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ARTICLE

Bambusicolous mycopathogens in China with an update on taxonomic diversity, novel species, pathogenicity, and new insights

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Abstract

Bambusicolous fungi inhabit bamboo tissues and play vital roles in bamboo ecosystems, mostly composed of saprobes, epiphytes, pathogens, and endophytes. Each category of fungus plays a distinct role: saprobes aid in decomposition, endophytes and epiphytes enhance plant health by establishing biochemical defense barriers, while pathogens can cause harmful effects like abnormal growth or death, thereby significantly influencing the overall health and quality of bamboo forests. In China, there is a rich diversity of bambusicolous mycopathogens but the information is scattered across various literature. Therefore, there is a need to systematically consolidate and provide an updated list of bambusicolous mycopathogens. This paper presents a comprehensive taxonomic account of bambusicolous mycopathogens in China with the following objectives: 1) to describe new specimens collected from Sichuan Province based on morphology and multigene phylogeny; 2) to update our current knowledge on the biodiversity of mycopathogens from China; 3) to discuss further research directions or areas. We have systematically gathered taxonomic information from diverse literature sources, such as articles, monographs, taxonomic websites, and other materials, to identify and screen fungal species associated with various bamboo diseases, including culm base rot, culm/timber rot, culm/leaf rust, dieback, shoot blight, rhombic spot, branch blight, witch's broom, tar spot, and leaf spot/blight. We have documented a total of 336 bambusicolous mycopathogens, providing additional details on host species, geographical distribution, disease type, epiphytology, and phylogenetic relationships based on DNA sequence data. The bambusicolous mycopathogens belong to 161 genera, 89

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families, 41 orders, 11 classes and three phyla. *Ascomycota* (272 species, 133 genera), is predominant among these bambusicolous mycopathogens. Within this phylum, *Sordariomycetes* (159 species, 61 genera) have the most species, followed by *Dothideomycetes* (78 species, 50 genera), *Eurotiomycetes* (23 species, nine genera), *Ascomycota* genera *incertae sedis* (eight species, eight genera), *Leotiomycetes* (two species, two genera), *Lecanoromycetes* (one species, one genus), and *Pezizomycetes* (one species, one genus). Within the *Basidiomycota* (60 species, 25 genera), the majority of species (55%) are in *Pucciniomycetes* (33 species, five genera), followed by *Agaricomycetes* (25 species, 18 genera), *Exobasidiomycetes* (one species, one genus), and *Ustilaginomycetes* (one species, one genus). Only four species (three genera) in the *Mucoromycota* were recorded. The top five largest bambusicolous mycopathogenic orders include *Hypocreales*, *Phyllachorales*, *Pleosporales*, *Pucciniales*, and *Xylariales*, comprising 39, 39, 32, 30, and 22 species, respectively. The most species-rich genera are *Phyllachora* (33 species, *Sordariomycetes*), *Puccinia* (25 species, *Pucciniomycetes*), *Fusarium* (15 species, *Sordariomycetes*), *Apiospora* (12 species, *Sordariomycetes*), *Colletotrichum* (nine species, *Sordariomycetes*), *Aspergillus* (seven species, *Eurotiomycetes*), and *Penicillium* (seven species, *Eurotiomycetes*). In addition, our freshly collected specimens unveil 23 species across nine orders within four classes, including a new genus, 12 novel species, 11 previously unreported host associations, and seven new geographical records. These species are associated with diseases based on symptoms observed or based on previous studies reporting their potential pathogenicity. Future *in vitro* studies are needed to verify the pathogenic nature of these bambusicolous fungi via Koch's postulates.

Keywords – 12 new taxa – Bambusicolous mycopathogens – Mycopathogenic classification – Phylogeny – Taxonomy

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INTRODUCTION

Bamboo plants, regarded as “the second largest forest on Earth”, are precious bioresources worldwide (Zhang & Guo 2009, Abdul Khalil 2018). As the largest member of the subfamily *Bambusoideae* in *Poaceae*, these monocotyledons play an important role in regional ecosystems,

economies, societies, and cultures worldwide (Zhang et al. 2010, Liu 2019). A documentary investigation shows that about 1,750 bamboo species in about 140 genera are abundant resources globally. In China, there are about 770 bamboo species, along with 5 hybrids and 203 forms or varieties, across 42 genera (Abdul Khalil 2018, Zhong et al. 2019, Shi et al. 2020, Tong et al. 2020, Li et al. 2021a, Ni et al. 2021a, b, Vinh et al. 2023, Huang et al. 2024a, b, Li et al. 2024). Bamboo species live in diverse climates, and contribute to numerous roles, such as climate regulation, soil and water conservation, carbon sequestration and oxygen release, biodiversity conservation, forest products, and forest health regimen. China is an important distribution center of bamboo plants, with the area of more than 7 million hectares covered by bamboo forests. The total output value of the bamboo industry exceeds 320 billion RMB, and it ranks first among exporters of bamboo products in the world (Wen et al. 2001, Wang et al. 2020).

Pathogenic microorganisms, including fungi, bacteria, viruses, nematodes, and mites, affect bamboo to a large extent (Kuai 1996, Mohanan 2017, Xu 2017). The number of fungal species on bamboo are likely to exceed 1,500 species and they are known from terrestrial and aquatic habitats (Cai et al. 2003, Phookamsak et al. 2022, Yu et al. 2023a, Zhang et al. 2023a). Up to now, nearly 700 species of pathogenic fungi on bamboo have been recorded globally (Xu et al. 2006, Mohanan 2017, Xu 2017, Wang et al. 2021, Dai et al. 2022, Jiang et al. 2022). In general, bambusicolous mycopathogens, belonging to the *Ascomycota*, *Basidiomycota*, and *Mucoromycota*, are reported to cause diseases of living bamboo plants or can cause bamboo timber rot (Mohanan 2017, Xu 2017). Generally, fungi inhabiting bamboo timber are often categorized as pathogens and pose a threat to many industries, especially in construction, furniture manufacturing, paper-making, and related sectors, due to their potential detrimental impact on the chemical composition, physical structure, and mechanical strength of bamboo timber (Ma et al. 2012, Sun et al. 2017, Feng et al. 2019). Scattered data on bambusicolous mycopathogens are reported in various literatures, wherein species, substrates, geographical areas, and harmful aspects have been documented (Deng 1963, Tai 1979, Kuai 1996, Zhang & Wang 1999, Zhou et al. 2000, Hyde et al. 2002, Xu et al. 2006, Dai et al. 2017, Mohanan 2017, Xu 2017). The traditional methods used to describe and identify bambusicolous mycopathogens have significantly improved with the use of molecular techniques, and continuous exploration of bambusicolous mycopathogens has led to the establishment of new pathogenic species (Li et al. 2019, 2021b, Yang et al. 2019a–c, Wei et al. 2021a, Liu et al. 2022a). However, there is no published and updated compilation on the overall known species of bambusicolous mycopathogens in China.

This paper presents an updated classification of bambusicolous mycopathogens in China, along with the number of taxa recorded at each taxonomic level. New collections of bambusicolous mycopathogens are described based on morphological examinations of fresh specimens, combined with phylogenetic analysis of DNA sequence data. The paper is divided into three main sections: (1) Taxonomy of new collections, (2) current research status of bamboo pathogenic fungi in China based on extensive literature studies, and (3) potential areas of current or future research. This monograph will enhance our taxonomic understanding of fungi associated with bamboo plants and their diseases, and can provide a reference for pathogen identification.

MATERIALS AND METHODS

Sample collection, morphological and DNA based studies

Fungal specimens associated with bamboo were collected from different sites (Bazhong City, Chengdu City, Guang'an City, Guangyuan City, Leshan City, Luzhou City, Panzhihua City, and Ya'an City) in China. Pure strains were obtained from the fresh collections by the single spore isolation method (Senanayake et al. 2020). Morphological observations and photomicrographs were made following the method of Zeng et al. (2022). Ex-type or representative isolates were deposited in Sichuan Agricultural University Culture Collection (SICAUCC), China. The collected specimens were deposited in the Herbarium of Sichuan Agricultural University (SICAU), China. Index

Fungorum and Faces of fungi numbers were obtained as detailed in Index Fungorum (2024) and Jayasiri et al. (2015).

Genomic DNA was extracted from fresh mycelium grown from single spore cultures. For specimens that were not readily cultivable, direct DNA extraction was performed. The PCR amplification was performed in a total volume of 25 μL of PCR mixtures including 22 μL Master Mix (Beijing TsingKe Biotech Co., Ltd., Beijing, China), 1 μL of DNA template, 1 μL of each primer (10 μM). Gene regions sequenced and primers used for each genus are tabulated (Table 1) and were selected based on current publications. Purification and sequencing of PCR products were carried out at TsingKe Biological Technology Co., Ltd., Chengdu, China.

Table 1 Gene regions and primers.

Genera	**Gene regions**	**Primers**		**References**
		Forward	**Reverse**	
Aciculosporium	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*tub*2	T1	Bt2b	O'Donnell & Cigelnik (1997), Glass & Donaldson (1995)
Asterothyrium	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
Bifusisporella	ITS	ITS1	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*rpb*1	RPB1-Ac	RPB1-Cr	Castlebury et al. (2004)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Conidiocarpus	ITS	ITS1	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-728F	ef1-986R	Carbone & Kohn (1999)
Fitzroyomyces	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	mtSSU	mrSSU1	mrSSU3R	Zoller et al. (1999)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Heteroepichloe	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*tub*2	T1	Bt2b	O'Donnell & Cigelnik (1997), Glass & Donaldson (1995)
Mendogia	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Neosetophoma	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
Ophiosphaerella	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)

Table 1 Continued.

Genera	Gene regions	Primers		References
		Forward	Reverse	
	SSU	NS1	NS4	White et al. (1990)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*tub*2	T1	T22	O'Donnell & Cigelnik (1997)
Parakarstenia	ITS	ITS1	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	mtSSU	mrSSU1	mrSSU3R	Zoller et al. (1999)
Paralloneottiosporina	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
Paraphaeosphaeria	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*tub*2	Bt2a	Bt2b	Glass & Donaldson (1995)
	act	ACT-512F	ACT-783R	Carbone & Kohn (1999)
Parasitibambusa	ITS	ITS1	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*mcm*7	CARCA-F	M456-5R	Van der Linde et al. (2016)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*tub*2	T1	Bt2b	O'Donnell & Cigelnik (1997), Glass & Donaldson (1995)
Phyllachora	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
Puccinia	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*CO*3	CO3-F1	CO3-R1	Beenken et al. (2012)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Roussoella	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Scorias	ITS	ITS1	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
Shiraia	ITS	ITS5	ITS4	White et al. (1990)
	LSU	LR0R	LR5	Rehner & Samuels (1994)
	SSU	NS1	NS4	White et al. (1990)
	*tef*1-α	ef1-983F	ef1-2218R	Rehner & Buckley (2005)
	*rpb*2	fRPB2-5F	fRPB2-7cR	O'Donnell et al. (2007)

The phylogenetic analyses were performed based on ex-type or otherwise authentic sequence data available in GenBank. DNA sequences generated from individual genes were aligned and visually checked in BioEdit 7.0.5.3 (Hall 1999) and MAFFT v.7.407 (Katoh & Standley 2013). Individual DNA sequence alignments from different individual genes were concatenated and

analyzed for each group of fungi under study. Maximum likelihood and Bayesian analyses were used to infer the phylogenetic position of each isolated taxon, and generated by using the CIPRES Science Gateway web server (Miller et al. 2010). Trees were rooted with suitable outgroup taxa in each analysis. The best scoring trees were selected and visualized with FigureTree v. 1.4.3 and edited using Adobe Illustrator CS6 (Adobe Systems Inc., San Jose, CA, USA). All the newly generated sequences in this paper were deposited in GenBank. The genealogical concordance phylogenetic species recognition (GCPSR) approach, introduced by Taylor et al. (2000), is used to define phylogenetically close species through a pairwise homoplasy index (PHI) test. The resulting phylogenetic trees and split graphs are assigned to each relevant description. Decisions as to whether taxa were new species or new records follow the guidelines of Jeewon & Hyde (2016) and Chethana et al. (2021).

Database Collection and Analysis

The database used in this study was obtained through a thorough literature search including all years, such as web-search engines (e.g. https://scholar.google.com.hk; http://www.cnki.net; http://k.vipslib.com; https://xueshu.baidu.com; https://fungi.ars.usda.gov. Related terms include bamboo plants, timber, *Poaceae*, 42 bamboo genera (e.g. *Bambusa*, *Chimonobambusa*, *Dendrocalamus*, *Fargesia*, *Indocalamus*, and *Phyllostachys*), bambusicolous fungi, pathogens, pathogenic microorganism, fungi, pathogenic fungi, pathogenic ascomycetes, pathogenic basidiomycetes, and other phyla (e.g. *Chytridiomycota*, *Oomycota*, and *Mucoromycota*)), fungus name registration website (Fungal Names, https://nmdc.cn/fungalnames/; Index Fungorum, http://www.indexfungorum.org/; MycoBank, http://www.mycobank.org/), monograph, and other related approaches. Up to August 2023, there are around 400 papers and 23 monographs on bambusicolous fungi in China, and approximately 300 papers and 23 monographs associated with bambusicolous mycopathogens. Fungal names, hosts, substrates, geographical distribution, disease type, and epiphytology were extracted from literature and recognized websites in this study for further analysis. The classification criterion of fungi follows Wijayawardene et al. (2022) unless the taxonomy has been updated recently. The plant classification scheme follows The Plant List (http://www.theplantlist.org) and Plant Science Data Center (https://www.plantplus.cn). Heatmap clustering of the distribution of bamboo pathogenic fungi in different provinces at the genus level was computed using the TBtools v2.001 (Chen et al. 2020). Z-scores were applied to columns, which were clustered with Euclidean distance measurement and complete linkage clustering method. Upset plots of the distribution of bamboo pathogenic fungi in different genera of bamboo and different parts of the disease were pictured with UpSetR package (version 1.4.0) (Lex et al. 2014, Conway et al. 2017).

RESULTS AND DISCUSSION

Given the large amount of information analyzed in this paper and ensure a coherent and logical flow, it has been structured into three sections: (1) Taxonomy of new collections, (2) current research status of bamboo pathogenic fungi in China based on extensive literature studies (with a focus on history, classification and species diversity of bambusicolous mycopathogens, as well as disease types and epiphytology), and (3) potential areas of current or future research.

Taxonomy

The new fungal collections are showcased in the specified sequence mentioned in the TABLE OF CONTENTS. They represent a total of 18 genera in 13 families, nine orders, and four classes. Fungal taxa described and illustrated in this paper include 23 species, with one new genus, 12 new species, 11 new records on the host, and seven new geographical records.

Ascomycota
Dothideomycetes
Capnodiales Woron., Annls mycol. 23(1/2): 177 (1925)

Capnodiaceae Höhn. ex Theiss., Verh. Zool.-Bot. Ges. Wien 66: 363 (1916)

Capnodiaceae was introduced by von Höhnel (1910) with the generic type *Capnodium* Mont., and it is characterized by immersed, gregarious, subglobose to globose ascostromata, cylindrical, bitunicate asci, bi- to tri-seriate, multi-septate or muriform ascospores, and aseptate and ellipsoid conidia (Chomnunti et al. 2011, 2014, Hyde et al. 2013, Hongsanan et al. 2015, Abdollahzadeh et al. 2020, Li et al. 2020). Abdollahzadeh et al. (2020) included seven morphologically and phylogenetically well-supported genera, *viz*. *Capnodium*, *Chaetocapnodium*, *Conidiocarpus*, *Heteroconium*, *Leptoxyphium*, *Phragmocapnias*, and *Polychaeton*, in this family. *Capnodiaceae* members mostly occur on sugary exudates from insects growing on the surface of leaves, fruits, stems and other non-plant objects, and which can cause chlorosis and plant stunting disease, due to black mycelium coating the host surface (Hongsanan et al. 2015, Abdollahzadeh et al. 2020).

Conidiocarpus Woron., Ann. Mycol. 24 (3/4): 250 (1926)

Conidiocarpus was established by Woronichin (1917), with the type species *C. caucasicus* Woron. However, Hughes (1976) and Batista & Ciferri (1963) proposed *C. penzigii* Woron., which was introduced by Woronichin (1926), as the type species of this genus. It has been suggested that *Conidiocarpus* is the asexual form of *Phragmocapnias* (Hughes 1976). Following the principles of priority and "one fungus, one name" as outlined in the ICN code, Bose et al. (2014) opted for the use of *Conidiocarpus* and transferred species from *Phragmocapnias* to *Conidiocarpus*. Based on phylogenetic analyses, morphological data and following the views of Hughes (1976), Abdollahzadeh et al. (2020) resurrected *Phragmocapnias* for two species, *Phr. betle* and *Phr. plumeriae* with conidiocarpus-like pycnidia lacking necks. Tennakoon et al. (2021) described a new species *Conidiocarpus fici-septicae* Tennakoon, C.H. Kuo & K.D. Hyde from *Ficus septica* Burm. F. based on multigene phylogeny and following the arrangement proposed by Abdollahzadeh et al. (2020) for *Conidiocarpus* species. Marasinghe et al. (2023) provided re-descriptions of epifoliar fungi and treated *Conidiocarpus* and *Phragmocapnias* as separate genera. Thungdee et al. (2023) synonymized *Conidiocarpus asiaticus* and *C. siamensis* under *C. caucasicus* based on morphology and phylogenetic analyses. In this paper, we support *C. siamensis* as a distinct species and report it causing sooty mould of *Phyllostachys sulphurea* (Carr.) A. et C. Riv in Sichuan Province, China.

1. *Conidiocarpus siamensis* (Chomnunti & K.D. Hyde) T. Bose, Mycologia 106(4): 753 (2014)
Figs 1, 2

Index Fungorum number: IF807059; Facesoffungi number: FoF07172

≡ *Phragmocapnias siamensis* Chomnunti & K.D. Hyde, Fungal Diversity 51(1): 112 (2011)

A sooty mould on leaves of *Phyllostachys sulphurea*. *Thallus* thin, dark brown, easily removed from the host surface, composed of cylindrical hyphae. *Superficial hyphae* 3–5 μm wide ($\overline{x}$ = 3.5 μm, n = 25), septate, constricted at the septum, branched, brown to dark brown, with subcylindrical hyphal cells. Sexual morph: *Ascomata* 70–130 × 65–110 μm ($\overline{x}$ = 95 × 80 μm, n = 25), superficial, solitary, globose to subglobose, narrowly rounded above, constricted at the base, brown to dark brown, thin-walled, with 3–4 ascomatal setae at the upper part of ascomata. *Setae*, dark brown to reddish-brown, but pale brown to hyaline at the apex. *Peridium* 13–17 μm wide, comprising cells of *textura angularis*, inner layer hyaline, outer layer dark brown. *Asci* 40–55 × 15–35 μm ($\overline{x}$ = 48 × 22 μm, n = 25), 8-spored, bitunicate, fissitunicate, subcylindrical to obovoid, short pedicellate or sometimes apedicellate, ocular chamber not observed. *Ascospores* 22–38 × 6–9 μm ($\overline{x}$ = 30 × 7.8 μm, n = 50), fasciculate, cylindrical to clavate, with rounded ends, hyaline, 3–5-septate, constricted at the septa, upper part wider than the lower part, guttulate, surrounded by an obscure mucilaginous sheath, smooth-walled. Asexual morph: *Conidiomata* pycnidial, 410–690 × 25–50 μm ($\overline{x}$ = 450 × 35 μm, n = 25), solitary to gregarious, superficial, blackish brown, cylindrical, swollen at the central part, stalk black, 45–70 × 25–50 μm ($\overline{x}$ = 55 × 35 μm, n = 15), wall comprising mostly cylindrical cells, the swollen part producing conidia inside. *Ostiolar neck* 8–14 μm ($\overline{x}$ = 12 μm, n = 25) diam, surrounded by hyaline hyphae. *Conidiogenous cells* formed in

the inner cells of the oval part. *Conidia* 3.8–5.1 × 2.1–2.6 µm ($\bar{x}$ = 4.5 × 2.3 µm, n = 50), cylindrical to oblong, ends round, hyaline, smooth-walled.

Culture characteristics – *Colonies* on PDA reaching 10 mm diam in 15 days at 25 ℃, under 12 h light/12 h dark, circular, convex, surface slightly rough, edge rules. Colonies from above: dark brown to black at the margin, black at the center; reverse: dark brown at the margin, dark brown to black at the center.

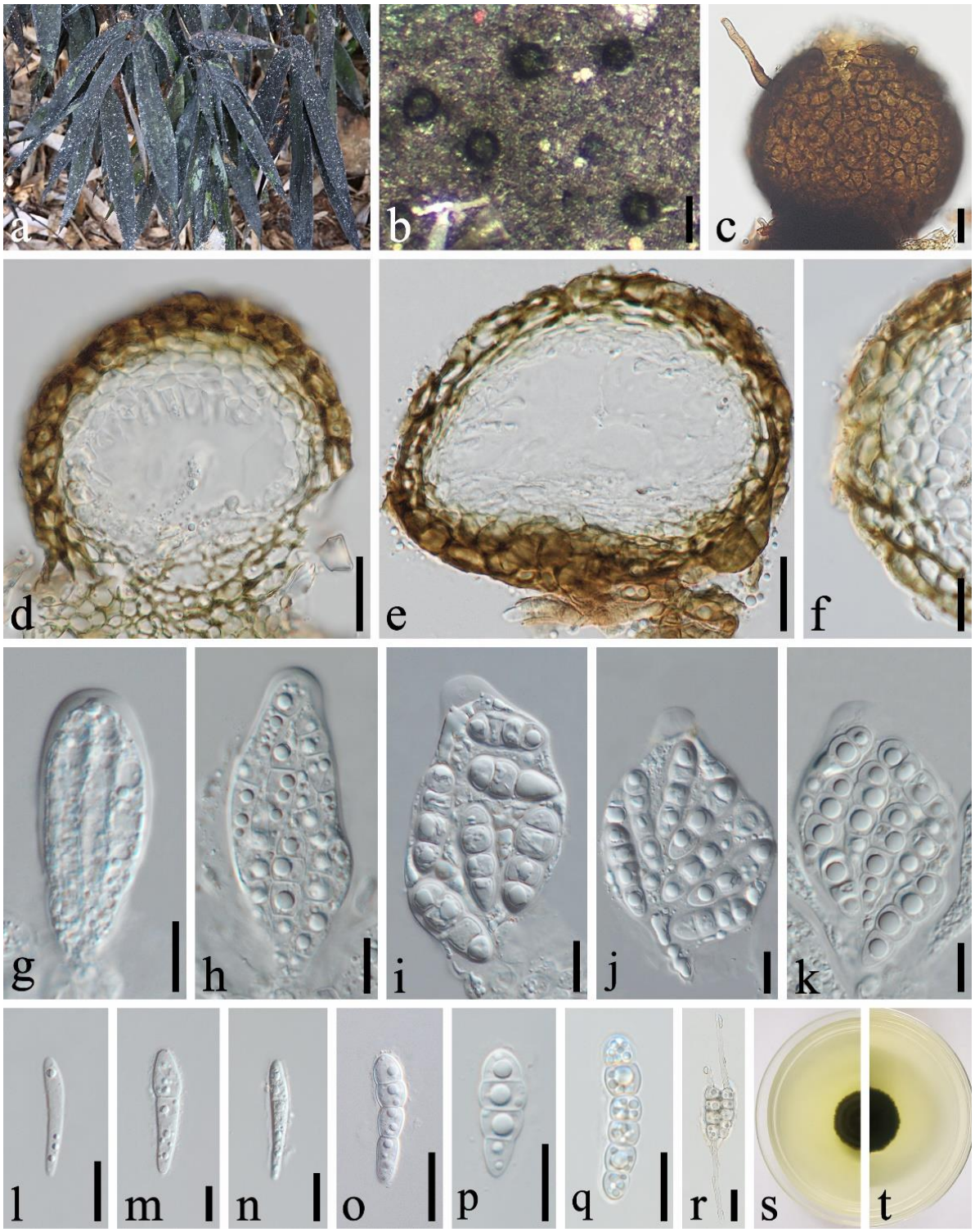

Figure 1 – Sexual morph of *Conidiocarpus siamensis* (SICAU 23-0011). a, b Appearance of ascomata on host. c Close-up of ascomata. d, e Section of ascoma. f Section of peridium. g–k Asci. l–q Ascospores. r Germinating ascospores. s, t Colonies on PDA (s obverse, t reverse). Scale bars: b = 100 µm, c–e = 20 µm, f–r = 10 µm.

Material examined – China, Sichuan Province, Panzhihua City, Miyi County, Baima Town, Longtang Village (26°59'29.53"N, 102°12'32.91"E, alt. 1574 m), on leaves of *Phyllostachys sulphurea*, 29 December 2022, Chunlin Yang, YCL202212001 (SICAU 23-0011), living culture SICAUCC 23-0010. *ibid*. YCL202212002 (SICAU 23-0012), living culture SICAUCC 23-0011.

GenBank numbers – SICAUCC 23-0010 – ITS = OR405901, LSU = OR405912, SSU = OR405927, *rpb*2 = OR465269, *tef*1-α = OR671432; SICAUCC 23-0011 – ITS = OR405901, LSU = OR405912, SSU = OR405927, *rpb*2 = OR531521, *tef*1-α = OR671433.

Notes – Phylogenetic analyses show the two new strains (SICAUCC 22-0010 and SICAUCC 22-0011) are closely related in a strongly supported clade (94% MLBS and 0.9 BYPP; Fig. 3), with *Conidiocarpus siamensis* (MFLUCC 10-0061, CPC 20464 and CPC 20468). *Conidiocarpus siamensis* (SICAUCC 23-0010) differs from *C. fici-septicae* (MFLUCC 19-0072, ex-type) and *C. caucasicus* (MFLUCC 10-0062) by its comparatively longer conidiomata (410–690 μm vs. 240–280 μm vs. 301–387 μm) with a wider ostiolar neck (8–14 μm vs. 6–9 μm vs. 4.9–6.5 μm), and wider conspicuous oval swellings (45–70 μm vs. 25–30 μm vs. 18–24 μm), and larger conidia (3.8–5.1 × 2.1–2.6 μm vs. 4–5 × 1–2 μm vs. 2.5–3.7 × 1–1.4 μm) (Chomnunti et al. 2011, Tennakoon et al. 2021). Comparisons of the ITS and LSU DNA sequence of *C. siamensis* (SICAUCC 23-0010) and *C. fici-septicae* (MFLUCC 19-0072) showed 98.92% (460/465, 0 gap) and 99.88% (853/854, 0 gap) similarity, respectively. The ITS sequence of *C. siamensis* (SICAUCC 23-0010) and *C. caucasicus* (MFLUCC 10-0062, MFLUCC 10-0063, SDBR-CMU478) showed 98.36% (361/367, 0 gap), 98.36% (361/367, 0 gap) and 97.84% (454/464, 5 gaps) similarity, respectively. The PHI test also showed no significant recombination events between *C. siamensis* and closely phylogenetically related species (Fig. 4). Therefore, we identify *C. siamensis* as a distinct species that differs from *C. caucasicus* and *C. fici-septicae*. Nucleotide comparisons of ITS, LSU from our collection (SICAUCC 23-0010) showed a high homology with the sequences of *C. siamensis* (MFLUCC 10-0061), with a similarity of 100% (367/367, 0 gap), and 99.42% (867/872, 0 gap), respectively. At the same time, nucleotide comparisons of ITS, LSU, *rpb*2, and *tef*1-α from our collection (SICAUCC 23-0010) revealed high homology with the sequences of *C. siamensis* (CPC 20464 and CPC 20468), with similarity of 100% (461/461, 0 gap), 100% (820/820 or 836/836, 0 gap), 98.97% (672/679, 0 gap), and 99.87% (756/757, 0 gap), respectively. *Conidiocarpus siamensis* was previously described in its asexual morph from living leaf of *Mangifera indica* L. in Thailand (Chomnunti et al. 2011). In the present study, the species is re-illustrated based on new collections of both sexual (Fig. 1) and asexual morph specimens (Fig. 2), and this is the first record from *Phyllostachys* (*Poaceae*) in China.

Scorias Fr., Syst. Mycol. (Lunde) 3(2): 269 (1832)

Scorias is characterized by 8-spored, bitunicate, oblong to saccate, apedicellate asci and fusiform, 3–4 transversely septate ascospores (Chomnunti et al. 2011). Chomnunti et al. (2011) epitypified *S. spongiosa* (Schwein.) Fr. based on a specimen isolated from a living leaf of *Entada* sp. (*Fabaceae*) in Thailand and verified its placement within the family *Capnodiaceae*. Hongsanan et al. (2015) also included *S. mangiferae* collected from a branch of *Mangifera* sp. (*Anacardiaceae*) in this family. Abdollahzadeh et al. (2020) described two new species, *S. aphidis* Abdollahz. & Crous and *S. camelliae* Abdollahz. & Crous, which were collected from aphids and *Camillia* sp. (*Theaceae*) in Indonesia.

2. *Scorias pseudoaphidis* Q. Zeng, Feng Liu, K.D. Hyde & C.L. Yang, sp. nov. Fig. 5

Index Fungorum number: IF900663; Facesoffungi number: FoF14774

Etymology – Refers to the similarity with *Scorias aphidis*.

Holotype – SICAU 23-0013

A sooty mould on branches, twigs, leaves and culm-sheaths of *Bambusa multiplex* (Lour.) Raeuschel ex J. A. et J. H. Schult. Sexual morph: Undetermined Asexual morph: Coelomycetous. Vegetative masses formed on substrate associated with *Pseudoregma bambucicola* (Takahashi), developed, consisting of cylindrical and septate hyphae, branched, thick wall, mucilaginous

between hyphae, and reduced to numerous pycnidia at apex. *Pycnidia* 220–340 × 37–79 μm ($\bar{x}$ = 273 × 59 μm, n = 20), a long neck 145–185 × 13–19 μm ($\bar{x}$ = 168.7 × 17.4 μm, n = 20), conspicuous oval or ellipsoidal central part 60–115 × 34–75 μm ($\bar{x}$ = 93.6 × 56 μm, n = 20), tapering to the apex, comprised of brown hyphae moderately helical twisting towards the apex surrounding the ostiole. *Pycnidial walls* 6.5–19 μm wide, composed of several layers of pale brown to dark brown cells of *textura angularis*, with inner light color layer, thick cell-wall at sides. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–14 × 1.8–3.5 μm ($\bar{x}$ = 9 × 2.4 μm, n = 20), cylindrical, blastic, enteroblastic, monophialidic, formed from the innermost layer of pycnidial wall, hyaline, smooth-walled. *Conidia* 3.6–5.7 × 2–2.9 μm ($\bar{x}$ = 4.6 × 2.4 μm, n = 50), ellipsoidal, occasionally reniform, unicellular, hyaline.

Culture characteristics – *Colonies* on PDA attaining 15–25 mm diam in 10 days, after 15 days at 25 °C, under 12 h light/12 h dark, sarcoid, spreading radially towards the edge, dark brown in the center, olive green towards the edge.

Material examined – China, Sichuan Province, Chengdu City, Wenjiang District, Chengdu Academy of Agricultural and Forestry Sciences (30°42'26.55"N, 103°51'24.61"E, alt. 472 m), on leaves and culm-sheaths of *Bambusa multiplex*, 5 September 2019, Chunlin Yang, YCL201904004 (SICAU 23-0013, holotype), ex-type culture SICAUCC 23-0012. *ibid*. YCL201904005 (SICAU 23-0014, paratype), ex-paratype culture SICAUCC 23-0013.

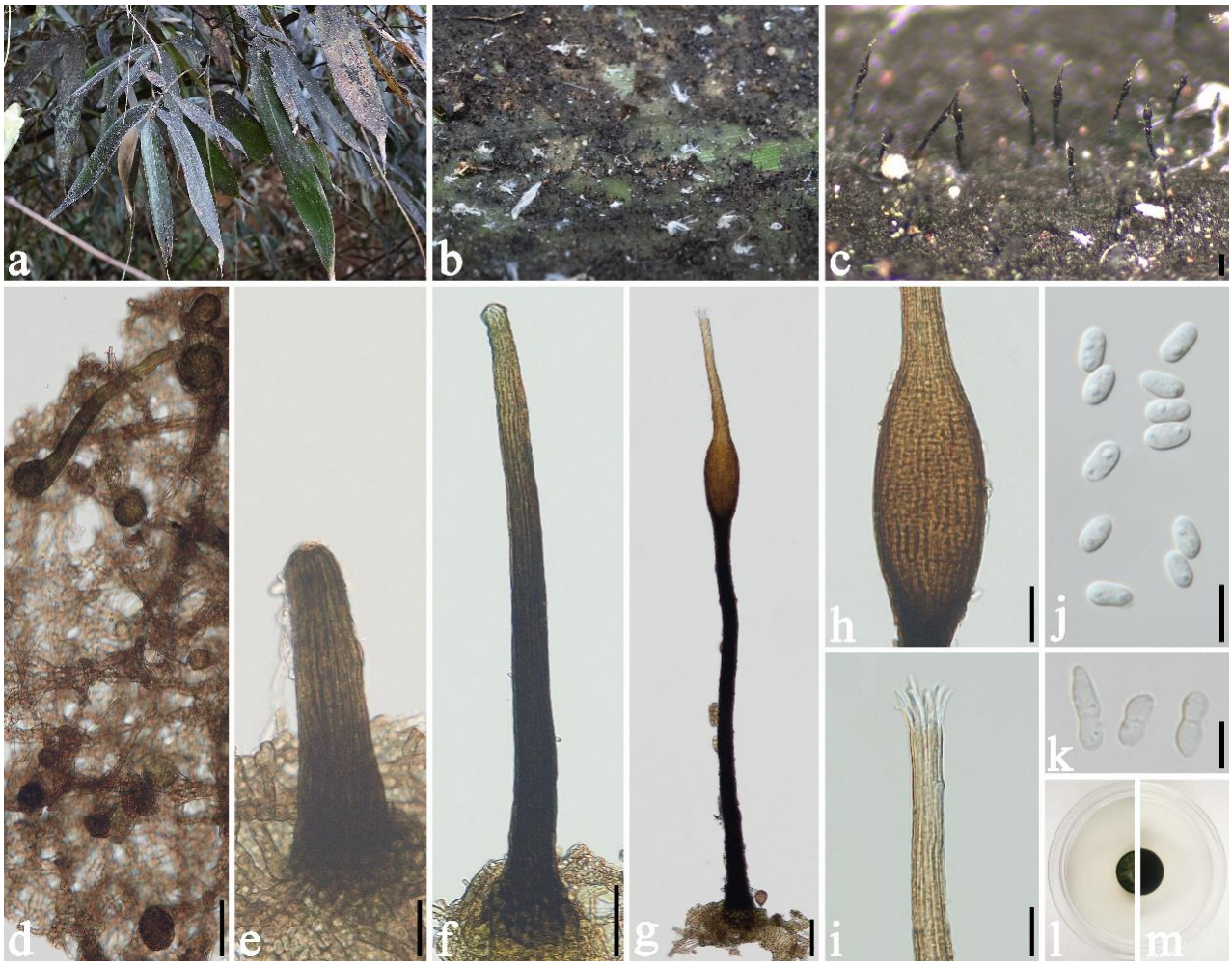

Figure 2 – Asexual morph of *Conidiocarpus siamensis* (SICAU 23-0012). a, b Sooty mould on the surface of host plant. c Pycnidia formed on the surface of leaf. d Network-like hyphae. e–g Pycnidia. h Cells wall of swollen part. i Ostiolar neck. j Conidia. k Germinating conidia. l, m Colonies on PDA (l obverse, m reverse). Scale bars: c = 100 μm, d, f, g = 50 μm, e = 20 μm, h–i = 10 μm, j, k = 5 μm.

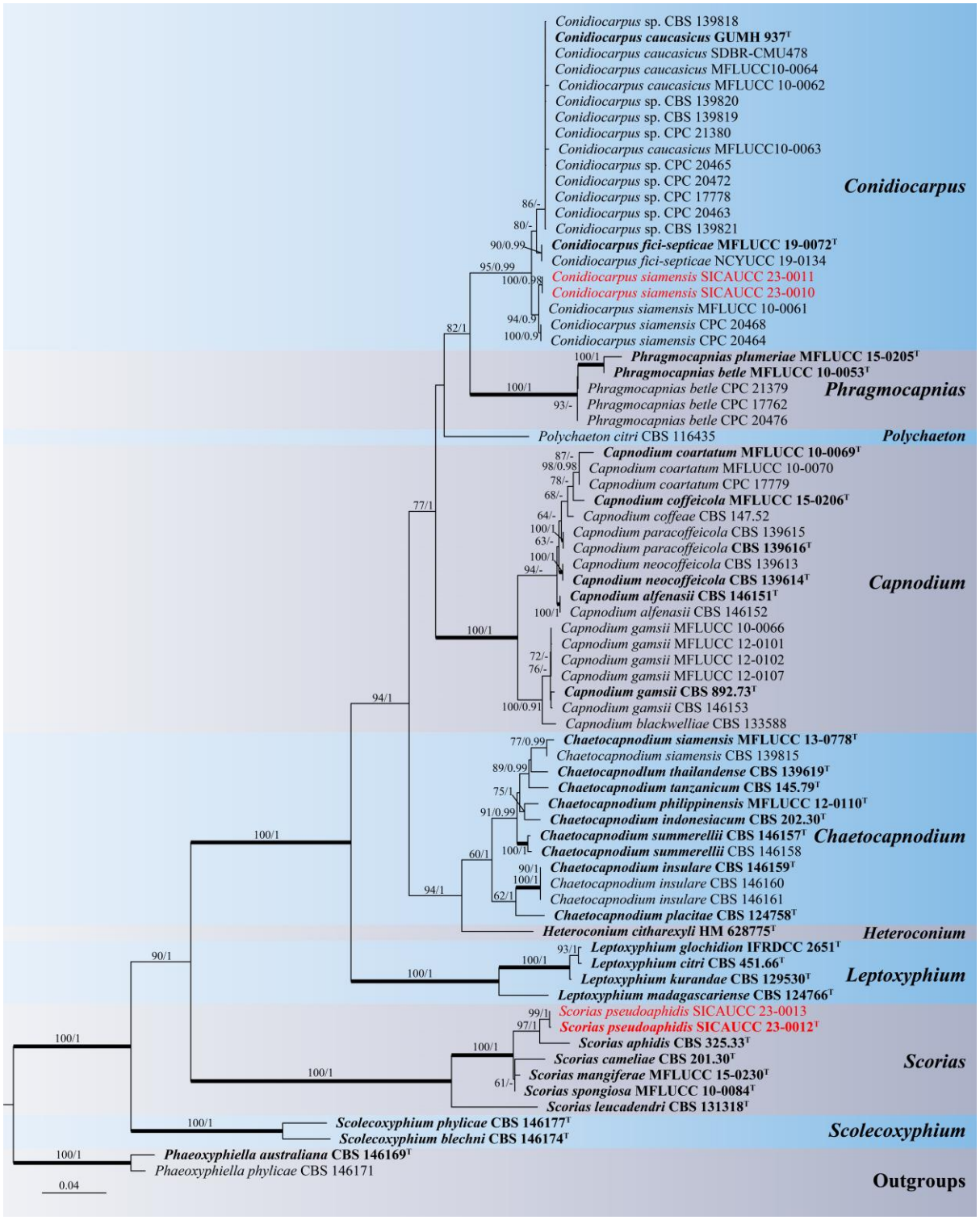

Figure 3 – Phylogenetic analyses of a concatenated aligned dataset (ITS, LSU, *rpb*2, and *tef*1-α), including 73 taxa within *Capnodiaceae*, were conducted and tree was rooted with *Phaeoxyphiella australiana* (CBS 146169) and *P. phylicae* (CBS 146171) (*Capnodiaceae*, *Capnodiales*). The alignment contained 3,353 characters, including gaps. The best scoring RAxML tree with a final likelihood value of -19,687.205716 is presented. The matrix had 1,103 distinct alignment patterns, with 19.98% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245159, C = 0.260447, G = 0.274255, T = 0.220139, with substitution rates AC = 1.284183, AG = 4.102790, AT = 1.804787, CG = 1.026708, CT = 9.408025, GT = 1.000000. The gamma distribution shape parameter α = 0.172907, and the tree length = 1.636231. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 60% and Bayesian posterior probabilities (BYPP,

right) ≥ 0.90 are indicated at the nodes, respectively. The ex-type strains are indicated with "T" in the end of the taxa labels. The newly generated sequences are highlighted in red. Bold lines in the tree represent MLBS = 100%, BYPP = 1.00.

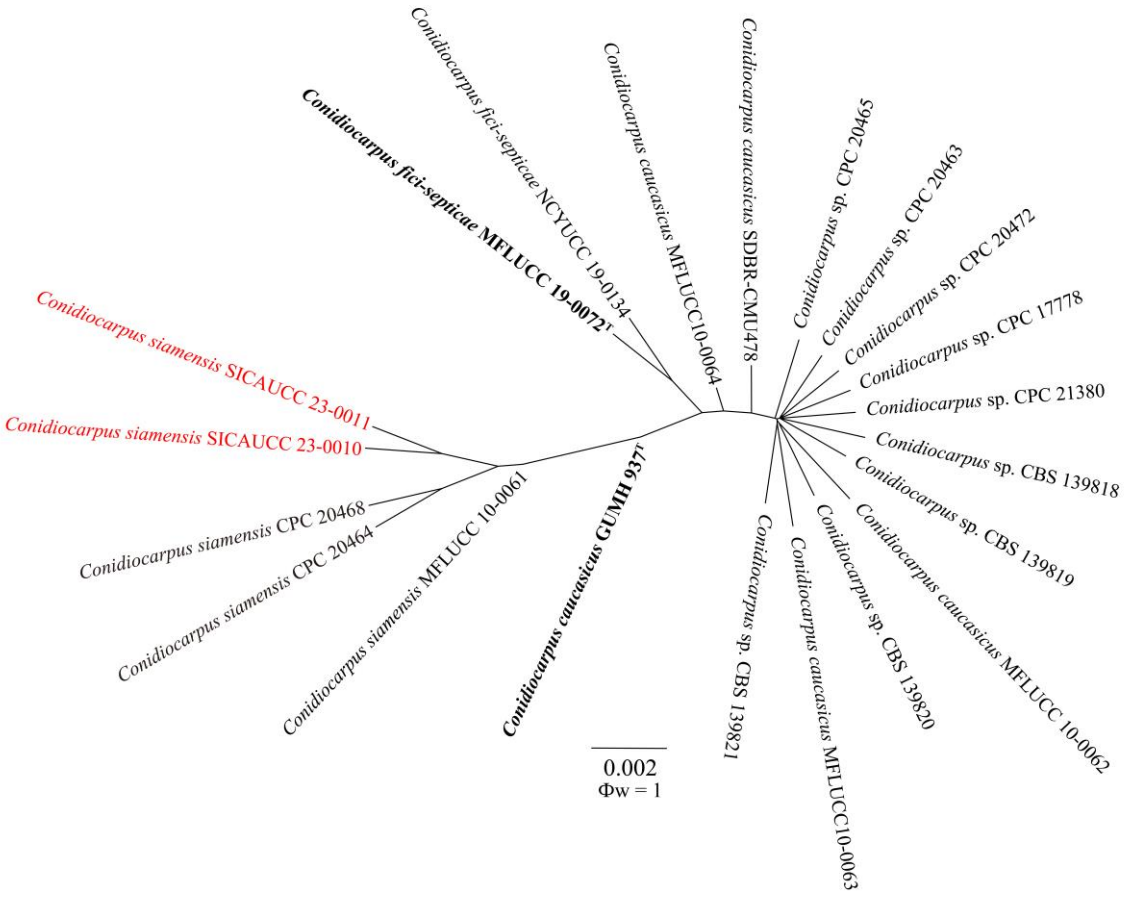

Figure 4 – The splits graph from the pairwise homoplasy index (PHI) test generated from the concatenated gene set of ITS, LSU, *rpb*2, and *tef*1-α sequence data of closely related species of *Conidiocarpus* using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The strains determined in this study are in red. The ex-type strains are marked with "T" after the strain number label.

GenBank numbers – SICAUCC 23-0012 – ITS = OR405903, LSU = OR405914, SSU = OR405929, *rpb*2 = OR465270, *tef*1-α = OR531512, *tub*2 = OR465276; SICAUCC 23-0013 – ITS = OR405904, LSU = OR405915, SSU = OR405930, *rpb*2 = OR465271, *tef*1-α = OR917086, *tub*2 = OR465277.

Notes – Multi-loci phylogenetic analyses based on a concatenated ITS, LSU, *tef*1-α and *rpb*2 sequence dataset show that *Scorias pseudoaphidis* (SICAUCC 22-0012 and SICAUCC 22-0013) forms a subclade with 99% MLBS and 1.00 BYPP support (Fig. 3), sister to *S. aphidis* (CBS 325.33). *Scorias pseudoaphidis* has a comparatively smaller central part of pycnidia (93.6 × 56 µm vs. 210 × 80 µm), and a longer pycnidial neck (145–185 µm vs. 50–185 µm) than *S. aphidis* (CBS 325.33) (Abdollahzadeh et al. 2020). A comparison of ITS, LSU, *tef*1-α and *rpb*2 sequence data of isolate *S. pseudoaphidis* and *S. aphidis* (CBS 325.33), shows that the nucleotide differences are 0.74% (4/542, 0 gap), 0.23% (2/876, 0 gap), 2.07% (19/917, 0 gap) and 4.08% (43/1052, 0 gap), respectively. Therefore, we identified *S. pseudoaphidis* as a new species of *Scorias*.

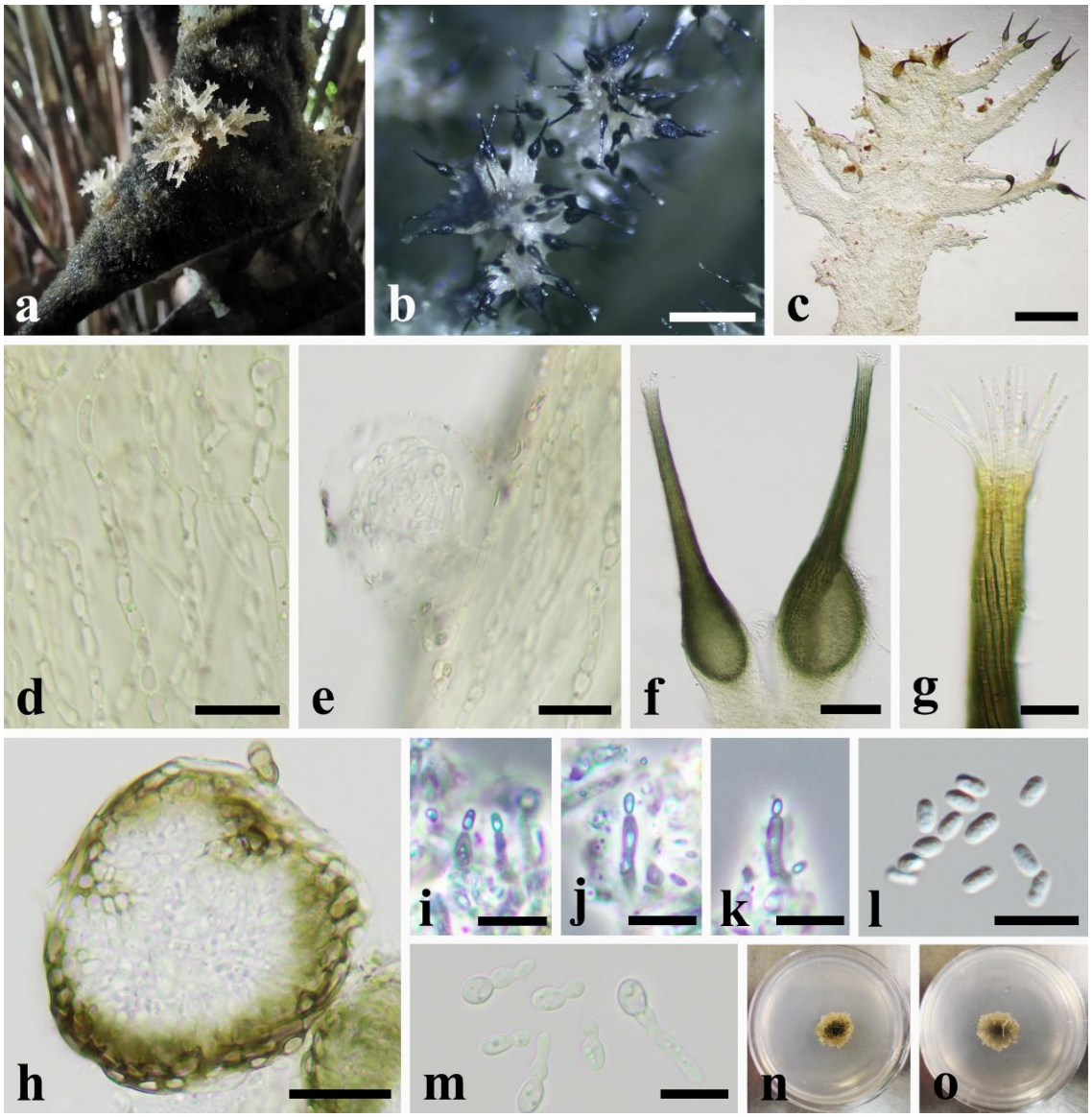

Figure 5 – *Scorias pseudoaphidis* (SICAU 23-0013, holotype). a, b Vegetative masses formed on the host. c Fruiting bodies with branches and pycnidia (synnemata). d Mycelial network in mucilaginous masses from stem of fruiting bodies. e Early differentiated branch from stem. f Flask-shaped conidiomata. g Ostiole surround by hyaline hyphae. h Cross section of a conidioma. i–k Conidiogenous cells with developing conidia. l Conidia. m Germinated conidia. n, o Colonies on PDA (n obverse, o reverse). Scale bars: b, c = 500 μm, f = 50 μm, d, e, g, h = 20 μm, i–m = 10 μm.

Pleosporales Luttr. ex M.E. Barr, Prodr. Cl. Loculoasc. (Amherst): 67 (1987)
Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953)

Didymosphaeriaceae was established by Munk (1953) and typified by *Didymosphaeria* O.E. Erikss. with *D. epidermidis* (Fr.) Fuckel as the type species (Gonçalves et al. 2019, Hongsanan et al. 2020a). After several taxonomic revisions, this family currently consists of 32 genera, which includes terrestrial, aquatic, endophytic, saprotrophic, parasitic, and hemibiotrophic from different hosts (Ariyawansa et al. 2014a, Dong et al. 2020, Hongsanan et al. 2020a). In addition, some species can cause disease in human beings (Hongsanan et al. 2020a). Species of *Didymosphaeriaceae* are mainly characterized by gregarious or scattered, immersed, globose to rarely subglobose, dark brown to black ascomata. The peridium is composed of two to three-layered dark brown to black cells of *textura angularis* or *textura intricata*. Asci are 2–8-spored, bitunicate, fissitunicate, cylindric or oblong, pedicellate, with an ocular chamber. Ascospores are

hyaline, brown to reddish-brown or dark yellowish-brown, one to several septa, oblong, phragmosporous or muriform, with or without a gelatinous sheath (Ariyawansa et al. 2014b). The asexual morphs are coelomycetous and hyphomycetous (Ariyawansa et al. 2014b, Crous et al. 2017a, Zhang et al. 2024).

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

Paraphaeosphaeria was introduced by Eriksson (1967) based on the type species *P. michotii*. To date, 38 taxa have been described (http://www.speciesfungorum.org/Index.htm, September 2024), of which some species have been transferred to *Phaeosphaeriopsis* (*Phaeosphaeriaceae*), *Leptosphaeria* (*Leptosphaeriaceae*), *Neophaeosphaeria* (*Neophaeosphaeriaceae*), *Chaetoplea* (*Phaeosphaeriaceae*) or *Heptameria* (*Dothideomycetes incertae sedis*) based on ascosporous and conidial morphology. *Paraphaeosphaeria* species are pathogens, saprobes or endophytes on a wide range of woody, herbaceous, lichens hosts, and soil (Kohlmeyer et al. 1999, Ramaley 1997, Tan & Shivas 2022, Verkley et al. 2014, Wanasinghe et al. 2018). They are frequently isolated from dead leaves, stems, senescent culms, twigs, and spines of *Yucca gloriosa* L., *Helianthus maximiliani* Schrad., *Typha latifolia* L., *Juncus roemerianus* Scheele, *Rosa canina* Gremli ex Christ, *Liatris scariosa* (L.) Willd., and *Picea abies* (L.) H. Karsten., which cause leaf spots and necrosis, canker or wood rot (Eriksson 1967, Barr 1992, Shearer 1993, Kohlmeyer et al. 1996, Verkley et al. 2014, Wanasinghe et al. 2018, Ding et al. 2019, Merwe et al. 2021). In this study, *Paraphaeosphaeria michotii* (Westend.) O.E. Erikss. was isolated from living leaves of *Chimonobambusa* sp., which is associated with leaf blight.

3. *Paraphaeosphaeria michotii* (Westend.) O.E. Erikss., Arch. Botan. 6: 405 (1967) Fig. 6

Index Fungorum number: IF335615; Facesoffungi number: FoF00058

≡ *Sphaeria michoti* Westend., Bull. Acad. R. Sci. Belg., Cl. Sci., sér. 2 7(5): 87 (1859)

Associated with leaf blight on leaves of *Chimonobambusa* sp. Sexual morph: *Ascomata* 70–150 μm long × 60–110 μm width × 80–120 μm high ($\overline{x}$ = 118 × 94 × 99 μm, n = 30), solitary to gregarious, immersed, globose to subglobose, dark brown to black, unilocular, glabrous. *Peridium* 6.2–13 μm ($\overline{x}$ = 9.7 μm, n = 25) wide, composed of 3–5 layers of brown to hyaline cells of *textura angularis*. *Asci* 55–66 × 11–15 μm ($\overline{x}$ = 61 × 13 μm, n = 50), 8-spored, bitunicate, broadly cylindrical to long clavate, with a short pedicel, slightly curved, apically rounded. *Ascospores* 12–19 × 4.3–5.4 μm ($\overline{x}$ = 16 × 5.1 μm, n = 50), 2-septate, constricted at the septum, elliptical, brown, smooth-walled, with many guttules, upper cell longer than the lower cell, surrounded by a thick mucilaginous sheath. Asexual morph: see Tanaka et al. (2015).

Culture characteristics – *Ascospores* germinated on PDA within 24 h at 25 ℃, under 12 h dark/12 h light, and germ tubes produced from sides. *Colonies* growing slowly, attaining 4.5 cm diam after 20 days at 25 ℃, cottony, circular, with a regular edge, brown.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Haihong Village (31°6'44.27"N, 103°44'37.75"E, alt. 781 m), on leaves of *Chimonobambusa* sp., 30 June 2022, Qian Zeng, ZQ202206010 (SICAU 23-0008), living culture, SICAUCC 23-0007.

GenBank numbers – SICAUCC 23-0007 – ITS = OR134752, LSU = OR134742, SSU = OR162594, *tef*1-α = OR134879, *tub*2 = OR134882, *act* = OR134883.

Notes – In the phylogenetic tree, the new strain SICAUCC 23-0007 is nested within *Paraphaeosphaeria michotii* strains with 100% MLBS/1.00 BYPP support (Fig. 7), and the specimen was similar to the description of *P. michotii* reported by Ariyawansa et al. (2014a). Nucleotide comparisons of ITS and LSU (SICAUCC 23-0007) also showed a high homology with the sequences of *P. michotii* (MFLUCC 13-0349, ex-type), with a similarity of 99.3% (545/549, 0 gap), and 100% (1286/1286, 0 gap), respectively.

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

Barr (1979) established *Phaeosphaeriaceae*, a large and important family in the order *Pleosporales* with diverse lifestyles mainly being saprobic, parasitic, endophytic or hyperparasitic

(Hongsanan et al. 2020b). Apart from their cosmopolitan distribution, *Phaeosphaeriaceae* taxa are morphologically and phylogenetically highly diverse. Currently, more than 80 genera are accommodated in this family, collected on stems, culms, branches, leaves, and flowers of a wide range of herbaceous and woody hosts (Phookamsak et al. 2014, Yang et al. 2019a). Some species in this family are pathogens of economically important plants and humans (Phookamsak et al. 2014, 2017, Hongsanan et al. 2020b). The morphological characters of *Phaeosphaeriaceae* are often ambiguous, with overlapping characters of *Leptosphaeriaceae* and *Pleosporaceae* (Ariyawansa et al. 2015). *Phaeosphaeriaceae* has been subjected to various taxonomic changes since its establishment. However, genera in this family can be distinguished based on multi-gene phylogenetic analyses coupled with morphology, and many new taxa have been introduced (Crous et al. 2018, Hyde et al. 2020a, b).

