

Endophytic fungi associated with medicinal ferns in Guizhou Province, China I: Morpho-molecular characterization of culturable endophytic fungi associated with *Dicranopteris* spp.

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Abstract

Endophytic fungi, a subject of increasing interest among researchers, possess the unique ability to produce a diverse array of compounds with significant biological activities, including anti-tumor, anti-bacterial, anti-viral, and anti-oxidant effects. What sets these fungi apart is their capacity to synthesize compounds that are identical or similar to those found in their host plants. This intriguing characteristic has made endophytic fungi in medicinal plants a key area of scientific exploration. Our current study, a pioneering systematic investigation of endophytic fungi associated with medicinal ferns in Guizhou Province, China, is the first in a series focusing on the morpho-molecular taxonomy

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of culturable endophytic fungi associated with *Dicranopteris* species. We isolated 84 endophytic fungal strains from various tissues and identified them as 59 distinct species based on both morphological characteristics and multi-locus phylogenetic analysis. A new family, *Massicellisporaceae*, three new genera viz. *Massicellispora*, *Miniglobosispora*, and *Pseudopopulomyces*, and 24 new species viz. *Amorocoelophoma dicranopterisis*, *Arxiella ellipsoidea*, *Castanediella dicranopteridis*, *Cladophialophora globosa*, *Colletotrichum dicranopterisis*, *C. guttulatisporum*, *Dactylonectria dicranopteridis*, *Diaporthe dicranopteridis*, *Geniculoseta dicranopteridis*, *Hypoxylon dicranopteridis*, *Ilyonectria dicranopteridis*, *Massicellispora dicranopteris*, *M. globosa*, *Miniglobosispora guizhounises*, *Neopestalotiopsis dicranopteridis*, *Nigrospora dicranopteridis*, *Periconia dicranopterisis*, *Pezicula dicranopteridis*, *Pseudodactylaria dicranopteridis*, *Omnidemptus dicranopteridis*, *Pseudopopulomyces dicranopteridis*, *Sphaerostilbella dicranopteridis*, *Trichocladium dicranopteridis*, and *Verruconis hyalina* are introduced. Additionally, 35 new host or geographical records are reported. Several species are also re-evaluated: *Diaporthe hainanensis* and *D. harriottiae* are synonymized under *D. arecae*, *Colletotrichum juglandis* is synonymized as *C. simulanticitri*, while, *C. gracile*, *C. oblongisporum*, and *C. nullisetosum* are consolidated into a single species, as *C. jiangxiense*, and *Cashiella sticheri* was transferred to *Pezicula* as *P. sticheri* based on morphological and phylogenetic evidence. Descriptions, illustrations, and phylogenetic analysis results are provided for all species introduced in this study. A checklist of fungi associated with *Dicranopteris* is also included. This study enhances our understanding of the diversity of endophytic fungi associated with medicinal *Dicranopteris* and lays a foundation for future research into their ecological roles and pharmacological potential.

Keywords – 29 new taxa – *Dothideomycetes* – Endophytes – *Massicellisporaceae* – Medicinal plants – *Sordariomycetes* – Taxonomy

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INTRODUCTION

Endophytic fungi inhabit healthy plant tissues without causing any visible disease symptoms, often forming a mutualistic relationship with their hosts (Petrini 1990, Saikkonen et al. 1998, Azevedo et al. 2000, Saikkonen et al. 2004). These fungi occupy a unique ecological niche, residing within plants for extended periods and relying on nutrient extraction from the host to support their

growth (Abeywickrama et al. 2023). In return, they produce specific metabolites that not only promote plant growth and development and enhance resistance to both biotic and abiotic stresses (Gao et al. 2010, Bhardwaj et al. 2014, Fontana et al. 2021, Poveda et al. 2021). One particularly important role of endophytic fungi is their ability to synthesize bioactive metabolites within the host, which can significantly influence the quality of medicinal plants (Jia et al. 2016). In recent years, researchers have isolated secondary metabolites from the endophytic fungi of various medicinal plants that are either identical or closely related to those produced by their hosts (Zhao et al. 2010, 2011, Kusari et al. 2013, Palanichamy et al. 2018), such as yew (Stierle et al. 2000, Tayung et al. 2011, Rivera-Orduña et al. 2011, Somjaipeng et al. 2015, Khan et al. 2022). This discovery has greatly expanded the potential of natural pharmaceutical resources. Moreover, the remarkable biological diversity of endophytic fungi enables them to produce a wide array of structurally diverse secondary metabolites with various bioactivities, including anti-bacterial, anti-tumor, stress resistance, insecticidal, immune-regulating, immunomodulatory, and anti-viral properties (Schulz et al. 2002, Kaul et al. 2012, Patil et al. 2016, Ratnaweera et al. 2017, Meena et al. 2019, Ancheeva et al. 2020). These compounds constitute a vast natural product library that continues to inspire and drive pharmaceutical innovation (Patil et al. 2016, Uzma et al. 2019).

Endophytes, with their remarkable adaptability, exhibit a range of behaviors, including saprobic and pathogenic, and may shift between these roles depending on environmental conditions and host interactions (Sturz et al. 2000, Newsham et al. 2011, De Silva et al. 2017, Bhunjun et al. 2024). Under specific environmental or physiological stresses, endophytes can transition from beneficial symbionts to pathogens or saprobes (Fisher & Petrini 1992, Promputtha et al. 2007, Hilário & Gonçalves 2023, Wang et al. 2024). As saprobes, they decompose dead or decaying organic matter, particularly after host tissue senescence, thereby recycling nutrients back into the ecosystem (Promputtha et al. 2007, Rodriguez et al. 2008). Conversely, endophytes may adopt a pathogenic role when the host plant experiences stress, such as nutrient deficiency or drought, enabling them to proliferate within plant tissues and potentially cause disease symptoms (Newsham et al. 2011). This function is driven by a combination of environmental triggers and complex and intriguing genetic interactions between the host and the endophyte (Photita et al. 2004, Promputtha et al. 2007, Hardoim et al. 2015). For example, *Neotyphodium* species typically maintain a mutualistic relationship with grasses, but can become harmful under stressful conditions (Yao & Liu 2012). This remarkable adaptability enables endophytes to alternative between beneficial and harmful states, allowing them to occupy diverse ecological niches and respond dynamically to changes in their environment.

In recent years, the diversity of endophytic fungi associated with medicinal plants has become a major focus of research; numerous studies have been conducted on endophytes from various medicinal species (Huang et al. 2008, de Siqueira et al. 2011, Bhagat et al. 2012, Mishra et al. 2021, Hussein et al. 2024). As a novel type of microbial resource, endophytes offer unique opportunities for the discovery of new bioactive compounds (Schulz et al. 2002, Kumar et al. 2012, Liu et al. 2018, Ancheeva et al. 2020). Through in-depth studies of plant endophytes, researchers are not only identifying new anti-bacterial agents effective against drug-resistant bacteria and discovering valuable natural products such as anti-tumor compounds, but also addressing broader challenges such as the scarcity of medicinal plant resources and the long growth cycles of these plants (Jia et al. 2016). Therefore, harnessing the symbiotic relationship between endophytes and host plants by isolating and screening strains that produce highly active compounds from abundant plant resources has become an important strategy for developing new drugs that are low in toxicity, environmentally friendly, and highly effective. This approach enriches the natural drug reservoir and addresses the issue of limited medicinal plant resources.

Dicranopteris is one of the medically important ferns known for its significant pharmacological properties (Li et al. 2006, 2007, Zakaria et al. 2008, Chen et al. 2014, Thomas et al. 2023). The genus belongs to the family *Gleicheniaceae*, comprises 12 species (Yang et al. 2021) and is widely distributed in tropical and subtropical regions around the world (Zhao et al. 2012, Xu et al. 2014, Yang et al. 2021). *Dicranopteris* is drought-resistant, highly tolerant of acidic conditions, extremely adaptable to its environment, and often grows spontaneously. It serves as an indicator plant for acidic soil and contributes and plays a role in maintaining soil and water quality. *Dicranopteris* is rich in active compounds such as flavonoids, terpenes, saponins, phenolic derivatives, and polysaccharides, which exhibit various pharmacological activities including anti-oxidant, anti-cancer, anti-bacterial, anti-inflammatory, anti-HIV, and analgesic properties (Li et al. 2006, 2007, Zakaria et al. 2006, 2011, Chen et al. 2014, Kale 2015, Aboshoufa et al. 2019, Baharuddin et al. 2021, Thomas et al. 2023). *Dicranopteris* holds significant therapeutic value and is traditionally used to promote blood circulation, stop bleeding, clear internal heat, promote diuresis, and reduce edema (Li et al. 2006, 2007, Zakaria et al. 2006, 2008, Kale 2015). Although, current research on *Dicranopteris* focuses primarily on its ecological and pharmacological properties, studies on its associated endophytic fungi remain limited (Kirschner & Liu 2014, Kirschner & Wang 2015, Guatimosim et al. 2016, Zhang et al. 2023a, Chen et al. 2024).

Guizhou Province, located in the southeast part of southwest China on the eastern side of the Yunnan-Guizhou Plateau, is one of the richest regions in China for fern diversity (Wang & Wang 2001, 2003). The province experiences a warm and humid climate, with rain and heat occurring in the same season, typical of a subtropical humid monsoon environment. These unique geographical and climatic conditions promote fern growth, with *Dicranopteris* being the most abundant fern in Guizhou. A total of 429 species of medicinal ferns, distributed in 48 families and 126 genera, have been reported in the province. Additionally, within the region, several new species of ferns have been discovered in karst microhabitats, such as caves, cliffs, and cracks (Lu et al. 2017, 2019, Zhang et al. 2019a). Endophytic fungi associated with medicinal plants found in karst microhabitats have likely evolved a distinct secondary metabolic network, different from common environmental fungi, through long-term co-evolution with their hosts (Tan et al. 2021, Zhou et al. 2022). However, prior to this study, no systematic investigations had been conducted on the diversity of endophytic fungi associated with medicinal ferns in Guizhou Province, China.

This study aims to systematically investigate the diversity of endophytic fungi associated with medicinal ferns, with a particular focus on three species of *Dicranopteris* viz. *D. ampla*, *D. linearis*, and *D. pedata*, which are widely distributed in Guizhou and are rich in active substances with potential for producing novel structural compounds. The objectives of this study are as follows: 1) to investigate the diversity of endophytic fungi associated with *Dicranopteris* in Guizhou Province; 2) to describe novel species, with illustrations and comparisons to similar species; 3) to collect cultures of endophytic fungi for further screening of novel bioactive compounds.

MATERIALS AND METHODS

Sample collection

Fresh healthy plant tissues such as leaves, rhizomes, roots, and stems of *Dicranopteris pedata*, *D. linearis*, and *D. pedata* were collected from Guizhou Province, China. After associated metadata such as date, locality, and host were noted (Rathnayaka et al. 2024), materials were kept in Ziplock bags and taken to the laboratory. Fungal isolation was carried out within 24 hours of collection.

Isolation of fungal endophytes

Tissues (leaves, stems, rhizomes, and roots) were washed with running tap water and surface sterilized to eliminate epiphytic microorganisms in a benchtop by immersing them in 75% (v/v) ethanol for 1–3 min (ca. 1 min for leaves and stems; ca. 3 min for rhizomes and roots, then rinsing with sterilized distilled water for 2 min, then soaked with 10% (v/v) NaClO for 0.5–2 min (ca. 0.5 min for leaves and stems; ca. 2 min for rhizomes and roots), and finally rinsing with sterile distilled water three times continuously. Materials were dried on sterilized filter papers and then cut into small cubes (ca. 3 mm in length of segments) and placed on fresh potato dextrose agar (PDA) containing antibiotic (50 µg/mL penicillin). Samples were incubated in a constant temperature incubator (25 °C). The plates were observed daily, and mycelia from the edge of fungal colonies were transferred to fresh PDA to obtain pure cultures. The specimens of dry cultures were deposited at the herbarium of the Cryptogams Kunming Institute of Botany Academia Sinica (KUN-HKAS) and the Guizhou Academy of Agriculture Sciences (Herb. GZAAS). Living cultures were deposited at the Kunming Institute of Botany Culture Collection (KUNCC) and Guizhou Culture Collection (GZCC).

Morphological study

The pure cultures were grown on PDA in a constant temperature incubator (26 °C) and observed every five days. Culture characteristics, such as size, shape, colour, and texture, were recorded and examined using a stereomicroscope (SMZ168-BL, Motic, China). Micro-morphological characteristics were photographed using an ECLIPSE Ni-U compound microscope (Nikon, Japan) fitted with an EOS 90D digital camera (Canon, Japan) fitted on to an ECLIPSE Ni-U compound microscope (Nikon, Japan). Measurements of morphological characteristics (conidiomata, conidiogenous cells, conidia, and mycelia) were made with the Tarosoft® Image Frame Work. Figures and the photo plates were processed by Adobe Illustrator CS6 (Adobe Systems, USA).

DNA extraction, PCR amplification, and sequencing

Fresh fungal mycelia were scraped with sterilized scalpels. Genomic DNA was extracted by the Biospin Fungus Genomic DNA Extraction Kit (BioFlux, China), following the manufacturer's protocol. The primers are summarized in Table 1. The amplification reactions were performed in 25 µL of PCR mixtures containing 12.5 µL of 2×Power Taq PCR Master Mix (a premix and ready-to-use solution, including 0.1 Units/µL Taq DNA Polymerase, 500 µm dNTP Mixture each (dATP, dCTP, dGTP, dTTP), 20 mM Tris-HCl pH 8.3, 100 mM KCl, 3 mM MgCl₂, stabilizer and enhancer), 1 µL of each primer, 1 µL DNA template and 9.5 µL nuclease-free water. PCR amplification was confirmed on 1% agarose electrophoresis gels stained with ethidium bromide. The PCR products were purified and sequenced with the same primers at TsingKe Biological Technology (Kunming) Co., China.

Table 1 Information on loci and primers used in this study

Loci	Primer pairs	Sequences of primers (5'-3')	References
ITS	ITS5	GGAAGTAAAAGTCGTAACAA	White et al. (1990)
	ITS4	GG TCCTCCGCTTATTGATATGC	
LSU	LR0R	ACCCG TGA ACTTAAGC	Vilgalys and Hester (1990)
	LR5	TCCTGAGGGAACTTCG	

Loci	Primer pairs	Sequences of primers (5'-3')	References
<i>rpb2</i>	fRPB2-5F	GAYGAYMGWGATCAYTTYG G	Liu et al. (1999)
	fRPB2-7cR	CCCATRGCTTGYTTRCCCAT	
<i>act</i>	ACT-512F	ATGTGCAAGGCCGGTTTCGC	Carbone & Kohn (1999)
<i>alt-α1</i>	ACT-783R	TACGAGTCCTTCTGGCCCAT	Hong et al. (2005)
	Alt-for Alt-rev	ATGCAGTTCACCACCATCGC ACGAGGGTGAYGTAGGCGTC	
<i>chs-1</i>	CHS-79F	TGGGGCAAGGATGCTTGGA GAAG	Carbone & Kohn (1999)
	CHS-345R	TGGAAGAACCATCTGTGAGA GTTG	
<i>tub2</i>	BT2a	GGTAACCAAATCGGTGCTGCT TT	Glass & Donaldson (1995)
	Bt2b	ACCCTCAGTGTAGTGACCCTT GGC	
<i>his3</i>	CYLH3F H3-1b	AGGTCCACTGGTGGCAAG GCGGGCGAGCTGGATGTCCTT	Crous et al. (2004)
<i>tef^{1-α}</i>	EF1-728F	CATCGAGAAGTTCGAGAAGG	Carbone & Kohn (1999)
	986R	TACTTGAAGGAACCCTTAC	
	EF2	GGARGTACCAGTSATCATG	O'Donnell et al. (2010)
	EF1	ATGGGTAAGGARGACAAGAC	
	983F	GCYCCYGGHCAYCGTGAYTT YAT	Rehner (2001)
<i>gapdh</i>	2218R	ATGACACCRACRGCACRGTY TG	Myllys et al. (2002)
	Gpd1-LM	ATTGGCCGCATCGTCTTCCGC AA	
	Gpd2-LM	CCCACTCGTTGTCGTACCA	
	GDF1	GCCGTCAACGACCCCTTCATT GA	Templeton et al. (1992)
	GDR1	GGGTGGAGTCGTACTTGAGC ATGT	
	GDP-1 GDP-2	CAACGGCTTCGGTCGCATTG GCCAAGCAGTTGGTTGTGC	Berbee et al. 1999

*Abbreviations: ITS – Internal Transcribed Spacer; LSU – Large Subunit ribosomal RNA; *rpb2* – RNA polymerase II second largest subunit; *act* – Actin; *alt-α1* – Alternaria major allergen; *chs-1* – Chitin synthase 1; *tub2* – beta-tubulin gene; *his3* – Histone3; *tef1-α* – translation elongation factor 1-α gene; *gapdh* – glyceraldehyde-3-phosphate dehydrogenase gene.

Phylogenetic Analyses

Unassembled sequences were checked in BioEdit version 7.0.5.3 (Hall 1999). BLAST searches

(Altschul et al. 1997) in GenBank yielded the remaining homogenous sequences, and the majority of the reference sequences came from earlier publications. Alignments for each locus were performed in the MAFFT v7.307 online version (Kato & Standley 2016) and manually verified in AliView v1.19-beta1k (Larsson 2014). The concatenation of different loci was done in SequenceMatrix 1.8 (Vaidya et al. 2011). The interleaved NEXUS files for Bayesian inference analyses were prepared by using AliView v1.19-beta1k (Larsson 2014). Phylogenetic analyses were conducted using maximum likelihood (ML) and Bayesian inference (BI) according to Dissanayake et al. (2020).

The Akaike information criterion (AIC), as implemented in MrModeltest v2 (Nylander 2004), was used to determine the best evolution models for each gene region. ML analyses were performed in raxmlGUI 2.0 (Edler et al. 2021) with RAxML v8.2.10 (Stamatakis 2014), using the ML + rapid bootstrap setting and the GTRGAMMAI (viz., GTR + GAMMA + I) substitution model with 1000 bootstrap replicates. Bayesian analysis was performed by MrBayes v3.1.2 (Ronquist et al. 2012). The model of evolution was estimated by MrModeltest 2.2 (Nylander 2004). Posterior probabilities (Rannala & Yang 1996) were performed by Markov Chain Monte Carlo Sampling (MCMC) in MrBayes v. 3.1.2. Six simultaneous Markov Chains were run for 1 billion generations, and trees were sampled every 1000th generation (resulting in 100,000 trees). The first 20000 trees representing the burn-in phase of the analyses were discarded and the remaining 80000 (post-burning) trees were used for calculating posterior probabilities (PP) in the majority rule consensus tree. Phylogenetic trees were drawn with FigTree v1.4.3 (Rambaut 2017).

RESULTS

The taxa presented below are arranged alphabetically. They encompass 59 species, distributed in 34 genera, 16 families, 18 orders, and four classes within the phylum Ascomycota. The classification follows the Outline of Fungi and fungus-like taxa (Hyde et al. 2024). The new species were identified following the guidelines provided by Jeewon & Hyde (2016), Chethana et al. (2021a), Jayawardena et al. (2021), and Maharachchikumbura et al. (2021).

Ascomycota Caval. -Sm

Pezizomycotina O.E. Erikss. & K. Winka

Dothideomycetes O.E. Erikss & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Botryosphaeriales was introduced by Schoch et al. (2006) to accommodate *Botryosphaeriaceae*. The order currently comprises six families: *Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Phyllostictaceae*, *Planistromellaceae*, and *Saccharataceae*. These families are well-supported by phylogenetic analysis and divergence time estimates (Phillips et al. 2019, Hongsanan et al. 2020a).

Botryosphaeriaceae Theiss. & Syd.

Botryosphaeriaceae was introduced by Theissen & Sydow (1918). Species of this family are endophytes, pathogens, and saprobes associated with a wide range of hosts with a worldwide distribution (Liu et al. 2012, Phillips et al. 2013, 2019). The taxonomy of *Botryosphaeriaceae* has long been complex until the molecular data were available and several authors have revised based on molecular data (Crous et al. 2006, Slippers et al. 2013, Dissanayake et al. 2016, Liu et al. 2017a, Phillips et al. 2019). The most comprehensive study of *Botryosphaeriaceae* was provided by Phillips et al. (2019) and accepted 22 genera based on ITS and LSU sequence data, and the divergence time estimates of this family are also provided. In this study, we follow the latest treatment and updated

accounts of *Botryosphaeriaceae* by Pem et al. (2024).

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

Neofusicoccum was established by Crous et al. (2006), with *N. parvum* as the type species. Members of this genus are recognized as endophytes, saprobes, and pathogens and are found on a wide range of hosts, including plants of agricultural, forestry, ecological, and economic significance (Lazzizera et al. 2008, Espinoza et al. 2009, Abdollahzadeh et al. 2013, Lopes et al. 2016). Initially, the species concept of *Neofusicoccum* was based solely on morphological characteristics. However, some species were incorrectly identified due to the minimal morphological differences. With advancements in molecular techniques, multi-locus DNA sequencing combined with morphological traits has become essential for accurately delineating *Neofusicoccum* species, leading to the discovery of many new species (Jayawardena et al. 2018, Hattori et al. 2021, Xu et al. 2022, Si et al. 2023). Currently, 71 species are listed in the Index Fungorum (2024), out of which 49 of them linked to sequence data.

Neofusicoccum sichuanense X.L. Xu & C.L. Yang, in Xu, Wang, Liu, Yang, Zeng, Wang, Liu & Yang, *Frontiers in Microbiology* 13(no. 1016548): 13 (2022) Fig. 1

Index Fungorum: IF 845074; Facesoffungi number: FoF 16289.

Endophytic in the stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: Colonies on MEA flat to slightly raised, reddish brown to dark brown with a velvety appearance. Mycelium 1.5–3.5 µm wide, superficial and immersed composed of septate, branched, brown to dark brown, verrucose and thick-walled hyphae, constricted at the septa, sometimes swollen at the septum, covered by a brown to dark brown sheath at the septa. Chlamydospores 11–17(–20) × 6–8 µm ($\bar{x}$ = 14 × 7 µm, n = 20), cylindrical to ellipsoidal, rounded at the apex, truncated at the base, hyaline when young, become dark greyish-brown when mature, septate, constricted at the septa, guttulate, thick and smooth walled.

Culture characteristics – Colonies on MEA reaching 60 mm diameter after 7 days at 25°C, colonies circular, margin wavy, flat, velvety appearance with greyish aerial mycelia in the middle, colony from above: brown to dark brown; reverse: dark brown to black.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stem of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS182–2 = GZAAS 25–0510), living culture (GZCC 25–0514).

GenBank numbers – ITS: PV138709, *tub2*: PV221998.

Notes – In our phylogenetic analysis (Fig. 2), our newly obtained strain (GZCC 25–0514) clustered with two strains of *Neofusicoccum sichuanense* (SICAUCC 22–0093 and SICAUCC 22–0099). We did not observe any sexual and asexual morphological structures for our strain, but the nucleotide of ITS and *tub2* sequence data of our new isolate are identical to the strains of *N. sichuanense* (SICAUCC 22–0093 and SICAUCC 22–0099). Thus, based on phylogenetic analysis, we identified our new strain as *N. sichuanense*. *Neofusicoccum sichuanense*, parasitic on the living twigs of *Juglans regia* was introduced by Xu et al. (2022). Our new isolate is an endophyte isolated from the stem of *Dicranopteris pedata*; thus, we report our new isolate as a new host record from *D. pedata*.

Phyllostictaceae Fr.

Phyllostictaceae was proposed by Fries (1849) to accommodate *Phyllosticta*. Subsequently, Schoch et al. (2006) placed *Phyllosticta* in *Botryosphaeriaceae* (*Botryosphaeriales*) based on

phylogenetic analysis, a classification that was accepted by Crous et al. (2006) and Liu et al. (2012). Wikee et al. (2013a) redefined the genus and showed that the genus clustered sister to *Botryosphaeriaceae*, they therefore resurrected *Phyllostictaceae* to accommodate *Phyllosticta*. Subsequently, a new genus *Pseudofusicoccum*, was added to the family by Phillips et al. (2019). Currently, only the two genera are accepted in the family (Wijayawardene et al. 2022, Wang et al. 2023a, Pem et al. 2024).

***Phyllosticta* Pers.**

Phyllosticta is a species-rich genus with more than 3000 epithets listed in the Index Fungorum (www.indexfungorum.org, accessed on 24 October 2024). The genus was introduced by Persoon (1818) with *P. convallariae* as the type species. The placement of this genus has long been debated until Wikee et al. (2013a), who redefined *Phyllosticta* and showed that the genus clustered sister with *Botryosphaeriaceae*, thus the family *Phyllostictaceae* was resurrected to accommodate *Phyllosticta*; this has been accepted by later studies (Slippers et al. 2013, Hongnan et al. 2020a, Wang et al. 2023a). *Phyllosticta* is characterized by pycnidial conidiomata containing aseptate conidia surrounded with a mucoid layer and bearing a single apical appendage; erumpent ascomata, 8-spored, clavate to broadly ellipsoid asci, and ellipsoid to limoniform ascospores (van der Aa 1973, van der Aa & Vanev 2002, Wikee et al. 2011). Previously, species identification criteria in *Phyllosticta* were based on morphology and host association (Wikee et al. 2011, Su & Cai 2012). However, many *Phyllosticta* species exhibit only minor morphological variation among species and lack any discernible host selectivity. Therefore, relying solely on host-specificity and morphological traits for identification is inaccurate (Wikee et al. 2011, Su & Cai 2012). In recent years, polyphasic taxonomic concepts, including multi-gene phylogenetic and morphological analyses, have been used for the taxonomy of *Phyllosticta* species, which have significantly improved the identification of *Phyllosticta* species. Currently, *Phyllosticta* is divided into six species complexes viz *P. capitalensis*, *P. concentrica*, *P. cruenta*, *P. owaniana*, *P. rhodora*, and *P. vaccinii* (Wang et al. 2023a). Species of this genus are mostly plant pathogens and endophytes from a broad range of hosts, with a worldwide distribution (Glience et al. 2011, Rashmi et al. 2019, Norphanphoun et al. 2020, Bhunjun et al. 2021a, 2022, Gomdola et al. 2022). In this study, *P. capitalensis* was isolated from *Dicranopteris*, and we reported it as a new host record for *Dicranopteris*.

***Phyllosticta capitalensis* Henn., Hedwigia 48: 13 (1908) [1909]**

Fig. 3

Index Fungorum: IF 168326; Facesoffungi number: FoF 06888.

Endophytic in the leaves of *Dicranopteris pedata*. Colonies on PDA flat to slightly raised, light brown in the middle, dark brown in the margin, with black fruiting bodies at the surface. Mycelium superficial and immersed composed of septate, branched, 4–6.5 μm wide, brown to dark brown, with smooth and thick-walled hyphae, slightly constricted at the septa. Chlamydospores 7–13.5(–18) $\times$ 7–11.5 μm ($\bar{x}$ = 10.4 $\times$ 9.4 μm , n = 20), globose to subglobose or irregular shape, hyaline to pale brown, smooth-walled.

Culture characteristics – Colonies on PDA reaching 55 mm diameter after 20 days at 25°C, colonies circular, velvety appearance with greyish brown aerial mycelia in the middle, flat to slightly raised, light brown in the middle, dark brown in the margin, with black fruiting bodies at the surface, colony from above: light brown to dark brown; reverse: dark brown to black.

Material examined – China, Guizhou Province, Ceheng County, Pomei Town, Southwest Guizhou Buyi and Miao Autonomous County, from the leave of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang (NS126–4 = GZAAS 25–0501), living culture (GZCC 25–0501); from the rhizome

of *D. linearis*, 16 March 2022, J.Y. Zhang (NS277–1 = GZAAS 25–0521), living culture (GZCC 25–0509); from a stem of *D. pedata*, 16 March 2022, J.Y. Zhang (NS253–6 = GZAAS 25–0519), living culture (GZCC 25–0507); from a stem of *D. linearis*, 16 March 2022, J.Y. Zhang, (NS269–1 = GZAAS 25–0520), living culture (GZCC 25–0508).

GenBank numbers – GZCC 25–0501: ITS: PV138733, LSU: PV138591, *tef1*- α : PV177121, *act*: PV188088. GZCC 25–0509: ITS: PV138734, LSU: PV138588, *tef1*- α : PV177124, *act*: PV188085. GZCC 25–0507: ITS: PV138735, LSU: PV138590, *tef1*- α : PV177122, *act*: PV188087. GZCC 25–0508: ITS: PV138736, LSU: PV138589, *tef1*- α : PV177123, *act*: PV188086

Notes – In this study, four strains were isolated from fresh leaves, stem, and rhizomes of *Dicranopteris* spp.; phylogenetic analysis showed that the four strains clustered with *P. capitalensis* (Fig. 4). We did not observe any sexual and asexual morph for our new isolates, only chlamydospores were observed from culture, but the comparisons of our new strains in ITS, LSU, *act* and *tef1*- α gene regions are almost identical to *P. capitalensis* (CBS 114751). Therefore, we identify our strain as *P. capitalensis* based on phylogenetic affinity. *Phyllosticta capitalensis* is an endophyte and plant pathogen with a wide range of hosts, having been reported from 70 plant families worldwide (Wikee et al. 2013b). However, this is the first time this species has been reported from *Dicranopteris* spp.

***Cladosporiales* Abdollahz. & Crous**

Abdollahzadeh et al. (2020) established *Cladosporiales* with the single family *Cladosporiaceae* Nann., based on phylogenetic analysis. In this study, we followed the treatment of Abdollahzadeh et al. (2020) for this order.

***Cladosporiaceae* Nann.**

Cladosporiaceae was introduced by Nannizzi (1934) with the type genus *Cladosporium*. Currently, eight genera viz. *Cladosporium*, *Cryoendolithus*, *Davidiellomyces*, *Graphiopsis*, *Neocladosporium*, *Rachicladosporium*, *Toxicocladosporium*, and *Verrucocladosporium* are accepted in the family (Wijayawardene et al. 2022; Hyde et al. 2024).

***Cladosporium* Link**

Cladosporium, one of the largest genera of dematiaceous hyphomycetes, was proposed by Persoon (1794) with *Dematium herbarum* Pers. as the type species, which was later described by Link (1816) as *C. herbarum* (Pers.:Fr.). *Cladosporium* is characterized by erect, straight, or geniculate conidiophores, coronate conidiogenous loci, conidial hila formed by a central convex dome surrounded by a raised periclinal rim, and acropetal branched chains of conidia (David 1997). *Cladosporium* species are similar in morphology; however, previous studies identified *Cladosporium* species primarily based on morphological characteristics, which has made the genus increasingly complex (David 1997, Heuchert et al. 2005, Schubert 2007, 2009, Bensch et al. 2012). With the molecular data available, various authors have continually revised this genus based on multi-locus phylogenetic analyses (Crous et al. 2007a, Sandoval-Denis et al. 2016, Iturrieta-González et al. 2021, Lee et al. 2023). Currently, three *Cladosporium* species complexes (*C. cladosporioides*, *C. herbarum* and *C. sphaerospermum*) have been identified.

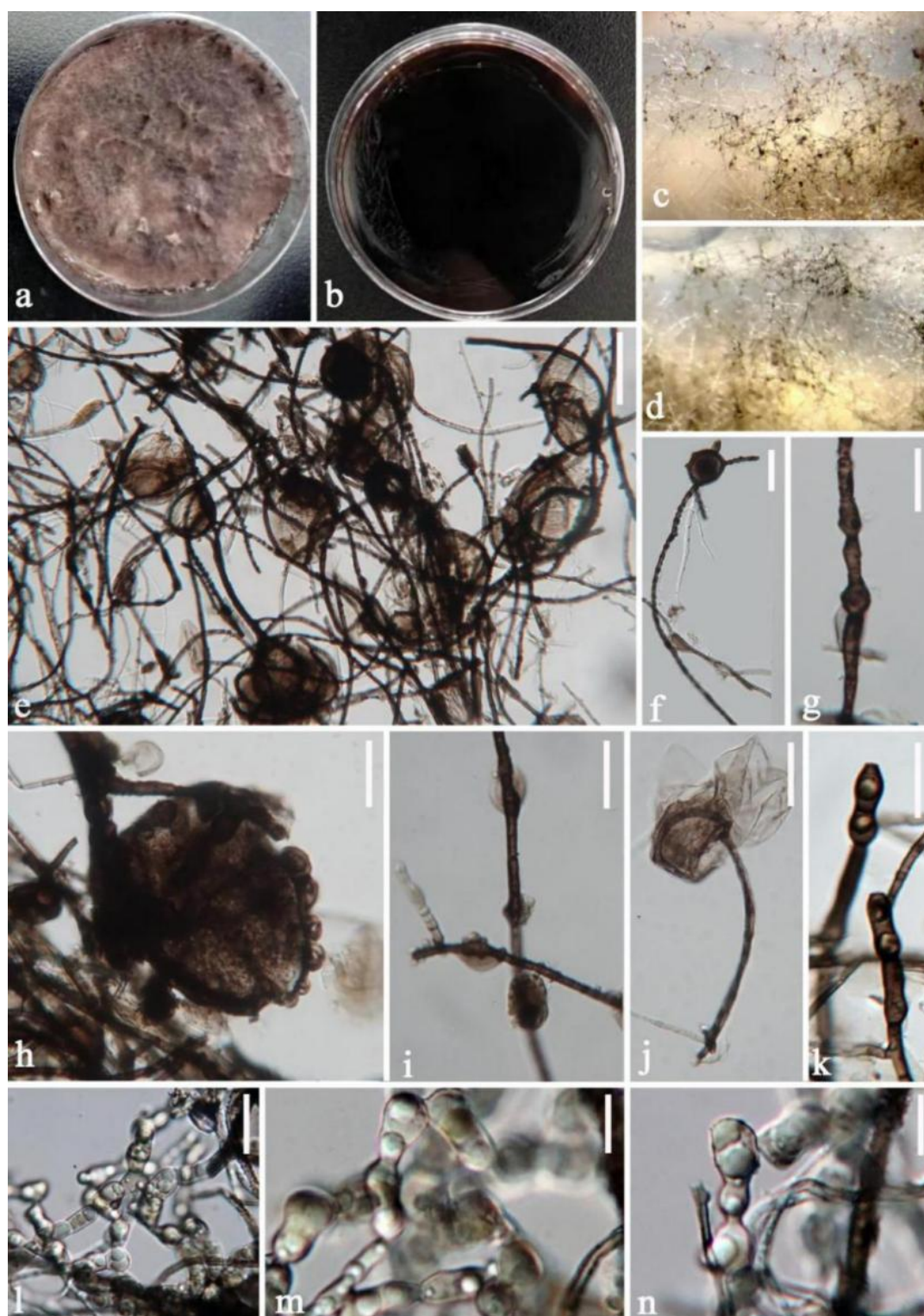


Figure 1 – *Neofusicoccum sichuanense* (GZAAS 25–0510, new host record) a, b Cultures on MEA from obverse and reverse. c, d Colonies on MEA. e–j Mycelium with sheath. k–n chlamydospores. Scale bars: e, f, j = 50 µm, g–i, k–l = 20 µm, m, n = 10 µm.



Figure 2 – Phylogram generated from maximum likelihood analysis based on combined ITS, *rpb2*,

tef1-α, and *tub2* sequence data. A total of 91 taxa were included in the combined analyses, which comprised 1875 characters after alignment. The best scoring RAxML tree with a final likelihood value of -8061.353437 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Botryosphaeria dothidea* (CBS 115476). The newly obtained strain is in red and the type strains are in bold.

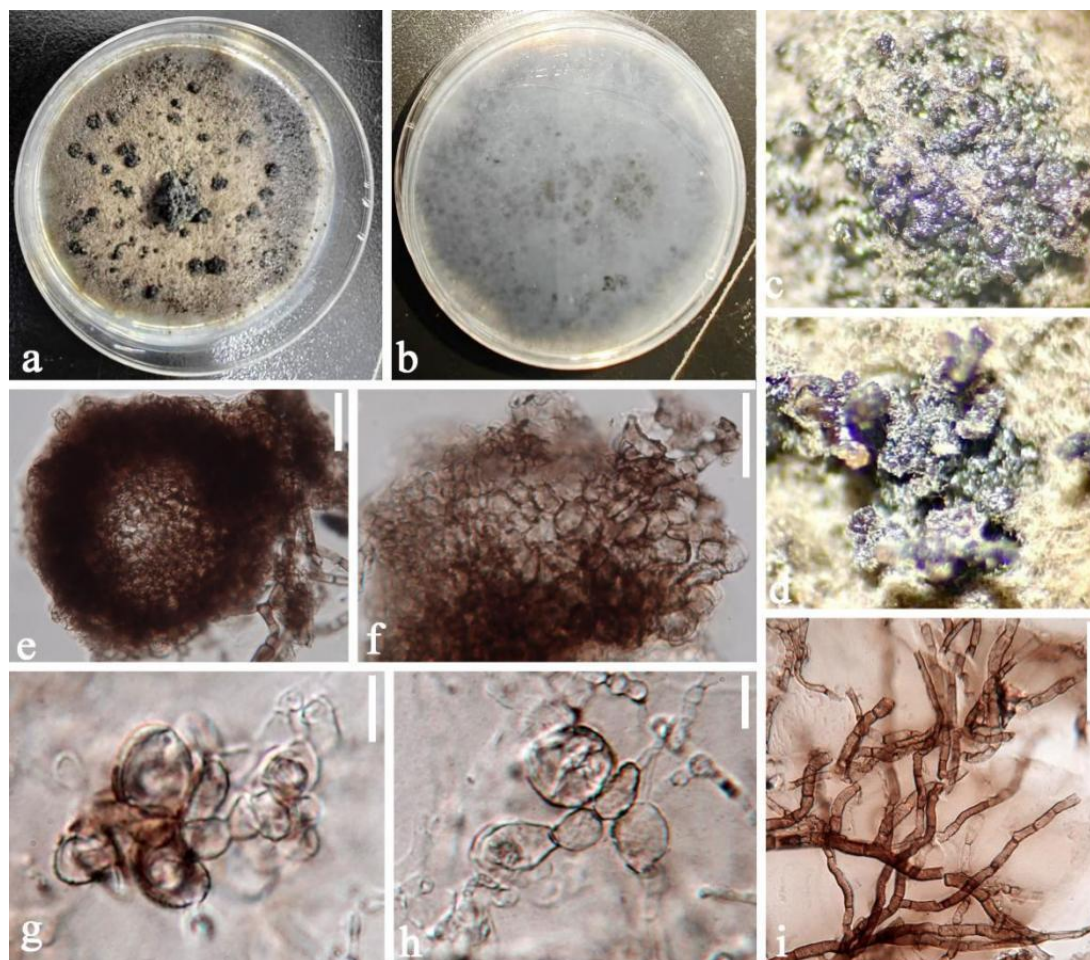


Figure 3 – *Phyllosticta capitalensis* (GZAAS 25–0501, new host record). a, b Cultures on PDA from above and below. c, d Fruiting bodies on PDA. e–f Ascomata. g–h Chlamydospores. i Mycelium. Scale bars: e, f = 30 μm , g, h = 10 μm , i = 50 μm .

Cladosporium angulosum Sand. -Den., Deanna A. Sutton & Guarro, in Sandoval-Denis, Gené, Sutton, Wiederhold, Cano-Lira & Guarro, Persoonia 36: 289 (2016) Fig. 5

Index Fungorum: IF 815333; Facesoffungi number: FoF 16495.

Endophytic in the stems of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Mycelium* superficial and immersed, composed of septate, branched, pale olivaceous brown, with smooth and thin-walled hyphae. *Conidiophores* 215–415(–507) $\times$ 3.5–6.5 μm ($\bar{x}$ = 314.3 $\times$ 4.9 μm , n = 15), macronematous, mononematous, erect, cylindrical, non-nodulose, septate, branched, frequently branching near the base, pale brown, smooth-walled. *Conidiogenous cells* terminal or intercalary, cylindrical, loci crowded at the apex forming clusters of pronounced scars, bearing up to two conidiogenous loci, darkened and refringent. *Conidia* 2.5–3.5 $\times$ 1–2 μm ($\bar{x}$ = 2.9 $\times$ 1.7 μm , n =40), in chains, subhyaline to pale brown, smooth and thin-walled, aseptate, with protuberant

conidial hila, not darkened.

Culture characteristics – Colonies on PDA reaching 53–55 mm after 15 days at 25 °C, brown to dark brown, flat, velvety to granular, with regular margin; reverse dark brown to black.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from a stem of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (292–1 = GZAAS 25–0523), living culture GZCC 25–0510.

GenBank numbers – ITS: PV138693, *act*: PV188077

Notes – Phylogenetic analysis showed that our isolate (GZCC 25–0510) grouped with two strains of *Cladosporium angulosum* (CPC 11526 and CBS 140692) with 96%ML and 1.00 PP (Fig. 6). The nucleotide comparisons of ITS and *act* gene regions between our new isolate (GZCC 25–0510) and *C. angulosum* (CBS 140692) revealed 0bp and 4bp differences respectively; GZCC 25–0510 differs from *C. angulosum* (CPC 11526) in ITS and *act* gene regions by 0bp and 6bp, respectively. This indicates that our new isolate was not significantly different from *C. angulosum* in molecular data. Morphologically, our new isolate is almost identical to *C. angulosum*. Therefore, we identified our new isolate as *C. angulosum*.

