* sp.	Plant	Malay Peninsula	USDA
	Atheliales	Atheliaceae	*Athelia*	*Athelia rolfsii*	*Coffea arabica*	Leaf	Brazil	USDA
	Cantharellales	Ceratobasidiaceae	*Ambrosiella*	*Ambrosiella xylebori*	*Coffea canephora*	NA	Africa, Cote d'Ivoire, India, Sri Lanka, Taiwan, United States	USDA
	Amylocorticiales	Amylocorticiaceae	*Agroathelia*	*Agroathelia rolfsii*-(*Sclerotium rolfsii*)	*Coffea arabica*	Plant	Kenya, Thailand	Oliveira et al. (2014)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Botryohypochnus	*Botryohypochnus isabellinus*-(*Pellicularia isabellina*)	*Coffea arabica*	Plant	Brazil	USDA
			Ceratobasidium	*Ceratobasidium* sp.*1*	*Coffea arabica*	Plant	Fiji	USDA
				Ceratobasidium sp.*2*	*Coffea canephora*	Plant	Fiji	USDA
				Ceratobasidium sp.*3*	*Coffea* sp.	Plant	Fiji, Samoa	USDA
			Davidsoniella	*Davidsoniella neocaledoniae*	*Coffea robusta*	NA	New Caledonia	USDA
			Pellicularia	*Pellicularia* sp.	*Coffea arabica*	Plant	Cambodia	USDA
			Rhizoctonia	*Rhizoctonia noxia*-(*Ceratobasidium noxium*)	*Coffea arabica*	Leaves	India	USDA
				Rhizoctonia noxia-(*Ceratobasidium noxium*)	*Coffea* sp.	NA	Colombia, India, Puerto Rico, Trinidad and Tobago	USDA
				Rhizoctonia noxia-(*Koleroga noxia*)	*Coffea arabica*	Plant	Cuba, Papua New Guinea	USDA
				Rhizoctonia noxia-(*Koleroga noxia*)	*Coffea canephora*	NA	Papua New Guinea	USDA
				Rhizoctonia noxia-(*Koleroga noxia*)	*Coffea* sp.	NA	Papua New Guinea	USDA
				Rhizoctonia solani	*Coffea arabica*	Seedlings	Brazil, China, Cuba, Florida, Mexico, Zimbabwe	USDA
				Rhizoctonia solani	*Coffea liberica*	Plant	Cuba	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Rhizoctonia solani-(*Pellicularia filamentosa*)	*Coffea arabica*	Roots, Stems	El Salvador, Jamaica, Tanzania	USDA
				Rhizoctonia solani-(*Rhizoctonia choussii*)	*Coffea arabica*	Plant	Cuba, El Salvador	USDA
				Rhizoctonia solani-(*Thanatephorus cucumeris*)	*Coffea arabica*	Plant	Taiwan	USDA
				Rhizoctonia solani-(*Thanatephorus cucumeris*)	*Coffea* sp.	NA	Papua New Guinea	USDA
				Rhizoctonia sp.*1*	*Coffea arabica*	Seedlings, Plant	China, Costa Rica, El Salvador, Haiti, Mexico, Panama	USDA
				Rhizoctonia sp.*2*	*Coffea canephora*	Plant	Fiji	USDA
				Rhizoctonia sp.*3*	*Coffea* sp.	Plant	Malawi, Philippines	USDA
	Corticiales	Corticiaceae	*Corticium*	*Corticium koleroga*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Corticium koleroga	*Coffea arabica*	Plant	Cuba, Dominican Republic, Jamaica, Mexico, Panama, Trinidad, Tobago, Venezuela	USDA
				Corticium koleroga	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Corticium koleroga-(*Pellicularia koleroga*)	*Coffea abeokutae*	NA	Puerto Rico, Virgin Islands	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Corticium koleroga- (*Pellicularia koleroga*)	*Coffea arabica*	Branches, Leaf	Bolivia, Brazil, Colombia, Costa Rica, Cote d'Ivoire, Cuba, Dominican Republic	USDA
				Corticium koleroga- (*Pellicularia koleroga*)	*Coffea canephora*	Plant	Fiji	USDA
				Corticium koleroga- (*Pellicularia koleroga*)	*Coffea* sp.	Plant	Samoa	USDA
				Corticium koleroga- (*Pellicularia koleroga*)	*Coffea stenophylla*	NA	Puerto Rico, Virgin Islands	USDA
				Corticium sp.	*Coffea arabica*	NA	Papua New Guinea	USDA
			Erythricium	*Erythricium salmonicolor*	*Coffea arabica*	Plant	Brazil, Sri Lanka	USDA
			Necator	*Necator salmonicolor*- (*Corticium salmonicolor*)	*Coffea canephora var. robusta*	NA	Guinea	USDA
				Necator salmonicolor- (*Corticium salmonicolor*)	*Coffea* sp.	Plant	Malay Peninsula	USDA
				Necator salmonicolor- (*Corticium salmonicolor*)	*Coffea arabica*	Plant	CostaRica, El Salvador, Guatemala, Honduras, Kenya, Mexico, Nicaragua, Panama, Puerto Rico, Taiwan, Virgin Islands	USDA
				Necator salmonicolor- (*Phanerochaete salmonicolor*)	*Coffea arabica*	NA	Papua New Guinea	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Necator salmonicolor-(*Phanerochaete salmonicolor*)	*Coffea canephora*	NA	Papua New Guinea	USDA
				Necator salmonicolor-(*Phanerochaete salmonicolor*)	*Coffea* sp.	Plant	Fiji, Papua New Guinea, Samoa	USDA
			Rhizoctonia	*Rhizoctonia solani*-(*Corticium solani*)	*Coffea arabica*	Plant	Jamaica, Kenya, Malay Peninsula, Malaysia, Tanzania	USDA
	Hymenochaetales	Hymenochaetaceae	*Hymenochaete*	*Hymenochaete coffeana*	*Coffea robusta*	NA	Central African Republic	USDA
				Hymenochaete noxia	*Coffea arabica*	NA	Kenya	Eida et al. (2009)
			Phellinus	*Phellinus lamaensis*	*Coffea robusta*	NA	New Caledonia	Eida et al. (2009)
				Phellinus lamaensis	*Coffea* sp.	Plant	Fiji, Papua New Guinea, Samoa	USDA
			Pyrrhoderma	*Pyrrhoderma noxium*	*Coffea arabica*	NA	Sri Lanka	Bongiorno et al. (2016)
				Pyrrhoderma noxium-(*Phellinus noxius*)	*Coffea arabica*	Fruit	Papua New Guinea, Taiwan	USDA
				Pyrrhoderma noxium-(*Phellinus noxius*)	*Coffea canephora*	NA	Papua New Guinea	USDA
				Pyrrhoderma noxium-(*Phellinus noxius*)	*Coffea* sp.	NA	Fiji	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Rigidoporaceae	*Rigidoporus*	*Rigidoporus lignosus*-(*Rigidoporus microporus*)	*Coffea liberica*	Plant	Brunei Darussalam	USDA
				Rigidoporus lignosus-(*Rigidoporus microporus*)	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Rigidoporus microporus	*Coffea* sp.	NA	Papua New Guinea	USDA
		Schizoporaceae	*Xylodon*	*Xylodon* sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
	Polyporales	Irpicaceae	*Flavodon*	*Flavodon flavus*-(*Irpex flavus*)	*Coffea robusta*	Plant	Malaysia	USDA
			Leptoporus	*Leptoporus lignosus*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Leptoporus lignosus	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Leptoporus lignosus	*Coffea liberica*	NA	Cote d'Ivoire	USDA
		Meruliaceae	*Phlebia*	*Phlebia subserialis*	*Coffea arabica*	Coffee Soil	Colombian andisols	USDA
			Physisporinus	*Physisporinus lineatus*-(*Polyporus zonalis*)	*Coffea arabica*	Plant	Brazil	USDA
		Polyporaceae	*Amauroderma*	*Amauroderma subrugosu*	*Coffea* sp.	NA	Papua New Guinea	USDA
			Fomes	*Fomes lamaoensis* -(*Fomes lamaensis*)	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Fomes lamaoensis -(*Fomes lamaensis*)	*Coffea arabica*	Roots	Ethiopia, Indonesia, Kenya, Uganda	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Fomes lamaoensis - (*Fomes lamaensis*)	*Coffea canephora var. robusta*	Roots	Indonesia, West Africa	USDA
				Fomes lamaoensis - (*Fomes lamaensis*)	*Coffea liberica*	Roots	Cote d'Ivoire, West Africa	USDA
				Fomes lignosus	*Coffea arabica*	Roots	Brazil, Congo, Ethiopia	USDA
				Fomes lignosus	*Coffea canephora var. robusta*	Roots	Congo, West Africa	USDA
				Fomes lignosus	*Coffea liberica*	Roots	Cote d'Ivoire	USDA
				Fomes lignosus	*Coffea* sp.	Plant	Malay Peninsula, Nigeria	USDA
				Fomes noxius - (*Phellinidium noxium*)	*Coffea arabica*	Plant	China, Taiwan	USDA
				Fomes noxius - (*Phellinidium noxium*)	*Coffea* sp.	Plant	Malay Peninsula, Nigeria	USDA
				Fomes sp.*1*	*Coffea canephora*	NA	Papua New Guinea	USDA
				Fomes sp.*2*	*Coffea* sp.	NA	Papua New Guinea	USDA
			Ganoderma	*Ganoderma lucidum*	*Coffea arabica*	NA	India	USDA
				Ganoderma philippii	*Coffea arabica*	Plant	Brazil	USDA
				Ganoderma philippii- (*Ganoderma pseudoferreum*)	*Coffea arabica*	Plant	East Indies	USDA
				Ganoderma philippii- (*Ganoderma pseudoferreum*)	*Coffea liberica*	Plant	Malay Peninsula	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Ganoderma philippii- (*Ganoderma pseudoferreum*)	*Coffea robusta*	Plant	Malay Peninsula	Lu et al. (2022d)
				Ganoderma sp.	*Coffea arabica*	NA	Papua New Guinea	Lu et al. (2022d)
			Hexagonia	*Hexagonia discopoda*	*Coffea canephora var. typica*	NA	Guinea	Lu et al. (2022d)
			Polyporus	*Polyporus coffeae*	*Coffea abeokutae*	NA	Cote d'Ivoire	Lu et al. (2022d)
				Polyporus coffeae	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Polyporus coffeae	*Coffea* sp.	NA	Papua New Guinea	USDA
				Polyporus depauperatus	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
				Polyporus rubidus	*Coffea arabica*	Roots	Indonesia	USDA
				Polyporus rubidus	*Coffea canephora var. robusta*	Roots	Indonesia	USDA
			Pycnoporus	*Pycnoporus cinnabarinus* (*Trametes cinnabarina*)	*Coffea dybowskii*	NA	Philippines	USDA
			Tinctoporellus	*Tinctoporellus* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Postiaceae	*Polystictus*	*Polystictus phaeus*	*Coffea arabica*	Plant	Taiwan	USDA
			Trametes	*Trametes polyzona-* (*Polystictus occidentalis*)	*Coffea arabica*	NA	Kenya, Tanzania	USDA
	Polyporales genera incertae sedis	Incertae sedis	*Diacanthodes*	*Diacanthodes novoguineensis*	*Coffea arabica*	NA	Papua New Guinea	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
	Russulales	Stereaceae	*Aleurodiscus*	*Aleurodiscus moquiniarum*	*Coffea arabica*	Plant	Brazil	USDA
	Sebacinales	Sebacinaceae	*Chaetospermum*	*Chaetospermum camelliae*	*Coffea canephora*	NA	India	USDA
Ascomycota order *incertae sedis*	Ascomycota families *incertae sedis*	Seuratiaceae	*Seuratia*	*Seuratia millardetii*	*Coffea* sp.	Leaves	Hawaii	USDA
		Ascomycota genera *incertae sedis*	*Annellophora*	*Annellophora* sp.	*Coffea liberica*	Plant	Malaysia	Djadjiti et al. (2020)
			Botryodiplodia	*Botryodiplodia* sp.	*Coffea* sp.	NA	Papua New Guinea	USDA
			Cephaleuros	*Cephaleuros mycoidea*	*Coffea liberica*	Plant	Sierra Leone, Tanzania	USDA
				Cephaleuros virescens	*Coffea arabica*	NA	Papua New Guinea	USDA
				Cephaleuros virescens	*Coffea canephora*	NA	Papua New Guinea	USDA
				Cephaleuros virescens	*Coffea* sp.	NA	Papua New Guinea	Vega et al. (2008)
			Chaetostroma	*Chaetostroma* sp.	*Coffea arabica*	Plant	Mexico	USDA
			Cladosporiella	*Cladosporiella deightonii*	*Coffea arabica*	Leaves	Cuba	USDA
			Clypeolum	*Clypeolum megalosporium*	*Coffea arabica*	NA	Costa Rica	USDA
			Diplocladiella	*Diplocladiella scalaroides*	*Coffea arabica*	NA	China, Japan, Taiwan	USDA
			Leptothyrium	*Leptothyrium discoideum*	*Coffea arabica*	NA	Venezuela	USDA
			Plenotrichopsis	*Plenotrichopsis coffeae*	*Coffea arabica*	Plant	Brazil	USDA
			Pleurodesmospora	*Pleurodesmospora* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Septogloeum	*Septogloeum concentricu*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Titaea	*Titaea hemileiae*	*Coffea arabica*	NA	Nigeria	USDA
			Vermicularia	*Vermicularia* sp.	*Coffea* sp.	Plant	Fiji	USDA
		Parodiopsidaceae	*Dimerosporina*	*Dimerosporina* sp.	*Coffea* sp.	Plant	Malaysia	USDA
Dacrymycetes	Dacrymycetales	Dacrymycetaceae	*Dacryopinax*	*Dacryopinax spathularia*	*Coffea arabica*	Plant	Venezuela	USDA
Dipodascomycetes	Dipodascales	Dipodascaceae	*Geotrichum*	*Geotrichum candidum*	*Coffea* sp.	Seed	Papua New Guinea	USDA
Dothideomycetes	Asterinales	Asterinaceae	*Asterina*	*Asterina coffeicola*	*Coffea arabica*	NA	Jamaica	USDA
			Dimerosporium	*Dimerosporium coronatun*	*Coffea arabica*	NA	Costa Rica	USDA
			Dinemasporium	*Dinemasporium coffeanum*	*Coffea arabica*	NA	Brazil	USDA
	Aulographales	Rhizodiscinaceae	*Rhizodiscina*	*Rhizodiscina coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Auriculariaceae	*Auricularia*	*Auricularia delicata*-(*Laschia delicata*)	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
				Auricularia nigricans-(*Auricularia polytricha*)	*Coffea arabica*	NA	Philippines	USDA
				Auricularia nigricans-(*Hirneola polytricha*)	*Coffea arabica*	Plant	Cuba	USDA
	Botryosphaeriales	Botryosphaeriaceae	*Barriopsis*	*Barriopsis coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Botryosphaeria	*Botryosphaeria* sp.	*Coffea arabica*	Leaves	Puerto Rico	Santamaría et al. (2005)
			Diplodia	*Diplodia coffeicola*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Diplodia coffeicola	*Coffea arabica*	Plant	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Diplodia sp.	*Coffea* sp., *Coffea arabica*	Leaves	Mexico, Papua New Guinea	USDA
			Diplodina	*Diplodina* sp.	*Coffea* sp.	NA	Haiti	USDA
			Dothiorella	*Dothiorella acericola*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Dothiorella camelliae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Dothiorella coffeae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Fusicoccum	*Fusicoccum* sp.	*Coffea arabica*	Plant	Mexico	USDA
			Guignardia	*Guignardia* sp.	*Coffea arabica*	Leaves	Puerto Rico	USDA
			Lasiodiplodia	*Lasiodiplodia coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Lasiodiplodia pseudotheobromae	*Coffea arabica*	Plant	Brazil, Thailand	USDA
				Lasiodiplodia pseudotheobromae	*Coffea* sp.	Plant	Congo, Democratic Republic	USDA
				Lasiodiplodia pseudotheobromae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Lasiodiplodia theobromae	*Coffea arabica*	Plant	Cuba, Fiji, Venezuela	USDA
				Lasiodiplodia theobromae	*Coffea canephora*	Plant	Fiji	USDA
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea arabica*	Plant	Cuba, Fiji, Ghana, Tanzania	USDA
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea canephora*	Plant	Cote d'Ivoire, Fiji, Papua New Guinea	USDA
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea liberica*	Plant	Brunei Darussalam, Cote d'Ivoire	USDA
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Lasiodiplodia theobromae-(*Botryodiplodia theobromae*)	*Coffea* sp.	Plant	Ghana, Malay Peninsula	USDA
			Macrophoma	*Macrophoma coffeae var. macrospora*	*Coffea arabica*	Plant	Brazil	USDA
			Macrophomina	*Macrophomina phaseolina*-(*Rhizoctonia bataticola*)	*Coffea arabica*	Plant	Uganda	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Macrophomina phaseolina-(*Rhizoctonia bataticola*)	*Coffea robusta*	Plant	Sri Lanka, Uganda	USDA
				Macrophomina phaseolina-(*Rhizoctonia lamellifera*)	*Coffea arabica*	NA	Kenya	USDA
				Macrophomina phaseolina	*Coffea arabica*	Root	Kenya	USDA
				Macrophomina phaseolina-(*Macrophom corchori*)	*Coffea arabica*	Plant	Thailand	USDA
				Macrophomina phaseolina-(*Macrophomina phaseoli*	*Coffea arabica*	Plant	Kenya, Tanzania, Thailand, Uganda	USDA
				Macrophomina phaseolina-(*Macrophomina phaseoli*	*Coffea canephora var. robusta*	Plant	Sri Lanka, Uganda	USDA
			Microdiplodia	*Microdiplodia* sp.	*Coffea robusta*	Plant	Malaysia	USDA
			Neofusicoccum	*Neofusicoccum parvum*	*Coffea arabica*	NA	Colombia	USDA
				Neofusicoccum podocarp	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neofusicoccum sichuanense	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Phyllostictaceae	*Phyllosticta*	*Phyllosticta bokensis*	*Coffea liberica*	NA	Congo, Democratic Republic of the	Oliveira et al. (2014)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Phyllosticta bokensis- (*Phyllosticta coffeae-arabicae*)	*Coffea arabica*	Plant	Taiwan	USDA
				Phyllosticta camoensis	*Coffea camoensis*	Leaves	Africa	USDA
				Phyllosticta capitalensis	*Coffea arabica*	Mature and Healthy Leaves	Brazil	USDA
				Phyllosticta coffeae-libericae	*Coffea robusta*	NA	India	USDA
				Phyllosticta coffeicola	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Phyllosticta coffeicola	*Coffea arabica*	NA	Brazil, China, Congo, Costa Rica, India, Panama	USDA
				Phyllosticta coffeicola	*Coffea canephora*	Plant	Cambodia	USDA
				Phyllosticta coffeicola	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Phyllosticta coffeicola	*Coffea* sp.	Plant	Fiji	USDA
				Phyllosticta sp.*1*	*Coffea arabica*	Plant	Brazil, Costa Rica, El Salvador, Eritrea, Florida, Guatemala, Mexico, Panama	USDA
				Phyllosticta sp.*2*	*Coffea* sp.	Plant	Ghana, Malay Peninsula	USDA
				Phyllosticta sp.*3*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Phyllosticta sp.*4*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Phyllosticta sp.*5*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Phyllosticta sp.*6*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Phyllosticta sp.*7*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Phyllosticta usteri	*Coffea arabica*	NA	Brazil, Czechoslovakia, Venezuela	USDA
	Capnodiales	Capnodiaceae	*Capnodium*	*Capnodium brasiliense*	*Coffea arabica*	Plant	Brazil, Kenya	USDA
				Capnodium brasiliense	*Coffea liberica*	Plant	Ghana	USDA
				Capnodium brasiliense	*Coffea* sp.	NA	Brazil, Colombia	USDA
				Capnodium citri- (*Aithaloderma citri*)	*Coffea arabica*	Plant	Brazil	USDA
				Capnodium coffeae	*Coffea arabica*	Plant	Costa Rica, El Salvador, Guatemala, Honduras, Mexico, Nicaragua, Panama	USDA
				Capnodium coffeae	*Coffea robusta*	Plant	Congo Democratic Republic	USDA
				Capnodium coffeicola	*Coffea* sp.	Leaves	Chiang Rai Thailand	Hongsanan et al. (2015)
				Capnodium sp.*1*	*Coffea arabica*	Plant	Cuba, Haiti, Mexico, Panama, Sudan, Tanzania, Zimbabwe	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Capnodium sp.*2*	*Coffea cassia*	Plant	Cuba	USDA
				Capnodium sp.*3*	*Coffea* sp.	Plant	Fiji, Hawaii	USDA
				Capnodium tanakae-(*Neocapnodium tanakae*)	*Coffea arabica*	Plant	China, Taiwan	USDA
				Capnodium tanakae-(*Neocapnodium tanakae*)	*Coffea liberica*	Plant	China, Taiwan	Monteiro et al. (2017)
			Chaetoscorias	*Chaetoscorias vulgaris*	*Coffea arabica*	Plant	China, Taiwan	USDA
			Leptoxyphium	*Leptoxyphium fumago*-(*Fumago vagans*	*Coffea arabica*	NA	China	USDA
			Paracapnodium	*Paracapnodium brasilense*	*Coffea arabica*	Leaves	Colombia	USDA
			Phragmocapnias	*Phragmocapnias asiaticus*	*Coffea arabica*	NA	Thailand	Monteiro et al. (2017)
		Readerielliopsidaceae	*Scorias*	*Scorias communis*	*Coffea liberica*	Plant	China, Taiwan	USDA
				Scorias sp.	*Coffea canephora*	NA	Papua New Guinea	USDA
	Cladosporiales	Cladosporiaceae	*Cladosporium*	*Cladosporium cf. sphaerospermum*	*Coffea arabica*	Leaves	USA, Maryland, Beltsville	Vega et al. (2008)
				Cladosporium cf.cladosporioides	*Coffea arabica*	Leaves	Puerto Rico, USA, Hawaii, Kona	Vega et al. (2008)
				Cladosporium cladosporioides	*Coffea arabica*	Leaves	Papua New Guinea	USDA
				Cladosporium cladosporioides	*Coffea* sp.	Leaf	Uganda	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Cladosporium cladosporioides complex	*Coffea arabica*	Mature and Healthy Leaves	Brazil	Oliveira et al. (2014)
				Cladosporium hemileiae	*Coffea robusta*	NA	Congo, Democratic Republic	USDA
				Cladosporium herbarum	*Coffea arabica*	NA	Mozambique	USDA
				Cladosporium herbarum	*Coffea canephora var. robusta*	Leaves, Young Seedlings	Indonesia	USDA
				Cladosporium herbarum	*Coffea* sp.	NA	Southern Africa	USDA
				Cladosporium oxysporum	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Cladosporium pseudocladosporioides	*Coffea* sp.	Plant	Uganda, United States	USDA
				Cladosporium sp.*1*	*Coffea arabica*	Plant, Peduncle, Beans	Australia, Brazil, Cuba, USA, Hawaii, Kona, Lavras, Minas Gerais.	USDA
				Cladosporium sp.*2*	*Coffea aurantii*	NA	Cyprus	USDA
				Cladosporium sp.*3*	*Coffea robusta*	Plant	Malawi	USDA
				Cladosporium sp.*4*	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Cladosporium sp.*5*	*Coffea arabica*	Leaves	Brazil	Bongiorno et al. (2016)
				Cladosporium sp.*6*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Cladosporium sp.*4*	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Cladosporium sp.*5*	*Coffea arabica*	Leaves	Brazil	Bongiorno et al. (2016)
				Cladosporium sp.*6*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Cladosporium sp.*7*	*Coffea arabica*	Leaves	China	USDA
				Cladosporium tenuissimum	*Coffea arabica*	Mature And Healthy Leaves	Brazil	Oliveira et al. (2014)
	Coniosporiales	Coniosporiaceae	*Coniosporium*	*Coniosporium* sp.	*Coffea arabica*	Leaves	Mexico	Saucedo-García et al. (2014)
	Dothideales	Dothioraceae	*Metasphaeria*	*Metasphaeria* sp.	*Coffea arabica*	NA	Eritrea	Gizaw et al. (2016)
		Saccotheciaceae	*Aureobasidium*	*Aureobasidium pullulans*	*Coffea arabica*	Mature And Healthy Leaves	Brazil	Gizaw et al. (2016)
	Dothideomycetes families incertae sedis	Vizellaceae	*Vizella*	*Vizella bingervilliana*	*Coffea liberica*	NA	Africa	USDA
		Trichosphaeriaceae	*Stachylidium*	*Stachylidium bicolor*	*Coffea arabica*	NA	Papua New Guinea	USDA
		Incertae sedis	*Auerswaldia*	*Auerswaldia excoriata*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Auerswaldia excoriata	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Auerswaldia excoriata	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Auerswaldia excoriata	*Coffea liberica*	NA	Cote d'Ivoire	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Eriomycopsis	*Eriomycopsis* sp.	*Coffea arabica*	Plant	Sudan	USDA
			Pseudomorfea	*Pseudomorfea coffeae*	*Coffea arabica*	NA	India	USDA
	Kirschsteiniotheliales	Kirschsteiniotheliaceae	*Kirschsteiniothelia*	*Kirschsteiniothelia puerensis*	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Hyde et al. (2023)
	Microthyriales	Microthyriaceae	*Trichopeltis*	*Trichopeltis pulchella*	*Coffea robusta*	Plant	Malaysia	USDA
	Muyocopronales	Muyocopronaceae	*Arxiella*	*Arxiella terrestris*	*Coffea arabica*	NA	Australia	USDA
			Muyocopron	*Muyocopron lithocarpi*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Setoapiospora	*Setoapiospora thailandica*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Mycosphaerellales	Dissoconiaceae	*Ramichloridium*	*Ramichloridium* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Mycosphaerellaceae	*Ascospora*	*Ascospora coffeae*	*Coffea robusta*	NA	Java	USDA
			Cercospora	*Cercospora coffeae–olivaceae*	*Coffea olivacea*	NA	India	USDA
				Cercospora coffeicola	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Cercospora coffeicola	*Coffea arabica*	Leaves, Berries	Australia, Brazil, Cambodia, China, Colombia, Congo, Democratic Republic, Cook Islands, Costa Rica, Cote d'Ivoire, Cuba, Dominican Republic, El Salvador, Fiji, Florida, Guatemala, Guinea, Haiti, Hawaii, Honduras, India, Indonesia, Jamaica, Japan, Kenya, Madagascar, Malawi, Mexico, Myanmar, New Caledonia, Nicaragua, Panama, Papua	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
							New Guinea, Peru, Philippines, Puerto Rico, Samoa, Sierra Leone, Sudan, Taiwan, Tanzania, Thailand, Trinidad and Tobago, Uganda, Venezuela, Virgin Islands, Zambia, Zimbabwe	
				Cercospora coffeicola	*Coffea bukobensis*	Leaves	Philippines	USDA
				Cercospora coffeicola	*Coffea canephora*	Plant	Cambodia, Fiji, Papua New Guinea, Samoa, Sierra Leone	USDA
				Cercospora coffeicola	*Coffea canephora var. robusta*	Leaves	Guinea, Sudan	USDA
				Cercospora coffeicola	*Coffea excelsa*	Leaves, Plant	China, Philippines, Sudan	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Cercospora coffeicola	*Coffea liberica*	Plant	Brunei Darussalam, China, Cote d'Ivoire, Cuba, Fiji, Sierra Leone	USDA
				Cercospora coffeicola	*Coffea* sp.	Leaves	Fiji, Ghana, Haiti, Jamaica, Malawi, Mauritius, Nicaragua, Nigeria, Papua New Guinea, Samoa, South Africa, Southern Africa, Thailand	USDA