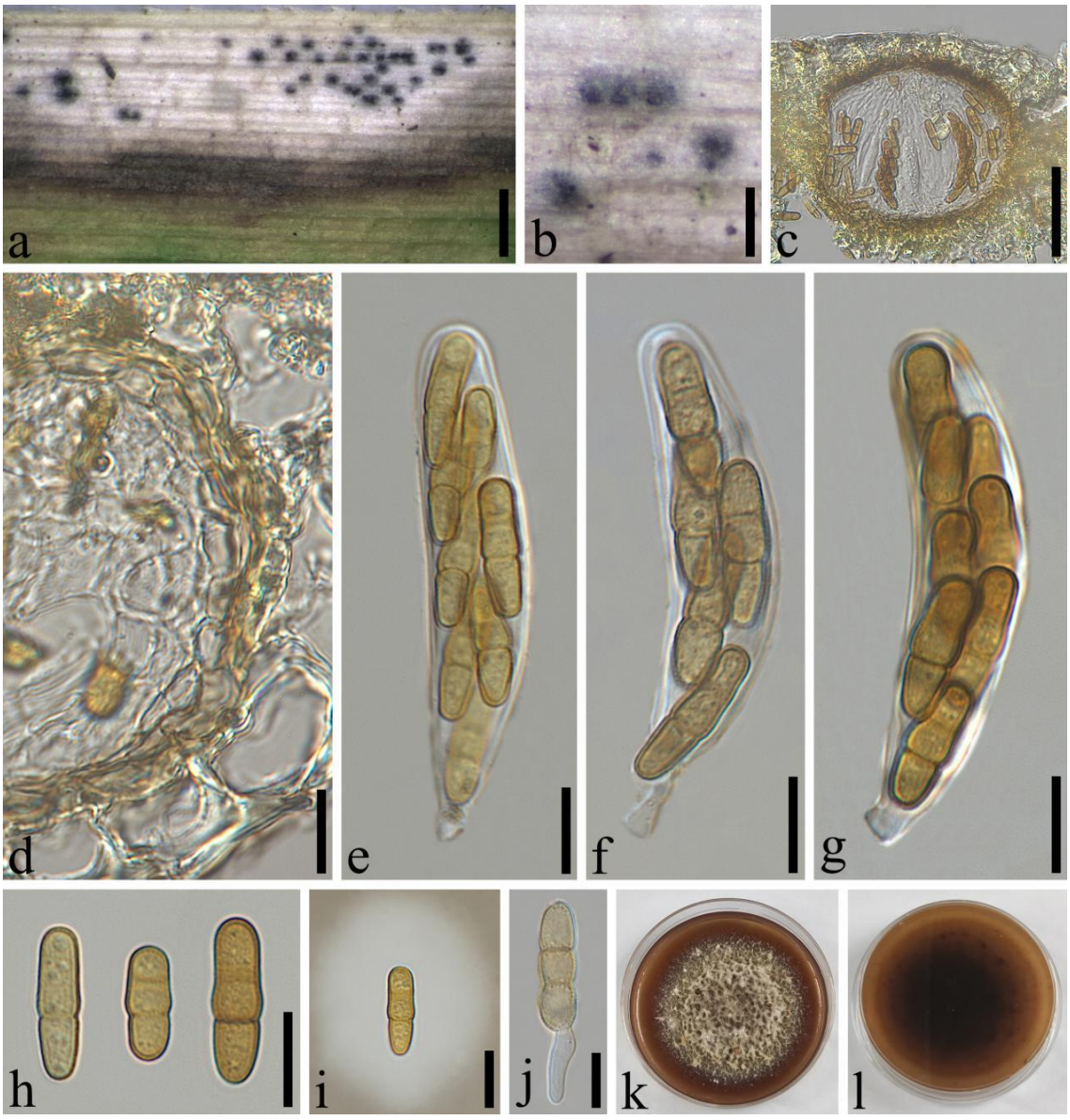

Figure 6 – *Paraphaeosphaeria michotii* (SICAU 23-0008). a, b Ascomata on host. c Vertical section of ascoma. d Peridium. e-g Asci. h, i Ascospores. j Germinating ascospore. k, l Colonies on PDA (k obverse, l reverse). Scale bars: a = 500 µm, b = 200 µm, c = 50 µm, d–j = 10 µm.

Neosetophoma Gruyter, Aveskamp & Verkley, Mycologia 102(5): 1075 (2010)

Neosetophoma was introduced by Gruyter et al. (2010) to accommodate *N. samarorum* (Desm.) Gruyter, Aveskamp & Verkley. *Neosetophoma* species are characterized by globose to

irregular conidiomata, with papillate ostioles and yellowish conidia, attenuate at one end (Liu et al. 2015, Wijayawardene et al. 2016). Tibpromma et al. (2017) introduced *N. garethjonesii* Tibpromma, E.B.G. Jones & K.D. Hyde as the first report of the sexual morph of *Neosetophoma*. To date, 25 species are known in this genus (http://www.speciesfungorum.org/Index.htm, September 2024), which has been often reported as a pathogen causing leaf spots of various hosts. In this paper, we provide a new host record of *N. xingrenensis*, which was collected from leaves of *Chimonobambusa* sp. as a pathogen associated with leaf blight.

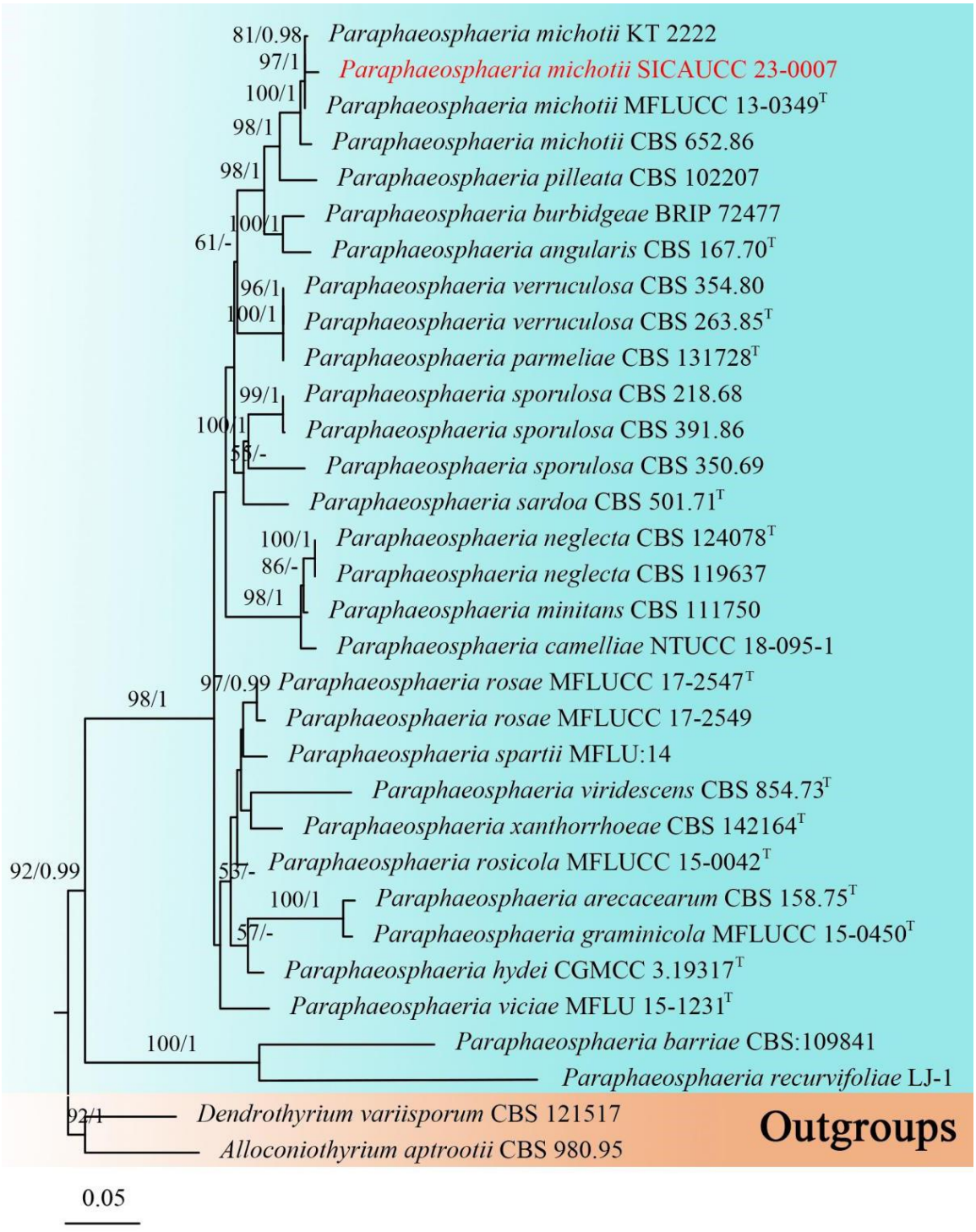

Figure 7 – Phylogenetic analysis of a concatenated aligned dataset (ITS, LSU, *tub*2, and *act*), including 32 taxa within *Paraphaeosphaeria* were conducted and rooted with *Alloconiothyrium aptrootii* (CBS 980.95) and *Dendrothyrium variisporum* (CBS 121517) (*Didymosphaeriaceae*, *Pleosporales*). The alignment contained 2,862 characters (ITS = 668, LSU = 1,370, *tub*2 = 538, *act*

= 286), including gaps. The best scoring RAxML tree with a final likelihood value of -11,570.714677 is presented. The matrix had 899 distinct alignment patterns, with 35.09% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232284, C = 0.256717, G = 0.276672, T = 0.234327, with substitution rates AC = 1.704827, AG = 3.561548, AT = 1.704242, CG = 1.149008, CT = 6.997958, GT = 1.000000. The gamma distribution shape parameter α = 0.182332, and the tree length = 2.125972. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequences are written in red.

4. ***Neosetophoma xingrenensis*** J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu [as '*xingrensis*'], Mycosphere 9(2): 335 (2018) Fig. 8

Index Fungorum number: IF662890; Facesoffungi number: FoF14786

Associated with leaf blight of *Chimonobambusa* sp. Sexual morph: *Ascomata* 90–165 μm long × 70–150 μm width × 90–120 μm high ($\bar{x}$ = 121 × 105 × 107 μm, n = 30), separate, gregarious to confluent, globose to subglobose, dark brown to black, superficial, unilocular, glabrous. *Ostiole* single, circular, centrally located. *Peridium* 4.6–12 μm ($\bar{x}$ = 9.1 μm, n = 30) wide, outer stratum comprising thick-walled, pseudoparenchymatous cells, and an inner stratum composed of 2–5 layers, with brown cells of *textura angularis*. *Hamathecium* 2.2–4.6 μm wide, numerous, embedded in a gelatinous matrix, hyaline, unbranched, septate. *Asci* 49–69 × 8.7–11 μm ($\bar{x}$ = 59 × 9.6 μm, n = 30), 8-spored, bitunicate, cylindrical, curved, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 16–24 × 3.7–4.7 μm ($\bar{x}$ = 20 × 4.2 μm, n = 50), overlapping biseriate, straight to slightly curved, hyaline when young and turn pale brown when mature, fusiform, 1–3-septate, not constricted at the septum, rough-walled, verruculose, with narrowly rounded ends, surrounded by gelatinous sheath attached. Asexual morph: Undetermined.

Cultural characteristics – Ascospores germinate in sterilized water within 24 h at 25 ℃, under 12 h light/12 h dark. Colonies grow slowly on PDA, reaching 3.5 cm after 15 days at 25 ℃, under 12 h light/12 h dark, circular, white aerial mycelium, brown.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Haihong Village (31°6'44.27"N, 103°44'37.75"E, alt. 781 m), on leaves of *Chimonobambusa* sp., 30 June 2022, Qian Zeng, ZQ202206011 (SICAU 23-0009), living culture SICAUCC 23-0008.

GenBank numbers – SICAUCC 23-0008 – ITS = OR134755, LSU = OR134746, SSU = OR162598, *tef*1-α = OR134880, *rpb*2 = OR424352.

Notes – *Neosetophoma xingrenensis* was described by Hyde et al. (2018) based on morphological characteristics and molecular phylogeny. The strain SICAUCC 23-0008 clustered with ex-type strain (GZCC 18-0110) with 91% MLBS and 0.99 BYPP support (Fig. 9). Morphological characteristics of the sexual morph in our materials are similar with the description reported by Hyde et al. (2018). However, the strain SICAU 23-0008 differs from *N. xingrenensis* (GZAAS 18-0100, holotype) in having rough-walled, verruculose ascospores, which are surrounded by a gelatinous sheath. Nucleotide comparisons of ITS and LSU (SICAUCC 23-0008) showed a high homology with the sequences of *N. xingrenensis* (GZCC 18-0110, ex-type), with a similarity of 98.7% (545/552, 0 gap), 99.8% (904/906, 0 gap), respectively. The PHI test, together with the ITS and LSU sequence data, also revealed statistically significant evidence for recombination between our collection (SICAUCC 23-0008) and closely phylogenetically related species (Fig. 10). Therefore, we identified our strain (SICAUCC 23-0008) as a new strain of *N. xingrenensis* based on morphology and phylogenetic evidence.

Ophiosphaerella Speg., Anal. Mus. nac. B. Aires, Ser. 3 12: 401 (1909)

Ophiosphaerella was introduced by Spegazzini (1909) and is typified with *O. graminicola* Speg. Barr (1987), who placed it in the *Phaeosphaeriaceae*, and this classification was supported by later authors (Zhang et al. 2012, Hyde et al. 2014, Phookamsak et al. 2014). The species of *Ophiosphaerella* are characterized by papillate ascomata bearing fissitunicate, cylindrical, pale

brown asci, frequently narrower near the base, with a short furcate pedicel, and filamentous, multi-septate ascospores (Zhang et al. 2023b). To date, 13 species are listed in Species Fungorum (http://www.speciesfungorum.org/Index.htm, September 2024). Most *Ophiosphaerella* species are found on leaves, sheaths, stolons, culms and stems as pathogens or saprobes of *Poaceae* and *Cyperaceae* worldwide (Câmara et al. 2000). Studies associated with plant diseases have shown that bermudagrass spring dead spot (SDS) caused by *Ophiosphaerella herpotricha*, *O. korrae*, and *O. narmari*, and root rot of *Hordeum vulgare* L. caused by *O. korrae* (Flores et al. 2015, Hong et al. 2018). In this study, we report our collections as new host records of *O. taiwanensis* from leaf-sheath of *Chimonobambusa purpurea* Hsueh & T. P. Yi and *Ophiosphaerella taiwanica* from a leaf-sheath of *C. pachystachys* Hsuch et W. P. Zhang.

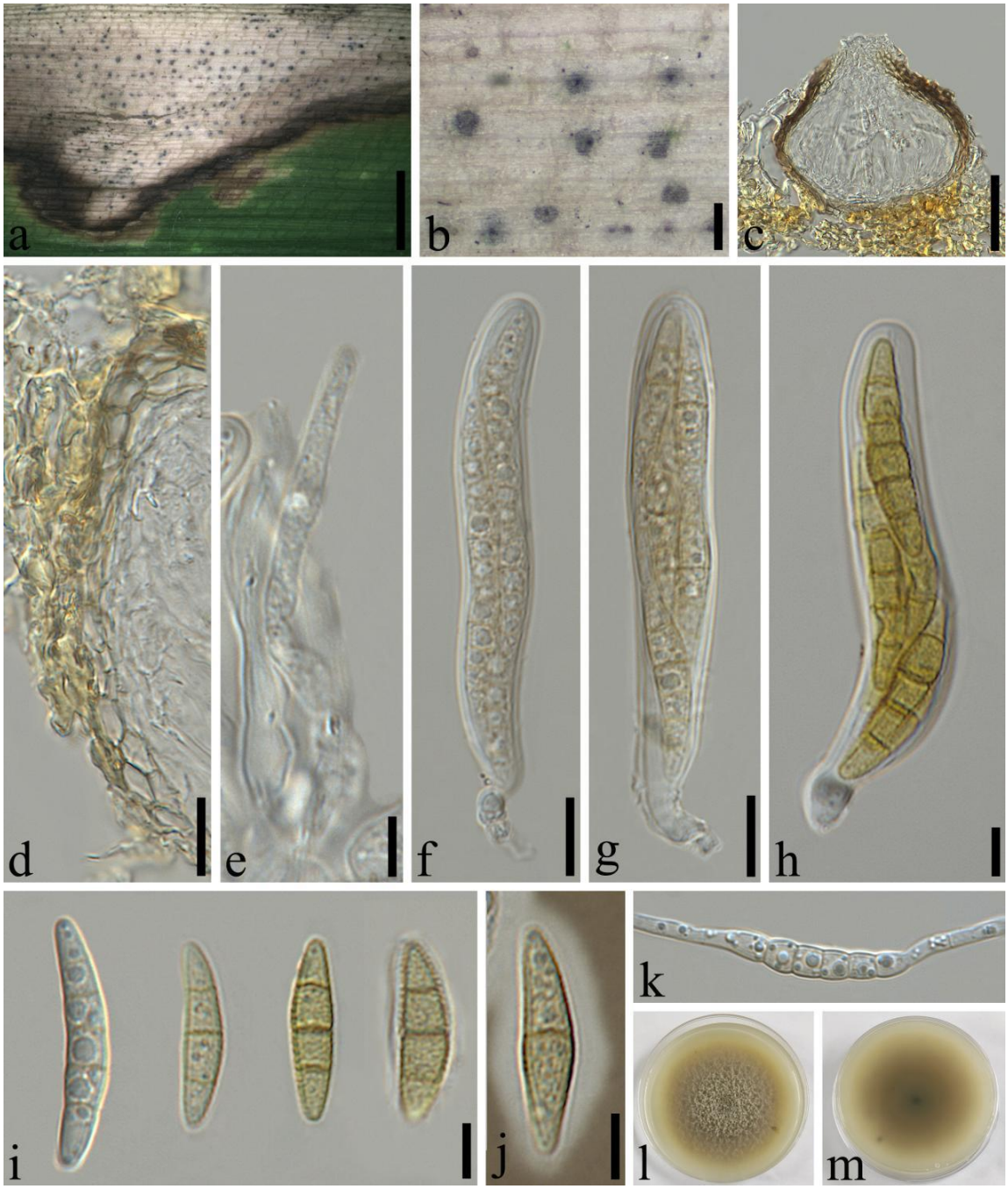

Figure 8 – *Neosetophoma xingrenensis* (SICAU 23-0009). a, b Ascomata on host. c Vertical sections of ascoma. d Peridium. e Paraphyses. f–h Asci. i Ascospores with echinate walls. j Ascospore with sheath in Indian ink. k Germinating ascospore. l, m Colonies on PDA (l obverse, m reverse). Scale bars: a = 2 mm, b = 200 µm, c = 50 µm, d, f–g, j = 10 µm, e, h–i = 5 µm.

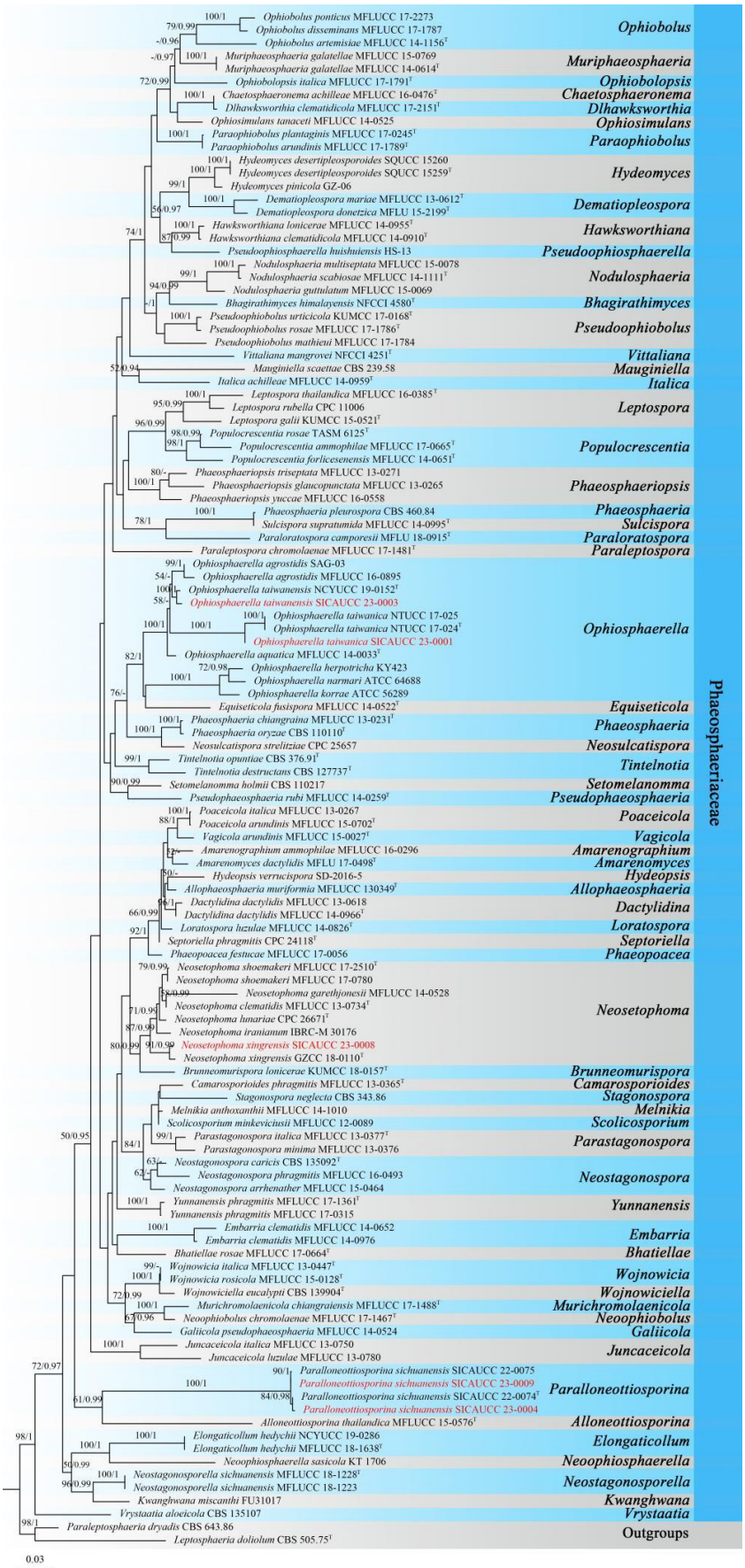

Figure 9 – Phylogenetic analyses of a concatenated aligned dataset (LSU, SSU, ITS, and *tef*1-α) comprising 118 taxa within *Phaeosphaeriaceae*, which is rooted with *Leptosphaeria doliolum* (CBS

505.75) and *Paraleptosphaeria dryadis* (CBS 643.86) (*Leptosphaeriaceae, Pleosporales*). The alignment contained 4,992 characters (LSU = 1,440, SSU = 1,550, ITS = 981, *tef*1-α = 1,021), including gaps. The best scoring RAxML tree with a final likelihood value of -37,360.918405 is presented. The matrix had 2,160 distinct alignment patterns, with 44.83% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246581, C = 0.237955, G = 0.264195, T = 0.251270, with substitution rates AC = 0.952193, AG = 2.965288, AT = 1.941930, CG = 0.746435, CT = 5.955386, GT = 1.000000. The gamma distribution shape parameter α = 0.188871, and the tree length = 4.757141. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequences are written in red.

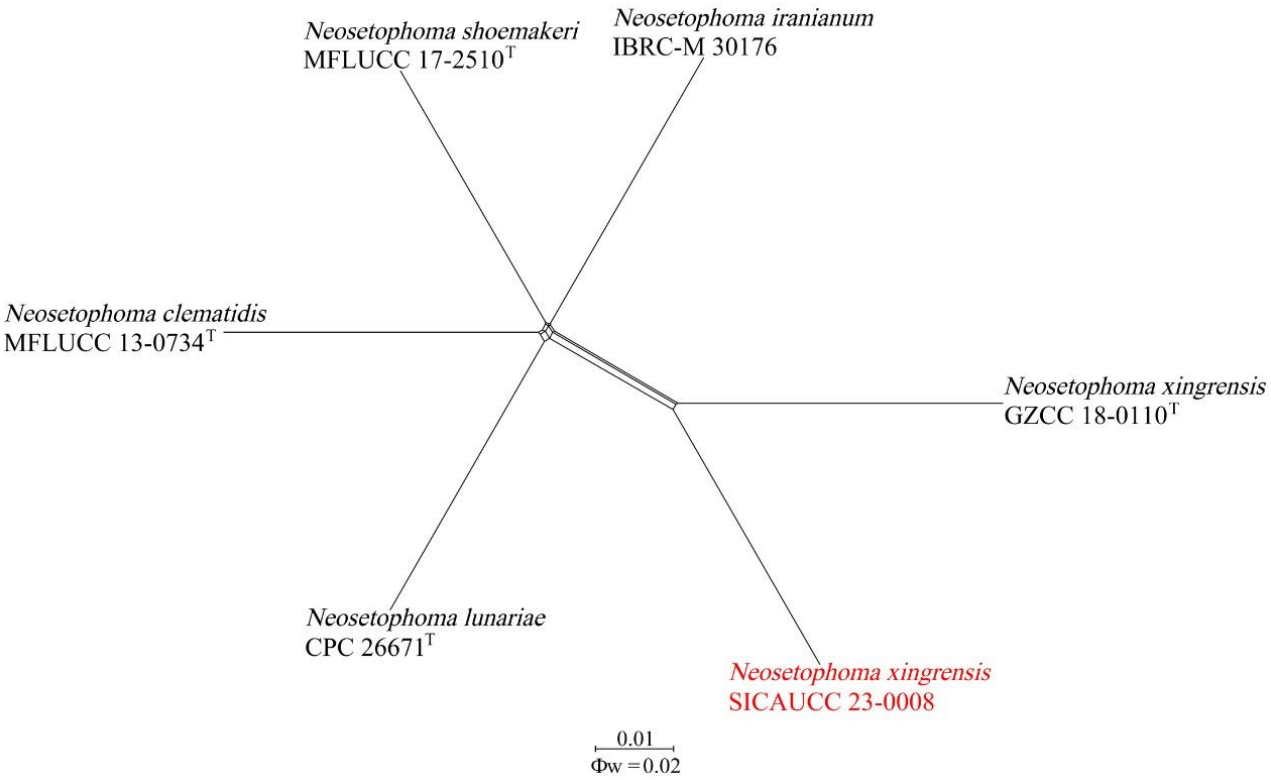

Figure 10 – The splits graph from the pairwise homoplasy index (PHI) test generated from the concatenated genes set of ITS and LSU sequence data of closely related species of *Neosetophoma* using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequence is written in red.

5. *Ophiosphaerella taiwanensis* Tennakoon, C.H. Kuo & K.D. Hyde, MycoKeys 70: 73 (2020) Fig. 11

Index Fungorum number: IF557488; Facesoffungi number: FoF14787

Associated with leaf blight on the tip of branches on leaf-sheath of *Chimonobambusa purpurea*, possibly associated with *Harmolita* spp. Sexual morph: *Ascomata* 320–400 μm high, 170–280 μm diam, solitary, scattered, pyriform, uniloculate, glabrous, dark brown to black, immersed to obviously erumpent through host epidermis with papilla, ostiole in center, periphysate. *Peridium* 10–24 μm thick, composed of brown to dark brown cells of *textura angularis*, hyaline towards the inside, usually fusing from the host tissues in outside. *Hamathecium* composed of anastomosed cellular pseudoparaphyses, 2.3–5.2 μm wide at base, narrower towards the apex, septate, embedded in a hyaline gelatinous matrix. *Asci* 140–180 × 8–10.5 μm ($\overline{x}$ = 158.5 × 9.2 μm, n = 50), 8-spored, bitunicate, cylindrical to cylindrical-clavate, short pedicellate, J- with Melzer's

reagent. *Ascospores* 140–180 × 2.4–3.1 μm ($\bar{x}$ = 155.3 × 2.8 μm, n = 50), 13–15-septate, fasciculate, spiraled, scolecosporous, filiform, pale brown to brown. Asexual morph: Undetermined.

Culture characteristics – *Ascospores* germinated with germ tubes developed from each cell of ascospores in sterilized water within 12 hours at 25 ℃. *Colonies* on PDA moderately grown, reaching 6 cm after incubation for 3 weeks at 25 ℃, and circle, raised, entire, white in margin, grayish white at the center, and reverse gray at the margin, brown to dark brown at the center.

Material examined – China, Sichuan Province, Chengdu City, Pengzhou City, Wenjingjiang Town, Shizhu Village (103°26'22.55"E 30°45'26.71"N, alt. 805 m), on leaf-sheath of *Chimonobambusa purpurea*, 29 October 2020, Chunlin Yang, YCL202010002 (SICAU 23-0003), living culture SICAUCC 23-0003.

GenBank numbers – SICAUCC 23-0003 – ITS = OR134753, LSU = OR134744, SSU = OR162596, *tef*1-α = OR134875, *rpb*2 = OR424348, *tub*2 = OR424349.

Notes – *Ophiosphaerella taiwanensis* was reported by Tennakoon et al. (2020). Morphologically, our observations are identical to the sexual descriptions provided by Tennakoon et al. (2020). Nucleotide comparisons of ITS, LSU, SSU, and *tef*1-α (SICAUCC 23-0003) showed a high homology with the sequences of *Ophiosphaerella taiwanensis* (NCYUCC 19-0152, ex-type), with a similarity of 98.8% (488/494, 0 gap), 100% (796/796, 0 gap), 100% (950/950, 0 gap), and 99.4% (615/619, 0 gap), respectively. In the phylogenetic trees, our strain SICAUCC 23-0003 clustered with the *Ophiosphaerella taiwanensis* in a clade with 100% MLBS and 1.00 BYPP support value (Fig. 9).

6. ***Ophiosphaerella taiwanica*** Ariyawansa & E.B.G. Jones, Phytotaxa 413(1): 44 (2019) Fig. 12

Index Fungorum number: IF831499; Facesoffungi number: FoF14788

Associated with leaf blight on leaf-sheath of *Chimonobambusa pachystachys*, possibly associated with *Harmolita* spp. Sexual morph: *Ascomata* 190–440 μm long × 150–350 μm width × 350–450 μm high ($\bar{x}$ = 299 × 278 × 408 μm, n = 20) (including neck), solitary to gregarious, globose, coriaceous, semi-immersed to immersed with erumpent neck, visible as black dots, unilocular, brown to dark brown, with centrally opening ostiole. *Ostioles* 132–232 μm ($\bar{x}$ = 165 μm, n = 20) diam, papillate; ostiolar canal filled with periphyses. *Peridium* 17–46 μm ($\bar{x}$ = 30 μm, n = 50) wide, comprising 2–6 layers of brown cells of *textura angularis*. *Hamathecium* of septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 84–180 × 5–8 μm ($\bar{x}$ = 135 × 6.8 μm, n= 20), 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 116–155 × 1.4–3 μm ($\bar{x}$ = 131 × 2.1 μm, n = 30), fasciculate, scolecosporous, parallel or spiral, filiform, pale brown, 10–14-septate, smooth-walled. Asexual morph: Undetermined.

Cultural characteristics – Ascospores germinate on PDA within 12 h at 25 ℃, under 12 h dark/12h light. Colonies grow slowly on PDA, reaching 1.5 cm after 2 weeks at 25 ℃, under 12 h light/12 h dark, and are circular, with cottony texture, surface smooth, dark grey at the center, near margin whitish grey.

Material examined – China, Sichuan Province, Chengdu City, Qionglai City (30°24'50.37"N, 103°8'54.18"E, alt. 1396 m), on leaf-sheath of *Chimonobambusa pachystachys*, 30 May 2022, Yu Deng, DY202205021 (SICAU 23-0001), living culture SICAUCC 23-0001.

GenBank numbers – SICAUCC 23-0001 – ITS = OR134751, LSU = OR134743, SSU = OR162595, *tef*1-α = OR134873, *rpb*2 = OR424346.

Notes – *Ophiosphaerella taiwanica* was described by Ariyawansa & Jones (2019) based on morphological characteristics and molecular phylogenies. The strain SICAUCC 23-0001 clustered with the ex-type strain (NTUCC 17-024) with 100% MLBS and 1.00 BYPP support (Fig. 9). Nucleotide comparisons of ITS, LSU, and *tef*1-α (SICAUCC 23-0001) showed a high homology with the sequences of *O. taiwanica* (NTUCC 17-024), with a similarity of 99.8% (521/522, 0 gap), 99.9% (832/833, 0 gap), and 98.7% (638/646, 0 gap), respectively.

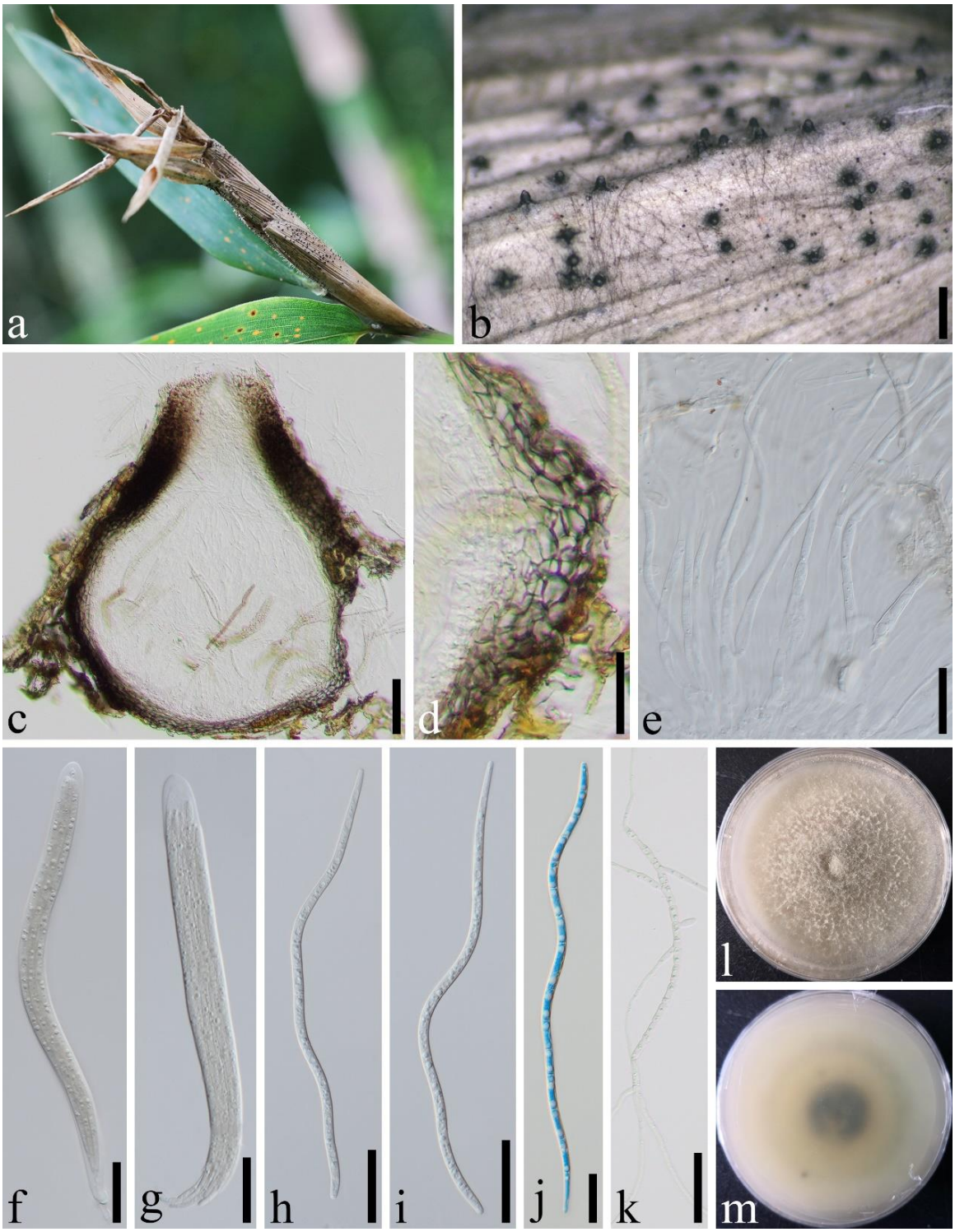

Figure 11 – *Ophiosphaerella taiwanensis* (SICAU 23-0003). a, b Ascomata on host. c Vertical sections of ascoma. d Peridium. e Pseudoparaphyses. f, g Asci with spirally arranged ascospores. h–j Ascospores. k Germinating ascospore. l, m Colonies on PDA (l obverse, m reverse). Scale bars: b = 500 µm, c = 50 µm, d–k = 20 µm.

Paralloneottiosporina Q. Zeng, Y.C. Lv & C.L. Yang, Journal of Fungi 8(702): 16 (2022)

Paralloneottiosporina was introduced by Zeng et al. (2022) for the single species *Pa. sichuanensis* which was found on living to nearly dead leaves of *Phyllostachys violascens* 'Prevernalis'. The genus is characterized by visible raised to superficial, dark brown to black, gregarious, globose to subglobose or dome-shaped ascomata on the host surface. Asci are 8-spored, bitunicate, rounded at the apex, cylindrical, curved, and with a short pedicel. Ascospores are

hyaline, fusiform, 1–2-septate, constricted at the septum, guttulate, smooth-walled, with narrowly rounded ends. Conidia are ellipsoid to ovoid, 1-septate, slightly constricted at the septum, smooth-walled, hyaline, with a rounded apex and a truncated base. *Paralloneottiosporina sichuanensis* can cause leaf blight of *Ph. violascens* 'Prevernalis', *Ph. edulis* and *Ph. tianmuensis* Wang et N. X. Ma, that eventually leads to leaf necrosis and plant decline in severe cases. In this study, *Pa. sichuanensis* was isolated from living culms, branches, and twigs of *Phyllostachys* spp.

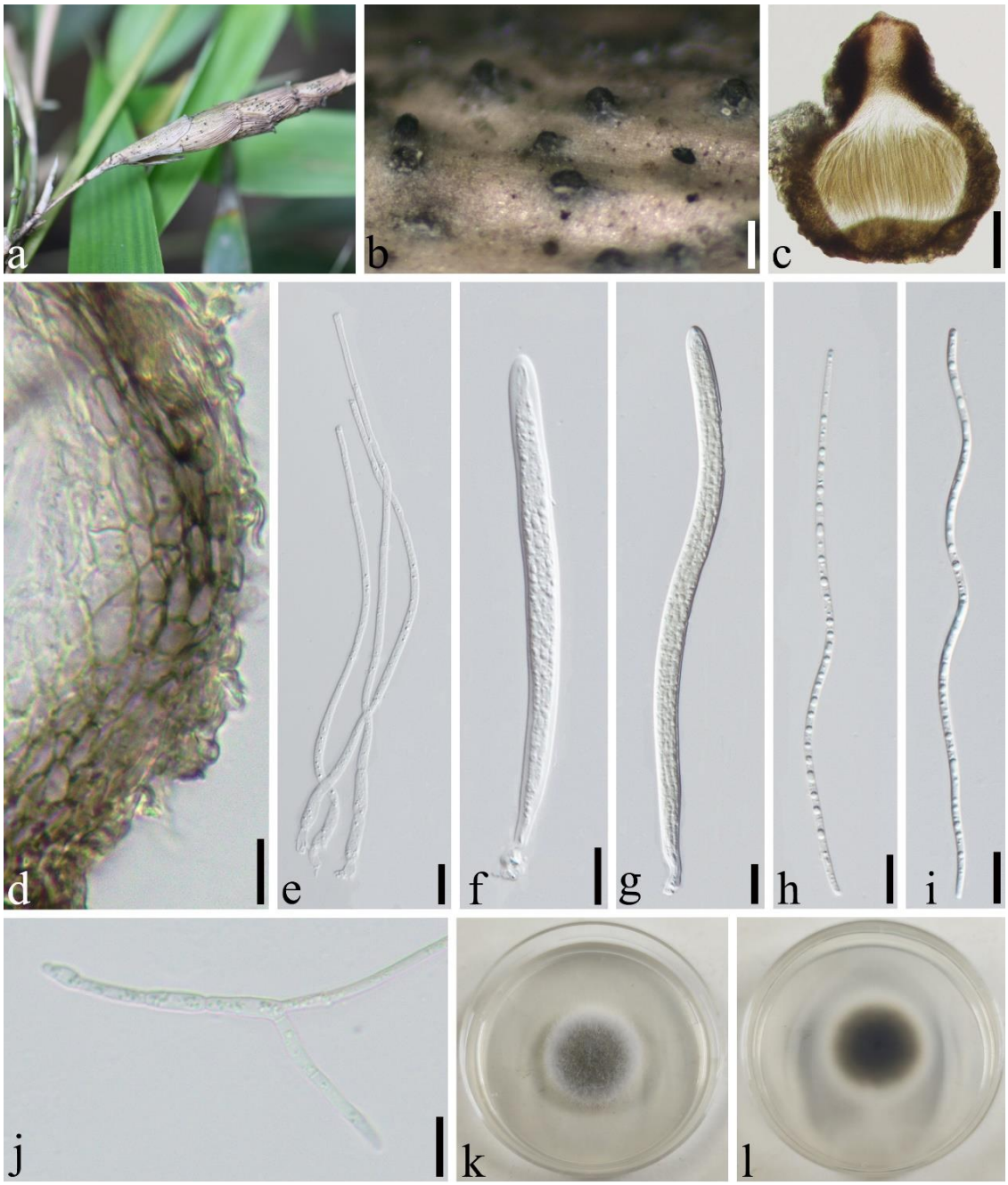

Figure 12 – *Ophiosphaerella taiwanica* (SICAU 23-0001). a, b Ascomata on host. c Vertical sections of ascoma. d Peridium. e Pseudoparaphyses. f, g Asci with spirally arranged ascospores. h, i Ascospores. j Germinating ascospore. k, l Colonies on PDA (k obverse, l reverse). Scale bars: b = 500 µm, c = 50 µm, d–j = 5 µm.

7. *Paralloneottiosporina sichuanensis* Q. Zeng, Y.C. Lv & C.L. Yang, Journal of Fungi 8(702): 16 (2022) Fig. 13

Index Fungorum number: IF559627; Facesoffungi number: FoF14789

Associated with the living and dying culms, branches and twigs of *Phyllostachys* sp. and leaves of *P. violascens* 'Prevernalis'. Sexual morph: see Zeng et al. (2022). Asexual morph: *Conidiomata* 140–340 µm long × 115–260 µm width × 55–120 µm high ($\overline{x}$ = 234 × 182 × 93 µm, n = 30), globose to long ellipsoid, coriaceous, semi–immersed, black, unilocular, gregarious, glabrous. *Pycnidial wall* 10–25 µm ($\overline{x}$ = 16 µm) wide, comprising 2–5 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, ampulliform to subcylindrical, smooth-walled. *Conidia* 12–19 × 5.9–6.9 µm ($\overline{x}$ = 15 × 6.4 µm, n = 50), ellipsoid to ovoid, 1–2-septate, slightly constricted at the septum, smooth, hyaline, with a rounded apex and a truncate base.

Cultural characteristics – Conidia germinated in sterilized water within 24 h at 25 ℃, under 12 h light/12 h dark. Cultures grow slowly on PDA, reach approximately 2.5 cm in 30 days at 25 ℃, under 12 h light/12 h dark, circular, raised, white aerial mycelium, whitish to bright orange-pink on the surface, and brown on the back.

Material examined – China, Sichuan Province, Bazhong City, Tongjiang County, Mashi Town (31°53'47.73"N, 107°19'54.96"E, alt. 685 m), on culms, branches and twigs of *Phyllostachys* sp., 13 July 2022, Qian Zeng, ZQ2022070109 (SICAU 23-0010), living culture SICAUCC 23-0009. China, Sichuan Province, Chengdu City, Chongzhou City, Yangma Base of Chengdu Academy of Agriculture and Forestry Science (30°40'44.94"N, 103°44'11.92"E, alt. 540 m), on the leaves of *P. violascens* 'Prevernalis', 30 April 2022, Chunlin Yang, YCL202204002 (SICAU 23-0004), living culture SICAUCC 23-0004.

GenBank numbers – SICAUCC 23-0009 – ITS = OR134756, LSU = OR134747, SSU = OR162599, *tef*1-α = OR134881, *rpb*2 = OR424353; SICAUCC 23-0004 – ITS = OR134754, LSU = OR134745, SSU = OR162597, *tef*1-α = OR134876, *rpb*2 = OR424350.

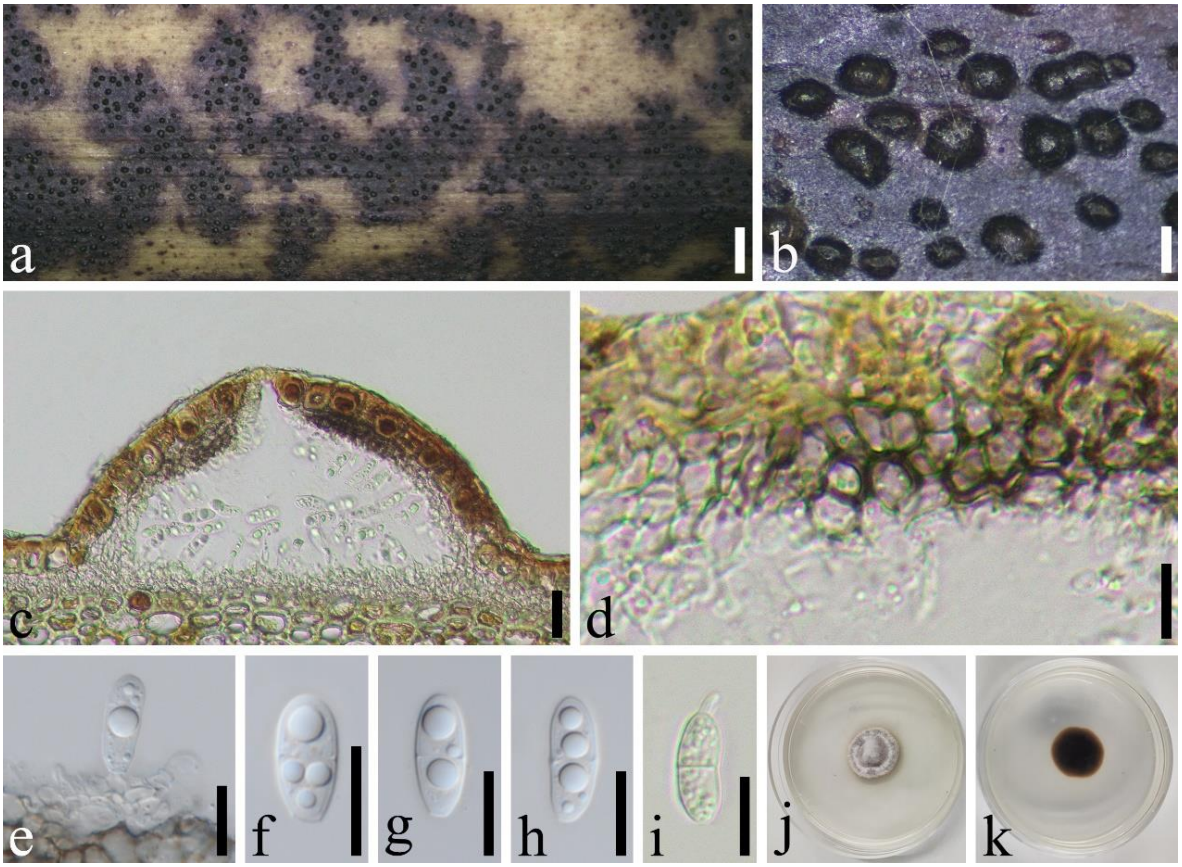

Figure 13 – *Paralloneottiosporina sichuanensis* (SICAU 23-0010). a, b Conidiomata on host. c Vertical section of conidioma. d Pycnidial wall. e Conidiogenous cell with a developing conidium. f–h Conidia. i Germinating conidium. j, k Colonies on PDA (j obverse, k reverse). Scale bars: a = 1 mm, b = 200 µm, c = 20 µm, d–i = 10 µm.

Notes – Our collections are identical to the descriptions of *Paralloneottiosporina sichuanensis* provided by Zeng et al. (2022). Nucleotide comparisons of ITS, LSU, SSU, and *tef*1-α (SICAUCC 23-0009) showed a high homology with the sequences of *P. sichuanensis* (SICAUCC 22-0074, ex-type), with a similarity of 99.8% (587/588, 0 gap), 99.9% (896/897, 0 gap), 99.9% (999/1000, 0 gap), and 100% (906/906, 0 gap). Nucleotide comparisons of ITS, LSU, SSU, and *tef*1-α (SICAUCC 23-0004) showed a high homology with the sequences of *P. sichuanensis* (SICAUCC 22-0074, ex-type), with a similarity of 99.8% (520/521, 0 gap), 99.8% (814/816, 0 gap), 100% (999/999, 0 gap), and 100% (888/888, 0 gap). Our strains (SICAUCC 23-0009 and SICAUCC 23-0004) clustered with *Paralloneottiosporina sichuanensis* in a clade with 100% MLBS and 1.00 BYPP support value (Fig. 9).

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

Liu et al. (2014) introduced the family to accommodate *Roussoella* Sacc., *Neoroussoella* J.K. Liu et al., and *Roussoellopsis* I. Hino & Katum, and the type genus is *Roussoella*. Jaklitsch & Voglmayr (2016) synonymized *Roussoellaceae* under *Thyridariaceae* based on phylogenetic analysis of limited taxa. However, Tibpromma et al. (2017) argued for the separation of *Roussoellaceae* and *Thyridariaceae* as distinct families within *Pleosporales*. Subsequent studies confirmed this separation using more taxa coupled with morphology and DNA sequences (Hyde et al. 2018, Jiang et al. 2019, Phookamsak et al. 2019, Mapook et al. 2020, Poli et al. 2020). The family is characterized by semi-immersed to immersed, solitary or gregarious, lightly raised, clypeate ascostromata containing trabeculate pseudoparaphyses embedded in a gel matrix, 4–8-spored, long cylindrical to clavate bitunicate asci, with or without obvious fissitunicate dehiscence, and brown to dark brown, 2-celled, ornamented ascospores (Thambugala et al. 2017). Members of this family are widely distributed on bamboo and palm hosts.

Roussoella Sacc., Atti Inst. Veneto Sci. lett., ed Arti, Sér. 6 6: 410 (1888)

Roussoella was introduced by Saccardo & Paoletti (1888) with *R. nitidula* Sacc. & Paol. as the type species. von Höhnel (1919) transferred an earlier species *Dothidea hysterioides* Ces. to *Roussoella*, and proposed *R. hysterioides* (Ces.) Höhn to be the type of the genus. Later researchers accepted this treatment (Eriksson 1984, Hyde et al. 1996, Tanaka et al. 2009, Hyde et al. 2013). However, Mycobank (2024) and Index Fungorum (2024) lists the type as *R. nitidula*. Miiller & von Arx (1962) placed *Roussoella* in *Amphisphaeriaceae*. Eriksson (1984) referred the genus to *Didymosphaeriaceae*. Liu et al. (2014) analyzed DNA sequences from the ITS, LSU, *tef*1-α, and *rpb*2 loci, and introduced the family *Roussoellaceae* to accommodate *Roussoella*. *Roussoella* is characterized by immersed, gregarious, clypeate ascostromata, containing trabeculate pseudoparaphyses embedded in a gel matrix. The asci are long cylindrical bitunicate without obvious fissitunicate dehiscence, and the ascospores are brown to dark brown, 2-celled ornamented. Currently, 47 taxa have been described in *Roussoella* (http://www.speciesfungorum.org/Index.htm, September 2024), mostly distributed on monocotyledons (mainly bamboos and palms).

8. *Roussoella siamensis* Phook., Jian K. Liu & K.D. Hyde, Phytotaxa 181(1): 18 (2014) Fig. 14

Index Fungorum number: IF550665; Facesoffungi number: FoF01984

Associated with *Bambusa multiplex*, causing culm blight. Sexual morph: *Ascomata* 495–900 μm long × 250–580 μm width × 130–265 μm high ($\bar{x}$ = 644 × 439 × 183 μm, n = 30), immersed, ellipsoid or dome-shaped on host surface, visible as raised, black, unilocular, gregarious, glabrous spots. *Peridium* 7.8–23 μm ($\bar{x}$ = 13 μm, n = 20) wide, with brown cells of *textura angularis*. *Hamathecium* composed of trabeculate pseudoparaphyses, 1.5–2.3 μm ($\bar{x}$ = 2 μm, n = 30) wide, hyaline, dense, numerous, smooth-walled, and embedded in a gelatinous matrix. *Asci* 80–110 × 5.3–7.1 μm ($\bar{x}$ = 98 × 5.8 μm, n = 30), 8–spored, cylindrical, curved, with a short to long pedicel. *Ascospores* 10–14 × 3.7–5 μm ($\bar{x}$ = 12 × 4.4 μm, n = 50), uni-seriate or overlapping, 1-septate, constricted at the septum, elliptical, straight, brown, rough-walled, longitudinally ribbed, with narrow rounded ends. Asexual morph: Undetermined.

Culture characteristics – *Ascospores* germinate in sterilized water within 24 h at 25 ℃, under 12 h dark/12 h light. *Colonies* grow slowly on PDA, reach approximately 2.5 cm in 20 days at 25 ℃, under 12 h dark/12 h light, circular, white aerial mycelium, black brown on the back.

Material examined – China, Sichuan Province, Luzhou City, Xuyong County, New District Yufu Park (28°9'11"N, 105°26'36"E, alt. 390 m), on culms of *Bambusa multiplex*, 26 June 2021, Qian Zeng, ZQ202107117 (SICAU 23-0007), living culture SICAUCC 23-0006.

GenBank numbers – SICAUCC 23-0006 – ITS = OR134757, LSU = OR134748, SSU = OR162600, *tef*1-α = OR134878.

Notes – *Roussoella siamensis* was described by Liu et al. (2014) based on morphological characteristics and molecular phylogeny. The strain SICAUCC 23-0006 clustered with ex-type strain (MFLUCC 11-0149) with high 100% MLBS and 1.00 BYPP support (Fig. 15). Morphologically, our collection is similar to the holotype specimen (MFLU 11-0185). Nucleotide comparisons of ITS LSU, and *tef*1-α (SICAUCC 23-0006) showed a high homology with the sequences of *R. siamensis* (MFLUCC 11-0149), with a similarity of 99.6% (533/535, 0 gap), 99.5% (847/851, 0 gap), and 99.1% (863/871, 0 gap), respectively.

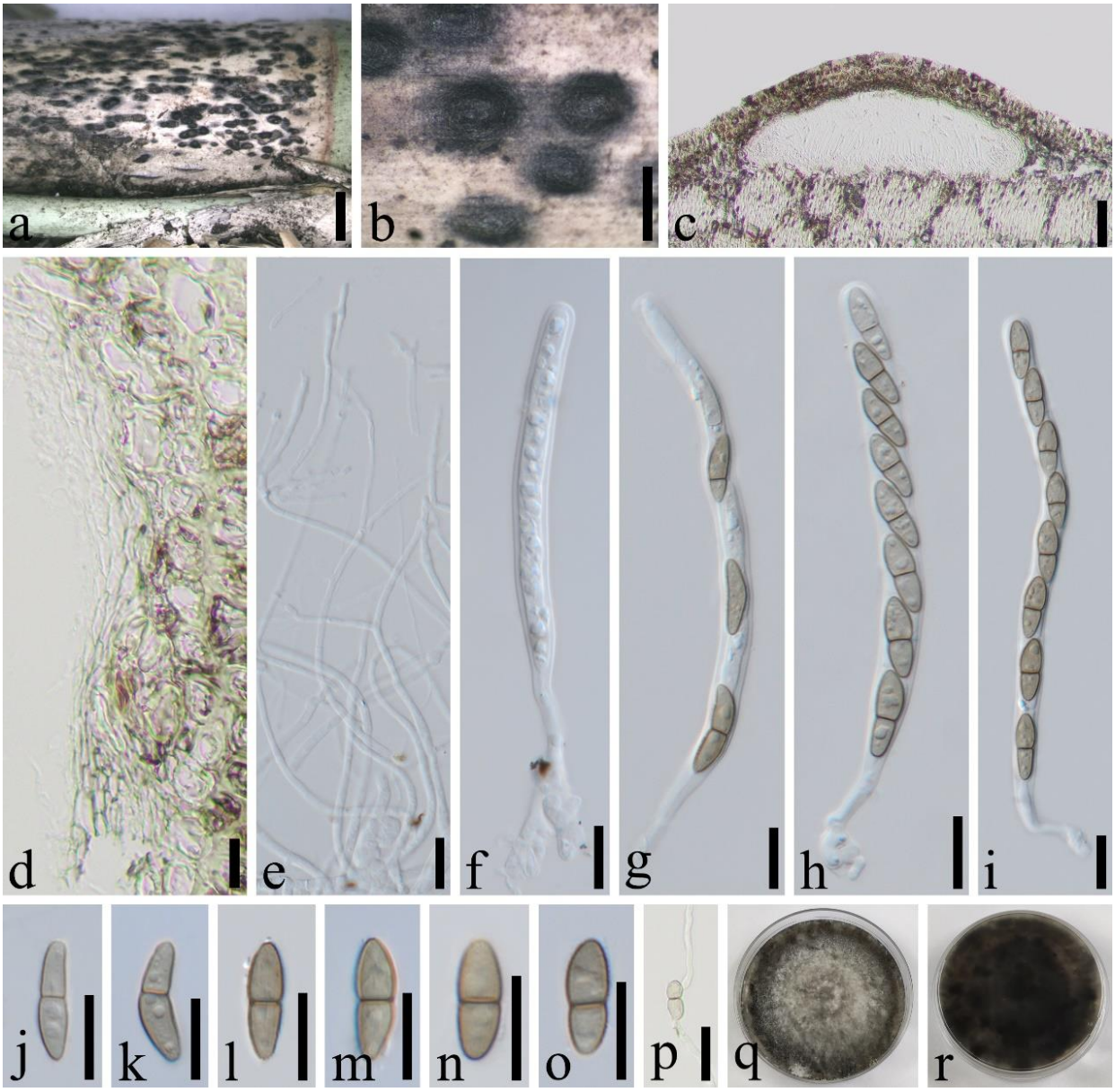

Figure 14 – *Roussoella siamensis* (SICAU 23-0007). a, b Ascomata on host. c Vertical section of ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–o Ascospores. p Germinating ascospore.

q, r Colonies on PDA (q obverse, r reverse). Scale bars: a = 2 mm, b = 500 µm, c = 50 µm, d–p = 10 µm.