Cladosporium angulosum, a human pathogen isolated from human bronchoalveolar lavage, was introduced by Sandoval-Denis et al. (2016). Subsequently, this species has been isolated from plants of *Camellia sinensis* (Lv et al. 2023), *Austropuccinia psidii* (da Silva et al. 2023), *Corymbia foelscheana* and indoor air (Bensch et al. 2018), which showed that this species is highly adapted to different environments. In this study, we report our new isolate from *Dicranopteris ampla* as a new host record.

Cladosporium benschieae P.P. Costa, A.W.C. Rosado & O.L. Pereira [as 'benschii'], Phytotaxa 560(1): 17 (2022) Fig.7

Index Fungorum: IF 845498; Facesoffungi number: FoF 17849.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Mycelium* sparse, pluriseptate, occasionally somewhat swollen and constricted at the septum, subhyaline to pale brown, irregularly rough-walled. *Conidiophores* 87–205 × 2.5–5.5 µm ($\bar{x}$ = 146.4 × 4 µm, n = 15), solitary, macronematous, rarely micronematous, arising laterally from the hypha, erect or flexuous, cylindrical-oblong, cylindrical attenuated toward the apex to filiform, non-geniculate, pale brown to brown, subhyaline, unbranched, pluriseptate, conspicuous, walls slightly thickened, pale brown. *Conidiogenous cells* integrated, terminal, cylindrical oblong or cylindrical slightly attenuated to apex, non-geniculate, sometimes swollen at apex, in terminal cells apex usually head-like swollen with pronounced subdenticulate to denticulate loci crowded at the tip, pale brown, with 1–5 loci at apex, conidiogenous loci non-protuberant or only slightly so, rarely thickened and darkened. *Ramoconidia* not observed. *Conidia* 3–5(–6) × 2–3.5 µm ($\bar{x}$ = 4.1 × 2.7 µm, n = 30) numerous, catenate, acrogenous, ellipsoid, limoniform, ovoid, subglobose, pale brown to brown.

Culture characteristics – Colonies on PDA attaining 55 mm diameter after 15 days at 25 °C, brown to dark brown, flat, dense, felty; reverse dark brown.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, 223–3 (GZAAS 25–0515, new record). *ibid*, (293–1 = GZAAS 25–0532, new record).

GenBank numbers – GZAAS 25–0515: ITS: PV138692, *tef1-α*: PV177093, *act*: PV188076. GZAAS 25–0532: PV138694, *tef1-α*: PV177092, *act*: PV188078.

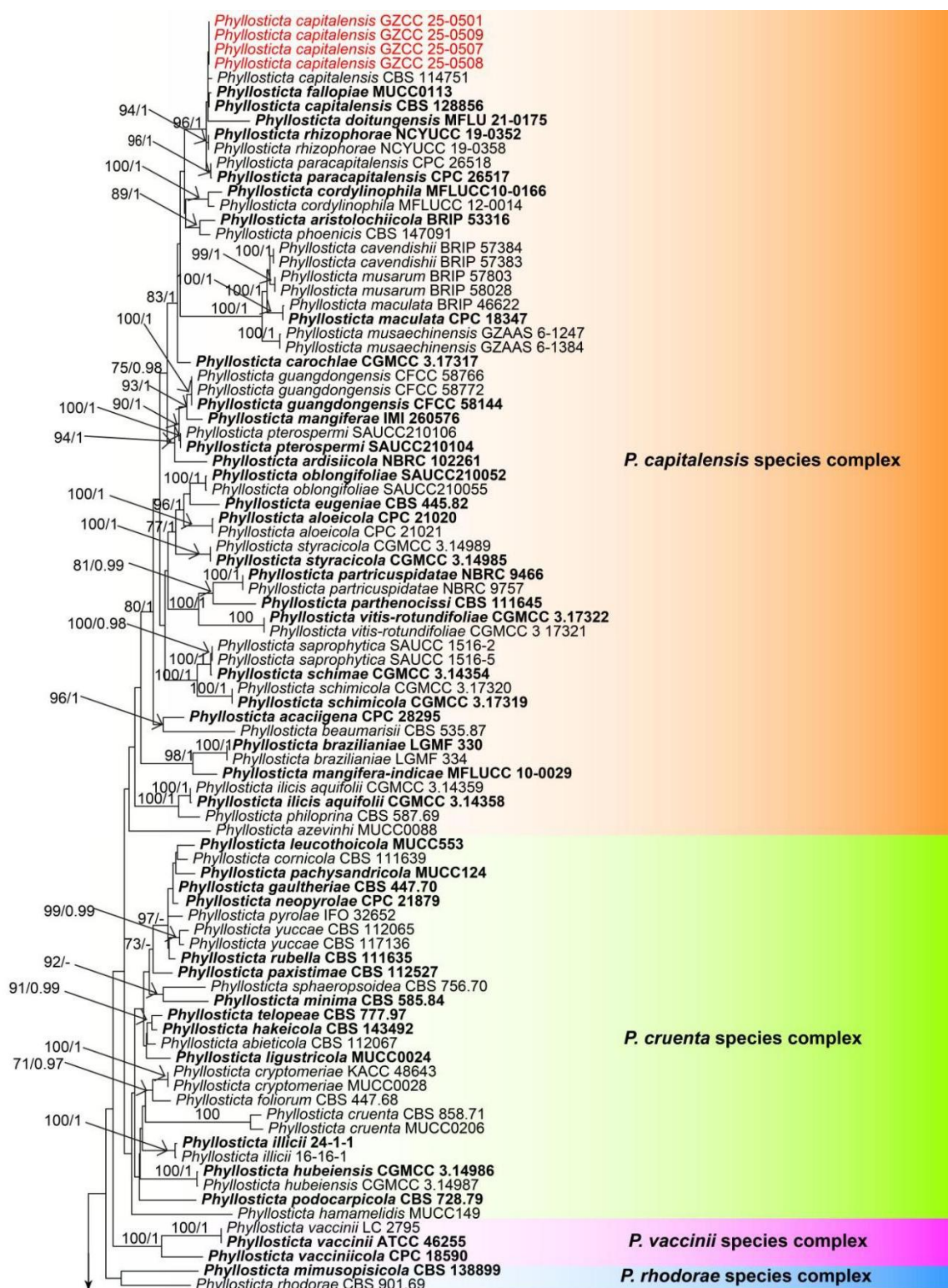


Figure 4 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *act*, *gapdh*, and *tef1-α* sequence data. A total of 147 taxa were included in the combined analyses, which comprised 2600 characters after alignment. The best scoring RAxML tree with a final likelihood value of -25751.617642 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Botryosphaeria obtusa* (CMW 8232) and *B. stevensii* (CBS 11255). The newly obtained strains are in red and the type strains are in bold.

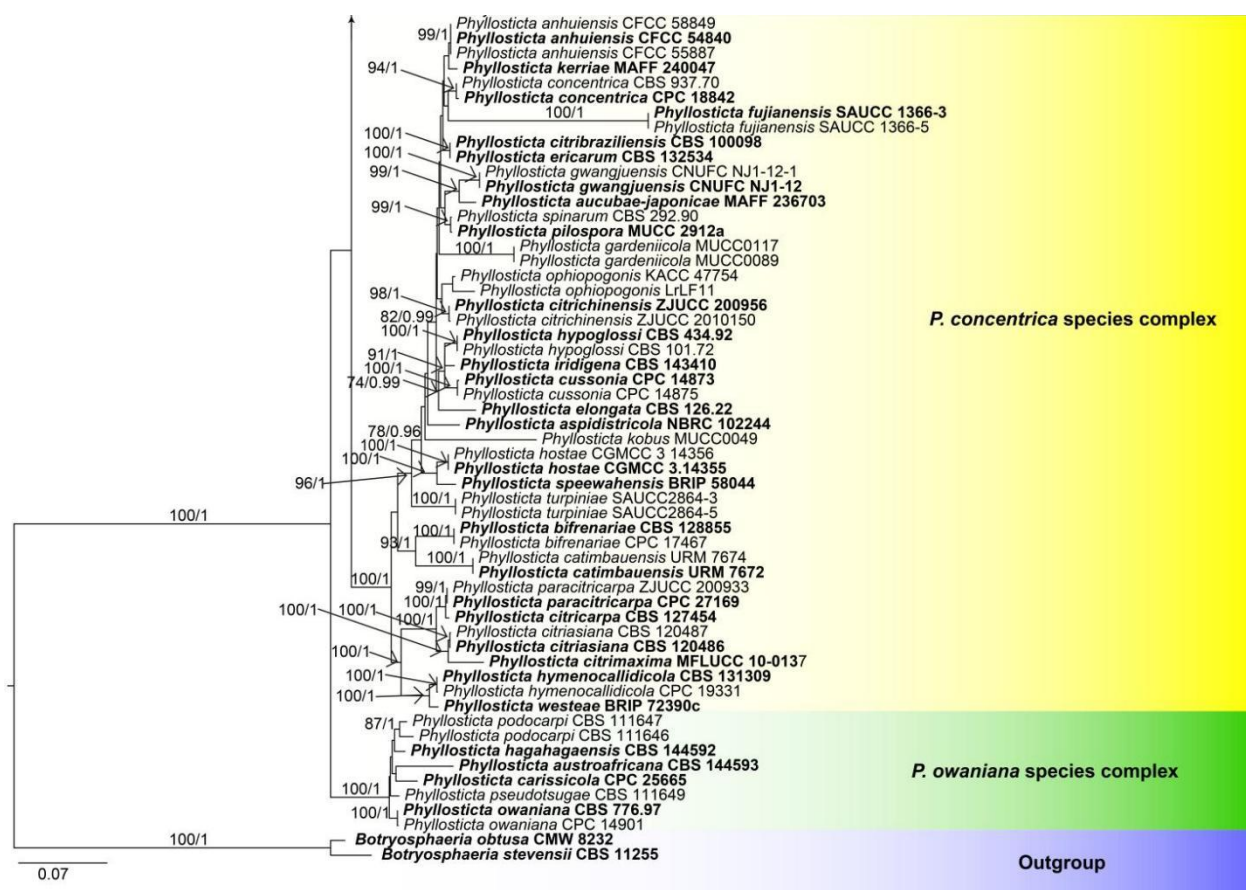


Figure 4 – Continued

Notes – Our phylogenetic analysis showed that the two new isolates (GZAAS 25–0515 and GZAAS 25–0532) grouped with *C. benschii* in an independent clade, but our two new isolates and *C. benschii* formed separate clades (Fig. 6). We compared the nucleotide sequences of our new isolates (GZAAS 25–0515 and GZAAS 25–0532) with the ex-type strain of *C. benschii* (COAD 2263). The results showed that the ITS sequence data of our new strains, GZAAS 25–0515 and GZAAS 25–0532, differ from *C. benschii* (COAD 2263) by 0 and 3 bp, respectively. The act sequence data of GZAAS 25–0515 and GZAAS 25–0532 differ from *C. benschii* (COAD 2263) by 2 bp and 3 bp, respectively. Additionally, the *tef1*-α sequence data of GZAAS 25–0515 are identical to *C. benschii* (COAD 2263), while GZAAS 25–0532 shows 3 bp differences from *C. benschii* (COAD 2263). The ITS, *act*, and *tef1*-α sequences of our two new strains are not significantly different from *C. benschii* (COAD 2263), which strongly suggests our new isolates are *C. benschii*. In addition, the morphology of our new isolate fits well with the description of *C. benschii* (Costa et al. 2022). Thus, we identified our new isolates as *C. benschii*, which was introduced by Costa et al. (2022) and collected on decaying leaves of *Aulonemia amplissima* from Brazil. This is the first geographic record of the species reported from China, isolated as an endophyte of *Dicranopteris pedata*.

Cladosporium chlamydosporiformans C.M. Pereira & R.W. Barreto, in Pereira et al., Fungal Systematics and Evolution 14: 22 (2023) Fig. 8

Index Fungorum: IF 850456; Facesoffungi number: FoF 17850.

Endophytic in the stems of *Dicranopteris ampla*. Sexual morph: Not observed. Asexual morph:

Mycelium superficial and immersed, composed of septate, branched, hyaline to pale brown, smooth-walled hyphae. *Conidiophores* $48\text{--}98 \times 2\text{--}4 \mu\text{m}$ ($\bar{x} = 72.7 \times 3.3 \mu\text{m}$, $n = 15$), mononematous, macronematous, solitary, erect to slightly flexuous, non-nodulose, sometimes subnodulose at the uppermost apex, unbranched or occasionally branched, septate, slightly constricted at septa, pale brown, smooth, sometimes somewhat irregularly rough-walled or verruculose. *Conidiogenous cells* terminal and intercalary, loci crowded at the apex forming clusters of pronounced scars, 1–2 conidiogenous loci formed at about the same level, loci often situated at lateral shoulders due to sympodial proliferation, *Conidia* $3\text{--}4.5(5.5) \times 2\text{--}3 \mu\text{m}$ ($\bar{x} = 3.8 \times 2.3 \mu\text{m}$, $n = 35$), solitary or in short unbranched chains, straight to slightly curved, cylindrical-oblong aseptate, sometimes slightly constricted at the septa, pale to pale medium olivaceous-brown.

Culture characteristics – Colonies on PDA attaining 45 mm diameter after 14 days at 25 °C, dark brown to greyish brown, velvety, furrowed; reverse dark brown to black.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyim, and Miao Autonomous County, from stems of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (181–4 = GZAAS 25–0509).

GenBank numbers – ITS: PV138691, *tef1-α*: PV177094, *act*: PV188075



Figure 5 – *Cladosporium angulosum* (GZAAS 25–0523, new host record). a, b Cultures on WA observed and reverse. c Colonies on WA. d–f Conidiophores. g–i Conidiogenous cells and conidia. j–o Conidia. Scale bars: d–f = 50 μm , g–o = 5 μm .

Notes – *Cladosporium chlamydosporiformans* was recently introduced by Pereira et al. (2024), it was isolated on uredinia of *Hemileia vastatrix* and leaves of *Coffea arabica* from Kenya. Our new isolate (GZAAS 25–0509) is phylogenetically related to *C. chlamydosporiformans* with 100% ML/1.00 BYPP support (Fig. 6). Morphologically, our new isolate is similar to *C. chlamydosporiformans* in having macronematous, solitary conidiophores which arise terminally or laterally from hyphae, integrated, terminal, subcylindrical conidiogenous cells with 1–5 loci at the apex, and aseptate, light brown to brown, smooth-walled conidia which are in acropetal and branched chains (Pereira et al. 2024). Thus, based on phylogenetic analysis and morphological characteristics, we identified our new isolate as *C. chlamydosporiformans* and reported it as a new host and geographical record from *Dicranopteris ampla* in China.

Cladosporium punicae Y.Q. Yang & Yong Wang bis, in Yang et al., Journal of Fungi 9(no. 250): 17 (2023) Fig. 9

Index Fungorum: IF 900113; Facesoffungi number: FoF 17851.

Endophytic in the stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Mycelium* superficial and immersed, hyphae branched, subhyaline to pale or medium olivaceous-brown, smooth and thin-walled. *Conidiophores* 55–132 × 2.0–4 µm ($\bar{x}$ = 93.9 × 3.3 µm, n = 15), macronematous, mononematous, solitary, arising terminally or laterally from plagiotropous or ascending and erect hyphae, erect, straight to slightly flexuous, cylindrical, sometimes slightly geniculate toward the apex, pale to medium brown, smooth to asperulate or minutely verruculose. *Conidiogenous cells* terminal or intercalary, cylindrical, loci crowded at the apex forming clusters of pronounced scars, bearing up to four conidiogenous loci. *Conidia* 2.5–4 × 1.5–2.5 µm ($\bar{x}$ = 3 × 2 µm, n = 40), forming chains, ovoid, ellipsoid, rounded at the apex, pointed at the base, somewhat darkened and refractive conidial hila, subhyaline to pale greyish-brown, smooth to minutely verruculose or irregularly rough-walled.

Culture characteristics – Colonies on PDA reaching 50 mm diameter after 15 days at 25 °C, greyish brown with abundant and dense aerial mycelium, velvety to granular, with regular margin. Reverse dark brown to black.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stems of *Dicranopteris pedata*, 17 March 2022, J.Y. Zhang, (179–2 = GZAAS 25–0507), living culture GZCC 25–0503. Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from leaves of *D. pedata*, 17 March 2022, J.Y. Zhang, (180–2 = GZAAS 25–0508), living culture GZCC 25–0504.

GenBank numbers – GZCC 25–0503: ITS: PV138689, *tef1-α*: PV177096, *act*: PV188073. GZCC 25–0504: ITS: PV138690, *tef1-α*: PV177095, *act*: PV188074.

Notes – Our two new strains (GZCC 25–0503 and GZCC 25–0504) grouped with the ex-type strain of *Cladosporium punicae* (GUCC 21271.5) in the phylogenetic analysis (Fig. 6). The ITS sequences of our strains (GZCC 25–0503 and GZCC 25–0504) were identical to those of *C. punicae* (GUCC 21267.1), with only 1 bp and 4 bp differences between strain GZCC 25–0504 and GUCC 21271.5, and strain GZCC 25–0503 and GUCC 21271.5, in the *act* and *tef1-α* gene regions, respectively. Morphologically, GUCC 21267.1 shares nearly identical colony morphology, conidiophores, conidiogenous cells, and conidia with the description of *C. punicae* (Yang et al. 2023a). Therefore, we report our new strains as a new host record of *C. punicae* on *Dicranopteris pedata*.

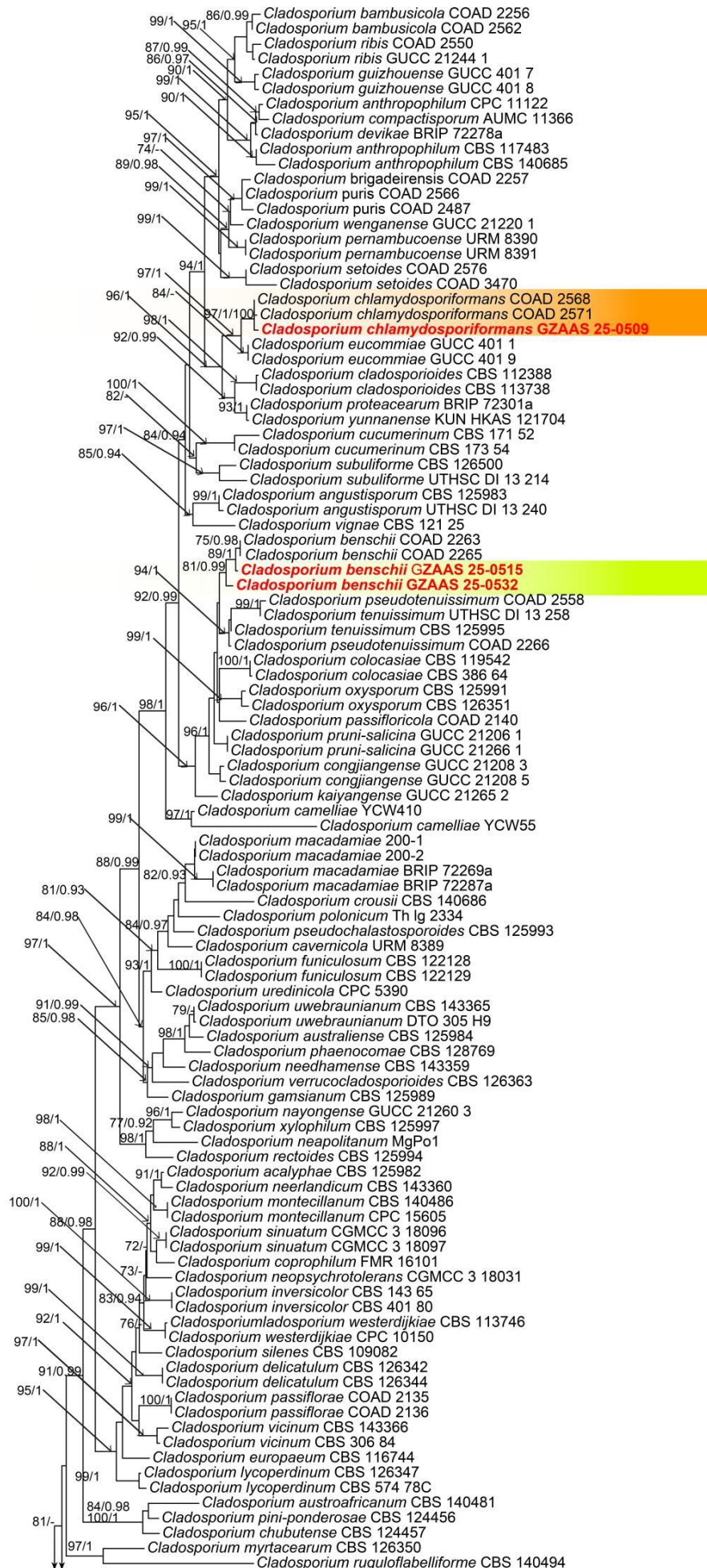


Figure 6 – Phylogram generated from maximum likelihood analysis based on combined ITS, *act*, and *tef1-α* sequence data. A total of 188 taxa were included in the combined analyses, which comprised 1028 characters after alignment. The best scoring RAxML tree with a final likelihood value of -19632.181468 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Cladosporium herbarum* (CBS 121621 and CBS 300.49). The newly obtained strains are in red and bold.

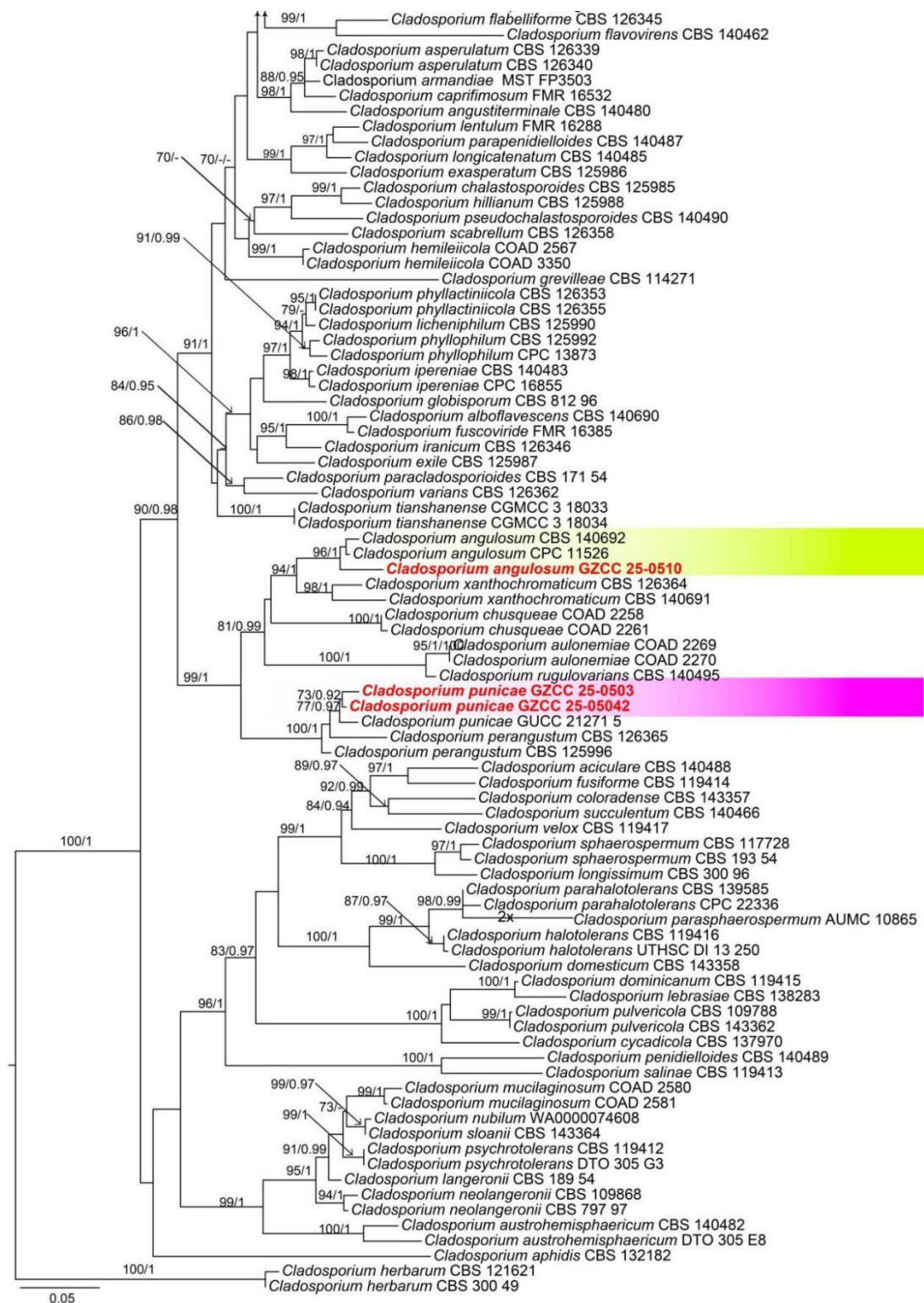


Figure 6 – Continued



Figure 7 – *Cladosporium benschieae* (GZAAS 25–0532, new host and geographic record). a, b Cultures on WA from above and below. c Colonies on WA. d–h Conidiophores. i–k Conidiogenous cells. l–o Conidia. Scale bars: d = 30 µm, e–h = 20 µm, i–o = 5 µm.

***Muyocoprionales* Mapook, Boonmee & K.D. Hyde**

Muyocoprionales was introduced by Mapook et al. (2016) to accommodate a single family *Muyocoprionaceae*, that formed a distinct clade within *Dothideomycetes* and is closely related to *Acrospermales* and *Dyfrlolomycetales*. However, *Muyocoprionaceae* is distinct from *Acrospermales* and *Dyfrlolomycetales* by superficial, flattened, carbonaceous, brittle ascomata, pseudoparaphyses that are longer than the asci and ellipsoidal to ovate, unicellular ascospores (Mapook et al. 2016). Hongsanan et al. (2020a) confirmed the status of this order based on phylogenetic analysis and divergence time. Currently, the order comprises a single family with 12 genera (Hongsanan et al.

2020a, Worobiec et al. 2020, Senwanna et al. 2021).

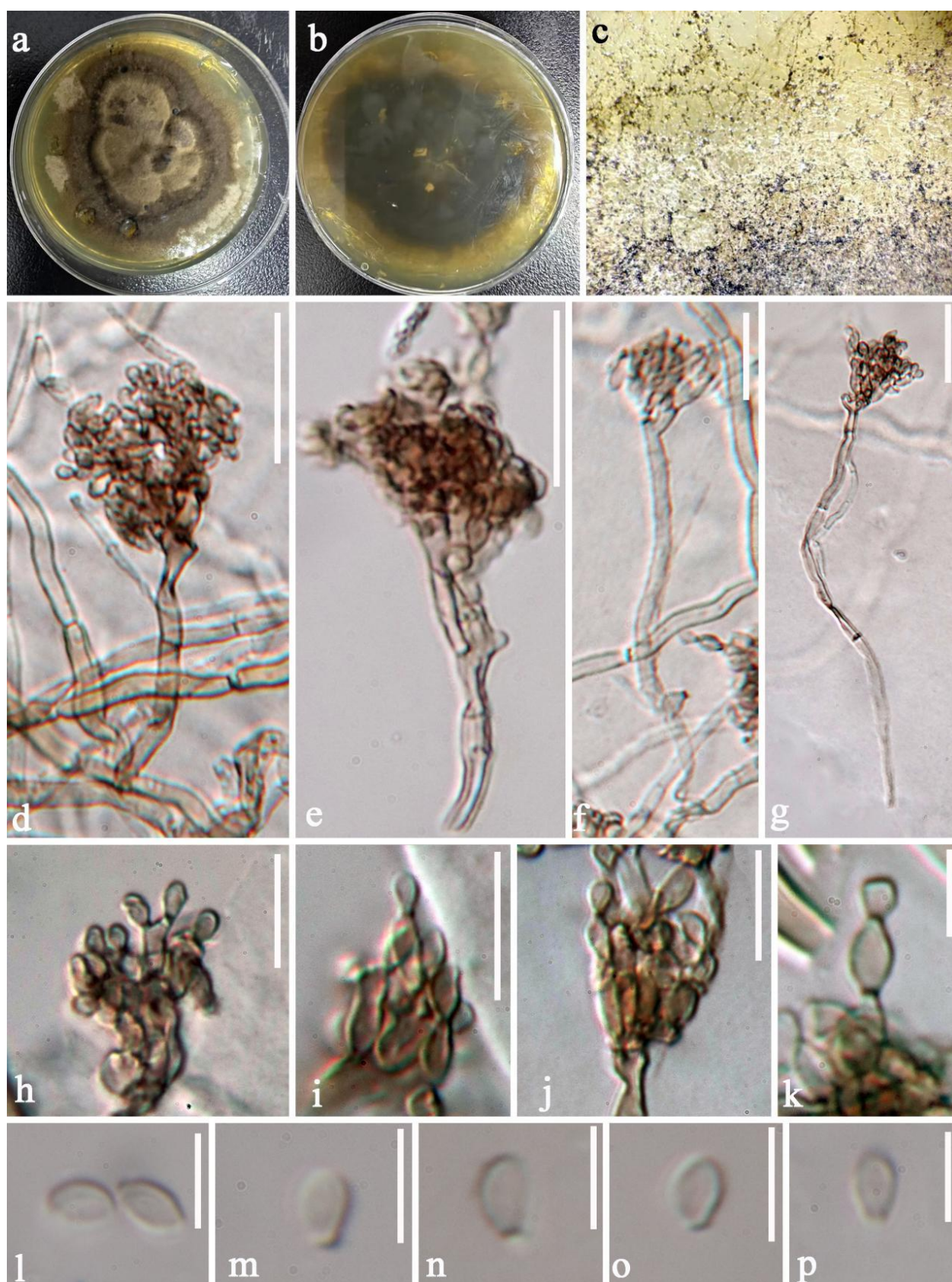


Figure 8 – *Cladosporium chlamydosporiformans* (GZAAS 25–0509, new host and geographical record). a, b Cultures on WA from above and below. c Colonies on WA. d–g Conidiophores,

conidiogenous cells, and conidia. h–k Conidiogenous cells and conidia. l–p Conidia. Scale bars: d–g = 20 μm , h–j = 10 μm , k–p = 5 μm .



Figure 9 – *Cladosporium punicae* (GZAAS 25–0507, new host record). a, b Cultures on WA from

above and below. c Colonies on WA. d–g Conidiophores. h–k Conidiogenous cells and conidia. l Conidiogenous cells. m–r Conidia. Scale bars: d–g = 20 µm, h–r = 5 µm.

***Muyocoproneae* K.D. Hyde**

Muyocoproneae was initially introduced by Luttrell (1951) and placed in *Hemisphaeriales* (Spegazzini 1881). Hyde et al. (2013) accepted it as a distinct family in *Dothideomycetes* with a single genus *Muyocopron*. Mapook et al. (2016) proposed a new order *Muyocoproneales*, to accommodate this family. Hongsan et al. (2020a) accepted nine genera viz. *Arxiella*, *Leptodiscella*, *Mycoleptodiscus*, *Muyocopron*, *Neocochlearomyces*, *Neomycoleptodiscus*, *Paramycoleptodiscus*, *Setoapiospora*, and *Pseudopalawania* in the family based on phylogenetic analysis. Subsequently, two new genera viz. *Muyocopromyces* and *Quadrisporella* were added to the family (Worobiec et al. 2020, Senwanna et al. 2021). We follow the latest updated accounts of this family provided by Hyde et al. (2024).

***Arxiella* Papendorf**

Arxiella was introduced by Papendorf (1967) for a hyphomycetous species *A. terrestris*, which has reniform conidia with obliquely cornute ends. Subsequently, four *Arxiella* species viz. *A. celtidis*, *A. dolichandrae*, *A. longispora* and *A. lunata* were introduced (Ruscoe 1970, Crous et al. 2014, Tennakoon et al. 2021, Xu et al. 2023). Except for *A. celtidis* (Tennakoon et al. 2021), all other species have been reported as asexual morphs, and characterized by 1- to multi-celled, simple or branched, hyaline to slightly olivaceous hyphae conidiophores, and reniform ends obliquely cornute, hyaline or faintly coloured, 1-septate, smooth conidia which are single or in short chains or in small irregular groups, usually with apical and basal horn-like appendages (Papendorf 1967, Ruscoe 1970, Crous et al. 2014). Only *A. celtidis* has been reported as sexual morphs, characterized by globose to subglobose, glabrous, ostiolate ascomata with minute papilla, bitunicate, cylindrical to cylindrical-clavate asci with an indistinct ocular chamber and uniseriate to bi-seriate, fusiform with acute ends, 1-septate, hyaline, guttulate, smooth-walled ascospores surrounded by a thin mucilaginous sheath (Tennakoon et al. 2021).

Recent studies showed that *A. celtidis*, *A. dolichandrae*, *A. longispora*, and *A. terrestris* formed a monophyletic clade within *Muyocoproneae*, while *A. lunata* clustered outside of the monophyletic *Arxiella* group; our analysis obtained a similar result (Fig. 11). Morphologically, *A. lunata* differs from other *Arxiella* species by its conidia with a curved inner side similar to a crescent, while others have a straight inner side similar to a boat (Papendorf 1967, Ruscoe 1970, Crous et al. 2014). Thus, the placement of this species needs to be clarified in the future.

***Arxiella ellipsoidea* J.Y. Zhang, K.D. Hyde, D.F. Bao & Y.Z. Lu, sp. nov.**

Fig.10

Index Fungorum: IF 903957; Facesoffungi number: FoF 17852.

Etymology – The name refers to its ellipsoidal conidia.

Holotype – KUN-HKAS 129879

Endophytic in the rhizome of *Dicranopteris pedata*. Sexual morph: undetermined. Asexual morph: *Mycelium* septate, branched, hyaline to brown, guttulate. *Conidiophores* 3–5 µm wide, macronematous to semi-macronematous, mononematous, solitary, straight or flexuous, cylindrical, brown, septate, guttulate, thick-walled. *Conidiogenous cells* monoblastic, integrated, terminal and intercalary, pale brown. *Conidia* 5–8 × 3–5 µm ($\bar{x}$ = 6.5 × 4 µm, n = 30), solitary or occasionally interconnected or irregular group with the members of interconnected, subglobose to ellipsoidal, pale to brown, aseptate, often with two or more distinct guttules, smooth-walled, sometimes with apical

and basal horn-like appendages, usually with a widely truncate and slightly raised hilum at the base where the basal appendage joins the conidium body.

Culture characteristics – *Colonies* on WA medium sporiferous, circular, immersed mostly, entire margin with filamentous margin, flat with thin aerial hyphae, white to brown, black spots visible at 1–2 spots.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi, and Miao Autonomous Prefecture, Chengheng County, isolated from the healthy rhizome of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS143–4 = KUN-HKAS 129879, holotype), ex-type living culture (KUNCC 23–14173).

GenBank numbers – ITS: PV138681, LSU: PV138578, *tef1-α*: PV177091

Notes – Our phylogenetic analysis showed that *A. ellipsoidea* (KUNCC 23–14173) grouped with *A. celtidis*, *A. dolichandrae*, *A. longispora*, and *A. terrestris* in a well-supported clade but formed a distinct lineage basal to *Arxiella* species, whereas *A. lunata* was placed outside of the monophyletic *Arxiella* group (Fig. 11). Thus, the placement of this species needs to be revised.

Conidia of *A. ellipsoidea* are single or in short chains or in small irregular groups with apical and basal horn-like appendages, which confirms the morphology of the generic conception in *Arxiella*. However, *A. ellipsoidea* differs from the existing species by its subglobose to ellipsoidal, brown conidia. While conidia of other *Arxiella* species are reniform or cylindrical, and hyaline (Xu et al. 2023, Crous et al. 2014). Among the *Arxiella* species, *A. ellipsoidea* is similar to *A. terrestris*; conidia of both species are solitary or occasionally interconnected or irregular groups with the members of interconnected, with apical and basal horn-like appendages, usually with a widely truncate and slightly raised hilum at the base where the basal appendage joins the conidium body (Papendorf 1967). However, *A. ellipsoidea* can be distinguished from *A. terrestris* in having subglobose to ellipsoidal, pale to brown, and aseptate conidia. In contrast, conidia of *A. terrestris* are 1-septate and reniform. Therefore, we introduce *A. ellipsoidea* as a new species based on phylogeny and morphology.

***Pleosporales* Luttr. ex M.E. Barr.**

Pleosporales is the largest order in the class *Dothideomycetes*. We follow the latest updated account of *Pleosporales* included in Hyde et al. (2024).

***Didymellaceae* Gruyter, Aveskamp & Verkley**

Didymellaceae was introduced by de Gruyter et al. (2009) and it is the largest family in *Pleosporales*, with 50 genera being accepted (Hyde et al. 2024). For a brief introduction to the family, see Hongsanan et al. (2020b).

***Paraboeremia* Qian Chen & L. Cai**

Paraboeremia was introduced by Chen et al. (2015) and placed in *Didymellaceae*. It is a well-studied genus with all species associated with sequence data. The genus is characterized by superficial or immersed, globose to subglobose or irregularly-shaped pycnidial conidiomata, ostiolate, sometimes with a short neck around the ostioles, phialidic, hyaline, smooth, globose to flask-shaped conidiogenous cells and ellipsoidal, hyaline or sometimes greenish, aseptate, guttulate conidia; pseudothecial, subglobose to pyriform, ostiolate ascomata and subcylindrical, hyaline ascospores with wider upper cell, constricted at the septum (Chen et al. 2015). Species of this genus have been isolated from soil, e.g., *P. yungensis*, *P. rekkeri*, and *P. truiniurum* (Jiang et al. 2017, Peralta et al. 2021), diseased plant leaves, such as, *P. camelliae* and *P. litseae* (Jiang et al. 2017, Peralta et al. 2021), and a few species have been found from submerged wood in freshwater habitats, e.g., *P. clausa*

(Magaña-Dueñas et al. 2021). *Paraboeremia* species have been reported in China, Spain, and the Netherlands (Chen et al. 2015, Jiang et al. 2017, Peralta et al. 2021, Magaña-Dueñas et al. 2021). Currently, 11 species are accepted in the genus (Index Fungorum 2024). In this study, we reported *P. litseae* as an endophytic fungus isolated from *D. pedata* in Guizhou Province, China.

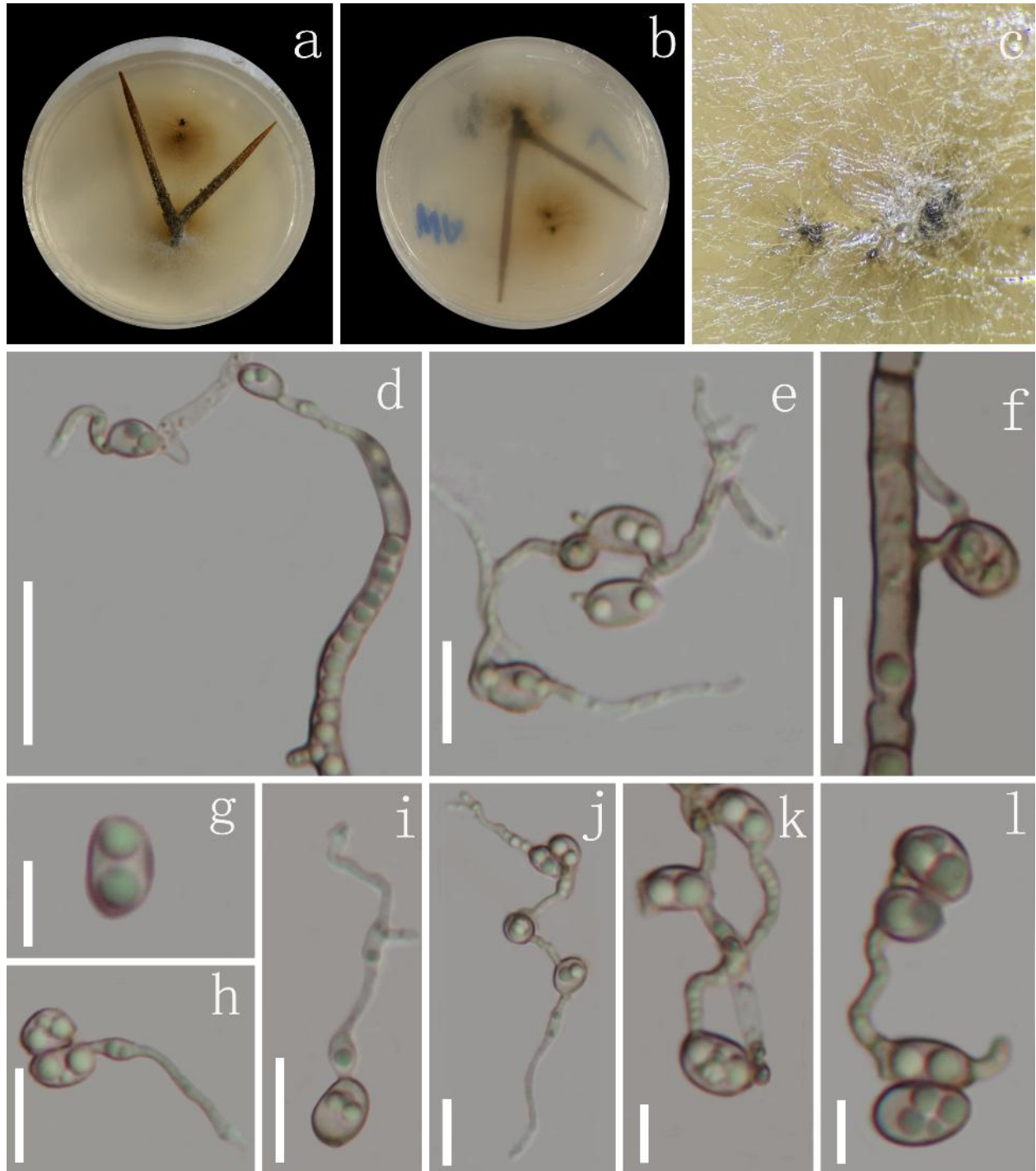


Figure 10 – *Arxiella ellipsoidea* (KUN-HKAS 129879, holotype). a, b Cultures on WA from above and below. c Colonies on WA. d–l Hyphae with conidiogenous cells, and conidia. Scale bars: d, j = 20 µm, e, f, i, k = 10 µm, g, h, l = 5 µm.