				Cercospora coffeicola	*Coffea robusta*	Plant	Brunei Darussalam, China, Hawaii, Malawi, New Caledonia, Sierra Leone, Sudan, Taiwan, Trinidad and Tobago	USDA
				Cercospora coffeicola	*Coffea stenophylla*	Leaves	Sierra Leone, Tanzania	USDA
				Cercospora coffeicola-(*Cercospora coffeae*)	*Coffea stenophylla*	NA	Africa	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Cercospora herrerana – (*Cercospora coffeicola*)	*Coffea arabica*	NA	Mexico	USDA
				Cercospora sp.	*Coffea arabica*	Leaves	Brazil, Japan	USDA
			Mycosphaerella	*Mycosphaerella coffeae*	*Coffea arabica*	Leaves	Brazil, Cuba, Samoa, Taiwan	USDA
				Mycosphaerella coffeae	*Coffea arabica var. myrtifolia*	Leaves	Congo, Democratic Republic, Congo Republic, Samoa	USDA
				Mycosphaerella coffeae	*Coffea robusta*	Plant	Taiwan	USDA
				Mycosphaerella coffeae	*Coffea* sp.	NA	Samoa	USDA
				Mycosphaerella coffeicola	*Coffea arabica*	Leaves	Africa, Cambodia, El Salvador, India, Jamaica, Mexico, Puerto Rico, Virgin Islands	USDA
				Mycosphaerella coffeicola	*Coffea* sp.	Plant	Mauritius, South Africa	USDA
				Mycosphaerella coffeicola-(*Sphaerella coffeicola*)	*Coffea* sp.	NA	Venezuela	USDA
				Mycosphaerella sp.	*Coffea arabica*	Leaves	Bolivia, Brazil	USDA
			Pseudocercospora	*Pseudocercospora coffeigena*	*Coffea arabica*	Plant	China	Culliao and Barcelo (2015)
			Septoria	*Septoria berkeleyi*	*Coffea arabica*	Plant	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Septoria berkeleyi	*Coffea arabica*	Plant	South America	USDA
				Septoria coffeae	*Coffea arabica*	NA	Uganda	USDA
				Septoria coffeicola	*Coffea liberica*	Leaves	Cameroon	USDA
				Septoria sp.	*Coffea arabica*	Plant	Brazil	USDA
			Sphaerella	*Sphaerella* sp.	*Coffea arabica*	Plant	Mexico	USDA
			Sphaerulina	*Sphaerulina coffeicola*	*Coffea arabica*	NA	Dominican Republic, Eritrea, Haiti	Eida et al. (2009)
			Zasmidium	*Zasmidium coffeae*	*Coffea bengalensis*	NA	India	USDA
				Zasmidium sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Neodevriesiaceae	*Tripospermum*	*Tripospermum gardneri*	*Coffea arabica*	Plant	Malay Peninsula	USDA
				Tripospermum gardneri	*Coffea liberica*	Plant	Malay Peninsula	USDA
		Teratosphaeriaceae	*Hyweljonesia*	*Hyweljonesia* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Stenella	*Stenella coffeae*	*Coffea bengalensis*	Leaves	India	
	Patellariales	Patellariaceae	*Patellaria*	*Patellaria coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Pleosporales	Acrocalymmaceae	*Acrocalymma*	*Acrocalymma coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Acrocalymma daliense	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Acrocalymma jinghongense	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Acrocalymma walkeri	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Amorosiaceae	*Neoamorocoelophoma*	*Neoamorocoelophoma coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Anteagloniaceae	*Anteaglonium*	*Anteaglonium parvulum*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Astrosphaeriellaceae	*Caryospora*	*Caryospora coffeae*	*Coffea* sp.	NA	Venezuela	USDA
		Bambusicolaceae	*Corylicola*	*Corylicola coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Leucaenicola	*Leucaenicola baoshanensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Leucaenicola coffeae	*Coffea arabica*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2025a)
		Coniothyriaceae	*Coniothyrium*	*Coniothyrium coffeae*	*Coffea arabica*	NA	Brazil, Haiti, Philippines	USDA
				Coniothyrium coffeae	*Coffea liberica*	NA	India	USDA
				Coniothyrium coffeae	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Coniothyrium coffeae	*Coffea* sp.	Plant	Philippines	USDA
				Coniothyrium fuckelii	*Coffea arabica*	Plant	Venezuela	USDA
				Coniothyrium sp.*1*	*Coffea liberica*	Plant	Malaysia	USDA
				Coniothyrium sp.*2*	*Coffea robusta*	Plant	Malaysia	USDA
		Corynesporascaceae	*Corynespora*	*Corynespora cassiicola*	*Coffea canephora*	Leaf, Berry	Brazil	Souza et al. (2011)
		Cyclothyriellaceae	*Vaginomyces*	*Vaginomyces yunnanensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Dacampiaceae	*Aaosphaeria*	*Aaosphaeria arxii*	*Coffea excelsa*	NA	Central African Republic	USDA
		Dictyosporiaceae	*Aquadictyospora*	*Aquadictyospora yunnanensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Han et al. (2024)
			Dictyocheirospora	*Dictyocheirospora chiangmaiensis*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Dictyocheirospora nabanheensis	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Pseudocoleophoma	*Pseudocoleophoma puerensis*	*Coffea arabica var. catimor*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022a)
				Pseudocoleophoma yunnanensis	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022a)
		Didymellaceae	*Allophoma*	*Allophoma nicaraguensis*	*Coffea* sp.	Twig	Nicaragua	USDA
				Allophoma nicaraguensis	*Coffea arabica*	NA	Nicaragua	USDA
			Ascochyta	*Ascochyta* sp.*1*	*Coffea arabica*	Plant	Brazil, Eritrea	USDA
				Ascochyta sp.*2*	*Coffea canephora var. robusta*	NA	Guinea	USDA
				Ascochyta sp.*3*	*Coffea robusta*	Plant	Brunei Darussalam	USDA
			Boeremia	*Boeremia coffeae-*(*Ascochyta coffeae*)	*Coffea arabica*	Leaves	Brazil	USDA
				Boeremia coffeae-(*Boeremia exigua var. coffeae*)	*Coffea arabica*	Leaves, Branches	Ethiopia, Malawi	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Boeremia exigua var. coffeae	*Coffea arabica*	Leaves	Brazil, Cameroon	USDA
				Boeremia exigua var. heteromorpha	*Coffea arabica*	NA	Brazil	USDA
			Didymella	*Didymella coffeae–arabicae*	*Coffea arabica*	NA	Ethiopia	USDA
				Didymella coffeae-arabicae-(*Peyronellaea coffeae–arabicae*)	*Coffea arabica*	NA	Ethiopia	USDA
			Ectophoma	*Ectophoma pomi*	*Coffea arabica*	Leaf	India	USDA
				Ectophoma pomi-(*Phoma pereupyrena*)	*Coffea arabica*	Leaf	India	USDA
			Epicoccum	*Epicoccum sorghi-*(*Epicoccum sorghinum*)	*Coffea* sp.	Fruit	India	USDA
				Epicoccum sorghinum-(*Phoma sorghina*)	*Coffea* sp.	Fruit	India	USDA
				Epicoccum sp. *1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Epicoccum sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Epicoccum sp.*3*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Microsphaeropsis	*Microsphaeropsis* sp.	*Coffea arabica*	Leaves	/	USDA
			Phoma	*Phoma coffeae*	*Coffea arabica*	NA	China	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Phoma coffeae-arabicae- (*Didymella coffeae-arabicae*)	*Coffea arabica*	NA	Ethiopia	USDA
				Phoma coffeicola	*Coffea abeokuta*	NA	Cote d'Ivoire	USDA
				Phoma coffeicola	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Phoma coffeicola	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Phoma costaricensis	*Coffea arabica*	Plant	Costa Rica, Guatemala, Papua New Guinea, Venezuela	USDA
				Phoma costaricensis	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Phoma costarricensis	*Coffea arabica*	Plant	Brazil, Costa Rica, India, Mexico, New Guinea, Nicaragua	USDA
				Phoma costarricensis	*Coffea* sp.	NA	Nicaragua	USDA
				Phoma eupyrena	*Coffea arabica*	Mature And Healthy Leaves	Brazil	Oliveira et al. (2014)
				Phoma exigua var. exigua	*Coffea arabica*	Leaves	/	Fernandes et al. (2009)
				Phoma herbarum	*Coffea arabica*	Leaves	/	Fernandes et al. (2009)
				Phoma leveillei	*Coffea arabica*	NA	Papua New Guinea	USDA
				Phoma sp.*1*	*Coffea arabica*	Plant	Brazil, Cuba, India	USDA
				Phoma sp.*2*	*Coffea canephora*	Plant	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Phoma sp.*3*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Phoma tarda	*Coffea arabica*	Coffee Berry	Brazil, Cameroon, Ethiopia, Kenya	USDA
			Stagonosporopsis	*Stagonosporopsis* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Xenodidymella	*Xenodidymella coffeae*	*Coffea arabica*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2025a)
		Didymosphaeriaceae	*Austropleospora*	*Austropleospora keteleeriae*	*Coffea arabica var. catimor*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2022a)
			Deniquelata	*Deniquelata yunnanensis*	*Coffea* sp.	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2022a)
			Didymosphaeria	*Didymosphaeria* sp.*1*	*Coffea canephora*	NA	Papua New Guinea	USDA
				Didymosphaeria sp.*2*	*Coffea robusta*	Plant	Malaysia	USDA
			Montagnula	*Montagnula coffeae*	*Coffea arabica*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2025a)
				Montagnula donacina-(*Munkovalsaria donacina*)	*Coffea arabica*	NA	Paraguay	USDA
				Montagnula donacina-(*Munkovalsaria donacina*)	*Coffea robusta*	NA	Central African Republic	USDA
				Montagnula thailandica	*Coffea arabica var. catimor*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2022a)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Paraconiothyrium	*Paraconiothyrium brasiliense*	*Coffea arabica*	Fruit	Brazil	USDA
				Paraconiothyrium fici	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Paraconiothyrium yunnanensis	*Coffea* sp.	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2022a)
			Phaeodothis	*Phaeodothis winteri*	*Coffea arabica*	Leaves	Brazil, India	USDA
				Phaeodothis winteri	*Coffea robusta*	Leaves	Malaysia	USDA
			Spegazzinia	*Spegazzinia meliolae*	*Coffea stenophylla*	Plant	Ghana	USDA
			Xenocamarosporium	*Xenocamarosporium acaciae*	*Coffea* sp.	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2022a)
		Halotthiaceae	*Halotthicoffea*	*Halotthicoffea coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Hermatomycetaceae	*Hermatomyces*	*Hermatomyces tucumanensis*	*Coffea liberica*	NA	Sierra Leone	USDA
		Leptosphaeriaceae	*Leptosphaeria*	*Leptosphaeria africana*	*Coffea robusta*	NA	South Africa	USDA
				Leptosphaeria canephorae	*Coffea canephora*	NA	Congo, Democratic Republic	USDA
				Leptosphaeria centrafricana	*Coffea excelsa*	NA	Central African Republic	USDA
				Leptosphaeria coffaeicida	*Coffea* sp.	NA	Costa Rica	USDA
				Leptosphaeria coffeicola	*Coffea arabica*	Plant	Malawi, Tanzania	USDA
				Leptosphaeria coffeicola	*Coffea robusta*	Plant	Malaysia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Leptosphaeria coffeigena	*Coffea arabica*	Plant	Cuba, Mexico, Venezuela	USDA
				Leptosphaeria coffeigena var. longirostrata	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Leptosphaeria cylindrospora	*Coffea robusta*	NA	Central African Republic	USDA
				Leptosphaeria excelsa	*Coffea excelsa*	NA	Central African Republic	Fernandes et al. (2009)
				Leptosphaeria gigaspora	*Coffea robusta*	NA	Central African Republic	de Almeida et al. (2019)
				Leptosphaeria lobayensis	*Coffea excelsa*	NA	Central African Republic	USDA
				Leptosphaeria longispora	*Coffea excelsa*	NA	Central African Republic	USDA
				Leptosphaeria macrorostra	*Coffea robusta*	NA	Central African Republic	USDA
				Leptosphaeria oubanguiensis	*Coffea robusta*	NA	Central African Republic	USDA
				Leptosphaeria pusilla	*Coffea* sp.	NA	Costa Rica	USDA
				Leptosphaeria sp.*1*	*Coffea arabica*	Plant, Leaves	Tanzania	USDA
				Leptosphaeria sp.*2*	*Coffea robusta*	Plant	Brunei Darussalam	USDA
				Leptosphaeria tetraspora	*Coffea robusta*	NA	Central African Republic	USDA
				Leptosphaeria tonduzi	*Coffea* sp.	NA	Costa Rica	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Longiostiolaceae	*Loculimurus*	*Loculimurus baoshanensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Loculimurus coffeae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Loculimurus lincangensis	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Longiostiolum	*Longiostiolum coffeae*	*Coffea arabica*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2025a)
				Longiostiolum puerense	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Lophiostomataceae	*Flabellascoma*	*Flabellascoma coffeae*	*Coffea arabica*	Dead and Decaying Twigs	Yunnan, China	Lu et al. (2025a)
			Oraniella	*Oraniella coffeicola*	*Coffea* sp.	NA	Hawaii	USDA
		Macrodiplodiopsidaceae	*Pseudochaetosphaeronema*	*Pseudochaetosphaeronema baoshanense*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Pseudochaetosphaeronema coffeae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Massariaceae	*Massarioramusculicola*	*Massarioramusculicola chiangraiensis*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China; Chiang Rai, Thailand	Hyde et al. (2024), Lu et al. (2025b)
		Massarinaceae	*Helminthosporium*	*Helminthosporium canephorae*	*Coffea canephora*	NA	Congo, Democratic Republic	USDA
				Helminthosporium coffeae	*Coffea* sp.	Plant	Ghana	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Helminthosporium coffeae	*Coffea arabica*	Plant	Ghana	USDA
				Helminthosporium densum-(*Imimyces densus*)	*Coffea excelsa*	NA	Sierra Leone	USDA
				Helminthosporium glabroides	*Coffea arabica*	NA	Ethiopia	USDA
				Helminthosporium puerensis	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025a)
				Helminthosporium sp.*1*	*Coffea arabica*	Plant	Nicaragua	USDA
				Helminthosporium sp.*2*	*Coffea* sp.	NA	Papua New Guinea	USDA
				Helminthosporium ubangiense	*Coffea* sp.	Leaves	Tropical Africa	USDA
		Melanommataceae	*Byssosphaeria*	*Byssosphaeria chiangraiensis*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
				Byssosphaeria coffeae	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Camposporium	*Camposporium antennatum*	*Coffea arabica*	NA	Australia	USDA
			Phragmocephala	*Phragmocephala atra*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
		Neohendersoniaceae	*Crassiparies*	*Crassiparies yunnanensis*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022b)
		Neomassariaceae	*Neomassaria*	*Neomassaria asexualis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Neomassaria coffeae	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025a)
				Neomassaria coloradensis	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neomassaria formosana	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neomassaria palmae	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neomassaria puerensis	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neomassaria yunnanensis	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Pseudohelminthosporium	*Pseudohelminthosporium clematidis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Nigrograna ceae	*Nigrograna*	*Nigrograna asexualis*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022c)
				Nigrograna coffeae	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022c)
				Nigrograna daliensis	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Nigrograna puerensis	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2022c)
		Occultibambusaceae	*Brunneofusispora*	*Brunneofusispora baoshanensis*	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Liu et al. (2024b)
				Brunneofusispora baoshanensis	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Brunneofusispora chiangraiensis	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
				Brunneofusispora coffeae	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Neooccultibambusa	*Neooccultibambusa coffeae*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025a)
		Paradictyoarthriniaceae	*Paradictyoarthrinium*	*Paradictyoarthrinium diffractum*	*Coffea* sp.	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
		Periconiaceae	*Periconia*	*Periconia byssoides*	*Coffea arabica*	Plant	Venezuela	USDA
				Periconia sp.	*Coffea arabica*	Leaves	/	USDA
		Phaeosphaeriaceae	*Banksiophoma*	*Banksiophoma coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Hendersonia	*Hendersonia coffeae*	*Coffea arabica*	Plant	Mexico	USDA
				Hendersonia sp.	*Coffea arabica*	NA	Eritrea	USDA
			Melnikia	*Melnikia coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Ophiosphaerella	*Ophiosphaerella chiangraiensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Phaeosphaeria	*Phaeosphaeria musae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Phaeosphaeria sp.*1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Phaeosphaeria sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Pleosporaceae	*Alternaria*	*Alternaria alternata*	*Coffea arabica*	Leaves	/	USDA
				Alternaria alternata-(*Alternaria tenuis*)	*Coffea* sp.	NA	Southern Africa	USDA
				Alternaria citri	*Coffea arabica*	Leaves	Mexico	USDA
				Alternaria sp.	*Coffea arabica*	Plant	Mexico	Oliveira et al. (2014)
			Bipolaris	*Bipolaris coffeana*	*Coffea arabica*	Leaves	Kenya	USDA
				Bipolaris zeicola	*Coffea arabica*	Plant	Brazil	USDA
			Curvularia	*Curvularia geniculata*	*leaf spot disease*	Coffea Sp.	South Korea	Nam et al. (2024)
				Curvularia prasadii	*Coffea arabica*	NA	Kenya	USDA
				Curvularia sp.*1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Curvularia sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Curvularia tropicalis	*Coffea arabica*	Leaves	India	USDA
				Curvularia tropicalis-(*Bipolaris tropicalis*)	*Coffea arabica*	Leaves	India	USDA
			Drechslera	*Drechslera biseptata*	*Coffea arabica*	Mature and Healthy Leaves	Brazil	USDA
				Drechslera sp.*1*	*Coffea arabica*	Plant	Brazil	USDA
				Drechslera sp.*2*	*Catuai variety*	Corticous Roots Tissues	Piumhi, Brazil	USDA
		Pleurotremataceae	*Melomastia*	*Melomastia puerensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Melomastia thamplaensis	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Pyrenochaetopsidaceae	*Pyrenochaetopsis*	*Pyrenochaetopsis microspora*	*Coffea arabica*	Leaf	Brazil	USDA
				Pyrenochaetopsis setosissima	*Coffea arabica*	Leaf	Brazil	USDA
		Roussoellaceae	*Pararoussoella*	*Pararoussoella coffeae*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025a)
			Roussoella	*Roussoella mexicana*	*Coffea arabica*	Leaves	Mexico	USDA
			Similrousoella	*Similrousoella jinghongensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Sporormiaceae	*Preussia*	*Preussia pseudominima*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Preussia sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
		Sulcatisporaceae	*Loculosulcatispora*	*Loculosulcatispora thailandica*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Thyridariaceae	*Cycasicola*	*Cycasicola coffeae*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025a)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Liua	*Liua muriformis*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Torulaceae	*Dendryphion*	*Dendryphion verrucosum*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Torula	*Torula mackenziei*	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2025b)
	Venturiales	Venturiaceae	*Antennaria*	*Antennaria setosa*	*Coffea arabica*	NA	Belgium	USDA
			Limacinia	*Limacinia* sp.	*Coffea arabica*	Plant	Mexico	USDA
				Limacinia spinigera-(*Triposporiopsis spinigera*)	*Coffea arabica*	Plant	China, Japan, Taiwan	USDA
				Limacinia spinigera-(*Triposporiopsis spinigera*)	*Coffea liberica*	Plant	China, Taiwan	USDA
			Venturia	*Venturia coffeicola*	*Coffea arabica*	Plant	Brazil	USDA
Entomophthoromycetes	Entomophthorales	Entomophthoraceae	*Entomophthora*	*Entomophthora fresenii*	*Coffea arabica*	NA	India	USDA
			Claroideoglomus	*Claroideoglomus etunicatum*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
Eurotiomycetes	Chaetothyriales	Chaetothyriaceae	*Aithaloderma*	*Aithaloderma longisetum*	*Coffea* sp.	Plant	Philippines	USDA
				Aithaloderma longisetum	*Coffea arabica*	NA	Belgium, Colombia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aithaloderma setosum	*Coffea* sp.	Plant	Indonesia	USDA
				Aithaloderma setosum	*Coffea arabica*	NA	Belgium	USDA
				Aithaloderma setosum	*Coffea excelsa*	NA	Philippines	USDA
				Aithaloderma setosum	*Coffea liberica*	Plant	Brunei Darussalam, Philippines	USDA
				Aithaloderma setosum	*Coffea robusta*	Plant	Brunei Darussalam	USDA
			Ceramothyrium	*Ceramothyrium coffeanum*	*Coffea robusta*	NA	New Guinea	USDA
			Chaetothyrium	*Chaetothyrium boedijnii*	*Coffea arabica*	NA	Papua New Guinea	USDA
				Chaetothyrium javanicum- (*Phaeosaccardinula javanica*)	*Coffea arabica*	Plant	China, Taiwan	USDA
				Chaetothyrium javanicum- (*Phaeosaccardinula javanica*)	*Coffea liberica*	Plant	China, Taiwan	USDA
				Chaetothyrium javanicum- (*Phaeosaccardinula javanica*)	*Coffea robusta*	Plant	China, Taiwan	USDA
				Chaetothyrium setosum	*Coffea arabica*	NA	Colombia	USDA
			Phaeosaccardinula	*Phaeosaccardinula coffeicola*	*Coffea arabica*	Leaves	Chiang Mai Thailand.	Maharach chikumbura et al. (2018)
				Phaeosaccardinula sp.	*Coffea arabica*	NA	Eritrea	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Coccodiniaceae	*Microxiphium*	*Microxiphium coffeanum*	*Coffea arabica*	Plant	Brazil	USDA
				Microxyphium sp.*1*	*Coffea arabica*	Plant	Cuba, Sudan	USDA
				Microxyphium sp.*2*	*Coffea canephora*	NA	Papua New Guinea	USDA
			Tephrosticta	*Tephrosticta ficina*-(*Deslandesia ficina*)	*Coffea liberica*	NA	Indonesia	USDA
		Trichomeriaceae	*Trichomerium*	*Trichomerium chiangmaiensis*	*Coffea arabica*	Leaves	Chiang Mai Thailand.	Monteiro et al. (2017)
		Incertae sedis	*Bahusutrabeeja*	*Bahusutrabeeja dwaya*	*Coffea arabica*	NA	India	USDA
			Staninwardia	*Staninwardia* sp.	*Coffea arabica*	Leaves	/	USDA
		Chaetothyriaceae	*Chaetothyrium*	*Chaetothyrium javanicum*	*Coffea* sp.	NA	Indonesia	USDA
	Eurotiales	Aspergillaceae	*Aspergillus*	*Aspergillus aculeatinu*	*Coffea arabica/robusta*	Beans	Chiang Mai, Chumphon	Estupiñan-López et al. (2018)
				Aspergillus alliaceus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus amstelodami-(*Eurotium amstelodami*)	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus amstelodami-(*Eurotium amstelodami*)	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus auricomus	*Coffea arabica*	Beans	Brazil, Minas Gerais	Sousa et al. (2019)
				Aspergillus awamori	*Arabica parchment coffee /green coffee*	Beans	Chiang Mai, Thailand	Kuntawee et al., (2015)
				Aspergillus brasiliensis	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus caespitosus	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus candidus	*Arabica parchment coffee/green coffee*	Beans	Chiang Mai, Thailand	Kuntawee et al. (2015)
				Aspergillus carbonarius	*Coffea arabica*	Beans	Minas Gerais	Sousa et al. (2019)
				Aspergillus carbonarius	*Coffea robusta*	Beans	Chiang Mai, Thailand	Noonim et al. (2008)
				Aspergillus carbonarius	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus chevalieri- (*Eurotium chevalieri*)	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus clavatus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus elegans	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus flavus	*Coffea* sp.	Root	Indonesia	Sari et al. (2025)
				Aspergillus Flavus	*Coffea arabica*	Beans	Saudi Arabia, Brazil	Batista et al. (2003b) Bokhari (2007)