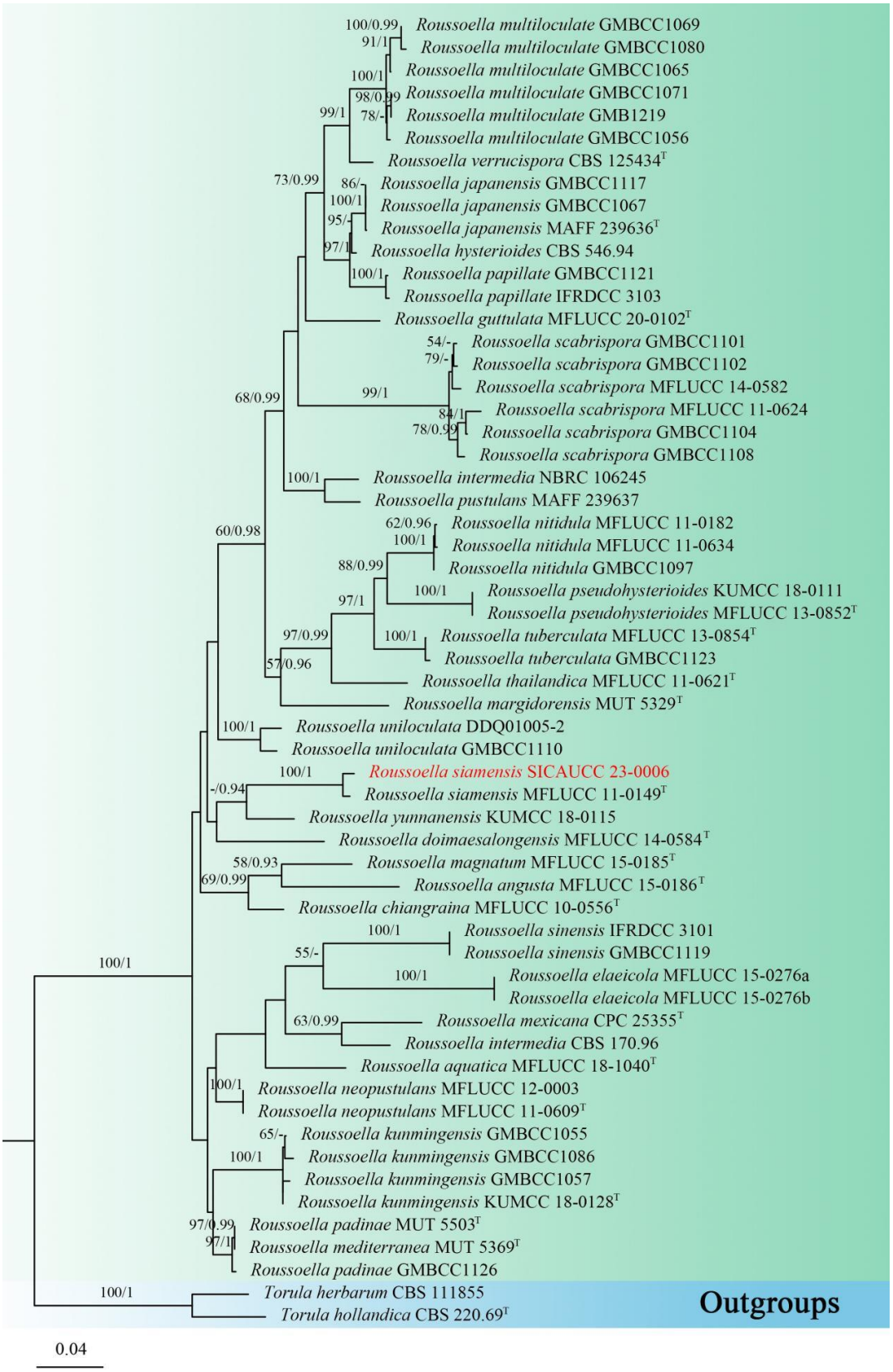

Figure 15 – Phylogenetic analyses of a concatenated aligned dataset (ITS, LSU, and *tef*1-α) comprising 58 taxa within *Roussoella* were conducted for the study, with *Torula herbarum* (CBS

111855) and *T. hollandica* (CBS 220.69) (*Torulaceae*, *Pleosporales*) as outgroup taxa. The alignment contained 3,865 characters (LSU = 1,478, LSU = 1,367, *tef*1-α = 1,020), including gaps. The best scoring RAxML tree with a final likelihood value of -17,527.013013 is presented. The matrix had 1,321 distinct alignment patterns, with 40.70% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234138, C = 0.273406, G = 0.273995, T = 0.218461, with substitution rates AC = 1.099309, AG = 2.459316, AT = 1.508551, CG = 0.883473, CT = 4.730499, GT = 1.000000. The gamma distribution shape parameter α = 0.184117, and the tree length = 2.040260. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequence is written in red.

Shiraiaceae Y.X. Liu, Z Y. Liu & K.D. Hyde, Phytotaxa 103(1): 53 (2013)

Shiraiaceae was introduced by Liu et al. (2013) which is typified by *Shiraia* Henn., and later Ariyawansa et al. (2013) added *Grandigallia* to this family. *Shiraiaceae* differs from other families in *Pleosporales* by forming large fleshy ascostromata on bamboo as an endophyte or parasite. Asci are bitunicate, 6-spored, and ascospores are muriform. This family currently comprises four genera, namely *Grandigallia* M.E. Barr, et al., *Neoshiraia* H.A. Ariyaw., *Rubroshiraia* D.Q. Dai & K.D. Hyde, and *Shiraia*.

Shiraia Henn., Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 28(3): 274 (1900)

Shiraia was introduced by Hennings (1900) and currently includes a single species *S. bambusicola*, which is parasitic on living bamboo branches. The ascostromata are conspicuous large, pinkish, fleshy structures with multiple-locules located near the periphery. The asci are fissitunicate and ascospores are hyaline, and muriform (Liu et al. 2013). *Shiraia bambusicola* is parasitic on branches, leading to the formation of tabasheer in several bamboo species, including *Brachystachyum densiflorum* (Rendle) Keng, *B. densilorum* (Rendle) Keng var. *villosum* S.L., *B. albostriatum* G.H. Lai, and *Sinobambusa yixingensis* C.S. This fungus is found in temperate regions of Asia, such as China and Japan (Kishi et al. 1991). Fruiting bodies of *S. bambusicola* are used as a traditional Chinese medicine. The metabolite hypocrellin has promising applications for anti-cancer treatments (Deininger et al. 2002, Miller et al. 2008).

9. *Shiraia bambusicola* Henn., Bot. Jb. 28(3): 274 (1900) Fig. 16

Index Fungorum number: IF158454; Facesoffungi number: FoF06203

Parasitic, endophytic or symbiotic on branches of *Phyllostachys violascens* 'Prevernalis'. Sexual morph: see Dai et al. (2019). Asexual morph: *Conidiostromata* 1.9–3.6 cm long, 1–2.5 cm wide, 0.7–2 cm high, solitary, superficial, subglobose, long ellipsoid to irregular, tuberculate, fleshy, white to pinkish. *Conidiomata tissue* thick, pinkish, composed of wide, woven hyphae of *textura intricata*. *Locules* in vertical section 185–590 × 145–340 µm ($\overline{x}$ = 343 × 236 µm, n = 20), globose to subglobose, immersed in the peripheral layer of conidiomata. *Wall of locules* 20–57 µm ($\overline{x}$ = 32 µm, n = 20) thick, composed of several layers of hyaline to light brown, small cells of *textura intricata*. *Conidiogenous cells* blastic, cylindrical, hyaline, smooth-walled. *Conidia* 59–80 × 19–36 µm ($\overline{x}$ = 69 × 29 µm, n = 20), fusiform, muriform, hyaline, with irregularly transverse and longitudinal septa, straight to curved, smooth-walled.

Cultural characteristics – Conidia germinated in sterilized water within 8 hours at 25 ℃, under 12 h dark/12 h light. Colonies growing slowly, attaining 3.4 cm diam after 15 days at 25 ℃, under 12 h dark/12 h light, circular, with even margin, floccose at the center, drift white at margin, brown to dark brown from below.

Material examined – China, Sichuan Province, Ya'an City, Yucheng District, Qingjiang Community (30°3'17.52"N, 103°3'48.98"E, alt. 687 m), on living branches of *Phyllostachys*

violascens ‘Prevernalis’, 13 May 2020, Qian Zeng, ZQ202005007 (SICAU 23-0005), living culture SICAUCC 23-0005.

GenBank numbers – SICAUCC 23-0005 – ITS = OR134758, LSU = OR134749, SSU = OR162601, *tef*1-α = OR134877, *rpb*2 = OR424351.

Notes – Morphological features of the asexual morph in our material agree well with the description of *Shiraia bambusicola* reported by several authors (Morakotkarn et al. 2008, Liu et al. 2013, Dai et al. 2019). Nucleotide comparisons of ITS and LSU (SICAUCC 23-0005) showed a high homology with the sequences of *S. bambusicola* (GZAAS2.0708, ex-type), with a similarity of 100% (492/492, 0 gap), and 99.9% (843/844, 0 gap), respectively. In the phylogenetic tree, the new strain SICAUCC 23-0005 clustered in the clade of *S. bambusicola* with 100% MLBS/1.00 BYPP support value (Fig. 17).

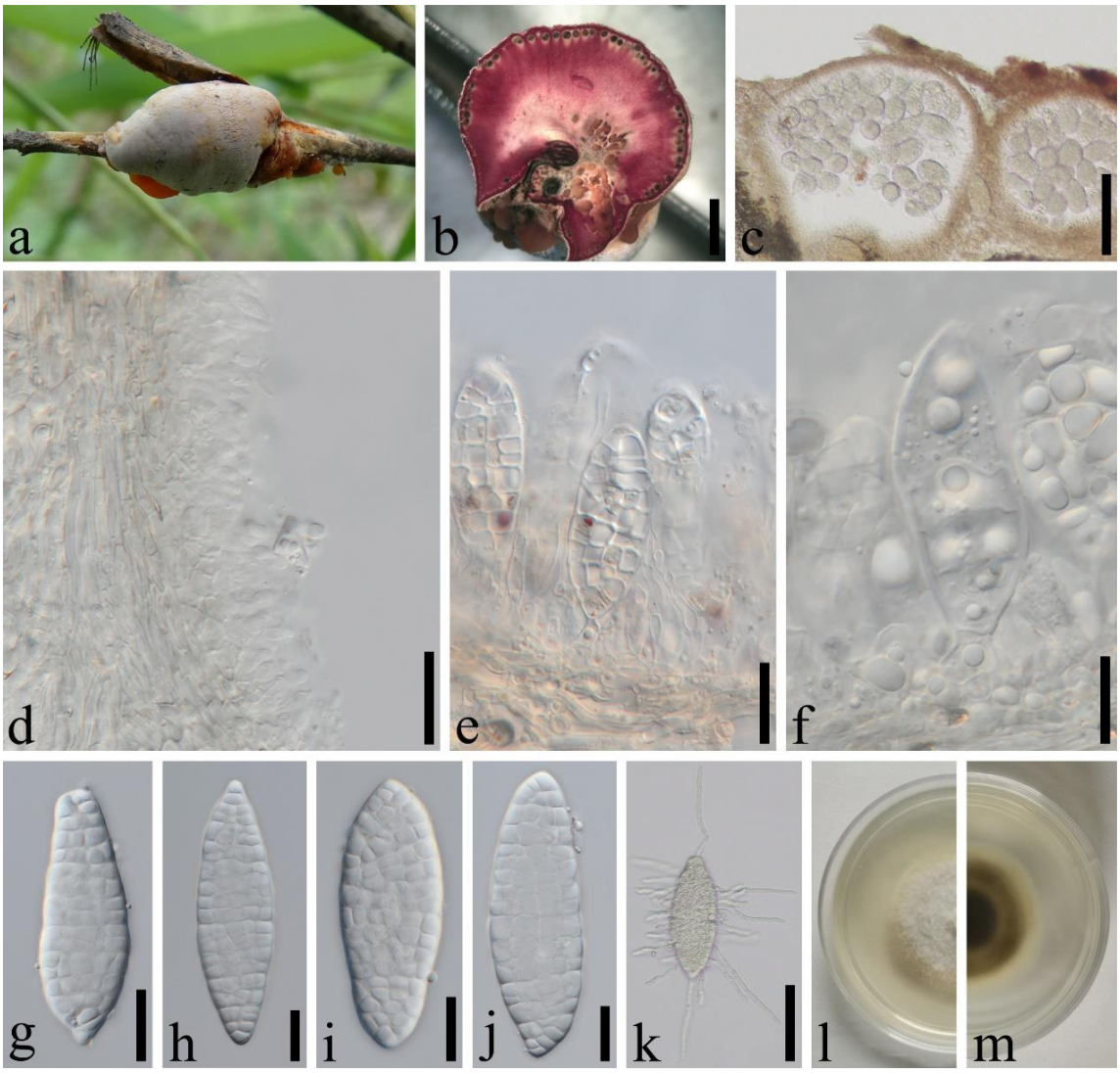

Figure 16 – *Shiraia bambusicola* (SICAU 23-0005). a Fruiting bodies. b, c Vertical sections through conidiostroma d Wall of locule. e, f Conidiogenous cells with developing conidia. g–j Conidia. k Germinating conidium. l, m Colonies on PDA (l obverse, m reverse). Scale bars: b = 3 mm, c = 100 µm, d–k = 20 µm.

Lecanoromycetes

Graphidales Bessey, Univ. Stud. Nebraska 7: 298 (1907)

Gomphillaceae Walt. Watson: 31 (1929)

Gomphillaceae was introduced by Watson (1929) and is an important component of tropical lichen communities, with some genera and species also found in temperate regions (Vězda & Poelt

1987, Lücking 1997, Tønsberg 2016, Xavier-Leite et al. 2018). More than 400 species are recognized, with the majority growing on living leaves of vascular plants in tropical forests and shrublands. Non-foliicolous taxa are typically found on ephemeral substrates, less frequently on bark and rock, and a few lineages are lichenicolous or even mycoparasitic (Etayo 2017, Lendemer 2017, Lücking et al. 2017, Diederich et al. 2018, Suija et al. 2018, Xavier-Leite et al. 2018, Guterres et al. 2020). Members of this family are characterized by apothecioid ascomata with hemiangiocarpous development, a hamathecium consisting of thin, strongly gelatinized and richly branched and anastomosing paraphyses, and nonamyloid asci corresponding to the annelasceous type (Vězda & Poelt 1987, Lücking 1997).

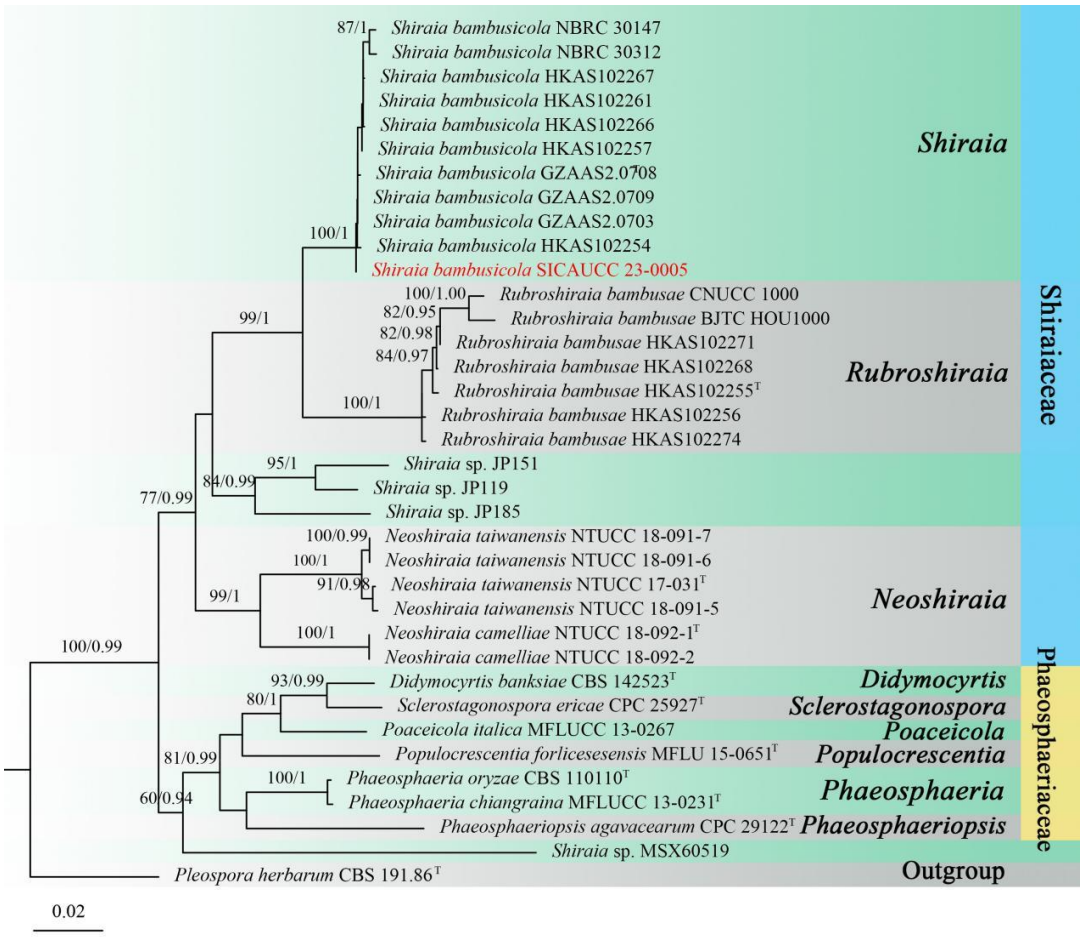

Figure 17 – Phylogenetic analyses were performed on a concatenated aligned dataset comprising combined ITS, LSU, SSU, and *tef*1-α sequence data from *Shiraiaceae* and *Phaeosphaeriaceae*. The alignment contained 4,259 characters (ITS = 679, LSU = 1,057, SSU = 1,494, *tef*1-α = 1,029), including gaps. The best scoring RAxML tree with a final likelihood value of -12,669.208970 is presented. The matrix had 822 distinct alignment patterns, with 38.28% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246263, C = 0.234179, G = 0.262847, T = 0.256710, with substitution rates AC = 1.081601, AG = 2.586788, AT = 1.991793, CG = 0.707425, CT = 4.995270, GT = 1.000000. The gamma distribution shape parameter α = 0.095975, and the tree length = 0.723311. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequence is written in red.

Asterothyrium Müll. Arg., Lichenes Epiphylli Novi: 12 (1890)

Asterothyrium was introduced by Müller (1890) which is typified by *A. argenteum* Müll. Arg. To date, about 15 epithets are known in this genus (http://www.speciesfungorum.org/Index.htm,

September 2024). The majority of *Asterothyrium* species are primarily found in tropical regions, but some are also distributed in temperate regions. They often grow on leaves of vascular plants of dicotyledons (*Lauraceae* and *Annonaceae*), with a few occurrences on poaceous hosts (Hennings 1904a, Lücking 1999, Ferraro & Lücking 2007, Flakus & Lücking 2008, Suto & Ohtani 2018). Most *Asterothyrium* species are primarily known through their sexual morphology, with less information available regarding their asexual characteristics (Hiern & Rendle 1901, Lücking 1992, Ferraro & Lücking 2007, Flakus & Lücking 2008). Due to the absence of DNA based and systematic studies, the phylogeny and classification of *Asterothyrium* have remained largely uncertain.

10. ***Asterothyrium bambusicola*** Q. Zeng & C.L. Yang, sp. nov. Fig. 18

Index Fungorum number: IF901125; Facesoffungi number: FoF14782

Etymology – The specific epithet refers to the bamboo host.

Holotype – SICAU 23-0040

Epiphytic on leaves of *Lingnania intermedia* (Hsueh & Yi) T.P. Yi, causing lichen-spot on leaves. *Thallus* epiphyllous, dispersed into rounded to irregular, scattered, sometimes confluent patches, pale green to green, greyish in margins, corticate, smooth-walled; cortex composed of rectangular cells, 3–7.5 μm × 3–6.5 μm ($\overline{x}$ = 5.7–4.4 μm, n = 50), thick-walled, hyaline, with radiating rows, usually living in symbiosis with algae; pycnidia formed when matured, randomly scattered in thallus. Sexual morph: Undetermined. Asexual morph: *Pycnidia* marginal, adnate, conical with a distinctly coniform beak in the center and a subcircular base, 80–170 μm diam, 85–130 μm high without beak, brown to black. *Pycnidial wall* 14–31 μm thick at the sides, 7–16 μm thick at the base, formed of hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.3–7.2 × 2–3.9 μm ($\overline{x}$ = 6.5–2.8 μm, n = 20), enteroblastic, phialidic, coniform or cylindrical, hyaline, smooth-walled. *Conidia* 6.1–9.3 × 2.4–3.7 μm ($\overline{x}$ = 7.7–3.2 μm, n = 50), ellipsoidal or cylindrical, sometimes slightly flexuous, unicellular, hyaline. Photobiont algae: *Photobiont cells* green, with a subparietal chloroplast bearing a conspicuous central pyrenoid, ellipsoidal to spherical, 7–15.5 × 6–13.5 μm ($\overline{x}$ = 10.4 × 8.7 μm, n = 30) diam.

Culture characteristics – *Conidia* germinated in sterilized water within 12 hours at 25 ℃. *Colonies* on PDA very slowly grown, reaching 0.5 cm after incubation for 70 days at 25 ℃, and subcircle, slightly raised, pulvinate, dense, yellowish, and reverse red pigments produced in PDA.

Material examined – China, Sichuan Province, Leshan City, Jingyan County, Fuxin Town, Fenshanpo (29°1'54.91"N, 103°54'47.74"E, alt. 376 m), on leaves of *Lingnania intermedia*, 11 Mar. 2021, C.L. Yang, YCL202103002 (SICAU 23-0040, holotype), ex-type culture SICAUCC 23-0024.

GenBank numbers – SICAUCC 23-0024 – ITS = OR583158, LSU = OR583159, *rpb*2 = OR587859.

Notes – The taxonomic status of the species in this genus is uncertain because most lack molecular data and have poorly described morphological characteristics. In the phylogenetic tree (Fig. 19), the novel species *Asterothyrium bambusicola* (SICAUCC 23-0024) is closely related to *A. microsporum* (23084) in a subclade (99% MLBS/1.00 BYPP). The PHI test results indicate the absence of significant recombination events between *A. bambusicola* and closely related phylogenetic species (Fig. 20). Comparisons of LSU sequence data of isolate *A. bambusicola* (SICAUCC 22-0040) and *A. microsporum* (23084), the nucleotide differences, after removing unaligned ends, are 1.61% (9/559, 1 gap). Most *Asterothyrium* species lack asexual descriptions, making it challenging to morphologically compare them to *A. bambusicola*, with around 13 species having asexual characteristics documented. *Asterothyrium bambusicola* displays morphological resemblances to *A. atromarginatum* Herrera-Camp. & Lücking, *A. microsporum* R. Sant., and *A. septemseptatum* Lücking, both exhibiting conidia of similar size (Lücking 1999, Herrera-Campos & Lücking 2002, Ferraro & Lücking 2007), but the conidial width of *A. bambusicola* is greater than that of the other three species (6.1–9.3 × 2.4–3.7 μm, 6–8 × 1.8–2

μm, 6–8 × 2–2.5 μm, and 6–9 × 1.5 μm, respectively), and the conidia of *A. bambusicola* are ellipsoidal or cylindrical, while that of *A. atromarginatum* and *A. microsporum* are ellipsoidal to oblong, fusiform for *A. septemseptatum*. In this study, *A. bambusicola* is proposed as a new species mainly based on DNA based differences.

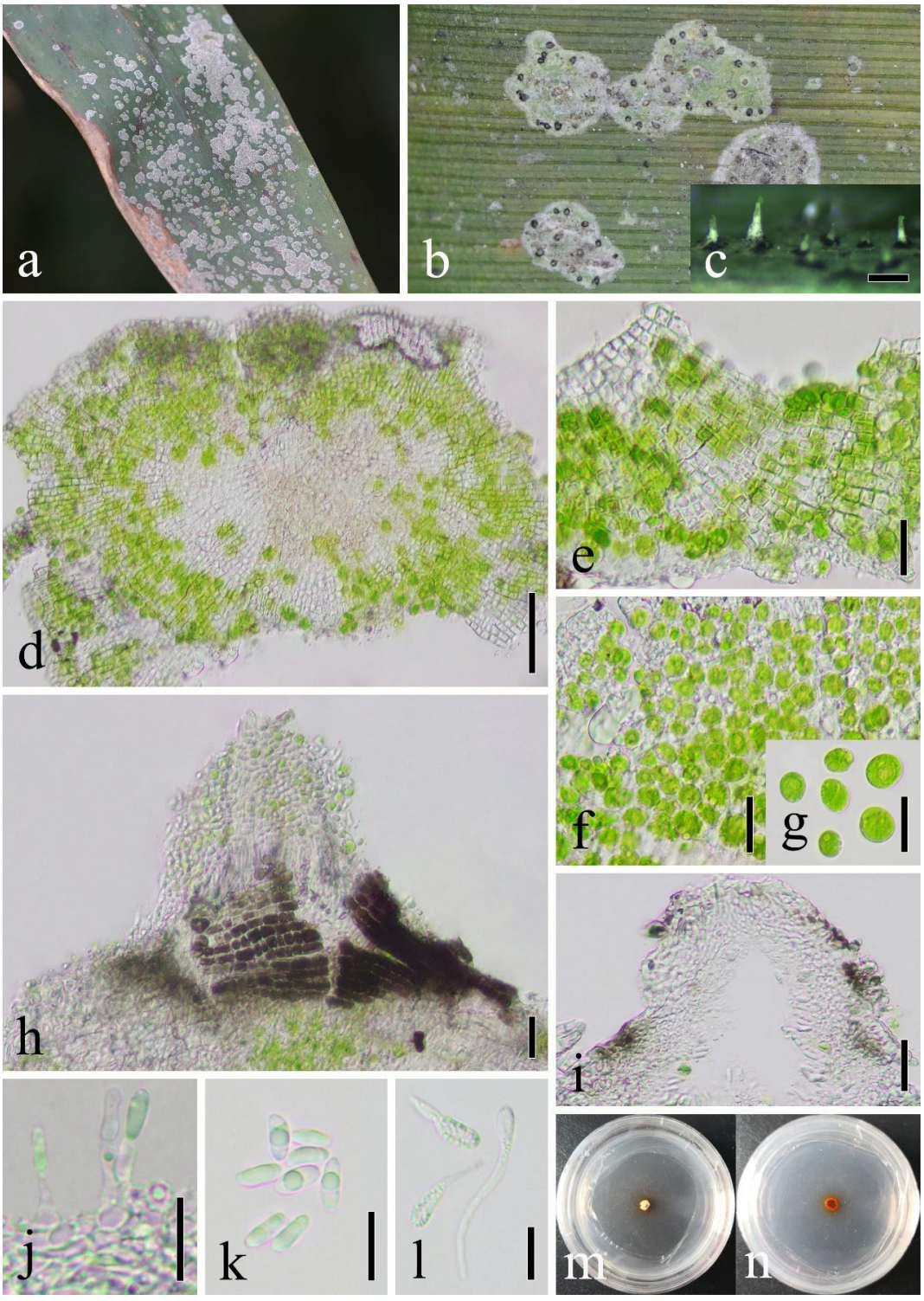

Figure 18 – *Asterothyrium bambusicola* (SICAU 23-0040, holotype). a, b Thallus with conidiomata fixed on the surface of leaves. c Conidiomata with coniform beak. d, e Cortex composed of rectangular cells f, g Photobiont cells mixed in between cortical cells. h, i Vertical sections through conidiomata. j Conidiogenous cells with developing conidia. k Conidia. l Germinating conidia. m, n Colonies on PDA (m obverse, n reverse). Scale bars: c = 200 μm, d = 50 μm, e–i = 20 μm, j–l = 10 μm.

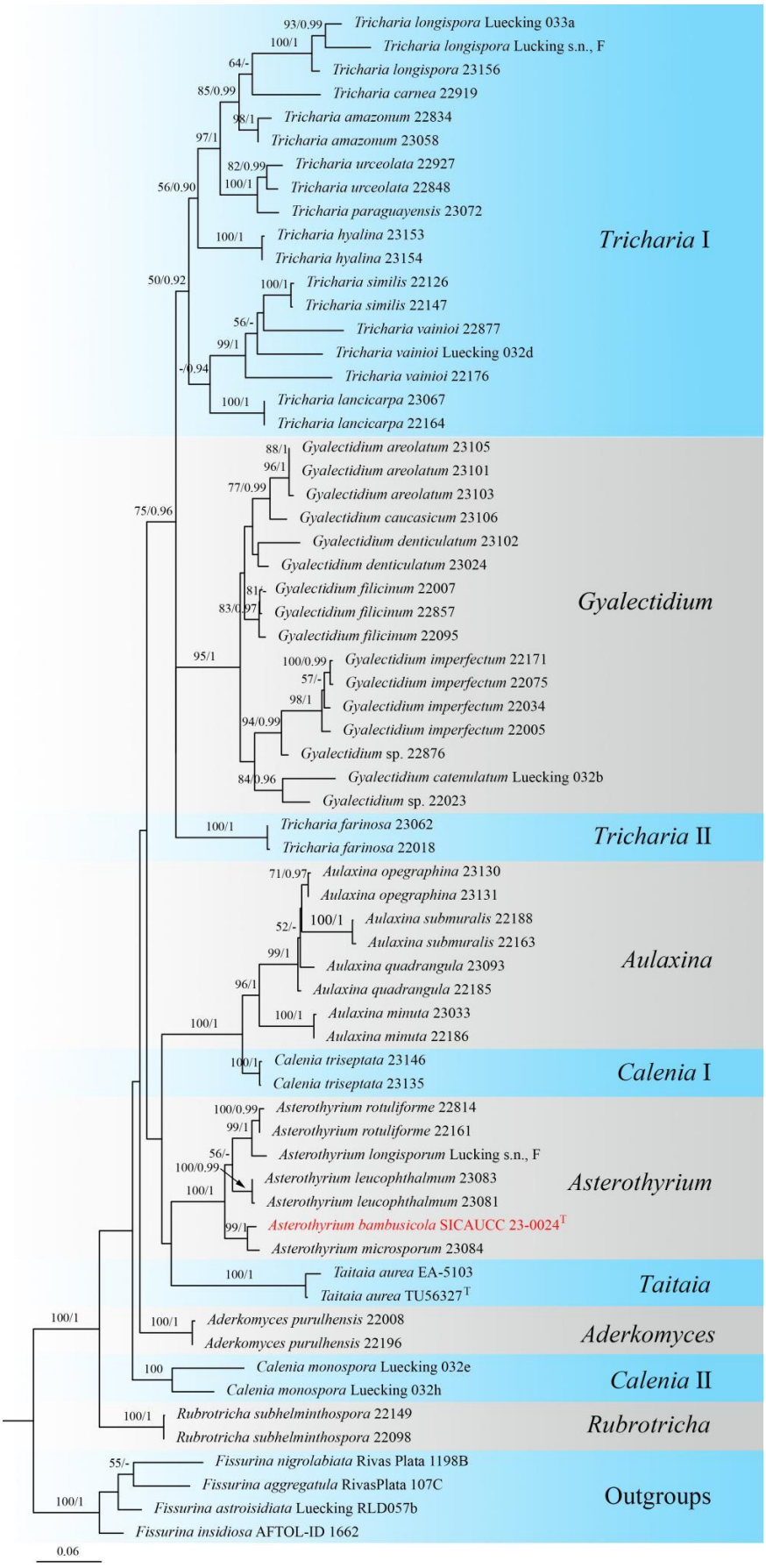

Figure 19 – Phylogenetic analyses of a concatenated aligned dataset (LSU and mtSSU), including 65 taxa within *Gomphillaceae*, were conducted and tree was rooted with *Fissurina aggregatula*

(RivasPlata 107C), *F. astroisidiata* (Luecking RLD057b), *F. insidiosa* (AFTOL-ID 1662), and *F. nigrolabiata* (Rivas Plata 1198B) (*Graphidaceae*, *Ostropales*). The alignment contained 1,898 characters (LSU = 703, mtSSU = 1,195), including gaps. The best scoring RAxML tree with a final likelihood value of -15,000.257300 is presented. The matrix had 939 distinct alignment patterns, with 39.97% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.326406, C = 0.161239, G = 0.228607, T = 0.283748, with substitution rates AC = 1.218158, AG = 4.082530, AT = 2.062913, CG = 0.735637, CT = 6.514119, GT = 1.000000. The gamma distribution shape parameter α = 0.327776, and the tree length = 2.981078. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The ex-type strains are indicated with "T" after the strain number. The newly generated sequence is written in red.

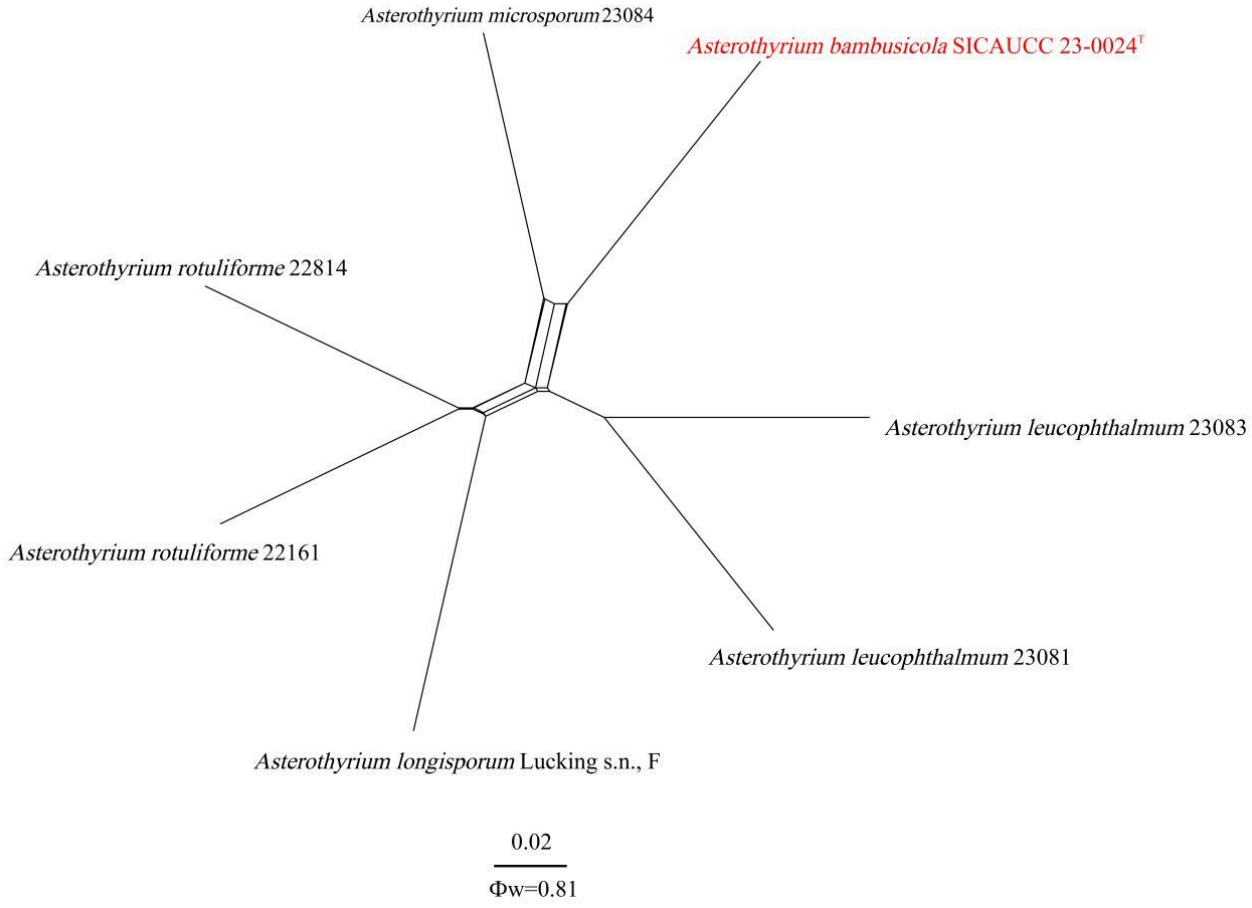

Figure 20 The splits graph for the pairwise homoplasy index (PHI) test was generated from LSU sequence data of closely related species of *Asterothyrium* using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The strain determined in this study is in red. The ex-type strain is marked with "T" after the strain number label.

Odontotrematales Lücking, Critical Reviews in Plant Sciences 38(3): 233 (2019)
Odontotremataceae D. Hawksw. & Sherwood, Mycotaxon 16 (1): 263 (1982)

Odontotremataceae was introduced by Hawksworth & Sherwood (1982) and later treated in detail by Sherwood-Pike (1987). The species of *Odontotremataceae* are mainly saprobes on various dead herbaceous plants and wood or grow as commensals or parasites on lichens and mosses. The apothecia are small and dark with an ascohymenium. Upon maturation, the circular ascocarps open with a radiate fissured pore that exposes a deeply urceolate disk. In some species, the apothecia

become erumpent. The exciple is hyphal, usually dark, with periphysoids. The asci are cylindrical, functionally unitunicate with a thickened apex. The hyaline ascospores can have a variety of different shapes and sizes (Sherwood-Pike 1987).

Parakarstenia C.L. Yang, H.O. Baral & X.L. Xu, Mycological Progress 18(6): 839 (2019)

Parakarstenia was introduced by Yang et al. (2019b) and currently includes a single species *Pa. phyllostachydis*, which is parasitic on living bamboo culms of *Phyllostachys heteroclada*, causing culm rhombic-spot disease. *Parakarstenia* is characterized by initially immersed, later erumpent, sessile and gregarious apothecia with a flat to slightly convex, greyish white or pale brown disc; hairless, cylindrical clavate asci with conical apex and a hemiamyloid (type RR) outer wall; ascospores are narrowly cylindrical-clavate to fusoid, vermiform, straight to medium curved, initially aseptate, and transversely multi-septate at maturity. This study establishes a new host record for *Pa. phyllostachydis*, found on living leaves of *Chimonobambusa pachystachys*.

11. *Parakarstenia phyllostachydis* C.L. Yang, H.O. Baral & X.L. Xu, Mycological Progress 18(6): 841 (2019) Fig. 21

Index Fungorum number: IF829066; Facesoffungi number: FoF14785

Associated with leaf blight of *Chimonobambusa pachystachys*. Sexual morph: *Apothecia* 350–1150 μm long × 250–800 μm width × 200–450 μm high ($\overline{x}$ = 701 × 591 × 290 μm, n = 30), sessile, separate or gregarious, spread or slightly convex, white to grayish white when fresh, sunken when dry, brown to dark brown, usually also at margin with some small adherent host residues. *Ectal excipulum* 35–120 μm, composed of several layers of brown to dark brown cells of *textura angularis*. *Medullary excipulum* 70–300 μm composed of several layers of hyaline cells of *textura angularis*. *Paraphyses* 1.5–4.2 μm wide, filiform, hyaline, sporadically branched below apex, twisted into coils or spirals at the apex. *Asci* 92–134 × 8.5–16 μm ($\overline{x}$ = 112 × 12 μm μm, n = 30), 8–spored, stipitate, cylindrical, entire outer wall and apical thickening deep red in IKI (I+ hemiamyloid, type RR), KOH/IKI deep blue. *Ascospores* 37–56 × 2.3–4.1 μm ($\overline{x}$ = 46 × 3.2 μm, n = 50), 2–4-septate (frequently 3-septate), narrow cylindrical to club-shaped, hyaline, parallel or intertwined, containing a medium amount of lipids. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Chengdu City, Qionglai City (30°26'56.5" N, 103°18'59.32" E, alt. 492 m), on living leaves of *Chimonobambusa pachystachys*, 20 August 2020, Qian Zeng, ZQ202008010 (SICAU 23-0006).

GenBank numbers – SICAU 23-0006 – ITS = OR583157, LSU = OR125603, SSU = OR162589, mtSSU = OR162590.

Notes – This collection is similar in morphology to the descriptions of *Parakarstenia phyllostachydis* provided by Yang et al. (2019b). Nucleotide comparisons of ITS, LSU and mtSSU (SICAU 23-0006) showed a high homology with the sequences of *P. phyllostachydis* (SICAU 16-0002, holotype), with a similarity of 99% (201/203, 0 gap), 99.2% (829/836, 0 gap), and 99.8% (1000/1002, 0 gap), respectively. In the phylogenetic tree, the strain SICAU 23-0006 clustered with *Parakarstenia phyllostachydis* (SICAU 16-0002) with 100% MLBS and 1.00 BYPP support (Fig. 22).

Ostropales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 68 (1932)

Stictidaceae Fr. (as 'Stictei'), Summa Veg. Scand., Sectio Post. (Stockholm): 345 (1849)

The family *Stictidaceae* was introduced by Fries (1849), with *Stictis* Pers. as the type genus (Persoon 1800). The asexual morph is characterized by pycnidial conidiomata, conidiogenous cells are phialidic, sympodial, retrogressive, conidia one-celled to multi-septate, ellipsoidal to long cylindrical and occasionally tetraradiate (Wei et al. 2021b). The sexual morph is characterized by open ascomata, unbranched paraphyses, non-amyloid cylindrical asci, and ellipsoid to filiform ascospores (Ekanayaka et al. 2019). *Stictidaceae* species are parasitic on bark, leaves and stems of plant hosts (Ekanayaka et al. 2019, Xu et al. 2022). To date, more than 50 genera are accepted under *Stictidaceae* (Thiyagaraja et al. 2021a, Wei et al. 2021b).

Fitzroyomyces Crous, Persoonia 39: 389 (2017)

Fitzroyomyces was introduced by Crous et al. (2017b) with *F. cyperacearum* Crous as the type species, which was recorded from the leaves of *Cyperaceae* in Australia. *Fitzroyomyces* species are mainly saprobic, and the asexual morph is characterized by immersed, globose to disc-shaped conidiomata, with acentral ostiole, and hyaline, cylindrical, multi-septate, conidia with a flexuous, obtuse apex, and truncate base (Crous et al. 2017b). The sexual morph is characterized by cupulate apothecia immersed in the substrate, whitish to cream disc, numerous, long filiform, aseptate, and unbranched paraphyses, 8-spored asci, filiform, multi-septate, and hyaline ascospores. *Fitzroyomyces* comprises five species, viz. *F. cyperacearum*, *F. pandanicola*, *F. hyaloseptisporus*, *F. xishuangbannaensis*, and *F. yunnanensis* (Crous et al. 2017b, Tibpromma et al. 2018, Lu et al. 2021, Wei et al. 2021b, Xu et al. 2022). In this study, we introduce *F. heterocladae* as a new species based on morphological and phylogenetic analyses.

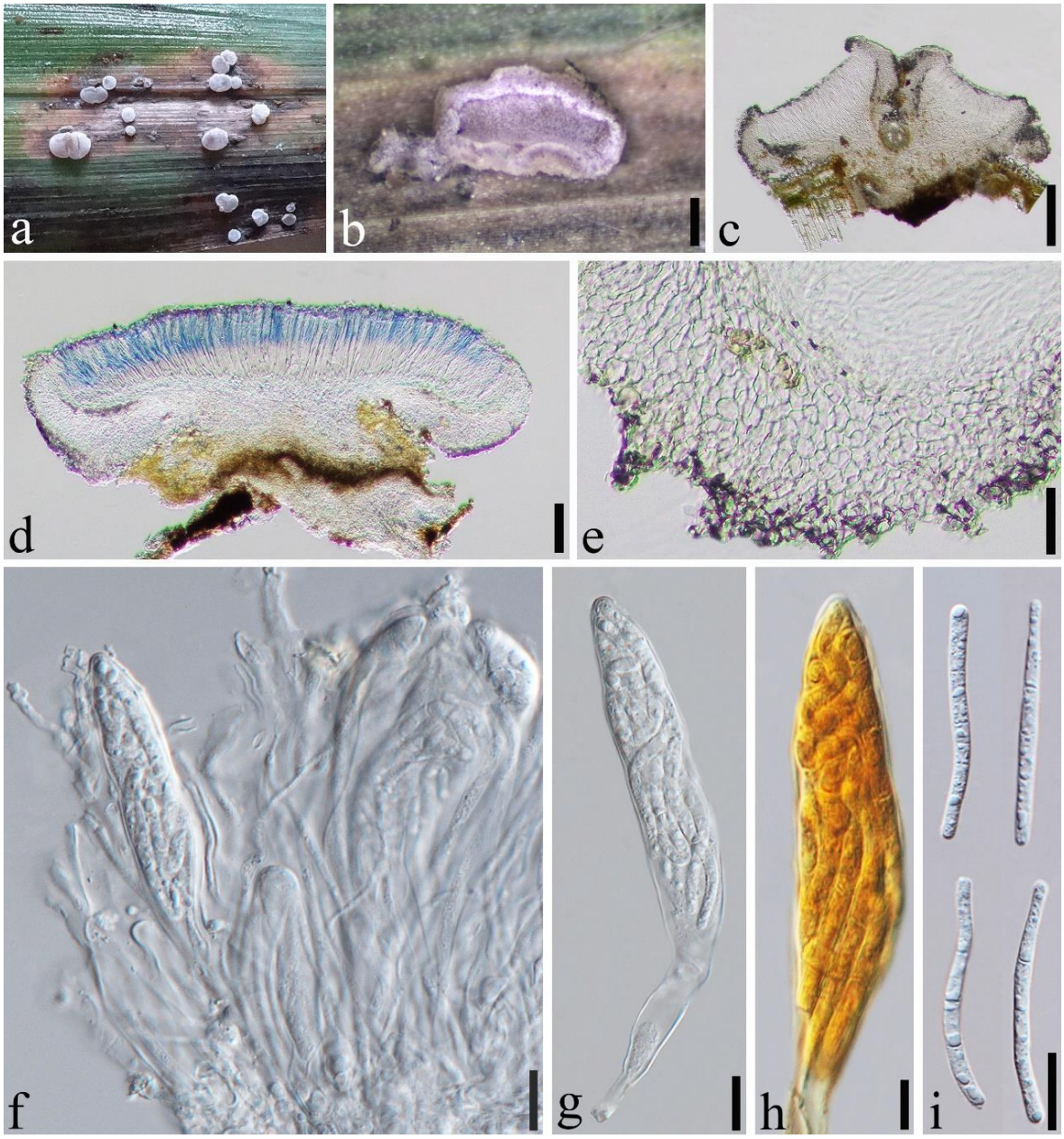

Figure 21 – *Parakarstenia phyllostachydis* (SICAU 23-0006). a, b Apothecia on host. c, d Vertical sections through apothecia (c in water, d in KOH/MLZ). e Ectal excipulum. f Asci interspersed among paraphyses. g, h Asci (g in water, h in MLZ). i Ascospores. Scale bars: b = 200 µm, c = 150 µm, d = 40 µm, e–g, i = 10 µm, h = 5 µm.

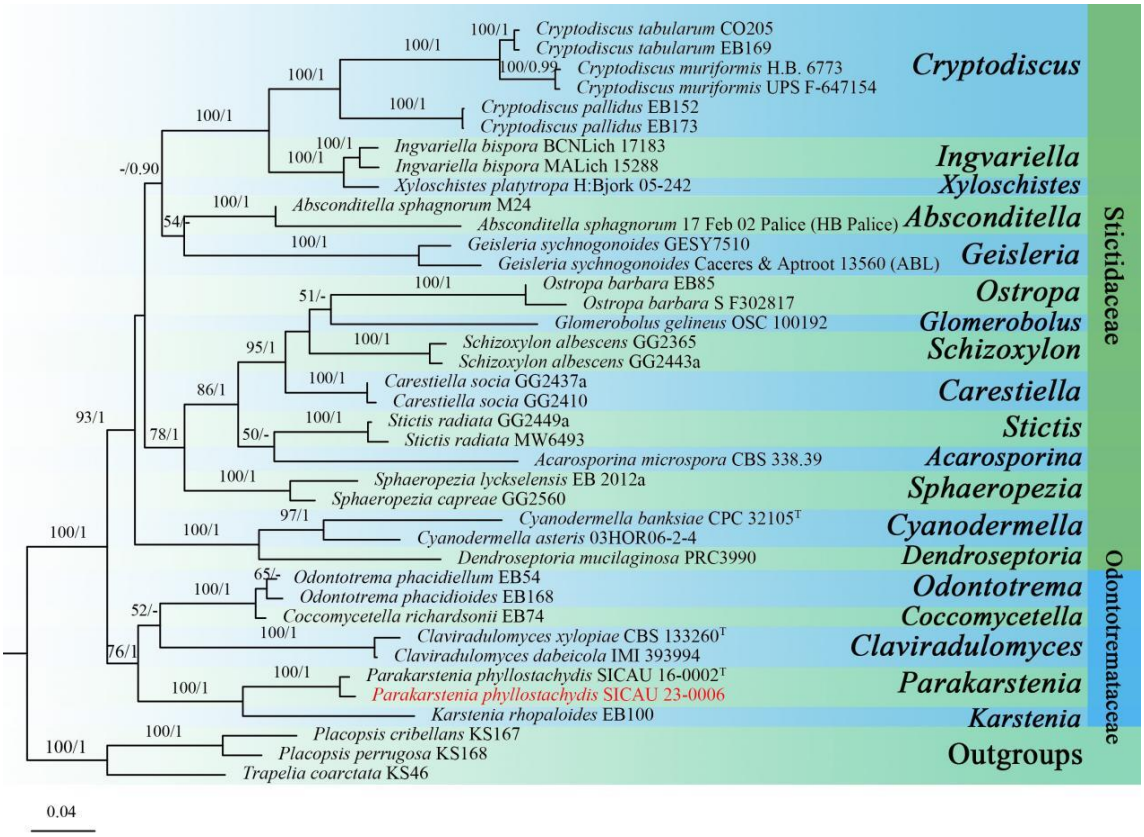

Figure 22 – Phylogenetic analyses based on the final concatenated dataset included 4,428 characters (LSU = 2,261, mtSSU = 1,033, ITS = 1,134) from 39 taxa. *Trapelia coarctata* (KS46), *Placopsis cribellans* (KS167) and *P. perrugosa* (KS168) from the *Trapeliaceae* family in *Baeomycetales* are included as outgroup taxa for rooting the tree. The best scoring RAxML tree with a final likelihood value of -25,298.184600 is presented. The matrix had 1,954 distinct alignment patterns, with 59.72% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.282152, C = 0.207914, G = 0.258934, T = 0.251000, with substitution rates AC = 1.032683, AG = 2.146219, AT = 1.871979, CG = 0.813712, CT = 4.737716, GT = 1.000000. The gamma distribution shape parameter α = 0.440970, and the tree length = 3.055348. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequence is written in red.

12. *Fitzroyomyces heterocladae* C.L. Yang & Q. Zeng, sp. nov. Fig. 23

Index Fungorum number: IF900589; Facesoffungi number: FoF14796

Etymology – Refers to the host species, *Phyllostachys heteroclada*, from which the new taxon was collected.

Holotype – SICAU 23-0002

Associated with twig blight of *Phyllostachys heteroclada*, causing twigs to fall leaves and death. Sexual morph: *Apothecia* 240–260 μm long × 180–240 μm width × 275–390 μm high ($\bar{x}$ = 251 × 209 × 321 μm, n = 5), arising singly, subglobose, sessile, immersed from the substrate, cupulate, margin often with a white rim, slightly protruding. *Disc* deeply cupulate, whitish to cream, with white margin. *Exciple* 8–17 μm ($\bar{x}$ = 11.5 μm, n = 20) thick, thin, comprising hyaline cells of *textura intricate*, usually separated from hymenium at upper part with some crystallites, with periphysoidal layer. *Periphyses* 3.5–13.8 μm ($\bar{x}$ = 8.4 μm, n = 20) long, 1–2-septate, enclosed in a gelatinous matrix, longer towards the apex, with an obtuse and slightly enlarged apical cells. *Hymenium* 160–250 μm ($\bar{x}$ = 198 μm, n = 20) thick, embedded in a gelatinous matrix, comprising paraphyses and asci. *Subhymenium* 9.6–29.7 μm ($\bar{x}$ = 23.7 μm, n = 20) thick, consisting of hyaline cells of *textura angularis*. *Epithecium* inconspicuous or absent. *Paraphyses* 1.2–2 μm ($\bar{x}$ = 1.6 μm,

n = 20) wide, hyaline, filiform, unbranched, septate, sometimes constricted at septum, apically cohering, narrower towards the apex. *Asci* 145–195 × 8–13 μm ($\overline{x}$ = 170 × 10.7 μm, n = 30), 8-spored, unitunicate, cylindrical-clavate, often broadest at middle part, short sessile, rounded at the apex. *Ascospores* 170–195 × 2.4–3.2 μm ($\overline{x}$ = 182.6 × 2.8 μm, n = 50), multiseriate, filiform, hyaline, 20–30-septate, slightly constricted at septum, sometimes breaking into part spores, 4–10 μm ($\overline{x}$ = 6.5 μm, n = 50) long in each cell of ascospores. Asexual morph: Undetermined.

Culture characteristics – *Ascospores* germinated in sterilized water within 12 h at 25 ℃, under 12 h dark/12 h light, with germ tubes developed from each cell of ascospores. *Colonies* on PDA slowly grown, only 2 cm after incubation for 30 days at 25 ℃, under 12 h dark/12 h light, and subcircle, wavy, dense, irregularly raised, radial plicated, leathery, flesh pink in center, white in margin, and reverse reddish.

Material examined – China, Sichuan Province, Ya'an City, Lushan County, Shuangshi Town (30°15'23.22"N, 102°55'58.08"E, alt. 1115 m), on twigs of *Phyllostachys heteroclada*, 10 Jun 2020, ChunLin Yang, YCL202006010 (SICAU 23-0002, holotype), ex-type culture SICAUCC 23-0002.

GenBank numbers – SICAUCC 23-0002 – ITS = OR134759, LSU = OR134750, SSU = OR162602, mtSSU = OR162603, *tef*1-α = OR134874, *rpb*2 = OR424347.

Notes – In the phylogenetic tree, our collection *Fitzroyomyces heterocladae* (SICAUCC 23-0002) is basal to *F. cyperacearum* with 91% MLBS/1.00 BYPP support, while also showing a relationship to *F. hyaloseptisporus* but with poor statistical support (Fig. 24). However, *F. heterocladae* differs from *F. cyperacearum* (MFLU 17-2072) in having a thinner excipulum, septate paraphyses, longer asci and finely guttulate ascospores (Table 3). *Fitzroyomyces heterocladae* can be distinguished from *F. hyaloseptisporus* (MFLU 21-0114, holotype) by its larger apothecia, different excipulum structure, smaller asci and ascospore with fewer septa (Table 2). The sequence comparisons show 6.09% (63/1034, 0 gap), 1.5% (9/605, 0 gap) differences in the LSU and ITS, respectively, between *F. heterocladae* and the type strain of *F. cyperacearum* (CBS 143170, ex-type). The nucleotide differences between *F. heterocladae* and *F. hyaloseptisporus* (MFLUCC 21-0111, ex-type) were 4.59% (38/827, 0 gap), 6.62% (39/589, 0 gap), 2.94% (22/749, 0 gap) in the LSU, ITS, and mtSSU, respectively. The morphological characteristics and molecular phylogenies support the establishment of a new species.