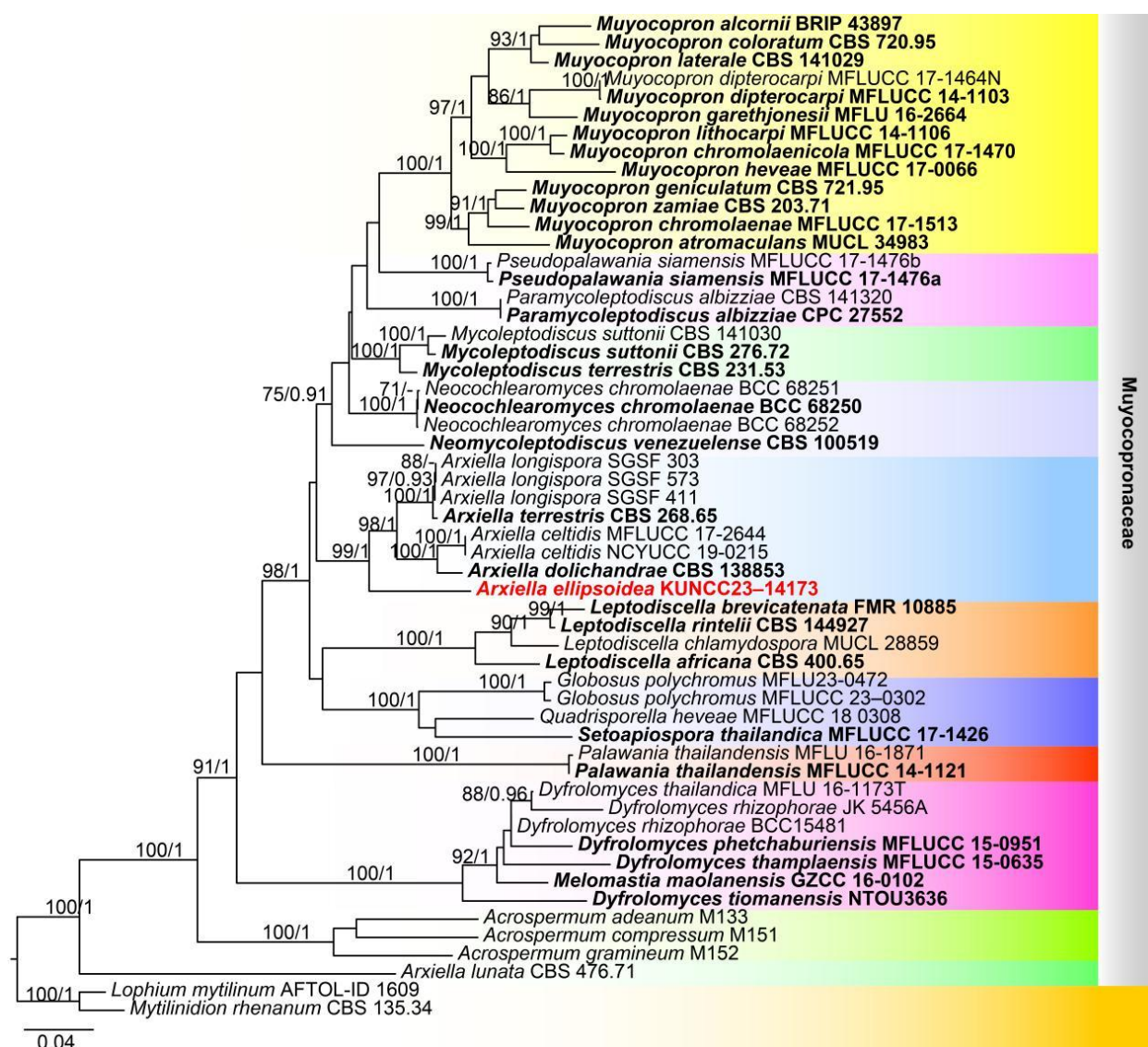


Figure 11 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, and *tef1-α* sequence data. A total of 55 taxa were included in the combined analyses, which comprised 3557 characters after alignment. The best scoring RAxML tree with a final likelihood value of -23665.622673 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Lophium mytilinum* (AFTOL-ID 1609) and *Mytilinidion rhenanum* (CBS 135.34). The newly obtained strain is in red and the type strains are in bold.

Paraboeremia litseae J.R. Jiang & L. Cai, in Jiang, Chen & Cai, Mycol. Progr. 16(4): 291 (2016) [2017] Fig. 12

Index Fungorum: IF 818243; Facesoffungi number: FoF 17853.

Endophytic in the rhizome of *Dicranopteris pedata*. Sexual morph: undetermined. Asexual morph: *Conidiomata* pycnidial in culture on MEA, gregarious, semi-immersed or nearly superficial, globose to subglobose, black. *Conidiomatal wall* pseudoparenchymatous, composed of semi-immersed or nearly superficial isodiametric cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform. *Conidia* $2.5\text{--}3.5 \times 1\text{--}2 \mu\text{m}$ ($\bar{x} = 3.1 \times 1.6 \mu\text{m}$, $n = 40$), ellipsoidal to

cylindrical with round ends, aseptate, hyaline, smooth-walled, guttulate. *Chlamydospores* not observed in culture.

Culture characteristics – Colonies on MEA reaching 55–60 mm diameter after one month at room temperature 25 °C, flattened, velvety, margin regular, grayish brown; reverse dark reddish brown.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi, and Miao Autonomous Prefecture, Cengheng County, isolated from the rhizome of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (85–1 = GZAAS 25–0530), living culture (GZCC 25–0513). Tongren City, Songtao County, from the rhizome of *D. pedata*, 21 February 2022, J.Y. Zhang, (78–1 = GZAAS 25–0528), living culture (GZCC 25–0512). *ibid*, (78–6 = GZAAS 25–0529).

GenBank numbers – GZCC 25–0512: ITS: PV138728, *tub2*: PV222014. GZAAS 25–0529: ITS: PV138729, *tub2*: PV222015. GZCC 25–0513: ITS: PV138730, *tub2*: PV222016.

Notes – In our phylogenetic analysis of combined ITS, *rpb2*, and *tub2* sequence data, three new isolates (GZCC 25–0513, GZAAS 25–0529 and GZCC 25–0512) clustered with *Paraboeremia litseae* CGMCC 3.18109 as the same species (Fig. 13). Our new isolates share similar morphological characters with *P. litseae* in having semi-immersed or nearly superficial, globose to subglobose conidiomata, ellipsoidal to cylindrical, aseptate, hyaline, smooth-walled conidia (Jiang et al. 2017). Therefore, based on both phylogeny and morphology, we identified our new isolates as *P. litseae*. *Paraboeremia litseae* was described by Jiang et al. (2017), isolated from diseased leaves of *Litsea* sp. (*Lauraceae*) in China. Our new isolate was obtained from *Dicranopteris pedata* and is the first *Paraboeremia* species recorded on *Dicranopteris*.

***Periconiaceae* Nann.**

Periconiaceae was introduced by Nannizzi (1934) with *Periconia* as the type genus. This family has long been ignored in modern taxonomic treatments and was placed as a member of *Massarinaceae*. Tanaka et al. (2015) showed that *Periconiaceae* formed a strongly supported clade sister to *Massarinaceae*. They, therefore, resurrected this family with the acceptance of four genera viz. *Bambusistroma*, *Flavomyces*, *Noosia* and *Periconia*. However, the phylogenetic status of *Bambusistroma* and *Noosia* remains questionable as they clustered with *Periconia* species in *Periconiaceae*. Yang et al. (2022) re-evaluated the taxonomic status of *Bambusistroma* and *Noosia* based on morphological and multi-gene phylogenetic analyses. Their results showed that *Bambusistroma* has similar morphology to the sexual morph of *Periconia* species, and *Noosia* is not significantly different from *Periconia* species that sporulated in vitro. Hence, these two genera were synonymized under *Periconia*. Currently, *Periconiaceae* comprises two genera, *Flavomyces* and *Periconia*. Nevertheless, as *Flavomyces* lacks morphological characteristics and clusters with *Periconia* species, its generic position is likewise dubious and needs to be clarified.

***Periconia* Tode**

Periconia was introduced by Tode (1791) with *P. lichenoides* Tode as the type. Most *Periconia* species are only known as asexual morphs, which are characterized by macronematous, mononematous, branched, or unbranched, and pale to dark brown conidiophores, monoblastic to polyblastic conidiogenous cells that are discrete on the terminal or intercalary of the stipe and globose to ellipsoidal, catenate or solitary, smooth or verruculose, and pale brown to brown conidia (Tanaka et al. 2015, Liu et al. 2017b). Several species have been reported as sexual morphs, characterized by scattered or grouped, globose ascomata with a central ostiole, hyaline periphyses, 8-spored asci, and broadly fusiform, 1-septate, hyaline, and smooth ascospores with an entire sheath (Hongsan et al.

2020b). *Periconia* species are widely distributed and mainly occur as saprobes and endophytes on various hosts, with a few being plant and human pathogens (Ellis 1971, 1976, Markovskaja & Kačergius 2014, Liu et al. 2017b, Hongsanan et al. 2020b, Yu et al. 2024). For example, *P. circinata* was reported as a pathogen causing blackening and rotting of wheat roots and stem bases (Goga 2000), while *P. keratitis* is a human pathogen causing mycotic keratitis in India (Sarkar et al. 2019).

There are 230 records of *Periconia* listed in the Index Fungorum of which 30 have been transferred to other genera (<http://www.indexfungorum.org>, accessed 28 November 2024). However, most species have been accepted in the genus based on morphological characters; only 46 species are correlated with molecular data, with most species only having ITS and LSU sequence data, which are insufficient to separate them at the species level (Yang et al. 2022). Hence, more phylogenetic markers are required to better understand the species boundaries in this highly diverse genus. In this study, a new species *P. dicranopterisis* is introduced based on morphological and multi-locus phylogenetic analyses.

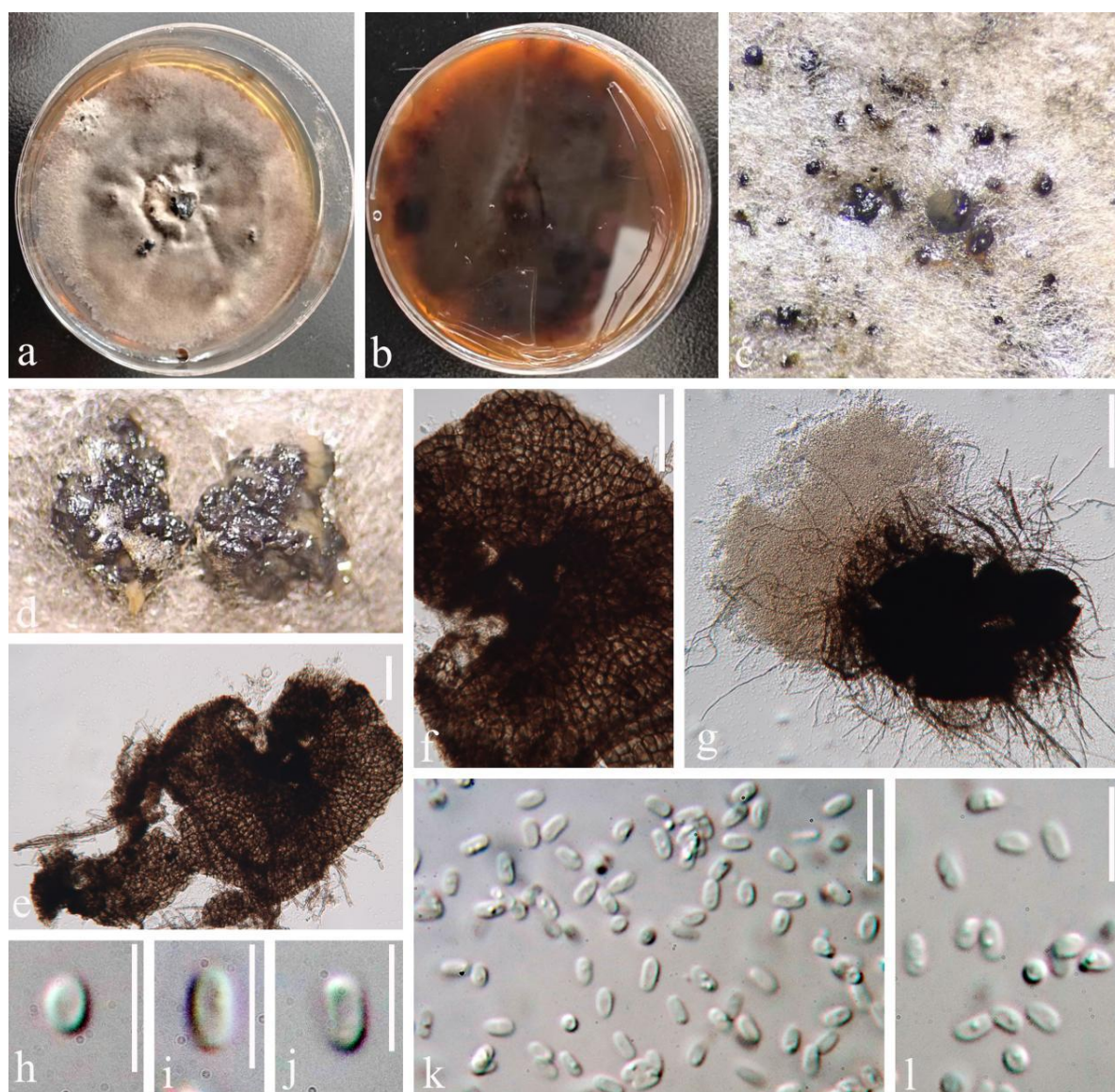


Figure 12 – *Paraboeremia litseae* (GZAAS 25–0530, new host record). a, b Culture on PDA from above and below. c, d Conidiomata on MEA. e, f Conidiomatal wall. g Conidiomata. h–l Conidia. Scale bars: e, f = 50 μ m, g = 100 μ m, h–j, l = 5 μ m, k = 10 μ m.

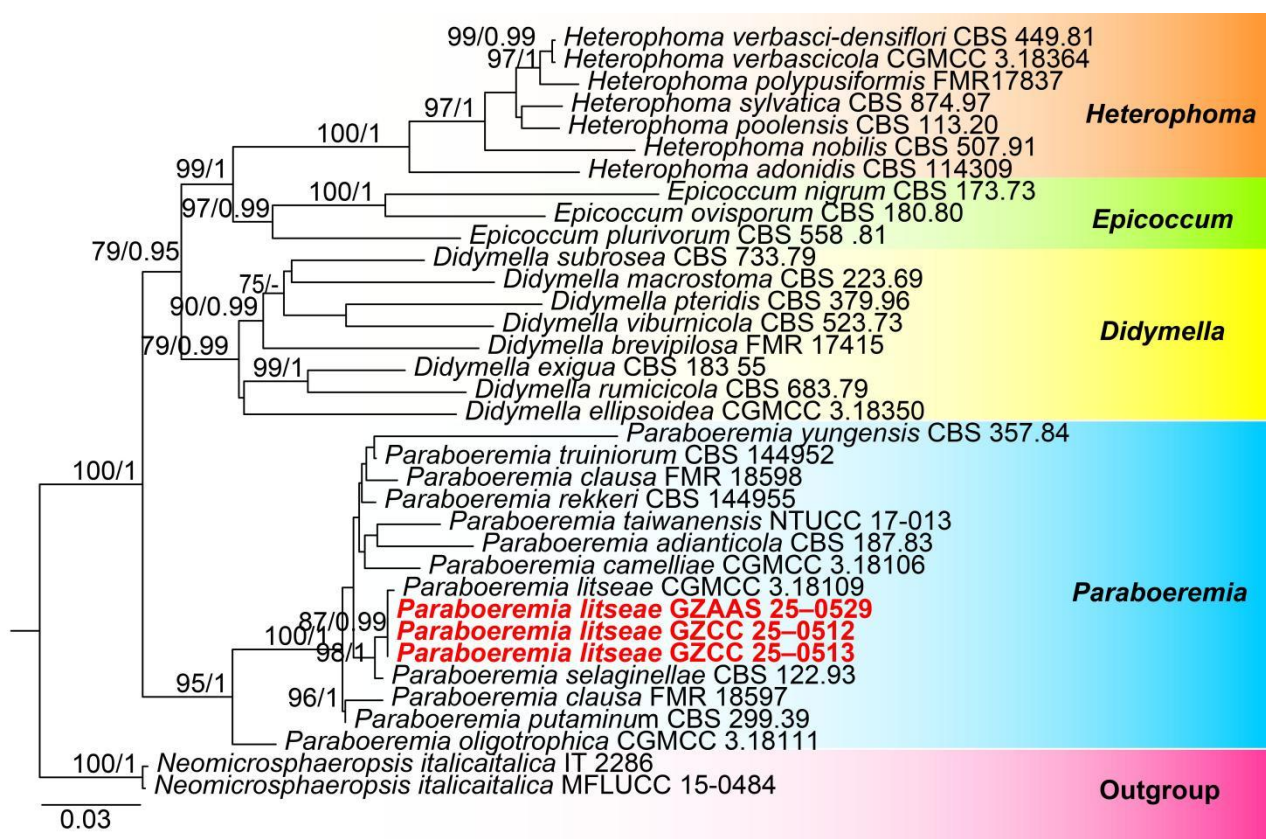


Figure 13 – Phylogram generated from maximum likelihood analysis based on combined ITS, *rpb2*, and *tub2* sequence data. 35 taxa were included in the combined analyses, which comprised 1414 characters after alignment. The best scoring RAxML tree with a final likelihood value of -8294.983988 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Neomicrosphaeropsis italicaitalica* (MFLUCC 15-0484 and IT 2286), the newly obtained strains are in red and bold.

Periconia dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & J.C. Kang, sp. nov.

Fig. 14

Index Fungorum: IF 903958; Facesoffungi number: FoF 17854.

Etymology – the specific epithet *dicranopteridis* refers to *Dicranopteris*, the fern genus from which the type strain was isolated.

Holotypes – KUN-HKAS 129916

Endophytic in the roots of *Dicranopteris pedata*. Sexual morph: undetermined. Asexual morph: *Mycelium* 1.5–6 µm wide, hyaline to pale brown, branched, septate, smooth, thick-walled. *Conidiophores* reduced to conidiogenous cells, cylindrical, brown, aseptate or septate, thick-walled. *Conidiogenous cells* monoblastic to polyblastic, discrete or integrated, determinate, or inconspicuous, cylindrical, brown. *Conidia* 8–11 µm diam ($\bar{x}$ = 9 µm, n = 30), solitary or in short chains, globose, brown to dark brown, aseptate, smooth to verrucose, sometimes with short spines, thick-walled, guttulate.

Culture characteristics – Colonies on MEA reaching 25 mm diameter after seven days at 25°C, irregular, medium dense, flattened, dull, dry, velvety appearance, white hyphal, with pink pigmented at the surface, reverse dark pink at the middle, paler towards the edge.

Material examined – China, Guizhou Province, Sanhe Town, Sandu Shui Autonomous County, Qiannan Buyi, and Miao Autonomous Prefecture, from the roots of *Dicranopteris pedata*, 11 April 2022, J.Y. Zhang, NS364–3 (KUN-HKAS 129916, holotype).

GenBank numbers – ITS: PV138731, LSU: PV138587, SSU: PV138560, *tef1*- α : PV177119

Notes: Our phylogenetic analysis showed that *P. dicranopteridis* clustered as a sister taxon to *P. prolifica* (Fig. 15). However, *P. dicranopteridis* can be easily distinguished from *P. prolifica* in having guttulate, verrucose conidia with spines. In contrast, conidia of *P. prolifica* are smooth-walled. Only ITS sequence data is available for *P. prolifica*, and the pairwise nucleotide comparisons showed that *P. dicranopteridis* (KUN-HKAS 129916) is significantly different from *P. prolifica* (MFLUCC 21–0155) in 26/508 bp (4.5%) of the ITS. In addition, the PHI test revealed no significant recombination event between our strain and the closely related taxa ($\Phi_w = 1$) (Fig. 16). Thus, we introduce *P. dicranopteridis* as a new species based on phylogeny and morphology.

The morphology of *P. dicranopteridis* matches the generic concept of *Periconia* in having holoblastic, monoblastic, or polyblastic conidiogenous cells and catenate or solitary, brown, spherical to sub-spherical, and aseptate conidia. However, most *Periconia* species have macronematous conidiophores, while conidiophores of *P. dicranopteridis* are micronematous and mostly reduced to conidiogenous cells. Yang et al. (2022) found that *Periconia* species sporulated in cultures resulted in micronematous conidiophores, as opposed to macronematous conidiophores in natural substrates. Our study is consistent with Yang et al. (2022); the new species is an endophyte that sporulates in culture and lacks conspicuous conidiophores. This suggests that the morphology of the same species on natural substrates may differ from the sporulates in culture.

***Phaeosphaeriaceae* M.E. Barr**

Phaeosphaeriaceae is a highly diverse family comprising 87 genera within *Dothideomycetes* (Hyde et al. 2024). The family was introduced by Barr (1979) with *Phaeosphaeria* as the type genus, which originally comprised 15 genera. Phookamsak et al. (2014) revised this family, accepting 28 genera based on generic type studies, representative specimens, and multi-gene phylogenetic analyses. Since then, many new genera have been consequently introduced to this family; up to now, 87 genera are included in this family (Wijayawardene et al. 2022, Wanasinghe & Maharachchikumbura 2023, Hyde et al. 2024).

***Stagonospora* (Sacc.) Sacc.**

Stagonospora is a species-rich genus with more than 500 entries listed in Index Fungorum (Index Fungorum 2024). However, only about 220 species are currently accepted in *Stagonospora* (Wijayawardene et al. 2022, Bhagya et al. 2024). The genus is characterized by erumpent, globose, brown ascomata with a minute ostiole, bitunicate, clavate asci, and ellipsoidal, 1-septate, ascospores with guttules in each cell (Quaedvlieg et al. 2013); immersed, globose to subglobose pycnidia with a single ostiole, conidiophores are reduced to conidiogenous cells with percurrent proliferations and holoblastic conidiogenesis, hyaline, cylindrical to ellipsoidal conidia with minute guttules (Brahmanage et al. 2020). Members of this genus are cosmopolitan, and exhibit diverse lifestyles as saprobes, endophytes, and pathogens of economically important plants with a worldwide distribution (Kobayashi et al. 2005, Quaedvlieg et al. 2013, Thambugala et al. 2017, Bhagya et al. 2024). In this study, five strains were isolated from *Dicranopteris*, and the five strains were identified as *S. tainanensis* based on phylogenetic analysis. This is the first species of *Stagonospora* reported from *Dicranopteris*. In addition, our phylogenetic analysis showed that *Stagonospora* is polyphyletic, and *S. pseudopaludosa* is clustered out of the genus, which is consistent with Bhagya et al. (2024).

Therefore, further studies are needed to clarify the accurate placement of this species.

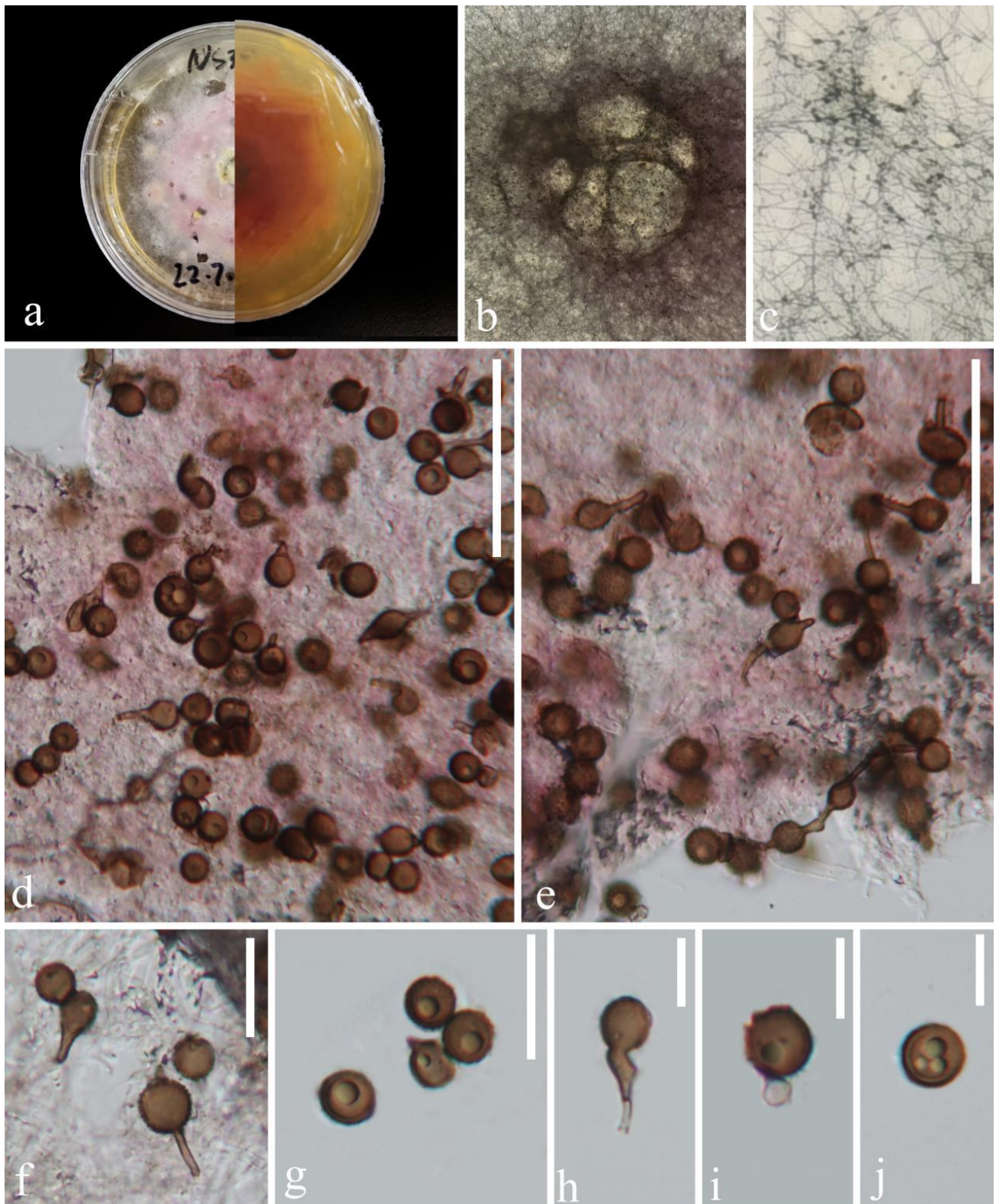


Figure 14 – *Periconia dicranopteridis* (KUN-HKAS 129916, holotype). a Culture on PDA obverse and reverse. b, c Colonies on PDA. d–j Conidiogenous cells and conidia. Scale bar: d, e = 50 µm, f, g = 20 µm, h–j = 10µm.

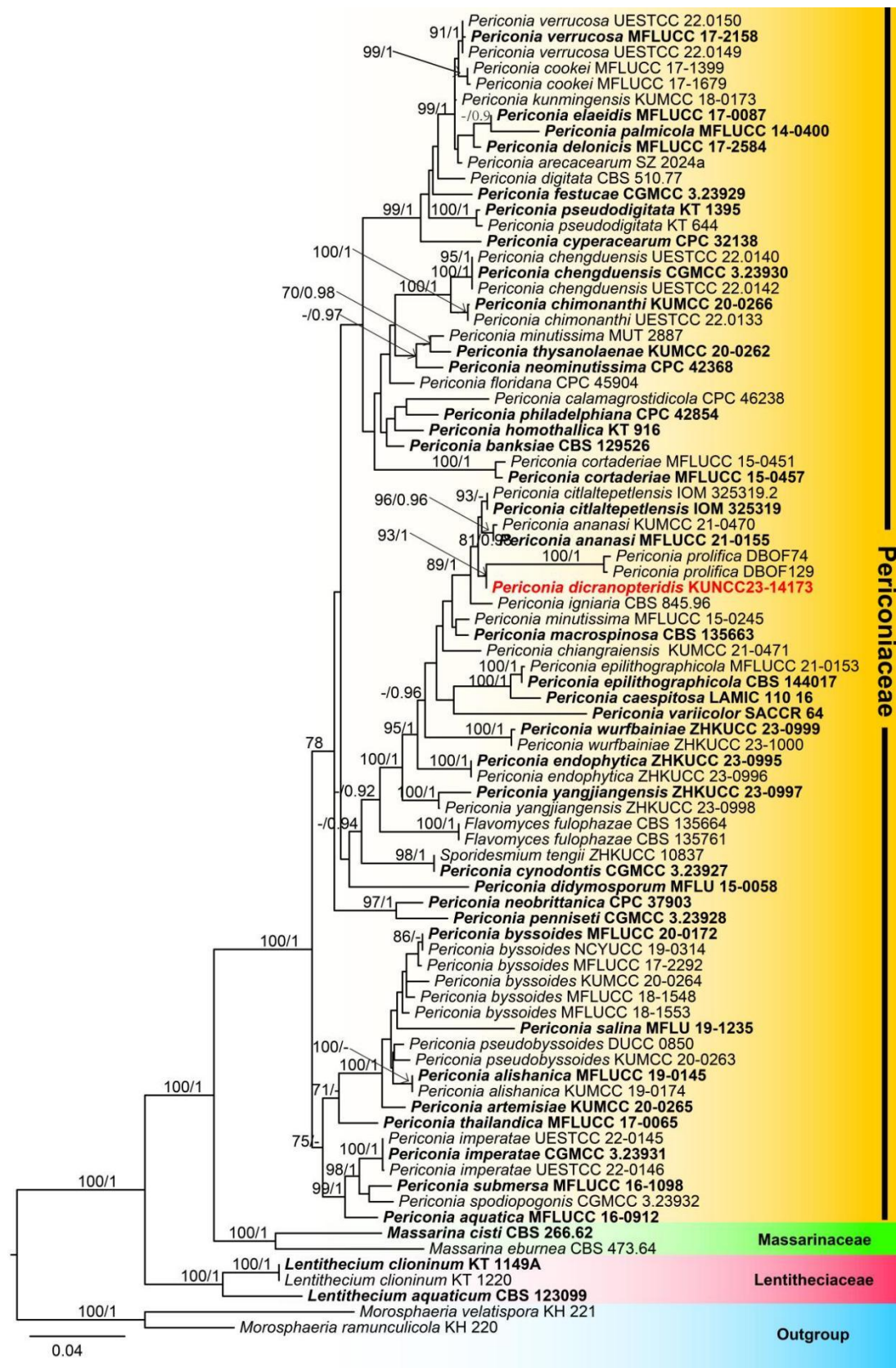


Figure 15 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, and *tef1-α* sequence data. 84 taxa were included in the combined analyses, which comprised 3400 characters after alignment. The best scoring RAXML tree with a final likelihood value of -8294.983988 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater

than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Morosphaeria ramunculicola* (KH 220) and *M. velatispora* (KH 221); the newly obtained strain is in red and the type strains are in bold.

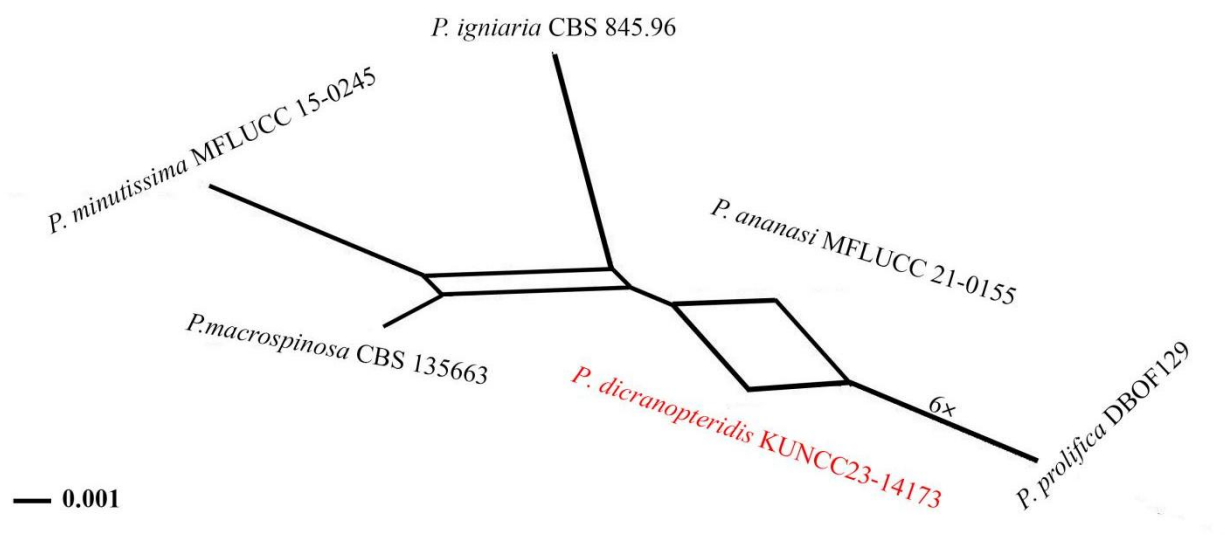


Figure 16 – Results of the PHI test of *Periconia dicranopteridis* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φ_w) < 0.05 indicate significant recombination within the dataset.

Stagonospora tainanensis W.H. Hsieh, Mycologia 71(5): 893 (1979)

Fig. 17

Index Fungorum: IF 324010; Facesoffungi number: FoF 17855.

See description in Bensch et al. (2010)

Culture characteristics: Colonies on PDA occupied the whole plate after 20 days at 25 °C, colonies circular, margin wavy, flat, velvety appearance with cream to greyish aerial mycelia in the middle, colony from above: greyish brown; reverse: dark brown centre and brown margin.

Material examined: China, Guizhou Province, Songtao County, Tongren City, from the roots of *D. pedata*, 21 February 2022, J.Y. Zhang, (NS285–5 = GZAAS 25–0522), living culture (GZCC 25–0516); Zhengfeng County, Southwest Guizhou Buyi and Miao Autonomous County, from the rhizome of *D. ampla*, 17 March 2022, J.Y. Zhang, (137–3 = GZAAS 25–0505); Chengheng County, Qianxinan Buyi and Miao Autonomous Prefecture, from a stem of *D. pedata*, 16 March 2022, J.Y. Zhang, (NS182–3 = GZAAS 25–0511). *ibdb* (NS 253–3 = GZAAS 25–0531); from a stem of *D. ampla*, 16 March 2022, J.Y. Zhang, (NS311–3 = GZAAS 25–0533).

GenBank numbers – GZAAS 25–0505: ITS: PV138739, LSU: PV138598, SSU: PV138561. GZAAS 25–0511: ITS: PV138740, LSU: PV138597, SSU: PV138562. GZAAS 25–0531: ITS: PV138741, LSU: PV138596. GZAAS 25–0522: PV138742, LSU: PV138595, SSU: PV138563. GZAAS 25–0533: ITS: PV138743, LSU: PV138594, SSU: PV138564.

Notes – Based on the combined ITS, LSU, and SSU phylogeny, our new isolates grouped together sister to *Stagonospora tainanensis* (KT 1866 and ATCC 38204) with 100% ML, 99% MP, and 1 BYPP support (Fig. 18). We were unable to observe the asexual or sexual morph characters in the culture. There were only 7bp, 1, and 0 bp differences in ITS, LSU, and SSU, respectively, between

our new strains and *Stagonospora tainanensis* (KT 1866), which does not significantly support our new strains to be a new species. Thus, based on phylogenetic analysis, we identified our new strains as *S. tainanensis*.

Stagonospora tainanensis is a significant pathogen infecting sugarcane, and causes a disease known as sugarcane leaf blight, which causes high cane yield and sugar losses in susceptible cultivars (Xu et al. 2022, Wang et al. 2021, Huang et al. 2023). In this study, we isolated *S. tainanensis* from *Dicranopteris pedata* as an endophyte and it is reported as a new host record.

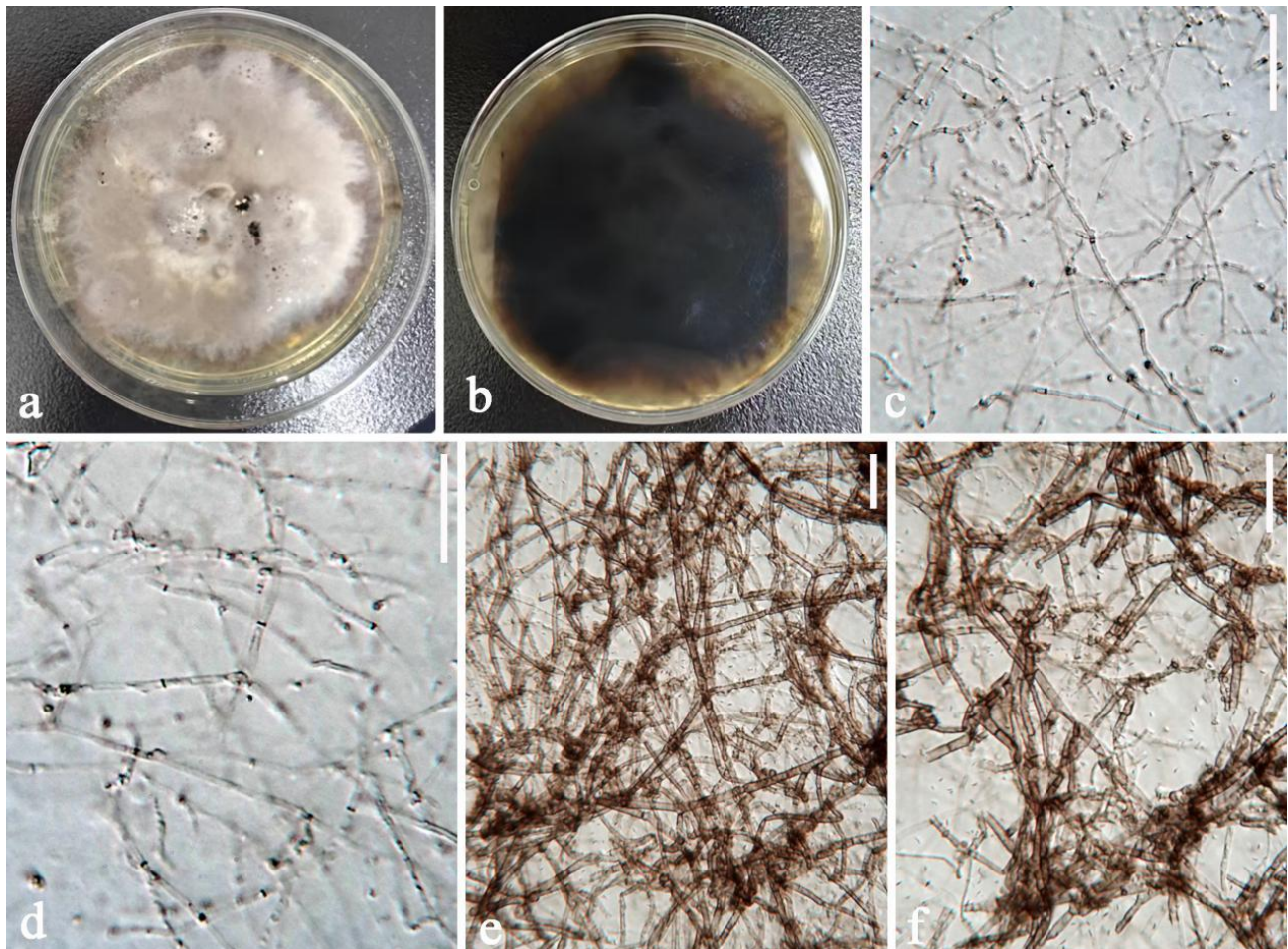


Figure 17 – *Stagonospora tainanensis* (GZAAS 25–0522, new host record). a, b Cultures on WA from above and below. c–f hyphae. Scale bars: c = 30 μm , d–f = 20 μm .

***Pleosporaceae* Nitschke**

Pleosporaceae is the largest family in *Pleosporales* (Wijayawardene et al. 2014, Ariyawansa et al. 2015). *Pleosporaceae* species occur worldwide as endophytes and saprobes on various plants or opportunistic human and plant pathogens (Ariyawansa et al. 2015, Hongsanan et al. 2020b). The classification of this family has been a major challenge due to the lack of molecular data and reference strains (Ariyawansa et al. 2015). Hyde et al. (2013) accepted 23 genera in this family based on morphology and molecular data. Ariyawansa et al. (2015) provided a backbone tree for *Pleosporaceae* and accepted 18 genera. To date, the family includes 28 genera (Hyde et al. 2024).