				Aspergillus Flavus	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus flavus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus foetidus	*Coffea arabica*	Beans	Brazil, Chiang Mai, Chumphon	Batista et al. (2003a)
				Aspergillus fumigatus	*Coffea arabica*	Beans	Brazil, India, Viet Nam	de Almeida et al. (2019)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus fumigatus	*Gorilla's Coffee*	Coffee Powder	Abuja	Djadjiti et al. (2020)
				Aspergillus fumigatus	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	Eida et al. (2009)
				Aspergillus fumigatus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus fumigatus	*Coffea* sp.	Root	Indonesia	Sari et al. (2025)
				Aspergillus glaucus	*Coffea arabica*	NA	Ethiopia	USDA
				Aspergillus granulosus	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus insulicola	*Coffea arabica*	Beans	Brazil, Minas Gerais	Batista et al. (2003), Sousa et al. (2019)
				Aspergillus japonicus	*Coffea arabica*	Beans	Minas Gerais	Sousa et al. (2019)
				Aspergillus japonicus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus lanosus	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus lanosus	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus melleus	*Coffea arabica*	Beans	Brazil, Minas Gerais, Chiang Mai, Chumphon	Pasin et al. (2009), Noonim et al. (2008), Batista et al. (2019)
				Aspergillus niger	*Coffea arabica*	Beans	Brazil, Kenya, Viet Nam, Local markets in Nayarit and Mexico, Lavras, Minas Gerais	Casas-Junco et al. (2018), de Almeida et al. (2019)
				Aspergillus niger	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas), Malaysia	da Silva et al. (2020)
				Aspergillus niger	*Coffea arabica/robusta*	Beans	Chiang Mai, Chumphon	Noonim et al. (2008)
				Aspergillus niger	*Coffea canephora*	NA	Cote d'Ivoire	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus niger	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Aspergillus niger	*Coffea liberica*	Plant	Cote d'Ivoire, Ghana	USDA
				Aspergillus niger	*Arabica/robusta/ liberica/excelsea*	Plant	Philippines	Alvindia et al. (2016)
				Aspergillus niger	*Coffea* sp.	Root	Indonesia	Sari et al. (2025)
				Aspergillus niger aggregate	*Coffea arabica*	Beans	Minas Gerais	Sousa et al. (2019)
				Aspergillus niger agregado	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus niger var. awamor	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus niger var. niger	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus ochraceus	*Arabica parchment coffee/green coffee*	Beans	Chiang Mai, Thailand	Kuntawee et al. (2015)
				Aspergillus ochraceus	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus ochraceus	*Coffea arabica*	Beans	Lavras, Minas Gerais, Brazil, Saudi Arabia	Bokhari (2007), Almeida et al. (2009)
				Aspergillus ochraceus	*Catuai variety*	Corticous Roots Tissues	Piumhi, Brazil	Estupiñan-López et al. (2018)
				Aspergillus ochraceus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus oryzae	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus oryzae	*Coffea arabica*	Leaves	Chinchiná, Caldas, Colombia	Chaves et al. (2012)
				Aspergillus ostianus	*Arabica parchment coffee/green coffee*	Beans	Chiang Mai, Thailand	Kuntawee et al. (2015)
				Aspergillus ostianus	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus ostianus	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus parasiticus	*Arabica parchment coffee/green coffee*	Beans	Chiang Mai, Thailand, Saudi Arabia	Bokhari (2007), Kuntawee et al. (2015)
				Aspergillus petrakii	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus pseudodeflectus	*Coffea arabica*	Beans	Papua New Guinea, Viet Nam	Vega et al. (2008)
				Aspergillus sclerotiicarbonarius	*Coffea robusta*	Beans	Chiang Mai, Chumphon	Noonim et al. (2008)
				Aspergillus sclerotiorum	*Arabica parchment coffee/green coffee*	Beans	Chiang Mai, Thailand, Brazil, Chiang Mai, Chumphon	Batista et al. (2003), Kuntawee et al. (2015)
				Aspergillus sclerotiorum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Aspergillus sp.	*Coffea arabica*	Beans	Saudi Arabia, Brazil	Bokhari (20007), de Almeida et al. (2019)
				Aspergillus sp. *seção Circumdati*	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus steynii	*Coffea arabica*	Beans	Chiang Mai, Chumphon	Noonim et al. (2008)
				Aspergillus sulphureus	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus sulphureus	*Coffea arabica*	Beans	Brazil, Minas Gerais	Sousa et al. (2019)
				Aspergillus sumatrense	*Coffea arabica*	Beans	Puerto Rico	Vega et al. (2008)
				Aspergillus sydowii	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Aspergillus tamarii	*Coffea arabica*	Beans	Brazil	de Almeida et al. (2019)
				Aspergillus tamarii	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Aspergillus terreus	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines, Chiang Mai, Thailand	Kuntawee et al. (2015), Alvindia and Guzman (2016)
				Aspergillus tubingensis	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Aspergillus tubingensis	*Coffea arabica/robusta*	Beans	Chiang Mai, Chumphon	Noonim et al. (2008)
				Aspergillus tubingensis	*Coffea arabica*	Beans	Colombia, Kenya	Vega et al. (2008)
				Aspergillus versicolor	*Coffea arabica*	Beansnaroasted Coffee	Local markets in Nayarit and Mexico, Brazil	Casas-Junco et al. (2018)
				Aspergillus westerdijkiae	*Arabica/robusta/ liberica/excelsea*	Beans	Thailand, Philippines	Noonim et al. (2008), de Almeida et al. (2016)
			Eurotium	*Eurotium rubrum*	*Coffea arabica*	Beans	India	Vega et al. (2008)
			Penicillium	*Penicillium aurantiogriseum*	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium brevecompactum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium brevicompactum	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Penicillium chrysogenum	*Coffea arabica*	Beans	Saudi Arabia, Brazil	Batista et al. (2003b) Bokhari (2007)
				Penicillium citrinum	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Penicillium citrinum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium citrinum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium coffeae	*Coffea arabica*	Plant	Hawaii	USDA
				Penicillium commune	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Penicillium corylophilum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium corylophylum	*Coffea arabica*	Beans	Saudi Arabia	Bokhari (2007)
				Penicillium corylophylum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Penicillium crustosum	*Coffea arabica*	Beans	Guatemala	Vega et al. (2008)
				Penicillium decumbens	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium digitatum	*Coffea arabica*	Plant	Brazil	USDA
				Penicillium digitatum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium expansum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium funiculosum	*Coffea arabica*	Beans	Lavras, Minas Gerais.	Pasin et al. (2009)
				Penicillium glabrum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)
				Penicillium implicatum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium italicum	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Penicillium jantinelum	*Coffea arabica*	Coffee Soil	Colombian andisols	González-Osorio et al. (2020)
				Penicillium montanense	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium olsonii	*Coffea arabica*	Beans	Colombia	Vega et al. (2008)
				Penicillium olsonii	*Coffea congensis*	Plant	Hawaii	Vega et al. (2008)
				Penicillium olsonii	*Coffea dewevrei*	Plant	Hawaii	Vega et al. (2008)
				Penicillium olsonii	*Coffea liberica*	Plant	Hawaii	Vega et al. (2008)
				Penicillium oxalicum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium pelutatum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium Rugulosum	*Coffea arabica*	Beans	Lavras, Minas Gerais.	Pasin et al. (2009)
				Penicillium solitum	*Coffea arabica*	Beans	Brazil	Batista et al. (2003a)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Penicillium sp.*1*	*Coffea arabica*	Beans, Coffee Soil	Brazil, Saudi Arabia, India, Colombian andisols	USDA
				Penicillium sp.*2*	*Catuai variety*	Corticous Root Tissues	Brazil, Piumhi	Estupiñan-López et al. (2018)
				Penicillium sp.*3*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Penicillium sp.*4*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Penicillium sp.*5*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Penicillium sp.*6*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Penicillium ubiquetum	*Coffea arabica*	Coffee Soil	Colombian andisols	González-Osorio et al. (2020)
				Penicillium Variable	*Coffea arabica*	Beans	Lavras, Minas Gerais.	Pasin et al. (2009)
				Penicillium verruculosum	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	Eida et al. (2009)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Penicillium verruculosum	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
				Penicillium waksmanii	*Arabica/robusta/ liberica/excelsea*	Beans	Philippines	Alvindia et al. (2016)
		Thermoascaceae	*Paecilomyces*	*Paecilomyces cf. fumosoroseus*	*Coffea arabica*	Crown	PUERTO RICO	Vega et al. (2008)
				Paecilomyces cf. javanicus	*Coffea arabica*	Peduncle	COLOMBIA, Caldas, Chinchina,	Vega et al. (2008)
				Paecilomyces sp.	*Coffea arabica*	Epicarp, Seedling, Root	MEXICO, Chiapas, Cacahoatan, Rancho El Paraı so, USA. Hawaii, Kona Experimental Station	Vega et al. (2008)
				Paecilomyces variotii- (*Byssochlamys spectabilis*)	*Coffea arabica*	Roasted Coffee	Local markets in Nayarit and Mexico	Casas-Junco et al. (2018)
		Trichocomaceae	*Talaromyces*	*Talaromyces* sp.*1*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Talaromyces sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
Exobasidiomycetes	Exobasidiales	Brachybasidiaceae	*Meira*	*Meira* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
Glomeromycetes	Diversisporales	Acaulosporaceae	*Acaulospora*	*Acaulospora flava*	*Coffea arabica*	Soil	Peru	USDA
				Acaulospora foveata	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Acaulospora mellea	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Acaulospora rugosa	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Acaulospora sp.	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
		Diversisporaceae	*Diversispora*	*Diversispora versiforms*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
	Gigasporales	Gigasporaceae	*Gigaspora*	*Gigaspora gigantea*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Gigaspora margarita	*Coffea arabica*	Plant	Brazil	USDA
				Gigaspora sp.	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
		Scutellosporaceae	*Scutellospora*	*Scutellospora* sp.*1*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Scutellospora sp.*2*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Scutellospora sp.*3*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
	Glomerales	Glomeraceae	*Funneliformis*	*Funneliformis coronatum*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Funneliformis geosporum	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
			Glomus	*Glomus dussi*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Glomus sp.*1*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Glomus sp.*2*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Glomus sp.*3*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Glomus sp.*4*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Glomus sp.*5*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Glomus sp.*6*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
			Rhizoglomus	*Rhizoglomus clarum*	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Rhizoglomus intraradices	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
				Rhizoglomus microaggregatum	*Coffea arabica*	Coffee Roots	Mexico	Lara-Capistran et al. (2021)
Lecanoromycetes	Caliciales	Physciaceae	*Physcia*	*Physcia* sp.	*Coffea arabica*	Plant	Venezuela	USDA
	Graphidales	Graphidaceae	*Graphis*	*Graphis* sp.	*Coffea arabica*	Plant	Venezuela	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
	Micropeltidales	Micropeltidaceae	*Micropeltis*	*Micropeltis applanata*	*Coffea arabica*	Leaves	El Salvador	USDA
				Micropeltis longispora-(*Scolecopeltella longispora*)	*Coffea arabica*	NA	Puerto Rico	USDA
				Micropeltis longispora-(*Scolecopeltis longispora*)	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
				Micropeltis mucosa	*Coffea arabica*	NA	Philippines	USDA
				Micropeltis mucosa	*Coffea excelsa*	NA	Philippines	USDA
				Micropeltis mucosa	*Coffea* sp.	Plant	Philippines	USDA
				Micropeltis mucosa-(*Dictyothyriella mucosa*)	*Coffea excelsa*	NA	Dominican Republic	USDA
				Micropeltis mucosa-(*Dictyothyriella mucosa*)	*Coffea* sp.	Plant	Philippines	USDA
				Micropeltis tonduzii-(*Micropeltidium tonduzii*)	*Coffea arabica*	NA	Costa Rica	Fernandes et al. (2009)
			Parapeltella	*Parapeltella coffeicola*	*Coffea arabica*	NA	Guatemala	USDA
			Scolecopeltidium	*Scolecopeltidium coffeae*	*Coffea arabica*	Plant	Brazil	Bongiorno et al. (2016)
			Scolecopeltopsis	*Scolecopeltopsis aeruginea*-(*Scolecopeltis aeruginea*)	*Coffea liberica*	NA	Indonesia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
Leotiomycetes	Helotiales	Drepanopezizaceae	*Gloeosporium*	*Gloeosporium coffeanum*	*Coffea arabica*	NA	Kenya	USDA
				Gloeosporium coffeicola	*Coffea arabica*	Plant	Taiwan	USDA
				Gloeosporium coffeicola	*Coffea* sp.	NA	Samoa	USDA
				Gloeosporium coffeicola var. ramulicola	*Coffea arabica*	NA	China	USDA
				Gloeosporium sp.	*Coffea arabica*	Plant	Mexico	USDA
				Gloeosporium sp.	*Coffea* sp.	NA	Hawaii	USDA
		Helotiales genera incertae sedis	*Dactylaria*	*Dactylaria acanthacearum*-(*Isariopsis acanthacearum*)	*Coffea liberica*	Plant	Malaysia	USDA
		Mollisiaceae	*Phialocephala*	*Phialocephala mexicana*	*Coffea arabica*	Leaves	Cote d'Ivoire	USDA
		Sclerotiniaceae	*Botrytis*	*Botrytis cinerea*	*Coffea arabica*	Seedlings, Leaves	China, Kenya, Tanzania	USDA
				Botrytis cinerea f. sp. *coffeae*	*Coffea arabica*	NA	Papua New Guinea	USDA
				Botrytis cinerea-(*Botryotinia fuckeliana*)	*Coffea arabica*	Plant	Hawaii	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Sclerotium	*Sclerotium coffeicola*	*Coffea arabica*	Leaves, Fruits	Brazil, Costa Rica, Guyana	USDA
				Sclerotium coffeicola	*Coffea dewevrei*	Leaves, Fruits	Guyana	Fernandes et al. (2009)
				Sclerotium coffeicola	*Coffea liberica*	Leaves, Fruits	Guyana, Trinidad and Tobago	USDA
				Sclerotium coffeicola	*Coffea robusta*	NA	Trinidad and Tobago	USDA
				Sclerotium coffeicola	*Coffea* sp.	Plant	Costa Rica, Suriname	Oliveira et al. (2014)
				Sclerotium sp.	*Coffea* sp.	Plant	Philippines	USDA
		Incertae sedis	*Dactylaria*	*Dactylaria haptospora*	*Coffea arabica*	NA	Australia	USDA
			Triposporium	*Triposporium* sp.	*Coffea canephora*	NA	Papua New Guinea	USDA
	Phacidiales	Phacidiaceae	*Ceuthospora*	*Ceuthospora coffeicola*	*Coffea arabica*	NA	Reunion	USDA
	Rhytismatales	Triblidiaceae	*Triblidium*	*Triblidium rufulum var. microsporum-* (*Tryblidiella rufula var. microspora*)	*Coffea canephora var. typica*	NA	Guinea	USDA
Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	*Rhodosporidiobolus*	*Rhodosporidiobolus* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Rhodotorula	*Rhodotorula aurantiaca*	*Coffea arabica*	Mature And Healthy Leaves	Brazil	USDA
				Rhodotorula aurantiaca A	*Coffea* sp.	Coffee Waste	Ethiopia (Sidama and Gedio)	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Rhodotorula hylophila	*Coffea* sp.	Coffee Waste	Ethiopia (Sidama and Gedio)	USDA
Mucoromycetes	Mucorales	Lichtheimiaceae	*Lichtheimia*	*Lichtheimia ramosa*	*Coffea arabica*	Beans	/	USDA
		Mucoraceae	*Choanephora*	*Choanephora infundibulifera f. infundibulifera*- (*Choanephora conjuncta*)	*Coffea arabica*	Plant	Japan	USDA
			Mucor	*Mucor* sp.	*Coffea arabica/robusta*	Beans	Philippines	
		Rhizopodaceae	*Rhizopus*	*Rhizopus oryzae*	*Coffea arabica*	Beans	/	USDA
				Rhizopus sp.	*Arabica/robusta*	Beans	Philippines	USDA
Myxomycetes	Physarales	Didymiaceae	*Diachea*	*Diachea leucopodia*	*Coffea arabica*	NA	India	USDA
		Physaridaeae	*Physarum*	*Physarum cinereum*	*Coffea arabica*	NA	Kenya	Fernandes et al. (2009)
				Physarum leucopus	*Coffea arabica*	NA	India	USDA
				Physarum luteolum	*Coffea arabica*	NA	India	USDA
Orbiliomycetes	Orbiliales	Arthrobotryaceae	*Trinacrium*	*Trinacrium indicum*- (*Trinacrium indica*)	*Coffea arabica*	Leaves	India	USDA
	Ostropales	Stictidaceae	*Fitzroyomyces*	*Fitzroyomyces yunnanensis*	*Coffea* sp.	Dead Wood	China	Lu et al. (2021)
			Karstenia	*Karstenia chrysophaea*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Neohormodochis	*Neohormodochis septispora*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
			Ostropomyces	*Ostropomyces pruinosella*	*Coffea arabica*	Dead Wood	China	Lu et al. (2021)
Peronosporomycetes	Peronosporales	Peronosporaceae	*Phytophthora*	*Phytophthora palmivora*	*Coffea arabica*	NA	China	USDA
				Phytophthora sp.	*Coffea arabica*	NA	Panama	USDA
		Pythiaceae	*Globisporangium*	*Globisporangium splendens*	*Coffea arabica*	NA	Zambia	USDA
				Globisporangium splendens-(*Pythium splendens*)	*Coffea arabica*	Soil	South Africa	USDA
			Pythium	*Pythium periilum*	*Coffea arabica*	Soil	South Africa	Gizaw et al. (2016)
				Pythium sp.	*Coffea arabica*	Roots	Florida, Guatemala, Mexico	Gizaw et al. (2016)
	Peronosporomycetes genera incertae sedis	Incertae sedis	*Trachysphaera*	*Trachysphaera fructigena*	*Coffea abeokutae*	NA	Cote d'Ivoire	Oliveira et al. (2014)
				Trachysphaera fructigena	*Coffea canephora*	NA	Cote d'Ivoire	Bongiorno et al. (2016)
				Trachysphaera fructigena	*Coffea liberica*	Fruits	Congo, Democratic Republic of the, Congo, Ghana	USDA
Pezizomycetes	Pezizales	Incertae sedis	*Zukalina*	*Zukalina* sp.	*Coffea stenophylla*	Plant	Ghana	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
Pichiomycetes	Pichiales	Pichiaceae	*Pichia*	*Pichia amenthionina var. menthionina*	*Coffea* sp.	Coffee Waste	Ethiopia (Sidama and Gedio)	USDA
				Pichia fermentans	*Coffea arabica var. Bourbon*	Coffee Beans	Australia	Elhalis et al. (2020)
				Pichia kudriavzevii	*Coffea arabica var. Bourbon*	Coffee Beans	Australia	Elhalis et al. (2020)
	Serinales	Debaryomycetaceae	*Candida*	*Candida albicans*	*Café Najjar*	Coffee Powder	Abuja	USDA
				Candida railenensis	*Coffea arabica var. Bourbon*	Coffee Beans	Australia	Elhalis et al. (2020)
				Candida xylopsoci	*Coffea arabica var. Bourbon*	Coffee Beans	Australia	Elhalis et al. (2020)
			Hyphopichia	*Hyphopichia burtonii A*	*Coffea* sp.	Coffee Waste	Ethiopia (Sidama and Gedio)	USDA
			Meyerozyma	*Meyerozyma* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
Pucciniomycetes	Helicobasidiales	Helicobasidiaceae	*Helicobasidium*	*Helicobasidium compactum*	*Coffea arabica*	Plant	East Indies, El Salvador, Guatemala	USDA
				Helicobasidium longisporum	*Coffea* sp.	NA	United States	USDA
	Pucciniales	Pucciniales genera incertae sedis	*Aecidium*	*Aecidium nobile*	*Coffea arabica*	NA	India	USDA
				Aecidium travancoricum	*Coffea travancorensis*	Leaves	India	USDA
		Zaghouaniaceae	*Hemileia*	*Hemileia coffeicola*	*Coffea arabica*	Leaves	Cameroon, Gabon	USDA
				Hemileia coffeicola	*Coffea* sp.	Leaves	Cameroon, India	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Hemileia vastatrix	*Coffea arabica*	Leaves	Africa, Angola, Asia, Brazil, Cambodia, Central America, China, Colombia, Congo, Cook Islands, Costa Rica, East Africa, Ethiopia, Fiji, India, Indonesia, Japan, Kenya, Madagascar, Malawi, Malay Peninsula, Mexico, New Caledonia, Nigeria, Pacific Islands, Pakistan, Panama, Papua New Guinea, Philippines, Puerto Rico Rwanda, Samoa, South Africa, South America, Southern Africa, Sri Lanka, Sudan, Taiwan, Tanzania, Thailand, Uganda Venezuela, Viet Nam, Zimbabwe	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Hemileia vastatrix	*Coffea arabica var. mokka*	Leaves	South Africa	USDA
				Hemileia vastatrix	*Coffea arabica var. myrtifolia*	Leaves	Congo	USDA
				Hemileia vastatrix	*Coffea bengalensis*	NA	India	USDA
				Hemileia vastatrix	*Coffea canephora*	Leaves	Asia, Brazil, Cambodia, Cameroon, India, Indonesia, Philippines, South America, Sri Lanka, Tanzania, Uganda, West Africa	USDA
				Hemileia vastatrix	*Coffea canephora var. robusta*	Leaves	India, Indonesia, Madagascar, Philippines, Sudan, Tanzania, Uganda	USDA
				Hemileia vastatrix	*Coffea congensis*	Leaves	India, Madagascar	USDA
				Hemileia vastatrix	*Coffea congensis var. chalotii*	Leaves	Uganda	USDA
				Hemileia vastatrix	*Coffea eugenioides*	Leaves	India, Kenya	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Hemileia vastatrix	*Coffea excelsa*	Leaves	China, Ethiopia, India, Philippines, Tanzania, Uganda	USDA
				Hemileia vastatrix	*Coffea laurina*	Leaves	Indonesia	USDA
				Hemileia vastatrix	*Coffea liberica*	Leaves	Africa, Asia, Brunei Darussalam, Cambodia, Central America, China, Fiji, India, Indonesia, Japan, Madagascar, Malay Peninsula, Malaysia, Samoa, Tanzania, Uganda, West Africa	USDA
				Hemileia vastatrix	*Coffea quillon*	Leaves	Indonesia	USDA
				Hemileia vastatrix	*Coffea robusta*	Leaves	Africa, China, India, Japan, Malay Peninsula, Malaysia, Philippines, Sudan, Taiwan, Tanzania, Thailand	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Hemileia vastatrix	*Coffea* sp.	Leaves	Africa, Asia, Australia, Brazil, China, Central America, China, Cook Islands, Costa Rica, Ethiopia, Fiji, Guinea, Malawi, Malaysia, Mauritius, New Guinea, Philippines, Samoa, South Africa, South America, Thailand, Vanuatu	USDA
				Hemileia vastatrix	*Coffea stenophylla*	Leaves	Sri Lanka	USDA
				Hemileia vastatrix	*Coffea arabica-canephora*	Leaves	Brazil, Colombia, Indonesia	USDA
				Hemileia vastatrix	*Coffea arabica-liberica*	Leaves	Uganda	USDA
Saccharomycetes	Ascoideales	Wickerhamomycetaceae	*Wickerhamomyces*	*Wickerhamomyces anomalus*	*Coffea arabica var. Bourbon*	Coffee Beans	Australia	Elhalis et al. (2020)
	Saccharomycetales	Saccharomycetaceae	*Eremothecium*	*Eremothecium coryli-* (*Nematospora coryli*)	*Coffea arabica*	Plant	Kenya, Tanzania	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Eremothecium coryli-(*Nematospora coryli*)	*Coffea* sp.	Plant	Malawi	USDA
				Eremothecium gossypii-(*Nematospora gossypii*)	*Coffea arabica*	NA	Kenya	USDA
			Saccharomyces	*Saccharomyces cerevisiae*	*Coffea* sp.	Root	Indonesia	Sari et al. (2025)
				Saccharomyces ellipsoideus	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