Sordariomycetes

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

Clavicipitaceae (Lindau) Earle ex Rogerson, Mycologia 62(5): 900 (1970)

Clavicipitaceae is regarded as one of the most diverse fungal families within the order *Hypocreales* (*Ascomycota*), exhibiting associations with insects, plants, fungi, and invertebrates (Spatafora et al. 2007, Sung et al. 2007, Steiner et al. 2011). Clavicipitaceous taxa associated with plants have been described in various species including *Aciculosporium*, *Atkinsonella*, *Balansia*, *Claviceps*, *Epichloë*, *Heteroepichloe*, *Myriogenospora*, *Periglandula*, *Shimizuomyces*, and *Ustilaginoidea*. Mongkolsamrit et al. (2021) isolated a similar asexual taxon from seed plant and introduced a new genus *Morakotia*. In this paper, we provide a multi-gene (ITS, LSU, SSU, *rpb*2, *tef*1-α, and *tub*2) phylogenetic tree for *Clavicipitaceae* (Fig. 29).

Aciculosporium I. Miyake, Bot. Mag., Tokyo 22: (307) (1908)

Aciculosporium was introduced by Miyake (1908) and is typified by *A. take* I. Miyake. This genus is characterized by cylindrical asci, thickened ascus apices, and filiform ascospores, which in many species disarticulate into part-spores. *Aciculosporium take* and *A. sasicola* have been identified as the causal agents of the economically significant witches' broom disease affecting bamboo in Japan and China (Tsuda et al. 1997, Oguchi 2001, Tanaka et al. 2003). *Aciculosporium* now consists of seven species, viz. *A. monostipum*, *A. oplismeni*, *A. phalaridis*, *A. sasicola*, *A. siamense* and *A. take*, including *A. chimonobambusae*, the new species described in this paper. Among these, *A. phalaridis* is known to produce stromata on sclerotia of commercially grown herb (*Phalaris aquatica* L.) in southern New South Wales and Victoria (Walker 2004). Mongkolsamrit

et al. (2021) introduced a new species *A. siamense*, which occurred on leaf sheaths (*Poaceae*). Tanaka et al. (2021) introduced a new species *A. oplismeni*, which occurred on wavy leaf basket grass (*Oplismenus undulatifolius* (Ard.) Roem. & Schult.), based on phylogenetic analyses of ITS, LSU, SSU, *tef*1-α, *rpb*1, and *ATP*6 sequence data.

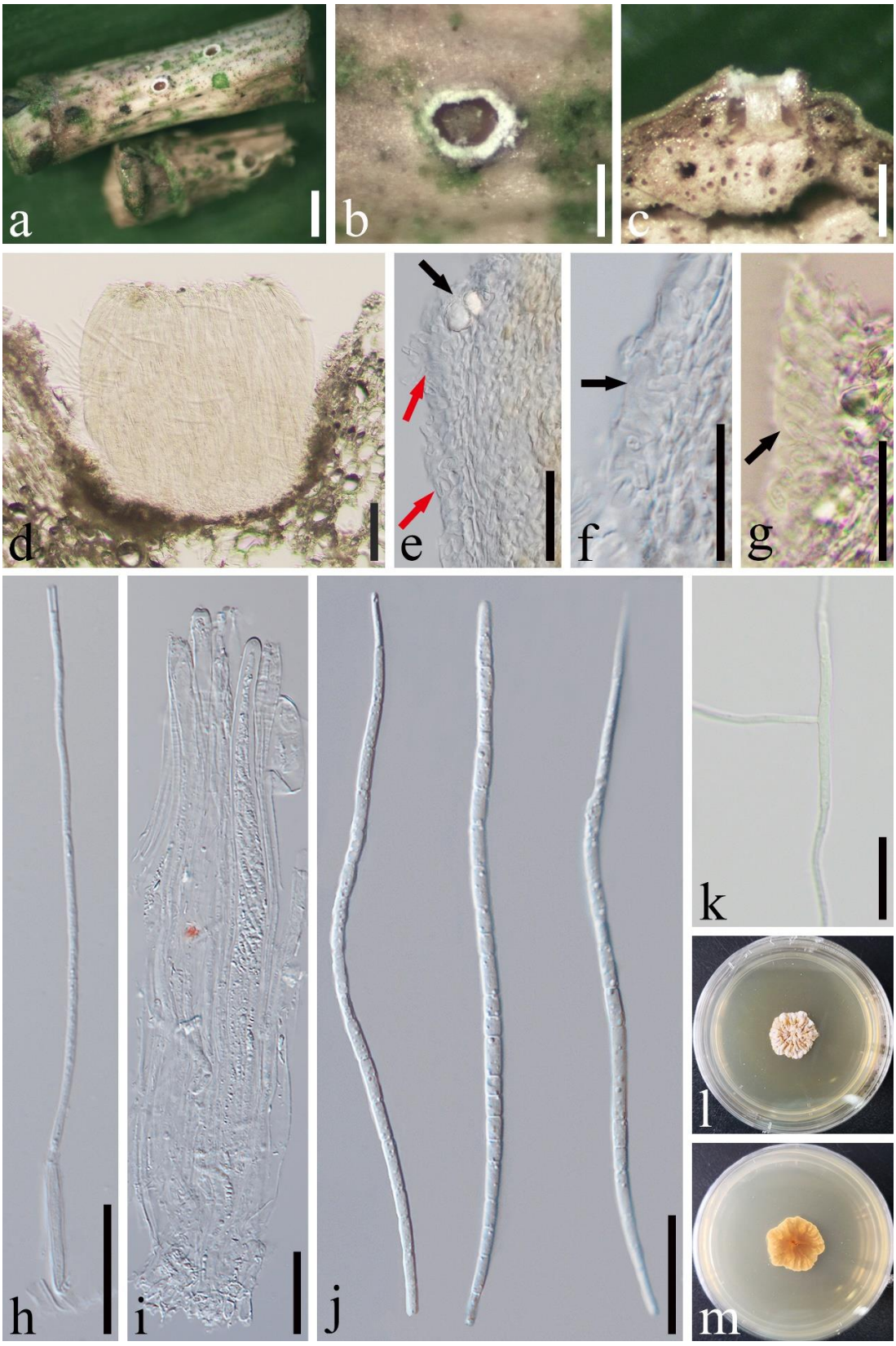

Figure 23 – *Fitzroyomyces heterocladae* (SICAU 23-0002, holotype). a–c Apothecia on host. d Vertical section of an apothecium. e Lateral structure of the exciple at upper part (periphysoidal

layer highlighted in red arrow; crystallites highlighted in black arrow). f, g Periphysoid surrounded by mucilaginous sheath. h Paraphyses. i Asci growing from subhymenium. j Ascospores. k Germinating ascospore. l, m Colonies on PDA (l obverse, m reverse). Scale bars: a = 500 µm, b, c = 200 µm, d = 60 µm, e–k = 20 µm.

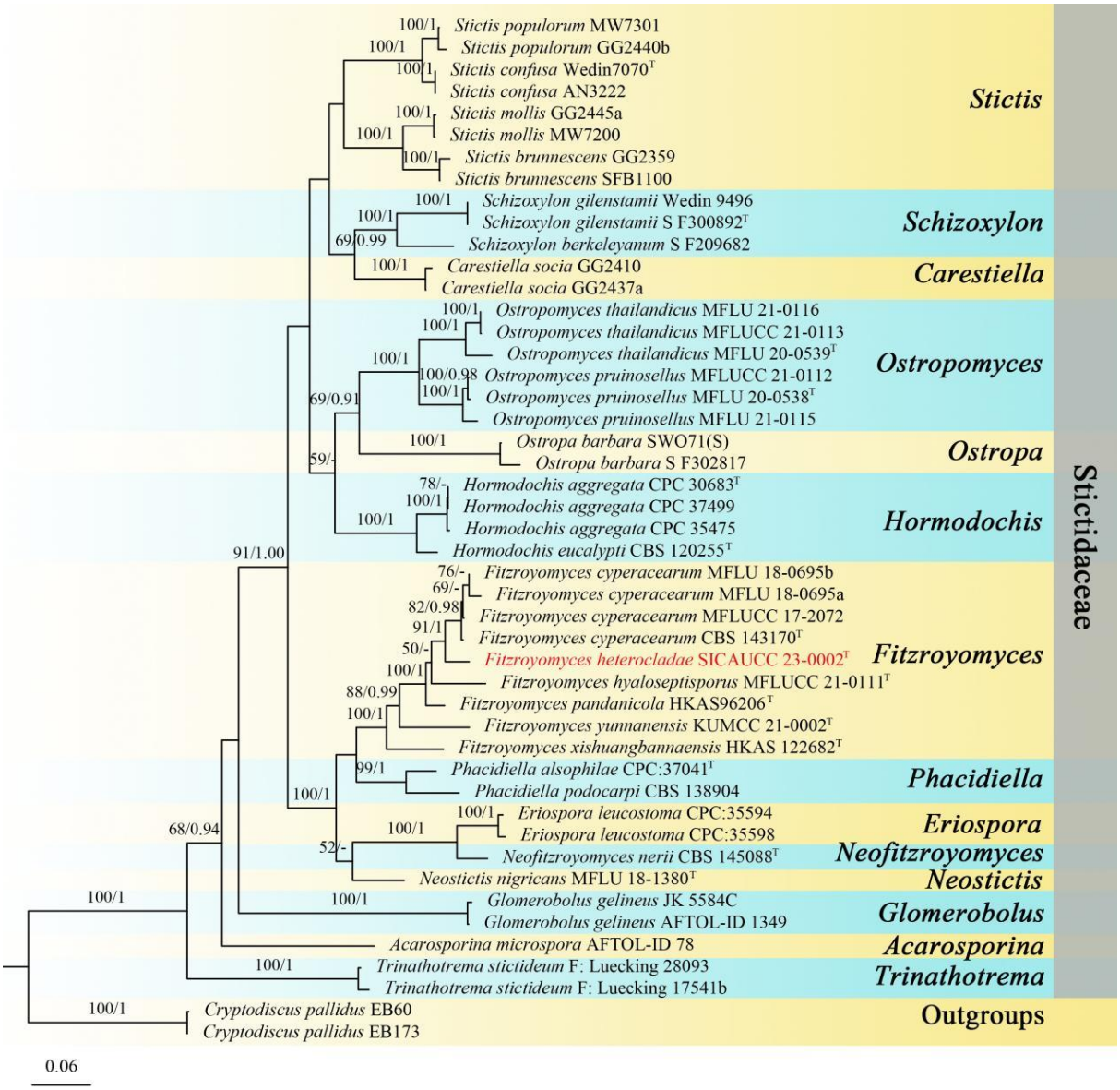

Figure 24 – Phylogenetic analyses based on a combined dataset (LSU, ITS, and mtSSU) comprising 47 taxa within *Stictidaceae*, which is rooted with *Cryptodiscus pallidus* (EB60) and *C. pallidus* (EB173) (*Stictidaceae*, *Ostropales*), were conducted for the study. The alignment contained 4,168 characters (LSU = 2,074, ITS = 996, mtSSU = 1,098), including gaps. The best scoring RAxML tree with a final likelihood value of -22,364.416669 is presented. The matrix had 1,762 distinct alignment patterns, with 56.19% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.277355, C = 0.215041, G = 0.260218, T = 0.247386, with substitution rates AC = 1.091494, AG = 2.403071, AT = 1.979246, CG = 0.804658, CT = 4.856222, GT = 1.000000. The gamma distribution shape parameter α = 0.320010, and the tree length = 3.041036. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequences are written in red.

Table 2 Morphological comparisons of *Fitzroyomyces* species.

Taxa	Specimens	Apothecia (µm)	Exciple (µm)	Asci (µm)	Ascospores (µm)	Septation	References
F. cyperacearum	MFLU 17-2072	201–260 × 210–310	17–70, *textura intricata*	110–150 × 10–20	100–145 × 2.5–3.5, eguttulate	17–21	Phukhamsakda et al. (2020)
F. hyaloseptisporus	MFLU 21-0114	140–200 × 150–200	6–20, *textura angularis*	165–200 × 10–25	150–200 × 3.5–6, finely guttulate	up to 58	Wei et al. (2021b)
F. heterocladae	SICAU 23-0002	240–260 × 180–240	8–17, *textura intricate*	145–195 × 8–13	170–195 × 2.4–3.2, guttulate	20–30	This study

Table 3 Morphological comparisons of *Mendogia* species.

Species	Ascostromata (mm)	Asci (µm)	Ascospores (µm)	Asci formation Type	Ascospore septation	Distribution	References
M. bambusina	0.98–1.85	55–90 × 17–25	13.5–25 × 5–8	Type I	3–5 transverse and 1–2 longitudinal septa	Indonesia	Raciborski (1900), Dai et al. (2017)
M. chiangraiensis	2–5	75–165 × 30–40	25–35 × 12–16	Type I	4–7 transverse and multi-longitudinal septa	Thailand	Jiang et al. (2020)
M. diffusa	0.22–0.4	45–70 × 25–35	15–25 × 6–10	Type II	5–6 transverse and 3–6 longitudinal septa	Thailand	Thiyagaraja et al. (2021b)
M. macrostroma	10–20 × 5–15	72–85 × 28–33.5	20–27 × 9–11	Type I	4–6 transverse and 2–4 longitudinal septa	Thailand	Dai et al. (2017)
M. manaosensis	1–2	85–120 × 10–12	30–55 × 3.5–4.5	Unknown	3–6 transverse septa	Brazil	Hennings (1904b)
M. philippinensis	2–4	42–55 × 16–19	16–18 × 5–6	Type II	5–6 transverse and longitudinal septa	Philippines	Sydow & Sydow (1917), von Arx & Müller (1975), Jiang et al. (2020)
M. sichuanensis	1.8–3.5	55–95 × 12–19	21–26 × 9–11	Type II	3–6 transverse and 1 longitudinal septum	China	In this study
M. yunnanensis	1.5–4.5	55–75 × 25–30	19–23 × 8.5–10.5	Type I	3–5 transverse and 2–3 longitudinal septa	China	Jiang et al. (2020)

13. ***Aciculosporium chimonobambusae*** Q. Zeng, Feng Liu, K.D. Hyde & C.L. Yang, sp. nov. Fig. 25

Index Fungorum number: IF900669; Facesoffungi number: FoF14775

Etymology – The specific epithet refers to the host genus *Chimonobambusa*.

Holotype – SICAU 23-0026

Parasitic associated with twigs of *Chimonobambusa tumidissinoda* J. R. Xue et T. P. Yi ex Ohrnb, causing leaf wilt disease. Sexual morph: *Ascostromata* 1.6–2.1 mm in diam, 1.4–2.2 mm high, hemispherical perithecial plates, sessile, surface snow white, pulvinate, fleshy pseudoparenchymatous. *Perithecia* 420–665 × 103–260 μm ($\overline{x}$ = 605 × 163 μm, n = 30), immersed, obovate, tips opened toward outside. *Asci* 340–385 × 5.4–6.3 μm ($\overline{x}$ = 360 × 5.6 μm, n = 40), 8-spored, unitunicate, filiform, thin-walled, with caps 3–5 μm thick. *Ascospores* 244–350 × 1.5–1.7 μm ($\overline{x}$ = 315 × 1.6 μm, n = 40), filiform, hyaline, multi-septate, easily producing fragmented part spores. Asexual morph: *Conidia* formed in PDA after 2 weeks, holoblastic, hyaline, narrowly cylindrical to filiform, 35–65 × 1.6–2 μm ($\overline{x}$ = 48 × 1.8 μm, n = 20), 1–2-septate, with apical branching appendages.

Culture characteristics – *Colonies* on PDA attaining 5–7 mm diam in 14 days at 25 ℃, under 12 h light/12 h dark, slow growing, yeast-like, convex, surface slightly rough, irregular edge, snow white mycelium on the surface and the back of colonies is beige.

Material examined – China, Sichuan Province, Luzhou City, Xuyong County, Fenshui Town (27°54'59"N, 105°16'14"E, alt. 1770 m), on living twigs of *Chimonobambusa tumidissinoda*, 26 July 2021, Qian Zeng, ZQ202107123 (SICAU 23-0026, holotype), ex-type culture SICAUCC 23-0020.

GenBank numbers – SICAUCC 23-0020 – ITS = OR405905, LSU = OR405916, SSU = OR405931, *rpb*2 = OR465274, *tef*1-α = OR531519.

Notes – In the phylogenetic analysis, *Aciculosporium chimonobambusae* is closely related to *A. take* and *A. sasicola* (100% MLBS/1.00 BYPP) (Fig. 26). The PHI test results indicate the absence of significant recombination events between *A. chimonobambusae* and closely related phylogenetic species (Fig. 27). Based on a comparison of their morphological characteristics, the perithecia of *A. chimonobambusae* (420–665 × 103–260 μm) are comparatively larger than those of *A. take* (375–525 × 100–125 μm) and *A. sasicola* (350–520 × 90–180 μm), while the asci of the new collection (340–385 × 5.4–6.3 μm) are longer compared to those in *A. take* (270–330 × 5–6 μm) and *A. sasicola* (112–275 × 5–7.5 μm) (Mongkolsamrit et al. 2021, Tanaka et al. 2021). Comparisons of the ITS, *rpb*2, and *tef*1-α sequences of *A. chimonobambusae* (SICAUCC 23-0020) and *A. take* (MAFF 241223) revealed 0.64% (3/462 bp, 1 gap), 1.69% (10/592 bp, 0 gap) and 1.46% (13/894 bp, 0 gap) sequence difference, respectively. The ITS, *rpb*2 and *tef*1-α sequences of *A. chimonobambusae* (SICAUCC 23-0020) differ from *A. sasicola* (MAFF 246967) by 0.44% (2/462 bp, 1 gap), 1.69% (10/592 bp, 0 gap) and 1.35% (12/894 bp, 0 gap), respectively. Therefore, based on morphology and phylogenetic evidence, we introduce our collection as a new species, *A. chimonobambusae*.

Heteroepichloe E. Tanaka, C. Tanaka, Gafur & Tsuda, Mycoscience 43(2): 92 (2002)

Heteroepichloe was introduced by Tanaka et al. (2002), and is typified by *H. bambusae* (Pat.) E. Tanaka et al. Tanaka et al. (2002) conducted morphological and phylogenetic studies on the causal agents of witches' broom of bamboo plants in East Asia based on ITS sequence data, and introduced a new genus *Heteroepichloe*, with two new species, viz. *H. bambusae* and *H. sasae*.

14. ***Heteroepichloe sichuanensis*** Q. Zeng, Feng Liu, K.D. Hyde & C.L. Yang, sp. nov. Fig. 28

Index Fungorum number: IF900901; Facesoffungi number: FoF14776

Etymology – The specific epithet "sichuanensis" refers to Sichuan Province, China, where the holotype was collected.

Holotype – SICAU 23-0025

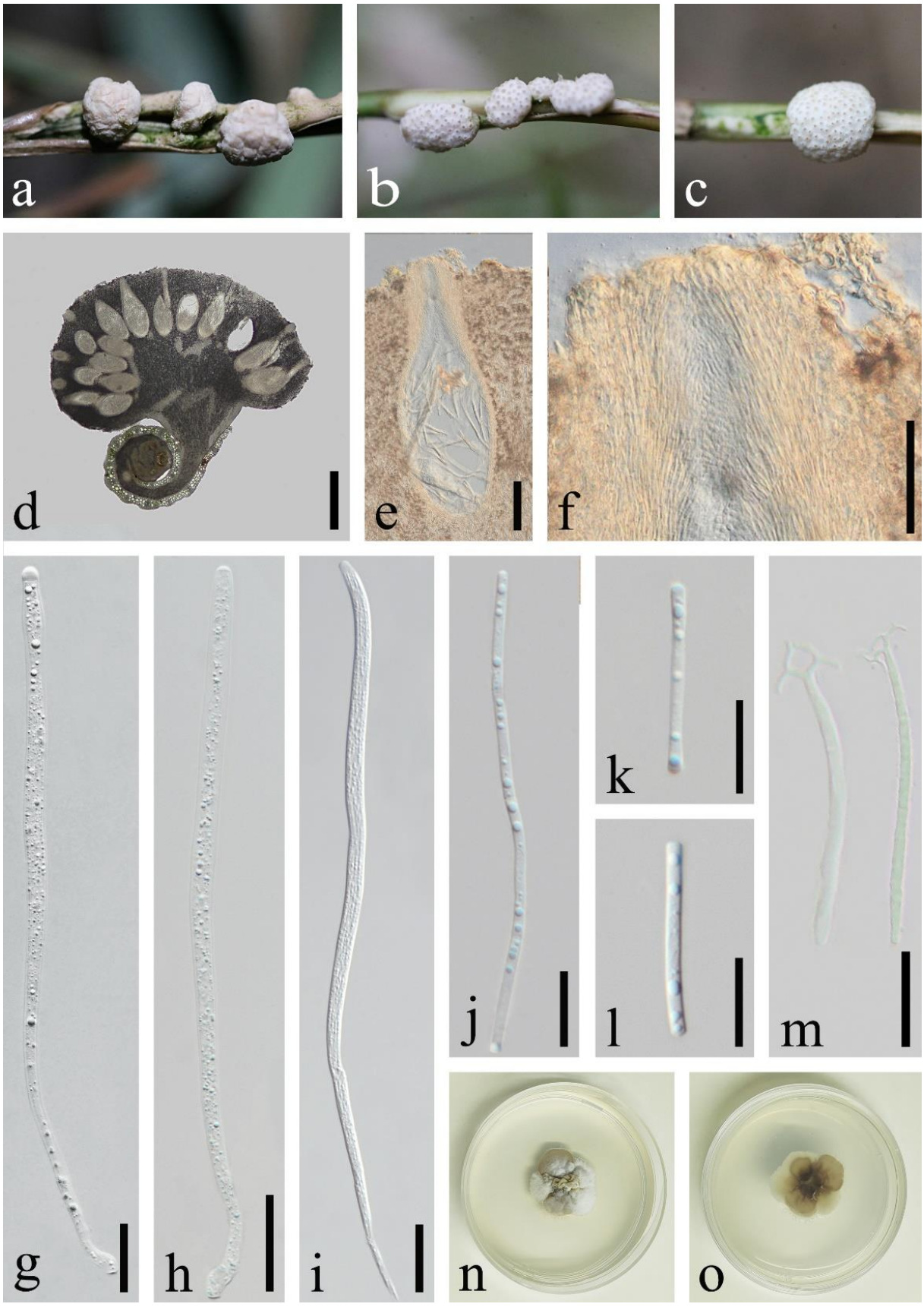

Figure 25 – *Aciculosporium chimonobambusae* (SICAU 23-0026, holotype). a–c Stromata on shoot apex of *Chimonobambusa tumidissinoda*. d Vertical section of ascostroma. e Vertical section of ascoma. f Ostiole of ascoma. g–i Asci. j Ascospores. k, l Part spores. m Apical appendaged conidia on PDA. n, o Colonies on PDA (n obverse, o reverse). Scale bars: d = 500 μm, e = 100 μm, f–i = 20 μm, j–m = 10 μm.

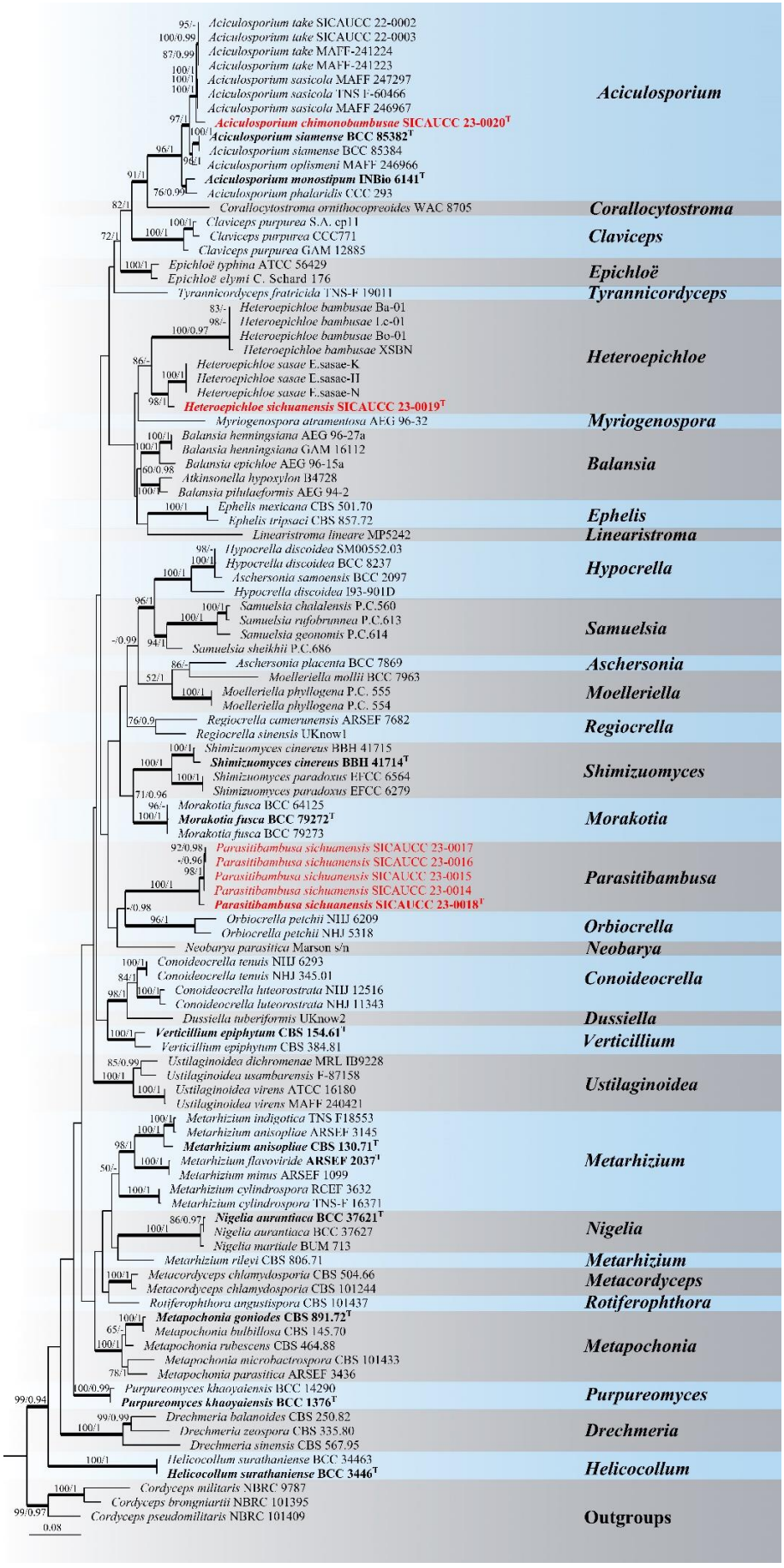

Figure 26 – Phylogenetic analyses of *Clavicipitaceae* combined ITS, LSU, SSU, *rpb*2, *tef*1-α, with *tub*2 sequence alignment, including 110 taxa within *Clavicipitaceae*, were conducted and tree was

rooted with *Cordyceps brongniartii* (NBRC 101395), *C. militaris* (NBRC 9787), and *C. pseudomilitaris* (NBRC 101409) (*Cordycipitaceae*, *Hypocreales*). The alignment contained 3,951 characters (ITS = 1,755, LSU = 2,178, SSU = 2,613, *rpb*2 = 1,194, *tef*1-α = 1,953, *tub*2 = 1,559), including gaps. The best scoring RAxML tree with a final likelihood value of -68,957.558503 is presented. The matrix had 3,774 distinct alignment patterns, with 71.68% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.235025, C = 0.269427, G = 0.271021, T = 0.224527, with substitution rates AC = 1.285959, AG = 3.715779, AT = 1.082659, CG = 1.389391, CT = 7.115114, GT = 1.000000. The gamma distribution shape parameter α = 0.212560, and the tree length = 4.835267. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90% are indicated at the nodes, respectively. Bold lines in the tree represent MLBS ≥ 90%, BYPP ≥ 0.9. The newly generated sequences are marked in red. The ex-type strains are indicated with "T" in the end of the taxa labels.

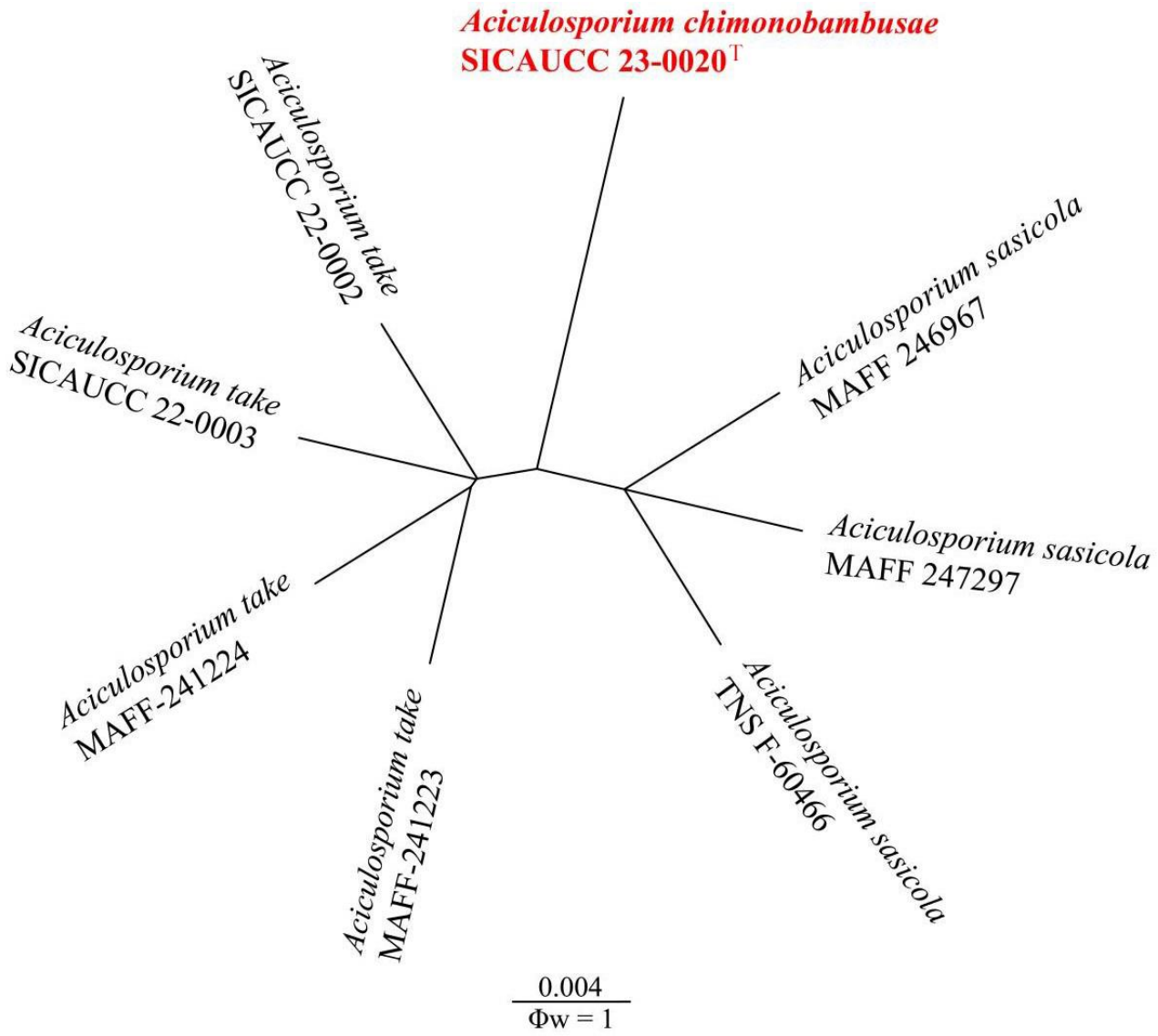

Figure 27 – The splits graph from the pairwise homoplasy index (PHI) test generated from the concatenated gene set of ITS, LSU, SSU, *rpb*2, *tef*1-α, and *tub*2 sequence data of closely related species of *Aciculosporium* using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The strain determined in this study is in bold and red. The ex-type strain is highlighted with "T" after the strain number label.

Associated with twigs and leaf sheaths of *Phyllostachys heteroclada* Oliver, causing the twigs to excessive growth and forming long, curved stromata at the tips of twigs. Sexual morph: *Stromata*, scattered, wrapping the leaf sheath, cylindrical, straight to curved, thin to both ends, dark purple to black, in cross-section approximately-circular. *Locules* 320–400 × 110–230 μm ($\overline{x}$ = 365 × 175 μm, n = 25), regularly buried in peripheral layer of stromata, oviform or oval, surface with ostioles when mature. *Asci* 190–285 × 4.7–9.8 μm ($\overline{x}$ = 241 × 6.9 μm, n = 30), filiform, with thickened rounded apex, hyaline. *Ascospores* filiform, hyaline, multi-septate and easily fragmented to dumbbell-shaped part spores in the ascus. *Part spores* 11.8–14.7 × 1.6–2.1 μm ($\overline{x}$ = 13.3 × 1.8 μm, n = 50), dumbbell-shaped, one-celled, hyaline, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – *Colonies* on PDA attaining 30 mm diam in 14 days, circular, convex, surface slightly rough, circular, irregular edge, flocculent, snow white from above and below. Mycelium superficial to immersed in media, branched, septate, smooth.

Material examined – China, Sichuan Province, Ya'an City, Lushan County, Shuangshi Town (31°15'24.01"N, 102°55'57.79"E, alt. 1096 m), on twigs of *Phyllostachys heteroclada*, 10 June 2020, Qian Zeng, ZQ202006018 (SICAU 23-0025, holotype), ex-type culture SICAUCC 23-0019.

GenBank numbers – SICAUCC 23-0019 – ITS = OR405906, LSU = OR405917, SSU = OR405932, *rpb*2 = OR531523, *tef*1-α = OR531518.

Notes – The multi-gene phylogenetic analysis of combined ITS, LSU, SSU, *rpb*2, *tef*1-α, and *tub*2 sequence data revealed that *Heteroepichloe sichuanensis* is a lineage sister clade to *H. sasae* with 98% MLBS/1.00 BYPP support (Fig. 26). This species is morphologically similar to *H. sasae* and *H. bambusae* with scleroid stromata, cylindrical asci and filiform ascospores. However, *H. sichuanensis* has hyaline stromata but the stromata are yellowish in *H. bambusae* and purplish in *H. sasae* (White & Reddy 1998, Tanaka et al. 2002). The nucleotide differences between our collection (SICAUCC 23-0019) and the ex-type strains of *H. sasae* (E. sasae-H, E. sasae-K, E. sasae-N) were 3.2% (16/504, 4 gaps), 3.19% (16/504, 3 gaps), 3.19% (16/504, 3 gaps) in the ITS, respectively. However, the latter lacks *rpb*2, LSU, SSU, *tef*1-α, and *tub*2 sequences for further comparisons. They are separate taxa based on the sequence data recommended by Chethana et al. (2021). Ecologically, *H. sichuanensis* was found only on *Phyllostachys* in subtropical regions, while *H. sasae* was only found on *Sasa* in temperate areas (White & Reddy 1998, Tanaka et al. 2002). Therefore, we introduce *H. sichuanensis* as a novel species based on phylogenetic evidence.

Parasitibambusa C.L. Yang, Feng Liu, K.D. Hyde & Q. Zeng, gen. nov.

Index Fungorum number: IF900767; Facesoffungi number: FoF14777

Etymology – Parasiti means parasitic in Latin, and refers to members of this genus parasitic on bamboo substrates.

Associated with twigs of bamboo. Sexual morph: Undetermined. Asexual morph*:* *Conidiomata* solitary, crumbly structure, succulent, expanded spherical, tightly wrapped around bamboo twigs, dark brown on the surface, yellowish brown in longitudinal section. Conidiomatal wall comprises tissue, densely packed, with several layers composed of dark brown to black, pseudoparenchymatous cells of *textura angularis* or *textura globulosa*. Fertile part clavate. *Conidiogenous cells* monophialidic, phialidic, determinate, compact, cylindrical to ampulliform, arranged in an ordinal manner, brown at the apex, lighter at the base, septate, smooth-walled. *Conidia* ovoid to long ovoid, hyaline to hazel, aseptate, smooth-walled.

Type species – *Parasitibambusa sichuanensis* C.L. Yang, Feng Liu & Q. Zeng

Notes – *Parasitibambusa* is characterized by dark, crumby structure, with dense cracks on the surface. The genus is commonly found on bamboo. *Parasitibambusa* differs from other genera in the family *Clavicipitaceae* due to the unique position of its conidiomata. The asexual morphs of *Parasitibambusa* produce ellipsoidal to spherical, hyaline to hazel conidia. These characters are not observed in other genera of the family *Clavicipitaceae*. According to the phylogenetic tree (Fig. 29), *Parasitibambusa* isolates form a highly supported clade within the family *Clavicipitaceae*, and is phylogenetically separated from *Orbiocrella*.

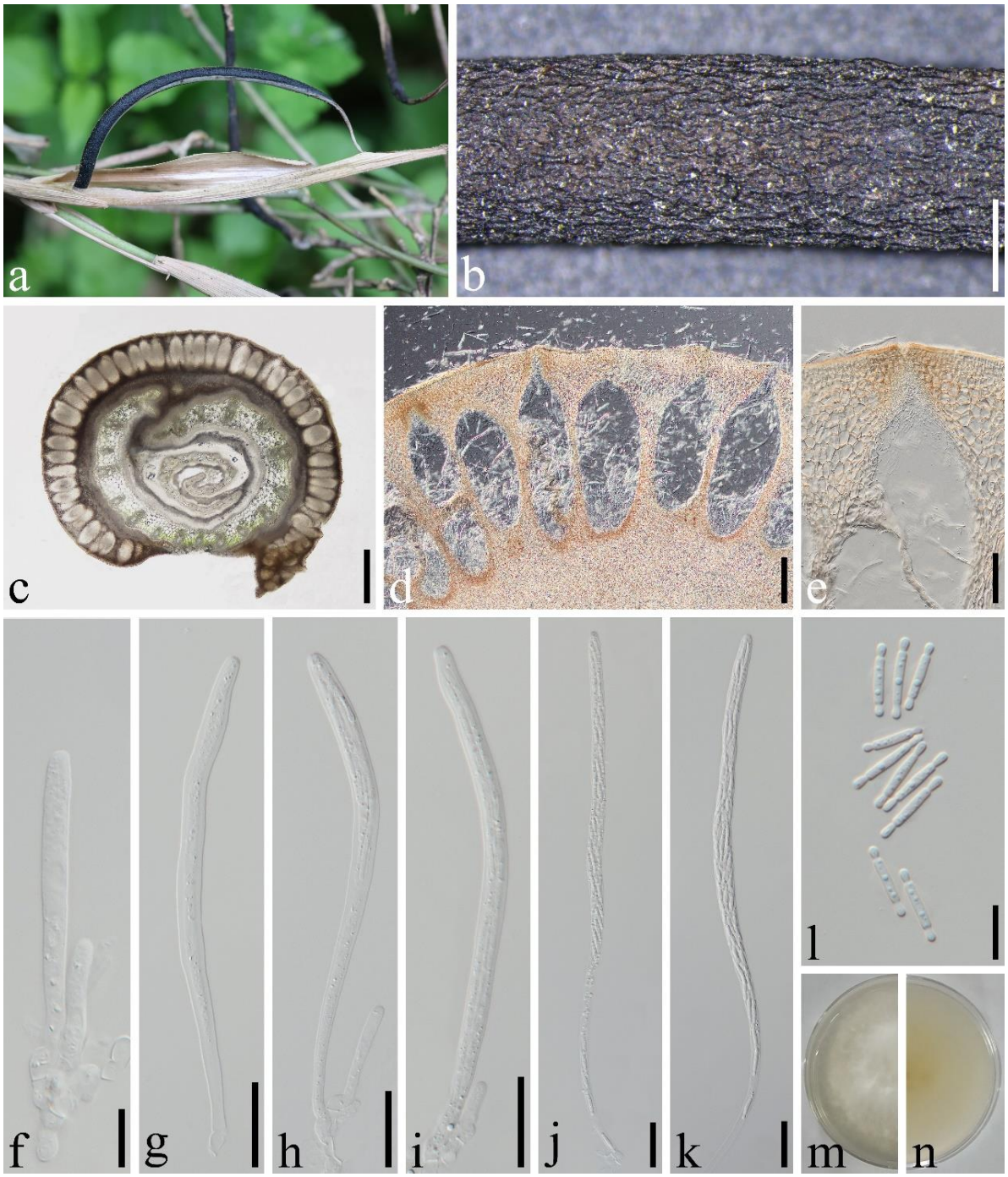

Figure 28 – *Heteroepichloe sichuanensis* (SICAU 23-0025, holotype). a, b Ascostromata on leaf sheaths of bamboo. c Vertical sections of ascostroma. c, d Vertical section of locules. e Ostiole of ascoma. f–k Asci. l Part spores. m, n Colonies on PDA (m obverse, n reverse). Scale bars: b = 1000 μm, c = 500 μm, d = 200 μm, e = 50 μm, g–k = 20 μm, f, l = 10 μm.

15. ***Parasitibambusa sichuanensis*** C.L. Yang, Feng Liu, K.D. Hyde & Q. Zeng, sp. nov. Fig. 29

Index Fungorum number: IF900768; Facesoffungi number: FoF14778

Etymology – The specific epithet "sichuanensis" refers to Sichuan Province, China, where the holotype was collected.

Holotype – SICAU 23-0024

Associated with withered twigs and leaves of *Phyllostachys heteroclada* and *P. violascens* 'Prevernalis' S.Y. Chen et C.Y. Yao, causing them to fall off. Sexual morph: Undetermined. Asexual morphs: *Conidiostromata* 3.5–6.5 cm in diam, 3–5 cm high, as irregular lumps, surface with cracks, initially caesious to gray, then dark grey to crineous, in cross-section yellow to

brownish-yellow, and eventually often dry and falling off. *Internal tissues* multi-layered, pseudoparenchymatous, composed of light brown cells of *textura angularis* or *textura globulosa*. *Conidiophores* bifurcate, forming a compact, brown palisade, arranged densely, septate, apex with catenulate conidia. *Conidiogenous cells* phialidic, 15–27 × 4.1–5.5 μm ($\overline{x}$ = 20 × 4.7 μm, n = 30), single or in terminated pairs, clavate to cylindrical, straight or flexuous, brown at apex, the base lighter, with a tapered and truncated terminated apex, with a smooth-walled collarette. *Conidia* 3.9–6.4 × 3.4–5.1 μm ($\overline{x}$ = 5.3 × 4.3 μm, n = 50), ellipsoidal to spherical, pale brown to brown, smooth-walled.

Cultural characteristics – Conidia germinate in sterilized water within 8 h at 25 ℃. Colonies growing slowly, attaining 3.4 cm diam after 14 days at 25 ℃, under 12 h light/12 h dark, circular, with even margin, dark brown at margin, brown yellow to dark brown from below.

Material examined – China, Sichuan Province, Ya'an City, Yucheng District, Zhongli Town (30°15'23.22"N, 102°55'58"E, alt. 1115 m), 12 June 2020, on twigs of *Phyllostachys heteroclada*, Chunlin Yang, YCL202006007 (SICAU 23-0024, holotype), ex-type culture SICAUCC 23-0018. *ibid*. Ya'an City, Yucheng District, Yashang Road (30°8'10.14"N, 103°3'23.28"E, alt. 902 m), 28 November 2019, on twigs of *P. violascens* 'Prevernalis', YCL201911008 (SICAU 23-0020, paratype), ex-paratype culture SICAUCC 23-0014. *ibid*. Ya'an City, Zhongli Town (130°7'51"N, 03°3'14"E, alt. 912 m), 28 November 2019, on twigs of *P. violascens* 'Prevernalis', YCL201911010 (SICAU 23-0021, paratype), ex-paratype culture SICAUCC 23-0015. *ibid*. Ya'an City, Yucheng District, Zhongli town (30°8'5.84"N, 103°3'19.38"E, alt. 878 m), 28 November 2019, on twigs of *P. violascens* 'Prevernalis', YCL202003002 (SICAU 23-0022, paratype), ex-paratype culture SICAUCC 23-0016. *ibid*. Ya'an City, Zhongli town (30°8'10.65"N, 103°3'23.46"E, alt. 875 m), 28 November 2019, on twigs of *P. violascens* 'Prevernalis', YCL202006006 (SICAU 23-0023, paratype), ex-paratype culture SICAUCC 23-0017.

GenBank numbers – SICAUCC 23-0014 – ITS = OR405907, LSU = OR405918, *mcm*7 = OR917087, SSU = OR405933, *rpb*2 = OR465272, *tef*1-α = OR531513; SICAUCC 23-0015 – ITS = OR405908, LSU = OR405919, *mcm*7 = OR465279, SSU = OR405934, *tub*2 = OR917088, *tef*1-α = OR531514; SICAUCC 23-0016 – ITS = OR405909, LSU = OR405920, *mcm*7 = OR465280, SSU = OR405935, *tub*2 = OR465278, *tef*1-α = OR531515; SICAUCC 23-0017 – ITS = OR405910, LSU = OR405921, *mcm*7 = OR465281, SSU = OR405936, *tef*1-α = OR531516; SICAUCC 23-0018 – ITS = OR405911, LSU = OR405922, *mcm*7 = OR465282, SSU = OR405937, *rpb*2 = OR531522, *tef*1-α = OR531517.

Notes – *Parasitibambusa sichuanensis* is described from living twigs of bamboo in China, where the fruiting body (conidiostromata) is a distinctly crumby structure, conidiogenous cells are phialidic, and conidia are hyaline, ellipsoidal to spherical, aseptate and with smooth perispores. These distinguishing features are not observed in other genera of *Clavicipitaceae*. The combined phylogeny shows that five isolates of *P. sichuanensis* form a distinct clade in *Clavicipitaceae* (Fig. 26).

Magnaporthales Thongk., Vijaykr. & K.D. Hyde, Fungal Diversity 34: 168 (2009)
Magnaporthaceae P.F. Cannon, Systema Ascomycetum 13: 26 (1994)

The family *Magnaporthaceae* was introduced by Cannon (1994), with the type genus *Magnaporthe* R.A. Krause & R.K. Webster, to accommodate taxa with globose to subglobose perithecial ascomata with long necks, unitunicate cylindrical asci, and morphologically variable ascospores. Silva et al. (2019) isolated an asexual taxon from leaves of *Sorghum bicolor* (L.) Moench and introduced a new genus *Bifusisporella*. Magnaporthaceous taxa are found in various plant parts, including leaves, stems, roots, and wood (Shearer 1989, Yuan et al. 2010), and also include saprobic species associated with the decomposition of debris in bamboo (Liu et al. 2015). This family comprises several important plant pathogenic taxa, for example, *Magnaporthe oryzae* commonly causes rice blast (Dean et al. 2012), while *Gaeumannomyces radicicola* causes stalk rot on maize in Brazil (Carraro et al. 2021), *Bifusisporella sichuanensis* causes leaf spot disease of *Phyllostachys edulis* (Carriere) J. Houzeau (Zeng et al. 2022).

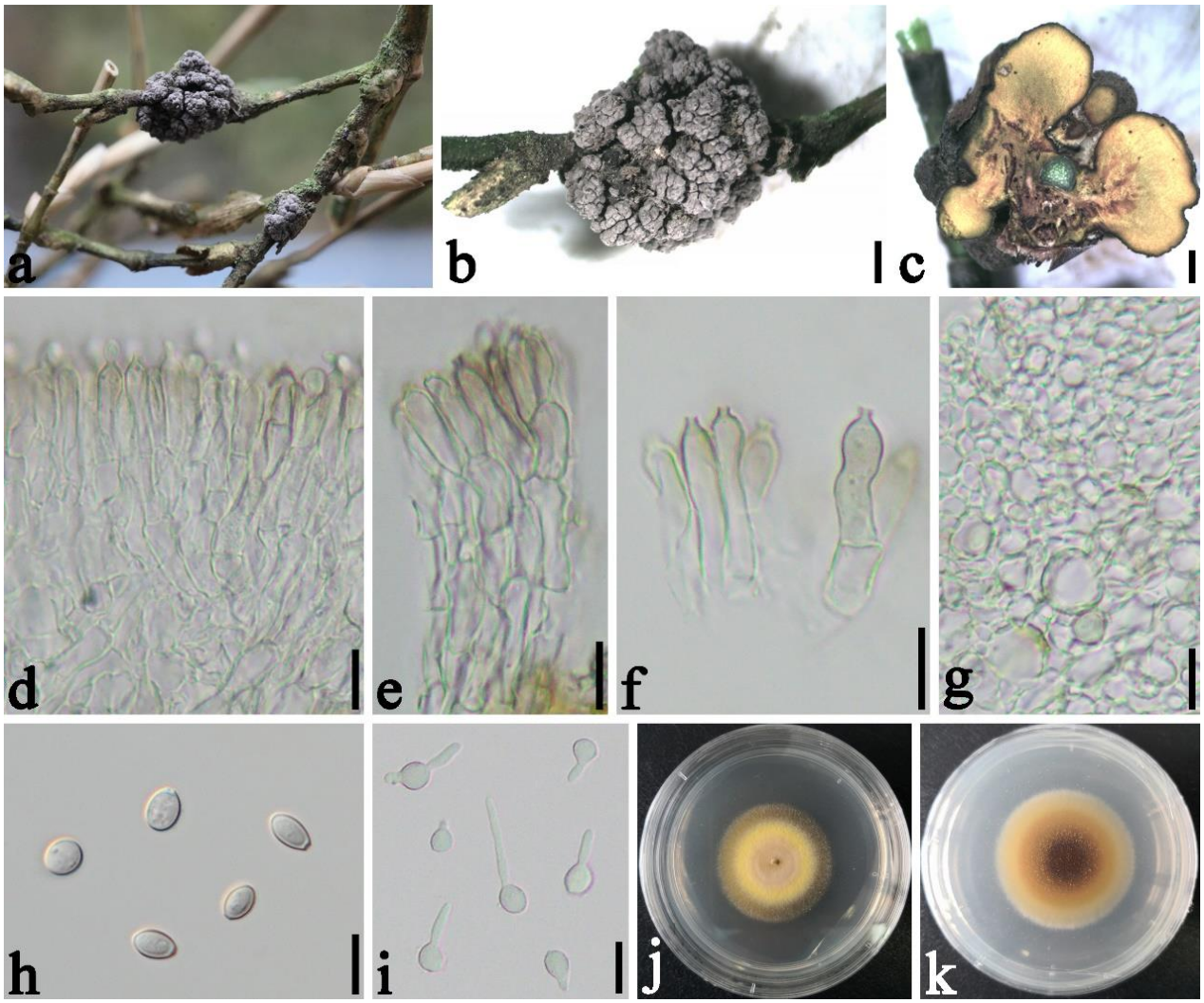

Figure 29 – *Parasitibambusa sichuanensis* (SICAU 23-0024, holotype). a, b Fruiting bodies. c Vertical sections through conidiostromata. d–f Conidiogenous cells. g Internal organizational structure of conidiomata. h Conidia. i Germinating conidia. j, k Colonies on PDA (j obverse, k reverse). Scale bars: b, c = 100 μm, d-i = 10 μm.

Bifusisporella R.M.F. Silva, et al., Mycological Progress 18(6): 852 (2019)

Bifusisporella was introduced by Silva et al. (2019) and is typified by *B. sorghi* R.M.F. Silva, et al., which was collected from leaves of *Sorghum bicolor* in Brazil. Zeng et al. (2022) isolated *B. sichuanensis* from living leaves of *Phyllostachys edulis* in China. This genus is characterized by the asexual morph typified by phialidic, curved, elongated conidiogenous cells and dimorphic conidia, and the sexual morph typified by subglobose ascomata, 8-spored, cylindrical asci and biseriate, fusiform, distinctly septate ascospores (Silva et al. 2019, Zeng et al. 2022).

16. *Bifusisporella fusispora* Q. Zeng, Feng Liu & C.L. Yang, sp. nov. Fig. 30

Index Fungorum number: IF900664; Facesoffungi number: FoF14783

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

Holotype – SICAU 23-0027

Associated with upper branches and culms of *Phyllostachys heteroclada*, causing dieback. Sexual morph: *Ascostromata* 700–1100 μm long × 370–600 μm width × 180–260 μm high ($\bar{x}$ = 855 × 460 × 215 μm, n = 10), separate or gregarious, fusiform, ellipsoid or irregular, black, coriaceous, semi-immersed, medium raised when matured, unilocular or multilocular, glabrous, a long fissure in center with numerous internal paraphyses. *Peridium* 9.5–31.1 μm wide, brown to black outer cells, thicker at the sides, with hyaline to brown of inner cells, composed of multi-layer cells of

textura angularis. *Paraphyses* 5–7.9 μm wide at base, numerous, cellular, constricted at the septa, usually swollen cells at base, narrowed towards the apex. *Asci* 75–100 μm × 11–15 μm ($\overline{x}$ = 87.5 × 12.7 μm, n = 20), bitunicate, fissitunicate, cylindrical, with a short stipe, apically rounded with an ocular chamber, 8-spored. *Ascospores* 25–45 × 5–7 μm ($\overline{x}$ = 33.5 × 6.3 μm, n = 50), overlapping, biseriate, fusiform, usually curved, 3-septate, slightly constricted at the septa, hyaline, smooth-walled, with large guttules in the cells, without a gelatinous sheath. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Ya'an City, Lushan County, Mount Zhifang (30°15'44.94"N, 102°59'15.56"E, alt. 875 m), on branches and culms of *Phyllostachys heteroclada*, 12 September 2017, Chunlin Yang, YCL201709001 (SICAU 23-0027, holotype).

GenBank numbers – SICAU 23-0027 – ITS =OR405944, LSU = OR405925, SSU = OR405946, *tef*1-α = OR947488.

Notes – Multigene analyses show that the new fungus *Bifusisporella fusispora* (SICAU 23-0027) is sister to *B. sichuanensis* (SICAUCC 22-0073) with 89% MLBS support (Fig. 31). *Bifusisporella fusispora* is similar to *B. sichuanensis* in having cylindrical asci and fusiform, hyaline ascospores, but they differ in the size of asci and ascospores. *Bifusisporella fusispora* has comparatively shorter asci (75–100 μm vs. 79–126 μm) and larger ascospores (25–45 × 5–7 μm vs. 22–35 × 5–6.5 μm) (Zeng et al. 2022). In addition, striking base-pair differences are noted, viz. 10.4% (55/528, 0 gap), 3.1% (27/852, 0 gap), 9.6% (88/917, 0 gap), in the ITS, LSU, and *tef*1-α, respectively. Hence, our collection is proposed as a new species.

Myriangiaceae Nyl., Mém. Soc. Sci. nat. Cherbourg 2: 9 (1854)

The family *Myriangiaceae* was introduced by Nylander (1854) with two species, *Myriangium duriaei* Mont. & Berk. and *M. curtisii* Berk. & Mont. (Montagne 1849). To date, the asexual morphs of species in this family have remained elusive and undiscovered (Hyde et al. 2013, Dissanayake et al. 2014, Jiang et al. 2020). Species are saprobic on dead leaves, stems, or bark of various plants (Hyde et al. 2013, Dissanayake et al. 2014, Jayawardena et al. 2014). However, certain genera within this group exhibit a parasitic or epiphytic lifestyle, residing on the surface of living plants (Dissanayake et al. 2014, Jayawardena et al. 2014, Dai et al. 2017). There are two types of ascus formation observed in this family. Type I is characterized by scattered and irregularly distributed asci within the ascostromata. In contrast, Type II exhibits asci that are localized and typically found at the base of the ascostromata (Miller 1940, Dissanayake et al. 2014, Dai et al. 2017).