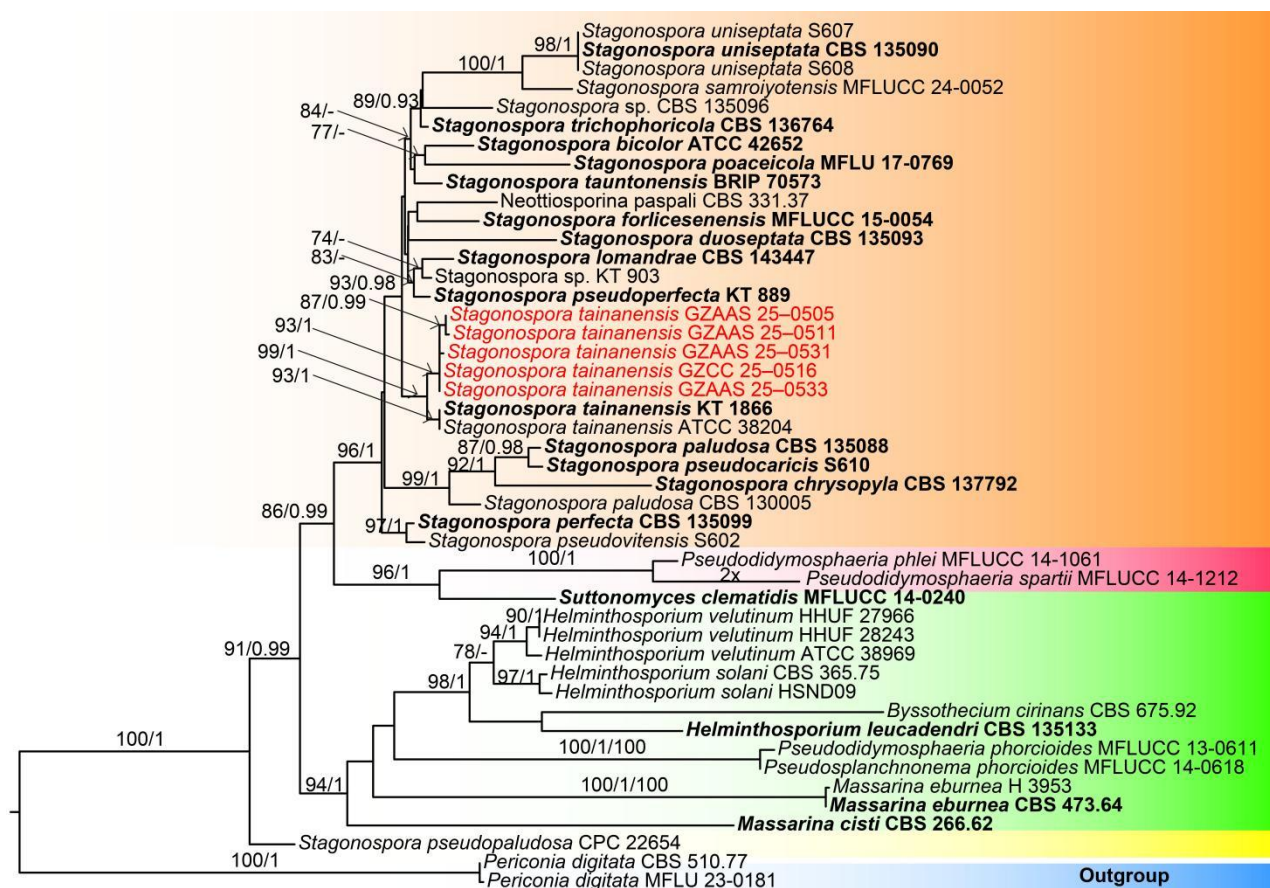


Figure 18 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and SSU sequence data. 46 taxa were included in the combined analyses, which comprised 2426 characters after alignment. The best scoring RAxML tree with a final likelihood value of -9635.061423 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Periconia digitata* (MFLU 23-0181 and CBS 510.77). The newly obtained strains are in red and the type strains are in bold.

Alternaria Nees

Alternaria is a species-rich dematiaceous hyphomycete genus, with over 800 species epithets (Index Fungorum 2024); however, only about 417 species are accepted in the genus (Li et al. 2022, 2023). *Alternaria* species are ubiquitous and exist in a variety of ecological niches, including endophytes on asymptomatic plant tissues, saprobes on diverse hosts and substrates, and pathogens of plants and animals, worldwide (Thomma 2003, Woudenberg et al. 2013, 2015, Gannibal & Lawrence 2016, Li et al. 2022, 2023). The genus is characterized by mononematous, macro- or micronematous, unbranched or branched conidiophores, mono- to polytretic, integrated to discrete, conidiogenous cells, solitary or catenate, phragmo- or dictyoseptate, straight or curved, medium brown to dark brown, smooth or verrucose, conidia with rounded or narrowly-beaked tips (Li et al. 2022, 2023). *Alternaria* species delimitation has long been disputed and challenging; multi-locus phylogeny has considerably improved species delimitation in the genus and allows for a better resolution of this group (Woudenberg et al. 2013, 2015, Gannibal & Lawrence 2016, Ghafri et al. 2019, Li et al. 2023). Lately, Li et al. (2023) updated the species limits, evolution, multi-locus phylogeny, and classification of *Alternaria*; currently, 29 sections have been identified in the genus.

Alternaria longipes (Ellis & Everh.) E.W. Mason, Mycological Papers 2: 19 (1928)

Fig. 19

Index Fungorum: IF 269712; Facesoffungi number: FoF 14360.

Endophytic in fresh leaves of *Dicranopteris pedata*. Sexual morph: undetermined. Asexual morph: *Mycelium* hyaline to brown, branched, septate, smooth, thick-walled. *Conidiophores* 25–85 × 3–4 µm ($\bar{x}$ = 49.5 × 3.5 µm, n = 10), macronematous, mononematous, straight, or flexuous, cylindrical, brown to dark brown, septate, branched, smooth, thick-walled. *Conidiogenous cells* 4–12 × 2.5–4.5 µm ($\bar{x}$ = 6 × 3.5 µm, n = 20), mono- to polytretic, integrated, terminal, cylindrical, brown, smooth, with a distinct apical conidiogenous loci. *Conidia* 16–27 × 8–14 µm ($\bar{x}$ = 20.5 × 11.5 µm, n = 30), acrogenous, catenate, formed in acropetal chains, subglobose, ovoid to obpyriform, beakless, brown to dark brown, 1–4 transversely euseptate, with 1–2 longitudinal or oblique septa in some transverse divisions, smooth, formed apically secondary conidiophores with 1–2 conidiogenous loci.

Culture characteristics – *Colonies* on PDA circular, with flat surface, edge entire, superficial and partially immersed, reaching 50 mm diameter. in 10 days at 26 °C, dark brown, and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi and Miao Autonomous Prefecture, Zhenfeng County, isolated from the leaves of *Dicranopteris pedata*, 17 March 2022, J.Y. Zhang, (NS189–1 = KUN-HKAS 129888).

GenBank numbers – ITS: PV138679, LSU: PV138576, SSU: PV138557, *tef1-α*: PV177090, *rpb2*: PV188064

Notes – Mason (1928) introduced *Alternaria longipes*, a plant pathogen that causes leaf spots (Hou et al. 2016, Wang et al. 2020). In the phylogenetic analyses, our strain clustered with *A. longipes* as the same species (Fig. 20). In addition, our strain matches well with *A. longipes* in morphology (Ellis 1971). Based on morphology and phylogeny, we identify our strain as *A. longipes* and report it as a new host record in Thailand.

Amorosiaceae Thambug. & K.D. Hyde

Amorosiaceae was proposed for a hyphomycete genus *Amorosia* (type genus), along with a newly established genus *Angustimassarina*, by Thambugala et al. (2015) based on phylogenetic analysis and morphological characteristics. Five additional genera viz. *Alfoldia*, *Amorocoelophoma*, *Neoangustimassarina*, *Neothyrostroma* and *Podocarpomyces* were subsequently introduced to the family (Crous et al. 2019a, Jayasiri et al. 2019, Yu et al. 2022). Currently, six genera are included in *Amorosiaceae*, except *Amorocoelophoma* and *Angustimassarina*; all other genera are monotypic and comprise a single species.

Amorocoelophoma Jayasiri, E.B.G. Jones & K.D. Hyde

Amorocoelophoma was established to accommodate a coelomycetous fungus, *A. cassiae*, which was collected on fallen pods of *Cassia* sp. (*Fabaceae*) from Thailand (Jayasiri et al. 2019). Three species, viz. *A. camelliae*, *A. neoregeliae* and *A. sinensis* were subsequently added to the genus based on morphological characteristics and phylogenetic analyses. *Amorocoelophoma camelliae* was collected from leaves of *Camellia sinensis* (*Theaceae*) (Ariyawansa et al. 2020), *A. neoregeliae* from leaf spots of *Neoregelia* sp. (*Bromeliaceae*) (Crous et al. 2021a), while *A. sinensis* was isolated from soil (Zhang et al. 2024a). Only coelomycetous asexual morphs are known for *Amorocoelophoma*, which is characterized by pycnidial, solitary to gregarious, ovoid to globose, brown conidiomata, phialidic, doliiform, hyaline conidiogenous cells and hyaline, cylindrical, aseptate conidia (Jayasiri et al. 2019). Recent studies showed that *Amorocoelophoma* is polyphyletic. Yu et al. (2022) showed

that *A. cassiae* and *A. neoregeliae* clustered with *Alfoldia vorosii* and *Neothyrostroma cassiae* in a weakly supported clade, while *A. camelliae* formed a distinct lineage within the family. The phylogenetic analysis of Zhang et al. (2024a) obtained a similar result as Yu et al. (2022). Their result showed that *A. camelliae* clustered into a single clade and separated from *A. cassiae*, *A. neoregeliae*, and *A. sinensis*. Thus, the genus is polyphyletic and the placement of *A. camelliae* needs to be re-evaluated. In this study, we introduce a new endophytic species, *A. dicranopterisis* isolated from *Dicranopteris linearis*.

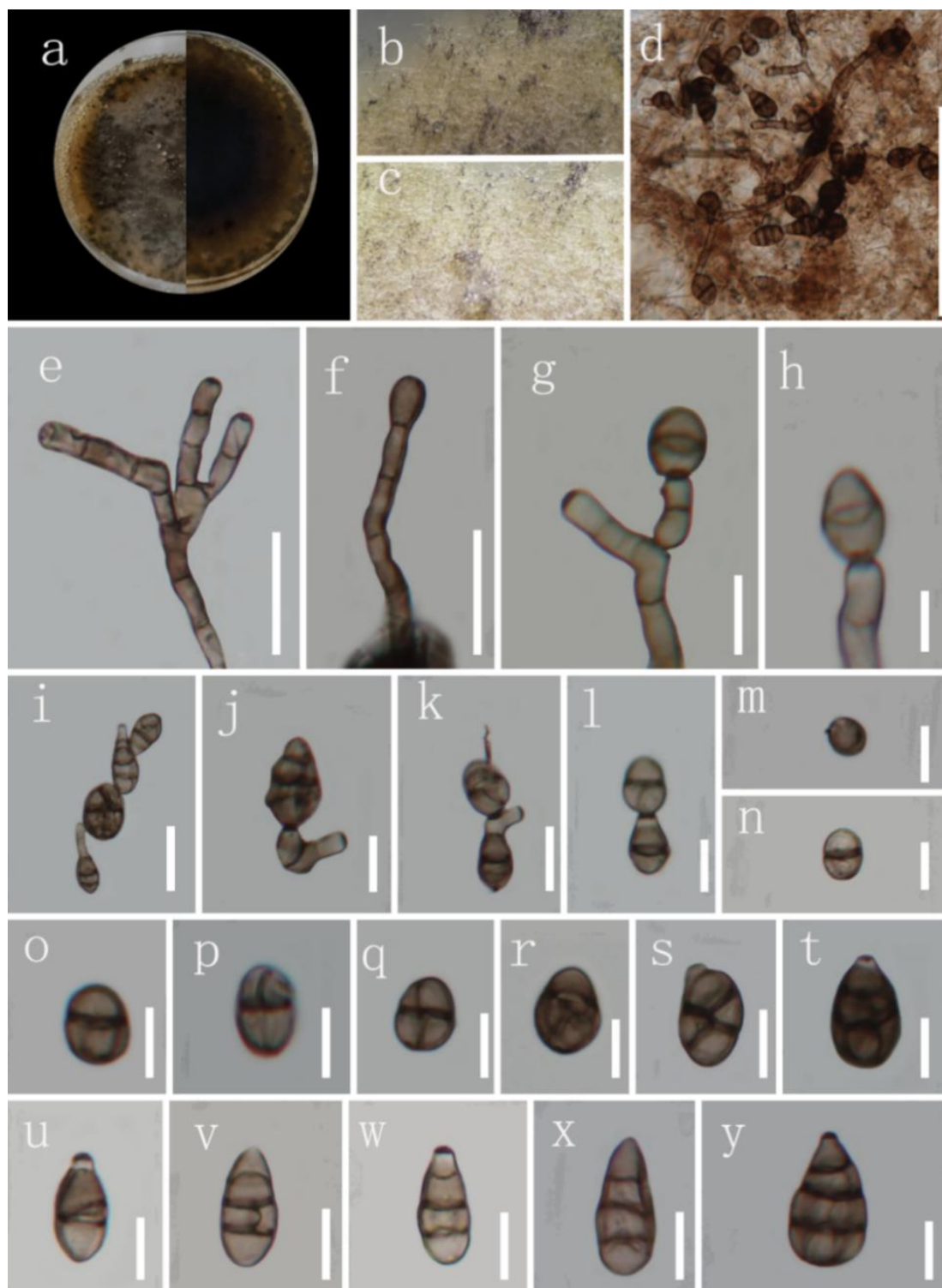


Figure 19 – *Alternaria longipes* (KUN-HKAS 129888, new host record). a, b Cultures on PDA. c Colonies on PDA. d–f Conidiophores. g, h Conidiogenous cells with conidia. i–y Conidia. Scale bars: d = 100 μ m, e–g, i = 20 μ m, j–y = 10 μ m, h = 5 μ m.

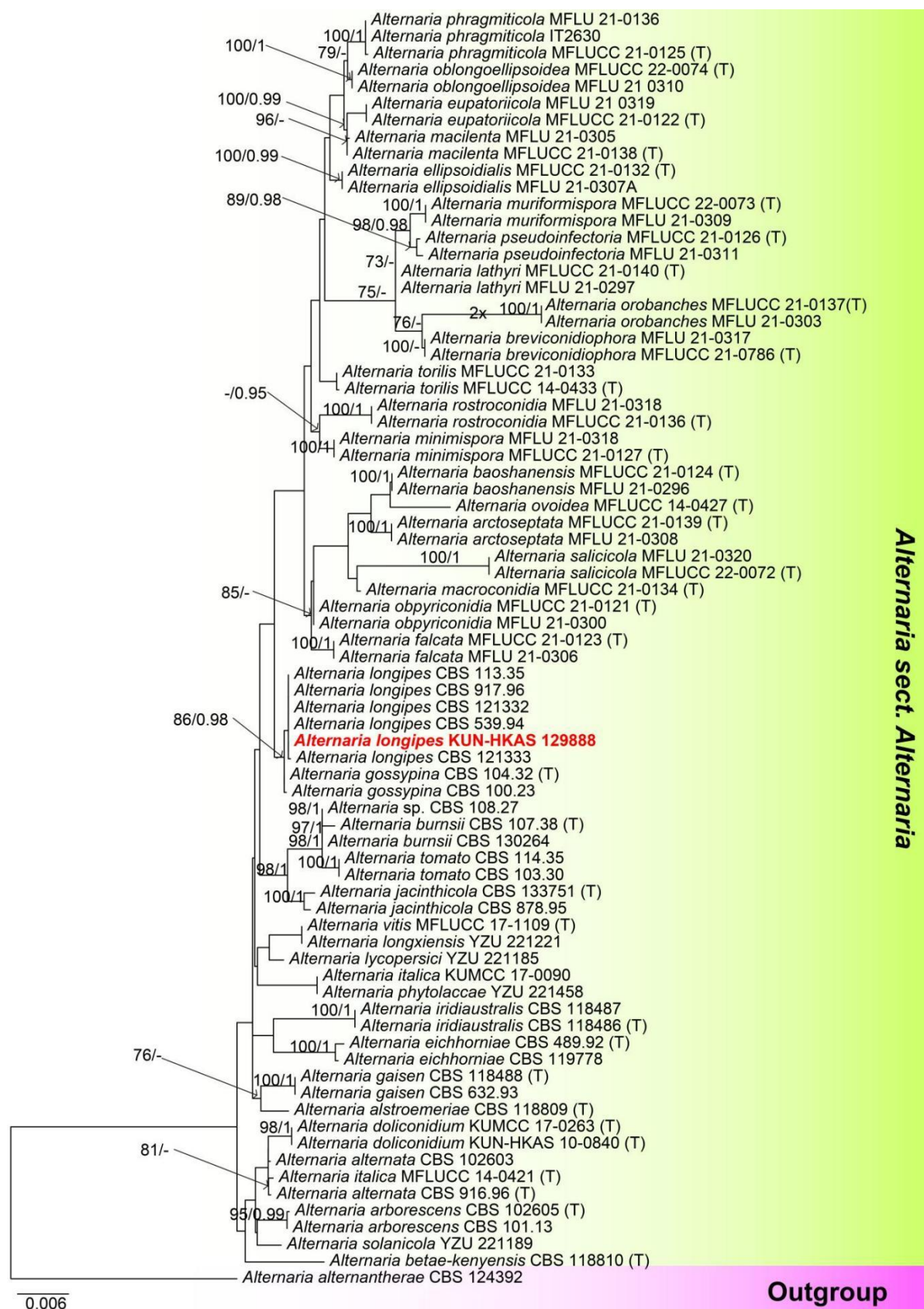


Figure 20 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *rpb2*, *gadph*, *tefl-α* and *alt-α* sequence data. 76 taxa were included in the combined analyses, which comprised 4317 characters after alignment. The best scoring RAxML tree with a final likelihood value of -11707.157540 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Alternaria alternantherae* (CBS 124392). The newly obtained strains are in red and bold.

Amorocoelophoma dicranopteridis J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov

Fig. 21

Index Fungorum: IF 903959; Facesoffungi number: FoF 17856.

Etymology – the specific epithet *dicranopteridis* refers to *Dicranopteris*, the fern genus from which the type strain was isolated.

Holotype – KUN-HKAS 129908

Endophytic in the root of *Dicranopteris linearis*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* dark brown to black, solitary to gregarious or confluent, stromatic, erumpent, globose, pycnidial, multilocular or unilocular. *Conidiomatal wall* composed two cell types; outer layers of *textura angularis* to *textura globosa* to with brown to dark brown cells, inner layers of *textura globosa* with pale brown to hyaline, cells. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells, hyaline, smooth. *Conidiogenous cells* 5–8 × 2–3 μm ($\bar{x}$ = 6.6 × 2.5 μm, n = 20), hyaline, phialidic, determinate, ampulliform to subcylindrical, or obovoid, smooth. *Conidia* 2.5–3.5 × 1–2 μm ($\bar{x}$ = 3.2 × 1.6 μm, n = 40), solitary, ellipsoid, subglobose to globose, hyaline, smooth-walled, guttulate.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the root of *Dicranopteris linearis*, 16 March 2022, J.Y. Zhang, (NS276–3 = KUN-HKAS 129908, holotype), ex-type living culture (KUNCC 23–14198).

Culture characteristics – Colonies on PDA medium reach 40–50 mm diameter. after 2 weeks at 25 °C, colonies circular, medium dense, flattened, dull, sponge-like areas in middle, from above, brown to dark brown, rough; from below pale brown at the margin, dark brown at the center.

GenBank numbers – ITS: PV138680, LSU: PV138577, SSU: PV138558, *rpb2*: PV188065

Notes – Our phylogenetic analysis showed that *Amorocoelophoma* is polyphyletic, which is consistent with Yu et al. (2022), and the new isolate (KUNCC 23–14198) formed a distinct clade sister to *A. neoregeliae* in *Amorosiaceae*, while *Amorocoelophoma camelliae* clustered out of *Amorocoelophoma*, sister to *Neothyrostroma encephalarti* (Fig. 22). Thus, the placement of this species needs to be clarified based on further phylogenetic and morphological analyses.

Our new isolate is similar to *A. neoregeliae* in having pycnidial, solitary to gregarious, ovoid to globose, brown conidiomata, hyaline, phialidic conidiogenous cells, and hyaline, aseptate conidia. However, it differs from *A. neoregeliae* in having ellipsoid, subglobose to globose, and smaller conidia (2.5–3.5 × 1–2 vs. (3–)3.5–4.5(–5) × (1.5–)2(–2.5) μm) (Crous et al. 2021a). In contrast, the conidia of *A. neoregeliae* are cylindrical. Based on morphology and phylogeny, we introduce a new species, *A. dicranopteridis*.

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde

Venturiales was introduced by Zhang et al. (2011), and it comprises two families, viz. *Sympoventuriaceae* and *Venturiaceae* (Shen et al. 2020, Hongsanan et al. 2020a, Wijayawardene et al. 2022). We followed the latest updated accounts of this order provided by Wijayawardene et al. (2022).

Sympoventuriaceae Y. Zhang et al., C.L. Schoch & K.D. Hyde

Sympoventuriaceae, a highly diverse family in *Venturiales* (*Dothideomycetes*, *Ascomycota*), was erected by Zhang et al. (2011) with *Sympoventuria* as the type genus. The classification of *Sympoventuriaceae* has long been controversial and the generic boundaries remain unresolved due to the lack of molecular data and a high level of morphological plasticity. Wei et al. (2022a) redefined the generic boundaries of *Sympoventuriaceae* and accepted 22 genera based on seven loci (SSU, ITS, LSU, *act*, *tub2*, *tefl-α* and *rpb2*) phylogenetic analysis and morphological characteristics. Members of this family are saprobes, endophytes, plant pathogens, and opportunistic pathogens in humans and animals (e.g., *Neofusicladium cameroonensis* and *Verruconis gallopava*) with a wide geographical distribution (Zhang et al. 2011, Seyedmousavi et al. 2013, Liu et al. 2017a, Wijayawardene et al. 2018, Wei et al. 2022a).

Verruconis Samerp., H.J. Choi, van den Ende, Horré & de Hoog

Verruconis, a well-studied genus, was introduced by Samerpitak et al. (2014) to accommodate *V. gallopava* and *V. verruculosa*, which were transferred from *Ochroconis* and *Scolecobasidium*, respectively. *Verruconis gallopava* was designated as the type. Since then, several new species have been introduced to the genus; currently, 15 species are accepted in the genus, and all of them have sequence data available in the GenBank (Qiao et al. 2019, Shen et al. 2020, Shao et al. 2022, Wei et al. 2022a).

Most *Verruconis* species are only known as the asexual morphs, characterized by micronematous, mononematous, septate conidiophores, holoblastic, determinate, conidiogenous cells and clavate to cylindrical, verrucose to smooth-walled conidia (Samerpitak et al. 2014, Shen et al. 2020, Shao et al. 2022). Only *Verruconis mangrovei* has been reported by the sexual morph, characterized by superficial to semi-immersed, clustered, or solitary, globose to subglobose, coriaceous, pale brown to dark brown, setae ascomata, bitunicate, broadly clavate, asci with an ocular chamber and dictyosporous, ellipsoidal to oblong, hyaline to pale brown ascospores (Hyde et al. 2020a). Species of *Verruconis* have been found in a variety of habitats, including soil, roots and leaves of plants, hot spring water, and decaying wood and industrial effluents (Qiao et al. 2019, Shen et al. 2020, Shao et al. 2022). While *V. gallopava* is a human and animal pathogen, which is the primary agent of human brain infections and causes encephalitis in poultry and wild birds, dogs, and cats (Geltner et al. 2015). This study introduces a novel endophytic species, *V. hyalinus* isolated from *Dicranopteris pedata* based on phylogeny and morphology.

Verruconis hyalina J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov.

Fig. 23

Index Fungorum: IF 903960; Facesoffungi number: FoF 17857.

Etymology – The name refers to its hyaline conidia

Holotype – KUN-HKAS 129902

Endophytic in the healthy rhizome of *Dicranopteris pedata*. Sexual morph: Undetermined. Asexual morph: *Mycelium* hyaline, branched, septate, 1–4 µm wide. *Conidiophores* arising from vegetative hyphae, micronematous, mononematous, solitary, cylindrical, hyaline, simple or branched, septate, slightly constricted at the septa, thin-walled. *Conidiogenous cells* 5–18 × 2–3.5 µm ($\bar{x}$ = 10 × 3 µm, n = 25), monoblastic, integrated, terminal, hyaline. *Conidia* 9–16.5 × 4.5–9.5 µm ($\bar{x}$ = 11.5 × 6 µm, n = 25), acrogenous, solitary, subglobose, ellipsoidal, obovoid, oblong, or irregular, hyaline, aseptate or 1–3-septate, strongly constricted at the septa, smooth.

Culture characteristics – Colonies on MEA medium under natural light, reaching 18 mm

diameter in 20 days at 26 °C, circular with entire margin, umbonate with a knobby protuberance in the center, cottony to fluffy, without veined and wrinkle, taupe with pale edge from above; black or dark brown in reverse side, and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi, and Miao Autonomous Prefecture, Chengheng County, isolated from the healthy rhizome of *D. pedata*, 16 March 2022, J.Y. Zhang, (NS267–6 = KUN-HKAS 129902, holotype), ex-type living culture (KUNCC 23–14194).

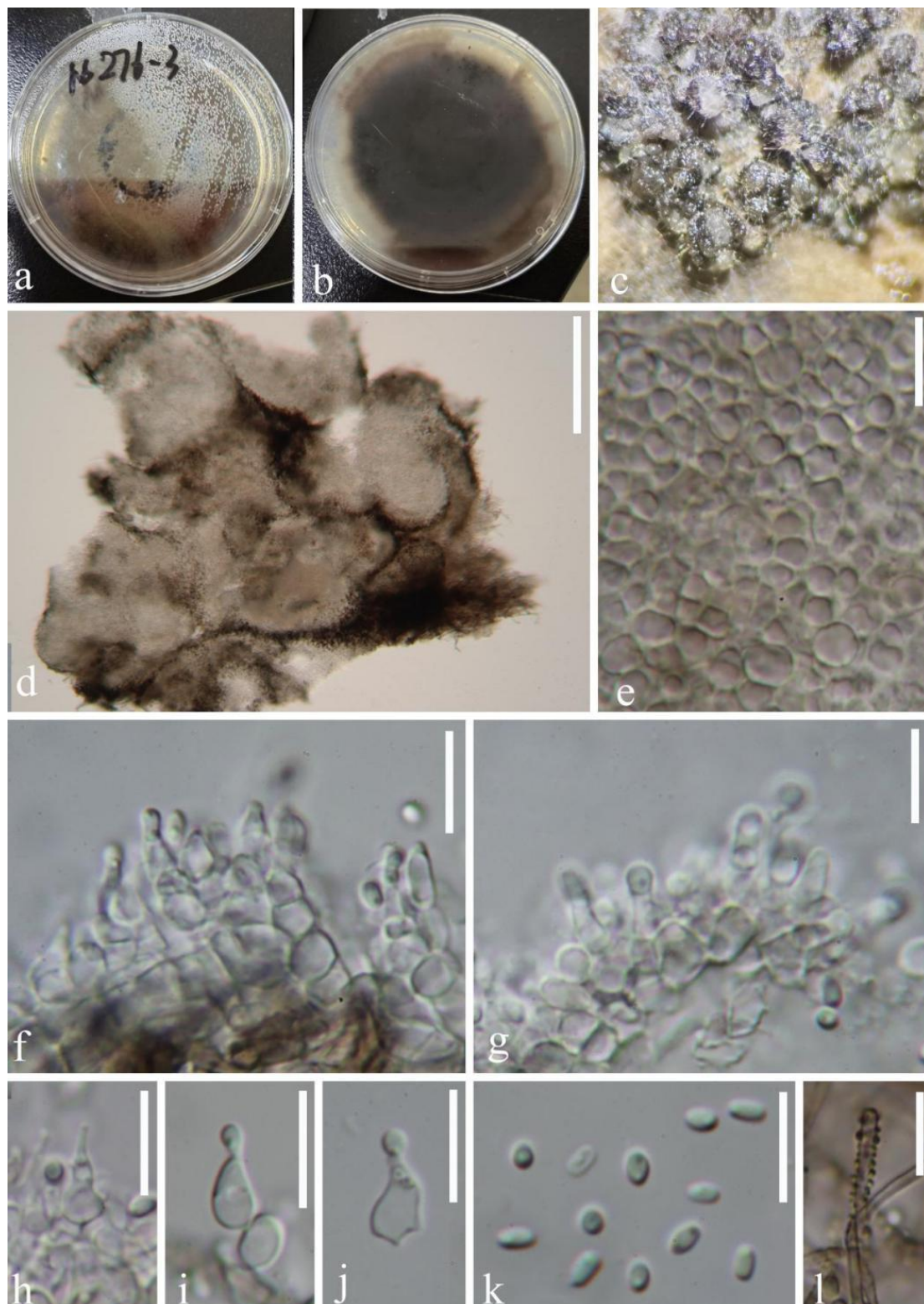


Figure 21 – *Amorocoelophoma dicranopteridis* (KUN-HKAS 129908, holotype). a, b Culture on PDA from above and below. c Colonies on PDA. d Section through conidiomata. e Peridium f–j Conidiogenous cells and Conidia. k Conidia. l Mycelium. Scale bar: d = 200 μ m, e–l = 10 μ m.

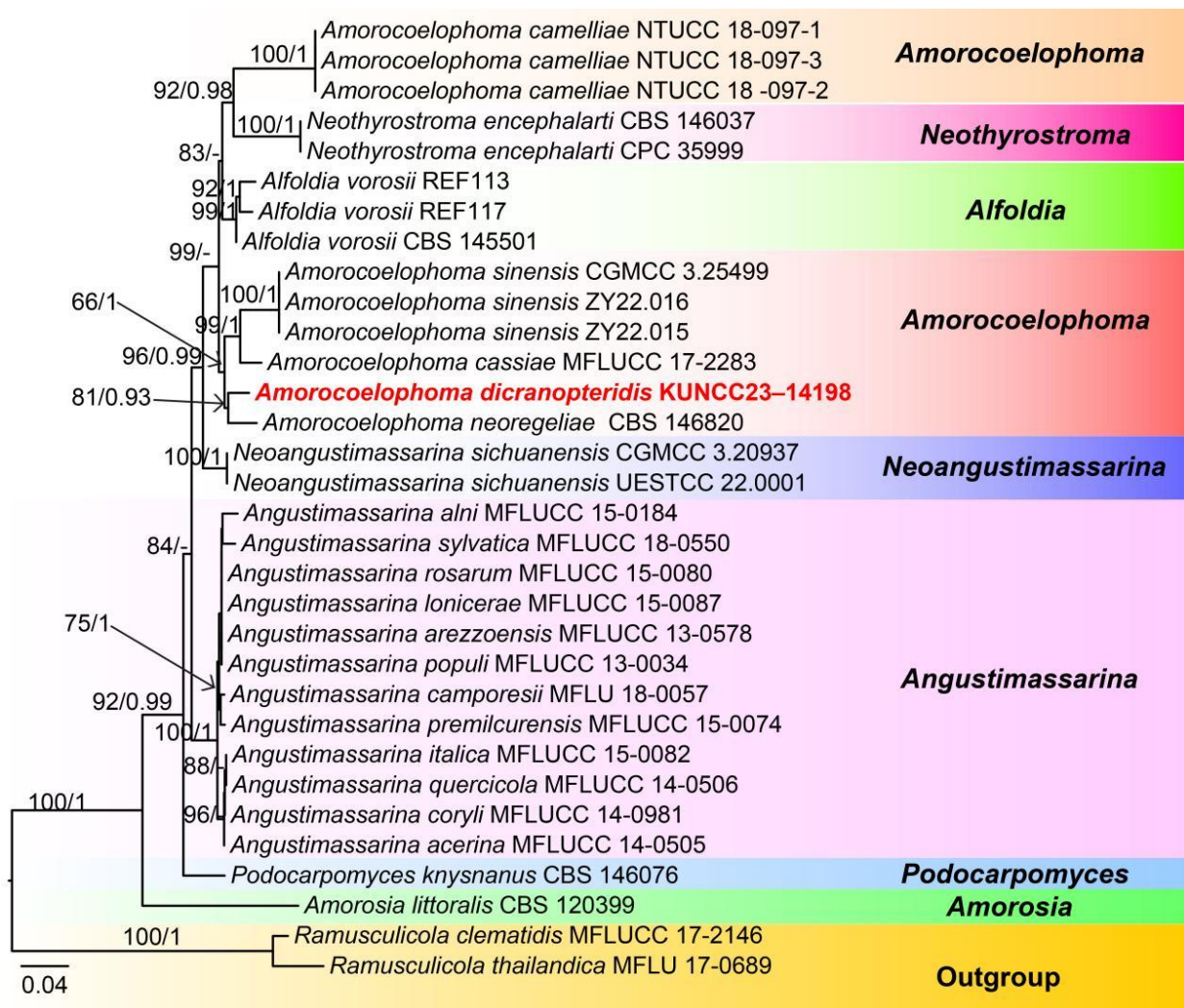


Figure 22 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *rpb2*, and *tef1- α* sequence data. A total of 32 taxa were included in the combined analyses, which comprised 4051 characters after alignment. The best scoring RAxML tree with a final likelihood value of -13214.885791 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Ramusculicola clematidis* (MFLUCC 17–2146) and *R. thailandica* (MFLU 17–0689); the newly obtained strains are in red and bold.

GenBank numbers – ITS: PV138744, LSU: PV138599

Notes – Phylogenetic analysis showed that our new collection shares a sister relationship with *V. mangrovei* with 100% ML/1.00 PP support (Fig. 24). *Verruconis mangrovei* is the only sexual species in *Verruconis*, which was introduced by Hyde et al. (2020), and it is a saprobe found on dead mangrove wood from marine habitats. Our collection is an endophyte isolated from *Dicranopteris*

pedata and only an asexual morph was reported for this species; thus, we were unable to compare the morphology of our new collection and *V. mangrovei*, but phylogenetically, they are distinct. Comparisons of the ITS and LSU sequences of our new collection and the ex-type of *V. mangrovei* revealed 99bp and 58bp differences, respectively, which strongly support our new collection as a new species. In addition, our collection is distinct from other asexual *Verruconis* species by its hyaline, smooth-walled conidia and diverse conidial shapes. Thus, *V. hyalina* is introduced as a new species.

In this study, we found significant differences in the ITS and LSU regions between our new species and the closely related *V. mangrovei*. However, despite these differences, our new species clusters within the same genus. This raises questions about the standardization of evaluating new species solely based on nucleotide variations within the genus.



Figure 23 – *Verruconis hyalina* (KUN-HKAS 129902, holotype). a, b Cultures on MEA from above

and below. c Colonies on MEA. c Colonies on MEA. d–k Conidiophores, conidiogenous cells, and conidia. l–s Conidia. Scale bars: d–g = 20 μ m, h–s = 10 μ m.

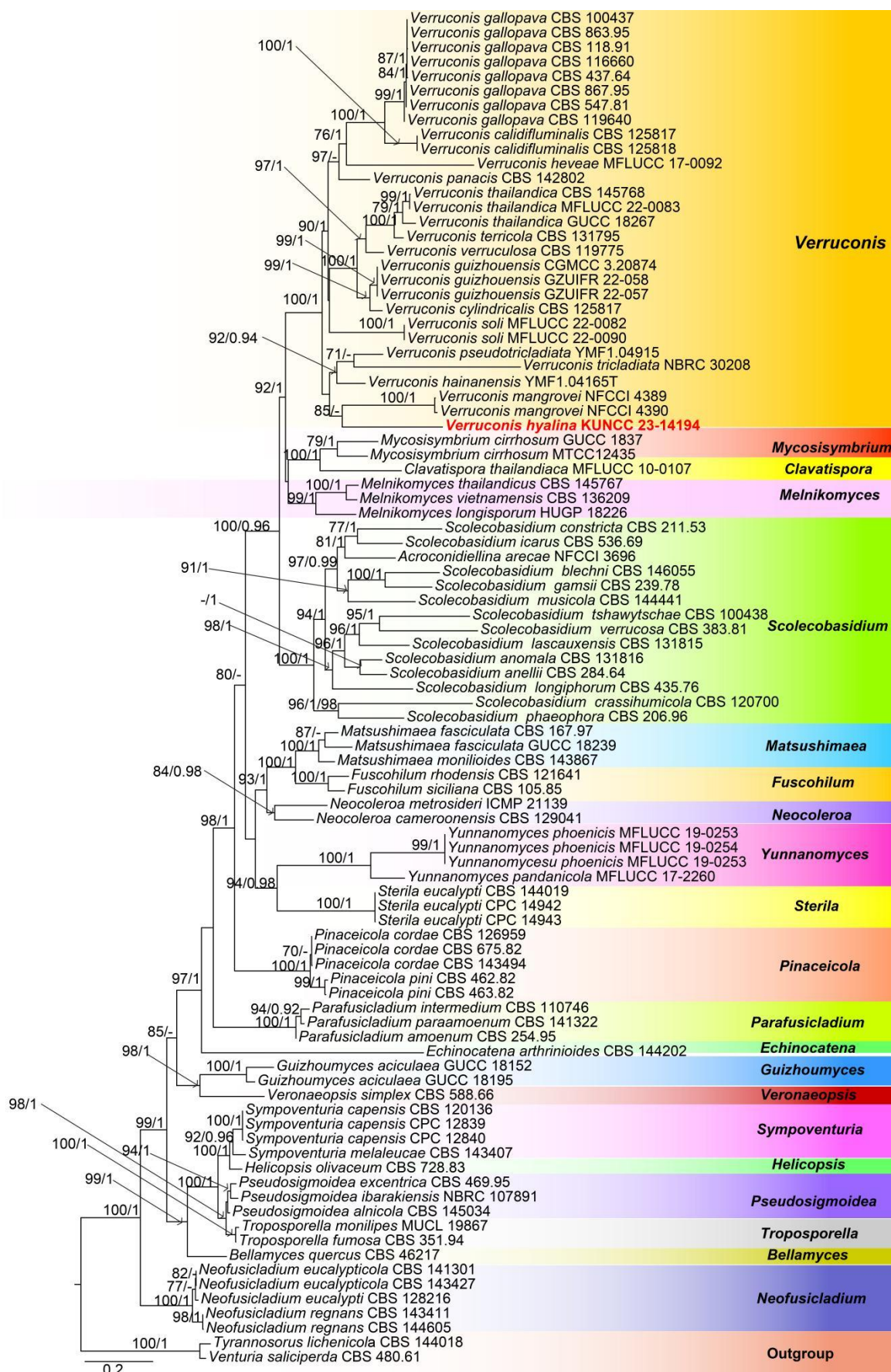


Figure 24 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. A total of 93 taxa were included in the combined analyses, which comprised 1514 characters after alignment. The best scoring RAxML tree with a final likelihood value of -44337.473498 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Tyrannosorus lichenicola* (CBS 144018) and *Venturia saliciperda* (CBS 480.61), the newly obtained strain is in red and bold.

Eurotiomycetes O.E. Erikss. & Winka

Chaetothyriales M.E. Barr

Barr (1987) introduced *Chaetothyriales*. Tian et al. (2021) provided phylogenetic analysis and morphological reappraisal of *Chaetothyriales* and accepted ten families: *Chaetothyriaceae*, *Coccodiniaceae*, *Cyphellophoraceae*, *Epibryaceae*, *Herpotrichiellaceae*, *Lyrommataceae*, *Microtheliopsidaceae*, *Paracladophialophoraceae*, *Pyrenotrichaceae* and *Trichomeriaceae*, with 55 genera.

Herpotrichiellaceae Munk

Herpotrichiellaceae was established by Munk (1953) and placed in *Chaetothyriales* (*Eurotiomycetes*), with *Herpotrichiella* as the type genus. *Herpotrichiellaceae* species are distributed all over the world and can be found in a wide range of environments, such as air, insects, plants, rocks, and soil (Feng et al. 2014, Sun et al. 2020, Tian et al. 2021, Thitla et al. 2023). *Herpotrichiellaceae* is characterized by setose, ostiolate ascomata, bitunicate asci with a thickened endotunica and greenish-grey to brown, 1-multi transversely septate ascospores, rarely with longitudinal septa (Munk 1953, Untereiner et al. 1995, Tian et al. 2021). The asexual morph of *Herpotrichiellaceae* is dematiaceous hyphomycetes, commonly referred to as black yeast, including *Capronia*, cladophialaphora-like species, *Exophiala*, *Fonsecaea*, and *Philaphora*. (Gueidan et al. 2014). Currently, 20 genera are accepted in the family (Tian et al. 2021, Thitla et al. 2023).

Cladophialophora Borelli

Cladophialophora is an asexual genus of simple hyphomycetes, characterized by branched or unbranched chains of conidia with hyaline conidial scars produced through blastic conidiogenesis (Sutton et al. 2009, Obase et al. 2016, Chang et al. 2023). *Cladophialophora* species are regularly reported as human pathogens, causing a range of illnesses from moderate cutaneous lesions to deadly encephalitis (Badali et al. 2009, 2010). Some are also endophytes, plant or human pathogens (de Hoog et al. 2007, Crous et al. 2007b, Obase et al. 2016), lichenicolous fungi (Diederich et al. 2013, Chang et al. 2023) and rock-inhabiting fungi (Fu et al. 2023). Currently, over 45 species are accepted in the genus with diverse ecological habitats from various substrates, such as plants, soil, rock, sports drinks, humans, and lichens (Badali et al. 2008, Obase et al. 2016, Tang et al. 2017, Chang et al. 2023, Fu et al. 2023). This study introduces a novel endophytic species, *C. globosa* based on phylogenetic analysis and morphological characteristics.