Sordariomycetes	Amphisphaeriales	Apiosporaceae	*Apiospora*	*Apiospora* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Arthrinium	*Arthrinium arundinis*	*Coffea arabica*	NA	Malawi	USDA
				Arthrinium phaeospermum	*Coffea arabica*	NA	Japan	USDA
				Arthrinium sp.*1*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Arthrinium sp.*2*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
			Nigrospora	*Nigrospora oryzae*	*Coffea arabica*	Plant	Japan	USDA
				Nigrospora oryzae-(*Khuskia oryzae*)	*Coffea arabica*	Mature And Healthy Leaves	Brazil	USDA
				Nigrospora sp.*1*	*Coffea arabica*	Plant	Brazil	USDA
				Nigrospora sp.*10*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sp.*11*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sp.*2*	*Coffea* sp.	Plant	Malay Peninsula	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Nigrospora sp.*3*	*Coffea* sp.	Cofee Leaf Rust Lesions	Hawai'i Island, HI, USA	Luiz et al. (2024)
				Nigrospora sp.*4*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Nigrospora sp.*5*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Nigrospora sp.*6*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sp.*7*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sp.*8*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sp.*9*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Nigrospora sphaerica	*Coffea robusta*	Plant	Brunei Darussalam	USDA
		Beltraniaceae	*Beltrania*	*Beltrania rhombica*	*Coffea arabica*	Plant	Venezuela	USDA
			Pseudosubramaniomyces	*Pseudosubramaniomyces fusisaprophyticus*-(*Subramaniomyces fusisaprophyticus*)	*Coffea* sp.	Dead, Fallen Leaves	Ethiopia	USDA
		Hyponectriaceae	*Physalospora*	*Physalospora* sp.	*Coffea robusta*	Plant	Malaysia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Sporocadaceae	*Pestalotia*	*Pestalotia coffeicola*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Pestalotia coffeicola	*Coffea arabica*	Plant	Brazil, Taiwan	USDA
				Pestalotia coffeicola	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Pestalotia elasticae	*Coffea arabica*	NA	Congo, Democratic Republic	USDA
				Pestalotia sp.*1*	*Coffea arabica*	Leaves	Puerto Rico	Santamaría et al. (2005)
				Pestalotia sp.*2*	*Coffea arabica*	Plant	Cuba, Mexico	USDA
				Pestalotia sp.*3*	*Coffea liberica*	Plant	Ghana	USDA
			Pestalotiopsis	*Pestalotiopsis albomaculans*-(*Pestalotia albomaculans*)	*Coffea liberica*	NA	Brazil	USDA
				Pestalotiopsis batatas	*Coffea robusta*	NA	China	USDA
				Pestalotiopsis coffeae	*Coffea excelsa*	NA	China	USDA
				Pestalotiopsis coffeae-(*Pestalotia coffeae*)	*Coffea arabica*	NA	Indonesia, Mexico	USDA
				Pestalotiopsis coffeae-(*Pestalotia coffeae*)	*Coffea robusta*	NA	New Caledonia	USDA
				Pestalotiopsis coffeae-arabicae	*Coffea arabica*	Leaves	China	USDA
				Pestalotiopsis disseminata	*Coffea arabica*	NA	Ghana	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Pestalotiopsis elasticae	*Coffea arabica*	NA	China	USDA
				Pestalotiopsis funerea	*Coffea arabica*	NA	Kenya	USDA
				Pestalotiopsis kenyana	*Coffea* sp.	Branches	Kenya	USDA
				Pestalotiopsis maculans	*Coffea arabica*	Plant	Brazil	USDA
				Pestalotiopsis royenae	*Coffea* sp.	Plant	Mauritius	Santamaría et al. (2005)
				Pestalotiopsis sp.*1*	*Coffea arabica*	Plant	Mexico	USDA
				Pestalotiopsis sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Pestalotiopsis versicolor	*Coffea arabica*	Plant	Venezuela	USDA
				Pestalotiopsis versicolor	*Coffea liberica*	Plant	Brunei Darussalam	USDA
			Pestalozzia	*Pestalozzia coffeae*-(*Pestalotia coffeae*)	*Coffea liberica*	Plant	Sierra Leone	USDA
			Pseudopestalotiopsis	*Pseudopestalotiopsis theae*-(*Pestalotiopsis theae*)	*Coffea robusta*	Plant	Brunei Darussalam	USDA
	Chaetosphaeriales	Chaetosphaeriaceae	*Lomaantha*	*Lomaantha brachypus*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Menisporopsis	*Menisporopsis dinemasporioides*	*Coffea* sp.	Decaying Branch	Yunnan, China and Chiang Rai, Thailand	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Sporoschisma	*Sporoschisma hemipsilum-* (*Melanochaeta hemipsila*)	*Coffea robusta*	NA	Central African Republic	USDA
		Helminthosphaeriaceae	*Hilberina*	*Hilberina hongheensis*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Coniochaetales	Coniochaetaceae	*Coniochaeta*	*Coniochaeta ligniaria*	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	Eida et al. (2009)
				Coniochaeta prunicola	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Coniochaeta velutina	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	Eida et al. (2009)
	Conlariales	Conlariaceae	*Conlarium*	*Conlarium aquaticum*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Coronophorales	Nitschkiaceae	*Fracchiaea*	*Fracchiaea heveae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Scortechiniaceae	*Neocryptosphaerella*	*Neocryptosphaerella coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Neocryptosphaerella guttulata	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Delonicicolales	Leptosilliaceae	*Leptosillia*	*Leptosillia coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Diaporthales	Cytosporaceae	*Cytospora*	*Cytospora baoshanensis*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Diaporthaceae	*Diaporthe*	*Diaporthe acutispora*	*Coffea* sp.	NA	China	USDA
				Diaporthe liquidambaris	*Coffea arabica*	Mature and Healthy Leaves	Brazil	Oliveira et al. (2014)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Diaporthe phaseoli	*Coffea arabica*	Mature and Healthy Leaves	Brazil	Oliveira et al. (2014)
				Diaporthe sp.*1*	*Coffea* sp.	Leaves	China	USDA
				Diaporthe sp.*2*	*Coffea arabica*	NA	Thailand	USDA
				Diaporthe sp.*3*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Diaporthe sp.*4*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Diaporthe sp.*5*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Diaporthe yunnanensis	*Coffea* sp.	Healthy Leaves	China	USDA
			Phomopsis	*Phomopsis arnoldiae*	*Coffea arabica*	Leaves	Mexico	Saucedo-García et al. (2014)
				Phomopsis coffeae	*Coffea arabica*	NA	India	USDA
				Phomopsis heveicola	*Coffea arabica*	Leaves	China	USDA
				Phomopsis sp.	*Coffea arabica*	Leaves	Florida, Hawaii, Mexico,Tanzania, Venezuela	USDA
				Phomopsis stipata	*Coffea arabica*	Leaves	/	Fernandes et al. (2009)
		Erythrogloeaceae	*Dendrostoma*	*Dendrostoma coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
		Gnomoniaceae	*Ophiognomonia*	*Ophiognomonia* sp.	*Coffea arabica*	Leaves	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Valsaceae	*Laestadia*	*Laestadia coffeicola*	*Coffea arabica*	Leaves	Costa Rico	USDA
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora*	*Distoseptispora crassispora*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Glomerellales	Glomerellaceae	*Colletotrichum*	*Colletotrichum acutatum*	*Coffea arabica*	Coffee Berries	Thailand Chiang Mai, Kenya, Papua New Guinea, Viet Nam	Prihastuti et al. (2009)
				Colletotrichum acutatum	*Cape Australia Coffee Estate*	Coffee Berries	Papua New Guinea	Prihastuti et al. (2009)
				Colletotrichum asianum	*Coffea arabica*	Coffee Berries	Thailand Chiang Mai	Prihastuti et al. (2009)
				Colletotrichum boninense	*Coffea arabica*	Leaves and Berries	Brazil, Viet Nam	Serrato-Diaz et al. (2020)
				Colletotrichum boninense	*Coffea canephora*	Leaves and Berries	Brazil	USDA
				Colletotrichum brassicicola	*Coffea arabica*	Leaves	Mexico	Saucedo-García et al. (2014)
				Colletotrichum brevisporum	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum capsici – (*Colletotrichum truncatum*)	*Coffea arabica*	Green Coffee Fruits	Florida, Venezuela, Viet Nam	USDA
				Colletotrichum capsici – (*Colletotrichum truncatum*)	*Coffea liberica*	Plant	Brunei Darussalam	USDA
				Colletotrichum cereale	*Coffea arabica*	Coffee Berries	Eritrea	USDA
				Colletotrichum coffeanum	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Colletotrichum coffeanum	*Coffea arabica*	Leaves, Green Coffee Fruits	Brazil, Cameroon, China, Congo, Democratic Republic, Costa Rica, Cuba, Dominican Republic, East Africa, El Salvador, Eritrea, Ethiopia, Florida, Guatemala, Honduras, Jamaica, Japan, Kenya, Malay Peninsula, Mexico, Myanmar, Nicaragua, Panama, Range of host, Tanzania	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum coffeanum	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Colletotrichum coffeanum	*Coffea liberica*	NA	China, Cote d'Ivoire	USDA
				Colletotrichum coffeanum	*Coffea robusta*	NA	China	USDA
				Colletotrichum coffeanum	*Coffea* sp.	Plant	Ghana, Malay Peninsula, Mauritius, Nigeria, Southern Africa	USDA
				Colletotrichum coffeanum-(*Guignardia coffeana*)	*Coffea arabica*	Plant	China, Taiwan	USDA
				Colletotrichum coffeophilum	*Coffea arabica*	Leaves	China, Costa Rica, Taiwan	USDA
				Colletotrichum costaricense	*Coffea arabica*	Coffee Berries	Costa Rica	USDA
				Colletotrichum costaricense	*Coffea* sp.	Coffee Berries	Costa Rica	USDA
				Colletotrichum crassipes	*Coffea arabica*	Leaves	/	Fernandes et al. (2009)
				Colletotrichum dematium	*Coffea arabica*	NA	Kenya	USDA
				Colletotrichum endophyticum	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum falcatum	*Coffea arabica*	Coffee Berries	Thailand Chiang Mai	Prihastuti et al. (2009)
				Colletotrichum fragariae – (*Colletotrichum theobromicola*)	*Coffea* sp.	NA	Angola, Brazil	USDA
				Colletotrichum fructicola	*Coffea arabica*	Leaves and Berries	China, Puerto Rico, Thailand	USDA
				Colletotrichum fructicola	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA
				Colletotrichum fructicola	*Coffea* sp.	NA	Angola	USDA
				Colletotrichum gigasporum	*Coffea arabica*	Unripe Fruit	Mexico	USDA
				Colletotrichum gigasporum	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA
				Colletotrichum gigasporum	*Coffea* sp.	NA	Viet Nam	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum gloeosporioides	*Coffea arabica*	Ripe Fruit	Brazil, China, Cuba, El Salvador, Guatemala, Indonesia, Jamaica, Kenya, Madagascar, Malawi, Mexico, Papua New Guinea, Peru, Puerto Rico, Sri Lanka, Venezuela, Viet Nam, Virgin Islands	USDA
				Colletotrichum gloeosporioides	*Coffea canephora var. robusta*	Plant	Sri Lanka	USDA
				Colletotrichum gloeosporioides	*Coffea liberica*	Plant	Indonesia	USDA
				Colletotrichum gloeosporioides	*Coffea* sp.	Berries	Brazil, South Africa, Sri Lanka	USDA
				Colletotrichum gloeosporioides	*Cape Australia Coffee Estate*	Berries	Papua New Guinea	Kenny et al. (2012)
				Colletotrichum gloeosporioides	*Coffea arabica*	Coffee Berries	Thailand Chiang Mai	Prihastuti et al. (2009)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea arabica*	Plant	Congo, Cuba, Fiji, Florida, India, Japan, Kenya, Madagascar, New Caledonia, Papua New Guinea, Range of host, Samoa, Tanzania, Uganda, Venezuela, Zimbabwe	USDA
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea bukobensis*	All–Aged Plants	Tanzania	Bongiorno et al. (2016)
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea canephora*	Plant	Fiji, Samoa	USDA
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea canephora var. robusta*	All–Aged Plants	Indonesia, Tanzania, Vanuatu	USDA
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea excelsa*	All–Aged Plants	Tanzania	USDA
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea liberica*	Plant	Brunei Darussalam	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea robusta*	Plant	Brunei Darussalam, New Caledonia, Tanzania	USDA
				Colletotrichum gloeosporioides-(*Glomerella cingulata*)	*Coffea* sp.	Plant	Fiji, Kenya, Malawi, Mauritius, Samoa, South Africa	USDA
				Colletotrichum kahawae	*Coffea arabica*	Berrirs	Angola, Burundi, Cameroon, Ethiopia, Kenya, Malawi, Rwanda, Tanzania, Thailand, Uganda, Zambia, Zimbabwe	USDA
				Colletotrichum kahawae	*Coffea* sp.	Berrirs	Kenya, Malawi	USDA
				Colletotrichum kahawae subsp. ciggaro	*Coffea* sp.	Fruit	Puerto Rico	Serrato-Diaz et al. (2020)
				Colletotrichum kahawae subsp. kahawae – (*Colletotrichum kahawae*)	*Coffea arabica*	Berrirs	Angola, Cameroon, Kenya, Malawi	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum kahawae subsp. kahawae – (*Colletotrichum kahawae*)	*Coffea* sp.	Plant	Africa, Kenya	USDA
				Colletotrichum karstii – (*Colletotrichum karsti*)	*Coffea arabica*	Leaf	Mexico	USDA
				Colletotrichum karstii – (*Colletotrichum karsti*)	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA
				Colletotrichum karstii – (*Colletotrichum karsti*)	*Coffea* sp.	Leaves	Viet Nam	USDA
				Colletotrichum ledongense	*Coffea canephora var. robusta*	Leaves and Berries	China	USDA
				Colletotrichum lupini	*Coffea arabica*	Leaves	Southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum magnisporum	*Coffea* sp.	Plant	Hawaii	USDA
				Colletotrichum musae	*Coffea arabica*	Leaves	Mexico	Saucedo-García et al. (2014)
				Colletotrichum plurivorum	*Coffea* sp.	Leaf	Viet Nam	USDA
				Colletotrichum queenslandicum	*Coffea* sp.	NA	Fiji	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum scovillei	*Coffea arabica*	Leaves	Southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum siamense	*Coffea arabica*	Leaves And Berries	Australia, China, Mexico, Puerto Rico, Thailand	USDA
				Colletotrichum siamense	*Coffea canephora*	Leaves	Australia	USDA
				Colletotrichum siamense	*Coffea canephora var. robusta*	Leaves And Berries	China	USDA
				Colletotrichum siamense	*Coffea* sp.	NA	Brazil, China, Colombia, Kenya, Malawi	USDA
				Colletotrichum siamense	*Coffea arabica*	Coffee Berries	Thailand Chiang Mai	Prihastuti et al. (2009)
				Colletotrichum sp.*1*	*Coffea arabica*	Leaves	Brazil, Puerto Rico	Santamaría et al. (2005), Bongiorno et al. (2016)
				Colletotrichum sp.*10*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum sp.*11*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*12*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*13*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*14*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*15*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*16*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*17*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*18*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*19*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*2*	*Coffea* sp.	Cofee Leaf Rust Lesions	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Colletotrichum sp.*20*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum sp.*21*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*22*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*23*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*24*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*25*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*26*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Colletotrichum sp.*3*	*Coffea arabica*	Leaves	Australia, Brazil, China, India, Mexico, Papua New Guinea, Venezuela	USDA
				Colletotrichum sp.*4*	*Coffea canephora*	Plant	Brazil	USDA
				Colletotrichum sp.*5*	*Coffea robusta*	Berries	India	USDA
				Colletotrichum sp.*6*	*Coffea* sp.	Plant	Malay Peninsula	USDA
				Colletotrichum sp.*7*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum sp.*8*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Colletotrichum sp.*9*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Colletotrichum theobromicola	*Coffea arabica*	Coffee Berries	Australia, Mexico, Puerto Rico	USDA
				Colletotrichum tropicale	*Coffea arabica*	Green Coffee Fruits	Puerto Rico	Serrato-Diaz et al. (2020)
				Colletotrichum tropicale	*Coffea canephora var. robusta*	Leaves And Berries	China	USDA
				Colletotrichum vietnamense	*Coffea* sp.	Leaf	Viet Nam	USDA
				Colletotrichum walleri	*Coffea arabica*	Leaf Tissue	Viet Nam	USDA
				Colletotrichum walleri	*Coffea* sp.	Leaf Tissue	Viet Nam	USDA
			Glomerella	*Glomerella coffeicola*	*Coffea arabica*	Leaves, Shoots	Brazil	USDA
				Glomerella phomoides	*Coffea arabica*	Plant	Fiji	USDA
				Glomerella phomoides	*Coffea canephora*	Plant	Fiji	USDA
		Plectosphaerellaceae	*Acrostalagmus*	*Acrostalagmus annulatus*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
	Hypocreales	Bionectriaceae	*Acremonium*	*Acremonium alternatum*	*Coffea arabica*	Epicarp	Colombia, Caldas, Chinchina	USDA
				Acremonium sp.	*Coffea arabica*	Green Coffee Seeds, Root	Puerto Rico, USA, Hawaii, Kona, Kona Experimental Station	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Acremonium sp.	*Coffea canephora*	NA	Papua New Guinea	USDA
			Clonostachys	*Clonostachys byssicola*	*Coffea arabica*	Stem	Bonga, Ethiopia	Kapeua-Ndacnou et al. (2023)
				Clonostachys rhizophaga	*Coffea canephora*	Leaves	Somalomo, Cameroon	Kapeua-Ndacnou et al. (2023)
				Clonostachys rosea	*Coffea arabica*	Leaves	COLOMBIA, Caldas, Chinchina	Vega et al. (2008)
				Clonostachys rosea f. catenulata-(*Gliocladium catenulatum*)	*Coffea arabica*	NA	Cuba	María del Carmen et al. (2021)
				Clonostachys rosea f. rosea	*Coffea arabica*	Stem	Bonga, Ethiopia	Kapeua-Ndacnou et al. (2023)
				Clonostachys sp. *2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Clonostachys sp.*1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Mycocitrus	*Mycocitrus zonatus*-(*Cephalosporium zonatum*)	*Coffea arabica*	Plant	Costa Rica, Puerto Rico, Virgin Islands	USDA
			Stephanonectria	*Stephanonectria chromolaenae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Stephanonectria sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Stilbella	*Stilbella* sp.	*Coffea arabica*	NA	Papua New Guinea	USDA
		Clavicipitaceae	*Aschersonia*	*Aschersonia coffeae*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Aschersonia sp.*1*	*Coffea arabica*	NA	Papua New Guinea	USDA
				Aschersonia sp.*2*	*Coffea robusta*	Plant	Malaysia	USDA
			Incertae sedis	*Clavicipitaceae* sp.	*Coffea arabica*	Green Coffee Seeds	Puerto Rico	Vega et al. (2008)
			Hypocrella	*Hypocrella scutata*	*Coffea canephora*	NA	Papua New Guinea	USDA
				Hypocrella sp.	*Coffea arabica*	NA	Papua New Guinea	USDA
		Cordycipitaceae	*Akanthomyces*	*Akanthomyces johnsonii*	*Coffea* sp.	Decaying Leaves	Ohio	Vincent et al. (1998)
				Akanthomyces sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Beauveria	*Beauveria bassiana*	*Coffea arabica*	Green Coffee Fruits	Puerto Rico	Saucedo-García et al. (2014)
				Beauveria bassiana	*Coffea arabica*	Seed, Epicarp, Peduncle, Crown	Colombia, Caldas, Chinchina	Vega et al. (2008)
				Beauveria brongniartii	*Coffea arabica*	Leaves	Mexico	Vega et al. (2008)
				Beauveria globulifera	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	Vega et al. (2008)
				Beauveria sp.*1*	*Coffea arabica*	Leaves	southern Ecuador	Vega et al. (2008)
				Beauveria sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Cordyceps	*Cordyceps cateniannulata*	*wild Coffea arabica*	Stem	Ethiopia	Pereira et al. (2024)
			Incertae sedis	*Cordycipitaceae* sp.*1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Cordycipitaceae sp.*2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Lecanicillium	*Lecanicillium lecanii*-(*Cephalosporium lecanii*)	*Coffea arabica*	NA	Puerto Rico, Venezuela, Virgin Islands	USDA
				Lecanicillium lecanii-(*Verticillium lecanii*)	*Coffea arabica*	NA	Papua New Guinea	USDA
				Lecanicillium lecanii-(*Verticillium lecanii*)	*Coffea canephora*	NA	Papua New Guinea	USDA
				Lecanicillium lecanii-(*Verticillium lecanii*)	*Coffea* sp.	NA	India	Estupiñan-López et al. (2018)
				Lecanicillium longisporum-(*Acrostalagmus aphidum*)	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
				Lecanicillium muscarium-(*Verticillium hemileiae*)	*Coffea arabica*	Plant	Brazil	USDA
			Simplicillium	*Simplicillium lanosoniveum*	*cofee leaf rust*	Coffea Sp.	Cuba	Baró Robaina et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Simplicillium sp.	*Coffea arabica*	Stem	Viçosa municipality, Minas Gerais, Brazil	Monteiro et al. (2017)
				Simplicillium sp. *1*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Simplicillium sp. *2*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Simplicillium sp. *4*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Simplicillium sp.*3*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Hypocreaceae	*Hypocrea*	*Hypocrea lixii*	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	María del Carmen et al. (2021)
				Hypocrea virens	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	María del Carmen et al. (2021)
			Trichoderma	*Trichoderma aethiopicum*	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma asperelloides	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma asperellum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma atroviride	*Coffea* sp.	Leaf	Kenya	María del Carmen et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Trichoderma bissettii	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma botryosum sp. *nov.*	*Coffea canephora*	Stem	Cameroon	María del Carmen et al. (2021)
				Trichoderma botryosum sp. *nov.*	*Coffea arabica*	Stem, Berries, Leaf	Ethiopia, Cameroon	María del Carmen et al. (2021)
				Trichoderma breve	*Coffea canephora*	Stem	Cameroon	María del Carmen et al. (2021)
				Trichoderma breve	*Coffea arabica*	Berry	Ethiopia	USDA
				Trichoderma brevicompactum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma caeruloviride sp. *nov.*	*Coffea arabica*	Stem	Ethiopia	USDA
				Trichoderma citrinoviride	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma erinaceum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma flagellatum	*Coffea arabica*	Roots	Ethiopia	María del Carmen et al. (2021)
				Trichoderma gamsii	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma guizhouense	*Coffea* sp.	Stem	Kenya	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Trichoderma hamatum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma hamatum	*Coffea arabica*	Stem, Berries	Ethiopia	USDA
				Trichoderma harzianum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma koningiopsis	*Coffea canephora*	Leaf, Stem	Cameroon	Lu et al. (2022d)
				Trichoderma koningiopsis	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma lentissimum sp. *nov*	*Coffea cf. arabica*	Stem	Kenya	Lu et al. (2022d)
				Trichoderma longibrachiatum	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma orientale	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma parareesei	*Coffea arabica*	Stem	Ethiopia	Oliveira et al. (2014)
				Trichoderma paratroviride	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma pseudopyramidale sp. *nov.*	*Coffea arabica*	Leaf, Stem	Ethiopia	Vega et al. (2008)
				Trichoderma reesei	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