Mendogia Racib., Parasit. Alg. Pilze Java's (Jakarta) 3: 31 (1900)

Mendogia was introduced by Raciborski (1900), and typified by *M. bambusina* Racib., which was collected from bamboo in Java and Indonesia. *Mendogia* is characterized by small to large, blackened, flattened, solitary to scattered, superficial ascostromata and subglobose to clavate asci, with eight muriform ascospores. *Mendogia* is predominantly associated with bamboo and palms, and it is distributed in tropical regions (Raciborski 1900, Hennings 1904b, Sydow & Sydow 1917, von Arx & Müller 1975, Dai et al. 2017). Dai et al. (2017) re-examined the type species *M. bambusina* and introduced a new species, *M. macrostroma* D.Q. Dai & K.D. Hyde, from a bamboo host. Jiang et al. (2020) introduced three new species, viz. *M. calami* Phookamsak, H.B. Jiang & K.D. Hyde, *M. chiangraiensis* H.B. Jiang, Phookamsak & K.D. Hyde, and *M. yunnanensis* from living bamboo twigs and culms in China, the Philippines, and Thailand. Thiyagaraja et al. (2021b) reported a new species, *M. diffusa* Thiyagaraja et al., from dead leaves of *Fagales* sp.

17. ***Mendogia sichuanensis*** Q. Zeng, Feng Liu & C.L. Yang, sp. nov. Fig. 32

Index Fungorum number: IF900665; Facesoffungi number: FoF14784

Etymology – The specific epithet "sichuanensis" refers to Sichuan Province, China, where the holotype was collected.

Holotype – SICAU 23-0028

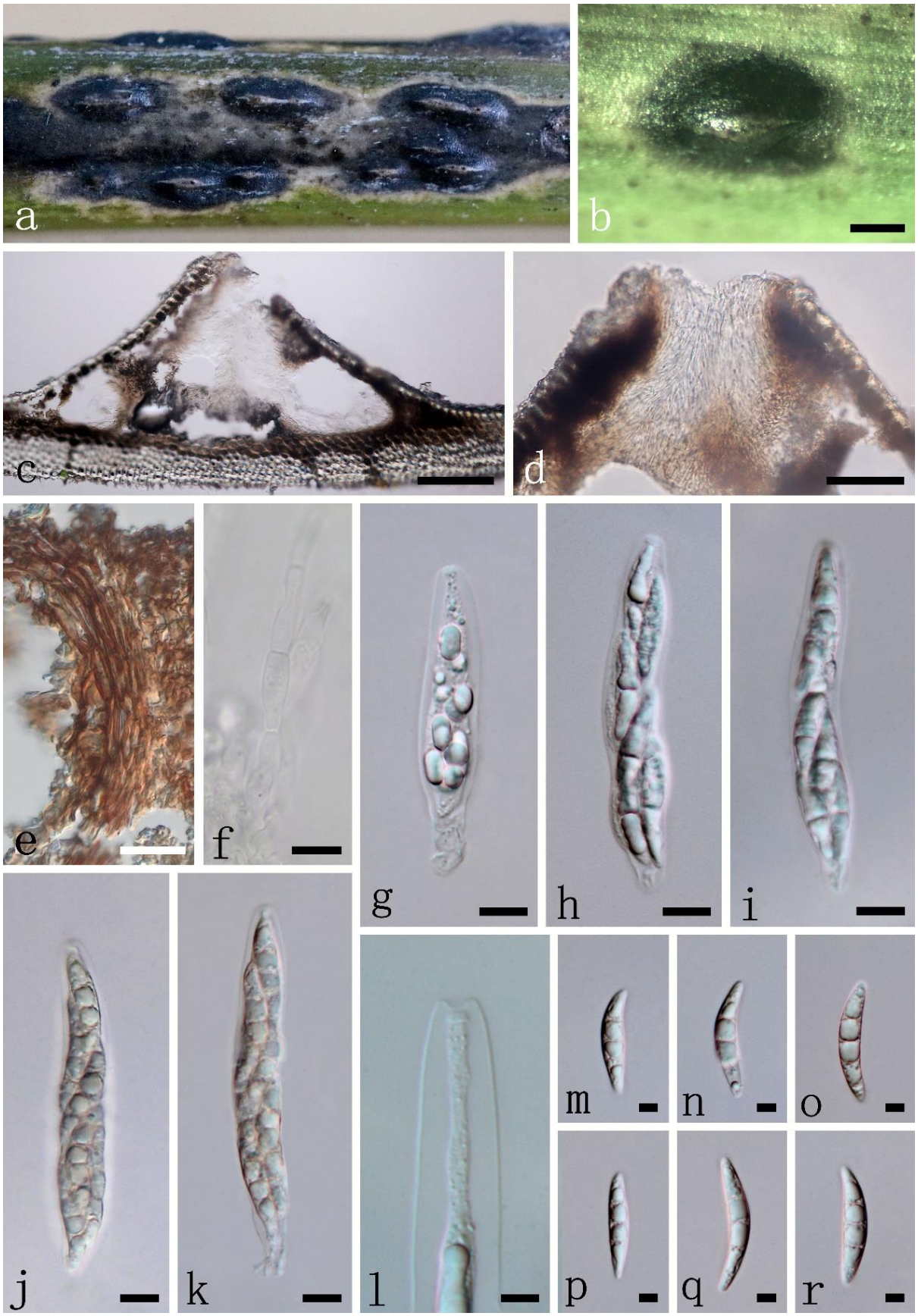

Figure 30 – *Bifusisporella fusispora* (SICAU 23-0027, holotype). a, b Ascostromata on host surface. c Section through ascostroma. d Close up of ostiole. e Peridium. f Paraphyses. g–k Asci. l Ascus apex. m–r Ascospores. Scale bars: b = 200 μm, c = 100 μm, d = 50 μm, e–k = 10 μm, l–r = 5 μm.

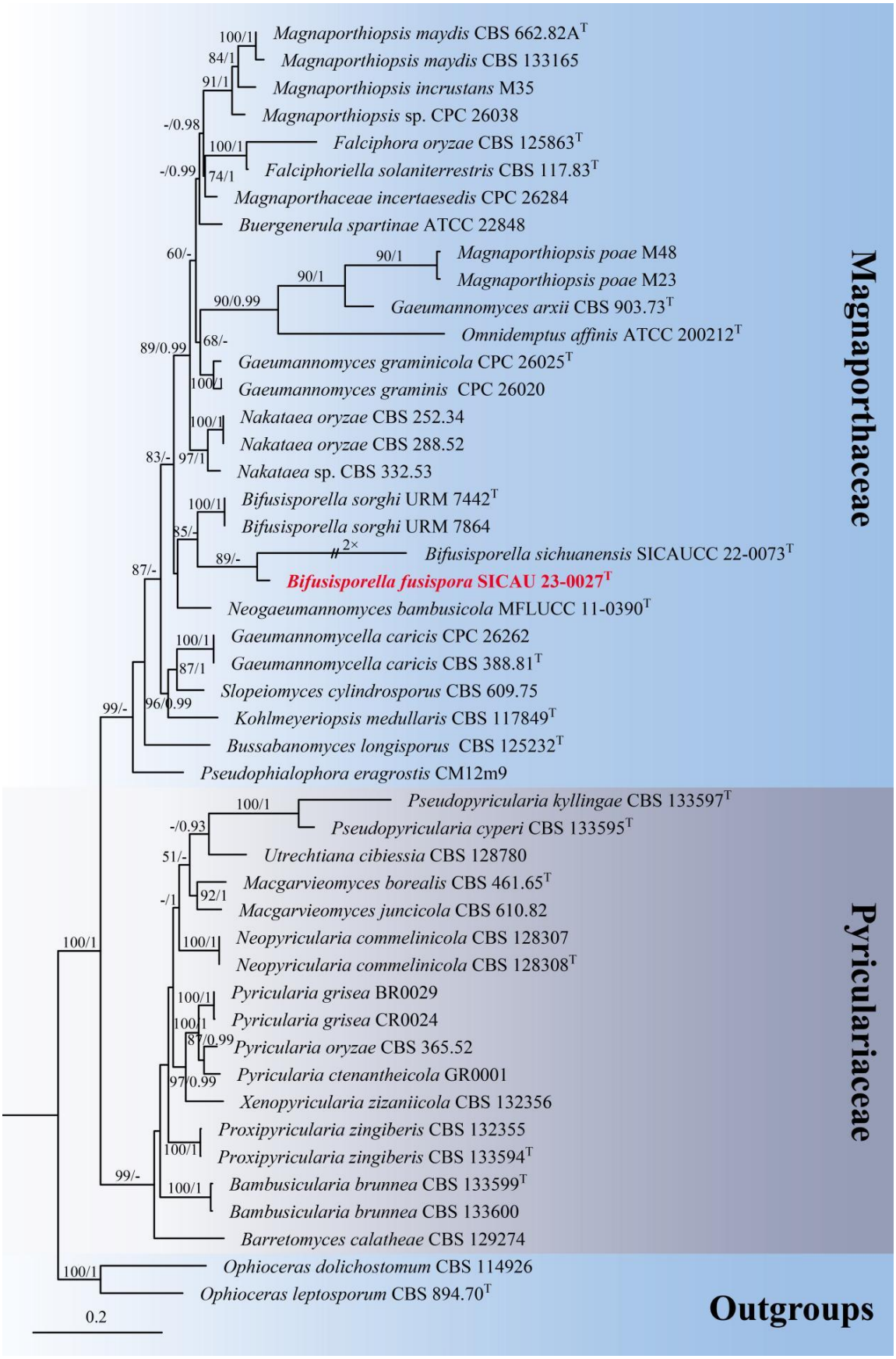

Figure 31 – Phylogenetic analyses of a concatenated aligned dataset (ITS, LSU, *rpb*1, and *tef*1-α), including 47 taxa within *Magnaporthaceae* and *Pyriculariaceae*, were conducted and tree was rooted with *Ophioceras dolichostomum* (CBS 114926) and *O. leptosporum* (CBS 894.70) (*Ophioceraceae*, *Magnaporthales*). The alignment contained 4,040 characters (ITS = 858, LSU =

1,304, *rpb*1 = 1,289, *tef*1-α = 1,085), including gaps. The best scoring RAxML tree with a final likelihood value of -33,754.245612 is presented. The matrix had 2,069 distinct alignment patterns, with 41.91% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245405, C = 0.272352, G = 0.280135, T = 0.202109, with substitution rates AC = 1.278688, AG = 2.333487, AT = 1.537577, CG = 1.121551, CT = 5.700157, GT = 1.000000. The gamma distribution shape parameter α = 0.513984, and the tree length = 4.39872. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The ex-type strains are indicated with "T" after the strain number label. The newly generated sequence is written in red.

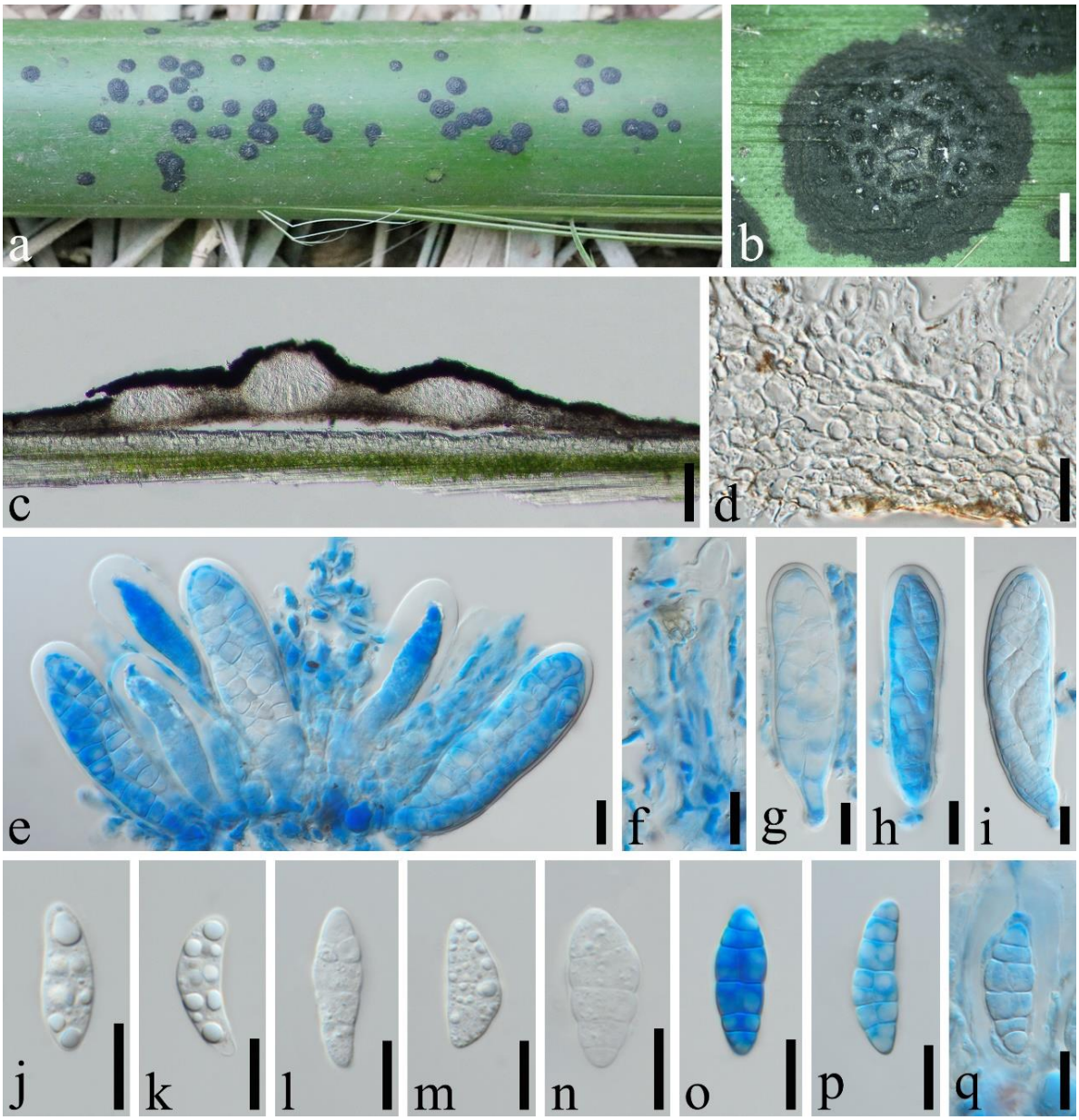

Figure 32 – *Mendogia sichuanensis* (SICAU 23-0028, holotype). a, b Ascostromata on bamboo host. c Section through ascostroma showing locules. d Peridium. e Asci with cellular pseudoparaphyses stained by cotton blue. f Cellular pseudoparaphyses. g–i Asci. j–q Ascospores. Scale bars: b = 500 μm, c = 100 μm, d–q = 10 μm.

Obligate epiphytic on culms of *Bambusa multiplex*. Sexual morph: *Ascostromata* 1.8–3.5 mm diam, 105–150 μm high, solitary, or gregarious, scattered, superficial, round to elliptical, black, coriaceous, flattened, low convex, and central peripheral wall of stromata cracking, with irregular

edge, rugose to rugulose at surface, easily removed from the host surface. *Peridium* thick-walled, composed of two type cells, outer layer 30–40 μm thick, thin-walled, composed of black tissue and easily breaking, inner layer 20–35 μm thick, thick at the base towards the sides and apex, composed of hyaline to brown, pseudoparenchymatous cells of *textura angularis*. *Asci* arranged in type II, 55–95 × 12–19 μm ($\overline{x}$ = 70 × 16 μm, n = 20), 8-spored, bitunicate, fissitunicate, subglobose to clavate, with short, rounded pedicel, apically rounded with well-developed ocular chamber. *Ascospores* 21–26 × 9–11 μm ($\overline{x}$ = 24 × 10 μm, n = 20), partially overlapping, irregularly arranged, hyaline, muriform, frequently ellipsoidal to ovoid, with rounded ends, with 3–6 transverse septa and 1 longitudinal septum, surrounded constricted at the septa, occasionally asymmetrical, constricted at the septa, smooth-walled, narrow at basal end, occasionally narrow at both ends, without a gelatinous sheath. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Luzhou City, Naxi District, Shangma Town, Jiangtian Village 2 Society (105°20'45"E, 27°31'41"N, alt. 270 m), on twigs and culms of *Bambusa multiplex*, 28 July 2021, Qian Zeng, ZQ202107185 (SICAU 23-0028, holotype).

GenBank numbers – SICAU 23-0028 – ITS = OR405945, LSU = OR405926, SSU = OR405947, *tef*1-α = OR947489.

Notes – *Mendogia sichuanensis* differs from other *Mendogia* species in the size of ascomata, asci and ascospores, having 3–6 transverse septa and 1 longitudinal septum (Table 3). Phylogenetic analyses based on a combined ITS, LSU, SSU, and *tef*1-α sequenced dataset (Fig. 33) showed that *M. sichuanensis* is distinct from *M. yunnanensis* (MFLU 19-006, holotype). Striking base-pair differences are also noted, viz. 5.67% (48/846, 0 gap), 3.41% (28/819, 0 gap), in the LSU and SSU. However, the latter lacks ITS and *tef*1-α sequences for further comparisons. The PHI test also revealed no significant genetic recombination levels between *M. sichuanensis* and closely phylogenetically related species occurred (Fig. 34), suggesting that they are not conspecific. In addition, *Mendogia sichuanensis* differs from *M. yunnanensis* by its slender asci (55–95 × 12–19 μm vs. 55–75 × 25–30 μm) with different ascus formation (Type II vs. Type I) and slightly larger ascospores (21–26 μm vs. 19–23 μm), and ascospores of *M. yunnanensis* are surrounded by shallow sheath at both ends, while in *M. sichuanensis*, sheaths are lacking (Jiang et al. 2020). Therefore, *M. sichuanensis* is introduced as a new species in there.

Phyllachoraceae Theiss., P. Syd., Annls mycol. 13(3/4):168 (1915)

The family *Phyllachoraceae* was introduced by Theissen & Sydow (1915). In subsequent taxonomic assessments, Hawksworth (1985) identified 23 genera, while Barr (1990) provided a key for genus of *Phyllachoraceae* with 12 included genera. Eriksson & Hawksworth (1993) expanded the recognition to 39 genera, and later Hawksworth et al. (1995) acknowledged 42 genera. Notably, Pearce & Hyde (2001) introduced the novel genus *Parberya*. In a more recent study, Maharachchikumbura et al. (2016) listed 59 genera within the *Phyllachoraceae*, based on available morpho-molecular data. *Phyllachoraceae* members are characterized by ascohymenial development accompanied by paraphyses, and thin-walled asci. These asci may possess an apical ring, which does not exhibit a blue stain in the presence of iodine (J-). The ascospores of these taxa are often hyaline and consist of a single cell (Cannon 1991). As for the asexual morphs, they are coelomycetes, spermatial, or disseminative in nature (Hawksworth et al. 1995). *Phyllachoraceae* species are obligate biotrophs, recognized as initial pathogens that facilitate pathways for secondary infections by other pathogens (Pearce et al. 1999).

Phyllachorales M.E. Barr, Mycologia 75(1): 11 (1983)

Phyllachora Nitschke ex Fuckel, Jb. nassau. Ver. Naturk. 23–24: 216 (1870) [1869–70]

Phyllachora was introduced from the herbarium in Fuckels exsiccate series ‘Fungi Rhenani’ with a single species, *P. agrostis* (Fuckel 1870). Later the genus was lectotypified with *Phyllachora graminis* as the generic type (Clements & Shear 1931), with the type genus of *Phyllachoraceae*, and accommodates species that grow immersed as a clypeate pseudostroma in leaf tissues, varying

from a subcuticular or intraepidermal condition, to a generalized infection of the entire section of the mesophyll, inducing characteristic black shiny superficial symptoms. The estimated number of *Phyllachora* species varies from 944 (Kirk et al. 2008) to 1,392 (Species Fungorum, September 2024). *Phyllachora* is characterized by black stromata of various shapes, but mostly rounded to oblong or elongated, superficial or subcuticular; globose, oval or irregular perithecia that are subcuticular or immersed in the host tissue; numerous paraphyses, that are slightly longer than asci;

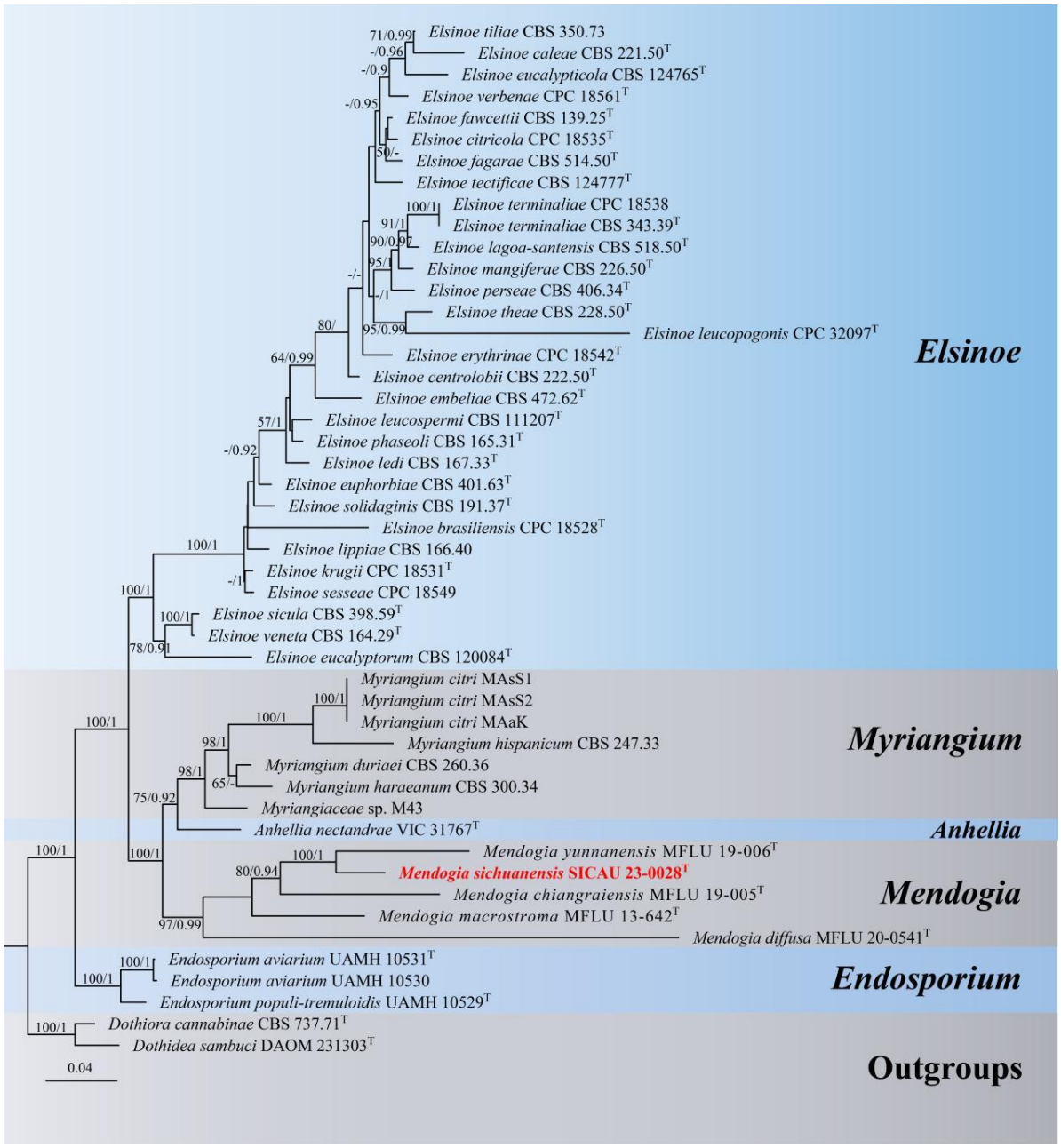

Figure 33 – Phylogenetic analyses of a concatenated aligned dataset (ITS, LSU, SSU, and *tef*1-α), including 48 taxa within *Myriangiales*, were conducted and tree was rooted with *Dothidea sambuci* (DAOM 231303) and *Dothiora cannabinae* (CBS 737.71). The alignment contained 5,685 characters (ITS = 939, LSU = 1,924, SSU = 1,784, *tef*1-α = 1,029), including gaps. The best scoring RAxML tree with a final likelihood value of -24,651.704027 is presented. The matrix had 1,559 distinct alignment patterns, with 60.15% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239775, C = 0.253020, G = 0.283172, T = 0.224033, with substitution rates AC = 1.434171, AG = 2.427343, AT = 1.495257, CG = 1.348550, CT = 6.854382, GT = 1.000000. The gamma distribution shape parameter α = 0.293327, and the tree

length = 1.816068. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 50% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The ex-type strains are indicated with "T" after the strain number label. The newly generated sequence is written in red.

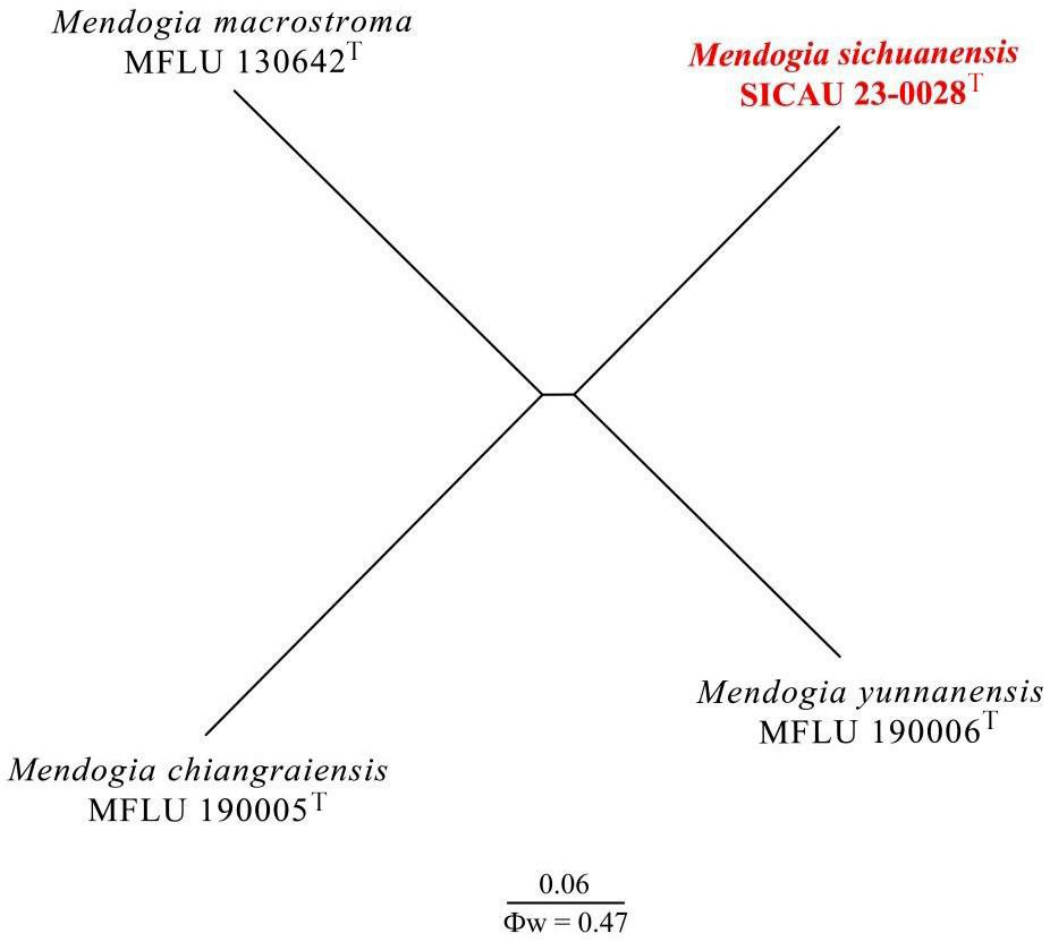

Figure 34 – The splits graph from the pairwise homoplasy index (PHI) test generated from the concatenated gene set of SSU, LSU, ITS, and *tef*1-α sequence data of closely related species of *Mendogia* using both LogDet transformation and splits decomposition. PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset. The ex-type specimens are indicated with "T" after the strain number label. The strain determined in this study is in bold and red.

asci 4–8-spored, persistent, cylindrical to fusiform, hyaline, short pedicellate, often with an apical ring; and 1–3-seriate ascospores that are round, ovate, oval or spindle-shaped, hyaline or faintly yellow, smooth or verrucose, and sometimes with a gelatinous sheath (Zhang et al. 2014, Maharachchikumbura et al. 2016, Santos et al. 2016, Dayarathne et al. 2017, Yang et al. 2019d). *Phyllachora* species are biotrophic obligate plant parasites with diverse hosts, especially grasses of tropical and subtropical distribution (Li et al. 2018, 2019, 2022a, Yang et al. 2019d).

18. *Phyllachora dendrocalami-membranacei* X.L. Li et al., Phytotaxa, 425(2): 82 (2019) Fig. 35

Index Fungorum number: IF831102; Facesoffungi number: FoF14790

Parasitic associated with leaves of *Bambusa emeiensis* L. C. Chia & H. L. Fung, causing tarspot on leaves. Tar spots 2–5 × 0.4–1.1 mm ($\overline{x}$ = 3.3 × 0.8 mm, n = 30) on the upper leaf surface, circular, black, shiny, with a yellow halo of discolored host tissue. Sexual morph: *Ascomata*, 400–1300 µm long × 260–750 µm width × 220–410 µm high ($\overline{x}$ = 747 × 483 × 291 µm, n = 50), immersed in the leaf tissue, occupying the entire leaf thickness, often developing next to adjacent

ascomata and confined by host vascular tissue, suboblate to subglobose with no obvious ostiole. *Peridium* composed of deeply melanised, dark-brown to black, host epidermal cells and occasionally cuticle and inner layers composed of several layers of hyaline, thin-walled, flattened cells. *Paraphyses* hyaline, filiform, unbranched, septate, not constricted at the septa, longer than asci, with tapering apices. *Asci* 148–184 × 10–15 μm ($\overline{x}$ = 170 × 13 μm, n = 50), 8-spored, unitunicate, long, cylindrical, short to medium pedicellate, apex obtuse to rounded. *Ascospores* 26–32 × 8–12 μm ($\overline{x}$ = 28 × 9.9 μm, n = 50), uniseriate, sometimes overlapping, and oblique, hyaline, dump-bell-shaped (with constrictions at the center), some are ellipsoidal, occasionally ovoid, one-celled, aseptate, some with one large fat globule in the centre. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Chengdu City, Qionglai City, Linji Town, Yinjiang Community (30°19'4.42"N, 103°17'23.6"E, alt. 518 m), on leaves of *Bambusa emeiensis*, 8 November 2020, Qian Zeng, ZQ202011002 (SICAU 23-0034).

GenBank numbers – SICAU 23-0034 – ITS = OR419576, LSU = OR419591, SSU = OR419583.

Notes – Phylogenetic analysis revealed that SICAU 23-0034 forms a sister clade with *Phyllachora dendrocalami-membranacei* (100% MLBS and 1.00 BYPP) (Fig. 36), specifically with *P. dendrocalami-membranacei* (MHYAU 222 and MHYAU 220). Sequence comparisons reveal a high similarity in their ITS (98.8%, 510/516, 0 gap) and LSU (99.1%, 775/782, 0 gap), signifying their close genetic relationship. In addition, our morphological analysis of the new collection was consistent with the species described by Li et al. (2019). The collection SICAU 23-0034 is therefore identified as *P. dendrocalami-membranacei*.

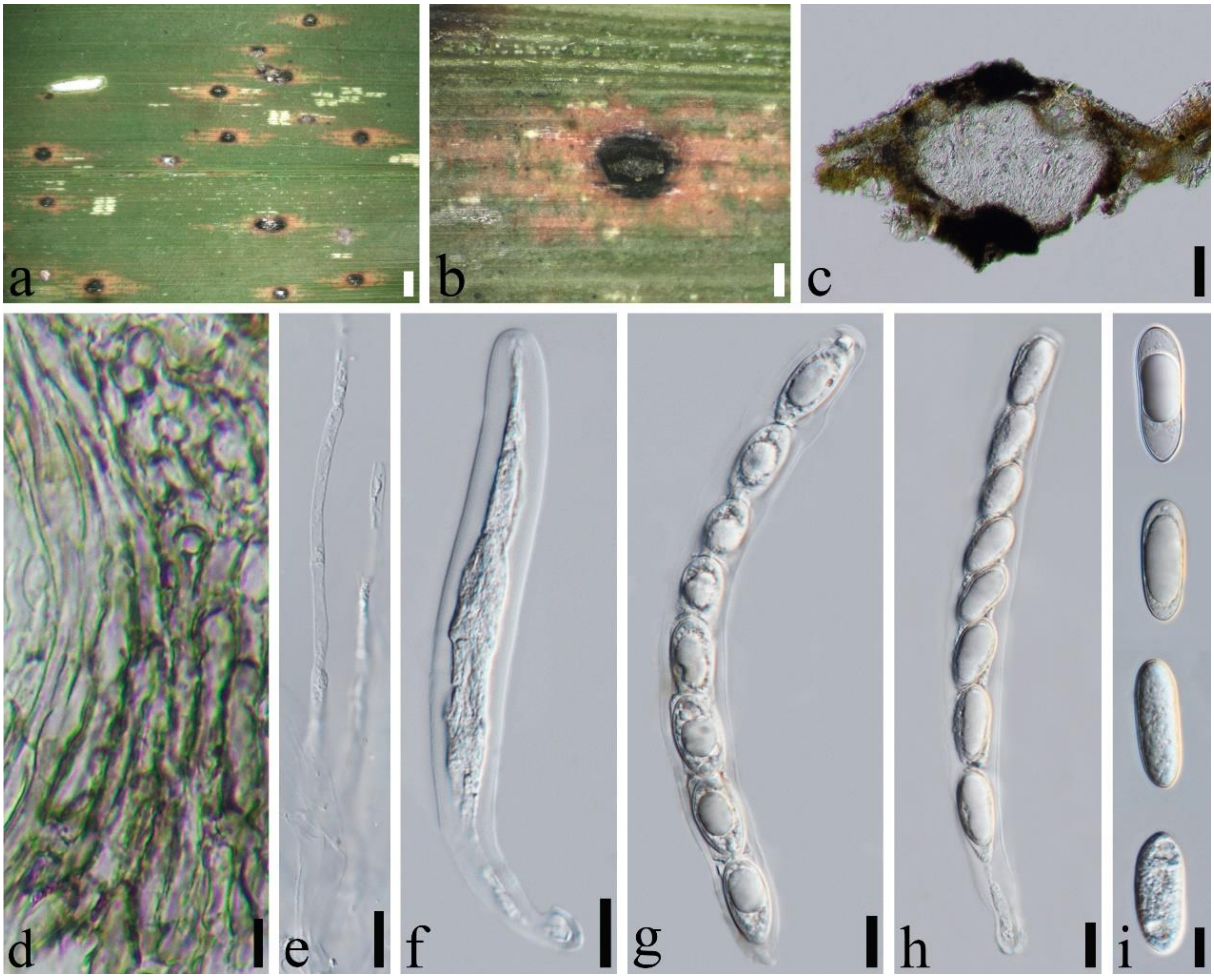

Figure 35 – *Phyllachora dendrocalami-membranacei* (SICAU 23-0034). a, b Appearance of ascomata on leaves. c Vertical section of ascoma. d Peridium. e Paraphyses. f–h Asci. i Ascospores. Scale bars: a = 1 mm, b = 200 μm, c = 100 μm, d–i = 5 μm.

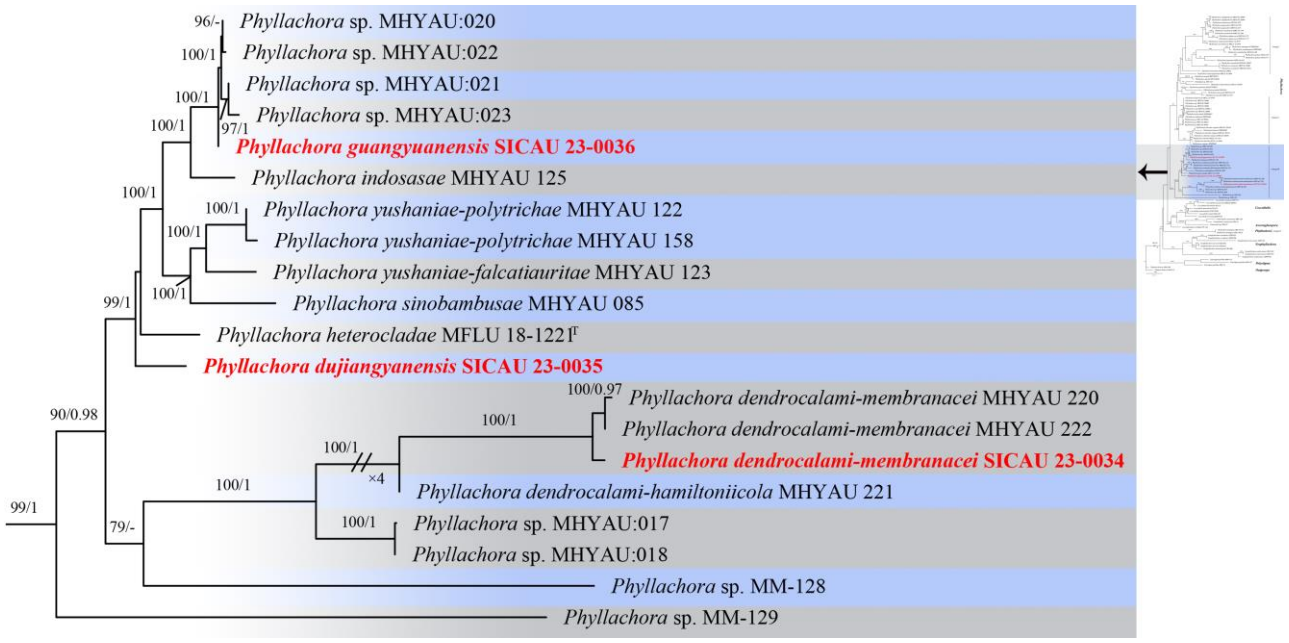

Figure 36 – Phylogenetic analyses of a combined dataset (LSU, ITS, and SSU), comprising 95 taxa within *Phyllachoraceae*, were conducted and tree was rooted with *Telimena bicincta* (MM-108) and *T. bicincta* (MM-133) (*Telimenaceae*, *Phyllachorales*). The alignment contained 4,442 characters (LSU = 1,182, ITS = 1,243, SSU = 2,017). The best scoring RAxML tree with a final likelihood value of -39,257.174 is presented. The matrix had 2,620 distinct alignment patterns. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250, with substitution rates AC = 1.00000, AG = 2.26764, AT = 1.00000, CG = 1.00000, CT = 3.40575, GT = 1.00000. The gamma distribution shape parameter α = 0.828, and the tree length = 6.797. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 75% and Bayesian posterior probabilities (BYPP, right) ≥ 0.90 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequences are written in red.

19. *Phyllachora dujiangyanensis* Y. Deng & C.L. Yang, sp. nov. Fig. 37

Index Fungorum number: IF900836; Facesoffungi number: FoF14791

Etymology – Referring to the collecting site, Dujiangyan City, Sichuan Province, China.

Holotype – SICAU 23-0035

Parasitic associated with leaves of *Chimonobambusa neopurpurea* 'Dujiangyan Fangzhu', causing tarspot on leaves. Tar spots 0.5–2 × 0.3–0.5 mm ($\bar{x}$ = 1.3 × 0.3 mm, n = 30) on the upper leaf surface, spindle-shaped, black, shiny, sometimes pale yellow to yellow stripe at the edge of tar spots. Sexual morph: *Ascomata* 320–1010 µm long × 170–480 µm width × 90–200 µm high ($\bar{x}$ = 647 × 300 × 128 µm, n = 50), immersed in the leaf tissue, occupying the entire leaf thickness, often developing next to adjacent ascomata and confined by host vascular tissue, suboblate to subglobose, sometimes irregular and no obvious ostiole. *Peridium* composed of dark-brown to black, host epidermal cells and occasionally cuticle and inner layers composed of several layers of hyaline, thin-walled, flattened cells. *Paraphyses* hyaline, filiform, unbranched, septate, not constricted at the septa, longer than asci. *Asci* 84–148 × 8–13 µm ($\bar{x}$ = 119 × 10.8 µm, n = 50), 8-spored, long, cylindrical, apex obtuse to rounded. *Ascospores* 12–21 × 4–8 µm ($\bar{x}$ = 15 × 6 µm, n = 50), uniseriate, sometimes overlapping and oblique, hyaline, some are ellipsoidal, occasionally ovoid, one-celled, aseptate, some with one large fat globule in the centre. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Haihong Community (31°6'26.87"N, 103°44'32.96"E, alt. 730 m), on leaves of *Chimonobambusa neopurpurea* 'Dujiangyan Fangzhu', 30 June 2022, Yu Deng, DY202206004 (SICAU 23-0035, holotype).

GenBank numbers – SICAU 23-0035 – ITS = OR419575, LSU = OR419590, SSU = OR419582.

Notes – In the phylogenetic tree, *Phyllachora dujiangyanensis* (SICAU 23-0035) constitutes an independent lineage within *Phyllachora*, with 99% MLBS/1.00 BYPP support (Fig. 36). Notably, *P. dujiangyanensis* displays distinct characteristics as compared to *P. heterocladae* (MFLU 18-1221, holotype) (Yang et al. 2019d). Specifically, it has smaller asci (84–148 × 8–13 μm vs. 167–190 × 9.9–17 μm) and smaller ascospores (12–21 × 4–8 μm vs. 17–27 × 6–8 μm). Furthermore, asci of *P. dujiangyanensis* lack a discernible apical ring. Nucleotide comparisons revealed notable genetic dissimilarities between *P. dujiangyanensis* and *P. heterocladae* (MFLU 18-1221), with sequence divergences of 10.39% (47/452, 0 gap), 3.72% (32/858, 0 gap), and 0.6% (6/887, 0 gap) observed in the ITS, LSU, and SSU, respectively. These findings strongly support the proposition of establishing *Phyllachora dujiangyanensis* as a new species based on both its morphological characteristics and phylogeny following the guidelines of Maharachchimbura et al. (2021).

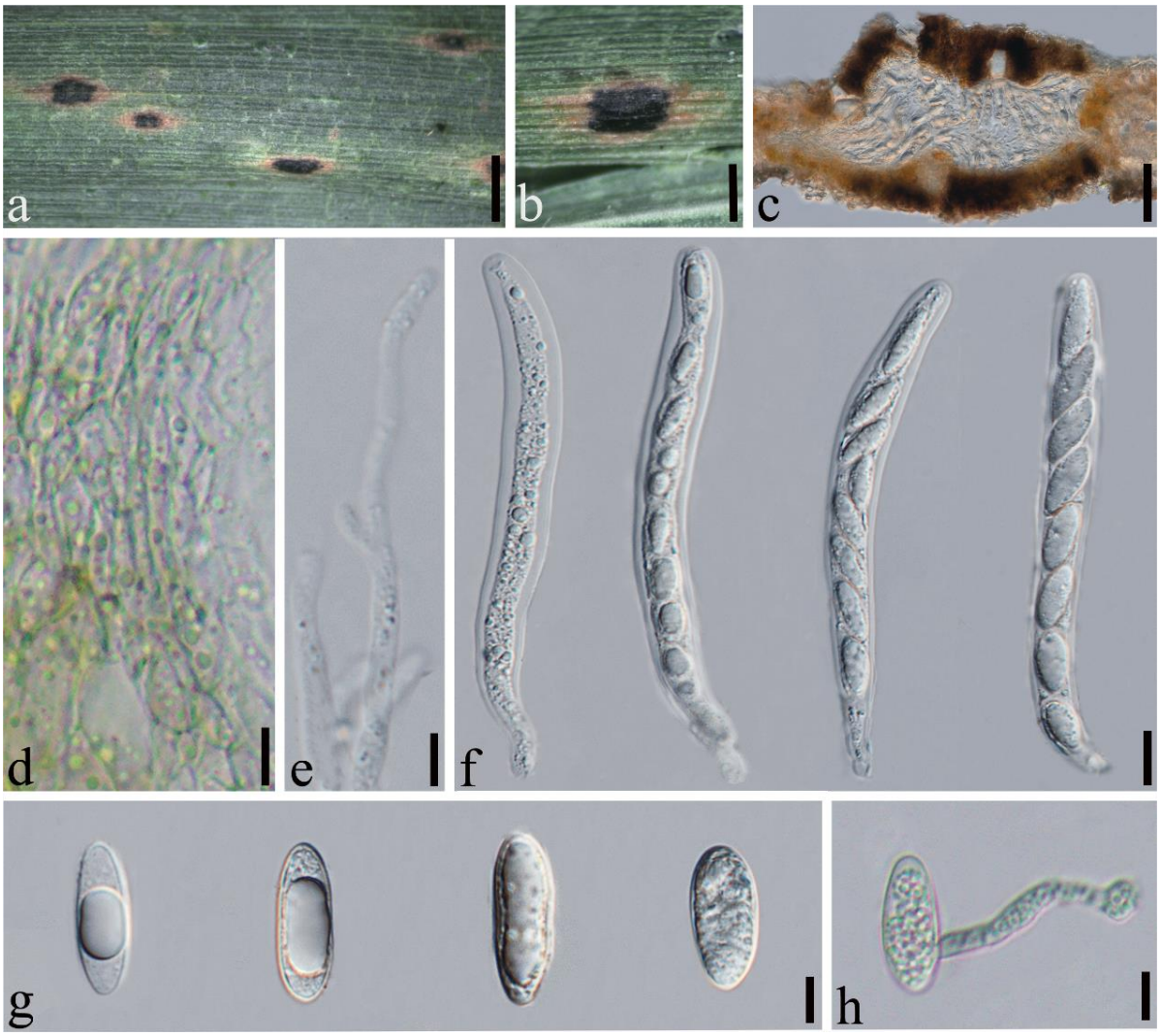

Figure 37 – *Phyllachora dujiangyanensis* (SICAU 23-0035, holotype). a, b Appearance of ascomata on leaves. c Vertical section of ascoma. d Peridium. e Paraphyses. f Asci. g Ascospores. h Germinating ascospore. Scale bars: a = 900 μm, b = 200 μm, c = 30 μm, f = 10 μm, d, e, g, h = 5 μm.

20. *Phyllachora guangyuanensis* Q. Zeng, Y. Deng & C.L Yang, sp. nov. Fig. 38

Index Fungorum number: IF900837; Facesoffungi number: FoF14792

Etymology – Referring to the collecting site, Guangyuan City, Sichuan Province, China.

Holotype – SICAU 23-0036

Parasitic associated with leaves of *Phyllostachys reticulata* f. *lacrima-deae* Keng f.et Wen, causing tarspot on leaves. Tar spots 1–4 × 0.4–0.9 mm ($\overline{x}$ = 2.3 × 0.7 mm, n = 30) on the upper leaf surface, elliptic or irregular, black, shiny, with a yellow halo of discolored host tissue. Sexual morph*: Ascomata* 550–1500 μm long × 110–670 μm width × 70–310 μm high ($\overline{x}$ = 1028 × 422 × 194 μm, n = 50), immersed in the leaf tissue, occupying the entire leaf thickness, often developing next to adjacent ascomata and confined by host vascular tissue, suboblate to subglobose and no obvious ostiole. *Peridium* composed of deeply melanised, dark-brown to black, host epidermal cells and occasionally cuticle, inner layers composed of several layers of hyaline, thin-walled, flattened cells. *Paraphyses* hyaline, filiform, branched, septate, not constricted at the septa. *Asci* 152–271 × 8–13 μm ($\overline{x}$ = 213 × 10 μm, n = 50) 8-spored, unitunicate, long, cylindrical, short to medium pedicellate, apex obtuse to rounded. *Ascospores* 15–32 × 5–11 μm ($\overline{x}$ = 26 × 7 μm, n = 50), uniseriate, sometimes overlapping and oblique, hyaline, ellipsoidal, occasionally ovoid, one-celled, aseptate, some with one or two large fat globules in the centre, surrounded by a gelatinous sheath. Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Guangyuan City, Lizhou District, Rongshan Town, Zhongkou Village (32°26'51.14"N 106°2'8.93"E, alt. 1285 m), on leaves of *Phyllostachys reticulata* f. *lacrima-deae*, 14 July 2022, Qian Zeng, ZQ202207137 (SICAU 23-0036, holotype).

GenBank numbers – SICAU 23-0036 – ITS = OR419577, LSU = OR419592, SSU = OR419584.

Notes – Multi-loci phylogenetic analyses based on a concatenated ITS, LSU, and SSU sequence dataset show that *Phyllachora guangyuanensis* forms a well-supported lineage (100% MLBS and 1.00 BYPP) (Fig. 36), sister to *P. indosasae* (MHYAU 125). *Phyllachora guangyuanensis* has larger ascomata (550–1500 × 110–670 μm vs. 285–434 × 127–231 μm), longer asci (213 μm vs. 129 μm) than *P. indosasae* (Wu et al. 2013). Comparison of LSU and ITS sequence data of *P. guangyuanensis* (SICAU 23-0036) and *P. indosasae* (MHYAU 125), revealed 25 bp (2.90%) across 853 LSU nucleotides and 24 bp (5%) across 480 ITS nucleotides without gaps. Therefore, we consider our collection (SICAU 23-0036) as a new species.

Basidiomycota

Pucciniomycetes

Pucciniales Caruel, Atti R. Accad. Naz. Lincei, Mem. Cl. Sci. Fis. Matem. Nat., sér. 5: 246 (1881)

Pucciniaceae Chevall. [as '*Puccinieae*'], Flore Générale des Environs de Paris 1: 413 (1826)

Pucciniaceae was proposed by Chevallier (1826) as the prototype family of *Pucciniales*, based on the characteristics of basidia and teliospores. Until this century, the classification of *Pucciniales* relied solely on morphological characteristics, which led to confusion in the categorization of genera within *Pucciniaceae*. Phylogenetic studies conducted by Aime et al. (2006), stimulated a revision of the classification within *Pucciniaceae*, and 23 genera have been documented in this family, namely *Baeodromus*, *Ceratocoma*, *Chardoniella*, *Chrycocelis*, *Cionothrix*, *Cumminsiella*, *Desmella*, *Didymopsora*, *Dietelia*, *Dipyxis*, *Edythea*, *Endophylloides*, *Endophyllum*, *Hapalophragmium*, *Leptopuccinia*, *Macropyxis*, *Miyagia*, *Puccinia*, *Pucciniosira*, *Sphenospora*, *Stereostratum*, *Uromyces*, and *Xenostele* (Aime et al. 2021). *Pucciniaceae* species are characterized by spermogonia group V (type 4) with aecia exhibiting aecidium-type characteristics, and uredinia predominantly displaying uredo-type traits, teliospores typically borne individually, mostly pedicellate, and usually with one or two cells, and basidia external. Most pucciniaceous species have a macrocyclic life cycle, although endocyclic and microcyclic species are also present. *Pucciniaceae* is the largest and most economically important family, with a diverse host range that includes *Berberidaceae*, *Ranunculaceae*, as well as various members of *Asteraceae*, *Euphorbiaceae*, *Fabaceae*, *Malvaceae*, *Orchidaceae*, *Poaceae*, and *Solanaceae* (Aime et al. 2018, Aime & Mctaggart 2021, Gautam et al. 2022).

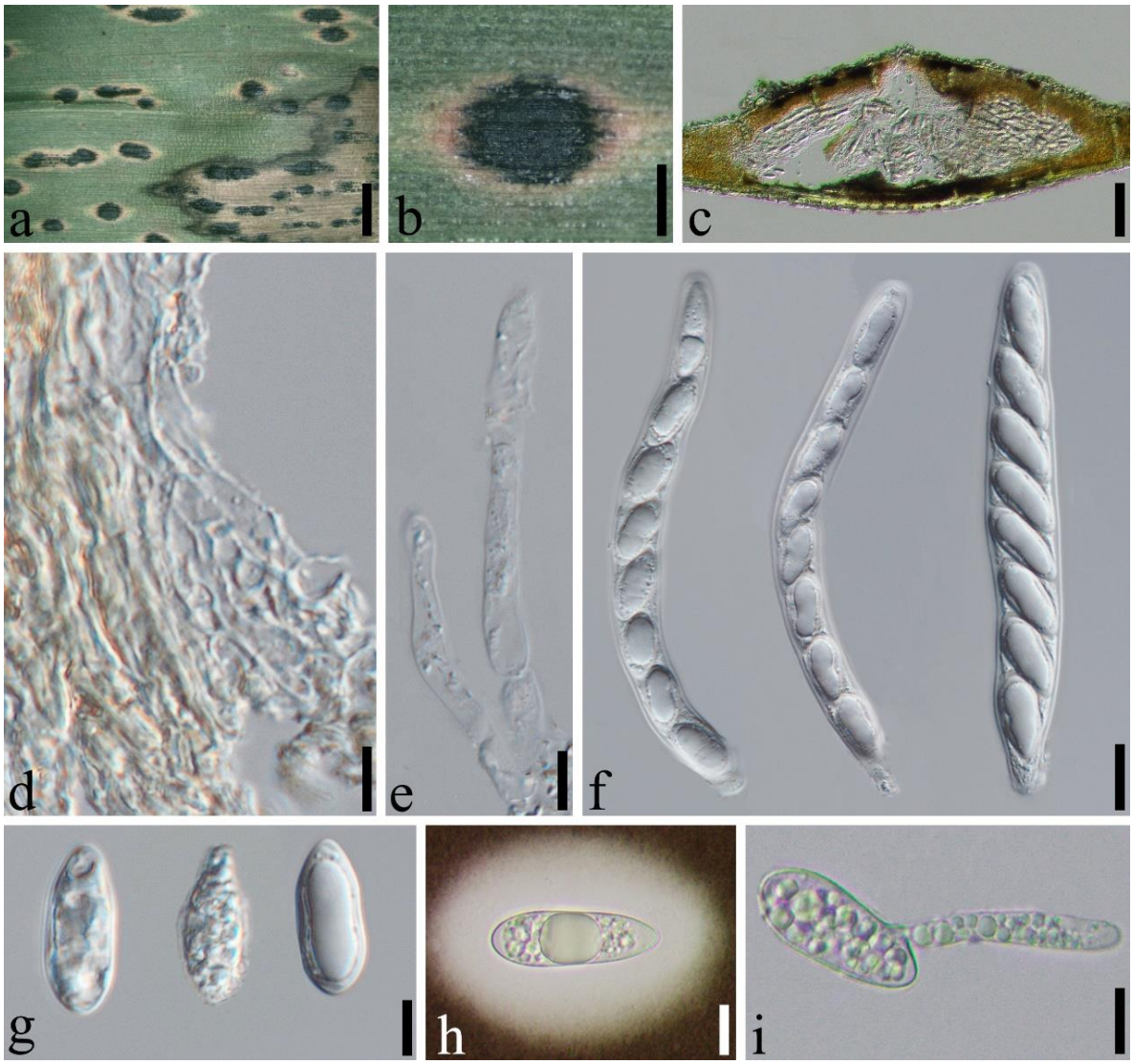

Figure 38 – *Phyllachora guangyuanensis* (SICAU 23-0036, holotype). a, b Appearance of ascomata on leaves. c Vertical section of ascoma. d Peridium. e Paraphyses. f Asci. g Ascospores. h Ascospore mounted in India ink. i Germinating ascospore. Scale bars: a = 2 mm, b = 500 μm, c = 100 μm, e = 10 μm, d, f–i = 5 μm.

Puccinia Pers., Neues Mag. Bot. 1: 118 (1794)

Puccinia was proposed by Persoon (1801), with *P. graminis* Pers. designated as the type species (Cunningham 1931). Subsequent research has revealed a rich diversity of *Puccinia*, with over 4,000 species identified, of which 3,300 species are currently recognized (Brondz 2014, Avasthi et al. 2023). *Puccinia* species may produce up to five distinct spore-producing structures, which differ both morphologically and cytologically. Their life cycle may involve two or more unrelated host plants (heteroecious rusts), or may be completed within a single host (autoecious rusts) plant (Avasthi et al. 2023).

These spore-producing structures, namely spermogonium, aecium, uredinium, telium, and basidium, represent the fundamental spore states in *Puccinia* species (Aime et al. 2021). *Puccinia* species typically manifest as yellow-orange or brown pustules on leaves, petioles, tender shoots, stems, and fruits. The pustules are often associated with chlorotic lesions, leading to premature wilting and senescence of infected leaves. The spore-producing pustules can be solitary, scattered, or grouped, and appear linear, concentric, or irregular, and are often erumpent. *Puccinia* members have a wide host range and distribution, and are particularly abundant on plant hosts belonging to the families *Asteraceae*, *Poaceae*, and *Ranunculaceae*. As with all rust fungi, *Puccinia* taxa are

obligate parasites that propagate through spores, primarily targeting the aerial parts of their host plants.

21. *Puccinia chimonobambusadis* Y. Deng & C.L. Yang, sp. nov. Fig. 39

Index Fungorum number: IF900838; Facesoffungi number: FoF14793

Etymology – Refers to the host genus, *Chimonobambusa*, from which the new taxon was collected.