Cladophialophora globosa J.Y. Zhang, D.F. Bao, & J.C. Kang, sp. nov.

Fig. 25

Index Fungorum: IF 903961; Facesoffungi number: FoF 17858.

Etymology – The name refers to its globose conidia.

Holotype – KUN-HKAS 129911

Endophytic in the rhizome of *Dicranopteris ampl*. Sexual morph: Undetermined. Asexual morph: *Mycelium* hyaline to pale brown, branched, septate, smooth-walled. *Conidiophores* 1.5–4 µm wide, micronematous, reduced to conidiogenous cells, terminal or lateral on undifferentiated hyphae, pale to brown, branched, septate, thick-walled. *Conidiogenous cells* 7.5–10 × 2–3.5 µm ($\bar{x}$ = 8.5 × 2.8 µm, n = 15), blastic, integrated, terminal, and intercalary, subcylindrical, denticulate. *Conidia* 3.5–6 × 2.5–4.5 µm ($\bar{x}$ = 4.5 × 3.5 µm, n = 30), solitary or catenate, globose to ovoid, subhyaline to brown, aseptate, smooth to verrucous, guttulate.

Culture characteristics – Colonies on medium of WA-carrot mixture under alternating natural and ultraviolet light, reaching ca. 52 mm diameter in 15 days at 26 °C, circular with filamentous margin, flat, without veined and wrinkle, dark brown to black, and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi and Miao Autonomous Prefecture, Zhenfeng County, isolated from the healthy rhizome of *Dicranopteris ampl*, 17 March 2022, J.Y. Zhang, (317–4 = KUN-HKAS 129911, holotype), ex-type living culture (KUNCC 23–14203).

GenBank numbers – ITS: PV138688, LSU: PV138585, SSU: PV138559

Notes – In the phylogenetic analyses, our strain KUNCC 23–14203 grouped with *C. exuberans*, *C. griseolivacea*, *C. matsushimae*, *C. molassis*, *C. mycetomatis*, *C. recurvata*, *C. tumbae*, and *C. tumulicola*, but in a distinct basal clade (Fig. 26). Morphologically, our new isolate has sub-hyaline to pale olivaceous, globose to ovoid, guttulate conidia. In contrast, conidia of the eight species are fusiform. Therefore, based on phylogeny and morphology, we introduce our new isolate as a new species, namely *C. globosa*.

Leotiomyces O.E. Erikss. & Winka

Helotiales Nannf.

Helotiales is a highly diverse order, containing over half of the described species within the class *Leotiomyces*. It also has the largest number of genera classified as *incertae sedis* at the familial level, indicating the need for further research to clarify their taxonomic placement (Baral et al. 2015, Quijada 2018, Johnston et al. 2019, Wijayawardene et al. 2022). The most recent list of *Helotiales* by Wijayawardene et al. (2022) recognized 36 families in *Helotiales*.

Massicellisporaceae D.F. Bao, J.Y. Zhang, K.D. Hyde & Y.Z. Lu, fam. nov.

Index Fungorum: IF 903998; Facesoffungi number: FoF 17859.

Type genus: *Massicellispora* D.F. Bao, J.Y. Zhang, Y.Z. Lu & J.C. Kang

Endophytic in dead plant tissues. Sexual morphs: Undetermined. Asexual morphs: *Colonies* on PDA media circular, flat, with an entire edge, pale grey to dark grey from above, reddish brown from below. *Mycelium* brown, branched, septate, wide. *Conidiophores* micronematous, reduced to conidiogenous cells, cylindrical, hyaline to pale brown, smooth-walled. *Conidiogenous cells* monophialidic, integrated, intercalary, doliform, subhyaline to brown. *Conidia* solitary or catenate and quickly become mass of cells, hyaline when young, becoming pale brown to dark-brown when mature, generally similar in shape, globose, subglobose, ellipsoidal to obovoid, rounded or with truncate base, smooth-walled.

Type genus: *Massicellispora* D.F. Bao, J.Y. Zhang, K.D. Hyde & Y.Z. Lu

Notes – Phylogenetic analysis showed that our two new isolates *Massicellispora globosa* (KUNCC 23–14165) and *M. dicranopteris* (KUNCC 23–14190), grouped with three strains of *Rhexocercosporidium* sp. (Dzf14, P5Es5, and TRXY 46) in a well-supported clade within *Helotiales*,

but did not belong to any family. (Fig. 27). Thus, *Massicellisporaceae* is introduced to accommodate a single genus *Massicellispora*, with two new endophytic species (*N. globosa* and *N. dicranopteris*) and three strains (Dzf14, P5Es5, and TRXY 46) based on phylogenetic analysis.

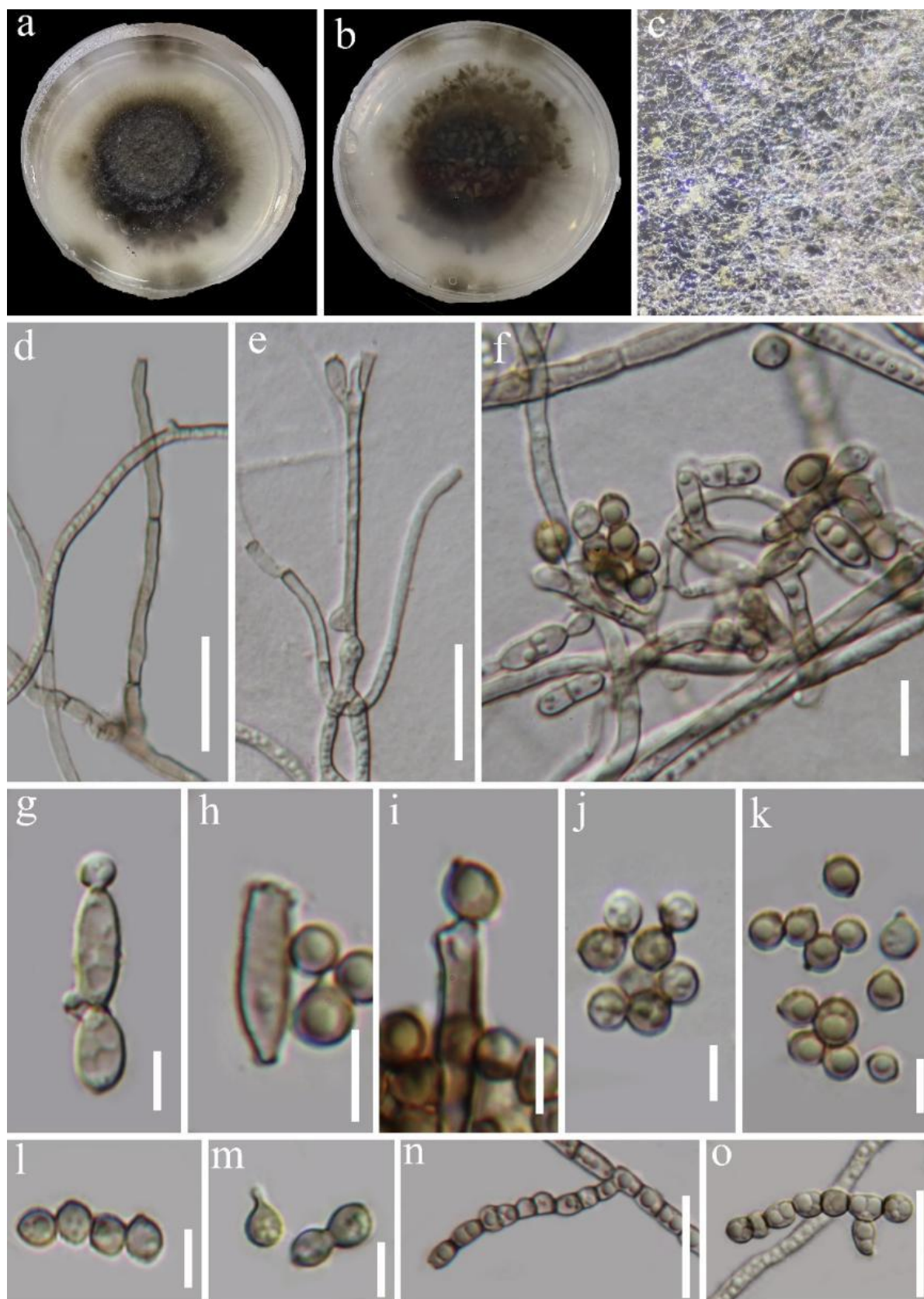


Figure 25 – *Cladophialophora globosa* (KUN-HKAS 129911, holotype). a, b Cultures on WA-carrot mixture from above and below. c Colonies on the WA-carrot mixture. d, e Conidiophores f Hyphae and conidia. g–i Conidiogenous cells and conidia. j–m Conidia. n, o Chlamydospore. Scale bars: d–f, n, o = 20 μ m, g–m = 5 μ m.

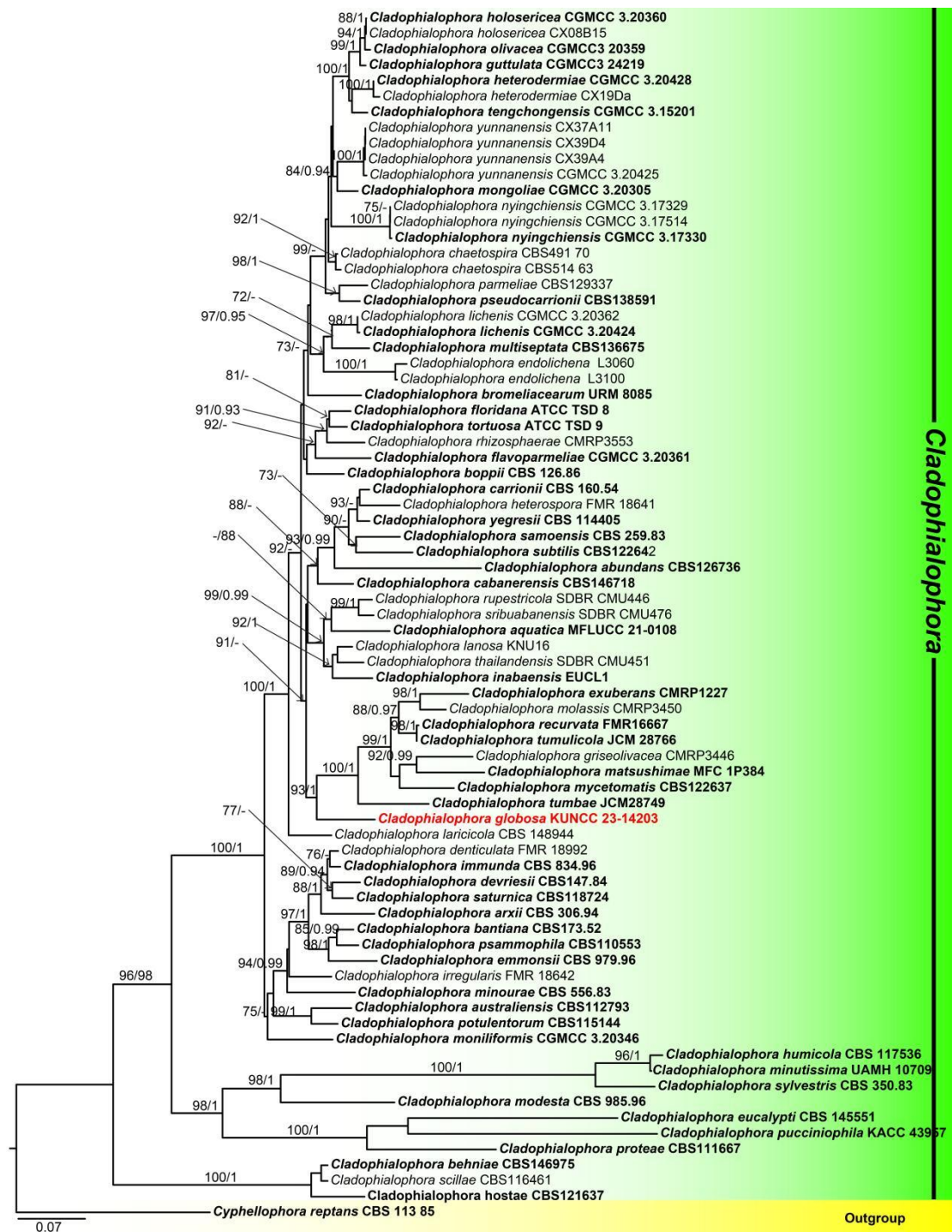


Figure 26 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1- α* , and *tub2* sequence data. A total of 77 taxa were included in the combined analyses, which comprised 3689 characters after alignment. The best scoring RAxML tree with a final likelihood value of -29313.948872 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Cyphellophora reptans* (CBS 113.85);

the newly obtained strains are in red and type strains are in bold.

Massicellispora D.F. Bao, J.Y. Zhang, K.D. Hyde & Y.Z. Lu, gen. nov.

Index Fungorum: IF 903962; Facesoffungi number: FoF 17860.

Etymology – Refers to the conidia quickly becoming a mass of cells

Endophytic in plant tissues. Sexual morphs: Undetermined. Asexual morphs: *Colonies* on PDA media circular, flat, with entire edge, pale grey to dark grey from above, reddish brown from below. *Mycelium* brown, branched, septate, wide. *Conidiophores* micronematous, reduced to conidiogenous cells, cylindrical, hyaline to pale brown, smooth-walled. *Conidiogenous cells*, monoblastic, integrated, intercalary, doliform, subhyaline to brown. *Conidia*, solitary or catenate and quickly become a mass of cells, hyaline when young, becoming pale brown to dark-brown when mature, generally similar in shape, globose, subglobose, ellipsoidal to obovoid, rounded or with a truncate base, smooth-walled.

Type species – *Massicellispora dicranopteridis* J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu

Massicellispora dicranopteridis J. Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 28

Index Fungorum: IF 903964; Facesoffungi number: FoF 17861.

Etymology – The specific epithet *dicranopteris* refers the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – KUN-HKAS 129894

Endophytic in the fresh root of *Dicranopteris linearis*. Sexual morph: Not observed. Asexual morph: *Mycelium* partly immersed, partly superficial, composed of hyaline to dark brown, smooth, thick-walled, septate, branched hyphae. *Conidiophores* not well-differentiated, micronematous, septate, hyaline to grayish brown, cylindrical to clavate. *Conidiogenous cells* 7–18(–27) × 3–4 µm ($\bar{x}$ = 12.3 × 3.5 µm, n = 20), monoblastic, integrated, pale brown, guttulate, smooth-walled. *Conidia* solitary, dry, septate, filamentous, helicoid; conidial filament indeterminate, with basipetal growth, pale to dark-brown, quickly becoming a coiled ball of cells; *Conidial cells* 5–7 × 4–5.5 µm ($\bar{x}$ = 6.1 × 4.9 µm, n = 30), similar in shape, globose to subglobose, subhyaline when young, becoming brown to dark brown at maturity, guttulate, smooth-walled.

Culture characteristics – Colonies on MEA attaining 15–20 mm diameter after 14 days at 25 °C, with smooth edge, circular, with fluffy, dense, brown to dark brown mycelium on the surface; in reverse dark brown with entire margin.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the root of *Dicranopteris linearis*, 16 March 2022, J.Y. Zhang, (212–2 = KUN-HKAS 129894, holotype), ex-type living culture (KUNCC 23–14190).

GenBank numbers – ITS: PV138668, LSU: PV138567, SSU: PV164581

Notes – Phylogenetic analysis showed that *Massicellispora globosa*, *M. dicranopteridis* and three unidentified strains (Dzfl4, P5Es5, and TRXY-46) formed a distinct clade within *Helotiales* (Fig. 27). To accommodate the two novel isolates and the three unidentified strains, a new genus, *Massicellispora* is introduced. Morphologically, both novel isolates have micronematous cylindrical, hyaline to pale brown, septate, smooth-walled conidiophores, monoblastic, subhyaline to brown conidiogenous cells and septate, filamentous, helicoid, subhyaline to brown, smooth-walled, globose, subglobose, ellipsoidal to obovoid, smooth-walled, subhyaline to brown conidia. However, the conidia of *M. dicranopteridis* are catenate and quickly become a mass of cells, which is different from those of *M. globosa*. In contrast, the conidia of *M. globosa* are solitary. Phylogenetically, *M. globosa* and *M. dicranopteridis* are sister taxa. As a result, we assigned the two species to the same

genus, *Massicellispora*. Nevertheless, whether the two species should be placed in the same or distinct genus requires further investigation with more taxonomic sampling and morphological characteristics.

Additionally, phylogenetic analysis showed that *Massicellispora dicranopteridis* (KUNCC 23–14190) clustered with an unidentified strain, *Rhexocerosporidium* sp. (Dzf14). This strain lacks morphological data, and only ITS sequence data is available, which is insufficient to identify it. Thus, additional phylogenetic and morphological data are required to rectify this strain.

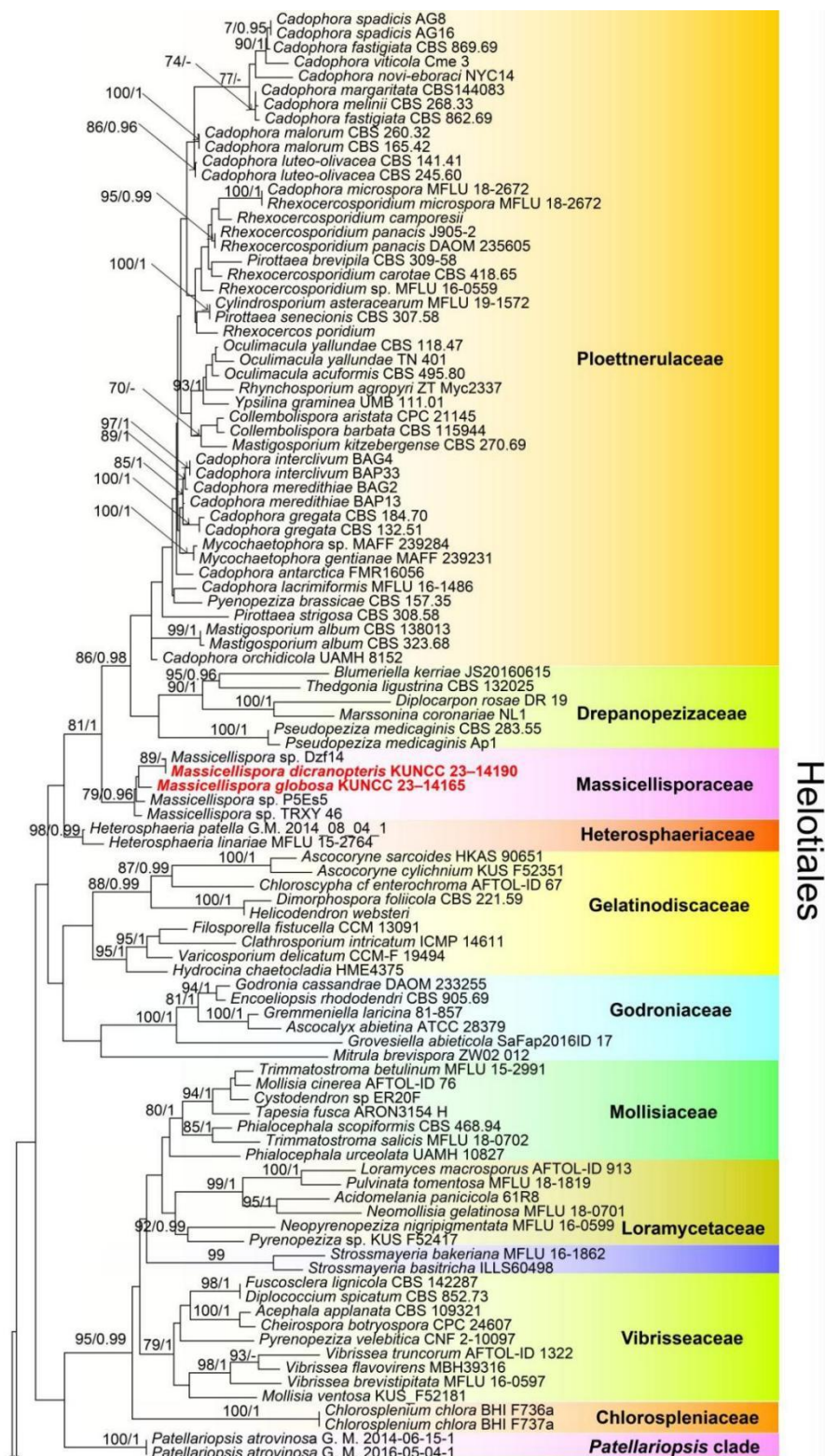


Figure 27 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. 168 taxa were included in the combined analyses, which comprised 1516 characters after alignment. The best scoring RAxML tree with a final likelihood value of -31039.487192 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Cyttaria hookeri* (isolate 60) and *C. johowii* (isolate 73); the newly obtained strains are in red and bold.

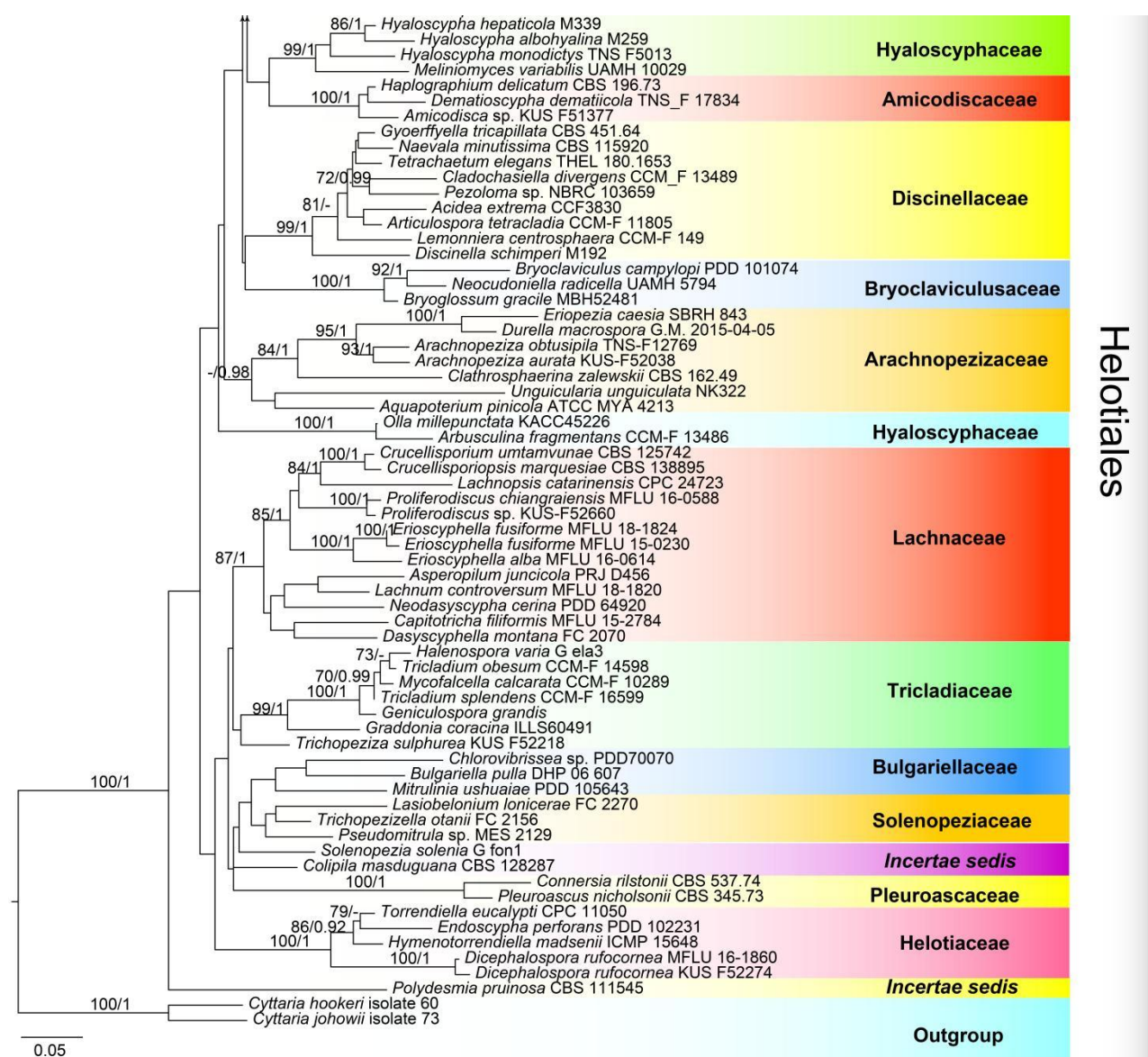


Figure 27 – Continued

Massicellispora globosa J. Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov.

Index Fungorum: IF 903965; Facesoffungi number: FoF 17862.

Etymology – The name refers to its globose conidia

Holotype – GZAAS 23–0792

Endophytic in the roots of *Dicranopteris ampla*. Sexual morph: Undetermined. Asexual morph: Colonies on PDA media circular, flat, with entire edge, pale grey to dark grey from above, reddish brown from below. *Mycelium* 1–3.5 μm wide, brown, branched, septate, smooth-walled.

Fig. 29

Conidiophores reduce to conidiogenous cells, cylindrical, hyaline to pale brown, smooth-walled. *Conidiogenous cells* $2.5\text{--}9.5 \times 2\text{--}4 \mu\text{m}$ ($\bar{x} = 6 \times 3 \mu\text{m}$, $n = 20$), monoblastic, integrated, intercalary, doliiform, subhyaline to brown. *Conidia* $5.5\text{--}7.5 \times 4.5\text{--}6 \mu\text{m}$ ($\bar{x} = 6.5 \times 5.5 \mu\text{m}$, $n = 25$), solitary, globose, ellipsoidal to obovoid, hyaline when young, brown when mature, aseptate, smooth.

Culture characteristics – Colonies on PDA medium under natural light, reaching 55 mm diameter in 14 days at 26 °C, circular with entire margin, flat with smooth surface, spread, with immersed mostly mycelia, without veined and wrinkle, gray to taupe towards edge from above; dark brown to brown from inside to the margin in reverse.

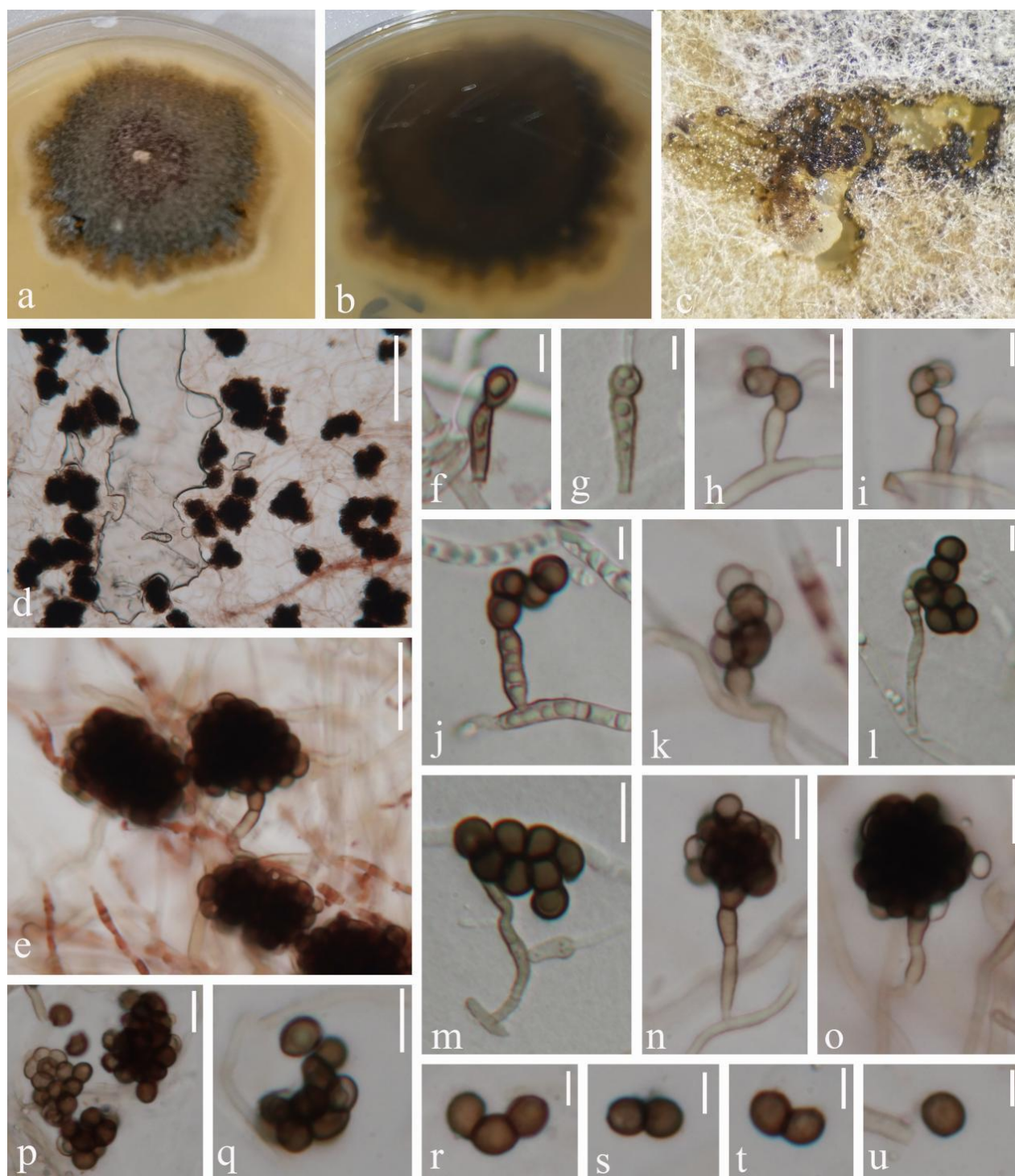


Figure 28 – *Massicellispora dicranopteridis* (KUN-HKAS 129894, holotype). a, b Culture on MEA

from above and below. c Colonies on MEA. d Conidial mass and mycelium. e–o Conidiophores, conidiogenous cells, and conidia. p–q Conidia. r–u Conidial cells. Scale bar: d = 100 μ m, e = 20 μ m, f–l, r–u = 5 μ m, m–q = 10 μ m

Material examined – China, Guizhou Province, Southwest Guizhou Buyi and Miao Autonomous Prefecture, Zhenfeng County, isolated from the healthy roots of *Dicranopteris ampl*a, 17 March 2022, J.Y. Zhang, (119–1 =GZAAS 23–0792, holotype), ex-type living culture (KUNCC 23–14165).

GenBank numbers – ITS: PV138667, LSU: PV138566, SSU: PV164580

Note – *Massicellispora globosa* is introduced as a new species based on its distinct morphology and phylogeny. *Massicellispora globosa* has solitary, globose, ellipsoidal to obovoid, aseptate, and hyaline to brown conidia, which are distinct from *M. dicranopteridis*. While *M. globosa* has guttulate and catenate conidia, which quickly become a mass of cells. Furthermore, we noticed that LSU sequence data is more valuable in discriminating between *M. dicranopteridis* and *M. globosa* than ITS. The ITS of these two species is almost identical, but the LSU sequence data differs by 26bp. Based on both phylogeny and morphology, we introduce *M. dicranopteridis* as a new species. However, the limited taxonomic sampling and morphological information available for this genus require further morphological and phylogenetic research based on more recent collections to comprehend it better.

***Medeolariales* Korf**

Medeolariales was introduced by Eriksson (1982) with a single family *Medeolariaceae*. Ekanayaka et al. (2019) showed that *Medeolariaceae* formed a monophyletic clade with *Ascodichaenaceae*, *Dermateaceae*, and a clade of *Coleophoma-Parafabreae*. Although *Ascocorticiaceae* do not have available sequence data in GenBank, species of this family have a similar morphology to *Medeolariales* taxa. Therefore, Ekanayaka et al. (2019) accepted *Ascodichaenaceae*, *Ascocorticiaceae*, *Dermateaceae*, and *Coleophoma-Parafabreae* clade in this order.

***Dermateaceae* Fr.**

Dermateaceae typified by *Dermea*, and members of this family can cause stem and fruit rots on vascular plants (Yuan and Verkley 2015, Chen et al. 2016, Michalecka et al. 2016, Cameldi et al. 2017, Pešicová et al. 2017, Romero et al. 2017, Lin et al. 2018a). *Dermateaceae* species have also been reported as endophytes and saprobes from various hosts (Chen et al. 2016). The family was initially placed in *Helotiales*; however, Ekanayaka et al. (2019) showed that *Dermateaceae* shares a close relationship with *Medeolariales*, placing this family in *Medeolariales*. The placement of this family remains problematic, as different authors treat it under different orders. Li et al. (2020a), following Ekanayaka et al. (2019), place this family in *Medeolariales*. However, more recently, Wijayawardene et al. (2022) and Iliushin & Kirtsideli (2023) placed the family back in *Helotiales*. In this study, we follow the treatment of Ekanayaka et al. (2019) and Li et al. (2020a), placing the family in *Medeolariales*, as phylogenetic analyses have shown that this family groups within *Medeolariales*.



Figure 29 – *Massicellispora globosa* (GZAAS 23–0792, holotype). a, b Cultures on PDA from above and below. c Colonies on PDA. d–m Conidiogenous cells with conidia. Scale bars: d = 20 μm , e–m = 10 μm .

The most recent list of *Dermateaceae* genera was provided by Hyde et al. (2024), which comprises 15 genera: *Chaetophiophoma*, *Coleophoma*, *Corniculariella*, *Davidhawksworthia*, *Dermea*, *Gelatinoamylaria*, *Neodermea*, *Neofabraea*, *Neogloeosporidina*, *Pezicula*, *Phlyctema*, *Pseudofabraea*, *Rhizodermea*, *Schizothyrioma* and *Verkleyomyces*. However, several genera within this family require further revisions due to the lack of sequence data and problematic phylogenetic affinities. For example, studies have shown that *Dermea* is polyphyletic within the family, and our phylogenetic analysis obtained a similar result (Jiang and Tian 2019). During our study on the diversity of endophytic fungi associated with *Dicranopteris*, we isolated a fungus, which we introduced as a new species placed in *Pezicula* based on phylogenetic and morphological analysis. Additionally, *Neofabraea actinidiae* was isolated from *Dicranopteris* for the first time.

***Neofabraea* H.S. Jacks.**

Neofabraea was introduced by Jackson (1913) with *N. malicorticis* as the type species (Jackson 1913). The genus was treated as a synonym of *Pezicula* by Nannfeldt (1932). However, Verkley (1999) accepted *Neofabraea* as a distinct genus based on phylogeny and morphology. Johnston et al. (2014) transferred related *Cryptosporiopsis* species to *Neofabraea*, and advocated for the use of *Neofabraea* over *Phlyctema*. *Neofabraea vagabunda* was introduced to accommodate *N. alba*. Chen et al. (2016) redefined the common endophytes and plant pathogens in *Neofabraea*, *Pezicula*, and related genera, emending the generic concept of *Neofabraea*. They accepted six species: *N. actinidiae*, *N. inaequalis*, *N. kienholzii*, *N. krawtzevii*, *N. malicorticis*, and *N. perennans* in the genus and all of which appear to be phytopathogenic. Five additional species, *N. brasiliensis*, *N. brunneipila*, *N. eucalyptorum*, *N. illicii*, and *N. salicina* were subsequently introduced to *Neofabraea* (Crous et al. 2015a, 2020, 2021b, Chen et al. 2016, Ekanayaka et al. 2019). Currently, 11 species are accepted in *Neofabraea*.

***Neofabraea actinidiae* (P.R. Johnst., M.A. Manning & X. Meier) P.R. Johnst., in Johnston, Seifert, Stone, Rossman & Marvanová, IMA Fungus 5(1): 102 (2014)** Fig. 30

Index Fungorum: IF 808962; Facesoffungi number: FoF 17863.

Endophytic in stems of *Dicranopteris ampla*. Sexual morph: Undetermined. Asexual morph: *Mycelium* mostly immersed, composed of hyaline, septate, smooth-walled. *Conidiophores* arise from single or slightly fasciculate aerial hyphae, hyaline, septate, smooth-walled. *Conidiogenous cells* 9–25 × 1.5–2.5 µm ($\bar{x}$ = 17 × 2 µm, n = 30), usually held on irregularly branched conidiophores, sometimes arising directly from hypha, sometimes with a conidiogenous loci, smooth-walled. *Conidia* 3.2–6.8 × 1.2–2.5 µm ($\bar{x}$ = 5 × 1.9 µm, n = 30), aseptate, elliptic to clavate, smooth-walled, ends widely rounded, with an indistinct scar at the base.

Culture characteristics – Colonies on PDA medium circular, aerial mycelium more or less, grow slowly, reaching 20 mm diameter after 10 days at 25 °C in natural light, circular, orange mycelium in the middle, pale orange to pink in the inner ring and white at the edge; orange in reverse, pale orange in narrow zone near margin, margin itself colorless similar variation in color from below.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Chengheng County, isolated from healthy stems of *Dicranopteris ampla* (*Gleicheniaceae*) collected from the rock crevices, 16 March 2022, J.Y. Zhang, (NS224–6 = KUN-HKAS 129897), living culture (KUNCC 23–14192).

GenBank numbers – ITS: PV138673, LSU: PV138572

Notes – Based on the phylogenetic tree, our new isolate clusters with two strains of *Neofabraea actinidiae* (CBS 121403 and CBS 194.69) (Fig. 31). There are no significant differences in ITS, LSU, and *rpb2* sequencing data between our new strain and *N. actinidiae* (CBS 121403 and CBS 194.69).

In addition, the morphology of our new isolate is almost identical to the holotype of *N. actinidiae*, except for the size of conidiogenous cells and conidia. Our isolate has larger conidiogenous cells ($9\text{--}25 \times 1.5\text{--}2.5$ vs. $8.5\text{--}14.5 \times 8\text{--}4$ μm) and smaller conidia ($3.2\text{--}6.8 \times 1.2\text{--}2.5$ vs. $9\text{--}14 \times 3\text{--}5.5$ μm) than the holotype (Johnston et al. 2004). Therefore, we identify our new isolate as *N. actinidiae* based on molecular data and morphological characteristics.

Neofabraea actinidiae was originally introduced by Johnston et al. (2004) as *Cryptosporiopsis actinidiae*. Subsequently, this species has been transferred to *Neofabraea* and synthesized as *N. actinidiae* based on phylogenetic analysis and morphological characteristics. *Neofabraea actinidiae* is a plant pathogenic fungus with a wide distribution, documented to cause ripe rots in the green kiwifruit cultivar, apple bull's-eye rot, and Cranberry fruit rot (Bogo et al. 2018, Tyson et al. 2019; Valentine et al. 2024). While our isolate is an endophyte isolated from *Dicranopteris ampla* stems. This is the first report of *N. actinidiae* isolation from *D. ampla*.

***Pezicula* Tul. & C. Tul.**

Pezicula, typified by *P. carpineae* was established in 1869. The genus is characterized by brightly colored, short-stalked apothecia with circular discs that are initially concave and surrounded by slightly elevated margins, but later become convex, inoperculate, and clavate or cylindric-clavate asci and broadly ellipsoid to elongate-ellipsoid to allantoid or fusoid ascospores (Ooki et al. 2003, Verkley 1999, Ekanayaka et al. 2016, Ma et al. 2021). The asexual morph of *Pezicula* has been linked to *Cryptosporiopsis* and Johnston et al. (2014) synonymized *Cryptosporiopsis* under *Pezicula*. Species of *Pezicula* are reported as endophytes, phytopathogens, or saprobes associated with diverse hosts from temperate regions of the world (Chen et al. 2016, Ma et al. 2021, Zheng & Zhuang 2022). In this study, we introduce a new species, *P. dicranopteridis*, which is an endophytic fungus isolated from *Dicranopteris*. In addition, *Cashiella sticheri* was transferred to *Pezicula* as *P. sticheri* based on phylogenetic analysis and morphological characters.

***Pezicula dicranopteridis* J. Y. Zhang, D.F. Bao & Y.Z. Lu, sp. nov.**

Fig. 32

Index Fungorum: IF 903966; Facesoffungi number: FoF 17864.

Etymology – Etymology: the specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – KUN-HKAS 129880

Endophytic in the healthy stem of *Dicranopteris pedata*. Sexual morph: Undetermined. Asexual morph: *Hyphae* $3.5\text{--}4.5$ μm , hyaline to pale brown, septate, branched, thin-walled, smooth. *Conidiophores* $6\text{--}8.5 \times 3.5\text{--}4.5$ μm ($\bar{x} = 7 \times 4$ μm , $n = 10$), micronematous, reduced to conidiogenous cells, hyaline, septate, thin-walled, unbranched, straight or flexuous. *Conidiogenous cells* holoblastic, hyaline to brown, terminal, cylindrical, flexuous, or coiled, bear a brown sheath at maturity. *Conidia* $12\text{--}15 \times 6\text{--}7$ μm ($\bar{x} = 13.3 \times 6.8$ μm , $n = 30$), aseptate, acropleuroacrogenous, oval to obovoid, fusiform, top-shaped, rounded at the base, tapering to a point at the apex, smooth-walled, guttulate, hyaline, differentiated within the conidiogenous cell.