				Trichoderma sp.	*Coffea arabica*	Leaves	Brazil	María del Carmen et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Trichoderma spirale	*Coffea canephora*	Stem	Cameroon	USDA
				Trichoderma theobromicola	*Coffea canephora*	Stem	Cameroon	Vega et al. (2008)
				Trichoderma virens	*Coffea brevipes*	Stem	Cameroon	USDA
				Trichoderma viride	*Coffea* sp.	Coffee Rhizospheric Soil	Ethiopia	Mulatu et al. (2022)
		Incertae sedis	*Cephalosporium*	*Cephalosporium deformans*	*Coffea arabica*	Plant	El Salvador	USDA
				Cephalosporium omnivorum	*Coffea arabica*	Plant	El Salvador	USDA
				Cephalosporium sp.	*Coffea arabica*	NA	Puerto Rico	USDA
		Myrotheciomycetaceae	*Trichothecium*	*Trichothecium roseum*	*Coffea arabica*	Plant	Florida	USDA
		Nectriaceae	*Albonectria*	*Albonectria rigidiuscula*-(*Fusarium decemcellulare*)	*Coffea canephora*	Plant	Brazil	USDA
			Calonectria	*Calonectria cylindrospora*-(*Cylindrocladium scoparium*)	*Coffea arabica*	NA	Taiwan	USDA
				Calonectria pyrochroa	*Coffea* sp.	NA	India	
				Calonectria sp.	*Coffea arabica*	NA	Uganda	Pasin et al. (2009)
			Cylindrocarpon	*Cylindrocarpon* sp.	*Coffea arabica*	NA	Venezuela	USDA
			Cylindrocladiella	*Cylindrocladiella parva*	*Coffea* sp.	NA	India	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Fusarium	*Fusarium acuminatum*	*Coffea* sp.	Coffee Residue Compost	Hiroshima prefecture	USDA
				Fusarium bostrycoides	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium camptoceras	*Coffea* sp.	Root of Wilting Coffea	Angola	USDA
				Fusarium coffeicola	*Coffea arabica*	NA	Brazil, El Salvador	USDA
				Fusarium concolor	*Coffea arabica*	Plant	Brazil	USDA
				Fusarium concolor	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium crassum	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium equiseti	*Coffea arabica*	Seed	Brazil	USDA
				Fusarium equiseti	*Coffea arabica*	Beans	Lavras /Minas Gerais	USDA
				Fusarium hengyangense	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium incarnatum- (*Fusarium semitectum*)	*Coffea arabica*	Plant	Venezuela	USDA
				Fusarium incarnatum- (*Fusarium semitectum*)	*Coffea liberica*	Plant	Malaysia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Fusarium lateritium	*Coffea arabica*	Berries, Twig, Bark	Brazil, El Salvador, Ethiopia, Malawi, New Caledonia, New Guinea, Papua New Guinea, Tanzania, Zimbabwe	Estupiñan-López et al. (2018)
				Fusarium lateritium	*Coffea canephora*	Plant	Brazil, Guinea	USDA
				Fusarium lateritium	*Coffea* sp.	Plant	Malawi	USDA
				Fusarium lateritium	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium lateritium subsp. lateritium	*Coffea arabica*	Plant	Brazil	USDA
				Fusarium lateritium var. longum – (*Fusarium stilboides*)	*Coffea arabica*	Plant	Costa Rica, Panama, Tanzania	USDA
				Fusarium meridionale	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium moniliforme	*Coffea arabica*	Plant	Brazil	Pasin et al. (2009)
				Fusarium nirenbergiae	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Cittition
				Fusarium oxysporum	*Coffea arabica*	Plant	Brazil, Costa Rica, El Salvador, Florida, Guatemala, Kenya, Mexico, Puerto Rico, Virgin Islands	USDA
				Fusarium oxysporum	*Coffea canephora*	Plant	Puerto Rico, Virgin Islands	
				Fusarium oxysporum	*Coffea canephora var. robusta*	Plant	Congo	Estupiñan-López et al. (2018)
				Fusarium oxysporum	*Coffea excelsa*	NA	Puerto Rico, Virgin Islands	USDA
				Fusarium oxysporum	*Coffea* sp.	Seed	Puerto Rico	USDA
				Fusarium oxysporum	*Catuai variety*	Corticous Roots Tissues	Piumhi, Brazil	USDA
				Fusarium oxysporum f. conglutinans	*Coffea stenophylla*	NA	Puerto Rico, Virgin Islands	USDA
				Fusarium oxysporum f. sp. *coffeae*	*Coffea arabica*	Plant	Brazil	USDA
				Fusarium pallidoroseum- (*Fusarium incarnatum*)	*Coffea arabica*	Plant	Brazil	USDA
				Fusarium pseudocircinatum	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium roseum	*Coffea arabica:*	NA	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Fusarium semitectum	*Coffea arabica*	Beans	Lavras, Minas Gerais.	USDA
				Fusarium solani	*Catuai variety*	Corticous Roots Tissues	Piumhi, Brazil	da Silva et al. (2020)
				Fusarium solani var. eumartii	*Coffea arabica*	Plant	Tanzania	USDA
				Fusarium solani-melongenae	*Coffee fruit rot*	Coffea Sp.	Puerto Rico (USA)	Serrato-Diaz et al. (2024)
				Fusarium sp.*1*	*Coffea arabica*	Plant	Brazil, Costa Rica, Cuba, Fiji, Florida, Malawi, Mexico, Panama, Papua New Guinea, Thailand, Venezuela	USDA
				Fusarium sp.*2*	*Coffea canephora*	Plant	Fiji	USDA
				Fusarium sp.*3*	*Coffea liberica*	Plant	Brunei Darussalam	USDA
				Fusarium sp.*4*	*Coffea robusta*	Plant	Brunei Darussalam, Malawi	USDA
				Fusarium sp.*5*	*Coffea* sp.	Beans, Plant	New Guinea, Zimbabwe	USDA
				Fusarium sp.*6*	*Coffea* sp.	Root	Indonesia	Sari et al. (2025)
				Fusarium sp.*7*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Fusarium sp.*8*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Fusarium sp.*9*	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
				Fusarium stilboides	*Coffea arabica*	Bark	Kenya, Malawi, Zimbabwe	USDA
				Fusarium stilboides	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	USDA
				Fusarium stilboides-(*Gibberella stilboides*)	*Coffea arabica*	NA	Papua New Guinea	USDA
				Fusarium xylarioides	*Coffea abeokutae*	NA	Cote d’Ivoire	USDA
				Fusarium xylarioides	*Coffea arabica*	Plant	Ethiopia, Uganda	USDA
				Fusarium xylarioides	*Coffea canephora*	Plant	Cote d’Ivoire, Uganda, Guinea	USDA
				Fusarium xylarioides	*Coffea liberica*	NA	Cote d’Ivoire	USDA
				Fusarium xylarioides	*Coffea robusta*	Plant	Uganda	USDA
				Fusarium xylarioides	*Coffea* sp.	Trunk	Cote d’Ivoire, Ivory Coast	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea abeokutae*	NA	Cote d’Ivoire	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea canephora*	NA	Cote d’Ivoire	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea canephora var. robusta*	Stems	Congo, Cote d’Ivoire, Guinea	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea canephora var. typica*	NA	Guinea	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea dewevrei*	Stems	Congo	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea excelsa*	Stems	Congo, Cote d'Ivoire	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Fusarium xylarioides-(*Gibberella xylarioides*)	*Coffea neoarnoldiana*	Stems	Congo	USDA
			Gibberella	*Gibberella* sp.	*Coffea arabica*	Beans, Plant	Colombia, Mexico	USDA
			Gliocladiopsis	*Gliocladiopsis tenuis*	*Coffea* sp.	NA	Viet Nam	USDA
				Gliocladiopsis tenuis-(*Cylindrocarpon tenue*)	*Coffea arabica*	NA	India	USDA
			Nectria	*Nectria bainii*	*Coffea arabica*	NA	Cuba	USDA
				Nectria cinnabarina	*Coffea* sp.	Plant	Malay Peninsula	USDA
				Nectria coffeigena	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Nectria coffeigena	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Nectria coffeigena	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Nectria dodgei	*Coffea arabica*	Plant	El Salvador	USDA
				Nectria dodgei	*Coffea arabica var. maragogipe*	Plant	Guatemala	USDA
				Nectria sp.	*Coffea arabica*	Plant	Costa Rica, El Salvador, Guatemala, Mexico	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Nectria tropica	*Coffea* sp.	NA	Colombia	USDA
			Neocosmospora	*Neocosmospora acutispora*	*Coffea arabica*	NA	Guatemala	USDA
				Neocosmospora ampla	*Coffea* sp.	NA	East Africa	USDA
				Neocosmospora brevicona-(*Hypomyces haematococcus var. breviconus*)	*Coffea abeokutae*	NA	Cote d'Ivoire	María del Carmen et al. (2021)
				Neocosmospora brevicona-(*Hypomyces haematococcus var. breviconus*)	*Coffea canephora*	NA	Cote d'Ivoire	María del Carmen et al. (2021)
				Neocosmospora brevicona-(*Hypomyces haematococcus var. breviconus*)	*Coffea liberica*	NA	Cote d'Ivoire	María del Carmen et al. (2021)
				Neocosmospora haematococca-(*Hypomyces haematococcus*)	*Coffea abeokutae*	NA	Cote d'Ivoire	María del Carmen et al. (2021)
				Neocosmospora haematococca-(*Hypomyces haematococcus*)	*Coffea canephora*	NA	Cote d'Ivoire	María del Carmen et al. (2021)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Neocosmospora haematococca-(*Hypomyces haematococcus*)	*Coffea liberica*	NA	Cote d'Ivoire	María del Carmen et al. (2021)
				Neocosmospora solani-(*Fusarium solani*)	*Coffea arabica*	Stem	Brazil, Haiti, Malaysia, Papua New Guinea, Viet Nam	USDA
				Neocosmospora solani-(*Fusarium solani*)	*Coffea canephora*	Plant	Brazil	USDA
				Neocosmospora solani-(*Fusarium solani*)	*Coffea* sp.	Seed	India, Papua New Guinea	USDA
			Ophionectria	*Ophionectria foliicola*	*Coffea liberica*	Leaves	Java	USDA
			Sarcopodium	*Sarcopodium coffeae*	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Sarcopodium flavolanatum-(*Lanatonectria flavolanata*)	*Coffea arabica*	NA	India	USDA
				Sarcopodium flavolanatum-(*Nectria flavo–lanata*)	*Coffea arabica*	NA	India	USDA
			Thelonectria	*Thelonectria veuillotiana*-(*Nectria veuillotiana*)	*Coffea arabica*	Crown	Dominican Republic	Estupiñan-López et al. (2018)
			Volutella	*Volutella* sp.	*Coffea arabica*	NA	Mexico, Nicaragua	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Ophiocordycipitaceae	*Purpureocillium*	*Purpureocillium lilacinum*	*Catuai variety*	Corticous Roots Tissues	Piumhi, Brazil	USDA
		Sarocladiaceae	*Sarocladium*	*Sarocladium bacillisporum*	*Coffea arabica*	Mature And Healthy Leaves	Brazil	USDA
		Stachybotryaceae	*Cymostachys*	*Cymostachys coffeicola*	*Coffea arabica*	NA	Cuba	USDA
			Didymostilbe	*Didymostilbe coffeae*	*Coffea arabica*	NA	Indonesia	USDA
				Didymostilbe coffeae	*Coffea* sp.	NA	Mexico Texas	USDA
			Myrothecium	*Myrothecium coffeae*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
				Myrothecium puerense	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Myrothecium sp.	*Coffea arabica*	Plant	Florida	USDA
			Paramyrothecium	*Paramyrothecium roridum*	*Coffea arabica*	Leaves	Mexico	USDA
				Paramyrothecium roridum	*Coffea* sp.	Twigs, Leaves	Colombia	USDA
				Paramyrothecium roridum	*infested coffee*	Coffea Sp.	India, Hawai	Giri et al. (2024)
				Paramyrothecium roridum-(*Myrothecium advena*)	*Coffea* sp.	Plant	Malay Peninsula	Fernandes et al. (2009)
				Paramyrothecium roridum-(*Myrothecium roridum*)	*Coffea arabica*	Stems, Leaves	Colombia, Costa Rica, Guatemala, Puerto Rico, Virgin Islands	USDA
				Paramyrothecium roridum-(*Myrothecium roridum*)	*Coffea canephora*	Leaves	Brazil	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Paramyrothecium roridum-(*Myrothecium roridum*)	*Coffea canephora var. robusta*	Stems, Leaves	Colombia	USDA
				Paramyrothecium roridum-(*Myrothecium roridum*)	*Coffea liberica*	Stems, Leaves	Colombia	USDA
			Peethambara	*Peethambara coffeae*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
			Stachybotrys	*Stachybotrys parvispora*	*Coffea liberica*	Plant	Malaysia	USDA
	Hysteriales	Hysteriaceae	*Rhytidhysteron*	*Rhytidhysteron coffeae*	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Du et al. (2023), Lu et al. (2025b)
				Rhytidhysteron rufulum-(*Tryblidiella rufula*)	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Rhytidhysteron rufulum-(*Tryblidiella rufula*)	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Rhytidhysteron rufulum-(*Tryblidiella rufula*)	*Coffea liberica*	NA	Cote d'Ivoire	USDA
	Magnaporthales	Pseudohalonectriaceae	*Pseudohalonectria*	*Pseudohalonectria lutea*	*Coffea arabica*	Leaves	/	USDA
	Meliolales	Meliolaceae	*Asteridiella*	*Asteridiella naucleae var. libericae*	*Coffea liberica*	NA	Sierra Leone	USDA
			Irenina	*Irenina coffeae*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Irenina glabra	*Coffea liberica*	Plant	Sierra Leone	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Irenina glabra	*Coffea* sp.	NA	Uganda	González-Osorio et al. (2020)
			Meliola	*Meliola coffeae*	*Coffea arabica*	NA	Ghana	USDA
				Meliola coffeae	*Coffea robusta*	Leaves	Ghana, Uganda	USDA
				Meliola psychotriae	*Coffea arabica*	NA	Ghana	USDA
				Meliola psychotriae var. coffeae	*Coffea stenophylla*	NA	Sierra Leone	USDA
				Meliola rogeri	*Coffea arabica*	NA	Ethiopia	USDA
				Meliola sp.*1*	*Coffea arabica*	Plant	Ghana	USDA
				Meliola sp.*2*	*Coffea liberica*	Plant	Ghana	USDA
	Microascales	Ceratocystidaceae	*Ceratocystis*	*Ceratocystis colombiana*	*Coffea arabica*	Wood	Colombia	USDA
				Ceratocystis colombiana	*Coffea* sp.	Wood	Colombia	USDA
				Ceratocystis fimbriata	*Coffea arabica*	Plant	Brazil, Colombia, Costa Rica, El Salvador, Guatemala, Nicaragua, Panama, Puerto Rico, Venezuela, Virgin Islands	USDA
				Ceratocystis fimbriata	*Coffea arabica*	Trunks, Branches	Bourbon Guatemala	USDA
				Ceratocystis fimbriata	*Coffea* sp.	Soil, Plant	Colombia	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Ceratocystis fimbriata-(*Ceratostomella fimbriata*)	*Coffea arabica*	Plant	China, Mexico	USDA
				Ceratocystis papillata	*Coffea arabica*	Plant	Colombia	USDA
				Ceratocystis papillata	*Coffea* sp.	Wood	Colombia	USDA
			Davidsoniella	*Davidsoniella neocaledoniae*-(*Chalara neocaledoniae*)	*Coffea robusta*	Leaf	New Caledonia	USDA
				Davidsoniella neocaledoniae-(*Thielaviopsis neocaledoniae*)	*Coffea robusta*	Wood	United States	USDA
			Thielaviopsis	*Thielaviopsis paradoxa*	*Coffea abeokutae*	NA	Cote d'Ivoire	USDA
				Thielaviopsis paradoxa	*Coffea arabica*	Plant	Brazil	USDA
				Thielaviopsis paradoxa	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Thielaviopsis paradoxa	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Thielaviopsis paradoxa-(*Ceratocystis paradoxa*)	*Coffea abeokutae*	Leaves, Stem	Cote d'Ivoire	USDA
				Thielaviopsis paradoxa-(*Ceratocystis paradoxa*)	*Coffea canephora*	Leaves, Stem	Cote d'Ivoire	USDA
				Thielaviopsis paradoxa-(*Ceratocystis paradoxa*)	*Coffea liberica*	Leaves, Stem	Cote d'Ivoire	USDA
		Microascaceae	*Microascus*	*Microascus* sp.	*Coffea arabica*	Leaves	/	USDA
	Phomatosporales	Phomatosporaceae	*Phomatospora*	*Phomatospora uniseriata*	*Coffea* sp.	Dead And Decaying Twigs	Yunnan, China	Hyde et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
	Pleurotheciales	Pleurotheciaceae	*Pleurotheciella*	*Pleurotheciella coffeae*	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
	Pseudodactylariales	Pseudodactylariaceae	*Pseudodactylaria*	*Pseudodactylaria coffeae*	*Coffea* sp.	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
	Savoryellales	Savoryellaceae	*Ascotaiwania*	*Ascotaiwania coffeae*	*Coffea arabica*	Dead And Decaying Twigs	Yunnan, China	Liu et al. (2024a)
	Sordariales	Chaetomiaceae	*Chaetomium*	*Chaetomium globosum*	*Coffea* sp.	Beans	Minas Gerais, Brazil (Cerrado and Sul de Minas)	da Silva et al. (2020)
				Chaetomium sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
		Lasiosphaeriaceae	*Incertae sedis*	*Lasiosphaeriaceae* sp.	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
		Podosporaceae	*Cladorrhinum*	*Cladorrhinum* sp.*1*	*Coffea arabica*	Leaves	China	Fernandes et al. (2009)
				Cladorrhinum sp.*2*	*Coffea arabica*	Leaves	China	de Almeida et al. (2019)
				Cladorrhinum sp.*3*	*Coffea arabica*	Leaves	China	Culliao and Barcelo (2015)
		Schizotheciaceae	*Triangularia*	*Triangularia aquilariae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Sporidesmiales	Sporidesmiaceae	*Sporidesmium*	*Sporidesmium coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Sporidesmium coffeicola	*Coffea* sp.	NA	New Guinea	USDA
				Sporidesmium hydei	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Sporidesmium pyriformatum	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Sporidesmium shoreicola	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Sporidesmium tropicale	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Sporidesmium yunnanense	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
	Thyridiales	Trichosphaeriaceae	*Musicillium*	*Musicillium* sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
	Togniniales	Togniniaceae	*Phaeoacremonium*	*Phaeoacremonium* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
	Tremellales	Bulleribasidiaceae	*Vishniacozyma*	*Vishniacozyma* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Cryptococcaceae	*Cryptococcus*	*Cryptococcus depauperatus*	*cofee leaf rust*	Coffea Arabica	Africa	Guterres et al. (2021)
				Cryptococcus sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
		Rhynchogastremaceae	*Papiliotrema*	*Papiliotrema* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
	Tubeufiales	Tubeufiaceae	*Helicoma*	*Helicoma olivaceum*	*Coffea arabica*	NA	Mexico	USDA
			Tubeufia	*Tubeufia baoshanensis*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Tubeufia chiangraiensis	*Coffea arabica*	Decaying Branch	Chiang Rai, Thailand	Lu et al. (2025b)
				Tubeufia coffeae	*Coffea arabica*	Decaying Branch	Yunnan, China and Chiang Rai, Thailand	Lu et al. (2025b)
	Xylariales	Cainiaceae	*Endocalyx*	*Endocalyx melanoxanthus*	*Coffea arabica*	Plant	Venezuela	USDA
		Coniocessiaceae	*Pseudoconiocessia*	*Pseudoconiocessia xishuangbannaensis*	*Coffea liberica*	Dead And Decaying Twigs	Yunnan, China	Lu et al. (2024)
		Diatrypaceae	*Allocryptovalsa*	*Allocryptovalsa truncata*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Allocryptovalsa xishuangbanica	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Anthostoma	*Anthostoma* sp.	*Coffea robusta*	Plant	Brunei Darussalam	USDA
			Eutypella	*Eutypella coffeicola*	*Coffea canephora*	NA	Cote d'Ivoire	USDA
				Eutypella coffeicola	*Coffea liberica*	NA	Cote d'Ivoire	USDA
			Libertella	*Libertella* sp.	*Coffea arabica*	Leaves	/	Fernandes et al. (2009)
			Peroneutypa	*Peroneutypa coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Peroneutypa multistromata	*Coffea canephora*	NA	Cote d'Ivoire	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
		Graphostromataceae	*Biscogniauxia*	*Biscogniauxia* sp.	*Coffea arabica*	NA	Hawaii	USDA
				Biscogniauxia sp.	*Coffea arabica*	Leaves	China	USDA
		Hypoxylaceae	*Annulohypoxylon*	*Annulohypoxylon cf. stygium*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Annulohypoxylon sp.*1*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Annulohypoxylon sp.*2*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Annulohypoxylon stygium-(*Hypoxylon stygium*)	*Coffea arabica*	NA	Puerto Rico, Virgin Islands	USDA
			Daldinia	*Daldinia* sp.*1*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*10*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*2*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*3*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*4*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*5*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*6*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Daldinia sp.*7*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*8*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Daldinia sp.*9*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
			Hypomontagnella	*Hypomontagnella coffeae*	*Coffea arabica*	Decaying Branch	Yunnan, China	Lu et al. (2025b)
			Hypoxylon	*Hypoxylon* sp. *1*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Hypoxylon sp. *2*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Hypoxylon sp. *3*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
		Lopadostomataceae	*Lopadostoma*	*Lopadostoma* sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
		Microdochiaceae	*Microdochium*	*Microdochium* sp.	*cofee leaf rust lesions*	Coffea Sp.	Hawai‘i Island, HI, USA	Luiz et al. (2024)
			Micropeltella	*Micropeltella mulleri*	*Coffea arabica*	Leaves	Brazil	Fernandes et al. (2009)
		Vamsapriyaceae	*Podosporium*	*Podosporium* sp.*1*	*Coffea* sp.	Plant	Ghana	USDA
				Podoxyphium sp.*2*	*Coffea arabica*	Plant	Myanmar,	USDA
		Xylariaceae	*Dematophora*	*Dematophora necatrix*	*Coffea arabica*	Plant	Brazil	USDA
			Kretzschmaria	*Kretzschmaria* sp.	*Coffea arabica*	Leaves	China	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Muscodor	*Muscodor coffeanum*	*Coffea arabica*	Leaf	Brazil, Minas Gerais, Viçosa municipality	USDA
				Muscodor puerensis	*Coffea* sp.	Decaying Branch	Yunnan, China	Lu et al. (2025b)
				Muscodor vitigenus	*Coffea arabica*	Stem	Brazil, Minas Gerais, Viçosa municipality	USDA
				Muscodor yucatanensis	*Coffea arabica*	Leaf	Brazil, Minas Gerais, Viçosa municipality	USDA
			Nemania	*Nemania* sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
			Nodulisporium	*Nodulisporium gregarium*	*Coffea arabica*	Mature and Healthy Leaves	Brazil	USDA
			Nodulisporium	*Nodulisporium* sp.	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
			Rosellinia	*Rosellinia aquila*	*Coffea arabica*	Roots	Guatemala	USDA
				Rosellinia arcuata	*Coffea excelsa*	NA	Central African Republic	USDA
				Rosellinia arcuata	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia asperata	*Coffea excelsa*	NA	Central African Republic	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Rosellinia asperata	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia boukokoae	*Coffea excelsa*	NA	Central African Republic	USDA
				Rosellinia boukokoae	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia bunodes	*Coffea arabica*	Roots	Brazil, Colombia, Indonesia, Jamaica, Mexico, Peru, Puerto Rico, Virgin Islands	USDA
				Rosellinia bunodes	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia bunodes	*Coffea* sp.	Plant	Colombia, Malay Peninsula, Trinidad and Tobago	USDA
				Rosellinia coffeae	*Coffea excelsa*	NA	Central African Republic	USDA
				Rosellinia coffeae	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia emergens	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia lobayensis	*Coffea excelsa*	NA	Central African Republic	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Rosellinia megalospora	*Coffea excelsa*	NA	Central African Republic	Santamaría et al. (2005), Fernandes et al. (2009)
				Rosellinia megalospora	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia necatrix	*Coffea arabica*	NA	China, Eritrea	USDA
				Rosellinia pepo	*Coffea arabica*	Roots	Brazil, Jamaica	USDA
				Rosellinia pepo	*Coffea* sp.	NA	Papua New Guinea	USDA
				Rosellinia saccasii	*Coffea robusta*	NA	Central African Republic	USDA
				Rosellinia sp.	*Coffea arabica*	Dead Hardwood	Brazil, Dominican Republic, Haiti, Mexico	USDA
			Stilbohypoxylon	*Stilbohypoxylon coffeicola*	*Coffea arabica*	NA	Guadeloupe	USDA
				Stilbohypoxylon quisquiliarum	*Coffea robusta*	NA	Central Africa	USDA
			Ustulina	*Ustulina deusta*	*Coffea arabica*	Plant	Fiji	USDA
				Ustulina deusta- (*Hypoxylon deustum*)	*Coffea arabica*	NA	Fiji	USDA
				Ustulina deusta- (*Hypoxylon deustum*)	*Coffea* sp.	NA	Fiji	USDA