Holotype – SICAU 23-0029

Parasitic on leaves of *Chimonobambusa utilis* (Keng) Keng f., causing leaf rust disease on host. *Spermogonia*, *aecia* and *telia*: undetermined. *Uredinia* hypophyllous, reddish, superficial, erumpent, subcircular or irregular, scattered in groups. *Urediniospores* 29–37.5 × 24–30 μm ($\overline{x}$ = 33.1 × 27.3 μm, n = 50), subglobose to globose, ellipsoidal or ovoid, yellow-brown, wall 0.8–2.8 μm ($\overline{x}$ = 2.0 μm, n = 50) thick, evenly thickened, echinulate, mostly 1–2 scattered germ pores.

Material examined – China, Sichuan Province, Guang'an City, Huayingshan City, Hongyan Village (106°49'35.81"E, 30°21'14.69"N, alt. 765 m), on leaves of *Chimonobambusa utilis*, 28 March 2019, Chunlin Yang, YCL201903014 (SICAU 23-0029, holotype); *ibid*. YCL201903016 (SICAU 23-0030).

GenBank numbers – SICAU 23-0029 – ITS = OR419570, LSU = OR419585, *CO*3 = OR540680; SICAU 23-0030 – ITS = OR419571, LSU = OR419586, SSU = OR419578, *CO*3 = OR540681.

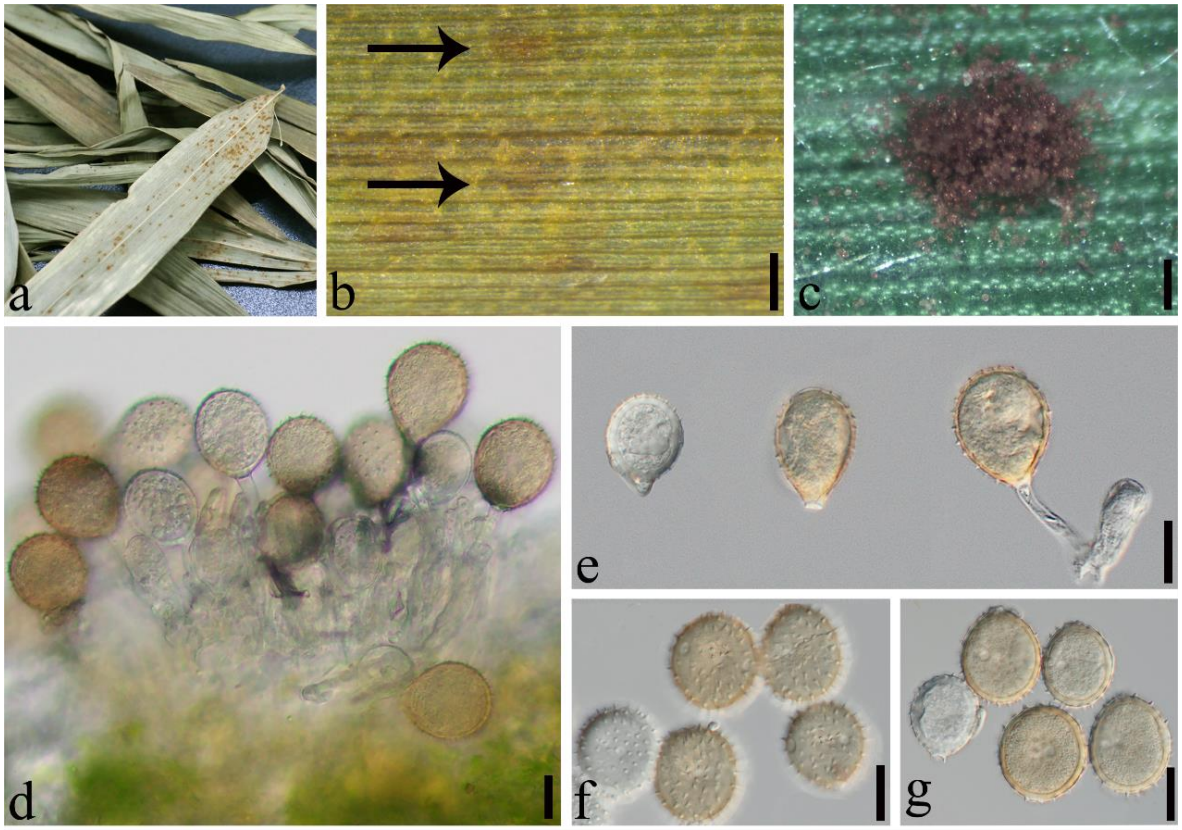

Figure 39 – *Puccinia chimonobambusadis* (SICAU 23-0029, holotype). a, b Uredinia on adaxial and abaxial leaves. c Uredinia. d Urediniospores with different developing stage. e, f Urediniospores. Scale bars: a = 1 mm, b = 150 μm, c–f = 20 μm.

Notes – In the phylogenetic tree, *Puccinia chimonobambusadis* constitutes a distinct subclade basal to *P. kusanoi*, *P. erianthi*, and *P. arundinariae* with high support (99% MLBS/0.98 BYPP) (Fig. 40). Despite a close phylogenetic relationship to these species, *P. chimonobambusadis* has only 1–2 germ pores whereas *P. arundinariae* has 3–5 scattered germ pores, *P. erianthi* has 3–4

scattered pores and *P. kusanoi* has (3–)4(–5) equatorial pores. The sequence comparisons show 3.7% (28/752 bp, 0 gap) differences in the LSU, between *P. chimonobambusadis* and the type strain of *P. erianthi* (HMAS350071). Therefore, we consider *P. chimonobambusadis* (SICAU 23-0029) to be a new species.

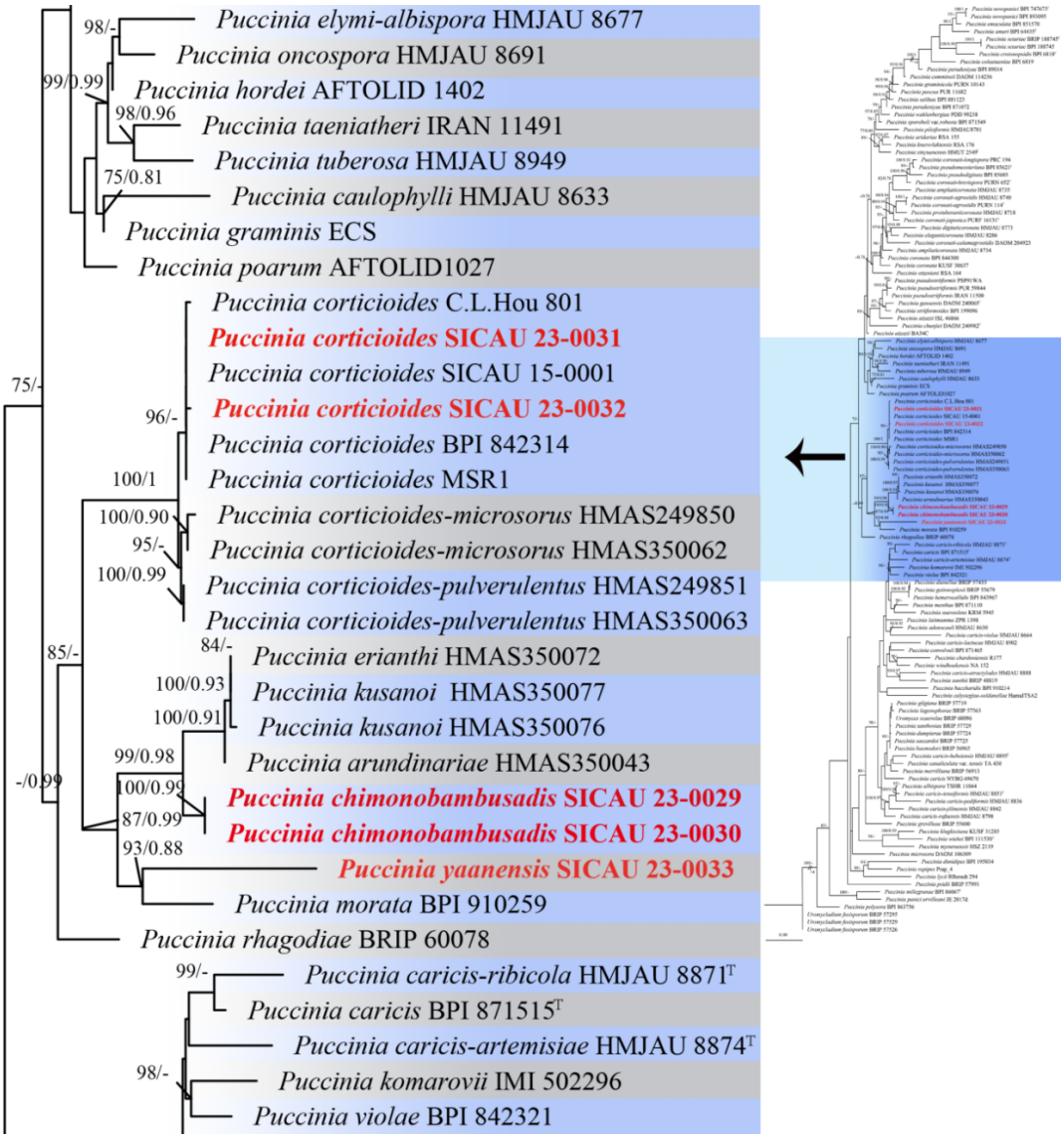

Figure 40 – Phylogeny of *Puccinia* reconstructed from a combined dataset (LSU and ITS) comprising 123 taxa within *Puccinia*, which is rooted with *Uromycladium fusisporum* (BRIP 57526, BRIP 57529, and BRIP 57295) (*Uromycladiaceae*, *Pucciniales*). The alignment contained 3,769 characters (ITS = 2,208, LSU = 1,561), including gaps. The best scoring RAxML tree with a final likelihood value of -25,623.690 is presented. The matrix had 1,709 distinct alignment patterns. Estimated base frequencies were as follows: A = 0.312, C = 0.163, G = 0.222, T = 0.303, with substitution rates AC = 1.77419, AG = 2.68716, AT = 2.07641, CG = 0.36875, CT = 4.26672, GT = 1.00000. The gamma distribution shape parameter α = 0.525, and the tree length = 4.714. Bootstrap support values for maximum likelihood (MLBS, left) ≥ 75% and Bayesian posterior probabilities (BYPP, right) ≥ 0.80 are indicated at the nodes, respectively. The sequences from ex-type strains are marked by a superscript symbol "T". The newly generated sequences are written in red.

22. ***Puccinia corticioides*** Berk. & Broome, J. Linn. Soc. Bot. 16 (89): 52 (1878) [1877] Fig. 41

Index Fungorum number: IF237523; Facesoffungi number: FoF14794

= *Stereostratum corticioides* (Berk. & Broome) H. Magn, Ber. dt. bot. Ges. 17: 181 (1899)

= *Dicaeoma corticioides* (Berk. & Broome) Kuntze [as '*corticiodes*'], Revis. gen. pl. (Leipzig) 3(3): 468 (1898)

Parasitic associated with culms of *Phyllostachys heteroclada* and *P. violascens* 'Prevernalis'. *Spermogonia* and *aecia*: undetermined. *Uredinia* in long series on the culms, stereum-like crusts, yellowish. *Urediniospores* 27–38 × 18–26 μm ($\bar{x}$ = 32.4 × 22.7 μm, n = 50), borne singly on pedicels, ellipsoidal, straw-yellow, wall 1–2.8 μm ($\bar{x}$ = 1.7 μm, n = 50) thick, evenly thickened, echinulate. *Telia* aggregated, in long series on culms and in stereum-like crusts, erumpent, pulvinate. *Teliospores* 20–34 × 12–25 μm ($\bar{x}$ = 27 × 18 μm, n = 50), 2-celled, occasionally 1-celled teliospores, buff, ellipsoidal or obovoid, walls 0.9–2.5 μm thick ($\bar{x}$ = 1.5 μm, n = 50) with unthickened at the apex, pedicels 125–246 μm ($\bar{x}$ = 177 μm, n = 20) length, hyaline.

Material examined – China, Sichuan Province, Ya'an City, Yucheng District, Yanchang Town (29°43'33.95"N 103°4'44.4"E, alt. 951 m), on culms of *Phyllostachys heteroclada*, 30 December 2015, Chunlin Yang, YCL201512001 (SICAU 23-0031); China, Sichuan Province, Ya'an City, Yucheng District, Zhongli Town (30°8'2.4"N 103°3'14.86"E, alt. 873 m), on culms of *P. violascens* 'Prevernalis', 16 March 2020, Chunlin Yang, YCL202003003 (SICAU 23-0032).

GenBank numbers – SICAU 23-0031 – ITS = OR419572, LSU = OR419587, SSU = OR419580; SICAU 23-0032 – ITS = OR419573, LSU = OR419588, SSU = OR419579, *tef*1-α = OR540683, *rpb*2 = OR540682.

Notes – This rust (SICAU 23-0031 and SICAU 23-0032) is similar to the known species *Puccinia corticioides* by its buff-coloured, smooth-walled, ellipsoidal or obovoid teliospores, and echinulate, ellipsoidal or obovoid urediniospores (Berkeley 1877, Okane 2020, Zhao et al. 2021). In addition, the phylogenetic analysis of a combination of ITS-LSU shows that our specimen is nested within *P. corticioides* complex with 96% MLBS/0.58 BYPP support (Fig. 40). The sequence comparison indicates a 99.76% (431/432, 0 gap) similarity in the ITS with *P. corticioides* (MSR1 and SICAU 23-0032), and 100% similarity (857/857, 0 gap) in the LSU with *P. corticioides* (BPI 842314 and SICAU 23-0032). Based on morphological characters and phylogenetic analyses, we determine our specimens as *P. corticioides.* Okane (2020) discovered that this rust produces spermogonia and aecia on *Choerospondias axillaris* (Roxb.) B. L. Burtt & A. W. Hill (*Anacardiaceae*).

23. *Puccinia yaanensis* Y. Deng & C.L. Yang, sp. nov. Fig. 42

Index Fungorum number: IF900839; Facesoffungi number: FoF14795

Etymology – Referring to the collecting site, Ya'an City, Sichuan Province, China.

Holotype – SICAU 23-0033

Parasitic on leaves of *Chimonobambusa szechuanensis* (Rendle) Keng f. causing leaf rust disease on host. *Spermogonia* and *aecia*: undetermined. *Urediniospores* 28–33 μm diam. ($\bar{x}$ = 30 μm, n = 20), globose, with translucent to distinctly brown walls, echinulate, with 1–2 equatorial germ-pores. *Telia* hypophyllous forming early exposed, 0.5–0.9 mm ($\bar{x}$ = 0.7 mm, n = 10) diam., covered with a layer of white basidia and basidiospores. *Teliospores* 20–52 × 6–16 μm ($\bar{x}$ = 35.46 ×10.78 μm, n = 50), with granular striae on the wall, fusiform or obovate, brown, constricted at the septum, with slender colorless thick-walled pedicels up to 150 μm long, with strongly thickened conical top, and a single apical germ pore, plus germ pore in lower cell immediately below septum. *Mesospores* 10–14 μm diam., spherical to ovate, smooth, thickened brown walls and with a single apical or subapical germ pore. *Basidia* 18–63 × 6.8–14 μm ($\bar{x}$ = 49 × 9.4 μm, n = 10), 4-celled, transparent, tubular or cruciform. *Basidiospores* 6.7–13 μm diam. ($\bar{x}$ = 10 μm, n = 20), transparent, ranging from wide oval to oval.

Material examined – China, Sichuan Province, Ya'an City, Yucheng District, Heilingang (29°50'5.38"N, 102°57'18.13"E, alt. 1245 m), on leaves of *Chimonobambusa szechuanensis*, 1 April 2023, Yu Deng, DY202304005 (SICAU 23-0033, holotype).

GenBank numbers – SICAU 23-0033 – ITS = OR419574, LSU = OR419589, SSU = OR419581.

Notes – In the phylogenetic analysis, *Puccinia yaanensis* (SICAU 23-0033) is closely related to *P. morata* (BPI 910259) with 93% MLBS/0.88 BYPP support (Fig. 40). However, *P. yaanensis* has smaller teliospores (20–52 × 6–16 μm vs. 50–75 × 14–20 μm) and conspicuous constrictive teliospores with a single septum. In addition, *P. morata* is parasitic on *Litsea* sp. (*Lauraceae*), completely different to bamboo (Cummins 1949). Sequence comparison reveals a divergence of 10.11% (36/356, 0 gap) in the LSU region between *P. yaanensis* and *P. morata*. Based on both morphological characteristics and phylogeny, the establishment of this new species is substantiated.

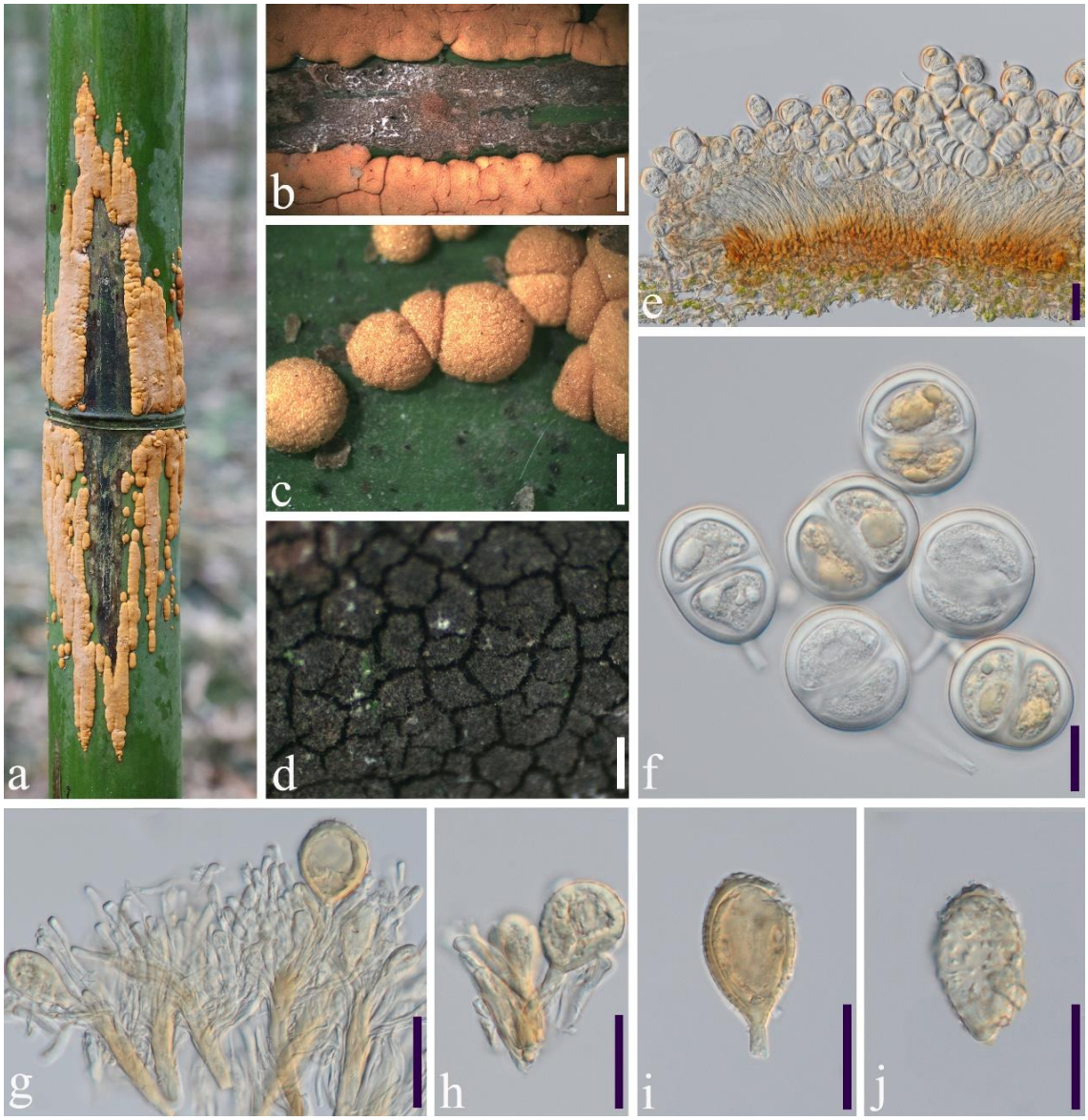

Figure 41 – *Puccinia corticioides* (SICAU 23-0032). a–b Uredinia and telia on the culm. c Telia. d Uredinia. e, f Teliospores. g, h Developing uredinia. i, j Urediniospores. Scale bars: b = 3.5 mm, c = 650 μm, d = 260 μm, e = 30 μm, f–j = 15 μm.

History of bambusicolous mycopathogens

The history of research into bambusicolous mycopathogens in China began with the description of *Oedocephalum glomerulosum* (Bull.) Sacc. (= *Oedocephalum glomerulosum* var. *cantonense* Teng) on culms of *Phyllostachys* sp. in Guangdong Province in 1932 (Teng 1996). For decades, the focus was not pathogenic fungi but rather on documenting bamboo fungi as a bioresource (Deng 1963, Tai 1979, Teng 1996, Zhang & Wang 1999). It was not until the 1960's that studies such as Zhao (1965), Chen (1980), Zhang (1982) and Zhu (1985) started paying

attention to bamboo diseases caused by fungi, *i.e.* culm rust, base rot, dieback and witches' broom. The period from 1960 to 2000 witnessed a significant expansion in the study of bambusicolous fungi. Kuai (1996) documented 191 pathogenic fungi in 118 genera. Zhou et al. (2000) conducted a comprehensive analysis of bambusicolous fungi in China, identifying 413 known species, among which 189 were from mainland China, 75 were from Hong Kong and 149 from Taiwan and their discussion predominantly centered on aspects such as the life history, host/substrate specialization and harmfulness of pathogens. Fungi causing bamboo timber decay and discoloration were investigated by some scholars (Zhao et al. 1994, Fu et al. 1999, Wang et al. 2000a, b). Xu et al. (2006) listed 208 species of pathogenic microorganisms and 183 species of fungi were recorded including 85 ascomycetes, 48 basidiomycetes and 50 hyphomycetes. Recent studies, such as those by Dai et al. (2022) and Jiang et al. (2022), have further documented the ascomycetes found on bamboo, highlighting a rich diversity of species but also pointing out the need for more specific studies on pathogens. Dai et al. (2022) documented 74 ascomycetes, predominantly saprobic taxa, found on bamboo in Yunnan and which were classified into *Sordariomycetes*, *Dothideomycetes*, *Eurotiomycetes* and *Leotiomycetes*. Jiang et al. (2022) summarized a checklist of bambusicolous ascomycetes in China, including 512 ascomycetous species, which belong to 50 orders, 116 families and 279 genera, but did not specifically address pathogens.

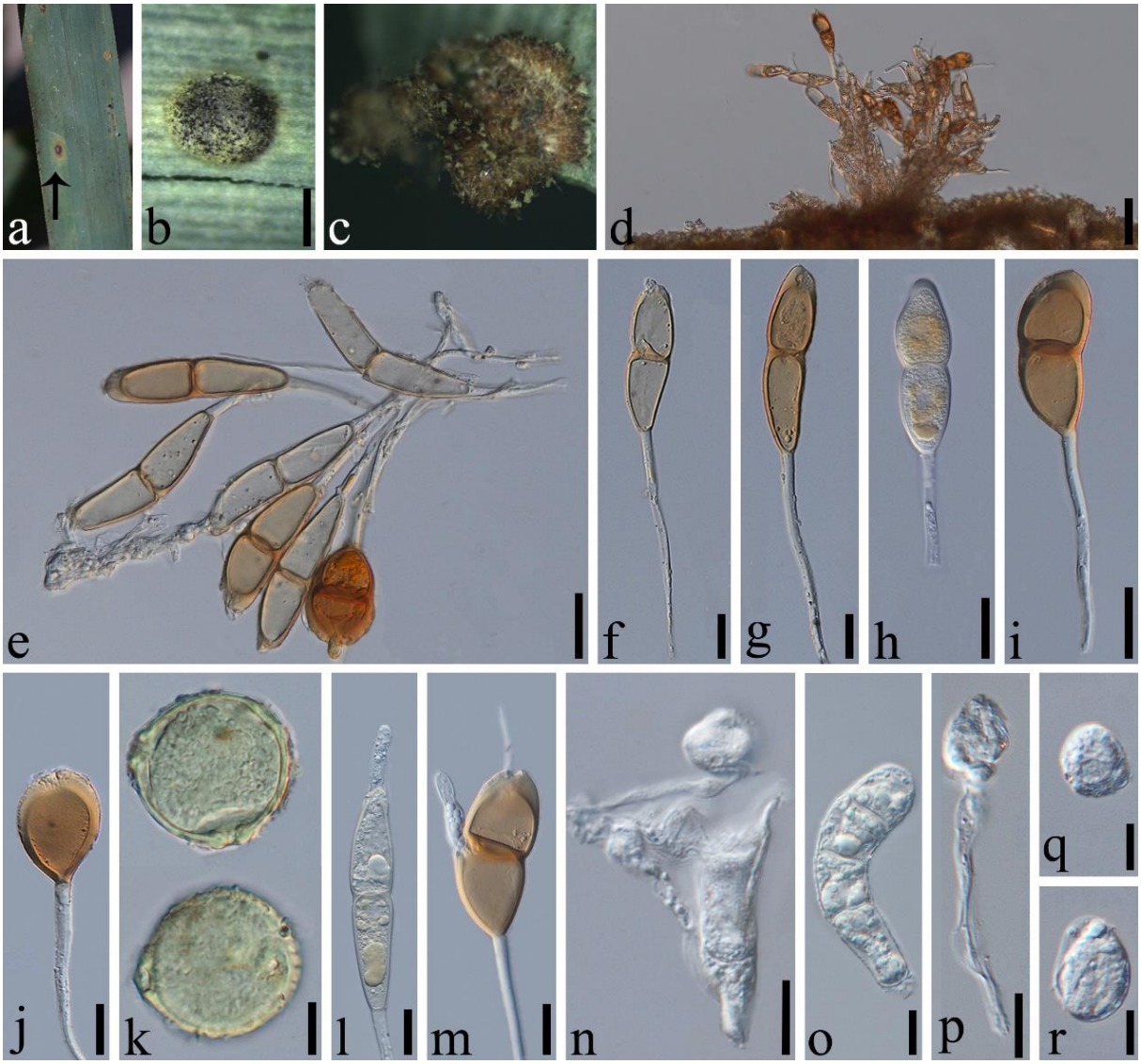

Figure 42 – *Puccinia yaanensis* (SICAU 23-0033, holotype). a–d Telia hypophyllous on leaves. e–i Teliospores. j Mesospores. k Urediniospores. l, m Germinating teliospores. n Developing

basidiospore on basidium. o Basidium. p Germinating basidiospore. q, r Basidiospores. Scale bars: b = 50 μm, c = 400 μm, d = 50 μm, e–h = 40 μm, i, l–n = 20 μm, j, k, o, p = 10 μm, q, r = 5 μm.

Studies on bambusicolous mycopathogens mainly focused on bioresource investigation, biological characteristics of pathogens, etiology and pathogenesis, disease control and management. Research results are mostly from the studies of economically important plants, e. g. *Bambusa pervariabilis* × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys edulis*, *P. heteroclada*, *P. sulphurea* var. *viridis* and *P. violascens* 'Prevernalis'. Dieback of *Phyllostachys edulis* caused by *Ceratosphaeria phyllostachydis* S. Zhang, first found in Ningbo of Zhejiang in 1959, was once epidemic and widespread in central and eastern provinces of China, resulting in severe economic losses and ecocatastrophe (Lin 2003). Nowadays, this disease has been well-understood with at least two generations of work and more than 70 papers published (Zhang 1982, Qiu et al. 1991, Lin 2001, Wei 2005). Hybrid bamboo (*Bambusa pervariabilis* × *grandis*) blight caused by '*Arthrinium*' *phaeospermum* (Corda) M.B. Ellis, which was initially reported in Sichuan in 2003, has been also studied systematically and comprehensively, culminating in 60 papers in various journals which dealt mostly on the pathogenesis of '*Arthrinium*' *phaeospermum* (Li et al. 2011, 2013, 2014a, 2015, Li & Zhu 2012, Fang et al. 2022), disease-resistance mechanism of the host (Li et al. 2018, Yan et al. 2022), and studies on antagonistic microbes (Xu et al. 2014, 2016, Zhang et al. 2014, Qiao et al. 2015). Culm rust and witch's broom on bamboos have been published in a variety of literature, but most of them are descriptive or investigative studies, lacking in-depth biological research at the molecular level (Zhu et al. 1983, Yang et al. 2001, Li et al. 2003, Yang & Wu 2011). In addition, some researchers focused on edible and medicinal value of bambusicolous mycopathogens, e. g. *Shiraia bambusicola* Henn., *Engleromyces goetzei* Henn., *Scorias spongiosa* (Schwein.) Fr., and *Rubroshiraia bambusae* D.Q. Dai & K.D. Hyde (Jia et al. 2006, He et al. 2012, Dai et al. 2019, Zhang et al. 2019a).

At least 400 scholars have so far worked on fungal diseases affecting bamboos, with approximately 35% being non-Chinese individuals mainly engaged as collaborators (Deng 1963, Tai 1979, Teng 1996, Zhou et al. 2000, Dai et al. 2017, 2022, Jiang et al. 2022, Zeng et al. 2022). Before 2000, systematic cataloging work on fungi in China, including bambusicolous fungi and mycopathogens, was mainly represented by Shuqun Deng, Fanglan Dai, Shiying Kuai, Ove E. Erriksson, and Liqin Zhang (Deng 1963, Tai 1979, Kuai 1996, Eriksson & Yue 1998, Zhang 2000). Subsequently, Dequn Zhou and Kevin D. Hyde analyzed the biodiversity of bambusicolous fungi in China, and indicated that abundant species resources distributed within the territory, but a few species known to us (Zhou et al. 2000, Hyde et al. 2002). C. Mohanan has published a monograph with two versions in 1997 and 2017 summarizing bamboo diseases in Asia with 580 mycopathogens across 300 genera, with only 75 species of fungi recorded in China (Mohanan 1997, 2017). Two main contents, pathogenetic characters and control measures, were summarized in this monograph. Following Shiying Kuai, Meiqing Xu has arranged pathogenic fungi on bamboos by species, hosts and geographical sites (Kuai 1996, Xu et al. 2006). Zhongyi Zhang and others focused on *Phyllachora* as pathogen of tar spot and described 27 species from bamboos (Zhang & Zhang 2014). Some researchers have studies mycopathogens on bamboo timbers, such as Guihua Zhao, and Wenjiu Wang (Zhao et al. 1994, Wang et al. 2000a, b). Despite the progress, challenges remain in understanding the full scope of bambusicolous mycopathogens. The research has often been fragmented, focusing on specific diseases or pathogens. The economic, ecological and cultural importance of bamboo in China and across Asia highlights the need for continued research, particularly in disease control and management strategies.

Classification of bambusicolous mycopathogens

This present study on the classification of bambusicolous mycopathogens offers a comprehensive update, drawing from a wide range of biodiversity studies, bamboo disease reports and related literature. This research has identified a total of 336 species of fungi (three phyla and 11 classes) that affect and colonize bamboos, excluding new collections described within the study

itself. A significant portion of these species, approximately 81%, are classified under the phylum *Ascomycota*, with another 17.9% under *Basidiomycota*, showcasing the dominance of these groups in bamboo pathology. The total number of bambusicolous mycopathogens in China accounted for 25% and 47% of bambusicolous fungi and mycopathogens in the world respectively, and ~76% of the total number of bambusicolous fungi in China (Zhou et al. 2000, Hyde et al. 2002, Xu et al. 2006, Mohanan 2017, Dai et al. 2022, Jiang et al. 2022, Zeng et al. 2022). In general, most mycopathogens have been reported before 2000 and then 109 new mycopathogens have been described, including 80 new taxonomic names (four new genera, 37 new species, 30 new combinations, and nine illegal names) (Table 4). Yunnan and Sichuan provinces emerge as hotspots for new discoveries, contributing 61 new species to the total count (Yang et al. 2019a, Wei et al. 2021a, Dai et al. 2022, Jiang et al. 2022, Zeng et al. 2022). This finding is notably intriguing, as over a third of these species were discovered within bamboo timber, highlighting the significant role that bamboo plays within the ecosystems and economy of these regions (Wu & Weng 1990, Fu et al. 1999, Ma et al. 2009a, b, Mohanan 2017). The most commonly reported mycopathogens belong to the orders *Phyllachorales*, *Hypocreales*, *Pleosporales*, *Pucciniales*, *Xylariales*, *Eurotiales*, and *Capnodiales*, especially in the families *Phyllachoraceae* and *Pucciniaceae*, which are almost distributed in all present distribution area of bambusicolous mycopathogens in China (Xu et al. 2006, Zhang & Zhang 2014, Mohanan 2017).

The most dominant species were recovered from the *Ascomycota* with 272 species (133 genera), followed by *Basidiomycota* with 60 species (25 genera), and *Mucoromycota* with four species (three genera) (Table 5). Within *Ascomycota*, *Sordariomycetes* was most common with 47.32% (159 species in 62 genera), followed by *Dothideomycetes* (78 species, 50 genera), *Eurotiomycetes* (23 species, nine genera), *Ascomycota incertae sedis* taxa (eight species, eight genera), *Leotiomycetes* (two species, two genera), *Lecanoromycetes* (one species, one genus), and *Pezizomycetes* (one species, one genus). *Pucciniomycetes* dominated the taxa under *Basidiomycota* with 33 species in five genera recorded, and then *Agaricomycetes* (25 species, 18 genera), *Exobasidiomycetes* (one species, one genus), and *Ustilaginomycetes* (one species, one genus). At present, *Mucoromycota* has the smallest number of taxa where only four species in three genera are documented. This present study not only updates the scientific community on the biodiversity of bambusicolous mycopathogens but also highlights the key areas for future research and conservation efforts, especially in terms of contribution to the global diversity of these organisms from China. The study also acknowledges limitations in the completeness of the data, indicating that some fungal species which are potential pathogens, along with their occurrence, pathogenicity, host substrates and geographical distribution, may have been previously overlooked, and there is a dire need to promote research in this area.

Table 4 New taxonomic names discovered after year 2000.

Taxonomic names	**Bamboo host names**	**Published year**
Alternaria bambusicola *#	*Fargesia nitida*	2007
Apiospora (*Arthrinium*) *pseudoparenchymatica* *+	*Dendrocalamus latiflorus*	2018/2021
Apiospora (*Arthrinium*) *arundinis* +	*Bambusa* sp., *Phyllostachys bissetii*, *Ph. violascens*	2021
Apiospora dongyingensis *	Bamboo	2023
Apiospora hainanensis *	Bamboo	2023
Apiospora (*Arthrinium*) *kogelbergensis* *+	*Bambusa intermedia*	2013/2021
Apiospora (*Arthrinium*) *locuta-pollinis* *+	*Phyllostachys aureosulcata* ‘Spectabilis’	2018/2021
Apiospora (*Arthrinium*) *pseudosinensis* *+	Bamboo	2013/2021
Apiospora (*Arthrinium*) *sacchari* +	*Phyllostachys edulis*	2021

Table 4 Continued.

Taxonomic names	Bamboo host names	Published year
Apiospora sphaerosperma ++ (= *Arthrinium phaeospermum*)	Bamboo, *Bambusa pervariabilis* × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys edulis*, *Ph. prominens*	2021
Apiospora (*Arthrinium*) *yunnana* *+	*Phyllostachys heteroclada*	2016/2021
Ascopolyporus tibetensis *	Bamboo	2023
Bambusicola subthailandica *	*Phyllostachys heteroclada*	2019
Bambusiomyces shiraianus +	*Arundinaria* sp., *Bambusa pervariabilis* × *grandis*, *Ba. emeiensis*, *Fargesia* sp., *Phyllostachys aurea*, *Ph. flexuosa*, *Ph. glauca*, *Ph. heteroclada*, *Ph. incarnata*, *Ph. nigra*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea*, *Ph. edulis*, *Ph. makinoi*, *Ph. nigra* var. *henonis*, *Ph. reticulata*, *Ph. rubicunda*, *Ph. sulphurea* var. *viridis*, *Pleioblastus amarus*, *Pleioblastus* sp., *Sasa chartacea*, *Sa. ramosa*	2011
Bifusisporella sichuanensis *	*Phyllostachys edulis*	2022
Botryobasidium rubiginosum +	Unknown bamboo	2016
Colletotrichum citricola *	Unknown bamboo	2013
Colletotrichum fructicola *	Unknown bamboo	2009
Colletotrichum siamense *	Unknown bamboo	2009
Cyphellophora sessilis +	*Phyllostachys meyeri*, *Yushania falcatiaurita*	2013
Dialonectria ullevolea *	*Phyllostachys* sp.	2011
Diaporthe guangxiensis *	*Dendrocalamus latiflorus*	2019
Didymella glomerata +	Unknown bamboo	2015
Ellisembia pseudoseptata +	*Phyllostachys heteroclada*	2001
Engleromyces sinensis *	*Arundinaria* sp.	2010
Epicoccum poaceicola *	*Phyllostachys sulphurea* var. *viridis*	2017
Epithele bambusae +	*Phyllostachys* sp., Unknown bamboo	2013
Fusarium bambusae +	Unknown bamboo	2017
Fuscoporia torulosa +	*Bambusa blumeana*	2001
Gibberella bambusae +	Unknown bamboo	2003
Heteroepichloe bambusae +	*Phyllostachys* sp., *Ph. glauca*, *Ph. edulis*, *Ph. sulphurea* var. *viridis*	2002
Heteroepichloe sasae +	*Semiarundinaria densiflora*, *Indocalamus tessellatus*, *Phyllostachys* sp.	2002
Longipedicellata aptrootii +	Unknown bamboo	2016
Lophiotrema neoarundinaria +	*Phyllostachys* sp., Unknown bamboo	2009
Mendogia yunnanensis *	Unknown bamboo	2020
Microdochium indocalami *	*Indocalamus longiauritus*	2020
Microdochium yunnanense *	*Indocalamus longiauritus*	2020
Nemania nummularioides +	Unknown bamboo	2001
Neocosmospora solani +	*Phyllostachys aureosulcata*, *Ph. edulis*, *Ph. glauca*, *Ph. sulphurea* f. *houzeauana*, *Ph. sulphurea* var. *viridis*	2015
Neokalmusia scabrispora +	Unknown bamboo	2014
Neonectria ditissima +	*Dendrocalamus latiflorus*	2006
Neostagonosporella sichuanensis *	*Phyllostachys heteroclada*	2019
Neopestalotiopsis clavispora +	Unknown bamboo	2014
Nigrospora osmanthi *	*Phyllostachys nigra*	2017
Parabambusicola bambusina +	Unknown bamboo	2015

Table 4 Continued.

Taxonomic names	Bamboo host names	Published year
Parakarstenia phyllostachydis *	*Phyllostachys heteroclada*	2019
Paralloneottiosporina sichuanensis *	*Phyllostachys violascens*	2022
Pestalotiopsis mangifolia +	*Cephalostachyum chinense*, *Dendrocalamus brandisii*, *De. giganteus*, *De. membranaceus*, *Lingnania intermedia*	2003
Phyllachora cephalostachyi *#	*Cephalostachyum pergracile*	2021
Phyllachora dendrocalami-hamiltoniicola *#	*Dendrocalamus hamiltonii*	2019
Phyllachora dendrocalami-membranacei *#	*Dendrocalamus membranaceus*	2019
Phyllachora hekouensis *#	*Indocalamus tessellatus*	2014
Phyllachora heterocladae *	*Phyllostachys heteroclada*	2019
Phyllachora indosasae *#	*Indosasa hispida* McClure cv. 'Rainbow'	2013
Phyllachora lushanensis *#	*Phyllostachys edulis*	2014
Phyllachora nanningensis *#	*Bambusa chungii*, *Ba. pervariabilis*, *Ba. rigida*	2014
Phyllachora yushaniae *#	*Dendrocalamus giganteus*, *De. semiscandens*, *Fargesia albocerea*, *Fa. solida*, *Indocalamus tessellatus*, *Phyllostachys nigra* var. *henonis*, *Sinobambusa tootsik*, *Yushania auctiaurita*, *Yu. niitakayamensis*	2014
Podonectria sichuanensis *	*Phyllostachys heteroclada*	2019
Rubroshiraia bambusae *	*Fargesia spathacea*	2019
Solicorynespora foveolate +	*Phyllostachys edulis*, *Phyllostachys* sp.	2008
Strigula sinoaustralis *	Unknown bamboo	2016
Serpula dendrocalami *	*Dendrocalamus* sp.	2019
Talaromyces rugulosus +	Unknown bamboo	2011

Notes: New generic names are visualized in bold. "*" indicates the new fungal names. "+" means the new combinations. "#" indicates illegal names, those which not registered in recognized platforms. "++" means *Apiospora sphaerosperma* as new combination needs to be further verified with type studies and additional data.

Table 5 Taxonomic classification and numbers of bambusicolous mycopathogens in China.

Class	Order	Family	Number of species
Classification of *Ascomycota*			
Dothideomycetes	*Asterinales*	*Asterinaceae*	1
	Botryosphaeriales	*Botryosphaeriaceae*	4
		Phyllostictaceae	3
	Capnodiales	*Capnodiaceae*	5
		Cladosporiaceae	5
		Mycosphaerellaceae	5
	Coniosporiales	*Coniosporiaceae*	1
	Dothideales	*Saccotheciaceae*	4
	Microthyriales	*Microthyriaceae*	1
	Myriangiales	*Myriangiaceae*	3
	Pleosporales	*Bambusicolaceae*	1
		Didymellaceae	6
		Didymosphaeriaceae	2
		Leptosphaeriaceae	4

Table 5 Continued.

Class	Order	Family	Number of species
		Longipedicellataceae	1
		Lophiotremataceae	1
		Massarinaceae	1
		Parabambusicolaceae	1
		Phaeosphaeriaceae	3
		Pleosporaceae	5
		Roussoellaceae	1
		Shiraiaceae	2
		Tetraplosphaeriaceae	1
		Pleosporales genera *incertae sedis*	3
	Strigulales	*Strigulaceae*	1
	Tubeufiales	*Tubeufiaceae*	4
	Dothideomycetes families *incertae sedis*	*Fenestellaceae*	1
		Parodiopsidaceae	2
		Pseudoperisporiaceae	1
		Schizothyriaceae	1
	Dothideomycetes genera *incertae sedis*	*Dothideomycetes* genera *incertae sedis*	4
Eurotiomycetes	*Chaetothyriales*	*Chaetothyriaceae*	3
		Cyphellophoraceae	1
		Trichomeriaceae	1
	Eurotiales	*Aspergillaceae*	17
	Eurotiomycetes genera *incertae sedis*	*Eurotiomycetes* genera *incertae sedis*	1
Lecanoromycetes	*Odontotrematales*	*Odontotremataceae*	1
Leotiomycetes	*Helotiales*	*Sclerotiniaceae*	1
		Tympanidaceae	1
Pezizomycetes	*Pezizales*	*Pezizales* genera *incertae sedis*	1
Sordariomycetes	*Amphisphaeriales*	*Amphisphaeriaceae*	3
		Pestalotiopsidaceae	4
	Chaetosphaeriales	*Chaetosphaeriaceae*	3
	Diaporthales	*Diaporthaceae*	2
		Gnomoniaceae	1
		Melanconidaceae	1
		Diaporthales genera *incertae sedis*	2
	Glomerellales	*Glomerellaceae*	9
	Hypocreales	*Bionectriaceae*	1
		Clavicipitaceae	7
		Cordycipitaceae	2
		Hypocreaceae	5
		Nectriaceae	20
		Niessliaceae	2
		Hypocreales genera *incertae sedis*	2
	Magnaporthales	*Ceratosphaeriaceae*	2
		Magnaporthaceae	1
	Meliolales	*Meliolaceae*	6

Table 5 Continued.

Class	Order	Family	Number of species
	Microascales	*Microascaceae*	1
	Phomatosporales	*Phomatosporaceae*	2
	Phyllachorales	*Phyllachoraceae*	39
	Sordariales	*Chaetomiaceae*	3
		Sordariaceae	1
	Xylariales	*Cainiaceae*	2
		Diatrypaceae	2
		Hyponectriaceae	2
		Hypoxylaceae	1
		Xylariaceae	15
	Sordariomycetes family *incertae sedis*	*Apiosporaceae*	13
	Sordariomycetes genera *incertae sedis*	*Sordariomycetes* genera *incertae sedis*	5
Ascomycota genera *incertae sedis*	*Ascomycota* genera *incertae sedis*	*Ascomycota* genera *incertae sedis*	8
Classification of *Basidiomycota*			
Agaricomycetes	*Agaricales*	*Hygrophoraceae*	3
		Mycenaceae	3
		Pterulaceae	1
		Tricholomataceae	1
	Atheliales	*Atheliaceae*	1
	Boletales	*Sclerodermataceae*	1
		Serpulaceae	2
		Tapinellaceae	1
	Cantharellales	*Aphelariaceae*	1
		Botryobasidiaceae	1
		Cantharellaceae	1
		Ceratobasidiaceae	2
	Corticiales	*Corticiaceae*	1
	Hymenochaetales	*Hymenochaetaceae*	1
	Phallales	*Phallaceae*	1
	Polyporales	*Ganodermataceae*	2
		Polyporaceae	1
	Thelephorales	*Thelephoraceae*	1
Exobasidiomycetes	*Exobasidiales*	*Brachybasidiaceae*	1
Pucciniomycetes	*Pucciniales*	*Phakopsoraceae*	3
		Pucciniaceae	25
		Pucciniales genera *incertae sedis*	2
	Septobasidiales	*Septobasidiaceae*	2
	Pucciniomycetes genera *incertae sedis*	*Pucciniomycetes* genera *incertae sedis*	1
Ustilaginomycetes	*Ustilaginales*	*Ustilaginaceae*	1
Classification of *Mucoromycota*			
Mucoromycetes	*Mucorales*	*Lichtheimiaceae*	2
		Mucoraceae	1
		Rhizopodaceae	1
		Overall total	336

Bambusicolous pathogenic ascomycetes

The classification of bambusicolous pathogenic ascomycetes reveals a diverse group encompassing six classes, *viz*. *Dothideomycetes*, *Eurotiomycetes*, *Lecanoromycetes*, *Leotiomycetes*, *Pezizomycetes* and *Sordariomycetes*. In addition, there are eight species belong to the *Ascomycota* genera *incertae sedis* each belonging to a distinct genus. The highest number of species come from the *Dothideomycetes* and *Sordariomycetes*, which make up about 87% of ascomycetes. Expanding research to classify pathogenic ascomycetes on additional hosts, considering that at least 80% (about 800 out of 973) of bamboo plants in China have no record of pathogenic ascomycetes, increases the probability of discovering a wider variety of pathogenic species. Given the situations mentioned above and the absence of a proper checklist on fungal pathogens associated with bambusicolous hosts, all extant published studies have been reviewed, culminating in the compilation of their data, including taxonomic name, substrate colonized, geographical distribution, DNA sequence data, and references, presented in Table 6.

So far, with 78 species identified from bamboo ecosystems, dothideomycetous taxa indicates a notably rich group. The pathogenic fungi within this class predominantly function as facultative parasitic pathogens, commonly leading to necrosis of host tissues and the formation of distinct patches of varying sizes. *Sordariomycetes*, the most abundant taxa of pathogenic fungi found in bambusicolous ecosystems, encompasses numerous pathogenic species, including *Aciculosporium take*, *Apiospora* spp., *Ceratosphaeria* spp., *Colletotrichum* spp., *Fusarium* spp., *Phyllachora* spp., and others. These fungi pose a significant threat to the health of bamboo forests, specifically by causing diseases such as *Ce. phyllostachydis*-induced dieback in *Phyllostachys edulis*, leading to extensive bamboo forest mortality (Zhang 1982, Wei 2005). The sordariomycetous pathogens, often parasitic or facultative saprobes, can cause localized bamboo forest diseases or damage entire bamboo forests under suitable conditions. Members of other classes within the *Ascomycota* phylum comprise 35 species primarily recognized for their pathogenic impact on bamboo timber.

The study and classification of these pathogenic ascomycetes have gradually advanced with the integration of molecular data, leading to an increase in the recognized species count (Dai et al. 2019, Yang et al. 2019a–f, Huang et al. 2020, Zeng et al. 2022). However, the challenge remains significant. Numerous fungi remain undocumented, especially in less explored areas, with similar challenges faced by various fungal groups. The reevaluation of the taxonomic status of certain species with molecular techniques emphasize the ongoing need for detailed investigation in this field. The classification and comprehensive documentation of this extensive fungal diversity pose significant challenges for mycologists and taxonomists, owing to the wide range of habitats in which these fungi reside.

Bambusicolous pathogenic basidiomycetes

These pathogens are categorized into four classes: *Agaricomycetes*, *Exobasidiomycetes*, *Pucciniomycetes* and *Ustilaginomycetes*. The majority, with 58 species are found within *Agaricomycetes* and *Pucciniomycetes* while only two species are identified under *Exobasidiomycetes* and *Ustilaginomycetes* (Table 7). Basidiomycetous taxa are noted for their wide-ranging substrates, including timber, root, fruit, seedling and other living tissues. Among these, obligate parasitic fungi, particularly *Pucciniomycetes*, are the primary group, found extensively on bamboo forest leaves. Bamboo timber, composed of lignin, cellulose and hemicellulose, provides a critical structural elements of bamboo timber and is vulnerable to decay (Kumar et al. 2020). Research indicates that the primary culm decay pathogens in bamboo are predominantly basidiomycetes, particularly *Agaricomycetes* (Schmidt et al. 2011, Möller & Mild 2019).