Culture characteristics – *Colonies* on PDA medium irregular, effuse, effuse, with little dark spots, flat with undulate edge, hyaline to pale brown.

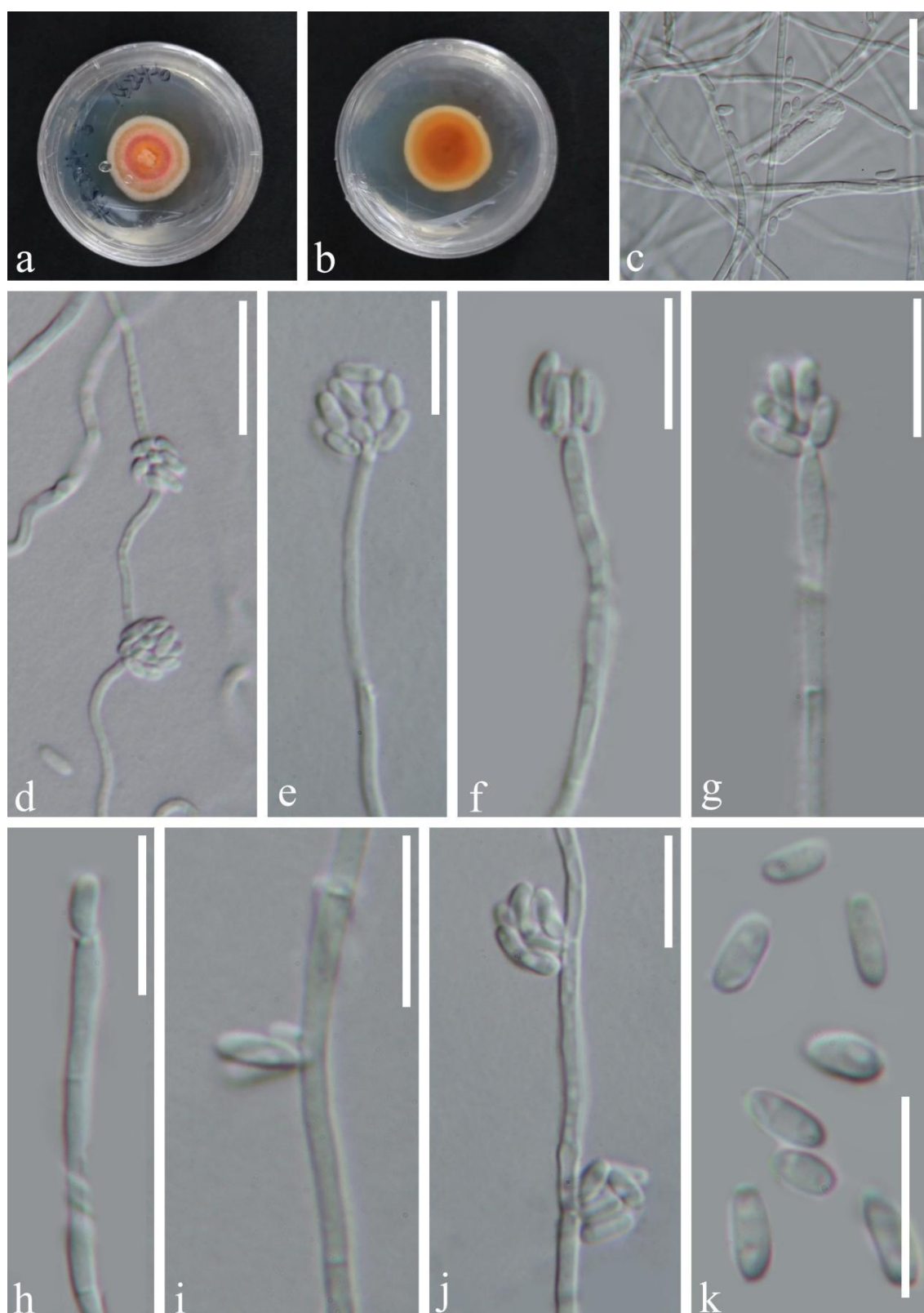
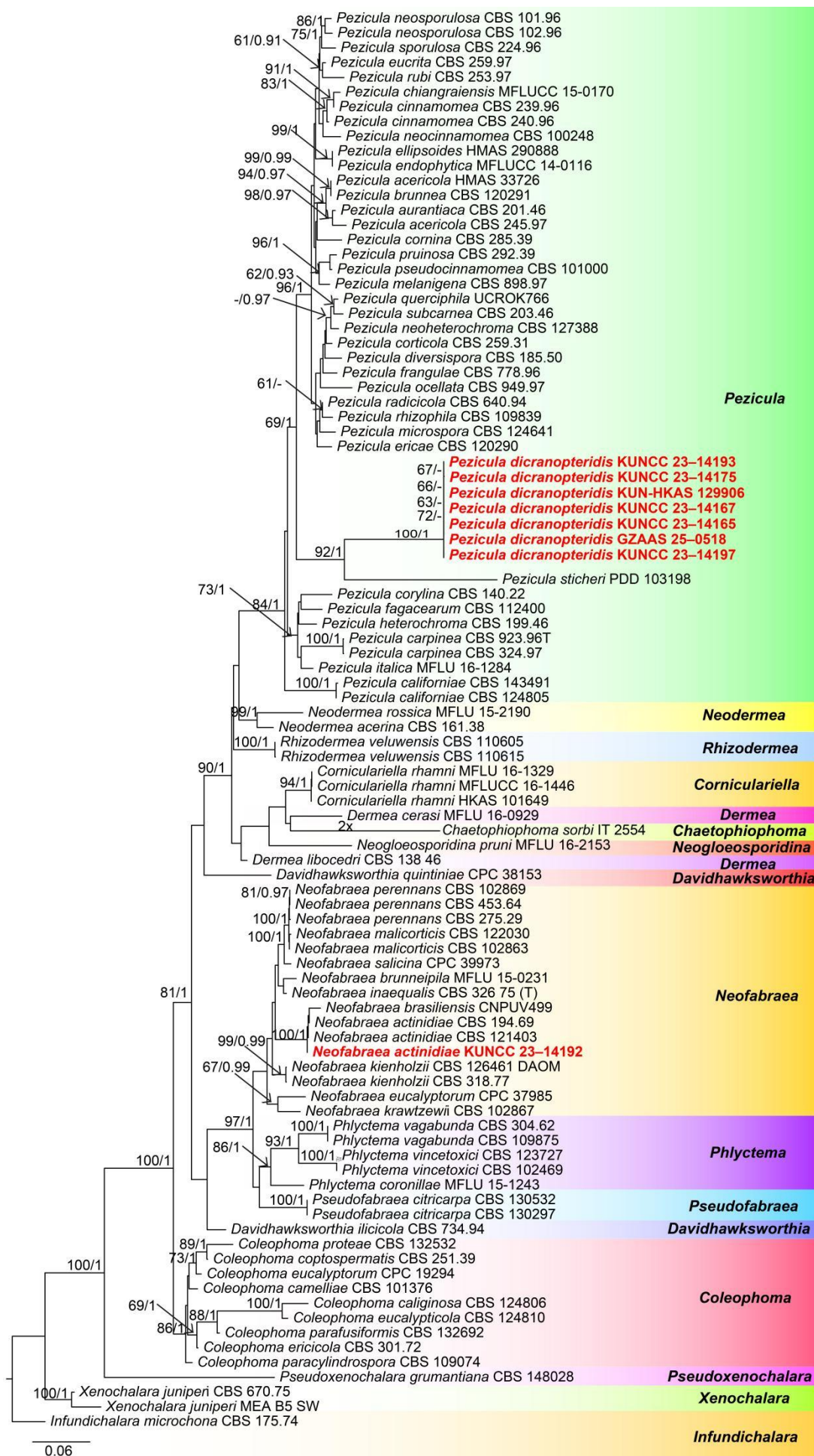


Figure 30 – *Neofabraea actinidiae* (KUN-HKAS 129897, new host record). a Colonies on PDA medium. b Conidiomata on PDA. c–j Conidiogenous cells bearing developing conidia. k Conidia. Scale bars: c–d = 20 μ m, e–k = 10 μ m.



Dermateaceae

Figure 31 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, and *tub2* sequence data. A total of 96 taxa were included in the combined analyses, which comprised 3103 characters after alignment. The best-scoring RAxML tree with a final likelihood value of -24627.151638 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Infundichalara microchona* (CBS 175.74). The newly obtained strains are in red and bold.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Chengheng County, isolated from the stem of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS152–3 = KUN-HKAS 129880, holotype), ex-type living culture (KUNCC23–14175). *ibid.* (NS253–2 = KUN-HKAS 129899), paratype, living culture (KUNCC23–14193). *ibid.*; isolated from the leaf of *D. linearis* near the roadside, 16 March 2022, J.Y. Zhang (NS275–3 = KUN-HKAS 129905), living culture (KUNCC23–14197). *ibid.* NS275–7 = KUN-HKAS 129906, paratype; isolated from the stem of *D. pedata* near the roadside, 16 March 2022, J.Y. Zhang (NS141–3 = GZAAS 23-0792), paratype, living culture (KUNCC23–14165). *ibid.* NS253–4 = GZAAS 25–0518, paratype; NS127–1 = GZAAS25–0502, paratype, living culture (KUNCC23–14167).

GenBank numbers – KUNCC 23–14175: ITS: PV138672, LSU: PV138571, RPB2: PV188061. KUNCC 23–14193: ITS: PV138674, LSU: PV138573. KUNCC 23–14197: ITS: PV138675, LSU: PV138574, RPB2: PV188063. KUN-HKAS 129906: ITS: PV138676, LSU: PV138575. KUNCC 23–14165: ITS: PV138671, LSU: PV138570. KUNCC 23–14167: ITS: PV138670, LSU: PV138569

Notes – In the phylogenetic analysis, our new isolates clustered with *Cashiella sticheri* (PDD 103198) in a well-supported clade basal to *Pezicula* (Fig. 31). *Cashiella sticheri* was introduced by Gadgil & Dick (1999), with only its sexual morph was known. Our isolates represent the asexual morphs, and the sexual morph was not observed in this study. Our isolates are phylogenetically distinct from *C. sticheri* (Fig. 31). Morphologically, *P. dicranopteridis* differs significantly from other *Pezicula* species, particularly in its formation and shape. *Pezicula dicranopteridis* produces oval to obovoid conidia, rounded at the base, tapering to a point at the apex, and formed within a brown sheath over time, a feature that was not observed in other *Pezicula* species. All other *Pezicula* species have cylindrical, ellipsoid, pyriform, claviform, or fusoid conidia (Verkley 1999, Chen et al. 2016, Zheng & Zhuang 2022). Notably, the endogenous conidial formation within a brown sheath in *P. dicranopteridis* is a unique feature.

Despite these morphological differences, our isolates and *Cashiella sticheri* are not significantly separated from *Pezicula* in the phylogenetic analyses. Therefore, based on both morphological and molecular evidence, we identify the eight newly obtained strains as a new species, *P. dicranopteridis* within *Pezicula*. However, further sampling and sequence data are required to confirm the precise placement of this new species.

Pezicula sticheri (Gadgil & M.A. Dick) D.F. Bao, Y.Z. Lu and J.C Kang, comb. nov.

≡ *Cashiella sticheri* Gadgil & M.A. Dick, N.Z. Jl For. Sci. 29(3): 447 (1999)

Index Fungorum: IF 903999; Facesoffungi number: FoF 17865.

Notes – *Cashiella sticheri* was introduced by Gadgil & Dick (1999) after being collected from *Sticheri cunninghamii* in New Zealand. It is characterized by black, cup-shaped apothecia that are sessile but narrowed at the base, gregarious, circular in outline, and glabrous, with clavate asci and uniseriate, ellipsoid, hyaline to pale brown, aseptate ascospores. These morphological characteristics align with the generic concept of *Pezicula*. Ekanayaka et al. (2019) demonstrated that *Cashiella*

sticheri grouped within *Dermateaceae*, a placement further supported by Wijayawardene et al. (2022).



Figure 32 – *Pezicula dicranopteridis* (KUN-HKAS 129880, holotype). a–b Cultures on WA from above and below. c Colonies on WA. d–i mycelium with a brown to dark brown sheath. j–n

Conidiogenous cells and conidia. o–s Conidia. Scale bars: d = 30 μm , e, f, h, i = 20 μm , g = 40 μm , j, k = 5 μm , l–s = 10 μm .

Our phylogenetic analysis showed that *Cashiella sticheri* clustered with our new isolates (*P. dicranopteridis*), forming a clade basal to *Pezicula*, and could not be significantly separated from *Pezicula* (Fig. 31). Thus, based on both phylogenetic and morphological analyses, we transfer *Cashiella sticheri* to *Pezicula*, synonymizing *P. sticheri* with *C. sticheri*. Currently, four species are accepted in *Cashiella*, but only *Cashiella sticheri* has sequence data available in GenBank. Therefore, further studies are needed to confirm whether the remaining *Cashiella* species should also be transferred to *Pezicula*.

***Rhytismatales* M.E. Barr ex Minter**

Based on the phylogenetic analyses, Ekanayaka et al. (2019) accepted three families, *Calloriaceae*, *Pezizellaceae*, and *Rhytismataceae*, in this order.

***Calloriaceae* Baral & G. Marson**

Ekanayaka et al. (2019) updated the classification of *Calloriaceae*, accepting 28 genera based on phylogenetic analysis and previous literature. Subsequently, Crous et al. (2021c) added a new genus, *Populomyces*. However, the majority of taxa in this family lack sequencing data in GenBank. Therefore, further studies are needed to better understand the classification of this family.

***Populomyces* Hern. -Restr.**

The monotypic genus *Populomyces* was introduced by Crous et al. (2021c) to accommodate *P. zwinianu* based on phylogenetic analysis and morphological characteristics. Tan et al. (2021) introduced the second species, *P. barnardiae* based solely on phylogenetic analysis, without any morphological description and illustration. Currently, two species are included in the genus, both of which have been isolated from soil (Crous et al. 2021c, Tan et al. 2021). *Populomyces* is characterized by micronematous conidiophores or mostly reduced to conidiogenous, monophialidic, hyaline, smooth, cylindrical to lageniform conidiogenous cells with a cylindrical collarette, and aseptate, cylindrical, solitary, hyaline, guttulate conidia (Crous et al. 2021c). In this study, *P. barnardiae* was isolated from the roots of *Dicranopteris pedata*, and detailed morphological descriptions, illustrations, and phylogenetic analysis results are provided for this species.

***Populomyces barnardiae* Y.P. Tan, Bishop-Hurley, Marney, R.G. Shivas, in Tan & Shivas, Index of Australian Fungi 3: 16 (2022)** Fig. 33

Index Fungorum: IF 900147; Facesoffungi number: FoF 17866.

Endophytic in the healthy roots of *Dicranopteris pedata*. Sexual morph: Undetermined. Asexual morph: *Hyphae* in medium, septate, hyaline, smooth-walled. *Conidiophores* micronematous, mostly reduced to conidiogenous cells. *Conidiogenous cells* 10–17 $\times$ 2.5–4.5 μm ($\bar{x}$ = 13.5 $\times$ 3.5 μm , n = 30), monophialidic, simple, ampuliform with swollen basal cell, smooth-walled, hyaline. *Conidia* 3.5–7 $\times$ 1.8–3.0 μm ($\bar{x}$ = 5.2 $\times$ 2.4 μm , n = 30), ellipsoidal with round ends, aseptate, hyaline, smooth-walled.

Culture characteristics – Colonies on PDA medium circular, entirely to slightly filamentous, growly fast, reaching 40 mm diameter after 7 days at 25 °C in natural light, cottony, velvety, dense, with creases, glutinous, pale yellow to bright orange from above; light orange-red in reverse, put in toothpicks to promote sporulation, spore production after two weeks.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Chengheng County, isolated from healthy roots of *Dicranopteris pedata* (Gleicheniaceae) collected from the rock crevices, 16 March 2022, J.Y. Zhang, (NS184–2 = KUN-HKAS 129886), living culture (KUNCC 23–14184).

GenBank numbers – ITS: PV138677, LSU: PV138602, SSU: PV164582, *rpb2*: PV188072.

Notes – Phylogenetic analysis showed that our new isolate (KUNCC 23–14184) was placed sister to *Populomyces barnardiae* (BRIP 74917a) (Fig. 34) which was isolated from soil in Australia by Tan et al. (2022). However, this species was introduced based on molecular analysis; there were no morphological descriptions or illustrations provided for this species. The nucleotide comparison of ITS and LSU sequence data from our new isolate and *P. barnardiae* (BRIP 74917a) revealed 5bp and 1bp differences, respectively. Which were not significantly different between the two species. Thus, we identified our new isolate as *P. barnardiae* and provided morphological descriptions, illustrations, and phylogenetic analysis results for this species.

Populomyces barnardiae is similar to the type species, *P. zwinianus* in having micronematous conidiophores, which are mostly reduced to conidiogenous cells, monophialidic, ampuliform smooth-walled, hyaline conidiogenous cells and aseptate, solitary, hyaline conidia. However, *P. barnardiae* is different from *P. zwinianus* by the shape and size of conidia (ellipsoidal with round ends vs. cylindrical, $3.5\text{--}7 \times 1.8\text{--}3$ vs. $9\text{--}12 \times 2\text{--}2.5$ μm) (Crous et al. 2021c). Furthermore, the phylogenetic analysis also strongly supports they are different species (Fig. 34).

Pseudopopulomyces D.F. Bao, K.D. Hyde & Y.Z. Lu, gen. nov.

Index Fungorum: IF 903984; Facesoffungi number: FoF 17868.

Etymology – Referring to its similarity with *Populomyces*.

Endophytic in the healthy plant tissue. Sexual morph: Undetermined. Asexual morph: *Conidiomata* sporodochial, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, terminal, cylindrical, hyaline, smooth. *Conidia* globose to suglobose, ellipsoidal with round ends, aseptate, hyaline, smooth-walled.

Pseudopopulomyces dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 35

Index Fungorum: IF 903967; Facesoffungi number: FoF 17867.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 25–0514

Endophytic in the root of *Dicranopteris pedata*. *Mycelium* mostly immersed composed of septate, branched, hyaline smooth hyphae. Sexual morph: Undetermined. Asexual morph: *Conidiomata* sporodochial, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $3.5\text{--}7 \times 1.5\text{--}2.5$ μm ($\bar{x} = 5.3 \times 2$, $n = 10$), monoblastic, terminal, cylindrical, hyaline, smooth. *Conidia* $3\text{--}4 \times 2\text{--}3$ μm ($\bar{x} = 3.7 \times 2.6$, $n = 30$), globose to suglobose, ellipsoidal with round ends, aseptate, hyaline, smooth-walled.

Culture characteristics – Colonies on PDA medium circular with entire margin, pale to bright yellow, reverse pure white, stenopsychrophile; aerial hyphae absent or sparse hyaline to white, and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the root of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS208–4 = GZAAS 25–0514, holotype).

GenBank numbers – ITS: PV138678, LSU: PV138603, SSU: PV164578, *tef1- α* : PV177125, *rpb2*: PV188070

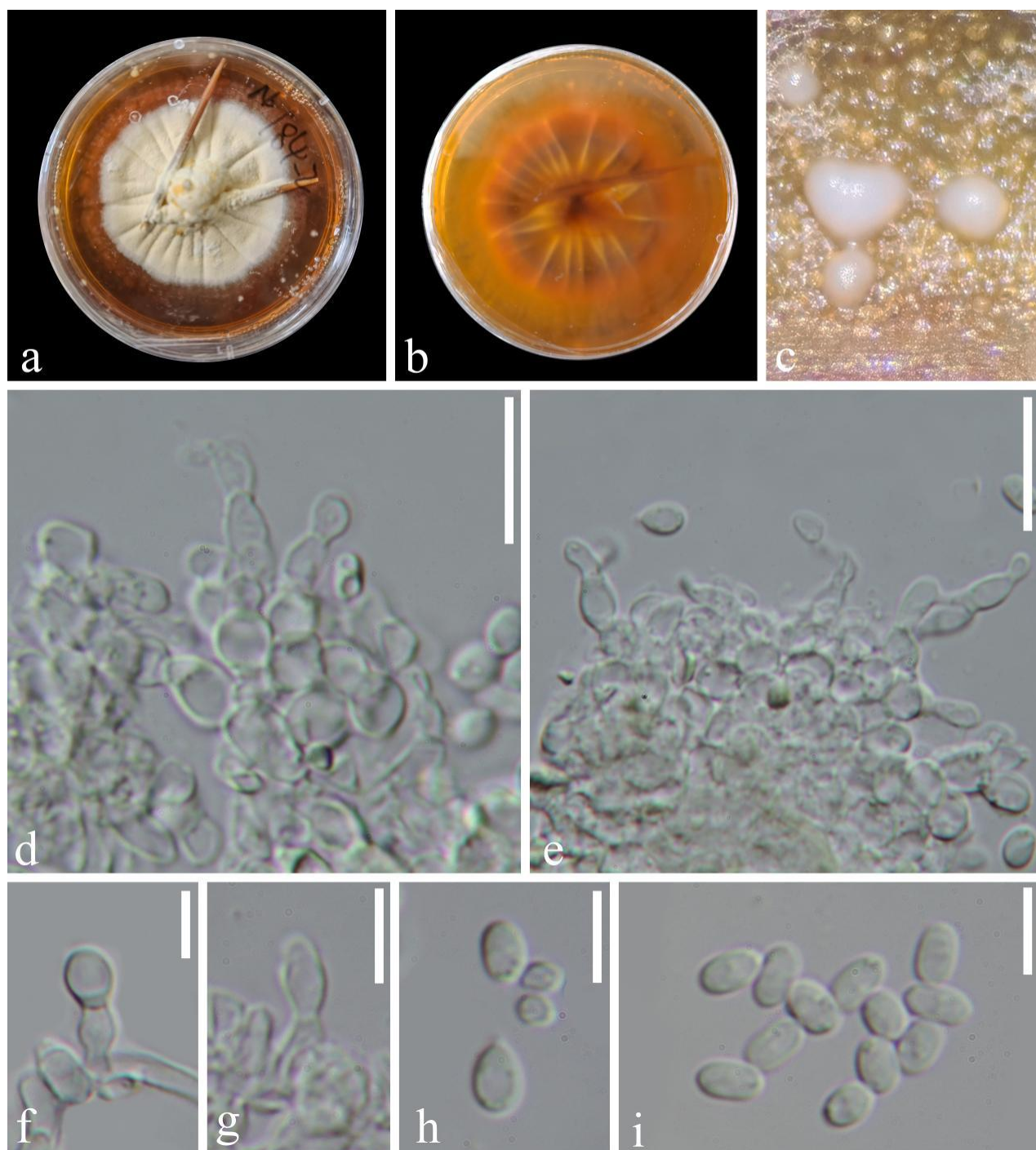


Figure 33 – *Populomyces barnardiae* (KUN-HKAS 129886, new host record). a, b Colonies on PDA medium. c Colonies on PDA. d, e Conidiogenous cells and Conidia. f–g Conidiogenous cells. h–i Conidia. Scale bars: d–e = 10 µm, f–i = 5 µm.

Notes – In a BLASTn search of NCBI GenBank, the closest matches of the ITS and LSU sequences of *Pseudopopulomyces dicranopteridis* (GZAAS 25–0514) with 83.93% and 95.22% similarities were *Tetracladium* sp. (B103) and *T. breve* (CCM F-12505), respectively. In our phylogenetic analysis, *P. dicranopteridis* grouped with *Calloria*, *Populomyces* and *Tricellula*, but in a distinct basal clade (Fig. 34). *Pseudopopulomyces dicranopteridis* is similar to *Tetracladium* in having 1-celled, hyaline, globose, ellipsoid, smooth-walled conidia (Wang et al. 2015). However, the

conidia of *Tetracladium* are directly borne on short, undifferentiated or sessile pedicels, or attach to the hyphae with very short conidiophores. In contrast, *P. dicranopteridis* has sporodochial conidiomata, reduced conidiophores and monoblastic, terminal, cylindrical, hyaline, smooth conidiogenous cells.

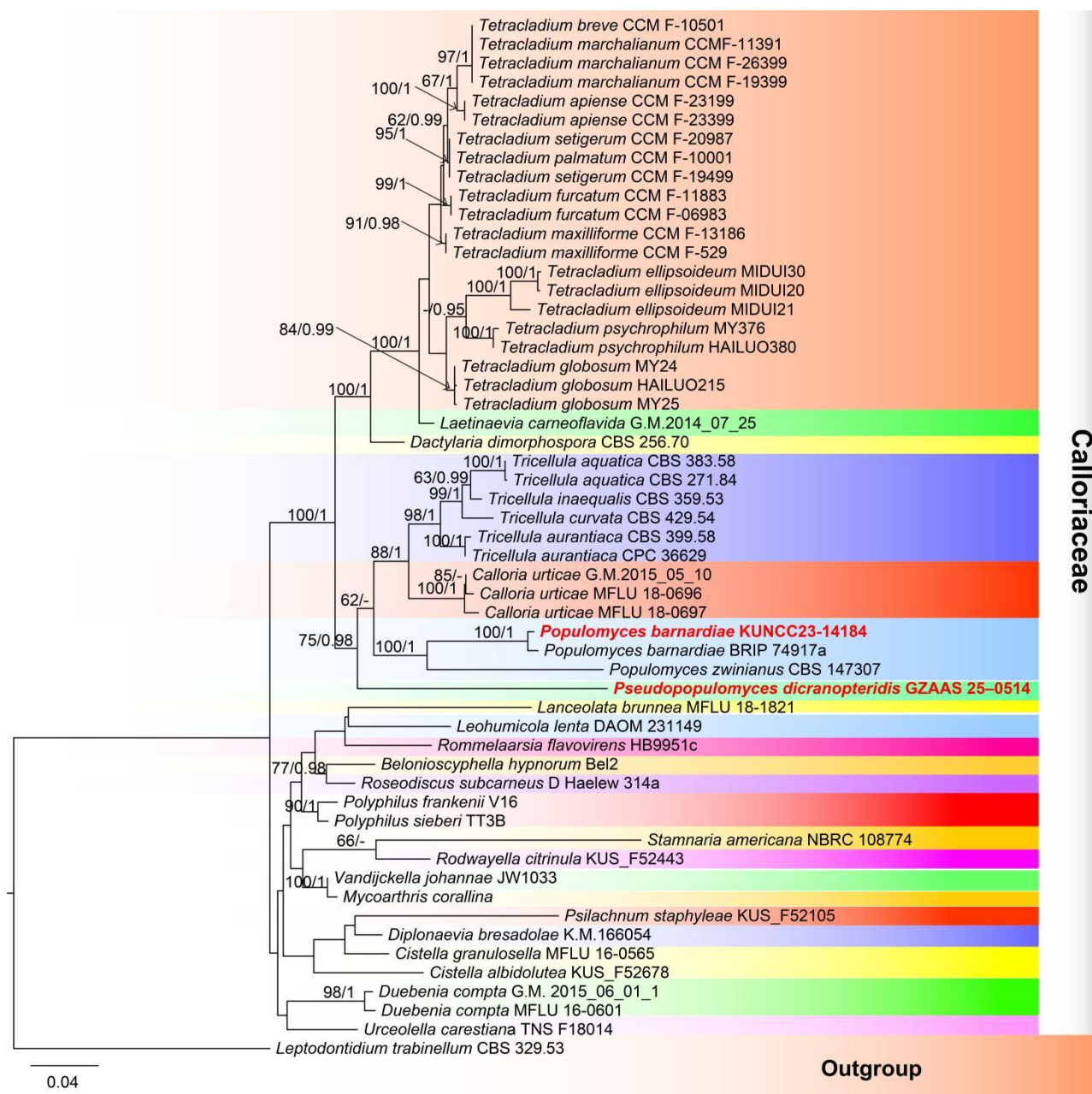


Figure 34 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. A total of 55 taxa were included in the combined analyses, which comprised 1464 characters after alignment. The best scoring RAxML tree with a final likelihood value of -9231.762549 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near branches as ML/PP. The tree is rooted with *Leptodontidium trabinellum* (CBS 329.53). The newly obtained strains are in red and bold.

Morphologically, *Pseudopopulomyces dicranopteridis* is similar to *Populomyces* in having

reduced conidiophores, monophialidic, simple, ampuliform with swollen basal cell, smooth-walled, hyaline conidiogenous cells and ellipsoidal, aseptate, hyaline, smooth-walled conidia. It is difficult to distinguish them from morphology. But phylogenetically, they are distinct, *Pseudopopulomyces dicranopteridis* formed a distinct lineage basal to *Tricellula*, *Calloria* and *Populomyces*. Thus, based on phylogenetic analysis and morphological differences, we introduce a new genus *Pseudopopulomyces* to accommodate our new isolate *Pseudopopulomyces dicranopteridis*.

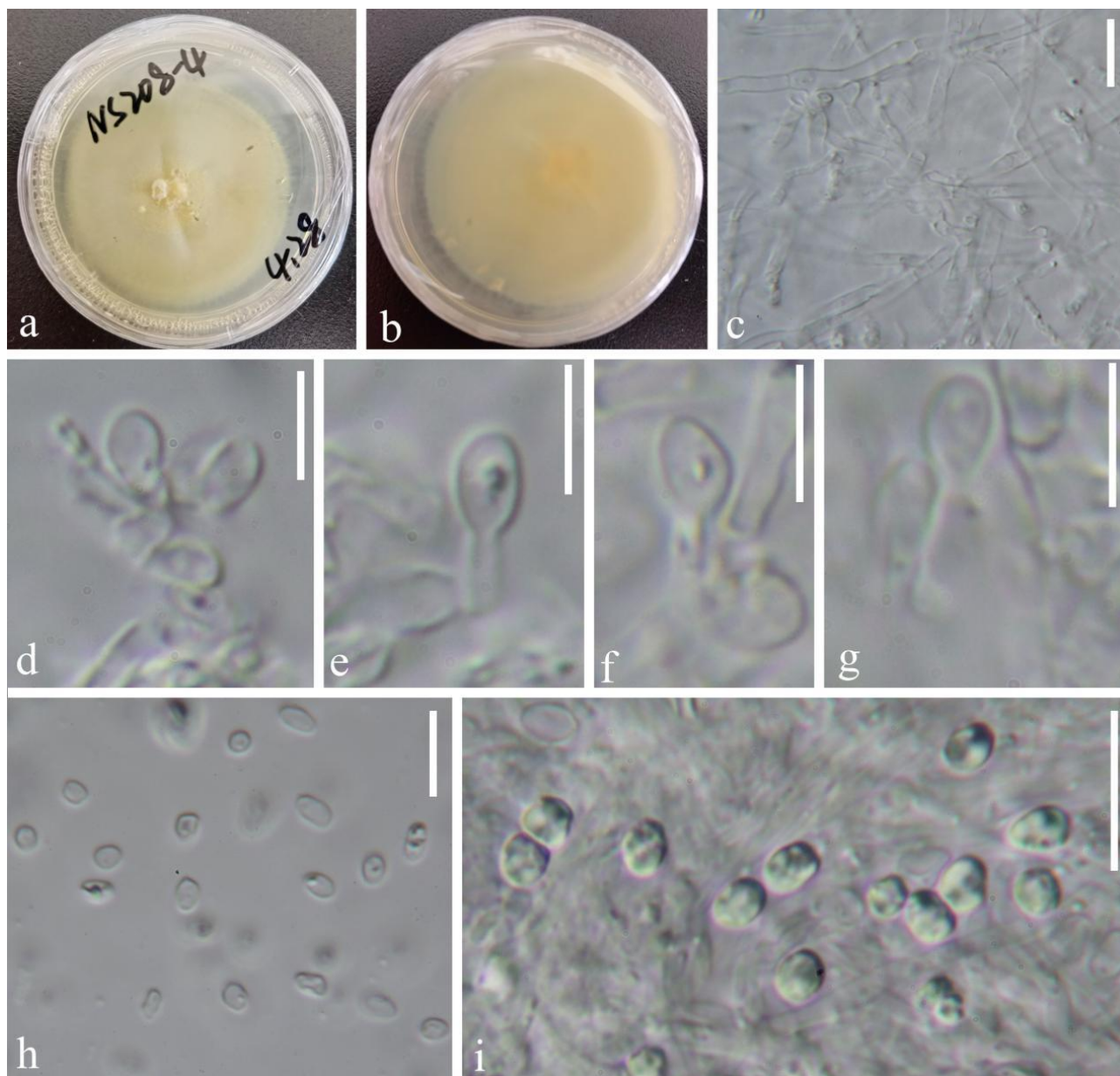


Figure 35 – *Pseudopopulomyces dicranopteridis* (GZAAS 25–0514, holotype) a, b Cultures on PDA from above and below. c Mycelium. d–g Conidiogenous cells and conidia. h–i Conidia. Scale bars: c, h, i = 10 μ m, d–g = 5 μ m.

Thelebolales Haeckel

Haeckel (1894) proposed the order *Thelebolales*, nevertheless, the classification of this order has long been disputed. Some studies mentioned that the order comprises two families, *Pseudeurotiaceae* and *Thelebolaceae* (Johnston et al. 2019, Batista et al. 2020). Ekanayaka et al.

(2019) treated *Pseudeurotiaceae* as a synonym of *Thelebolaceae*, as their phylogenetic analysis showed that *Pseudeurotiaceae* is nested within *Thelebolaceae*. Recently, Quijada et al. (2022) showed that *Thelebolaceae* is monophyletic, whereas *Pseudeurotiaceae* is polyphyletic and they introduced the third family, *Holwayaceae*, constituting three genera (*Holwaya*, *Patinella*, and *Ramgea*) previously placed in *Tympanidaceae*, *Thelebolaceae*, or *incertae sedis* in *Helotiales* or *Leotiomyces*.

Miniglobosispora D.F. Bao, Y.Z. Lu, K.D. Hyde & J.C. Kang, gen. nov.

Index Fungorum: IF 903968; Facesoffungi number: FoF 17870.

Etymology – The generic epithet refers to the small globose conidia

Endophytic in the rhizome of *Dicranopteris linearis*. Sexual morph: Not observed. Asexual morph: *Hyphae* hyaline to brown, septate, branched, aerial mycelium, thin-walled. *Conidiophores* hyaline to pale brown, septate, branched, slightly flexuous, with conidiogenous cell arising terminally or laterally. *Conidiogenous cells* polyblastic, integrated, hyaline, smooth-walled, cylindrical to oblong. *Conidia* single or catenate, hyaline, aseptate, thin-walled, smooth, obovoid to clavate, globose, subglobose, sometimes truncate at both ends or truncate at base and rounded at the apex, sometimes with one or more hilum at one end.

Type species – *Miniglobosispora guizhounises* D.F. Bao, J.Y. Zhang, Y.Z. Lu & J.C. Kang

Miniglobosispora guizhounises J. Y. Zhang, D.F. Bao, K.D. Hyde & J.C. Kang, sp. nov. Fig. 36

Index Fungorum: IF 903969; Facesoffungi number: FoF 17869.

Etymology – Refers to the Guizhou Province, where the holotype was collected.

Holotype – KUN-HKAS 129872

Endophytic in the root of *Dicranopteris ampla*. Sexual morph: not observed. Asexual morph: *Mycelium* in culture partly immersed, partly aerial, composed of hyaline to brown, septate, branched, aerial mycelium, thin-walled, hyphae *Conidiophores* hyaline to pale brown, septate, branched, slightly flexuous, with conidiogenous cells arising terminally or laterally. *Conidiogenous cells* monoblastic, polyblastic, integrated, hyaline, smooth-walled, cylindrical to oblong. *Conidia* 3.6–6.2 × 1.8–2.7 µm ($\bar{x}$ = 4.2 × 2.4 µm, n = 30), single or catenate, hyaline, aseptate, thin-walled, smooth, globose to subglobose, obovoid to clavate, or irregular, sometimes truncate at both ends or truncate at the base and rounded at the apex, sometimes with 1–3 hilum at the base, guttulate.

Culture characters – Colonies on PDA medium, growing fast, dense, covered with abundant, white, cottony to woolly aerial mycelia, reverse brown to dark brown.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi and Miao Autonomous County, from the root of *Dicranopteris ampla*, 2 August 2022, J.Y. Zhang, (116–2 = KUN-HKAS 129872 = GZAAS 23–0784, holotype).

GenBank numbers – ITS: PV138666, LSU: PV138565, SSU: PV164579, rpb2: PV188071

Notes – In our phylogenetic analysis, the new strain (KUN-HKAS 129872) grouped with *Alatospora*, *Gorgomyces*, and *Miniancora* as a monophyletic clade distinct from *Thelebolaceae*. However, our new isolate formed an independent clade that is distinct from the three genera (Fig. 37). Morphologically, our new strain is quite different from *Alatospora*, *Gorgomyces*, and *Miniancora* in having holoblastic to polyblastic and phialidic conidiogenous cells and single or catenate, hyaline, aseptate, clavate to short cylindrical, globose to subglobose conidia. Species in *Alatospora* and *Miniancora* have long conidiophores, phialidic conidiogenesis, and conidia that are tetra- or multi-radiate, T-shaped or flail-shaped conidia, with filiform, septate, main axis and 0–4 branches (Ekanayaka et al. 2019). *Gorgomyces* has solitary, filiform conidia with an apical appendage and a

stalk cell (Roldán 1989). Hence, based on its distinct morphology and phylogenetic analysis, we introduce a new genus, *Miniglobosispora*, to accommodate our new strain as *Miniglobosispora guizhounises*.

Sordariomycetes O.E. Erikss. & Winka

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde

Diaporthales Nannf.

Nannfeldt (1932) established *Diaporthales*. The order comprises saprobes, endophytes, and pathogens on plants, animals, or soil (Alvarez et al. 2016, Senanayake et al. 2017, 2018, Fan et al. 2018, Hyde et al. 2020a). We followed the latest treatment of *Diaporthales* by Wijayawardene et al. (2022), which accepted 32 families.

Diaporthaceae Höhn. ex Wehm.

Diaporthaceae was introduced by Höhnelt (1917) and placed in *Diaporthales*. Wehmeyer (1975) included *Diaporthe* and *Mazzantia* in this family, which was later confirmed by Castlebury et al. (2002) based on a phylogenetic analysis of LSU sequence data. Afterwards, several new genera and previously introduced genera have been confirmed in the family based on phylogenetic analysis (Lumbsch & Huhndorf 2010, Lamprecht et al. 2011, Dai et al. 2014, Voglmayr & Jaklitsch 2014, Maharachchikumbura et al. 2015). Maharachchikumbura et al. (2015) accepted 11 genera viz. *Allantoportha*, *Apioporthella*, *Clypeoporthella*, *Diaporthe*, *Diaporthella*, *Diaporthopsis*, *Leucodiaporthe*, *Mazzantia*, *Mazzantiella*, *Ophiodiaporthe* and *Pustulomyces* in *Diaporthaceae* based on phylogenetic analysis. However, *Mazzantiella* and *Clypeoporthella* have been synonymized under *Mazzantia* and *Diaporthe*, respectively. *Diaporthella* was excluded from the family by Senanayake et al. (2017, 2018) as the genus clustered out of *Diaporthaceae*. The latest treatment of *Diaporthaceae* was provided by Hyde et al. (2024) who accepted 15 genera: *Apioporthella*, *Apiosphaeria*, *Chaetoconis*, *Chiangraiomycetes*, *Diaporthe*, *Hyaliappendispora*, *Leucodiaporthe*, *Massariothea*, *Mazzantia*, *Ophiodiaporthe*, *Paradiaporthe*, *Phaeocystostroma*, *Phaeodiaporthe*, *Pseudophaeocystostroma*, *Pustulomyces*, *Pulvinaticonidioma*, *Stenocarpella* and *Subellipsoidispora*.

Diaporthe Nitschke

Diaporthe is a large and diverse genus, introduced by Nitschke (1870) and typified by *D. eres*. Initially, *Diaporthe* species were believed to be host-specific, leading to the identification of numerous species based on morphological characteristics and host association (Gomes et al. 2013, Gao et al. 2016). However, it is now understood that *Diaporthe* species exhibit significant inter- and intra-species diversity and are not host-specific, with many species occurring on multiple hosts. Consequently, morphological features and host association alone are insufficient for accurate species identification (Rehner & Uecker 1994, Wehmeyer 1933, Mostert et al. 2001, Gomes et al. 2013). Currently, multigene phylogenetic analyses (ITS, *tub2*, *tef1-α*, *cal* and *his3*), combined with morphological characteristics and ecological data, are employed to delimit *Diaporthe* species (Gao et al. 2017, Yang et al. 2020, Norphanphoun et al. 2022, Hongsanan et al. 2023, Liu et al. 2024, Dissanayake et al. 2024). Members of the genus *Diaporthe* function as endophytes, saprobes, or pathogens and are known to cause severe plant diseases, such as dieback, cankers, leaf spots, blights, rot, and wilt, affecting a variety of economically important agricultural crops (Gomes et al. 2013, Dissanayake et al. 2017, Bai et al. 2022, Hongsanan et al. 2023, Zhou et al. 2024).