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
			Xylaria	*Xylaria rhizocola*	*Coffea arabica*	NA	Colombia	USDA
				Xylaria sp. *10*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *11*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *12*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *13*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *14*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *15*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *16*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *17*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *18*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *19*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Xylaria sp. *2*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *20*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *21*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *22*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *23*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *24*	*Coffea arabica*	Leaves	China	Lu et al. (2022d)
				Xylaria sp. *3*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *4*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *5*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *6*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)

Table 5.1 (continued)

Class	Orders	Family	Genus	Species	Host	Isolation Part	Location	Citition
				Xylaria sp. *7*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *8*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp. *9*	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
				Xylaria sp.*1*	*Coffea arabica*	Leaves	Puerto Rico	USDA
		Xylariales genera incertae sedis	*Anthostomella*	*Anthostomella coffeae*	*Coffea liberica*	NA	Cote d'Ivoire	USDA
				Anthostomella sp.	*Coffea arabica*	Leaves	southern Ecuador	Poma-Angamarca et al. (2024)
Ustilaginomycetes	Ustilaginales	Ustilaginaceae	*Pseudozyma*	*Pseudozyma* sp.	*Coffea arabica*	Green Coffee Seeds	Puerto Rico	USDA

Note "NA" indicate the isolation part is unavailable, "USDA" = https://fungi.ars.usda.gov