The challenge in fully understanding the impact and diversity of basidiomycetous pathogens on bamboo lies in the complexity of their identification and the need for comprehensive species composition analysis. This complexity is compounded by the diverse ecological roles these fungi play, ranging from obligate parasites to decay agents. Despite the recognized significance of

Table 6 Classification of bambusicolous pathogenic ascomycetes with information on the type of substrates, geographical distribution, and molecular data.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Aciculosporium take	Branch, and twig: *Arundinaria fargesii*, *Bambusa blumeana*, *Ba. dolichoclada*, *Ba. multiplex*, *Ba. oldhamii*, *Bambusa* sp., *Ba. ventricose*, *Chimonobambusa quadrangularis*, *Dendrocalamus latiflorus*, *Phyllostachys aurea*, *Ph. reticulata*, *Ph. bissetii*, *Ph. edulis*, *Ph. glauca*, *Ph. heteroclada*, *Ph. lithocarpa*, *Ph. reticulata*, *Ph. makinoi*, *Ph. nigra* var. *henonis*, *Ph. nuda*, *Ph. sulphurea* var. *viridis*, *Ph. sulphurea*, *Ph. violascens* 'Prevernalis', *Ph. viridiglaucescens*, *Ph. vivax*, *Pleioblastus amarus*, *Semiarundinaria densiflora*	Shandong, Jiangsu, Zhejiang, Guangdong, Fujian, Anhui, Taiwan, Shanghai, Hubei, Hunan, Jiangxi, Henan, Shaanxi, Sichuan, Guizhou, Guangxi	ITS, LSU, SSU, *rpb*2, *tef*1-α, *mcm*7, *tub*2	Xu et al. (2006), Xue et al. (2007), Mohanan (2017), Tanaka et al. (2021), Liu et al. (2022b)
Aithaloderma bambusinum	Culm, and branch: *Bambusa* sp.	Zhejiang		Xu et al. (2006)
Alternaria alternata	Culm base, culm, timber, and leaf: *Cephalostachyum chinense*, *Dendrocalamus brandisii*, *De. giganteus*, *De. latiflorus*, *De. membranaceus*, *Lingnania intermedia*, *Phyllostachys edulis*, *Ph. glauca*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Pleioblastus amarus*, unknown bamboo	Jiangsu, Zhejiang, Anhui, Jiangxi, Yunnan	ITS	Fu et al. (1999), Wang et al. (2000a), Ma et al. (2009a, 2012), Zhang et al. (2011), Wang et al. (2012), Mohanan (2017)
Alternaria bambusicola	Leaf: *Fargesia nitida*	Yunnan		Zhang et al. (2007)
Alternaria sp. (3)	Timber, and leaf: *Bambusa pervariabilis* × *grandis*, unknown bamboo	Jiangsu, Guangdong, Hunan, Guizhou		Zhao et al. (1994), Ma et al. (2009a, b), Sang et al. (2012)
Alternaria viticola	Timber: Unknown bamboo	Jiangsu		Zhao et al. (1994)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Anthostomella mirabilis	Branch, and twig: Unknown bamboo	Zhejiang, Anhui, Guangdong, Fujian, Jiangxi, Hunan, Sichuan, Yunnan, Guangxi		Xu et al. (2006)
Anthostomella nitidissima	Branch, and twig: Unknown bamboo	Guangdong, Yunnan		Xu et al. (2006)
Anthostomella profunda	Branch, and twig: Unknown bamboo	Guangdong		Xu et al. (2006)
Anthostomella shiraiana?	Branch, and twig: Unknown bamboo	Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Sichuan, Guangxi		Xu et al. (2006)
Anthostomella striola?	Branch, and twig: Unknown bamboo	Yunnan		Xu et al. (2006)
Apiospora arundinis	Culm, timber, branch, twig, and leaf: *Bambusa* sp., *Phyllostachys bissetii*, *Ph. violascens*, unknown bamboo	Jiangsu, Guangdong, Hunan, Sichuan, Yunnan, Guangxi		Fu et al. (1999), Wang et al. (2000a), Xu et al. (2006), Chen et al. (2015), Mohanan (2017)
Apiospora dongyingensis	Leaf: Unknown bamboo	Shandong	ITS, LSU, *tef*1-α, *tub*2	Liu et al. (2023a)
Apiospora hainanensis	Leaf: Unknown bamboo	Hainan	ITS, LSU, *tef*1-α, *tub*2	Liu et al. (2023a)
Apiospora kogelbergensis	Culm: *Bambusa intermedia*	Sichuan	ITS, LSU, *tub*2	Yin et al. (2020)
Apiospora locuta-pollinis	Culm: *Phyllostachys aureosulcata* 'Spectabilis'	Sichuan	ITS, LSU, *tef*1-α, *tub*2	Liu et al. (2023b)
Apiospora pseudoparenchymatica	Top culm, branch, and twig from host: *Dendrocalamus latiflorus*	Sichuan	ITS, LSU, *tef*1-α, *tub*2	Yang et al. (2019f)
Apiospora pseudosinensis	Leaf: Unknown bamboo	Shandong, Hainan	ITS, LSU, *tef*1-α, *tub*2	Liu et al. (2023a)
Apiospora sacchari	Culm: *Phyllostachys edulis*	Jiangxi	ITS	Wang et al. (2012)
Apiospora shiraiana	Culm, branch, twig, and leaf: *Bambusa emeiensis*, *Bambusa* sp., *Fargesia dracocephala*, *Phyllostachys* sp., unknown bamboo	Jiangsu, Zhejiang, Anhui, Guangdong, Hunan, Sichuan, Guangxi		Xu et al. (2006)
Apiospora sphaerosperma (= '*Arthrinium*' *phaeospermum*)	Culm base, culm, and timber: *Bambusa pervariabilis* × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys edulis*, *Ph. prominens*, unknown bamboo	Beijing, Jiangsu, Zhejiang, Anhui, Jiangxi, Hubei, Hunan, Sichuan, Yunnan		Wu & Weng (1990), Fu et al. (1999), Wang et al. (2000a), Ma et al. (2003), Xu et al. (2006), Zhu et al. (2009), Zhang et al. (2011),

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
				Wu et al. (2014)
Apiospora sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Apiospora yunnana	Branch, and twig: *Phyllostachys heteroclada*	Sichuan	ITS, LSU, *tef*1-α	Yang et al. (2019e)
Arecophila bambusae	Timber: Unknown bamboo	Hongkong		Umali et al. (1999), Mohanan (2017)
Arecophila coronata	Timber: Unknown bamboo	Hongkong		Umali et al. (1999), Mohanan (2017)
Arthrobotryum rickii	Branch, and twig: Unknown bamboo	Guangxi		Xu et al. (2006)
Ascochyta lophanthi var. *osmophila*	Leaf: *Phyllostachys glauca*	Jiangsu		Xu et al. (2006)
Ascopolyporus tibetensis	Culm: Unknown bamboo	Tibet	ITS, LSU, *tef*1-α	Yu et al. (2023b)
Aspergillus candidus	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Aspergillus fumigatus	Timber: Unknown bamboo	Yunnan		Ma et al. (2009a)
Aspergillus ochraceus	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Aspergillus restrictus	Timber: Unknown bamboo	Jiangsu		Zhao et al. (1994)
Aspergillus sp. (2)	Culm, timber, and branch: *Bambusa pervariabilis* × *grandis*, unknown bamboo	Guangdong, Guizhou		Ma et al. (2009a), Sang et al. (2012)
Aspergillus versicolor	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Aspergillus wentii	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Asterinella hingensis	Culm: *Bambusa* sp., *Phyllostachys reticulata*	Shanxi, Shaanxi. Jiangsu, Zhejiang, Anhui, Fujian, Jiangxi, Henan, Hubei, Hunan, Yunnan, Guizhou, Guangxi		Xu et al. (2006), Mohanan (2017)
Asteroma argentea	Leaf: *Bambusa pervariabilis* × *grandis*	Guizhou		Sang et al. (2012)
Astrosphaeriella fusispora	Culm, and branch: Unknown bamboo	Guangdong, Sichuan, Guangxi		Xu et al. (2006)
Astrosphaeriella minima	Culm: Unknown bamboo	Guangdong, Hunan, Guangxi		Xu et al. (2006)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Astrosphaeriella stellata	Culm, and branch: Unknown bamboo	Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Guangdong, Sichuan, Guizhou, Guangxi		Xu et al. (2006)
Aureobasidium pullulans	Leaf: *Bambusa pervariabilis* × *grandis*	Guizhou		Sang et al. (2012)
Balladyna lelebae	Culm: *Bambusa multiplex* var. *shimadae*	Taiwan		Xu et al. (2006)
Bambusicola subthailandica	Leaf: *Phyllostachys heteroclada*	Sichuan	ITS, LSU, SSU, *rpb*2, *tef*1-α	Yang et al. (2019c)
Bifusisporella sichuanensis	Leaf: *Phyllostachys edulis*	Sichuan	ITS, LSU, *tef*1-α, *rpb*1	Zeng et al. (2022)
Botryodiplodia fabae	Timber: Unknown bamboo	Jiangsu		Zhao et al. (1994)
Botryodiplodia sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Botryosphaeria sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Botryotinia sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Capnophaeum ischurochloae	Culm: *Bambusa blumeana*, *Ba. emeiensis*	Guizhou, Taiwan		Xu et al. (2006)
Ceratosphaeria phyllostachydis	Culm: *Bambusa pervariabilis* × *grandis*, *Phyllostachys edulis*	Jiangsu, Zhejiang, Anhui, Jiangxi, Fujian, Shanghai, Hubei, Sichuan		Xu et al. (2006), Huang & Zhu (2007), Zhang et al. (2011), Mohanan (2017)
Ceratosphaeria silva-nigra	Culm, and branch: Unknown bamboo	Sichuan		Xu et al. (2006)
Cercosporidium bambusicola	Leaf: *Bambusa* sp.	Taiwan		Xu et al. (2006)
Chaetomium cochliodes	Timber: Unspecified	Yunnan		Fu et al. (1999), Wang et al. (2000a)
Chaetomium globosum	Culm: *Phyllostachys reticulata*, unknown bamboo	Beijing, Yunnan		Fu et al. (1999), Wang et al. (2000a), Ma et al. (2009a), Mohanan (2017)
Chaetomium sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b), Mohanan (2017)
Chaetosphaeria macrospora	Culm, and branch: Unknown bamboo	Taiwan		Xu et al. (2006)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Chaetosphaeria stenostachyae	Culm, and branch: *Bambusa blumeana*	Taiwan		Xu et al. (2006)
Chaetothyrium echinulatum	Unspecified: *Phyllostachys makinoi*	Taiwan		Xu et al. (2006)
Chaetothyrium javanicum	Culm: *Bambusa dolichoclada*, *Dendrocalamus latiflorus*, *Phyllostachys makinoi*	Taiwan		Xu et al. (2006)
Chaetothyrium spinigerum	Unspecified: *Bambusa dolichoclada*, *Ba. oldhamii*, *Dendrocalamus latiflorus*, *Phyllostachys makinoi*	Taiwan		Xu et al. (2006)
Cladosporium cladosporioides	Timber: Unspecified	Yunnan		Fu et al. (1999), Wang et al. (2000a), Mohanan (2017)
Cladosporium cucumerinum	Timber: Unspecified	Yunnan		Fu et al. (1999), Wang et al. (2000a)
Cladosporium herbarum	Timber, and leaf: *Indocalamus tessellatus*, *Phyllostachys edulis*, unspecified bamboo	Jiangsu, Zhejiang, Hubei, Yunnan		Zhao et al. (1994), Fu et al. (1999), Wang et al. (2000a), Xu et al. (2006)
Cladosporium oxysporum	Timber (Culm?): *Bambusa blumeana*, unspecified bamboo	Yunnan		Fu et al. (1999), Wang et al. (2000a), Xu et al. (2006)
Cladosporium sp. (1)	Timber: Unknown bamboo	Unspecified		Mohanan (2017)
Claviceps purpurea	Branch?: *Indocalamus* sp.	Zhejiang		Xu et al. (2006)
Coccodiella arundinariae	Culm?, and leaf: *Phyllostachys* sp., *Ph. edulis*, *Semiarundinaria densiflora*	Jiangsu, Zhejiang, Anhui, Fujian, Sichuan, Guangxi		Xu et al. (2006), Zhang (2007), Mohanan (2017)
Colletotrichum citricola	Unspecified: Unknown bamboo	Guangdong		Liu et al. (2022a)
Colletotrichum coccodes	Culm: *Bambusa pervariabilis*	Guizhou		Ren et al. (2008)
Colletotrichum fructicola	Unspecified: Unknown bamboo	Jiangxi		Liu et al. (2022a)
Colletotrichum hsienjenchang	Culm?: *Phyllostachys nigra* var. *henonis*, *Ph. edulis* f. *pubescens*	Unspecified	ITS, *act*, *chs*-1, *his*3	Sato et al. (2012)
Colletotrichum kahawae clade	Unspecified: Unknown bamboo	Jiangxi		Liu et al. (2022a)
Colletotrichum metake	Fruit: *Chimonobambusa quadrangularis*	Guizhou	ITS, *gapdh*, *chs*-1, *act*, *tub*2	Wang et al. (2021), Liu et al. (2022a)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Colletotrichum septorioides	Leaf: *Bambusa vulgaris*, *Phyllostachys edulis*, *Phyllostachys* sp.	Unspecified		Mohanan (2017)
Colletotrichum siamense	Unspecified: Unknown bamboo	Jiangxi		Liu et al. (2022a)
Colletotrichum sp. (3)	Culm, and leaf: *Bambusa pervariabilis* × *grandis*, *Bambusa vulgaris*, unknown bamboo	Guangdong, Guizhou		Sang et al. (2012), Mohanan (2017), Liu et al. (2022a)
Coniosporium saccardoanum	Culm?: *Phyllostachys bissetii*, *Ph. edulis*	Jiangsu, Henan, Hubei, Hunan, Sichuan, Guangxi		Xu et al. (2006)
Coniothyrium sp. (1)	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Curvularia sp. (1)	Timber: Unspecified	Jiangsu		Zhao et al. (1994)
Cyphellophora sessilis	Culm: *Phyllostachys meyeri*, *Yushania falcatiaurita*	Hubei	ITS	Zhuang et al. (2010)
Dialonectria ullevolea	Unspecified: *Phyllostachys* sp.	Jiangsu		Xu et al. (2006)
Diaporthe guangxiensis	Culm: *Dendrocalamus latiflorus*	Sichuan	ITS, *cal*, *tef*1-α, *tub*2	Wei et al. (2021a)
Didymella glomerata	Timber: Unknown bamboo	Yunnan		Ma et al. (2009a)
Didymella maculosa	Branch, and twig: Unknown bamboo	Jiangsu, Hunan, Sichuan, Yunnan, Guangxi		Xu et al. (2006)
Didymosphaeria bambusicola	Culm: Unknown bamboo	Guangdong, Guangxi		Xu et al. (2006)
Dimeriella dendrocalami	Unspecified: *Dendrocalamus latiflorus*	Taiwan		Xu et al. (2006)
Dimerina bambusicola	Culm, and leaf: *Phyllostachys dulcis*, *Ph. glauca*, *Ph. violascens*, *Ph. vivax*, unknown bamboo	Unspecified		Mohanan (2017)
Dinemasporium sp. (1)	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a), Ma et al. (2009b)
Ellisembia pseudoseptata	Culm: *Phyllostachys heteroclada*	Yunnan		Xu et al. (2006)
Engleromyces goetzei	Culm: Unknown bamboo	Sichuan, Yunnan, Tibet		Xu et al. (2006)
Engleromyces sinensis	Culm: *Arundinaria* sp.	Yunnan		Whalley et al. (2010)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Epicoccum nigrum	Leaf, and others: *Bambusa pervariabilis* × *grandis*, *Phyllostachys edulis*	Guizhou, unspecified location		Xu et al. (2006), Sang et al. (2012)
Epicoccum poaceicola	Leaf: *Phyllostachys sulphurea* var. *viridis*	Jiangsu	ITS, LSU, *rpb*2, *tub*2	Liu et al. (2020)
Eupenicillium sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Eurotium sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Eutypa kusanoi	Branch: *Bambusa blumeana*	Taiwan		Xu et al. (2006)
Eutypella bambusina	Branch, and twig: *Bambusa* sp., unknown bamboo	Jiangsu, Zhejiang, Anhui, Fujian, Guangdong, Hunan, Yunnan, Guizhou, Guangxi		Xu et al. (2006)
Fenestella bambusicola	Culm: Unknown bamboo	Zhejiang		Xu et al. (2006)
Fusarium acuminatum	Root, and culm base: *Phyllostachys edulis*	Zhejiang		Xu et al. (2006)
Fusarium bambusae	Culm: Unknown bamboo	Guangdong		Xu et al. (2006)
Fusarium bambusicola	Unspecified: *Bambusa emeiensis*	Sichuan		Xu et al. (2006)
Fusarium camptoceras	Branch: *Phyllostachys edulis*	Zhejiang		Xu et al. (2006)
Fusarium equiseti	Culm, and branch: *Bambusa textilis*, *Phyllostachys edulis*, *Ph. glauca*, *Ph. viridis* f. *houzeauana*	Jiangsu, Zhejiang		Xu et al. (2006), Zhou et al. (2011a), Mohanan (2017)
Fusarium equiseti var. *meyeri*	Culm base: *Phyllostachys meyeri*	Zhejiang	ITS	Lou et al. (2009)
Fusarium fujikuroi	Shoot, culm base, and culm: *Bambusa balcooa*, *Ba. textilis*, *Dendrocalamus asper*, *De. strictus*, *Indosasa crassiflora*, *Ph. edulis*, *Phyllostachys* sp.	Jiangsu, Zhejiang, Anhui, Hubei, Hunan, Jiangxi, Guangdong, Sichuan, Yunnan, Guangxi		Chen (1980), Xu et al. (2006), Mohanan (2017)
Fusarium graminearum	Culm: *Phyllostachys edulis*	Jiangxi		Wang et al. (2012)
Fusarium heterosporum	Culm base: *Phyllostachys edulis*	Jiangsu, Zhejiang, Anhui, Jiangxi, Hubei, Hunnan, Sichuan		Jia et al. (2002), Xu et al. (2006)
Fusarium incarnatum	Culm: *Bambusa multiplex*,	Zhejiang, Fujian,	ITS, *tef*1-α, *rpb*2	Xu et al. (2006),

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
	Ba. pervariabilis × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys edulis*, *Ph. heteroclada*	Shanghai, Taiwan		Mohanan (2017), Huang et al. (2019)
Fusarium oxysporum	Root, culm base, and culm: *Bambusa pervariabilis* × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys dulcis*, *Ph. edulis*, *Ph. heteroclada*	Zhejiang, Jiangxi, Sichuan, Guizhou, Guangxi, unspecified location	ITS	Xu et al. (2006), Cai et al. (2010), Ren et al. (2011), Wang et al. (2012), Mohanan (2017)
Fusarium proliferatum	Culm base: *Bambusa pervariabilis* × *grandis*	Sichuan	ITS, *tef*1-α, *rpb*2, *tub*2, *his*, mtSSU	Li et al. (2022b)
Fusarium sambucinum	Culm, and others: *Bambusa pervariabilis* × *grandis*, *Bambusa sinospinosa*	Fujian, Hunan, Sichuan, Guizhou, Guangxi		Xu et al. (2006), Ren et al. (2009), Sang et al. (2012)
Fusarium sp. (3)	Shoot, timber, branch, and leaf: *Bambusa pervariabilis* × *grandis*, Phyllostachys sp., unknown bamboo	Beijing, Anhui, Fujian, Hunan, Yunnan, Guizhou		Wang et al. (2000a), Ma et al. (2009a), Sang et al. (2012), Mohanan (2017)
Fusarium stilboides	Culm: *Phyllostachys dulcis*, *Ph. edulis*, *Ph. elegans*, *Ph. iridescens*, *Ph. nuda*, *Ph. sulphurea* f. *houzeauana*, *Ph. sulphurea* f. *robertii*, *Ph. sulphurea* var. *viridis* 'Qingpi', *Ph. sulphurea* var. *viridis*, *Ph. violascens*	Zhejiang		Xu et al. (2006), Mohanan (2017)
Gibberella bambusae	Culm: Unknown bamboo	Jiangsu, Zhejiang, Anhui		Xu et al. (2006)
Gibberella sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Gliocladium sp. (1)	Culm?: *Phyllostachys edulis*	Zhejiang		Mohanan (2017)
Haraea japonica	Unspecified: *Phyllostachys* sp.	Unspecified		Mohanan (2017)
Helminthosporium arundinis	Leaf: *Bambusa emeiensis*	Guizhou		Xu et al. (2006)
Heteroepichloe bambusae	Twig: *Phyllostachys* sp., *Ph. glauca*, *Ph. edulis*, *Ph. sulphurea* var. *viridis*	Jiangsu, Zhejiang, Anhui, Guangdong, Guizhou		Xu et al. (2006), Zhang et al. (2011)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Heteroepichloe sasae	Twig: *Semiarundinaria densiflora*, *Indocalamus tessellatus*, *Phyllostachys* sp.	Anhui, unspecified location		Xu et al. (2006), Cheng et al. (2009), Mohanan (2017)
Hinoa bambusicola	Leaf: *Phyllostachys* spp., other bamboos	Uncertain distribution		Zhang (2000), Mohanan (2017)
Hypocrea sp. (1)	Timber: Unknown bamboo	Unspecified		Ma et al. (2009b)
Hypocrella bambusae	Culm?: Unknown bamboo	Yunnan, Tibet		Wang et al. (2015)
Hypoxylon rubiginosum	Culm: Unknown bamboo	Qinghai, Gansu, Inner Mongolia, Hebei, Shanxi, Shaanxi, Jining, Jiangsu, Zhejiang, Anhui, Jiangxi, Fujian, Hunan, Guangdong, Sichuan, Yunnan, Guizhou, Guangxi		Xu et al. (2006)
Isaria sp. (1)	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Konradia bambusina	Branch: *Bambusa* sp.	Fujian, Guangdong, Guangxi		Xu et al. (2006)
Lasiodiplodia theobromae	Timber: *Phyllostachys edulis*, unknown bamboo	Zhejiang, Anhui, Hunan, Guangdong, Yunnan		Ma et al. (2009a, 2012)
Lembosia tikusensis	Culm: *Phyllostachys nigra*	Unspecified		Mohanan (2017)
Leptosphaeria bambusae	Culm: Unknown bamboo	Hunan		Xu et al. (2006)
Leptosphaeria eumorpha	Branch: *Bambusa* sp.	Guangdong		Xu et al. (2006)
Leptosphaeria sp. (2)	Culm, and timber: *Bambusa pervariabilis* × *grandis*, unknown bamboo	Guizhou, unspecified location		Ma et al. (2009b), Sang et al. (2012)
Leptosphaeria tigrisoides	Culm, and branch: Unknown bamboo	Jiangsu, Zhejiang, Shaanxi		Xu et al. (2006)
Linochora howardii	Leaf: *Bambusa multiplex*	Guangdong		Xu et al. (2006)
Loculistroma bambusae	Culm, and twig: *Phyllostachys* sp.	Hubei, unknown location		Xu et al. (2006), Mohanan (2017)
Longipedicellata aptrootii	Timber: Unknown bamboo	Hongkong		Mohanan (2017)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Lophiotrema neoarundinaria	Culm: *Phyllostachys* sp., unknown bamboo	Guangdong, Yunnan		Xu et al. (2006)
Melanconium sp. (1)	Timber: Unspecified bamboo	Jiangsu		Zhao et al. (1994)
Melchioria tengii	Culm: Unknown bamboo	Sichuan		Xu et al. (2006)
Meliola acristae	Unspecified: *Bambusa* sp., *Phyllostachys dulcis*, *Ph. glauca*, *Phyllostachys* sp., *Ph. violascens*, *Ph. vivax*, *Pleioblastus cantori*?, *Sasa* sp.	Unspecified locations		Mohanan (2017)
Meliola arundinis	Unspecified: *Bambusa* sp., *Phyllostachys dulcis*, *Ph. glauca*, *Phyllostachys* sp., *Ph. violascens*, *Ph. vivax*, *Pleioblastus cantori*?, *Sasa* sp.	Unspecified locations		Mohanan (2017)
Meliola bambusae	Unspecified: *Bambusa* sp., *Indocalamus longiauritus*, *Phyllostachys dulcis*, *Ph. glauca*, *Phyllostachys* sp., *Ph. violascens*, *Ph. vivax*, *Pleioblastus cantori*?, *Sasa* sp.	Guangdong, Hainan, unspecified locations		Xu et al. (2006), Mohanan (2017)
Meliola phyllostachydis	Unspecified: *Indosasa crassiflora*, *Phyllostachys bissetii*, *Ph. edulis*, *Ph. glauca*, *Ph. makinoi*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Pseudosasa usawai*, unknown bamboo	Jiangsu, Zhejiang, Henan, Hubei, Hunan, Guangdong, Fujian, Jiangxi, Sichuan, Taiwan		Zhang (2000), Xu et al. (2006)
Meliola tenella	Unspecified: *Phyllostachys violascens*, *Ph. vivax*, *Ph. dulcis*, *Ph. glauca*, *Phyllostachys* sp., *Bambusa* sp., *Sasa* sp., *Pleioblastus cantori*?	Unspecified locations		Zhang 2000), Xu et al. 2006)
Mendogia yunnanensis	Culm: Unknown bamboo	Yunnan	LSU, SSU	Jiang et al. (2020)
Metasphaeria denata?	Culm, and branch: *Phyllostachys* sp.	Zhejiang		Xu et al. (2006)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Metasphaeria deviata	Unspecified: *Phyllostachys* sp.	Zhejiang, Hubei, Hunan		Xu et al. (2006)
Metasphaeria fusariispora	Leaf: *Phyllostachys sulphurea* var. *viridis*	Hunan		Xu et al. (2006)
Microascus brevicaulis	Timber: *Cephalostachyum chinense*, *Dendrocalamus brandisii*, *De. giganteus*, *De. membranaceus*, *Lingnania intermedia*, unspecified bamboo	Yunnan, unspecified locations		Fu et al. (1999), Wang et al. (2000a), Mohanan (2017)
Microdochium indocalami	Leaf: *Indocalamus longiauritus*	Yunnan	ITS, LSU, *rpb*2, *tub*2	Huang et al. (2020)
Microdochium sp. (1)	Leaf: *Indocalamus longiauritus*	Yunnan	ITS, LSU, *tub*2	Huang et al. (2020)
Microdochium yunnanense	Leaf: *Indocalamus longiauritus*	Yunnan	ITS, LSU, *rpb*2, *tub*2	Huang et al. (2020)
Miyakeomyces bambusae	Leaf: *Phyllostachys* sp.	Liaoning, Jiangsu, Guizhou		Xu et al. (2006)
Mycocitrus phyllostachydis	Culm, and branch: *Phyllostachys* sp., unknown bamboo	Jiangsu, Henan		Xu et al. (2006)
Mycosphaerella bambusifolia	Unspecified: *Phyllostachys* sp.	Shaanxi		Xu et al. (2006)
Mycosphaerella sp. (1)	Timber: Unknown bamboo	Unspecified locations		Ma et al. (2009b)
Mycosphaerella tassiana	Leaf: *Bambusa* sp.	Guangdong		Xu et al. (2006)
Myriangium bambusae	Leaf: *Bambusa multiplex*, *Bambusa* sp.	Jiangsu		Mohanan (2017)
Myriangium haraeanum	Culm?, and culm leaf?: *Bambusa multiplex* var. *riviereorum*, *Bambusa* sp., *Fargesia* sp., *Indocalamus tessellatus*, *Phyllostachys reticulata*, *Ph. bissetii*, *Ph. edulis*, *Ph. glauca*, *Ph. heteroclada*, *Ph. iridescens*, *Ph. nigra* var. *henonis*, *Ph. violascens*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Pleioblastus amarus*	Jiangsu, Zhejiang, Anhui, Fujian, Jiangxi, Shanghai, Hunan, Henan, Sichuan, Guizhou		Zhang (2000), Xu et al. (2006), Zhang et al. (2011), Mohanan (2017)
Myriangium sp. (1)	Twig: *Bambusa multiplex*	Unspecified location		Mohanan (2017)
Myriodiscus sparassoides	Culm: *Bambusa* sp., unknown bamboo	Guangdong, Guangxi, Hainan	ITS, LSU	Xu et al. (2006), Quijada et al. (2019)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Nemania nummularioides	Culm: Unknown bamboo	Guangdong		Xu et al. (2006)
Neocapnodium tanakae	Leaf, and unspecified tissues: *Bambusa dolichoclada*, *Ba. oldhamii*, *Phyllostachys makinoi*	Anhui, Taiwan		Xu et al. (2006), Mohanan (2017)
Neocosmospora solani	Culm: *Phyllostachys aureosulcata*, *Ph. edulis*, *Ph. glauca*, *Ph. sulphurea* f. *houzeauana*, *Ph. sulphurea* var. *viridis*	Jiangsu, Zhejiang, Anhui, Fujian		Zhang (2000), Xu et al. (2006), Mohanan (2017)
Neokalmusia scabrispora	Culm, and leaf: Unknown bamboo	Jiangsu, Zhejiang		Xu et al. (2006)
Neonectria ditissima	Culm: *Dendrocalamus latiflorus*	Fujian		Xu et al. (2006)
Neopestalotiopsis clavispora	Timber: Unknown bamboo	Anhui		Ma et al. (2009a)
Neostagonosporella sichuanensis	Root, culm, branch, and twig: *Phyllostachys heteroclada*	Sichuan	ITS, LSU, SSU, *tef*1-α	Yang et al. (2019a)
Nigrospora oryzae	Timber, and leaf: *Phyllostachys nigra*, unknown bamboo	Shandong, Anhui, unspecified location	ITS, *tef*1-α	Ma et al. (2009a), Wei (2014), Hao et al. (2020)
Nigrospora osmanthi	Leaf: *Phyllostachys nigra*	Shandong	ITS, *tef*1-α, *tub*2	Hao et al. (2020)
Nigrospora sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Oedocephalum glomerulosum	Culm: *Phyllostachys* sp.	Guangdong		Xu et al. (2006)
Papularia bambusina	Branch, and twig: *Bambusa* sp.	Fujian		Xu et al. (2006)
Parabambusicola bambusina	Culm: Unknown bamboo	Sichuan		Xu et al. (2006)
Parakarstenia phyllostachydis	Culm, and branch: *Phyllostachys heteroclada*	Sichuan	ITS, LSU	Yang et al. (2019b)
Paralloneottiosporina sichuanensis	Leaf: *Phyllostachys violascens*	Sichuan	ITS, LSU, SSU, *tef*1-a	Zeng et al. (2022)
Passalora aterrima	Unknown tissues: *Sinarundinaria* sp.?	Guangxi		Xu et al. (2006)
Penicillium chrysogenum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Penicillium citreonigrum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Penicillium citrinum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Penicillium oxalicum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Penicillium purpureogenum	Timber: *Phyllostachys edulis*	Zhejiang		Ma et al. (2012)
Penicillium sp. (1)	Timber: Unspecified bamboo	Jiangsu		Zhao et al. (1994)
Penicillium spinulosum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Pestalosphaeria sp.	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Pestalotiopsis adusta	Leaf: *Bambusa pervariabilis* × *grandis*	Guizhou		Sang et al. (2012)
Pestalotiopsis mangifolia	Timber: *Cephalostachyum chinense*, *Dendrocalamus brandisii*, *De. giganteus*, *De. membranaceus*, *Lingnania intermedia*	Unknown location		Mohanan (2017)
Phaeosphaeria bambusae	Leaf: *Bambusa lapidea*, *Phyllostachys aureosuleata* f. *spectabilis*, *Ph. reticulata*, *Ph. dulcis*, *Ph. edulis*, *Ph. glauca*, *Ph. iridescens*, *Ph. makinoi*, *Ph. meyeri*, *Ph. nidularia*, *Ph. violascens*, *Ph. sulphurea* f. *houzeauana*, *Ph. sulphurea* var. *viridis*, *Ph. sulphurea*, *Ph. vivax*	Jiangsu, Zhejiang		Xu et al. (2006)
Phaeostalagmus tenuissimus	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Phoma arundinacea	Culm: *Bambusa emeiensis*, *Phyllostachys glauca*, *Ph. sulphurea* var. *viridis*	Guangdong, Sichuan		Xu et al. (2006)
Phomatospora dinemasporium	Leaf: *Phyllostachys* sp.	Hebei, Jiangsu		Xu et al. (2006)
Phomatospora sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Phomopsis sp. (1)	Culm: *Bambusa pervariabilis* × *grandis*	Guizhou		Sang et al. (2012)
Phragmocarpella fusispora	Leaf: *Phyllostachys* sp.	Guangdong		Xu et al. (2006)
Phragmocarpella japonica	Leaf: *Bambusa* sp., *Phyllostachys edulis*	Fujian, Hubei		Xu et al. (2006)
Phyllachora bambusae	Leaf: *Bambusa* sp.	Guangdong, Hunan		Xu et al. (2006), Zhang & Zhang (2014)
Phyllachora bambusina	Leaf: *Bambusa* sp.	Hunan, Hainan, Yunnan, Guangxi		Li et al. (2014b), Zhang & Zhang (2014)
Phyllachora cephalostachyi	Leaf: *Cephalostachyum pergracile*	Yunnan	ITS, LSU	Li et al. (2021b)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Phyllachora chimonobambusae	Leaf: *Chimonobambusa quadrangularis*, *Ch. yunnanensis*	Yunnan		Li et al. (2014b), Zhang & Zhang (2014)
Phyllachora dendrocalami	Leaf: *Dendrocalamus giganteus*, *De. strictus*, unknown bamboo	Yunnan		Zhang & Zhang (2014)
Phyllachora dendrocalami-hamiltoniicola	Leaf: *Dendrocalamus hamiltonii*	Yunnan	LSU	Li et al. (2019)
Phyllachora dendrocalami-membranacei	Leaf: *Dendrocalamus membranaceus*	Yunnan	ITS, LSU	Li et al. (2019)
Phyllachora eximia	Leaf: *Arundinaria* sp., *Bambusa beecheyana*, *Ba. chungii*, *Ba. emeiensis*, *Ba. multiplex*, *Bambusa* sp., *Ba. spinosa*, *Indocalamus latifolius*, *In. tessellatus*, *Phyllostachys reticulata*, *Ph. edulis*, *Ph. glauca*, *Ph. heteroclada*, *Fargesia nitida*	Jiangsu, Zhejiang, Anhui, Fujian, Hubei, Hunan, Jiangxi, Guangdong, Hongkong, Henan, Sichuan, Yunnan, Guangxi, Taiwan		Xu et al. (2006), Zhang & Zhang (2014)
Phyllachora graminis	Leaf: *Arundinaria* sp., *Bambusa* sp., *Phyllostachys heteroclada*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*	Jiangsu, Hunan, Yunnan		Zhang & Zhang (2014), Mohanan (2017)
Phyllachora hekouensis	Leaf: *Indocalamus tessellatus*	Yunnan		Zhang & Zhang (2014)
Phyllachora heterocladae	Culm: *Phyllostachys heteroclada*	Sichuan	ITS, LSU, SSU	Yang et al. (2019d)
Phyllachora indocalami	Leaf: *Indocalamus tessellatus*, *Yushania niitakayamensis*	Zhejiang, Anhui, Taiwan		Parbery (1967), Xu et al. (2006)
Phyllachora indosasae	Leaf: *Indosasa hispida* cv. 'Rainbow '	Yunnan		Wu et al. (2013)
Phyllachora ischaemi	Leaf: *Chimonobambusa armata*	Yunnan		Zhang & Zhang (2014), Mohanan (2017)
Phyllachora lelebae	Leaf: *Bambusa multiplex*, *Ba. pachinensis*	Taiwan		Xu et al. (2006), Zhang & Zhang (2014)
Phyllachora leptotheca	Leaf: Unknown bamboo	Unspecified location		Mohanan (2017)
Phyllachora lushanensis	Leaf: *Phyllostachys edulis*	Jiangxi		Zhang & Zhang (2014)
Phyllachora maculans	Leaf: *Bambusa* sp.	Yunnan		Zhang & Zhang (2014)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Phyllachora malabarensis	Leaf: *Arundinaria faberi*, *Bambusa* sp., *Ba. textilis*, unknown bamboo	Zhejiang, Anhui, Guangdong, Hunan, Sichuan, Yunnan		Zhang & Zhang (2014)
Phyllachora megastroma	Leaf: Unknown bamboo	Yunnan		Zhang & Zhang (2014)
Phyllachora nanningensis	Leaf: *Bambusa chungii*, *Ba. pervariabilis*, *Ba. rigida*	Guangxi, Hainan		Zhang & Zhang (2014)
Phyllachora orbicula	Leaf: *Arundinaria japonica*, *Bambusa arundinaceae*, *Ba. multiplex* var. *riviereorum*, *Ba. pervariabilis* × *grandis*, *Bambusa* sp., *Fargesia dracocephala*, *Fa. mairei*, *Phyllostachys edulis*, *Ph. reticulata*, *Phyllostachys* sp., *Pseudosasa japonica*, unknown bamboo	Shandong, Zhejiang, Anhui, Hunan, Guangdong, Hongkong, Jiangxi, Yunnan, Guizhou		Sang et al. (2012), Zhang & Zhang (2014)
Phyllachora orbicularis	Leaf: *Bambusa chungii*, *Ba. emeiensis*, *Ba. multiplex*, *Bambusa* sp., *Ba. spinosa*, *Ba. blumeana*, *Phyllostachys bissetii*, *Ph. glauca*, *Ph. heteroclada*, *Ph. sulphurea* var. *viridis*, *Pseudosasa japonica*	Shandong, Zhejiang, Hunan, Fujian, Guangdong, Jiangxi, Sichuan, Yunnan, Guangxi		Xu et al. (2006)
Phyllachora orbiculata	Leaf: Unknown bamboo	Unspecified location		Zhang (2000), Mohanan (2017)
Phyllachora pachinensis	Leaf: *Bambusa pachinensis*, *Bambusa* sp., unknown bamboo	Jiangsu, Zhejiang, Jiangxi, Yunnan, Taiwan		Parbery (1967), Zhang & Zhang (2014)
Phyllachora phragmitis-karkae	Leaf: *Phyllostachys* sp., *Sasa* sp.	Unspecified location		Mohanan (2017)
Phyllachora phyllostachydis	Leaf: *Bambusa albo-lineata*, *Ba. lapidea*, *Ba. blumeana*, *Ba. textilis*, *Phyllostachys bambusoides* var. *castilloni*, *Ph. edulis*, *Ph. glauca*, *Ph. heteroclada*, *Ph. lithophia*?,	Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Henan, Jiangxi, Shaanxi, Chongqing, Yunnan, Guizhou, Guangxi,		Zhang (2000), Xu et al. (2006), Zhang & Zhang (2014), Mohanan (2017)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
	Ph. makinoi, *Ph. nigra* var. *henonis*, *Ph. nigra*, *Ph. nuda*, *Ph. reticulata*, *Phyllostachys* sp., *Semiarundinaria densiflora*, *Fargesia nitida*, unknown bamboo	Taiwan		
Phyllachora shiraiana	Leaf: *Arundinaria* sp., *Ar. japonica*, *Bambusa albo-lineata*?, *Ba. dolichomerithalla* cv. *green-stripestem*, *Ba. dolichomerithalla* cv. *siliverstripe*, *Ba. lapidea*, *Ba. multiplex*, *Bambusa* sp., *Ba. blumeana*, *Ba. textilis*, *Ba. ventricosa*, *Indosasa gigantea*, *Indocalamus longiauritus*, *Phyllostachys bissetii*, *Ph. edulis*, *Ph. glauca*, *Ph. makinoi*, *Ph. nidularia*, *Ph. nigra*, *Ph. nuda*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Pleioblastus amarus*, *Pl. simonii*, *Pleioblastus* sp., *Sasa japonica*, unknown bamboo	Shandong, Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Jiangxi, Guangdong, Hongkong, Shaanxi, Chongqing, Sichuan, Yunnan, Guizhou, Guangxi, Hainan, Taiwan		Xu et al. (2006), Zhang et al. (2011), Zhang & Zhang (2014), Mohanan (2017)
Phyllachora sinensis	Leaf: *Bambusa arundinaceae*, *Ba. beecheyana*, *Ba. blumeana*, *Ba. emeiensis*, *Ba. multiplex*, *Ba. pervariabilis*, *Bambusa* sp., *Dendrocalamus giganteus*, *Phyllostachys reticulata*, *Ph. edulis*, *Ph. glauca*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*	Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Jiangxi, Guangdong, Sichuan, Yunnan, Taiwan		Zhang et al. (2011), Zhang & Zhang (2014)
Phyllachora tetraspora	Leaf: *Sasa* sp.	Taiwan		Zhang & Zhang (2014)
Phyllachora tjangkorreh	Leaf: *Arundinaria japonica*, *Bambusa blumeana*,	Shandong, Anhui, Fujian, Guangdong,		Xu et al. (2006), Gong et al. (2008),

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
	Chimonobambusa quadrangularis, *Phyllostachys nidularia*, *Ph. reticulata*, *Phyllostachys* sp.	Shaanxi, Yunnan		Zhang & Zhang (2014)
Phyllachora tonkinensis	Leaf: *Yushania brevipaniculata*, *Phyllostachys reticulata*, *Bambusa* sp.	Fujian, Sichuan, Yunnan		Li et al. (2014b), Zhang & Zhang (2014)
Phyllachora yushaniae	Leaf: *Dendrocalamus giganteus*, *De. semiscandens*, *Fargesia albocerea*, *Fa. solida*, *Indocalamus tessellatus*, *Phyllostachys nigra* var. *henonis*, *Sinobambusa tootsik*, *Yushania auctiaurita*, *Yu. niitakayamensis*	Zhejiang, Guangdong, Yunnan, Taiwan		Zhang & Zhang (2014)
Phyllosticta bambusina	Leaf: *Phyllostachys glauca*	Jiangsu		Xu et al. (2006)
Phyllosticta necatrix	Timber: Unspecified bamboo	Jiangsu		Zhao et al. (1994)
Phyllosticta take	Leaf: *Bambusa emeiensis*, *Ba. textilis*	Sichuan		Xu et al. (2006)
Physalospora reinkingiana	Culm, and branch: Unknown bamboo	Fujian, Hunan, Guangdong, Guangxi		Xu et al. (2006)
Physalospora sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Podonectria sichuanensis	Root, culm, branch, and twig: *Phyllostachys heteroclada*	Sichuan	ITS, LSU, SSU, *tef*1-α, *tub*2	Yang et al. (2019g), Xu et al. (2021)
Prosthemiella bambusina	Leaf: *Bambusa multiplex* var. *riviereorum*	Guangdong		Xu et al. (2006)
Pseudolachnella scolecospora	Unknown tissue: *Phyllostachys* sp.	Zhejiang, Hunan		Xu et al. (2006)
Rosellinia culmicola	Culm: Unknown bamboo	Guangxi		Xu et al. (2006)
Rosellinia decipiens	Culm, and leaf?: Unknown bamboo	Hainan		Xu et al. (2006)
Rosellinia emergens	Culm, and branch: Unknown bamboo	Jiangsu, Fujian, Guangdong, Yunnan, Guangxi		Zhang (2000), Xu et al. (2006)
Rosellinia sp. (1)	Unknown tissue: Unknown bamboo	Unspecified location		Mohanan (2017)
Roussoella hysterioides	Timber: Unknown bamboo	Hongkong		Mohanan (2017)
Rubroshiraia bambusae	Branch: *Fargesia spathacea*	Yunnan	ITS, LSU, SSU, *tef*1-α	Dai et al. (2019)
Scolicotrichum phyllostachydis	Branch?: *Phyllostachys* sp.	Jiangsu		Xu et al. (2006)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Scorias capitata	Unknown tissue: *Bambusa emeiensis*	Sichuan		Xu et al. (2006)
Scorias communis	Unknown tissue: *Bambusa dolichoclada*, *Ba. oldhamii*, *Indocalamus latifolius*, *Phyllostachys makinoi*	Anhui, Taiwan		Xu et al. (2006)
Scorias spongiosa	Culm, branch, and leaf: Unknown bamboos	Jiangsu, Zhejiang, Sichuan	ITS	He et al. (2011)
Septocytella bambusina	Leaf: *Bambusa* sp.	Zhejiang, Hunan		Xu et al. (2006)
Septogloeum sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Shanoria bambusarum	Leaf: *Phyllostachys edulis*	Anhui		Xu et al. (2006)
Shiraia bambusicola	Branch, and twig: *Bambusa blumeana*, *Ba. emeiensis*, *Ba. intermedia*, *Bambusa* sp., *Chimonobambusa pachystachys*, *Fargesia* sp., *Indosasa shibataeoides*, *Phyllostachys edulis*, *Ph. glauca*, *Ph. heteroclada*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea*, *Ph. sulphurea* var. *viridis*, *Ph. violascens*, *Ph. violascens* 'Prevernalis', *Pleioblastus amarus*, *Semiarundinaria densiflora*	Jiangsu, Zhejiang, Anhui, Fujian, Hubei, Hunan, Henan, Jiangxi, Shanghai, Sichuan, Yunnan, Guizhou	ITS, LSU, SSU, *tef*1-α, *rpb*2	Zhang (2000), Xu et al. (2006), Zhang et al. (2011), Mohanan (2017), Dai et al. (2019)
Solicorynespora foveolata	Unknown tissue: *Phyllostachys edulis*, *Phyllostachys* sp.	Jiangsu, Hunan, Shaanxi, Sichuan, Yunnan, Guangxi		Xu et al. (2006)
Sordaria sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Sphaeropsis photiniae	Timber: Unspecified bamboo	Jiangsu		Zhao et al. (1994)
Sphaeropsis sapinea	Timber: Unknown bamboo	Anhui		Ma et al. (2009a)
Sporidesmium ehrenbergii	Timber: Unspecified bamboo	Jiangsu		Zhao et al. (1994)
Sporidesmium eupatoriicola	Culm: *Bambusa textilis*	Hongkong		Xu et al. (2006)
Sporidesmium uapacae	Culm: *Phyllostachys edulis*	Yunnan		Xu et al. (2006)
Strigula sinoaustralis	Leaf: Unknown bamboo	Guangxi	ITS	Jiang et al. (2016)
Talaromyces rugulosus	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)

Table 6 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Telimena graminis	Leaf: *Phyllostachys edulis*	Jiangxi		Xu et al. (2006)
Tetraploa aristata	Unknown tissue: *Bambusa* sp.	Guangdong		Xu et al. (2006)
Trichoderma harzianum	Timber: *Phyllostachys edulis*, unknown bamboo	Zhejiang, Yunnan		Xu et al. (2006), Ma et al. (2012)
Trichoderma sp. (1)	Timber: Unknown bamboo	Guangdong		Ma et al. (2009a)
Trichoderma viride	Timber: Unspecified tissue	Yunnan		Fu et al. (1999), Wang et al. (2000a)
Trichothecium roseum	Timber: Unknown bamboo	Yunnan		Wang et al. (2000a)
Trichothecium sp. (1)	Timber: Unknown bamboo	Unspecified location		Ma et al. (2009b)
Tubeufia javanica	Branch?: *Bambusa blumeana*	Taiwan		Xu et al. (2006)
Ustulina deusta	Culm: Unknown bamboo	Jiangsu, Zhejiang, Anhui, Fujian, Hunan, Jiangxi, Guangdong, Shaanxi, Yunnan, Guangxi, Taiwan		Xu et al. (2006)
Xenosporella berkeleyi	Unspecified tissue: *Phyllostachys* sp.	Zhejiang		Xu et al. (2006)
Xenosporella dendrocalami?	Unspecified tissue: *Dendrocalamus latiflorus*	Guangxi, Taiwan		Xu et al. (2006)
Xylaria scopiformis	Root?: Unknown bamboo	Hebei, Guangdong, Jiangxi, Yunan, Guangxi, Hainan		Xu et al. (2006)
Xylaria sp. (3)	Culm, and timber: *Phyllostachys edulis*, other unspecified bamboos	Jiangxi, Yunnan, unspecified location		Fu et al. (1999), Wang et al. (2000a), Ma et al. (2009b), Wang et al. (2012)
Xylosphaeria sp. (1)	Root: Unknown bamboo	Unspecified location		Mohanan (2017)

Notes – The information provided comprises valid data recorded in the literature. In instances where the literature lacks clear or unexplained information, the table should incorporate terms such as "?", "unknown" or "unspecified". Molecular data pertains to precise molecular information explicitly mentioned in the existing literature and data registered in the NCBI database. In cases where pathogens are documented in the literature without species identification, the taxon is only being referred to the genus level as one species, with the numbers in parentheses denoting the frequency of occurrence in the literature. This note is also applicable to Table 7 presented below.

basidiomycetes in bamboo pathology, research into their specific species composition and ecological impact remains somewhat constrained. Factors such as limited access to diverse specimens, variability in anatomical morphology and the ecological interactions within bamboo ecosystems contribute to these challenges. As with ascomycetes, the taxonomy of basidiomycetes associated with bamboo requires thorough reevaluation. This necessitates a detailed and multidisciplinary approach, incorporating morphology, molecular data and ecological traits to accurately define species boundaries and understand their roles within bamboo ecosystems.

Table 7 Classification of bambusicolous pathogenic basidiomycetes with information on the type of substrates, geographical distribution, and molecular data.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Aphelaria dendroides	Culm, and leaf?: Unknown bamboo	Yunnan		Xu et al. (2006)
Athelia rolfsii?	Fruit, seedling, and branch: *Phyllostachys aureosulcata*, *Ph. edulis*, *Ph. glauca*, *Ph. reticulata*, *Ph. sulphurea* var. *viridis*	Unspecified location		Mohanan (2017)
Bambusiomyces shiraianus	Shoot, branch, twig, and inflorescence: *Arundinaria* spp., *Bambusa pervariabilis* × *grandis*, *Ba. emeiensis*, *Fargesia* sp., *Phyllostachys aurea*, *Ph. flexuosa*, *Ph. glauca*, *Ph. heteroclada*, *Ph. incarnata*, *Ph. nigra*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea*, *Ph. edulis*, *Ph. makinoi*, *Ph. nigra* var. *henonis*, *Ph. reticulata*, *Ph. rubicunda*, *Ph. sulphurea* var. *viridis*, *Pleioblastus amarus*, *Pl. makinoi*?, *Pleioblastus* sp., *Sasa chartacea*, *Sa. ramosa*	Jiangsu, Zhejiang, Anhui, Fujian, Hubei, Hunan, Henan, Jiangxi, Shaanxi, Sichuan, Yunnan, Guizhou, Taiwan		Zhu (1988), Xu et al. (2006), Zhang et al. (2011), Sang et al. (2012), Mohanan (2017)
Botryobasidium rubiginosum	Culm: Unknown bamboo	Hebei, Jiangsu, Anhui, Fujian, Hunan, Guangdong, Guangxi		Xu et al. (2006)
Clavulina sp. (1)	Root: Unknown bamboo	Unspecified location		Mohanan (2017)
Corticium centrifugum	Root: *Dendrocalamus latiflorus*	Taiwan		Xu et al. (2006)
Dicellomyces sp. (1)	Leaf: Unknown bamboo	Unspecified location		Xu et al. (2006)
Epithele bambusae	Culm, and culm leaf: *Phyllostachys* sp.	Zhejiang, Henan, Sichuan, Yunnan, Hainan		Xu et al. (2006)
Favolaschia pustulosa	Culm: Unknown bamboo	Fujian, Guangdong, Yunnan		Xu et al. (2006)
Favolaschia staudtii	Culm: Unknown bamboo	Sichuan		Xu et al. (2006)

Table 7 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Favolaschia tonkinensis	Culm: Unknown bamboo	Sichuan		Xu et al. (2006)
Fuscoporia torulosa	Culm: *Bambusa blumeana*	Taiwan		Xu et al. (2006)
Ganoderma applanatum	Culm: *Bambusa blumeana*, *Ba. dolichoclada*, unknown bamboo	Jilin, Heilongjiang, Hebei, Shanxi, Shaanxi, Jiangsu, Zhejiang, Anhui, Fujian, Jiangxi, Hunan, Henan, Inner Mongolia, Gansu, Qinghai, Xinjiang, Sichuan, Yunnan, Guizhou, Guangxi, Hainan, Taiwan		Xu et al. (2006)
Ganoderma lucidum	Root, and culm base: *Bambusa blumeana*, *Ba. oldhamii*, *Ba. vulgaris*, *Ba. vulgaris* f. *vittata*	Taiwan		Xu et al. (2006), Mohanan (2017)
Hygrocybe chlorophana	Root: Unknown bamboo	Unspecified location		Mohanan (2017)
Hygrocybe coccinea	Root: Unknown bamboo	Unspecified location		Mohanan (2017)
Hygrocybe miniata	Root: Unknown bamboo	Unspecified location		Mohanan (2017)
Kweilingia bambusae	Leaf, and leaf-sheath: *Oligostachyum lubricum*, unknown bamboo	Zhejiang, Guangxi		Xu et al. (2006)
Kweilingia divina?	Leaf: *Bambusa albolineata*, *Ba. arundinaceae*, *Ba. beecheyana* var. *pubescens*, *Ba. beecheyana*, *Ba. blumeana*, *Ba. dolichoclada* f. *stripe*, *Ba. dolichoclada*, *Ba. dolichomerithalla* cv. 'Silverstripe', *Ba. multiplex* f. *fernleaf*, *Ba. multiplex* f. *stripestem-fernleaf*, *Ba. multiplex* var. *shimadae*, *Ba. multiplex*, *Ba. odashimae*, *Ba. oldhamii*, *Ba. pachinensis* var. *hirsutissima*, *Ba. pachinensis*, *Ba. utilis*, *Ba. ventricosa*, *Ba. vulgaris* 'Wamin', *Ba. vulgaris* f. *vittata*, *Dendrocalamus latiflorus* f. *meinung*,	Taiwan		Xu et al. (2006), Mohanan (2017)

Table 7 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
	De. latiflorus f. *subconvex*, *De. latiflorus*, *Fargesia dracocephala*, *Pseudosasa* sp.			
Phallus cinnabarinus	Root: *Dendrocalamus latiflorus*	Taiwan		Xu et al. (2006)
Physopella inflexa	Leaf: *Bambusa blumeana*, *Phyllostachys* sp., unknown bamboo	Zhejiang, Hubei, Henan, Shanghai		Xu et al. (2006), Mohanan 2017)
Pterula penicellata	Culm leaf?: Unknown bamboo	Yunnan		Xu et al. (2006)
Puccinia arundinariae	Leaf: *Phyllostachys sulphurea* var. *viridis*	Shaanxi		Xu et al. (2006)
Puccinia bambusicola	Leaf: *Bambusa* sp.	Hunan		Xu et al. (2006), Mohanan 2017)
Puccinia brachystachyicola	Leaf: *Fargesia spathacea*, *Semiarundinaria densiflora*	Jiangsu, Zhejiang, Sichuan		Xu et al. (2006)
Puccinia corticioides	Culm: *Arundinaria* sp., *Bambusa beecheyana*, *Ba. blumeana*, *Bambusa* sp., *Ba. vulgaris* f. *vittata*, *Chimonobambusa quadrangularis*, *Chimonobambusa* sp., *Indocalamus* sp., *Phyllostachys bissetii*, *Ph. dulcis*, *Ph. edulis*, *Ph. glauca*, *Ph. heteroclada*, *Ph. meyeri*, *Ph. nidularia*, *Ph. nigra* var. *henonis*, *Ph. nuda*, *Ph. propinqua*, *Ph. propinque*?, *Ph. reticulata*, *Ph. rubicunda*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Ph. sulphurea*, *Ph. violascens*, *Ph. vivax*, *Pleioblastus amarus*, *Pseudosasa amabilis*, *Ps. japonica*, *Sasa longiligulata*, *Sasa* sp., *Semiarundinaria densiflora*, *Se. fastuosa*, *Semiarundinaria* sp.	Shandong, Jiangsu, Zhejiang, Anhui, Hubei, Hunan, Henan, Jiangxi, Guangdong, Shaanxi, Shanghai, Sichuan, Yunnan, Tibet, Guizhou, Guangxi, Taiwan	ITS, LSU	Xu et al. (2006), Zhang et al. (2011), Zhuang (2012), Mohanan (2017)
Puccinia dispori	Leaf: *Phyllostachys edulis*, *Ph. aurea*	Jiangsu, Zhejiang, Henan, Guangdong		Mohanan (2017)
Puccinia ditissima	Leaf: *Dendrocalamus giganteus*, *De. latiflorus*, *Schizostachyum* sp.	Taiwan, unspecified location		Xu et al. (2006), Mohanan (2017)

Table 7 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Puccinia flammuliformis	Leaf: *Bambusa* sp., *Indocalamus tessellatus*, unknown bamboo	Unspecified location		Xu et al. (2006), Mohanan (2017)
Puccinia ignava	Leaf: *Bambusa bambos*, *Ba. oldhamii*, *Ba. ventricosa*, *Ba. vulgaris*, *Ba. vulgaris* f. *vittatam*, *Dendrocalamus giganteus*, *De. latiflorus*, *Neosinocalamus* sp., *Schizostachyum* sp.	Jiangsu, Fujian, Guangdong, Taiwan		Ma et al. (2005), Xu et al. (2006), Zhou et al. (2010), Mohanan (2017)
Puccinia kusanoi	Leaf: *Bambusa* sp., *Fargesia spathacea*, *Nipponobambusa* sp.?, *Phyllostachys aurea*, *Ph. edulis*, *Phyllostachys* sp., *Pleioblastus* sp., *Pseudosasa* sp., *Sasa* sp., *Sasaella* sp., *Semiarundinaria* sp., *Sinobambusa* sp., *Yushania niitakayamensis*	Zhejiang, Anhui, Fujian, Shaanxi, Sichuan, Yunnan, Guangxi, Taiwan	ITS, LSU, SSU	Xu et al. (2006), Mohanan (2017), Shen et al. (2017)
Puccinia kwanhsienensis	Leaf: *Bambusa* sp., *Sasa masamuneana*	Anhui, Fujian, Sichuan, Yunnan, Guangxi		Xu et al. (2006), Mohanan (2017)
Puccinia longicornis	Leaf: *Bambusa arundinaceae*, *Bambusa* sp., *Indocalamus* sp., *Nipponobambusa* sp.?, *Phyllostachys* sp., *Pleioblastus* sp., *Pseudosasa* sp., *Sasaella* sp., *Sasa* sp.	Jiangsu, Zhejiang, Anhui, Fujian, Guangdong, Shaanxi, Sichuan, Yunnan, Guangxi		Xu et al. (2006), Mohanan (2017)
Puccinia machilicola	Leaf: Unknown bamboo	Zhejiang		Xu et al. (2006)
Puccinia melanocephala	Leaf: *Arundinaria* sp., *Bambusa* sp., *Sasa masamuneana*	Sichuan		Mohanan (2017)
Puccinia neoporteri	Leaf: Unknown bamboo	Jiangsu		Xu et al. (2006)
Puccinia nigroconoidea	Leaf: *Phyllostachys* sp.	Anhui		Xu et al. (2006), Mohanan (2017)
Puccinia phyllostachydis	Leaf: *Arundinaria* sp., *Bambusa blumeana*, *Ba. emeiensis*, *Bambusa* sp., *Drepanostachyum suberecta*?, *Fargesia* sp., *Fa. spathacea*, *Phyllostachys aurea*, *Ph. edulis*, *Ph. glauca*, *Ph. makinoi*, *Ph. nigra* var. *henonis*, *Ph. nigra*, *Ph. nuda*, *Ph. reticulata*, *Phyllostachys* sp., *Ph. sulphurea* var. *viridis*, *Ph. sulphurea*, *Sasa borealis*	Jiangsu, Zhejiang, Fujian, Henan, Shaanxi, Jiangxi, Sichuan, Yunnan, Guizhou, Guangxi, Taiwan		Xu et al. (2006), Mohanan (2017)

Table 7 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Puccinia polliniae	Leaf: *Phyllostachys edulis*, *Ph. aurea*, *Sasa masamuneana*	Anhui, Fujian, Yunnan, Guangxi		Mohanan (2017)
Puccinia polliniae-imberbis	Leaf: *Bambusa* sp., *Phyllostachys aurea*, *Ph. edulis*	Anhui, Fujian, Yunnan, Guangxi		Mohanan (2017)
Puccinia polliniicola	Leaf: *Bambusa oldhamii*, *Bambusa* sp., *Ba. vulgaris*, *Indocalamus tessellatus*, *Ischurchola spinosa*?	Anhui, Fujian, Shaanxi, Yunnan, Guangxi		Mohanan (2017)
Puccinia recondita	Leaf: *Bambusa pervariabilis* × *grandis*	Guizhou		Sang et al. (2012)
Puccinia scabrida	Leaf: *Phyllostachys* sp.	Jiangsu		Xu et al. (2006), Mohanan (2017)
Puccinia sinarundinariae	Leaf: *Fargesia nitida*	Sichuan		Xu et al. (2006), Mohanan (2017)
Puccinia sinarundinariicola	Leaf: *Yushania brevipaniculata*	Sichuan		Xu et al. (2006)
Puccinia tenella	Leaf: *Bambusa* sp.	Hongkong		Xu et al. (2006), Mohanan (2017)
Puccinia xanthosperma	Leaf: *Bambusa* sp., *Himalayacalamus collaris*	Tibet, unspecified location		Xu et al. (2006), Mohanan (2017)
Rhizoctonia fumigata	Unknown tissue: *Bambusa* sp.	Taiwan		Xu et al. (2006)
Rhizoctonia solani	Seedling: *Bambusa bambos*, *Ba. blumeana*, *Dendrocalamus brandisii*, *De. strictus*, *Phyllostachys* sp., *Thyrsostachys siamensis*	Unspecified location		Mohanan (2017)
Scleroderma verrucosum	Root, culm, and culm base: *Bambusa bambos*	Unspecified location		Mohanan (2017)
Septobasidium albidum	Culm: *Phyllostachys* sp.	Zhejiang		Xu et al. (2006)
Septobasidium bogoriense	Culm: *Phyllostachys glauca*, *Ph. sulphurea* var. *viridis*	Zhejiang, Henan		Xu et al. (2006)
Serpula dendrocalami	Culm: *Dendrocalamus* sp.	Yunnan	ITS	Wang et al. (2019)
Serpula similis	Culm, and culm base: *Bambusa bambos*, *Thyrsostachys oliveri*, unknown bamboo	Guangdong		Xu et al. (2006), Mohanan (2017)
Tapinella atrotomentosa	Culm: Unknown bamboo	Jilin, Hebei, Jiangsu, Anhui, Fujian, Henan, Hunan, Guangxi		Xu et al. (2006)
Thelephora terrestris	Root: Unknown bamboo	Unspecified location		Mohanan (2017)
Tricholomopsis sp. (1)	Root: Unknown bamboo	Unspecified location		Mohanan (2017)

Table 7 Continued.