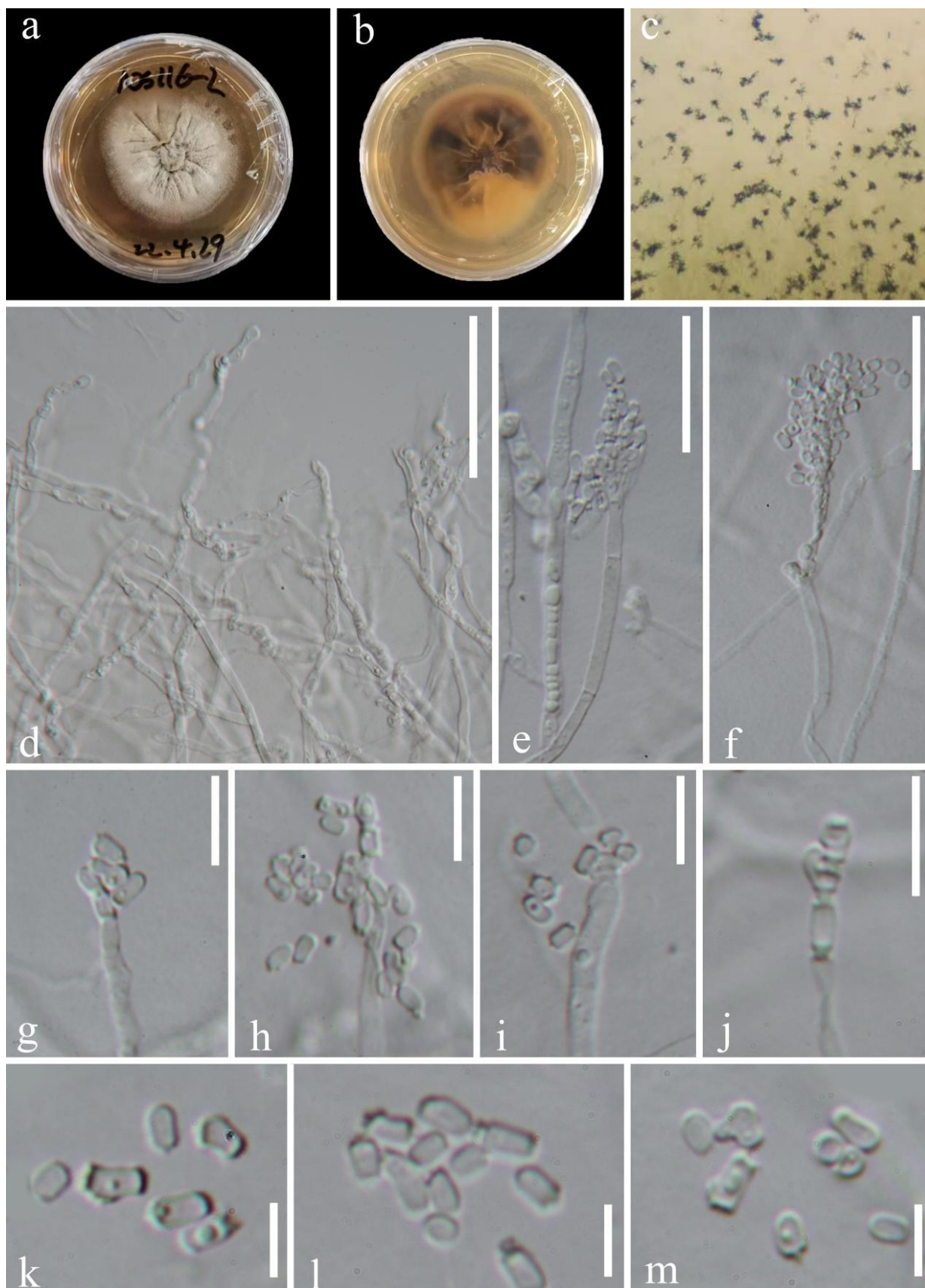


Figure 36 – *Miniglobospora guizhounises* (KUN-HKAS 129872, holotype). a, b Culture on PDA from above and below. c Colonies on PDA. d Mycelium. e, f Conidiophores, conidiogenous cells, and conidia. g–j Conidiogenous cells with conidia. k–m Conidia. Scale bar: e, d = 50 μ m, f = 100 μ m, g–j = 20 μ m, k–m = 10 μ m.

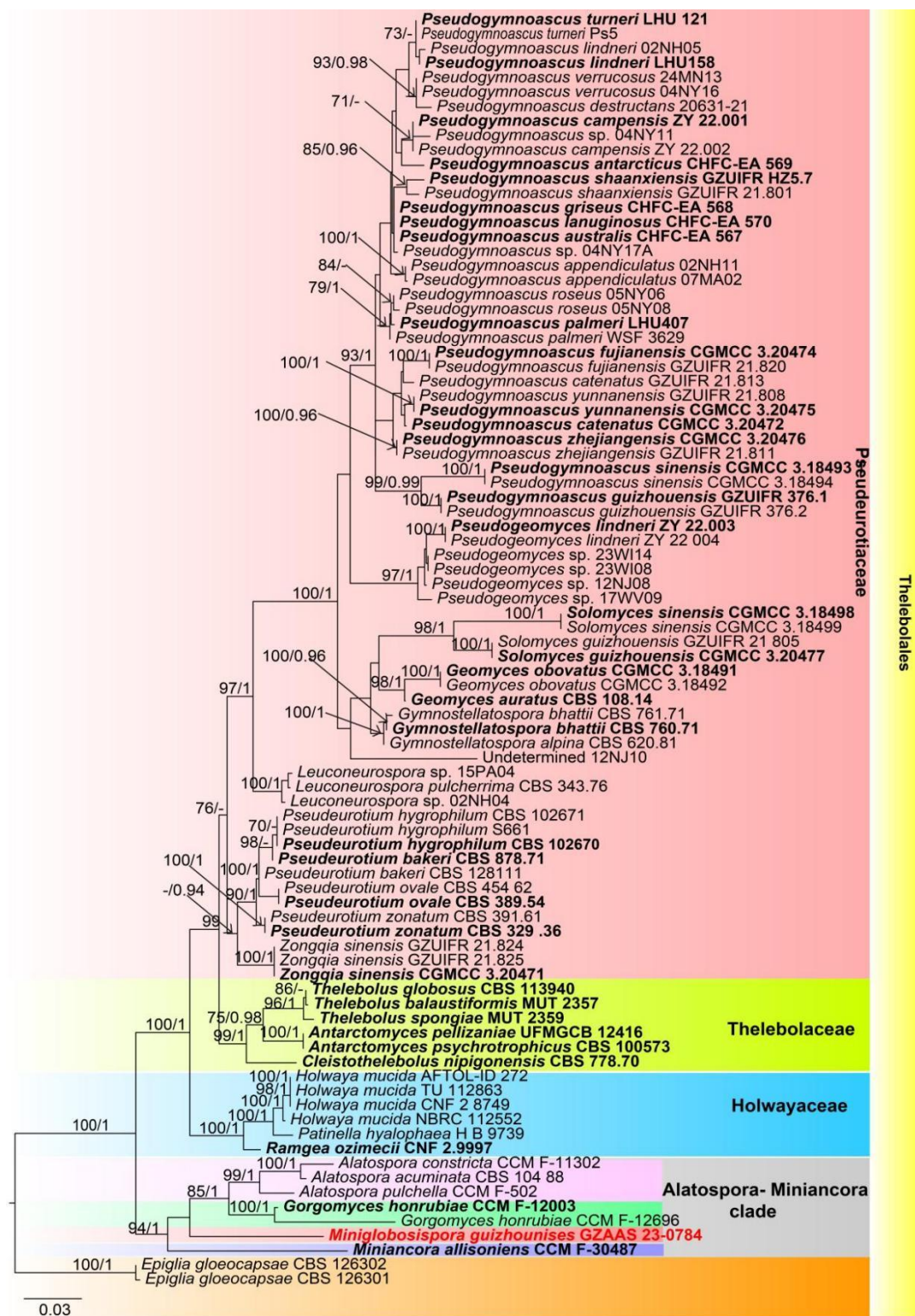


Figure 37 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. 88 taxa were included in the combined analyses, which comprised 1530 characters after alignment. The best scoring RAxML tree with a final likelihood value of -8632.476251 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near branches as ML/PP. The tree is rooted with *Epiglia gloeocapsae* (CBS 126302 and CBS 126301). The newly obtained strains are in red and the type strains are in bold.

There are currently 1,299 *Diaporthe* species listed in Index Fungorum (2024) (accessed 1 November 2024), though only about one-fifth of these species have been linked to molecular data (Zhou et al. 2024). Recently, Dissanayake et al. (2024) re-evaluated the genus, refining species boundaries and dividing *Diaporthe* into seven sections (*Crotalariae*, *Eres*, *Foeniculina*, *Psoraleaepinnatae*, *Rudis*, and *Sojae*) and proposing 15 species complexes. In this study, following the treatment of Dissanayake et al. (2024), four *Diaporthe* species belonging to two sections (*Foeniculina* and *Sojae*) were identified based on phylogenetic and morphological analyses. In addition, two new recently published species *D. hainanensis* and *D. harriottiae* are synonymized under *D. arecae* based on phylogenetic analysis and morphological characteristics. Interestingly, *D. xishuangbanica* was reported for the first time as a hyphomycete with brown conidia in this study. In contrast, the conidia of *Diaporthe* are typically hyaline. We speculate that this difference may be due to various morphotypes; specifically, our species is a hyphomycete, while other species are coelomycetes. Additionally, the same species may exhibit different characteristics depending on the conditions.

Diaporthe arecae (H.C. Srivast., Zakia & Govindar.) R.R. Gomes, Glienke & Crous, Persoonia 31: 16 (2013) Fig. 38

= *Diaporthe hainanensis* Qin Yang, in Liu, Luo, Huang & Yang, MycoKeys 102: 235 (2024)

= *Diaporthe harriottiae* Y.P. Tan, in Tan & Shivas, Index of Australian Fungi 44: 1 (2024)

Index Fungorum: IF 802924; Facesoffungi number: FoF 08405.

Endophytic in the fresh stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose or irregular, brownish to black, solitary or in groups, embedded, erumpent, cream to pale luteous conidial droplets exuding from the central ostioles. *Conidiophores* 13–20 × 2–3 µm ($\bar{x}$ = 16.6 × 2.3 µm, n = 10) reduced to conidiogenous cells, cylindrical to subcylindrical, truncate at the apex, (0)1–2 septate, densely aggregated, hyaline, smooth-walled. *Conidiogenous cells* 9–11 × 2–3 µm ($\bar{x}$ = 10.2 × 2.4 µm, n = 10), phialidic, terminal, cylindrical to subcylindrical, hyaline. *Alpha conidia* not observed. *Beta conidia* 25–30 × 1.5–2.5 µm ($\bar{x}$ = 28 × 1.6 µm, n = 36), filiform, slightly curved, tapering towards the ends, aseptate, hyaline, not guttulate. *Gamma conidia* not observed.

Culture characters – Colonies on PDA medium occupied the whole plate in 15 days at 25 °C. Colony at first white, becoming cream to yellowish, flat, with dense and felted mycelium, white to cream with brownish dots with age, with visible solitary or aggregated conidiomata at maturity, reverse pale brown to yellowish brown.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the fresh stem of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (108–1 = KUN-HKAS 136229), living culture (KUNCC 24–17928).

GenBank numbers – ITS: PV138705, *tefl-α*: PV177101, *tub2*: PV221994

Notes – Dissanayake et al. (2024) recently re-evaluated the species within *Diaporthe*, combining and synonymizing many species. Approximately 50 species were merged into a single species, *D. arecae*, based on both phylogenetic and morphological analyses. Following the treatment by Dissanayake et al. (2024), our phylogenetic analysis showed that our new isolate grouped within the *D. arecae* clade (Fig. 39). Morphologically, the new isolate also matches the characteristics of *D. arecae*. Therefore, we have identified our new isolate as *D. arecae* and report it as a new host record for *Dicranopteris pedata*.

Recently, two new species, *D. hainanensis* and *D. harriottiae*, were introduced by Liu et al. (2024) and Tan & Shivas (2024), respectively. However, these two species were not included in the

phylogenetic analysis of Dissanayake et al. (2024). Our phylogenetic analysis revealed that both species clustered within the *D. arecae* clade. Following the treatment of Dissanayake et al. (2024), we synonymize these two species under *D. arecae*.

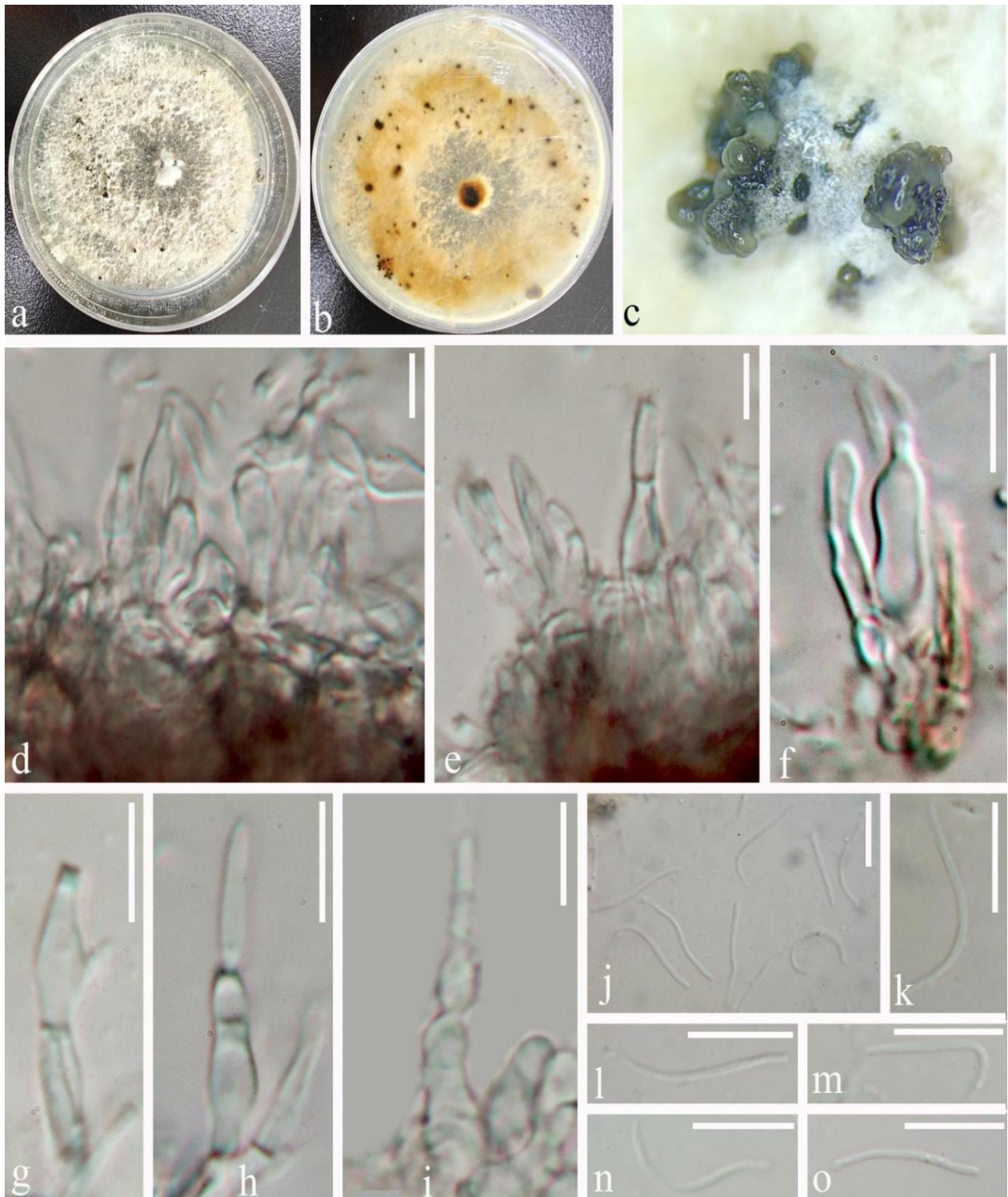


Figure 38 – *Diaporthe arecae* (KUN-HKAS 136229, new host record). a, b Front and reverse colony on PDA. c Conidiomata on the PDA. d Mycelium. d–g Conidiophores. h, i Conidiogenous cells with beta conidia. j–o Beta conidia. Scale bars: Scale bars: d–i = 5 µm, j–o = 10 µm.

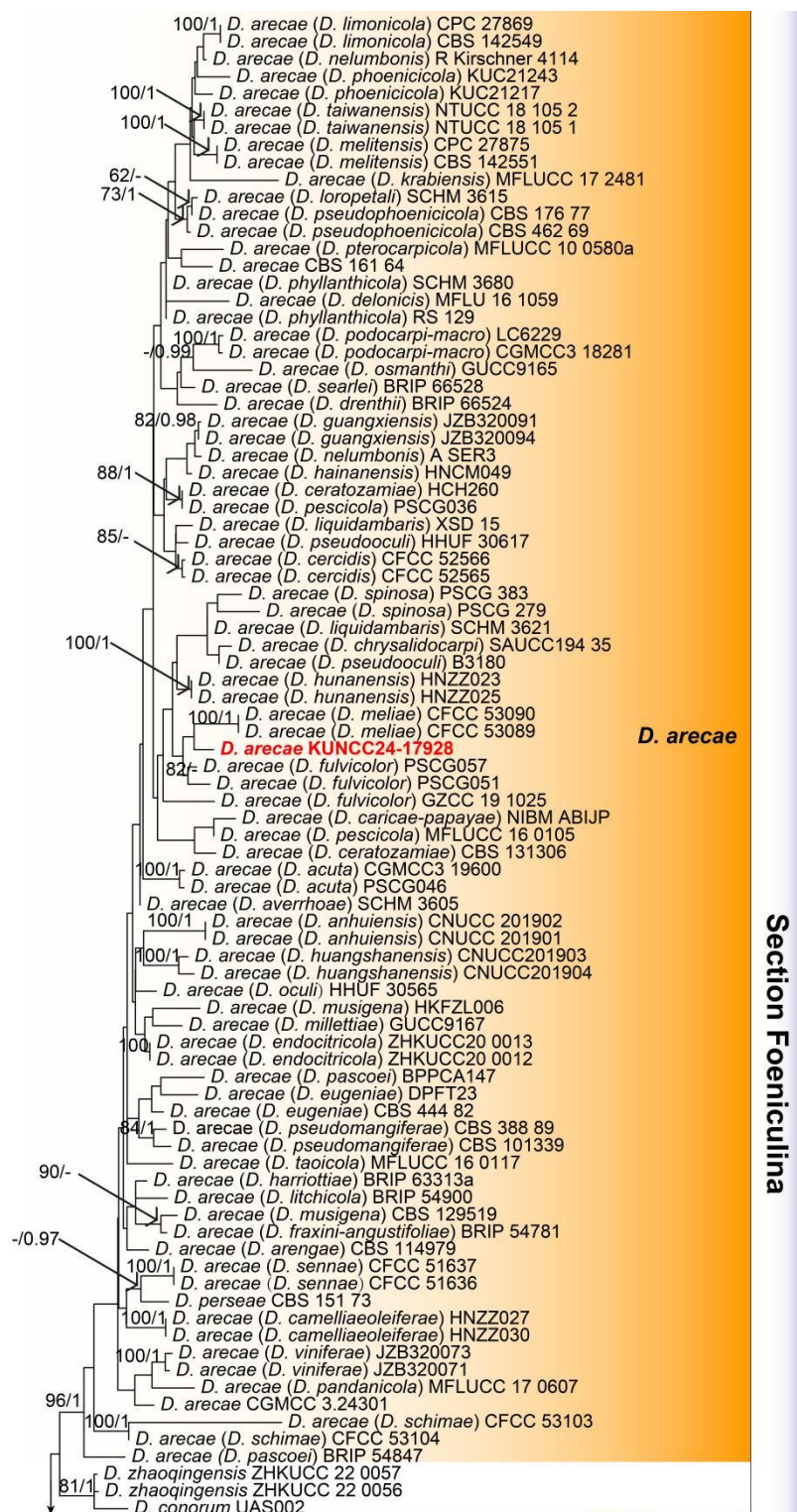


Figure 39 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1*- α , *cal*, and *tub2* sequence data. 210 taxa were included in the combined analyses, which comprised 2131 characters after alignment. The best scoring RAxML tree with a final likelihood value of -38334.068800 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near branches as ML/PP. The tree is rooted with *D. amygdali* (CBS 126679). The newly obtained strains are in red and bold.

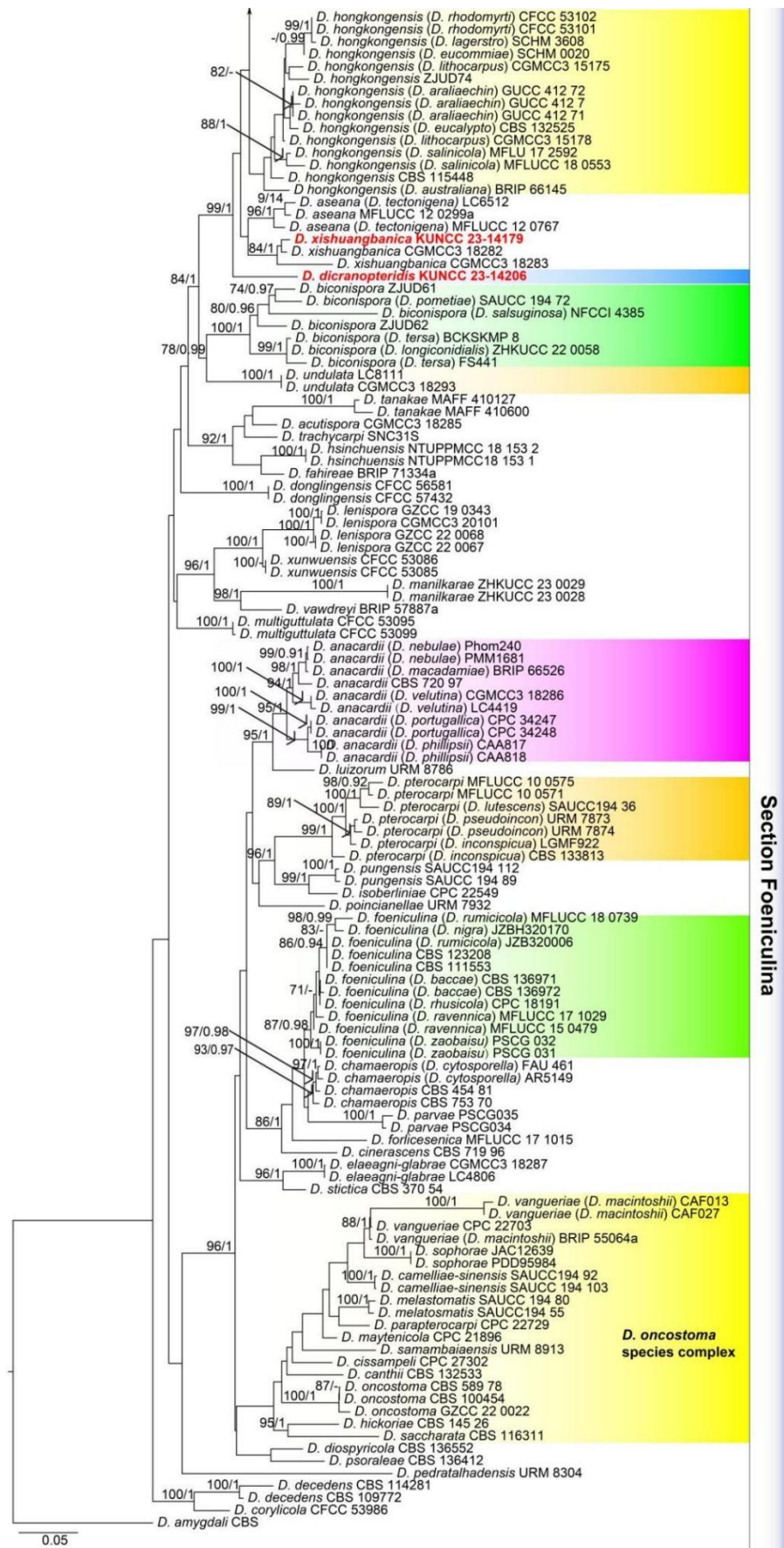


Figure 39 – Continued

Diaporthe dicranopteridis J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov.

Fig. 40

Index Fungorum: IF 903970; Facesoffungi number: FoF 17871.

Etymology – Refers to the host fern *Dicranopteris*, on which the holotype was isolated.

Holotype – GZAAS 25–0527

Endophytic in the fresh stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose or irregular, dark brown to black, solitary or in groups, embedded, erumpent, white to cream conidial drops exuded from ostioles. *Conidiomatal wall* brown to dark brown, composed several layers of brown to dark brown cells of *textura angularis*. *Conidiophores* 31–53 × 2–3 µm ($\bar{x}$ = 42.4 × 2.5 µm, n = 25), cylindrical to subcylindrical, truncate at the apex, (0)1–2 septate, densely aggregated, hyaline, smooth-walled. *Conidiogenous cells* 13–24 × 1.5–2.5 µm ($\bar{x}$ = 18.8 × 2.2 µm, n = 34), phialidic, terminal, cylindrical to subcylindrical, hyaline. *Alpha conidia* not observed. *Beta conidia* 12–15 × 2–2.5 µm ($\bar{x}$ = 13.7 × 2.1 µm, n = 34), filiform, slightly curved, tapering towards the ends, aseptate, hyaline, not guttulate. *Gamma conidia* not observed.

Culture characters – Colonies on PDA medium grow rapidly, forming dense, compact masses. The surface is densely covered with abundant white mycelial growth and bears distinct black fruiting bodies; the reverse side appears dark grey with scattered white spots.

Material examined – China, Guizhou Province, Libo County, Southwest Guizhou Buyi and Miao Autonomous County, from the fresh stem of *Dicranopteris pedata*, 8 April 2022, J. Y Zhang, (379–2 = GZAAS 25–0527, holotype), ex-type culture (KUNCC 23–14206).

GenBank numbers –ITS: PV138703, *tefl-α*: PV177099, *tub2*: PV221992, *his3*: PV188093

Notes – In our phylogenetic analysis, *Diaporthe dicranopteridis* (KUNCC 23–14206) formed a distinct lineage within *Diaporthe* (Section Foeniculina) (Fig. 39), which can be recognized as a new species. Morphologies of *Diaporthe* species are quite similar to each other; thus, it is difficult to identify them without multi-locus phylogenetic analysis. Our new species, *D. dicranopteridis* is phylogenetically closely related to *D. xishuangbanica*, *D. tectonigena*, and *D. aseana*. But *D. dicranopteridis* differs from *D. tectonigena* in having longer conidiophores (31–53 vs. 9–32 µm) and shorter *Beta conidia* (12–15 vs. (16–)29–30(–34) µm) (Doilom et al. 2016). *Diaporthe dicranopteridis* is different from *D. xishuangbanica* and *D. aseana* in having longer conidiophores (31–53 µm in *D. dicranopteridis*, 13–34.5 µm in *D. xishuangbanica* and 8–15 µm in *D. aseana*) (Hyde et al. 2016, Gao et al. 2017). Thus, *D. dicranopteridis* is introduced as a new species, based on phylogeny and morphological analyses.

Diaporthe tulliensis R.G. Shivas, Vawdrey & Y.P. Tan, in Crous et al., Persoonia 35: 301 (2015)

Fig.41

Index Fungorum: IF 812896; Facesoffungi number: FoF 16300;

Endophytic in stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose or irregular, dark brown to black, solitary or in groups, embedded, erumpent, white to cream conidial drops exuded from ostioles. *Conidiophores* densely aggregated, reduced to conidiogenous cells, hyaline to brown, smooth-walled. *Conidiogenous cells* phialidic, terminal, cylindrical to subcylindrical, hyaline. *Alpha conidia* 11–14 × 3–4 µm ($\bar{x}$ = 12.9 × 3.6 µm, n = 30), ellipsoidal to cylindrical, acute at both ends, straight, hyaline, aseptate, smooth-walled, small-guttulate. *Beta conidia* and *Gamma conidia* not observed.

Culture characters – Colonies on PDA reach 50–60 mm diameter within 15 days at 25 °C, flat, white to grey on the surface, bears distinct black fruiting bodies and produce red pigmentation; brown to dark gray with red pigment.

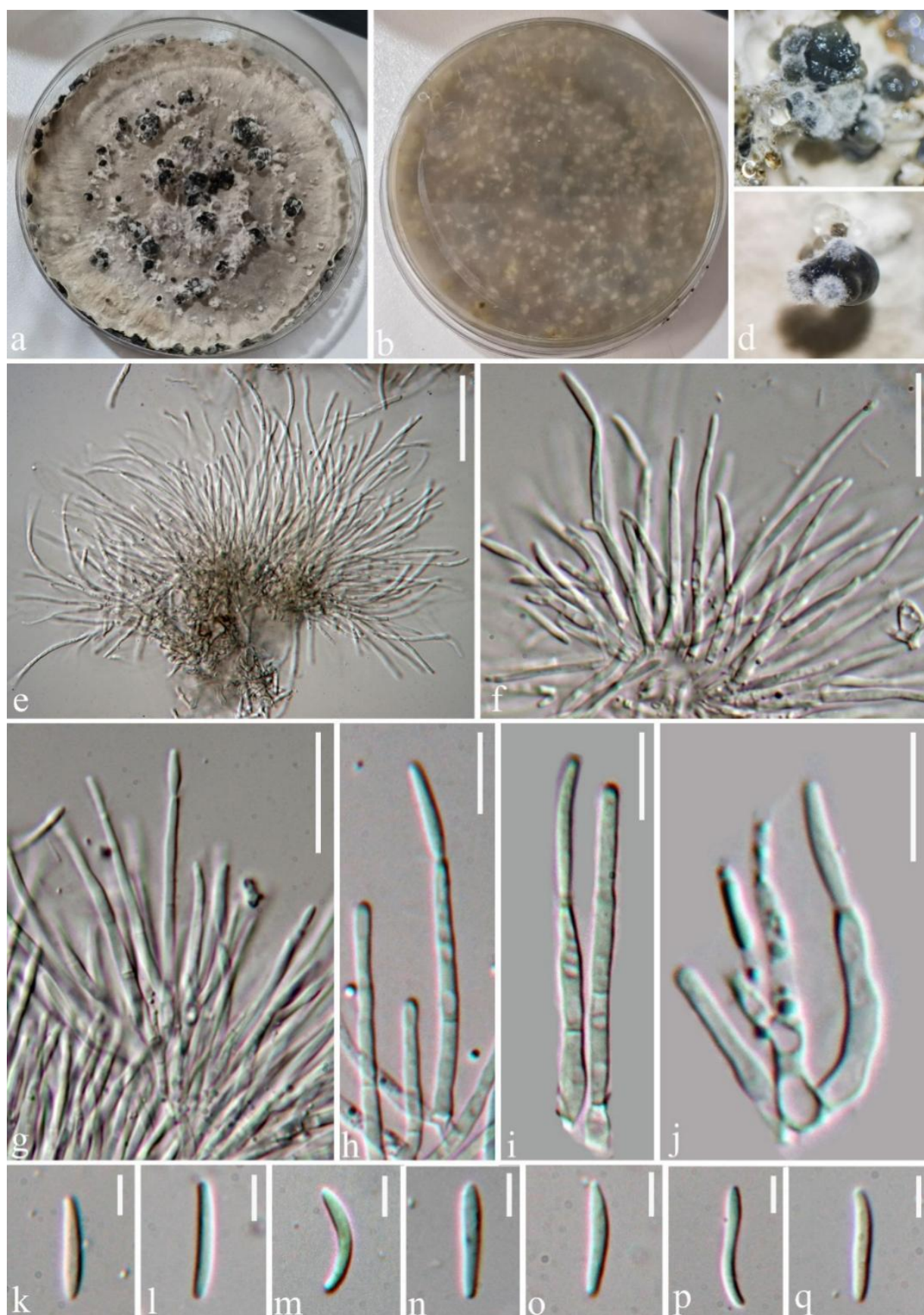


Figure 40 – *Diaporthe dicranopteridis* (GZAAS 25–0527, holotype). a, b Obverse and reverse colony on PDA. c, d Conidiomata on the PDA. e–j Conidiophores, conidiogenous cells, and conidia. k–q Beta conidia. Scale bars: Scale bars: e = 40 μm, f, g = 20 μm, h–j = 10 μm, k–q = 5 μm.

Material examined – China, Guizhou Province, Zhenfeng County, Southwest Guizhou Buyi and Miao Autonomous County, the stem of *Dicranopteris pedata*, 17 March 2022, J.Y. Zhang, (290–1 = KUN-HKAS 136235), living culture KUNCC 24–17933.

GenBank numbers – ITS: PV138706, *tef1-α*: PV177102, *tub2*: PV221995, *his3*: PV188092

Notes – In our phylogenetic analysis, the new isolate KUNCC 24–17933 clustered with two strains of *Diaporthe hubeiensis* (JZB320128 and JZB320123) (Fig. 39), which was introduced by Manawasinghe et al. (2019) from the diseased trunk of *Vitis vinifera* in China. Morphologically, the new isolate is nearly identical to *D. hubeiensis*, except for the conidia, which are small-guttulate and larger than those of the holotype of *D. hubeiensis*. The ITS, *tub2*, *his3*, *cal*, and *tef1-α* sequences of the new isolate (KUNCC 24–17933) show no significant differences from *D. hubeiensis* (JZB320123). However, Dissanayake et al. (2024) recently refined the species boundaries and complexes of *Diaporthe*, *D. hubeiensis* was synonymized as *D. tulliensis*. Following this treatment, we identified our new isolate as *D. tulliensis*. This is the first report of *D. tulliensis* from *Dicranopteris pedata*.

Diaporthe xishuangbanica Y.H. Gao & L. Cai, in Gao, Liu, Duan, Crous & Cai, IMA Fungus 8(1): 179 (2017). Fig. 42

Index Fungorum: IF 820685; Facesoffungi number: FoF 11356;

Endophytic in the rhizome of *Dicranopteris linearis*. Sexual morph: Not observed. Asexual morph: *Hyphae* hyaline to brown, septate, branched, aerial mycelium, thin-walled. *Conidiophores* cylindrical, straight or slightly flexuous, hyaline to pale brown, septate, branched, with conidiogenous cell arising terminally or laterally. *Conidiogenous cells* polyblastic, terminal, integrated, hyaline, smooth-walled, cylindrical to oblong. *Conidia* 4–6 × 2–3 μm ($\bar{x}$ = 4.9 × 2.8 μm, n = 40), single, in a short chain, aseptate, thin-walled, smooth, obovoid to clavate, or ellipsoidal to fusiform, rounded at the apex, truncate at the base, straight, hyaline when young, becoming olive brown when mature, aseptate, smooth-walled, guttulate.

Culture characters – Colonies on PDA medium, growing fast, dense, covered with abundant, white at the surface, cottony to woolly aerial mycelia; reverse dark grey.

Material examined – China, Guizhou Province, Zhenfeng County, Southwest Guizhou Buyi and Miao Autonomous County, the rhizome of *Dicranopteris pedata*, 17 March 2022, J.Y. Zhang, (171–1 = KUN-HKAS 129883), living culture KUNCC 23–14179.

GenBank numbers – ITS: PV138704, *tef1-α*: PV177100, *tub2*: PV221993, *his3*: PV188091.

Notes – The phylogenetic analysis showed that our new isolate KUNCC 23–14179 clustered sister to the ex-type strain of *D. xishuangbanica* (CGMCC 3.18282) with 83% bootstrap support (Fig. 43). The comparison of nucleotides of ITS, *tef1-α*, *tub2* and *his3* sequences between our new isolate and *D. xishuangbanica* (CGMCC 3.18282) revealed 8bp, 0bp, 1bp and 4bp differences, respectively, which were not significantly different from *D. xishuangbanica* (CGMCC 3.18282). Thus, we identified our new isolate as *D. xishuangbanica*.

Morphologically, our new isolate KUNCC 23–14179 was found as hyphomycetes, while the holotype of *D. xishuangbanica* was reported as coelomycetes (Gao et al. 2017). Our new isolate is similar to the holotype of *D. xishuangbanica* in having fusiform, multi-guttulate conidia. However, our new isolate has single or catenate, hyaline to olive brown conidia, which are different from the holotype; the occurrence of these differences may be due to the different morphs as our new isolate is a hyphomycetes, while the holotype is a coelomycete. It would be fascinating to look into the morphologies of the same fungus in different asexual morphs; there could be differences between the hyphomycetous and coelomycetous asexual morphs of the same fungus.

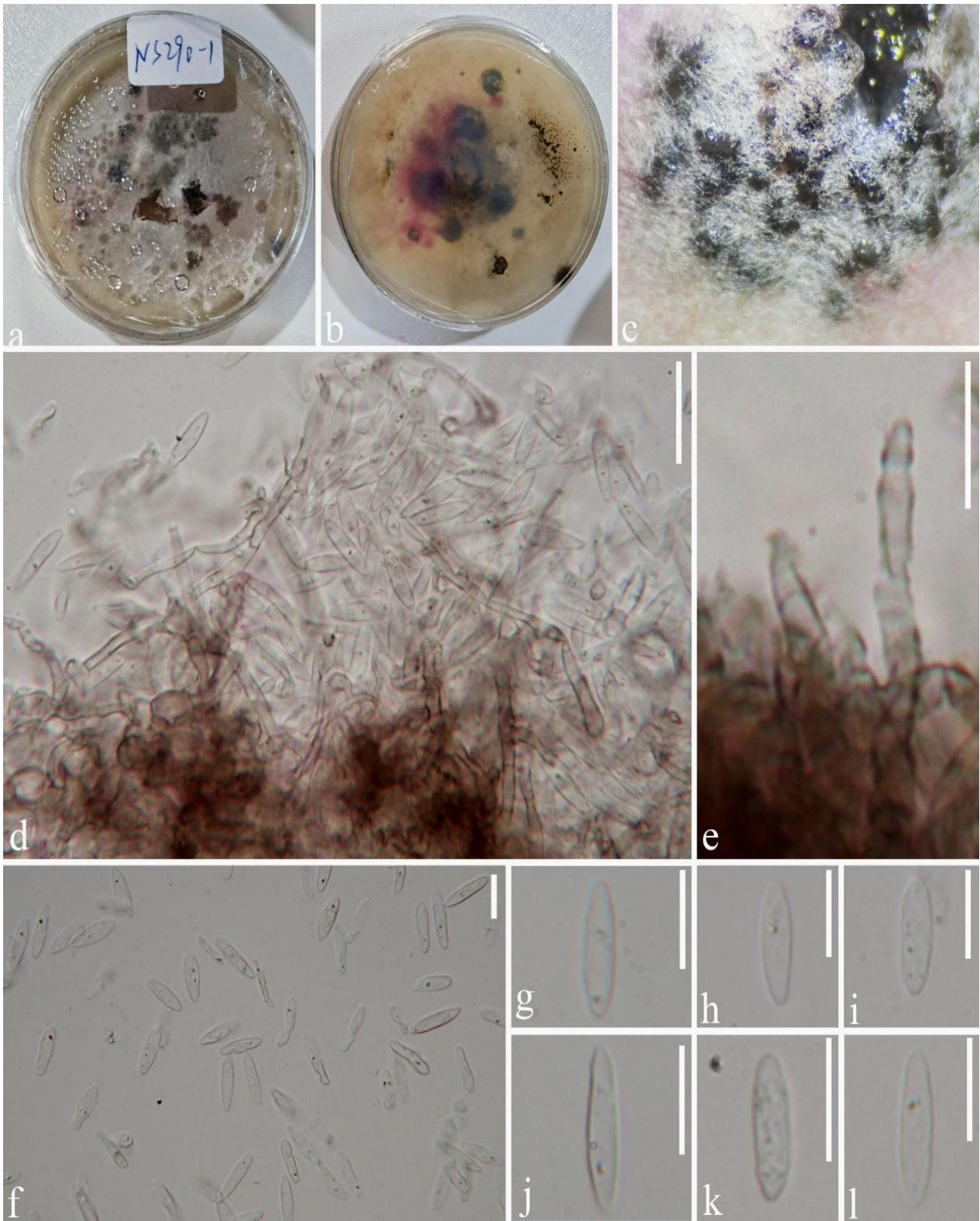
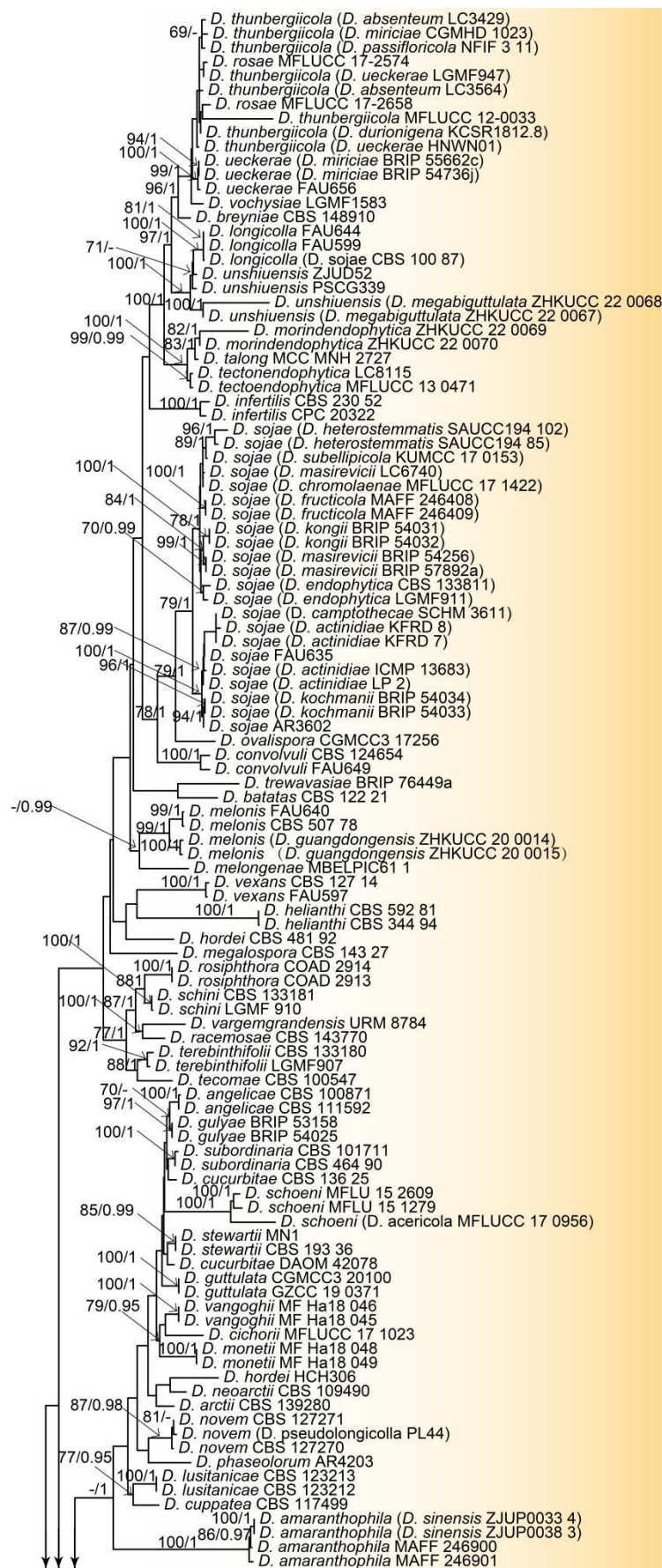


Figure 41 – *Diaporthe tulliensis* (KUN-HKAS 136235, new host record). a, b Front and reverse colony on PDA. c Conidiomata on the PDA. d Conidial mass, conidiophores with alpha conidia. e Conidiophores. f–l Alpha conidia. Scale bars: d = 20 μm. e–l = 10 μm.