CHAPTER 6

CONCLUSIONS

6.1 Overall Conclusion

This study focused on exploring the species diversity of saprobic fungi associated with coffee, using a combined approach of phylogenetic analyses and morphological examination. It also evaluated the biocontrol potential of coffee-associated endophytes and introduced a new pathogen that causes coffee sooty mold disease. Based on ITS sequence data, 360 saprobic fungal strains collected from Thailand and China were initially identified and diversity analyzed, representing seven classes, 37 orders, 83 families, and 137 genera. Detailed morphological descriptions, illustrations, and phylogenetic trees were provided for 138 strains, including six new genera, 76 new species, and 47 new records. In addition, 235 coffee-associated endophytic fungi were isolated, among which 61 strains were screened for disease resistance against four different pathogens, and potential biocontrol strains were identified. This study also presents a comprehensive global inventory of confirmed coffee-associated fungi.

6.1.1 Diversity of Coffee-associated Saprobic Fungi

A total of 360 saprobic fungal strains were collected from seven sites (Baoshan, Dali, Dehong, Jinghong, Lincang, Nujiang, and Pu’er) in China and one site (Chiang Rai) in Thailand (Figure 6.1). The high diversity of coffee-associated fungi in Pu’er and Baoshan, China, reflects the ecological richness of these regions. With its subtropical plateau climate characterized by abundant rainfall and moderate temperatures, Pu’er is ideal for cultivating predominantly Arabica coffee. The elevated Shannon Diversity Index (H') and Simpson Diversity Index (D) values indicate a wide variety of fungal species. At the same time, the lower Evenness Index (J) suggests an uneven species distribution, highlighting the dominance of particular taxa. In contrast, Baoshan's diverse microclimate ranges from subtropical to temperate, supporting robust coffee cultivation and contributing to its ecological diversity. High values for the Shannon,

Simpson, and Evenness indices indicate rich species diversity and a balanced distribution of taxa. Conversely, Nujiang has the lowest Shannon (H') and Simpson (D) indices among the eight sampling sites, indicating lower species richness. However, its Evenness Index (J) ranks third, suggesting a relatively even distribution of species and a stable ecosystem. Despite sampling coffee from only one site in Thailand, the diversity indices suggest a moderate level of fungal diversity, indicating a balanced ecosystem. These findings highlight the importance of Yunnan, China, and Thailand as key reservoirs of fungal diversity, particularly in biodiversity hotspots along the Greater Mekong River. Our study, with its rich insights into the fungal communities associated with coffee ecosystems and their adaptive capacity, offers valuable information about the diversity and ecological dynamics of saprobes in these regions. For example, the ability of these fungal communities to produce enzymes that break down organic matter, such as cellulose and lignin (Bucher et al., 2005), demonstrates their ecological resilience. This presents important opportunities for further research into the complex interactions between fungi and coffee ecosystems, informing sustainable coffee cultivation practices.

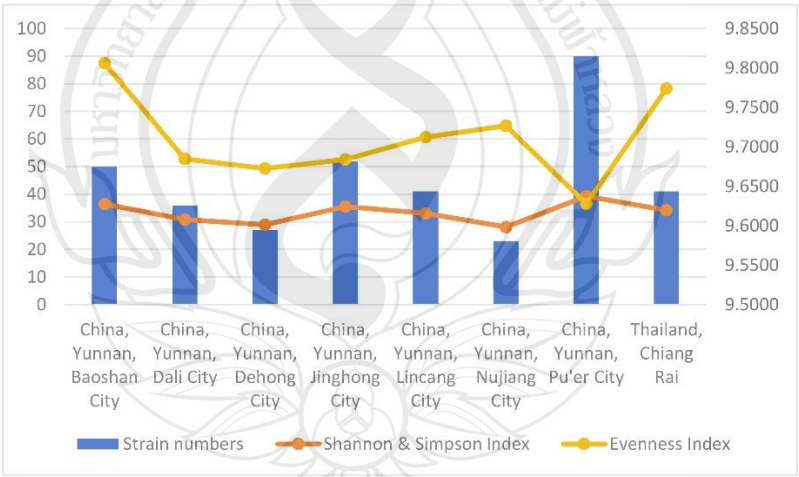


Figure 6.1 Diversity index analysis of 360 strains from 8 collection sites

Figure 6.1 To enhance visualization, the values of the Shannon Diversity Index (H'), Simpson Diversity Index (D), and Evenness Index (J) were multiplied by 10 and plotted as line graphs.

6.1.2 Taxonomy and Phylogeny of Coffee-associated Saprobic Fungi

In our research, Pleosporales emerged as the dominant fungal order, a finding that highlights its widespread occurrence as seen in Pem et al. (2024). As the largest order within the Dothideomycetes, it encompasses a wide range of fungal taxa, contributing to its ecological prominence (Wijayawardene et al., 2022; Hyde et al., 2024a; Pem et al., 2024). What's truly impressive is the adaptability of Pleosporales members to diverse environmental conditions, as they thrive in both terrestrial and aquatic habitats, including the microhabitats found in coffee plantations. This ability to flourish in various substrates likely facilitates their widespread occurrence in these ecosystems (Zhang et al., 2012; Lu et al., 2022a; Calabon et al., 2023). Lastly, many fungi within this order are saprobes, feeding on decomposing organic matter. The abundant organic material in coffee ecosystems, such as decaying leaves and rotting coffee cherries, provides a favorable environment for their growth (Zhang et al., 2012; Hoseini et al., 2021).

Our results, which are consistent with those for *Chromolaena odorata* (Siam weed), *Hevea brasiliensis* (Para rubber), and *Tectona grandis* (teak), with Dothideomycetes and Sordariomycetes as the dominant classes (Doilom et al., 2017; Mapook et al., 2020a; Senwanna et al., 2021; Figure 6.2), reveal both overlap and divergence in fungal assemblages. Most fungal species in coffee ecosystems reproduce sexually, with only a few exhibiting asexual morphs (Hyphomycetous/Coelomycetous). This trend may indicate that the coffee ecosystem environment preferentially favors sexual reproduction, potentially enhancing genetic diversity in fungal populations.

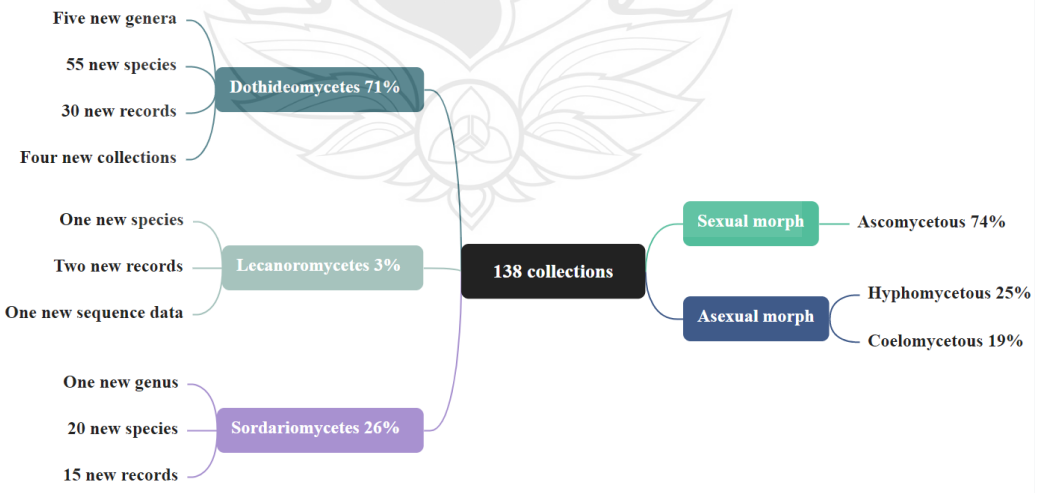


Figure 6.2 One hundred thirty-eight saprobic collections, morphology, and taxonomy distribution

6.1.3 Biocontrol Ability of Coffee-associated Endophytic Fungi

Endophytic fungi isolated from *Coffea* have shown promise as sources of bioactive compounds (Monteiro et al., 2017). Fulthorpe et al. (2020) reported the isolation of coffee root endophytes that have potential ecological roles with *Coffea arabica* based on next-generation sequencing, and *Burkholderia*, *Enterobacter*, and *Pantoea* were reported as the dominant bacterial genera, while *Cladosporium*, *Exidiopsis*, *Mycena*, *Penicillium*, and *Trechispora* were reported as the dominant fungal genera (Fulthorpe et al., 2020). Sette et al. (2006) employed a minimal inhibitory concentration (MIC) test to investigate the endophytic filamentous fungi against various human pathogenic bacteria isolated from coffee plants (*Coffea arabica* and *C. robusta*) in Pedreira, Mococa, and Pindorama counties, Brazil. The study revealed that 17 endophytic fungi were capable of inhibiting at least one of the bacterial pathogens. At the same time, *Guignardia* sp. (CBMAI 69), *Phomopsis* sp. (CBMAI 164), and *Trichoderma harzianum* (CBMAI 43) were able to inhibit four to five bacterial species. Furthermore, the study showed that *Aspergillus versicolor* (CBMAI 46), *Cladosporium* sp. (CBMAI 64 and CBMAI 66), *Fusarium oxysporum* (CBMAI 53), and *Glomerella* sp. (CBMAI 63) can inhibit all pathogenic bacteria (Sette et al., 2006). Previous studies have shown that coffee-endophytic fungi are diverse, and different groups of fungi are capable of inhibiting various fungal and bacterial pathogens (Sette et al., 2006). When comparing our study's results with those of Sette et al. (2006), we found that the endophytic fungi isolated in our study, including *Arthrinium* sp., *Biscogniauxia* sp., *Daldinia* sp., *Diaporthe* sp., and *Nigrospora* sp., can also inhibit the growth of pathogens. Still, they are not the same fungal genera that were reported in previous studies.

6.1.4 A New Sooty Mold Disease in Coffee

Sooty mold in coffee trees is indeed a common problem, often caused by fungal species that produce dark mycelial mats on leaf surfaces, affecting photosynthesis and overall plant health. Despite its prevalence, new fungal species associated with this mold are still being discovered, including the authors' recently identified species. Moving forward, it's crucial to distinguish between known, common sooty mold species and newly identified ones. This differentiation is vital for farmers to implement effective protective strategies against these fungal pathogens, ensuring the sustainability

and health of coffee plants. This study describes and characterizes *Trichomerium puerense* as a novel sooty mold pathogen affecting coffee plants, based on comprehensive morphological and multi-gene phylogenetic analyses. Pathogenicity assays confirmed its causal role in sooty mold disease, marking the first documented occurrence of this pathogen on coffee in China. This finding extends the known host range and geographic distribution of *Trichomerium* species, while also highlighting the potential for other underexplored fungal pathogens in coffee ecosystems.

The emergence of *T. puerense* poses potential threats to coffee plant health, berry development, and commercial yield, which may directly impact market value. Further research is urgently needed to elucidate the biology, epidemiology, and ecological drivers of this pathogen, as well as to develop targeted management strategies. Additionally, surveillance for similar sooty mold species in coffee-growing regions should be prioritized to mitigate future disease risks.

6.2 Research Advantages

6.2.1 This study makes a substantial contribution to the understanding of fungal biodiversity in southern China and northern Thailand, two regions recognized as important biodiversity hotspots, yet remain relatively underexplored in terms of fungal taxonomy. Through the discovery of six new genera, 76 new species, and 47 new records, our research significantly expands the known fungal diversity in these areas. These findings not only enhance regional species inventories but also offer valuable insights into fungal systematics, biogeography, and host associations, particularly with *Coffea* sp. The high number of novel taxa reported highlights the untapped mycological richness of these regions and emphasizes the need for continued exploration. Furthermore, documenting such diversity contributes to global efforts in biodiversity assessment and is crucial for developing informed conservation strategies in the face of ongoing environmental change.

6.2.2 The well-preserved axenic cultures obtained in this study, particularly the endophytic fungi isolated from coffee plants, represent a valuable resource for future research. Our results confirm that several coffee-associated endophytes possess

antagonistic activity against plant pathogens, highlighting their potential role as biological control agents. These collections not only contribute to the understanding of fungal biodiversity but also provide a solid foundation for applied studies aimed at developing sustainable disease management strategies. Moreover, they open promising avenues for the exploration of bioactive metabolites, with potential applications in agriculture, pharmacology, and beyond. Thus, this study bridges fundamental biodiversity research with practical implications for biocontrol and the discovery of natural products.

6.2.3 Yunnan is the core coffee-producing region in China, accounting for 98% of the nation's total coffee output. However, studies on the fungal communities associated with coffee in this region remain unreported. This study presents the first systematic investigation of the diversity of saprobic and endophytic fungi in coffee plants across Yunnan Province, and successfully identified multiple antagonistic strains with significant biocontrol potential against major coffee pathogens. The findings not only fill a critical knowledge gap in China's coffee-associated fungal resources but also substantially expand the diversity database of coffee-associated symbiotic fungi. More importantly, this work provides valuable candidate microbial resources for developing eco-friendly biocontrol agents, offering both scientific and practical significance for reducing chemical pesticide dependence and promoting sustainable green practices in the coffee industry.

6.3 Future Work

6.3.1 Biodiversity Exploration

Future studies should systematically expand fungal diversity surveys to major coffee-producing regions in Southeast Asia, particularly in biodiversity hotspots such as Laos and Myanmar. By comparing the composition and functional characteristics of coffee-associated fungal communities across geographical gradients, the study aims to address the following key scientific questions: (1) What are the biogeographical distribution patterns of coffee symbiotic fungi, and what environmental or ecological factors drive these patterns? (2) How do host specificity and ecological niche

differentiation influence the diversity and evolution of fungal taxa? (3) How do different locations affect the lifestyles and function of fungal communities associated with coffee?

6.3.2 Functional Characterization of Antagonistic Strains

Future work should focus on validating the biocontrol potential of the identified antagonistic strains through in planta assays. Greenhouse and field trials are necessary to evaluate their effectiveness against major coffee pathogens, including *Hemileia vastatrix* and *Colletotrichum kahawae*. Additionally, mechanistic studies should investigate whether the antagonistic effects are mediated by antibiosis, niche competition, mycoparasitism, or induction of systemic resistance in the host. Clarifying these mechanisms will enhance strain selection for biocontrol purposes and guide the formulation of effective and sustainable biological products.