Species name	Substrate and host	Geographical distribution	Molecular data	References
Uredo arundinis-donacis	Leaf: *Bambusa* sp., *Fargesia* sp., *Phyllostachys* sp., *Sasa borealis*, *Sa. septentrionalis*	Unspecified location		Mohanan (2017)
Uredo dendrocalami	Leaf: *Dendrocalamus latiflorus*, *De. strictus*	Guangdong		Xu et al. (2006), Mohanan (2017)
Uredo haloxyli?	Culm: *Bambusa arundinaceae*, *Ba. multiplex* 'Fernleaf', *Dendrocalamus* sp., *Phyllostachys* sp., *Sasa borealis*	Shaanxi, Guangdong, Guangxi		Xu et al. (2006)

Other bambusicolous pathogenic Fungi

In comparison to *Ascomycota* and *Basidiomycota*, a limited number of phyla have been documented to pose a threat to bamboo plants and only four species belonging to *Mucoromycota* have been reported to cause harm to bamboo timber (Ma et al. 2009b). However, the fungal kingdom is vast, comprising approximately 22 described phyla (Voigt et al. 2021, Zhao et al. 2022), indicating a potential for a broader diversity of bamboo pathogens that has been currently documented. Research on plant pathogenic fungi has traditionally focused on ascomycetes and basidiomycetes, given their widespread presence and notable impact on agriculture and forestry. However, instances of pathogenicity from other fungal phyla suggest that the scope of pathogenic threats to bamboo may extend beyond these well-studied groups. For instance, within *Entorrhizomycota*, the occurrence of root gall caused by *Juncorrhiza* spp. or *Entorrhiza* spp. is observed (Bauer et al. 2015, Riess et al. 2019). Similarly, the *Chytridiomycota* harbors *Synchytrium minutum* (Pat.) Gaum.) responsible for false rust disease (Yun et al. 2011), and other phyla such as *Sanchytriomycota* have been linked to plant pathogenic activity (Galindo et al. 2021). The relatively limited reporting on non-ascomycete and non-basidiomycete fungi suggests that there may be underexplored areas of fungal biology and ecology. Further investigations are necessary to determine whether other types of pathogenic fungi exist in bamboo plants and to understand their effects on the growth of bamboo plants and the bamboo forest ecosystem.

Species diversity of bambusicolous mycopathogens

Bambusicolous mycopathogens are distributed throughout the entire country, with a notably higher prevalence of species documented in the southern regions, specifically south of the Yellow River. Investigation of pathogenic fungi affecting Chinese bamboo is closely linked to the growth of the bamboo industry. In key bamboo-producing provinces like Guangdong, Jiangsu, Sichuan, Yunnan, and Zhejiang, extensive records of pathogenic fungi exist (Fig. 43). However, the identification and recognition of pathogenic species from other areas encounter challenges due to policy constraints, which limit the accessibility of information regarding these pathogens. Among the 26 provinces surveyed, 16 have documented ten or more species of pathogenic fungi. Notably, Anhui, Fujian, Guangdong, Guangxi, Hunan, Jiangsu, Sichuan, Yunnan, and Zhejiang have each recorded over thirty recorded species of pathogenic fungi. Clear heterogeneity in pathogenic fungal species was evident across different regions, leading to diverse structures and compositions of the pathogenic fungal communities. However, certain ubiquitous species, like the pathogens from *Apiosporaceae*, *Nectriaceae*, *Phyllachoraceae*, *Pucciniaceae*, and *Xylariaceae* families, exhibited widespread distribution across most provinces (Fig. 43).

Pathogenic fungi have been documented on over 120 bamboo species, belonging to at least 23 genera. These include *Arundinaria*, *Bambusa*, *Cephalostachyum*, *Chimonobambusa*, *Dendrocalamus*, *Drepanostachyum*, *Fargesia*, *Himalayacalamus*, *Indocalamus*, *Indosasa*,

Lingnania, *Oligostachyum*, *Phyllostachys*, *Pleioblastus*, *Pseudosasa*, *Sasa*, *Sasaella*, *Schizostachyum*, *Semiarundinaria*, *Sinobambusa*, *Thyrsostachys*, and *Yushania*. Among these, *Arundinaria*, *Bambusa*, *Dendrocalamus*, *Fargesia*, *Indocalamus*, *Phyllostachys*, *Pleioblastus*, and *Sasa* each have been reported to harbour more than ten pathogenic species and this indicates a reasonably high prevalence level of pathogenic fungi. Particularly, *Phyllostachys* (130 species), *Bambusa* (118 species) and *Dendrocalamus* (30 species) show an abundant diversity of pathogenic species (Fig. 44 a, b), with fewer than 20 species noted for remaining genera. Among the genera studied, the top three exhibit a remarkable diversity of pathogenic species. For instance, pathogens associated with *Phyllostachys* are diversified into eight classes, 27 orders, 44 families, and 73 genera. *Bambusa* harbours pathogens spanning eight classes, 28 orders, 46 families, and 61 genera. *Dendrocalamus* records pathogens from six classes, 14 orders, 18 families, and 20 genera. Simultaneously, substantial variations were evident in the species composition of pathogens across different bamboo species. Pathogenic fungi have the potential to affect all tissues of bamboo plants, showing a wide range of species and tissue specialization. The majority of recorded species, over 80%, are found in culms, branches/twigs and leaves, highlighting these parts as particularly susceptible to fungal attacks (Fig. 44 c, d).

Taxonomically, 336 species of bambusicolous pathogenic fungi have been documented, encompassing three phyla, 11 classes, 41 orders, 89 families, and 161 genera. The orders *Phyllachorales*, *Hypocreales*, *Pleosporales*, and *Pucciniales*, collectively account for over 40% of the total recorded species, demonstrate significant species richness and extensive geographic distribution (Fig. 45). The dominant species of pathogenic fungi was mainly from ascomycetes, including genera such as *Phyllachora*, *Fusarium*, *Apiospora*, *Colletotrichum*, *Aspergillus*, and *Penicillium*. Among the basidiomycetes, *Puccinia* is the dominant genus, with 25 recorded species (Fig. 45). *Aspergillus* and *Penicillium*, common pathogenic fungi found in bamboo timber, are the primary culprits causing harm.

Disease types and epiphytology

In China, more than 35 types of fungal diseases have been documented within bamboo forests (Figs 46 c–f, 47), predominantly affecting the culms, branches or twigs, and leaves (Fig. 46 a, b). Culm diseases are more diversified, mainly including timber rot, culm blight, culm rot, canker, spot, sooty mould, wilt, plaster disease, dieback, culm rust, anthracnose and shoot blight. The pathogen of culms includes 170 species, belonging to *Ascomycota* (five classes, 24 orders, 53 families, 86 genera, 150 species), *Basidiomycota* (two classes, seven orders, 10 families, 11 genera, 16 species) and *Mucoromycota* (one class, one order, three families, three genera, four species). Branch blight, spot, witch's broom, tube curl, tabasheer and sooty mould were common in branch/twig diseases and 43 ascomycetous pathogens documented reside in four classes, 11 orders, 19 families, 30 genera, 43 species, while only two species are from *Basidiomycota*. Leaf diseases are the most common ones in bamboo forests, especially leaf spot, tar spots, leaf rust, leaf blight, leaf mold and sooty mould. Leaf-associated pathogens include about 110 species, most of which belong to the phylum *Ascomycota* (three classes, 13 orders, 24 families, 36 genera, 80 species), and the remaining 30 species come from the *Basidiomycota* (two classes, two orders, three families, five genera). Data indicate a heterogeneous distribution of species among different types of diseases (Fig. 46 b), highlighting host specialization among many pathogens, for example, *Puccinia* spp. and *Phyllachora* spp. mostly found on leaves (Xu et al. 2006, Zhang & Zhang 2014, Mohanan 2017), *Aciculosporium* spp. and *Heteroepichloe* spp. target twigs (Cheng et al. 2009, Tanaka et al. 2021), *Shiraia bambusicola* and *Rubroshiraia bambusae* inhabit branches (Dai et al. 2019). These fungi typically exhibit a high degree of parasitism towards specific host tissues without inducing rapid mortality. In contrast, most pathogenic fungi such as *Apiospora*, *Colletotrichum*, and *Fusarium*, adopt a saprophytic or facultative saprophytic lifestyle and can infect different anatomical locations demonstrating a broader host range (Xu et al. 2006, Yang et al. 2019d, e).

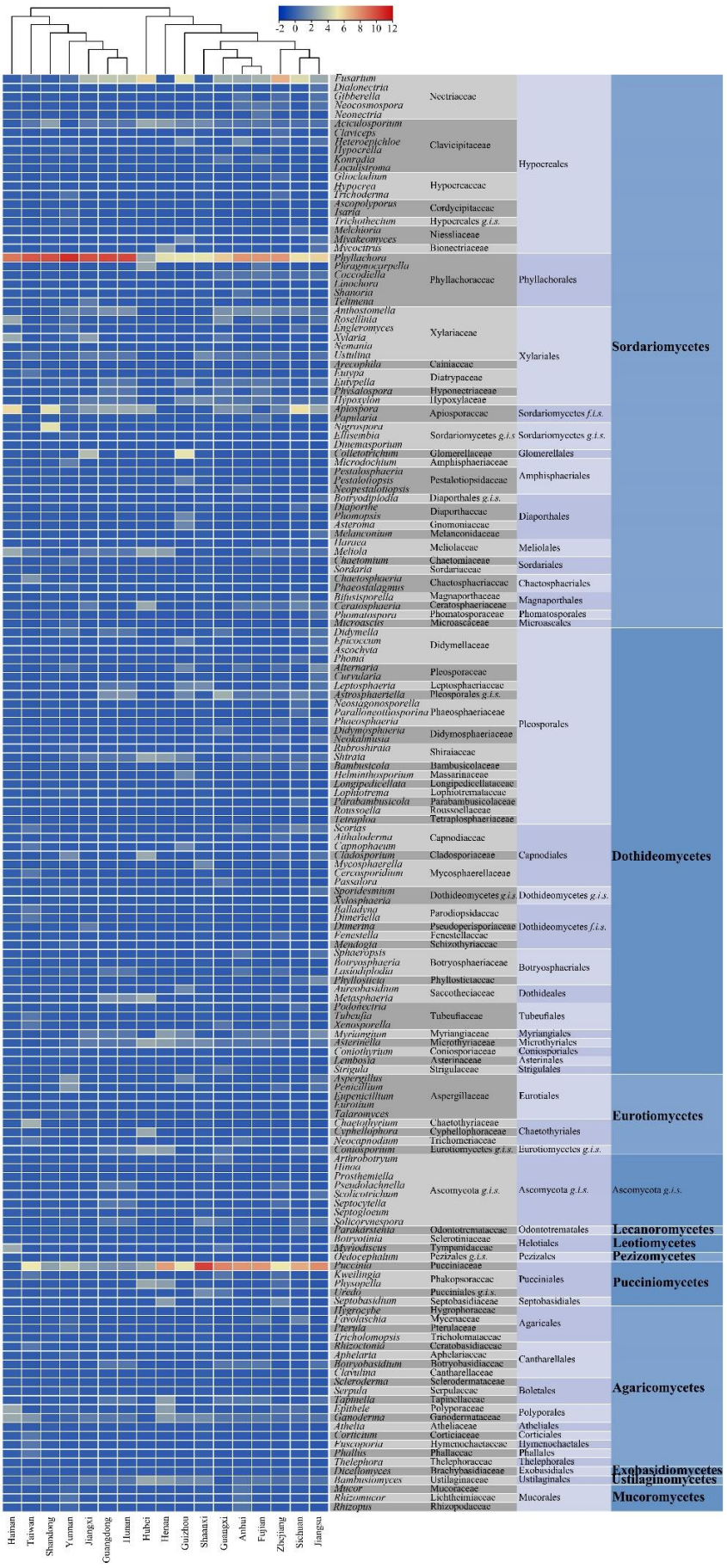

Figure 43 – Hierarchical clustering of the distribution of bamboo pathogenic fungi in different provinces at the level of genus. The color of each heatmap cell represents the relative abundance of

the corresponding bamboo pathogenic fungi in each province. The provinces recorded with equal to or greater than 10 species of bamboo pathogenic fungi were selected in the analysis, and the proportion of these fungi in each province at the genus level were calculated. The heatmap clustering were computed using the TBtools v2.001. Z-scores was applied to columns, which were clustered with Euclidean distance measurement and complete linkage clustering method. In the plate, "*f.i.s.*" is an abbreviation for *families incertae sedis*, and "*g.i.s.*" stands for *genera incertae sedis*.

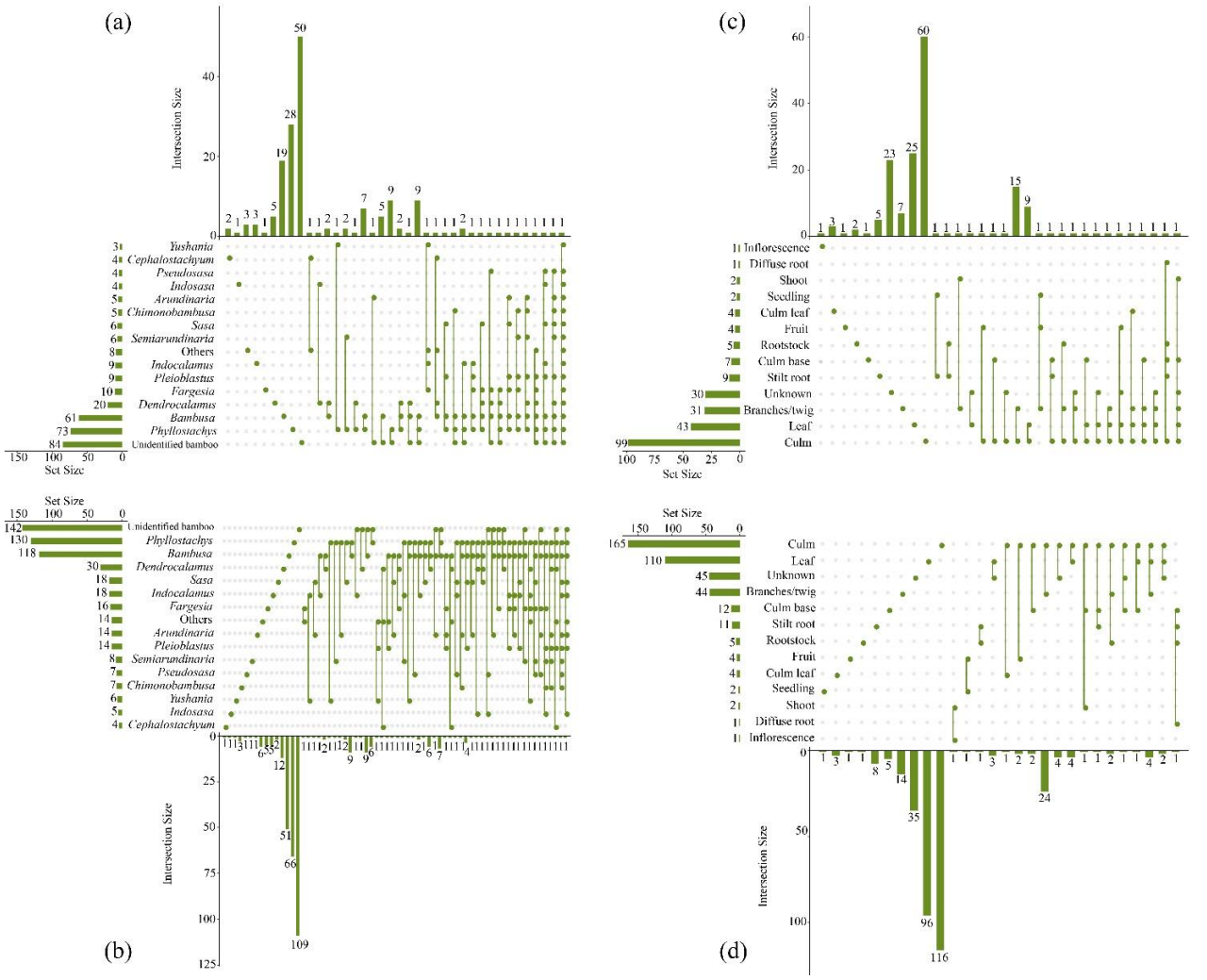

Figure 44 – Upset plots of the distribution of bamboo pathogenic fungi in genera (a) and species (b) levels of different genera of bamboo and in genera (c) and species (d) levels of different sites of bamboo. To date, the bamboo pathogenic fungi have been documented in 23 bamboo genera, and some genera with the number of bamboo pathogenic fungi species fewer than five species were categorized as "others", including *Cephalostachyum* (4 spp.), *Lingnania* (3 spp.), *Sinobambusa* (3 spp.), *Sasaella* (2 spp.), *Schizostachyum* (2 spp.), *Thyrsostachys* (2 spp.), *Drepanostachyum* (1 sp.), *Himalayacalamus* (1 sp.), and *Oligostachyum* (1 sp.). Statistics indicated that there were 12 tissue sites invaded by bamboo pathogenic fungi, including culm, leaf, branch/twig, culm base, stilt root, rootstock, culm leaf, fruit, shoot, seedling, inflorescence, and diffuse root. The upset plots of the distribution of bamboo pathogenic fungi in different treatment levels were pictured with UpSetR package.

The occurrence and prevalence of diseases in bamboo forests are shaped by various factors, including stand characteristics, climatic conditions, biochemical factors, and human activities. The disease bamboo blight, for instance, is caused by *Sarocladium oryzae* (Sawada) W. Gams &

D. Hawksw., and conditions such as high temperature and humidity in the local area are conductive to the infection. Factors such as poor stand management, soil properties and insect behaviors are

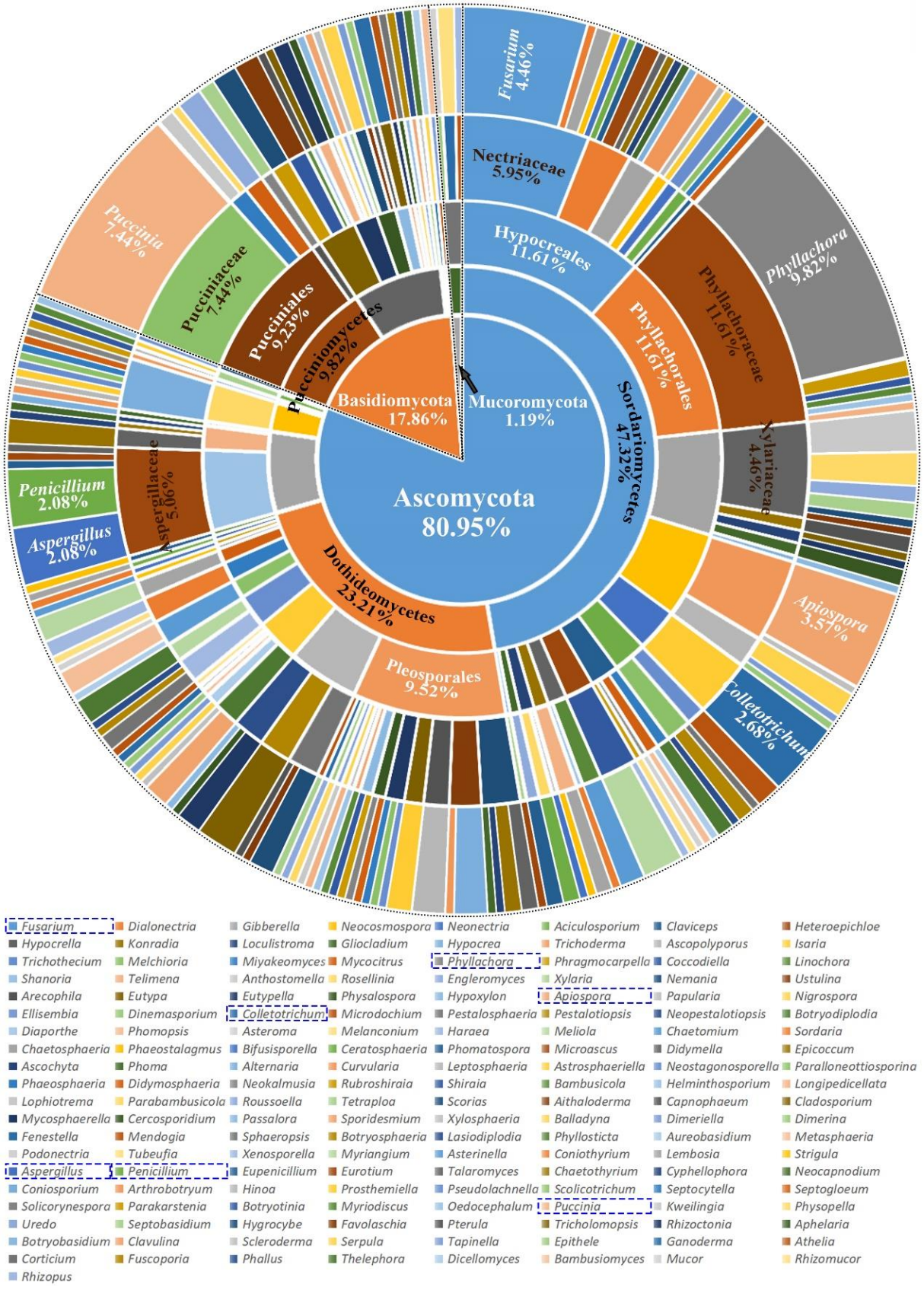

Figure 45 – The proportion of fungal species within each phylum (inner layer), class (second layer), order (third layer), family (fourth layer), and genus (outer layer) among bamboo pathogenic

fungi is presented, highlighting the top three to seven groups. The names of all 161 genera are listed below the pie chart, and highlighting the top seven genera.

responsible for the development and spreading of the disease (Mohanan 2017). For dieback of *Phyllostachys edulis*, as a pathogen-dominated disease, ascospores are the main source of infection, spreading through wind and rain within a short distance (typically up to 300 meters). Long-distance transmission occurs through the transportation of infected mother bamboo, timber, and bamboo shoots. Temperature, humidity, and light conditions are crucial for the formation of fruiting bodies and spore germination. The disease is common in wind gap, mountain ridge, and sunny slope, and its severity persists without proper management. High temperatures and drought in summer facilitate its occurrence and spread (Lin 2001, Wei 2005). The investigation of bamboo disease epidemiology plays a crucial role in bamboo forest management, serving as a vital tool to safeguard bamboo forests from pathogen infestations and enhance productivity. Currently, varying degrees of understanding have been achieved regarding the kinds of 11 types of bamboo diseases, such as culm base rot, culm/timber rot, culm rust, dieback, shoot blight, rhombic spot, branch blight, witch's broom, tar spot, leaf spot/blight, and leaf rust (Table 8). These findings represent a crucial foundation for further comprehensive investigations into the epidemiology of bamboo forest diseases.

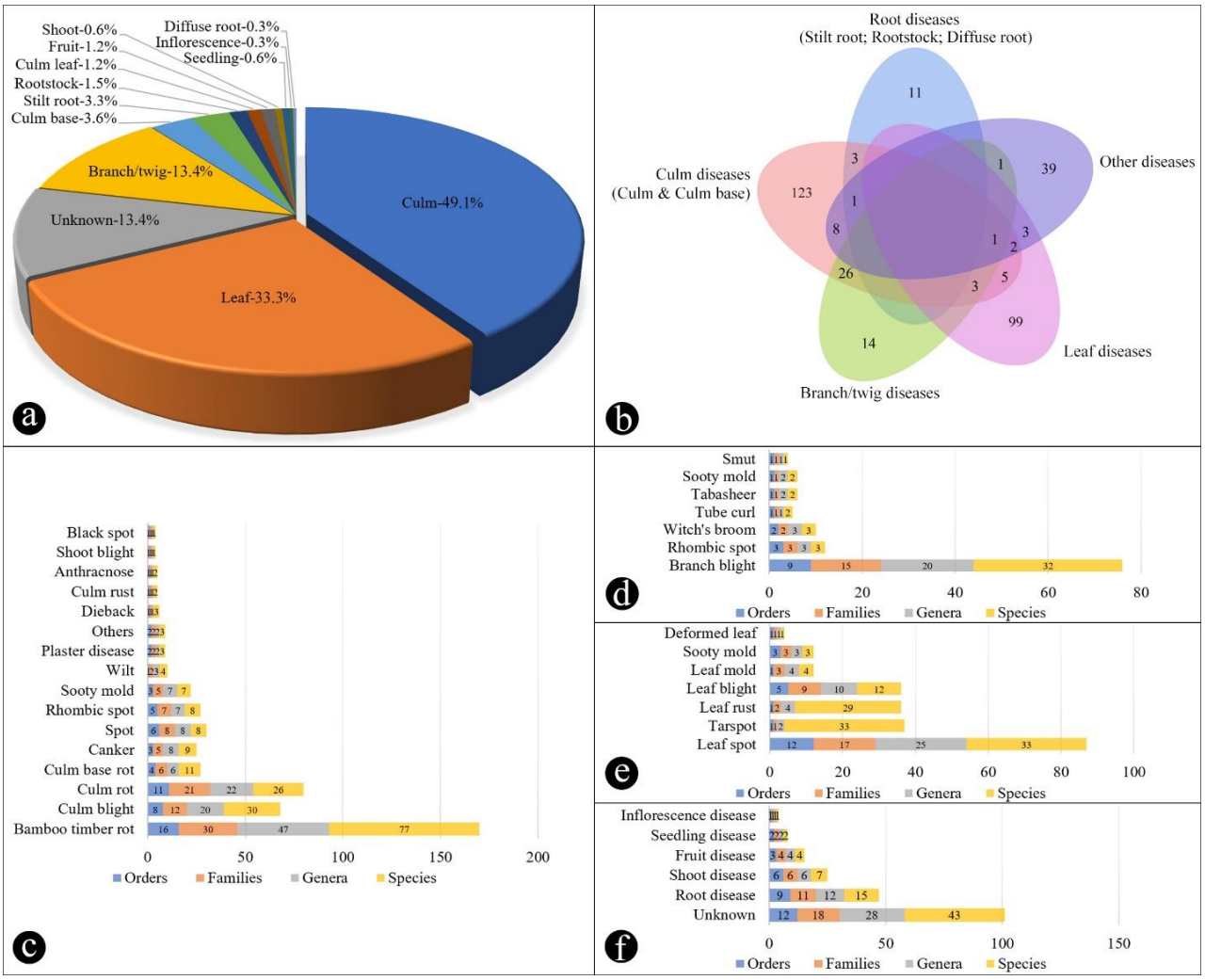

Figure 46 – Statistical results from different disease types. a Percentage of pathogenic fungi species in different tissues of bamboo plants; b Venn diagram of pathogenic fungi species in different tissues of bamboo plants; c–f Number of pathogenic fungi species in different orders on culms, branches or twigs, leaves, and others, respectively.

Figure 47 – Different disease types in bamboo forest. a Black spot in rootstocks of *Phyllostachys heteroclada*. b Bamboo shoot rot of *Dendrocalamus farinosus*. c Algae spot on culm of *Chimonobambusa neopurpurea* 'Dujiangyan Fangzhu'. d Spindle spot in culm of *Ch. pachystachys*. e Rhombic spot in culm of *Ph. bissetii*. f Culm blight of *Ph. sulphurea*. g Culm rot for new plant from the current year of *De. latiflorus*. h Culm rust of *Ph. edulis*. i Bamboo timber rot of *Ph. edulis*. j Culm blight of *Shibataea chinensis*. k Witch's broom of *Ph. violascens* 'Prevernalis'. l Branch blight of *Ph. elegans*. m Sooty mould on leaves of *Bambusa multiplex* 'Alphonse-Karr'. n Leaf blight of *Pseudosasa disticha*. o Leaf rust of *Ba. emeiensis*. p Tarspot of *Ph. sulphurea* var. *viridis*.

Table 8 An overview of the main fungal diseases of bamboo plants in China.

Type of diseases	Tissues	Species of main pathogens	Characteristics and regularity of bamboo diseases	References
Culm base rot	Rhizome; culm base	*Fusarium* spp.; *Alternaria alternata*; *Apiospora sphaerosperma* (= '*Arthrinium*' *phaeospermum*)	The pathogens primarily impact *Bambusa* and *Phyllostachys* plants. Considerable research has been conducted on culm-base rot in *Ph. edulis*, where *Apiospora sphaerosperma* serves as the principal pathogen, while *Fusarium* spp. acts as a secondary pathogen. This disease is heavily influenced by external factors. During the bamboo shoot growth stage, it infects the young culm base, leading to rot and depression of the culm base, thereby affecting the bamboo culm's wood grain. As the bamboo matures, it becomes more susceptible to wind damage, and in severe cases, the afflicted bamboo culms may experience withering and mortality. The present understanding of the disease's regularity is still unclear. However, it is generally recognized that the pathogens target the non-lignified young bamboo culms between March and May. The incidence and severity of the disease are facilitated by prolonged rainfall or favorable temperature conditions, which promote pathogen infection and disease epidemic. The diseased bamboo plants within the forest, along with the mycelia and spores of the pathogen present in the soil, constitute the primary sources of disease infection.	Chen (1980), Xu et al. (2006), Mohanan (2017), Crous et al. (2021), Li et al. (2022b)
Culm/timber rot	Living culm; timber; others	Ascomycetes (*Apiospora* spp.; *Arecophila* spp.; *Aspergillus* spp.; *Chaetomium* spp.; *Cladosporium* spp.; *Fusarium* spp.; *Leptosphaeria* spp.; *Penicillium* spp.), and basidiomycetes (*Botryobasidium rubiginosum*; *Epithele bambusae*; *Favolaschia* spp.; *Ganoderma* spp.; *Tapinella atrotomentosa*)	The affected plants, which include bamboo timbers and their products, mainly include plants belonging to the genera *Bambusa*, *Phyllostachys* and *Dendrocalamus*. The decay of living bamboo or bamboo timber usually involves two processes. In the initial stage, plant tissues undergo mildew or discoloration, where the pathogen utilizes nutrients such as starch, sugar, and protein present in bamboo culms to induce mildew growth or alter the color of the tissues. This results in the formation of nearly round or oval spots on the culms, impacting the appearance and quality of bamboo. Generally, this process has minimal effect on the strength of bamboo and is predominantly associated with pathogenic ascomycetes. The second stage entails the progressive decay of tissue. It involves the gradual breakdown of non-degradable components present in the bamboo culm tissue, such as lignin, cellulose, and hemicellulose. As a result, the grain and strength of the bamboo culm undergo a decline, along with a decrease in the overall longevity of bamboo products. Overall, due to the combined influence of various living fungi, plant diseased sections or bamboo timbers undergo a gradual process of dissolution and decay. Among these, pathogenic basidiomycetes play a significant role in the degradation of bamboo culm tissue. The decay of bamboo species in natural forests or bamboo timber is influenced	Umali et al. (1999), Wang et al. (2000a, b), Xu et al. (2006), Ma et al. (2012), Mohanan, (2017), Wei et al. (2021a), Sun et al. (2017), Cen et al. (2021)

Table 8 Continued.

Type of diseases	Tissues	Species of main pathogens	Characteristics and regularity of bamboo diseases	References
			by various factors, such as bamboo species, its age and growth state, climate, forest management, cutting season, and storage conditions.	
Culm rust	Culm; branch	*Puccinia corticioides*	More than 35 species of plants in the genera of *Bambusa*, *Phyllostachys*, *Chimonobambusa*, *Semiarundinaria*, and others were affected. *Puccinia corticioides*, a microcyclicform type, primarily affects the culms. While the teliospore and urediospore stages of its pathogen are found on bamboo culms, the remaining stages have yet to be observed in natural environments. The disease exhibited a defined progression: From October to February of the following year, teliospore masses formed on the culms, remaining dormant through the winter. From March to May, the teliospore masses gradually dried up, cracked, and fell off. Then, between May and June, urediospore masses developed in the same area. Mature urediospores dispersed and spread via wind and rain. Currently, the urediospores are considered the sole infection source for this disease, primarily entering through wounds and colonizing the bamboo tissue as mycelium. The host alternation of *Pu. corticioides* remains poorly understood, but experimental basidiospore inoculation has demonstrated the development of spermogonia and aecidia on the leaves of *Choerospondias axillaris*.	Zhou et al. (1995), Xu et al. (2006), Zhuang (2012), Mohanan, (2017), Okane et al. (2020)
Dieback	Culm; branch	*Ceratosphaeria phyllostachydis*	The main affected host was *Phyllostachys edulis*. Dieback disease of *Ph. edulis* is a highly damaging bamboo disease, primarily targeting new grown bamboo. It causes tongue-shaped or fusiform spots at the culm and branch junctions, resulting in bamboo plant mortality for 3-4 years. This disease can be observed in various forms within bamboo forests, including branch dieback, shoot blight, and complete plant dieback. The onset pattern followed this sequence: in April, ascocarps formed on infected tissues. From May to June, mature ascospores were released, primarily during rainy or high humidity conditions, penetrating through wounds or direct contact. The susceptible period occurred in May to June. Symptoms appeared at the infected site after a latent period of 1 to 3 months, typically from July to September. Overwintering in November involved mycelia, ascospores, and conidia. In the following year, the primary source of infection was predominantly ascospores originating from 1-3-year-old diseased bamboo.	Qiu et al. (1991), Lin et al. (1993), Zhang & Ou (1993), Liao (1994), Li (2003), Xu et al. (2006)
Shoot blight	Culm; branch	*Apiospora pseudoparenchymatica*;	The disease occurs in plants such as *Bambusa pervariabilis* × *grandis*, *Dendrocalamus latiflorus*, *Phyllostachys heteroclada*, and *Ph. prominens*.	Ma et al. (2003), Hu et al. (2005),

Table 8 Continued.

Type of diseases	Tissues	Species of main pathogens	Characteristics and regularity of bamboo diseases	References
		Ap. sphaerosperma (= '*Arthrinium*' *phaeospermum*); *Ap. yunnana*	Extensive studies have revealed that shoot blight of *Ba. pervariabilis* × *grandis* is mainly caused by the opportunistic pathogen *Apiospora sphaerosperma*. The disease damages sheath scars and areas between branches and culms, forming tongue-shaped or rhomboid spots. Severe cases result in withered, yellowed, and shed of leaves, even the death of plants. Within the forest, various manifestations are observed, including branch dieback, shoot blight, and complete plant dieback, with the latter being predominant. The pathogenesis unfolds as follows: From April to June, the pathogen invades through wounds or stomata, utilizing the mycelium and conidia in the infected bamboo as the main sources of infection. The disease reaches its peak incidence in August to September, gradually subsiding in October as it enters the overwintering period. The pathogenic fungi survive within the diseased bamboo tissue or soil as mycelia and conidia.	Zhu et al. (2009), Yang et al. (2019d, e)
Rhombic spot	Culm; branch; others	*Fusarium oxysporum*; *Neostagonosporella sichuanensis*	The disease mainly occurs in *Phyllostachys edulis*, *Ph. heteroclada*, and *Ph. bissetii*. Rhombic spot of *Ph. heteroclada*, a recently discovered bamboo disease, poses significant harm and exhibits rapid spread. It affects bamboo plants that are older than six months, resulting in the formation of rhomboid, nearly rhomboid, or irregular spots on the culms, branches, and exposed roots. The disease can result in blight and plant death for 2-4 years. The occurrence regularity of this disease is detailed in reference Qi et al. (2021).	Wang et al. (2012), Yang et al. (2019a), Qi et al. 2021)
Branch/twig blight	Branch	*Anthostomella* spp.; *Apiospora* spp.; *Astrosphaeriella* spp.; *Chaetosphaeria* spp.; *Fusarium* spp.; *Leptosphaeria* spp.	This disease is frequently observed in bamboo forests, primarily affecting plants of *Bambusa*, *Phyllostachys*, and other species. Branch or twig blight is primarily characterized by its localized infection nature. When it affects branches or twigs, it leads to inhibited growth, defoliation, wilting, or even death of the affected parts. In severe instances, it can cause desiccation and shedding of lateral branches. However, overall, its impact on bamboo plants is typically minimal. The pathogenesis of this disease is sparsely documented, and its occurrence and development are influenced by factors such as local temperature, humidity, and the growth stage of the host plant.	Xu et al. (2006), Zhang (2000), Mohanan (2017)
Witch's broom	Branch; twig	*Aciculosporium take*; *Heteroepichloe bambusae*; *He. sasae*; *Loculistroma bambusae*; *Phaeosphaeria bambusae*	It mainly affects the *Bambusa* and *Phyllostachys* plants. Witch's broom, a common ailment in bamboo forests, damages lateral branches, causing clustered and excessively grown twigs. This leads to the formation of distinctive spherical, bird's nest-like, broom-like, vine-like, and creeping branches. Severe cases weaken bamboo plant growth, reduce resistance, and hinder wood accumulation and bamboo shoot rates in the forest. *Aciculosporium take*, identified as the	Zhu & Huang (1988, 1989), Xue et al. (2005, 2006), Cheng et al. (2009), Yang & Wu (2011), Mohanan (2017),

Table 8 Continued.

Type of diseases	Tissues	Species of main pathogens	Characteristics and regularity of bamboo diseases	References
			predominant pathogen behind witch's broom in forests, and its occurrence regularity can be referred to in the paper by Liu et al. (2022b).	Liu et al. (2022b)
Tarspot	Leaf	*Bambusicola subthailandica*; *Phragmocarpella japonica*; *Phyllachora* spp.	This disease exhibits a remarkably wide host spectrum, encompassing over 65 plants from 15 genera. Notable among these are species belonging to *Arundinaria*, *Bambusa*, *Chimonobambusa*, *Dendrocalamus*, *Fargesia*, *Sasa*, *Phyllostachys*, *Pleioblastus*, *Yushania*, and other genera. Tarspot, primarily caused by *Phyllachora* spp., mostly affects the leaves, forming rhomboid, oval, round, angular, or irregular black spots. These spots are often dense, scattered, and accompanied by a light yellow to yellow halo. They can fluoresce and later lead to withered spots with the disease progress. When the spots merge, it can result in leaf death, impacting the growth and landscape of bamboo forests. The regularity of the disease remains uncertain. Typically, from July to May of the following year, stroma formation occurs on the leaves, with scattered spermogonia present within the stroma. During other periods, the development of sporogenous tissues or associated structures is infrequent, while mycelium may grow or lie dormant in the affected area.	Parbery (1967), Xu et al. (2006), Gong et al. (2008), Li et al. (2014b, 2019, 2021), Zhang & Zhang (2014), Mohanan (2017), Yang et al. (2019c, f)
Leaf spot/blight	Leaf	*Alternaria* spp.; *Apiospora* spp.; *Epicoccum* spp.; *Microdochium* spp.; *Nigrospora* spp.	Leaf spot or blight is a pervasive and common disease that impacts bamboo forests. It affects a wide range of bamboo species, including *Bambusa*, *Dendrocalamus*, *Fargesia*, *Indocalamus*, *Phyllostachys*, *Pleioblastus*, and *Sasa*. This disease manifests as a localized infection, typically resulting in the formation of black spots, leaf spots, necrotic spots, striped spots, mold spots, and other symptoms on the leaf surface. In severe cases, the disease spots densely cover the entire leaf, eventually leading to leaf death and detachment. The regularity of this disease is not well-established, with limited studies and reports available.	Zhang (2000), Xu et al. (2006), Zhang et al. (2007), Jiang et al. (2016), Mohanan (2017), Hao et al. (2020), Huang et al. (2020), Liu et al. (2020)
Leaf rust	Leaf	*Kweilingia* spp.; *Puccinia* spp.; *Uredo* spp.	Leaf rust is a common disease characterized by local infections in most bamboo plants. The pathogenic fungi, as typical obligate parasites, cause dense patches on leaves, resulting in leaf withering and death. The production of teliospores and urediospores by the pathogen occurs on leaves, while the other stages remain unknown. The regularity of leaf rust remains rarely understood. Urediospores are believed to be the primary source of infection, contributing to the occurrence and spread of this forest disease.	Tsai et al. (1985), Xu et al. (2006), Zhou et al. (2010), Mohanan (2017), Shen et al. (2017)

Potential areas of current or future research

Research on the species diversity of bambusicolous mycopathogens in China has often been characterized by its fragmented nature, with the majority of studies focused on small-scale site surveys or the examination of individual pathogens. There is a noticeable lack of comprehensive, multi-level system research that encompasses various crucial aspects, including the communities of pathogenic fungi, the diversity within bamboo species groups, the influence of different climatic factors and the impact of geographical variations. The interaction between pathogenic fungal communities, their hosts and the environment is essential for advancing our knowledge in this field. Future research needs to address several key topics to unravel the complexity of bambusicolous mycopathogen biodiversity (Fig. 48). These can include 1) clarifying the diversity of pathogenic fungal species, community structures and composition, and biogeographical distribution patterns; 2) Investigating the relationships between pathogenic fungal communities and habitat factors, including an understanding of the mechanisms that regulate these relationships; 3) Clearing the inherent pathogenicity patterns and pathogenesis, and developing control strategies for different pathogenic fungi; 4) Examining the effect of the biodiversity of pathogenic fungi on ecosystem services. Addressing these research areas through future studies will enhance our understanding of bambusicolous mycopathogens and their role in bamboo ecosystems. Data obtained will aid to the development of more effective conservation, management and mitigation strategies to protect these vital resources.

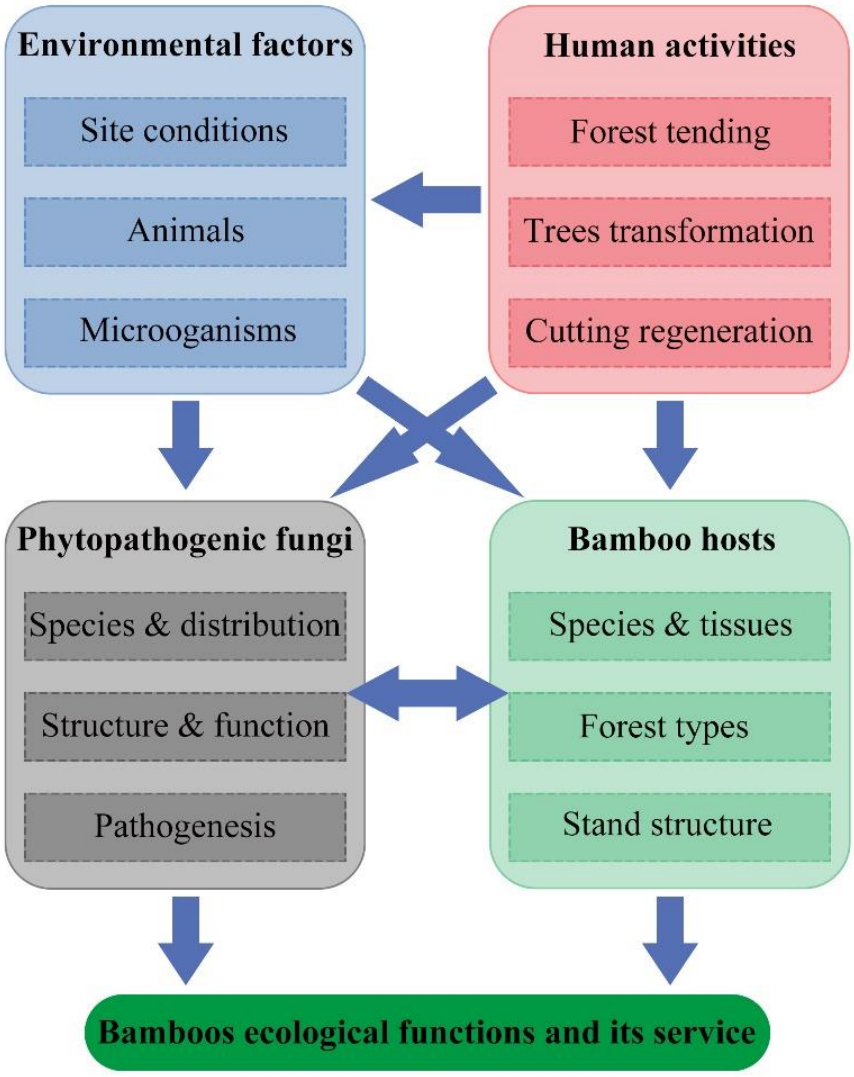

Figure 48 – Environmental factors, human activities and host plants affect the structure and function of bamboo forest ecosystems by regulating the biodiversity of bamboo pathogenic fungi.

The available list of bambusicolous mycopathogens compiled herein provides additional information to better aid in pathogen identification and disease monitoring, as well as targeting taxa that are valuable targets of biological resources such as new disease control agents. Many species of recordable pathogens (above 50%) lack necessary information or have incomplete data, viz. species boundaries are not clear, molecular data are missing or incomplete, the lack of related specimens, and pathogenesis regularity and characteristics are inadequate. There are abundant resources of bambusicolous fungi in China, and the total of 5,868–9,584 species exist in bamboo forests (Zhou et al. 2000, Hawksworth & Lücking 2017). It is estimated that roughly 2,400–4,200 pathogenic fungi have yet to be discovered, based on the existing conversion ratio (about 47%, with 700 out of 1,500 fungi documented in bamboo forests classified as pathogens). Nowadays, modern taxonomic studies of pathogenic fungi on bamboos are urgently needed, to enable species classification of pathogenic fungi to be scientific and reasonable based on the comprehensive evidence, such as macroscopic features, microscopic structure, culture characteristics, multi-gene genealogical concordance consistency, and ecological attributes (Taylor et al. 2000, Jeewon & Hyde 2016, Aime et al. 2021). A comprehensive species list is essential in order to uncover the community structure and distribution patterns of pathogenic fungi within bamboo forests.

There is a dearth of research on the relationship between plant pathogenic fungal communities and environmental factors. However, numerous studies have focused on fungal species diversity, relying primarily on high-throughput sequencing technology (*i.e.* NGS) to analyze the diversity of species in various environments or treatment groups (Nilsson et al. 2019, Liu et al. 2022c, Lin et al. 2023a, b), and to predict the potential ecological functions of different groups (Sun & Guo 2012, Geng et al. 2018, Zhang et al. 2019b). The ecological functions and regulatory roles of pathogenic fungal communities within forest ecosystems have received limited attention from researchers and the general public. In general, the main habitat factors affecting the species and composition of pathogenic fungi were environmental conditions, human disturbance and host attributes. Accumulating studies on environmental factor-induced in plant-associated mycobiomes have shown that those factors can regulate the structure and composition of pathogenic fungi community on plants (Doohan et al. 2003, Desprez-Loustau et al. 2006, Velásquez et al. 2018, Větrovský et al. 2019, Haddoudi et al. 2021, Lin et al. 2023b), such as the climate variables (temperature, moisture and drought), water availability, CO_2 concentrations, salt stress or heavy metal interference. Undoubtedly, human activity can impact pathogenic fungal communities by directly or indirectly altering or destroying their suitable environment, for example, through host removal, afforestation measures, nutrition strategy, or fungicide use. Differences in host species and genetic backgrounds can cause the diversity and specificity of pathogenic fungi (Ahlholm et al. 2002, Wang et al. 2017, Han et al. 2023). In addition, the pathogen can govern plant-associated microbiomes for enhancing plant health or to maximize forest production, such as with attracting beneficial microbes for rescue future generations (Gao et al. 2021, Liu et al. 2023c), and this could be intricately linked to the host plant's endogenous disease resistance mechanisms. Our understanding of the complex interactions between bamboo, pathogens, and the environment in the bamboo forest ecosystem is very limited.

To date, there are only six major bamboo diseases with well-established natural pathogenesis patterns worldwide (Rahman 1978, Zhu et al. 1983, Lin 2003, Zhu et al. 2009, Tanaka 2010, Yang & Wu 2011, Okane et al. 2020, Qi et al. 2021, Liu et al. 2022c, 2024, Liang et al. 2024), such as bamboo blight on *Bambusa* spp., culm rust on *Phyllostachys* spp., top branch blight (dieback) on *Ph. edulis*, witches' broom, hybrid bamboo blight on *B. pervariabilis* × *grandis*, and rhombic-spot on *Ph. heteroclada*. The pathogens responsible for these diseases are *Sarocladium oryzae*, *Puccinia corticioides* Berk. & Broome, *Ceratosphaeria phyllostachydis*, *Aciculosporium take* I. Miyake, '*Arthrinium*' *phaeospermum*, and *Neostagonosporella sichuanensis* C.L. Yang, X.L. Xu & K.D. Hyde, respectively. In general, while there have been extensive studies on the natural pathogenesis and harmful characteristics caused by bamboo diseases, more in-depth research is needed to understand the underlying mechanisms, such as whole genome sequencing and gene mining, pathogenic genes, effectors, and disease-resistant genes along with their corresponding resistance

factors or elicitors. Bamboo diseases are commonly attributed to a single pathogen-host system, implying that a single disease-causing agent infects a particular host. However, recent studies have suggested that the occurrence of poly-microbial microbiome may be prevalent in nature (Qi et al. 2021, Han et al. 2023, Lv et al. 2023). Effective management of bamboo diseases has always been a daunting task. While comprehensive management strategies are recommended, they are not always effectively implemented. Chemical control, direct felling, and neglect are commonly used, but they may not always be the most appropriate methods. In addition, given the widespread use of bamboo in various industries such as bamboo shoot production, product processing, and landscaping, implementing comprehensive management technology is the most sustainable and environmentally friendly approach (Lin 2003, Hu et al. 2005, Xue et al. 2005, Liu et al. 2022b). This will help control the biomass of pathogenic fungi and promote the healthy growth of bamboo forests. Apart from traditional methods such as water and fertilizer management, forest management initiatives, and chemical control, cultivating advantageous microbial communities can also be instrumental in controlling diseases and promoting plant growth (Verbon et al. 2016, Yuan et al. 2018, Fuke et al. 2021, Hladnik et al. 2022, Li et al. 2022c, Sun et al. 2022, van Dijk et al. 2022, Lin et al. 2023b). Zhou et al. (2022) constructed several synthetic communities of tomato plants comprising 205 unique strains to safeguard against soil-borne *Fusarium* wilt disease. Their findings indicate a significant negative correlation between the incidence of the disease and the diversity of rhizosphere bacteria and fungi. Moreover, these communities were found to significantly upregulated the expression of disease-resistance genes. Furthermore, recent research has proposed innovative strategies for mitigating bamboo forest diseases, such as the role of host root exudates in modulating rhizosphere microorganism function to bolster host growth and resilience against external factors (Feng et al. 2023); a rice lignin precursor, 4-hydroxycinnamic acid, regulated by the microbiome-shaping gene *OsPAL02*, orchestrates microbiome homeostasis on rice leaves by facilitating the recruitment of beneficial foliar microorganisms and inhibiting harmful pathogenic microorganisms (Su et al. 2024).

A systematic understanding on the impact of the pathogenic fungi community on the ecosystem function of bamboo forest remains unclear. Through varying multifaceted interactions, the structure and function of bamboo forest ecosystem are regulated by multi-pathogens invasion directly or indirectly (Fig. 49). Relevant studies suggested that diseases can lead to poor growth or death of hosts, which directly leads to the decrease of carbon sequestration and culm volume, bamboo shoots yield less or no production, and the loss of ornamental value (Zhou et al. 2011b, Mohanan 2017, Liu et al. 2022b, Das et al. 2023). Some studies indicated that disease-induced changes in taxonomic composition influence the functional adaptation of environmental organisms (Berendsen et al. 2018, Yuan et al. 2018). Generally, bamboo forest is a complex ecosystem, not only serving as an efficient source of ecological products to humans but also regulating organisms which includes animals, microbes, and protists. How pathogenic fungi affect the realization of the ecological function of bamboo forest, they can influence ecosystem function in many unexplained ways. Uncovering the elemental ecological patterns that regulate the assembly, co-occurrence patterns, and functions of plant-associated biomes and how do bamboos modulate their biomes under external stress are requisite for governing bamboo biomes to enhance bamboo health and to maximize production or ecological benefits. Currently, many studies often focused on soil microbiomes and their role, such as healthy bamboo plants, surrounded by basal rot disease caused by *Fusarium proliferatum*, can assemble more beneficial microbes in rhizosphere soil (Lin et al. 2023b). Accumulated studies have shown that soil microbes play a vital role in biogeochemical progress, including matter decomposition, nutrients mineralization, soil aggregation, heavy metals sequestration, and reducing the fitness of pathogens (Wagg et al. 2014, Gu et al. 2016, Jacoby et al. 2017, Fuke et al. 2021). However, within forest ecosystems, there remains a significant gap in our understanding of the structural and functional dynamics of biomes across the rhizosphere, phyllosphere, and endosphere, driven by mycobiomes.

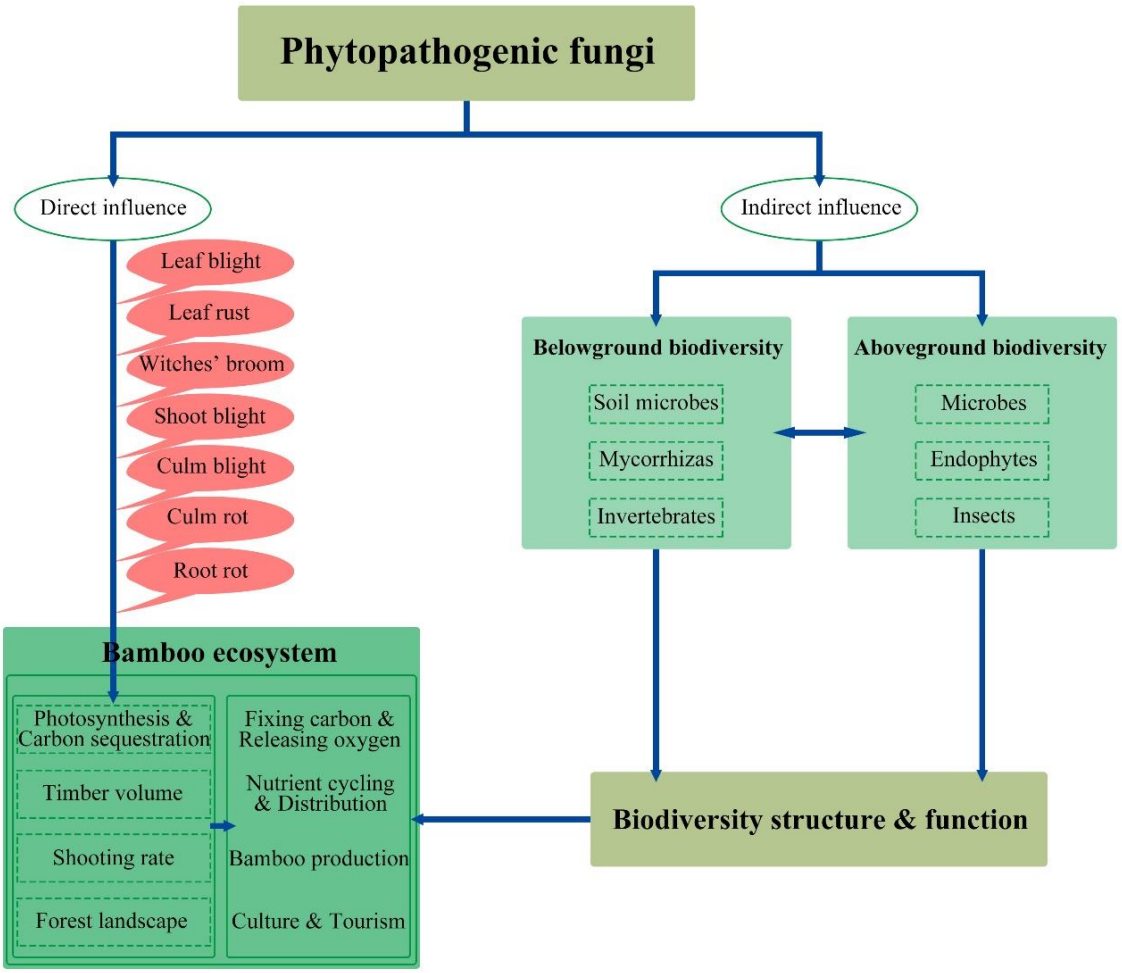

Figure 49 – Direct and indirect influence for the service of bamboo forest ecosystem regulated by phytopathogenic fungi.

CONCLUSION

The extensive investigation into bambusicolous mycopathogens in China represents a significant headway in the comprehension of fungal biodiversity and its interactions with bamboo ecosystems. This journey, starting from early 20th-century exploratory studies to modern, sophisticated analyses has revealed the critical role these pathogens play in health and productivity of bamboo forests. The progression from basic taxonomy to advanced disease management strategies emphasizes the economic and ecological importance of bamboo, highlighting the challenges and opportunities in preserving these vital ecosystems against pathogenic threats. The research highlights the rich diversity of pathogenic fungi within bamboo forests, especially in southern regions of China, where bamboo cultivation thrives. The documentation of over 336 pathogenic fungi species across various genera and the identification of more than 35 types of fungal diseases affecting bamboo culms, branches, twigs, and leaves, reflect the complex relationship between these pathogens and their bamboo hosts. This relationship demands targeted research and sophisticated management strategies to mitigate the impact of pathogens effectively. This study illuminates the necessity for a consolidated research approach to overcome the fragmented nature of current research efforts. This approach should aim to fill knowledge gaps in pathogen-host interactions and develop innovative strategies for disease management, emphasizing the need for multi-disciplinary collaboration among mycologists, ecologists, phytopathologists and bamboo industry stakeholders. The potential areas for future research outlined in the text call for a comprehensive exploration into the diversity, impact and management of bambusicolous mycopathogens. This includes enhancing our understanding of pathogen biodiversity, developing

effective disease control strategies, investigating the ecological roles of pathogenic fungi and exploring the use of synthetic microbial communities for disease resistance.

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