6.3.3 Metabolite Discovery and Characterization

The bioactive metabolites underlying fungal antagonism remain largely unexplored. Future studies should employ high-resolution metabolomics (e.g., LC-MS, GC-MS) coupled with bioassay-guided fractionation to isolate and identify compounds that stimulate antimicrobial activity or plant defense. These metabolites could serve as lead molecules for the development of next-generation biofungicides. Moreover, considering the historical significance of endophytic fungi in drug discovery (such as taxol production by *Taxomyces andreanae*), promising compounds produced by coffee fungi may also have potential for pharmaceutical development.

6.3.4 Fungal Community Differences Between Organic and Conventional Coffee Cultivation

Sternhagen et al. (2020) reported significant differences in fungal community composition between organically and conventionally managed coffee fields, primarily driven by variations in environmental conditions and agricultural practices. Organic management not only supports a higher overall fungal diversity but also promotes greater richness of saprotrophic, plant-pathogenic, and mycoparasitic fungi. These groups play critical roles in nutrient cycling and the regulation of plant pathogen populations within agricultural systems. Moreover, factors such as shade management, along with the application of fungicides and synthetic fertilizers, influence not only the

composition and richness of rhizosphere fungal communities but also alter the trophic structure of the coffee agroecosystem.

To better understand the mechanisms underlying these patterns, future studies should experimentally manipulate shade levels, synthetic fungicide applications, and fertilizer use within individual coffee farms. This would allow for the disentanglement of their individual and combined effects on fungal diversity and community composition. Given that shifts in fungal community structure and trophic dynamics directly impact coffee plant health and productivity, such knowledge is essential for optimizing sustainable cultivation practices and enhancing ecosystem services in coffee agroecosystems.

6.3.5 Challenges in Species-Level Identification

In our study, most species were identified only by ITS; however, ITS alone often provides resolution only at the genus level and is insufficient for accurate species-level identification, particularly in genera with species complexes such as *Colletotrichum*, *Diaporthe*, and *Fusarium*. These genera contain closely related species that cannot be distinguished solely using ITS sequences. Therefore, future studies should incorporate multilocus phylogenetic analyses, using additional gene regions such as LSU, SSU, *ACT*, *RPB2*, *TUB2*, and *TEF* to clarify species boundaries and ensure reliable identification. A more comprehensive molecular approach is essential for advancing fungal taxonomy and understanding the true diversity of fungi associated with coffee.

6.4 Publications

List of publications

6.4.1 First Author

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APPENDIX A

MEDIA AND CHEMICAL REAGENTS

1. Malt Extract Agar (MEA) used for fungal cultivation

Agar 15 g

Peptone 0.78 g

Glycerol 2.35 g

Dextrin 2.75 g

Maltose, Technical 12.75 g

Suspend 33.6 g of malt extract agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the power and bring volume to 1000 ml. Autoclave at 121ºC for 20 minutes.

2. Potato dextrose agar (PDA) used for fungal cultivation

Potato starch (from the infusion) 4 g

Dextrose 20 g

Agar 15 g

Suspend 39 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121ºC for 20 minutes.

3. Water Agar (WA) used for Fungal Isolation

Agar 15 g

Suspend 15 g of agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121°C for 20 minutes.

4. Melzer's Reagent used for identification of ascomycete fungi. Amyloid reaction of asci changed to blue or heavily purple colors.

5. Indian ink used for observing gelatinous appendages of ascospores in some species.

APPENDIX B

ABSTRACT OF PUBLICATIONS

pathogens

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Review

Comprehensive Review of Fungi on Coffee

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Abstract: Coffee is grown in more than 80 countries as a cash crop and consumed worldwide as a beverage and food additive. It is susceptible to fungal infection during growth, processing and storage. Fungal infections, in particular, can seriously affect the quality of coffee and threaten human health. The data for this comprehensive review were collected from the United States Department of Agriculture, Agricultural Research Service (USDA ARS) website and published papers. This review lists the fungal species reported on coffee based on taxonomy, life mode, host, affected plant part and region. Five major fungal diseases and mycotoxin-producing species (post-harvest diseases of coffee) are also discussed. Furthermore, we address why coffee yield and quality are affected by fungi and propose methods to control fungal infections to increase coffee yield and improve quality. Endophytic fungi and their potential as biological control agents of coffee disease are also discussed.

Keywords: endophytes; fungal diseases; fungal toxins; pathogens; postharvest diseases

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1. Introduction

Coffee has gained in popularity in modern times and is the second-best-selling beverage in the world [1]. As an important economic crop, it is central to the livelihoods of millions of people worldwide [2]; accordingly, more than 80 countries grow coffee and some countries use coffee as a major cash crop [3]. World coffee production for 2020/21 is forecast to be 5.5 million kg higher than the previous year, reaching a record 176.1 million kg [4]. Brazil is the largest exporter of coffee, and its exports account for one-third of the global total [5]. The Agricultural Trade Office in Sao Paulo (ATO) forecasts the Brazilian coffee production for 2020/21 at a record of 67.9 million kg, an increase of 15% over 2019 output. Finland is the largest per capita consumer of coffee, while China consumes the most coffee by volume [6]. *Coffea arabica* and *C. canephora* (robusta) are the two most-grown coffee species in the world [7], accounting for 60% and 40% of global production, respectively [8].

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Taxonomic and phylogenic appraisal of a novel species and a new record of Stictidaceae from coffee in Yunnan Province, China

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Abstract

Coffee, an important economic crop, is often threatened by fungal infections. During a survey of coffee fungi in Yunnan Province, China, two saprobic Stictidaceae species were collected. Maximum likelihood (ML) and Bayesian posterior probability of combined LSU, ITS and mtSSU genes supported the placement of our fungal collections within *Fitzroyomyces* and *Ostropomyces* with high statistical support. A new species, *Fitzroyomyces yunnanensis sp. nov.* and a new record, *Ostropomyces pruinosellus* are introduced. These two species were recorded on coffee wood in sexual and asexual states, respectively. Their taxonomic placements were further supported by detailed morphological and phylogenetic comparisons of allied taxa.

Keywords: 1 new species, China, coffee, new record, phylogeny, taxonomy

Introduction

Coffee is the second most consumed beverage in the world after tea, and is an important global crop (Murthy & Naidu 2012). Coffee is grown in over 80 countries, serving as the main source of income for farmers in many of them (Los Santos-Briones & Hernández-Sotomayor 2006). The top three coffee-producing countries are Brazil, Colombia and Vietnam (Lemma & Megersa. 2021). China is also one of the largest coffee producing countries, and its production is rapidly increasing (Zhang *et al.* 2014) with Yunnan Province accounting for more than 90% of coffee production in China (Neilson & Wang 2019). Fungal infections have significant impacts on the production of coffee (Adhikari *et al.* 2020). Endophytic and saprobic fungi in coffee have also attracted attention as they can improve the quality of coffee while also acting as biocontrol agents to prevent and treat coffee diseases (Angélico *et al.* 2017, Botrel *et al.* 2018). Approximately 136 endophytes, 30 saprobes and 297 pathogens have been reported from coffee (Lu *et al.* 2021).

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Endophytic Fungi Associated with Coffee Leaves in China Exhibited In Vitro Antagonism against Fungal and Bacterial Pathogens

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Abstract: Coffee endophytes have been studied for almost 74 years, and several studies have demonstrated coffee-endophytic fungi with antibacterial and antifungal potential for human and plant pathogens. In this study, we isolated and identified a total of 235 strains of endophytic fungi from coffee leaf tissues collected in four coffee plantations in Pu'er city, Yunnan province, China. Molecular identification was carried out using maximum likelihood phylogenetic analysis of nuclear ribosomal internal transcribed spacer (ITS1-5.8S rDNA-ITS2) sequences, while the colonization rate and the isolation frequency were also calculated. Two pathogenic fungi (*Alternaria alternata* and *Penicillium digitatum*) and two pathogenic bacteria (*Pseudomonas syringae* and *Salmonella enterica* subsp. *enterica*) were used for screening the antagonistic activities of 61 strains of coffee-endophytic fungi by a dual-culture test assay while maximum likelihood phylogenetic analysis confirmed their natural classification. This is the first study of coffee-leaf-endophytic fungal diversity in China, and the results revealed that coffee-endophytic fungi from this study belong to the Ascomycota, distributed among two classes, 10 orders, and 17 families. Concurrently, endophytic fungi isolates distributed in *Arthrinium*, *Biscogniauxia*, *Daldinia*, *Diaporthe*, and *Nigrospora* showed strong antagonistic activities against the pathogens. For the pathogens *Alternaria alternata* and *Pseudomonas syringae*, *Nigrospora* XCE-7 showed the best inhibitory effects with inhibition rates of 71.76% and 61.11%, respectively. For the pathogen *Penicillium digitatum*, *Daldinia* ME-9 showed the best inhibitory effect with a 74.67% inhibition rate, while *Biscogniauxia* PTE-7 and *Daldinia* T5E-1-3 showed the best inhibitory effect with a rate of 60.42% against the pathogen *Salmonella enterica* subsp. *enterica*. Overall, our study shows the diversity of coffee endophytes in four coffee-growing areas in Pu'er city, Yunnan province, China, and their potential use as biological control agents against two fungal and two bacterial pathogens.

Keywords: biocontrol agents; *Coffea*; coffee-endophytic fungi; pathogenic fungi; pathogenic bacteria

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Crassiparies yunnanensis sp. nov. (Neohendersoniaceae, Pleosporales) from dead twigs of *Coffea arabica* in China

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Abstract

Arabica coffee (*Coffea arabica*) accounting for about 60% of the world's coffee is popular all over the world as a refreshing beverage and food additive. During surveys of fungi occurring on coffee plants, we collected a species of Neohendersoniaceae on dead twigs of an Arabica coffee plant in Pu'er, Yunnan Province, China. Phylogenetic analyses of combined SSU, LSU, ITS, *rpb2*, and *tef* gene sequences confirmed that our fungus is a distinct new species within *Crassiparies*. Morphological characteristics also support this taxon to be a novel species in *Crassiparies*. Full description, photo plate, and a phylogenetic tree to show the placement of the new species in *Crassiparies* are provided.

Keywords: 1 new species, morphology, phylogeny, saprobes, taxonomy

Introduction

China successfully planted coffee for the first time in Taiwan Province in 1884 while French missionaries brought Arabica coffee (*Coffea arabica*) to Yunnan Province in 1982 (Zhang *et al.* 2014). The most successful provinces for coffee cultivation in China are Guangdong, Guangxi, Hainan, and Yunnan. In 2017, the coffee plantation area in Yunnan was about 125,000 hm^2, while the production reached 90,718–136,077 tonnes (Lin & Mo 2018). The planting area and yield of coffee in Yunnan account for 98% of the country's production. The main coffee-growing regions in Yunnan are Baoshan, Dehong, Lincang, Pu'er, Xishuangbanna, and Wenshan (Hou & Hu 2016, Li *et al.* 2017, Lin & Mo 2018).

Pleosporales, introduced by Luttrell & Barr in 1987, is the largest fungal order in Dothideomycetes (Hongsanan *et al.* 2020). The members of Pleosporales are characterized by immersed, erumpent to superficial, globose to subglobose, perithecioid ascomata usually with a papillate apex, ostioles with or without periphyses, hamathecium with cellular pseudoparaphyses, bitunicate asci, and ascospores of various shapes, pigmentation and septation (Barr 1987, Zhang *et al.* 2012). Pleosporales contains 91 families and 614 genera (Zhang *et al.* 2012, Hongsanan *et al.* 2020, Wijayawardene *et al.* 2022).

In phylogenetic analyses, Neohendersoniaceae formed a monophyletic clade within the Pleosporales and was introduced by Giraldo *et al.* (2017) with *Neohendersonia* as the type genus and *N. kickxii* as the type species. The characteristics of this family are ascomata that are immersed, globose to collabent, papillate, dark brown to black with

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Journal of *Fungi*

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Article

Description of Four Novel Species in *Pleosporales* Associated with Coffee in Yunnan, China

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Abstract: In Yunnan Province, the coffee-growing regions are mainly distributed in Pu'er and Xishuangbanna. During the surveys of microfungi associated with coffee in Yunnan Province, seven taxa were isolated from coffee samples. Based on molecular phylogenetic analyses of combined ITS, LSU, SSU, *rpb2*, and *tef1-α* sequence data and morphological characteristics, four new species viz. *Demiquelata yunnanensis*, *Paracamothyrium yunnanensis*, *Pseudocoleophoma puerensis*, and *Pse. yunnanensis*, and three new records viz. *Austropleospora keteleeriae*, *Montagnula thailandica*, and *Xenocamarosporium acaciae* in *Pleosporales* are introduced. In addition, *Paracamarosporium fungicola* was transferred back to *Paracamothyrium* based on taxonomy and DNA sequences. Full descriptions, illustrations, and phylogenetic trees to show the placement of new and known taxa are provided. In addition, the morphological comparisons of new taxa with closely related taxa are given.

Keywords: *Coffea*; *Demiquelata*; new species; new records; *Paracamothyrium*; phylogeny; *Pseudocoleophoma*; taxonomy

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1. Introduction

The coffee genus *Coffea*, belonging to the botanical family *Rubiaceae*, has about 170 varieties [1], and one of the varieties, *Coffea arabica*, is the most popular coffee variety around the world [2]. Coffee, as the world's second best-selling beverage and a food additive, sells all over the world, with many additional advantages such as refreshment, diuresis, invigorating the stomach, and stimulating appetite [3,4]. China's total production of coffee ranks 12th place in the world, and the annual export volume of coffee beans reaches 82.7 thousand tons [5], making it the fourth largest coffee exporter in Asia after Vietnam, Indonesia, and India [5,6]. In 2020, the export and import of coffee in China were worth $145 million and $310 million, respectively [7]. Yunnan Province is the largest coffee capital in China, and the planting area and total yield account for 95–98% of the total in China [5,8].

Coffee is susceptible to microfungi during pre-harvest and post-harvest processing, especially pathogenic fungi, which can affect coffee tree growth, fruit yield, and quality [9,10]. The most recent coffee fungi review in 2022 counted about 966 coffee-associated microfungi

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https://mycokeys.pensoft.net

RESEARCH ARTICLE

MycoKeys

Three new species of *Nigrograna* (Dothideomycetes, Pleosporales) associated with Arabica coffee from Yunnan Province, China

Li Lu[1,2,3], Samantha C. Karunarathna[1], Dong-qin Dai[1], Ruvishika S. Jayawardena[2,3], Nakarin Suwannarach[4], Saowaluck Tibpromma[1]

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Abstract

Coffee is one of the most important cash crops in Yunnan Province, China. Yunnan is ranked as the biggest producer of high-quality coffee in China. During surveys of microfungi from coffee plantations in Yunnan, six fungal strains that resemble Nigrograniaceae were collected. Multi-gene analyses of a combined SSU-LSU-ITS-*rpb2*-*tef1*-α sequence data matrix were used to infer the phylogenetic position of the new species in *Nigrograna* while morphological characteristics were used to deduce the taxonomic position of the new species. Six fungal strains isolated from decaying branches of *Coffea arabica* represent three new saprobic species in *Nigrograna*. The three new species, *N. asexualis*, *N. coffeae*, and *N. puerensis*, are described with full (macro and micro characteristics) descriptions, illustrations, and a phylogenetic tree that shows the phylogenetic position of new taxa.

Keywords

3 new taxa, *Coffea arabica*, Nigrogranaceae, phylogeny, saprobic fungi, taxonomy

IMA Fungus

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Research Article

Unveiling fungal diversity associated with coffee trees in China using a polyphasic approach and a global review of coffee saprobic fungi

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Abstract

Arabica coffee (*Coffea arabica*) is the most cultured and popular coffee bean in today's world. Yunnan Province is well known as China's largest arabica coffee cultivation region. Fungi represent an important group of microorganisms associated with coffee, profoundly influencing its yield and quality. In this study, twelve fungal collections growing on dead and decaying twigs of coffee were collected and isolated to systematically document microfungi associated with coffee plants in Yunnan Province. Ten novel species, each representing a unique family within *Pleosporales*, were identified and introduced, based on comprehensive morphological analyses and multigene phylogenetic studies. The ten new species belong to the families *Bambusicolaceae*, *Didymellaceae*, *Didymosphaeriaceae*, *Longiostiolaceae*, *Lophiostomataceae*, *Massarinaceae*, *Neomassariaceae*, *Occultibambusaceae*, *Roussoellaceae* and *Thyridariaceae* with each family containing one new species. Macro- and micro-characteristics, descriptions and phylogenetic trees indicating the placement of the new taxa are provided. In addition, pairwise homoplasy index (PHI) test results and morphological comparisons between the new species and closely-related taxa are given. This study also establishes a comprehensive global inventory of saprobic fungi associated with coffee, which is intended to help researchers and professionals worldwide with practical information. This research enhances the understanding of coffee-associated fungal diversity in China and underscores the importance of introducing new saprobic fungal taxa related to coffee.

Key words: *Coffea arabica*, Fungal diversity, new taxa, southwest China, taxonomy

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Pseudoconiocessia xishuangbannaensis gen. et *sp. nov.* in Coniocessiaceae, Xylariales from *Coffea liberica* in China

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Abstract

During a survey of saprobic fungi on coffee samples in Yunnan Province, China, in 2020 and 2022, fungal fruiting bodies on decaying Liberian coffee twigs were collected and isolated. Maximum likelihood and Bayesian analyses of combined ITS, LSU, and *RPB2* genes showed that the two isolated fungal strains belonged to a distinct species in Coniocessiaceae and were well separated from closely related genera with 73% ML and 0.92 PP statistical support. Morphologically, this distinct species can be differentiated from other genera in Coniocessiaceae by aseptate hamathecium, 4–8-spored asci with a flat apical ring, and fusiform ascospores, conical at the lower end. Based on morphology and phylogenetic analyses, the two fungal strains are described as a distinct new genus *Pseudoconiocessia*, within Coniocessiaceae. *Pseudoconiocessia* is introduced here with *Pseudoconiocessia xishuangbannaensis* as the type species.

Key words: 1 new genus, 1 new species, Liberian coffee, multi-gene, phylogeny, taxonomy

Introduction

More than 100 coffee varieties are available worldwide, while *Coffea liberica* (Liberian coffee) is one of the top three coffee species (Mugo 2010). *Coffea liberica*, indigenous across much of tropical West and Central Africa (Davis *et al.* 2006), was an important commercial crop during the 1930s–1950s (N'diaye *et al.* 2005). Nowadays, *C. liberica* has almost stopped selling and *C. arabica* (Arabica coffee) and *C. canephora* (Robusta coffee) currently account for almost all commercial coffee worldwide (N'diaye *et al.* 2005, Mannino *et al.* 2023). However, *C. liberica* is still cultivated to a minor extent, as it is perceived by coffee lovers as having a distinct taste and aroma (N'diaye *et al.* 2005, Herawati *et al.* 2022). *Coffea liberica* stands out as a resilient alternative, showcasing adaptability to changing climate scenarios (Lee 2023). Regarding the studies on fungi associated with coffee, only a few fungi studies have been carried out on *C. liberica*. For example, Kartika *et al.* (2019) found that Arbuscular Mycorrhizal Fungi (AMF) in Liberian coffee can improve coffee nutrient absorption, and increase plant resistance to pathogens and drought. Reportedly, the Liberian cultivars showed phenotypical resistance to coffee leaf rust (CLR) disease, which can be a source of resistant germplasm (Wahibah *et al.* 2023). Therefore, studying the fungi associated with Liberian coffee encourages future studies on the applications of fungi (Davis *et al.* 2022).

Sordariomycetes was introduced by Eriksson & Winka (1997), and is the second largest class in Ascomycota (Kirk *et al.* 2008, Hyde *et al.* 2013, Luo *et al.* 2019). Sordariomycetes are important for their role as plant and

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