Figure 42 – *Diaporthe xishuangbanica* (KUN-HKAS 129883, new host record). a, b Front and reverse colony on PDA. c Conidial mass on the PDA. d–h hyphae, conidiogenous cells and conidia. i–k Conidiogenous cells and conidia. l–t Conidia. Scale bars: Scale bars: d–h = 10 μm, i–t = 5 μm.



Section Sojae

Figure 43 – Phylogram generated from maximum likelihood analysis based on combined ITS, *cal*, *his3*, *tef1-α*, and *tub2* sequence data. 223 taxa were included in the combined analyses, which

comprised 2550 characters after alignment. The best scoring RAxML tree with a final likelihood value of -42468.030076 is presented. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near branches as ML/PP. The tree was rooted to *D. amygdali* (CBS126679 and CBS111811). The newly generated sequences are shown in red and bold.

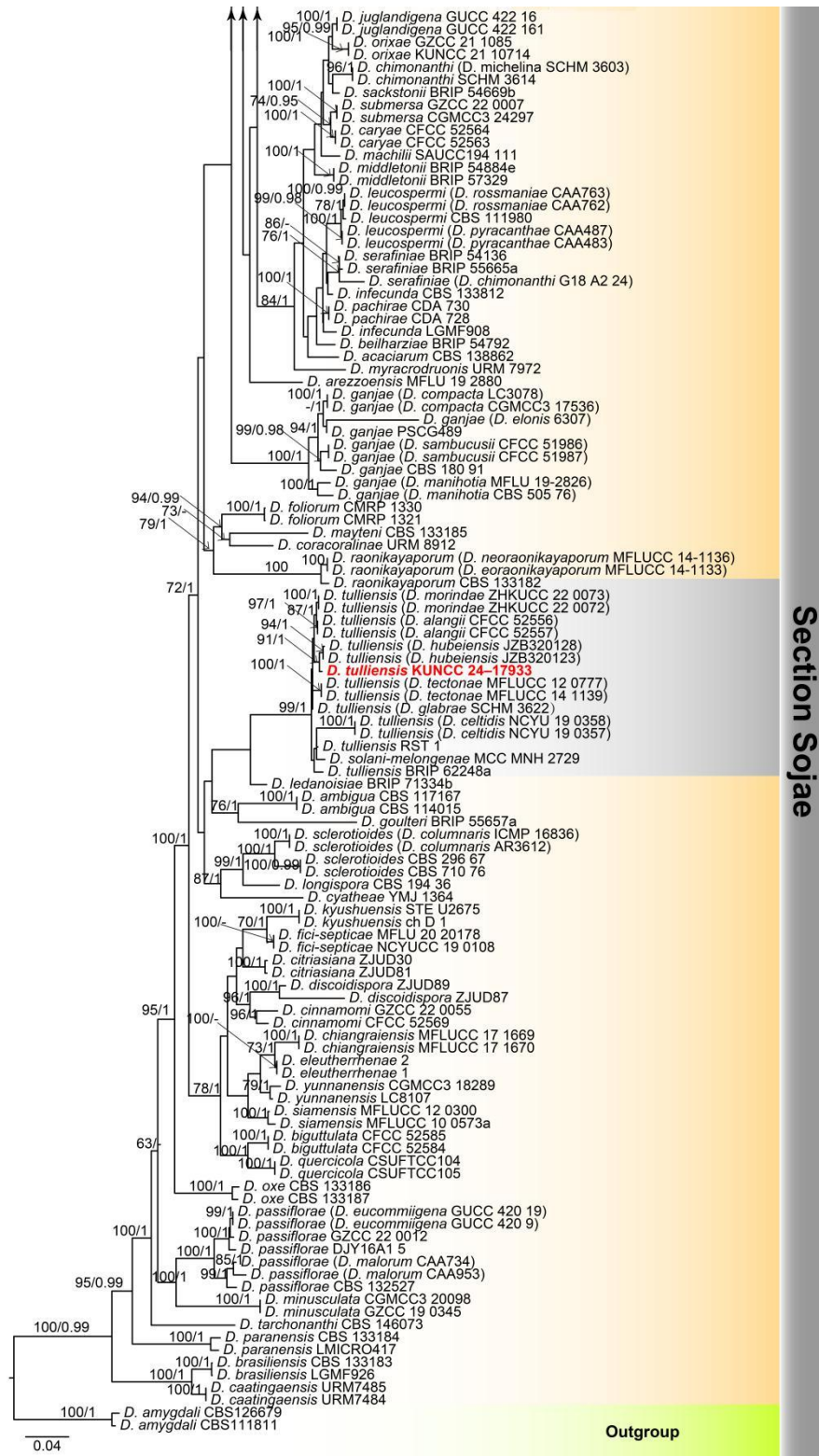


Figure 43 – Continued

Subclass *Hypocreomycetidae* O.E. Erikss. & Winka

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Glomerellales was validly introduced by Réblová et al. (2011); they have clarified the taxonomy of this order with accepted *Glomerellaceae* and two newly described families, *Australiascaceae* and *Reticulascaceae* based on morphology and a multi-locus phylogenetic analysis (LSU, SSU, and *rpb2*). Later, *Plectosphaerellaceae* and *Malaysiascaceae* were added to the order by Maharachchikumbura et al. (2016) and Tibpromma et al. (2018), respectively. However, the status of *Malaysiascaceae* may need further revision as the divergence time for *Malaysiascaceae* falls in the genus status (Hyde et al. 2020a).

Glomerellaceae Locq. ex Seifert & W. Gams

Glomerellaceae was initially introduced by Locquin (1984) it was not validated for publication. Zhang et al. (2006) accepted and formally introduced *Glomerellaceae* as a distinct family and placed it in *Hypocreomycetidae*. Maharachchikumbura et al. (2016) and Hyde et al. (2020) confirmed that *Glomerellaceae* is monophyletic with a single genus, *Colletotrichum*.

Colletotrichum Corda

Colletotrichum, the type genus of *Glomerellaceae*, is a speciose and ecologically diverse genus that includes endophytes, saprobes, plant pathogens, or can occur in several life modes, and a few species that are human pathogens and animal pathogens (Cai et al. 2009, Shivaprakash et al. 2011, Huang et al. 2013, Buchta et al. 2019, Liu et al. 2021, 2022, Jayawardena et al. 2021). Previously, *Colletotrichum* species were identified mainly based on host range and morphological characteristics. However, the characteristics of *Colletotrichum* species are not suitable for species-level identification due to their environmental dependencies, polyphyly, and the potential for multiple species to infect the same host plant (Than et al. 2008, Cai et al. 2009, Liu et al. 2022, Talhinhos & Baroncelli 2023, Zhang et al. 2024b). In recent years, a multi-locus phylogenetic approach has been presented for *Colletotrichum* species delimitation, which has greatly improved the identification of *Colletotrichum* species (Fu et al. 2019, Bhunjun et al. 2021b, Liu et al. 2022, Zhang et al. 2023b, Peng et al. 2023, Zhang et al. 2024b, Zhou et al. 2024, Sui et al. 2024). To date, 15 *Colletotrichum* species complexes have been identified (Liu et al. 2022, Zhou et al. 2024). Index Fungorum (2024) listed 2054 records of *Colletotrichum*; however, only about one-fifth have sequence data available in the GenBank database (Zheng et al. 2022). In this study, two new species and four new host records are described based on phylogeny and morphology.

Colletotrichum dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov.

Fig. 44

Index Fungorum: IF 903971; Facesoffungi number: FoF 17872.

Holotype – GZAAS 25–0524

Etymology – Refers to the host plant *Dicranopteris*, on which the holotype was collected.

Endophytic in fresh leaves of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Vegetative hyphae* hyaline or pale brown, smooth-walled, septate, branched. *Conidiomata* acervular, gregarious, pale luteous. *Setae* medium brown, paler towards the apex, smooth-walled, 2–4-septate, tip acute or round. *Conidiophores* 44–70 × 3.5–5 µm ($\bar{x}$ = 57 × 4.4 µm, n = 25), cylindrical, hyaline when young, becoming brown to dark brown when mature, hyaline to pale brown towards the apex, brown to dark brown at the base, branched, septate, smooth-walled. *Conidiogenous cells* 11–19 × 3–4.5 µm ($\bar{x}$ = 15.6 × 4 µm, n = 35), phialidic, integrated, terminal, hyaline, smooth-walled, cylindrical to clavate. *Conidia* 21–25 × 5–6 µm ($\bar{x}$ = 23.1 × 5.5 µm, n = 35), hyaline, aseptate,

guttulate, dry, cylindrical, straight or slightly curved, rounded or obtuse at the apex, obtuse at the end, straight or slightly curved, smooth-walled. *Appressoria*: not observed.

Cultural characteristics – Colonies on PDA reaching 68–70 mm diameter within 14 days at 25 °C, flat, entire margin, aerial mycelium white, cottony, conidiomata visible at maturity, white on the surface, brown to dark grey on reverse, without pigmentation,

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the fresh leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (292–4 = GZAAS 25–0524, holotype), ex-type culture (GZCC 23–0706).

GenBank numbers – ITS: PV138700, *tub2*: PV221989, *act*: PV188079, *gapdh*: PV221979.

Notes – In our phylogenetic analysis, our new isolate *Colletotrichum dicranopteridis* (GZCC 23–0706) clustered within *C. graminicola* species complex, and sister to *C. paraendophyllum* (LC13888) with 98% ML bootstrap support (Fig. 45). *Colletotrichum dicranopteridis* (GZCC 23–0706) is similar to *C. paraendophyllum* in having dark brown, smooth-walled, septate setae, branched conidiophores and hyaline, aseptate, guttulate, smooth-walled conidia. However, *C. dicranopteridis* (GZCC 23–0706) differs from *C. paraendophyllum* in having 2–4-septate setae and cylindrical, straight or slightly curved conidia with round or obtuse apex and obtuse end. While the setae of *C. paraendophyllum* are 1–2-septate, and conidia are gradually tapering towards a rounded apex and a usually truncate base, with a similar radian (Liu et al. 2022). A comparison of nucleotide in ITS, *tub2*, and *act* gene regions revealed 11bp, 19bp, and 29bp differences. Thus, based on phylogeny and morphological characteristics, we introduce our new isolate as a new species.

Colletotrichum fioriniae (Marcelino & Gouli) Pennycook, Mycotaxon 132(1): 150 (2017) [2016]
Fig. 46

Index Fungorum: IF 553097; Facesoffungi number: FoF 02891.

Endophytic in the stem of *Dicranopteris ampla*. Sexual morph: Not observed. Asexual morph: *Vegetative hyphae* hyaline or pale brown, smooth-walled, septate, branched. *Conidiomata* not observed. *Setae* 39–57 × 2.5–3 µm ($\bar{x}$ = 48.4 × 2.8 µm, n = 15), dark brown, smooth-walled, 3–4-septate, tip acute or round. *Conidiophores* cylindrical, hyaline to dark brown, branched, septate, smooth-walled. *Conidiogenous cells* 8–13 × 2–3 µm ($\bar{x}$ = 10.7 × 2.6 µm, n = 15), phialidic, integrated, terminal, hyaline to pale brown, smooth-walled, ampulliform. *Conidia* 10–13 × 3–3.5 µm ($\bar{x}$ = 12 × 3.2 µm, n = 35), fusiform with both ends acute, straight, or slightly curved, hyaline, aseptate, dry, guttulate, smooth-walled. *Appressoria*: not observed.

Cultural characteristics – Colonies on PDA reaching 30–40 mm diameter within 14 days at 25 °C, flat, entire margin, dark grey to greyish brown on the surface, brown to dark grey a reverse, without pigmentation,

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stem of *Dicranopteris ampla*, 2 March 2022, J.Y. Zhang, (118–1 = KUN-HKAS 136234), living culture (KUNCC 24–17929).

GenBank numbers – ITS: PV138695, *act*: PV188084, *gapdh*: PV221975

Notes – In the current phylogenetic analysis, our new isolate KUNCC 24–17929 clustered as a sister taxon to *Colletotrichum fioriniae* (Fig. 45). The nucleotide differences between isolate KUNCC 24–17929 and *C. fioriniae* (CBS 128517) in the ITS and *gapdh* gene regions are 0.04% (2/492 bp) and 1.8% (4/211 bp), respectively. The nucleotide sequences of the *act* gene between KUNCC 24–17929 and *C. fioriniae* are completely identical. These differences are not significant enough to separate our isolate from *C. fioriniae*. Morphologically, our new isolate is similar to *C. fioriniae*, having hyaline, ampulliform, smooth-walled conidiogenous cells and fusiform, hyaline, aseptate

conidia with acute ends. However, our isolate has setae, a feature not observed in *C. fioriniae*. Studies have shown that setae may be present or absent in different strains of the same species (e.g., *C. plurivorum*) (Damm et al. 2019). Therefore, this characteristic is insufficient to distinguish our new isolate from *C. fioriniae*. Based on both phylogenetic and morphological evidence, we identified our new isolate as *C. fioriniae*.

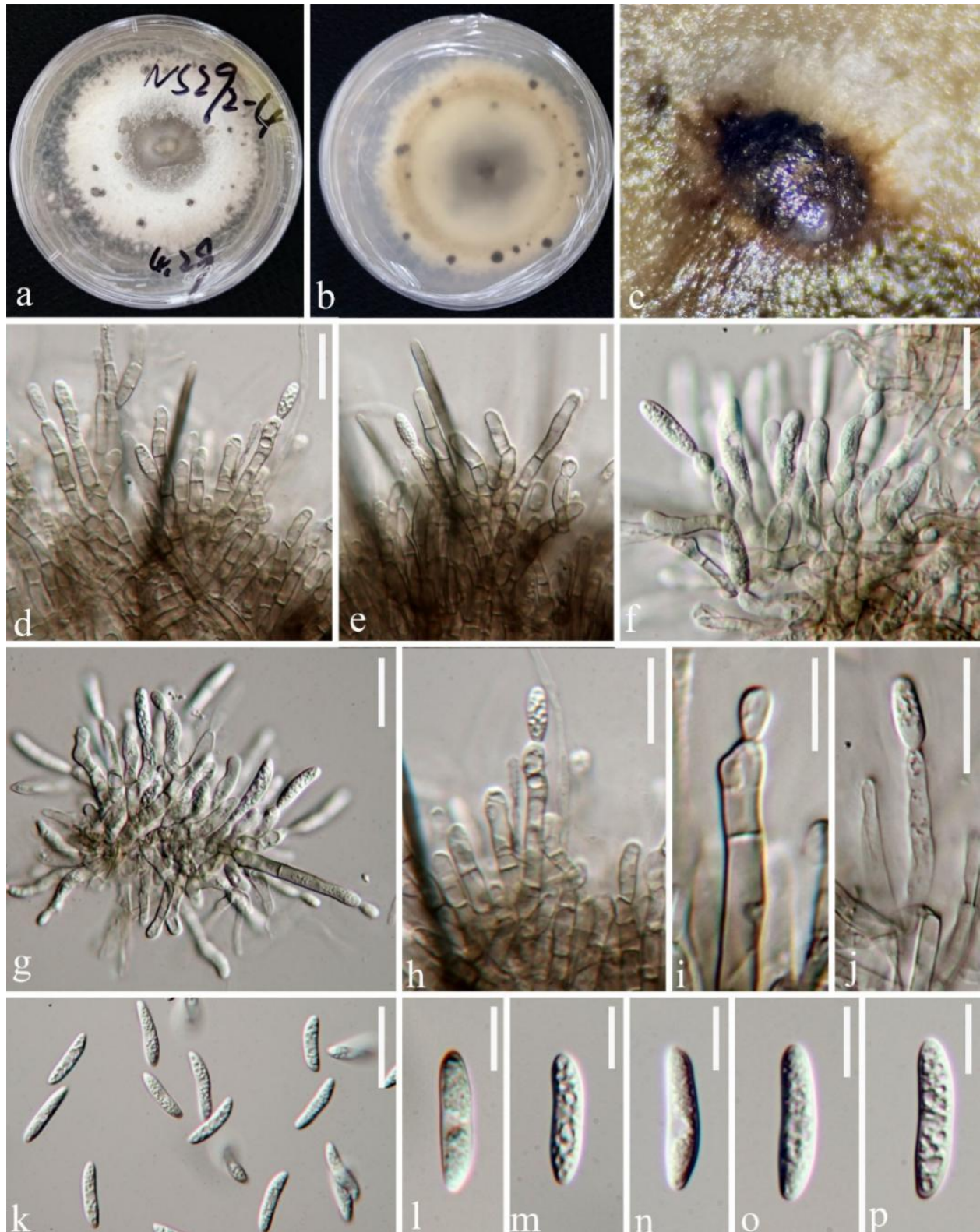


Figure 44 – *Colletotrichum dicranopteridis* (GZAAS 25–0524, holotype). a, b Front and reverse colony on PDA. c Conidiomata on the PDA. d, e Conidial mass with setae. g Conidiophores, conidiogenous cells, and conidia. h–j Conidiogenous cells and conidia. k–p Conidia. Scale bars: d–h, j = 20 µm, i, l–p = 10 µm, k = 30 µm.

Colletotrichum guttulatisporum J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov.

Fig. 47

Index Fungorum: IF 903972; Facesoffungi number: FoF 17873.

Etymology – Refers to the guttulate ascospores of the fungus.

Holotype – KUN-HKAS 136231

Endophytic in the leaves of *D. padata*. Sexual morph: *Ascomata perithecia*, solitary, or superficial or immersed in the agar medium, non-stromatic, subglobose, ostiolate, medium to dark brown. Hamathecium not observed. *Ascomatal wall* composed of several layers of pale brown *textura angularis*. *Asci* 47–67 × 4.5–6 µm ($\bar{x}$ = 57.4 × 13.3 µm, n = 20), unitunicate, 8-spored, cylindrical to clavate, tapering to apex and base, smooth-walled, the base broadly truncate. *Ascospores* 13–15 × 3.5–5 µm ($\bar{x}$ = 14.2 × 4.2 µm, n = 30), uni- or biserially arranged, aseptate, hyaline, smooth-walled, fusiform with round ends, straight or rarely very slightly curved, guttulate. Asexual morph: Not observed.

Cultural characteristics – Colonies on PDA reaching 45–50 mm diameter within 14 days at 25 °C. Colony entire, white to pale grey, with felted mycelium, brownish to black ascomata erumpent at maturity, coated with white hypha, granular at the margin, reverse pale brown, with brownish dots when maturity.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from fresh leaves of *D. padata*, 16 March 2022, J.Y. Zhang, (183–3 = KUN-HKAS 136231), living culture (KUNCC 24–17936).

GenBank numbers – ITS: PV138698, *act*: PV188081, *gapdh*: PV221977.

Notes – In our phylogenetic analysis, *Colletotrichum guttulatisporum* formed a distinct lineage within *Colletotrichum* and basal to *C. araujiae*, *C. capsicicola* and *C. brasiliense* (Fig. 45). *Colletotrichum guttulatisporum* is reported here only by the sexual morph, while only asexual morphs are known for the other species. *Colletotrichum guttulatisporum* is phylogenetically distinct from the three species (Fig. 45). Morphologically, *C. guttulatisporum* is quite similar to *C. plurivorum* in having astromatic, globose to obpyriform, ostiolate ascomata, a peridium of pale brown flattened *textura angularis* and uni- or biserially, aseptate, hyaline, smooth-walled, fusiform ascospores with round ends. However, *C. guttulatisporum* differs from *C. plurivorum* in having narrower asci (4.5–6 vs. 10.5–12.5 µm) and guttulate, smaller ascospores (13–15 × 3.5–5 vs. (13–)14.5–18(–22) × (4–)5–6(–7) µm) (Damm et al. 2019).

Colletotrichum jiangxiense F. Liu & L. Cai, in Liu, Weir, Damm, Crous, Wang, Liu, Zhang & Cai, Persoonia 35: 82 (2015)

Fig. 48

= *Colletotrichum gracile* Z.F. Yu, in Yu, Jiang, Zheng, Zhang & Qiao, Journal of Fungi 8(2, no. 185): 14 (2022)

= *Colletotrichum oblongisporum* Z.F. Yu, in Yu, Jiang, Zheng, Zhang & Qiao, Journal of Fungi 8(2, no. 185): 20 (2022)

= *Colletotrichum nullisetosum* Z.F. Yu, in Yu, Jiang, Zheng, Zhang & Qiao, Journal of Fungi 8(2, no. 185): 18 (2022)

Index Fungorum: IF 809161; Facesoffungi number: FoF 17277;

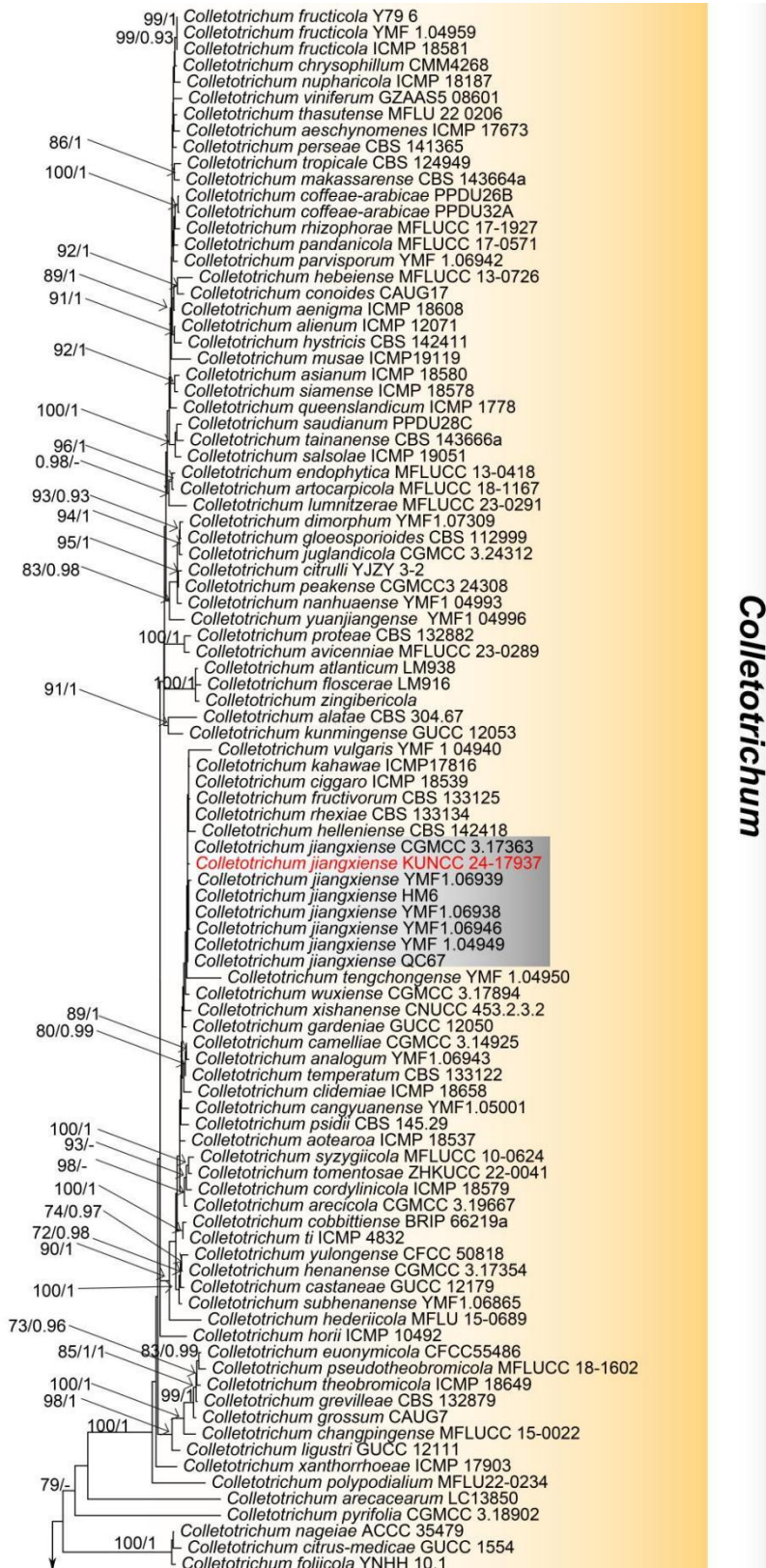


Figure 45 – Phylogram generated from maximum likelihood analysis based on combined ITS, *act*, *chs*, *gapdh*, and *tub2* sequence data. A total of 249 taxa were included in the combined analyses, which comprised 1981 characters after alignment. The best scoring RAxML tree with a final likelihood value of -50068.239269 is presented. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near

branches as ML/PP. The tree is rooted to *D. Monilochaetes infuscans* (CBS 86996). The newly generated sequences are shown in red.

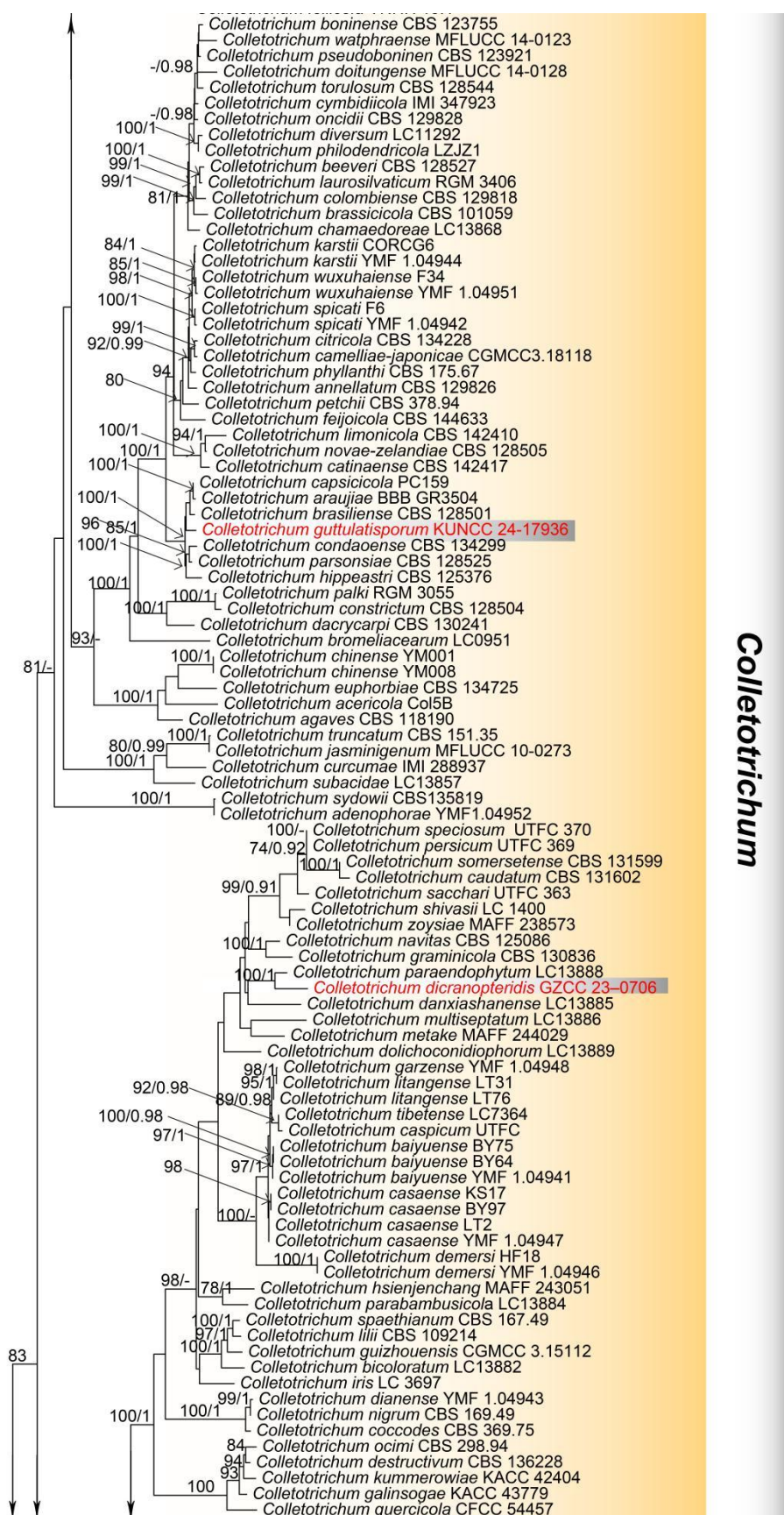


Figure 45 – Continued

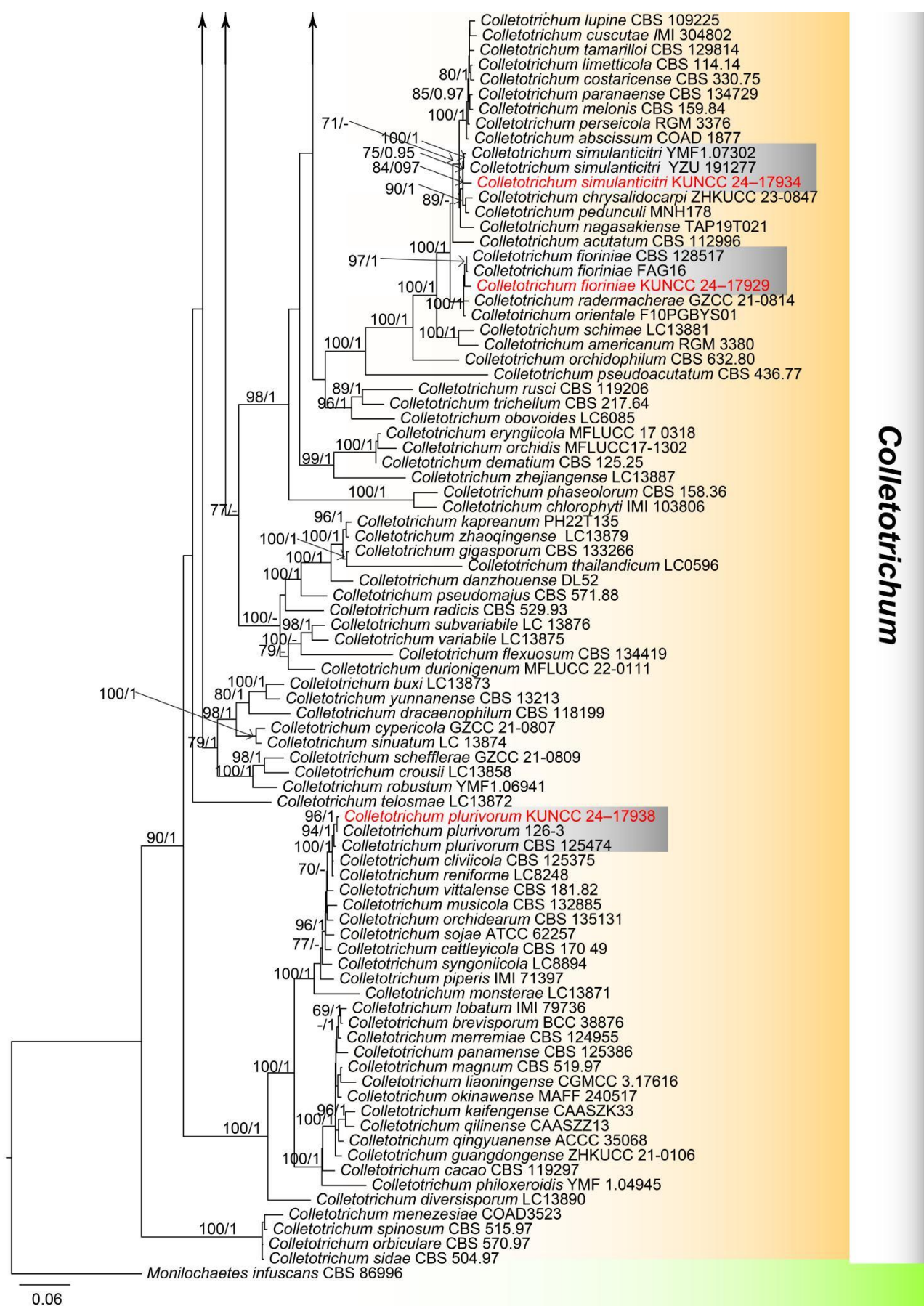


Figure 45 – Continued



Figure 46 – *Colletotrichum fioriniae* (KUN-HKAS 136234, new record). a, b. Obverse and reverse colony on PDA. c–f Conidiophores. g Setae. h–l Conidia. Scale bars: c, i–l = 5 μ m, d = 20 μ m, e–h = 10 μ m.

Endophytic in the leaves of *Dicranopteris ampla*. Sexual morph: Not observed. Asexual morph: *Vegetative hyphae* hyaline or pale brown, smooth-walled, septate, branched. *Conidiomata* not observed. *Setae* not observed. *Conidiophores* 24–40 $\times$ 2.5–3.5 μ m ($\bar{x}$ = 32.2 $\times$ 3.9 μ m, n = 15), hyaline to pale brown, branched. *Conidiogenous cells* 9–23 $\times$ 2–3.5 μ m ($\bar{x}$ = 16.1 $\times$ 2.8 μ m, n = 15). *Conidia* 14–18 $\times$ 3–4 μ m ($\bar{x}$ = 15.6 $\times$ 3.5 μ m, n = 30), hyaline, aseptate, smooth-walled, cylindrical, both ends bluntly rounded or one end bluntly rounded and one end acutely rounded. *Appressoria* single, brown to dark brown, smooth-walled, variable in shape, irregular unlobed or slightly lobed.

Culture characters – Colonies on PDA occupied the whole plate in 7 days at 25 $^{\circ}$ C. Colonies entirely white, reverse pale yellowish. Aerial mycelium white, velvety, margin well defined.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi and Miao Autonomous County, from the leaves of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (122–6 = KUN-HKAS 136232), living culture (KUNCC 24–17937).

GenBank numbers – ITS: PV138696, *tub2*: PV221986, *act*: PV188083, *gapdh*: PV221974

Notes – *Colletotrichum jiangxiense* was introduced by Liu et al. (2015). It is characterized by pale brown to brown chlamydospores, which are circular, ellipsoidal, or irregular in shape. Acervular

conidiomata are present, with hyaline to pale brown, branched conidiophores. The conidiogenous cells are hyaline to pale brown and cylindrical. The conidia are hyaline, aseptate, smooth-walled, and cylindrical, with both ends rounded or one end rounded and the other end acute. In our phylogenetic analysis, the newly obtained strain KUNCC 24–17937 grouped with *C. jiangxiense* (CGMCC 3.17363, HM6, YMF 1.04949, and QC67), *C. gracile* (YMF 1.06939), *C. oblongisporum* (YMF 1.06938), and *C. nullisetosum* (YMF 1.06946) (Fig. 45). Notably, *C. gracile* (YMF 1.06939), *C. oblongisporum* (YMF 1.06938), and *C. nullisetosum* were intermingled with the strains of *C. jiangxiense* (CGMCC 3.17363, HM6, YMF 1.04949, and QC67) in the phylogenetic tree (Fig. 44). We compared the sequence data of our new strain and these species, the results showed that they are identical in the ITS and *act* gene regions with minor differences in the *tub2* and *gapdh* gene regions (Table. 2). There were no significant morphological differences of these strains and our new strain (KUNCC 24–17937) (Table. 3). Although two conidial shapes were observed in *C. nullisetosum*, however, sometimes the conidial shapes may change in species, and one of the conidial shapes has also been found in the other three species, and phylogeny this species is also not significantly different from the other three species (Table 2). Therefore, we propose combining these taxa into a single species. *Colletotrichum gracile* (YMF 1.06939), *C. oblongisporum* (YMF 1.06938), and *C. nullisetosum* (YMF 1.06946) were recently introduced by Yu et al. (2022). To prioritize *C. jiangxiense*, we synonymize *C. gracile*, *C. oblongisporum*, and *C. nullisetosum* under *C. jiangxiense*. Additionally, our new isolate (KUNCC 24–17937) represents a new host record for *Dicranopteris ampla*.

Table 2 Comparison of nucleotide differences among our new strain (KUNCC 24–17937), *C. jiangxiense* (CGMCC 3.17363, HM6, YMF 1.04949 and QC67), *C. gracile* (YMF 1.06939), *C. oblongisporum* (YMF 1.06938), and *C. nullisetosum* (YMF 1.06946)

Species	Strain	<i>tub2</i>			<i>gapdh</i>			<i>chs</i>
<i>C. nullisetosum</i>	YMF1.06946	T	G	A	G	G	C	C
<i>C. oblongisporum</i>	YMF1.06938	T	G	T	A	G	C	C
<i>C. gracile</i>	YMF1.06939	T	T	T	A	A	T	T
<i>C. jiangxiense</i>	KUNCC 24–17937	C	G	T	A	G	C	-
<i>C. jiangxiense</i>	CGMCC 3.17363	C	G	T	A	G	C	-
<i>C. jiangxiense</i>	HM6	-	-	T	A	G	C	C
<i>C. jiangxiense</i>	QC67	-	-	T	A	G	C	C
<i>C. jiangxiense</i>	YMF 1.04949	-	-	T	A	G	C	C

“-” refers to the unavailability of the sequence data. The different base pairs are in bold font.

Colletotrichum plurivorum Damm, Alizadeh & Toy. Sato, in Damm, Sato, Alizadeh, Groenewald & Crous, Stud. Mycol. 92: 31 (2018) Fig. 49

Index Fungorum: IF 824228; Facesoffungi number: FoF 10691.

Endophytic in fresh leaves of *Dicranopteris ampla*. Sexual morph: Not observed. Asexual morph: *Vegetative hyphae* hyaline to brown, septate, branched, smooth-walled. *Conidiomata* gregarious, dark brown to black. *Setae* not observed. *Conidiophores* reduced to conidiogenous cells, hyaline to pale brown, smooth-walled, septate, branched. *Conidiogenous cells* 8.5–13 × 3–4.5 μm ($\bar{x}$ = 10.9 × 4 μm, n = 20), phialidic, integrated, terminal hyaline to pale brown, smooth-walled, cylindrical clavate to doliiform. *Conidia* 15–19 × 4.5–6 μm ($\bar{x}$ = 17.1 × 5.4 μm, n = 35), hyaline to brown, aseptate, guttulate, cylindrical, obtuse at both ends, smooth-walled. *Appressoria*: not

observed.

Cultural characteristics – Colonies on PDA reaching 55 mm diameter within 10 days at 25 °C, flat, dense, and raised in the center, cottony, dense, and regular to rhizoid and aerial mycelium scarce towards the periphery, greyish-pink on the surface, dark grey to greyish pink on reverse.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the fresh leaves of *Dicranopteris ampla*, 16 March 2022, J.Y. Zhang, (197–3 = KUN-HKAS 136230), living culture (KUNCC 24–17938).

GenBank numbers – ITS: PV138699, *tub2*: PV221988, *act*: PV188080, *gapdh*: PV221978

Notes – In the multi-gene phylogenetic tree, the new strain (KUNCC 24–17938) clustered with *Colletotrichum plurivorum* (CBS 125474) with 92% ML and 1.00 BYPP value (Fig. 45). Morphologically, our isolate is comparable to the holotype of *C. plurivorum*, except for the color of the conidia, which are hyaline to brown, whereas those of the holotype are hyaline (Damm et al. 2019). Therefore, we identified our isolates as *C. plurivorum*. This is the first report of *C. plurivorum* associated with *Dicranopteris ampla*.

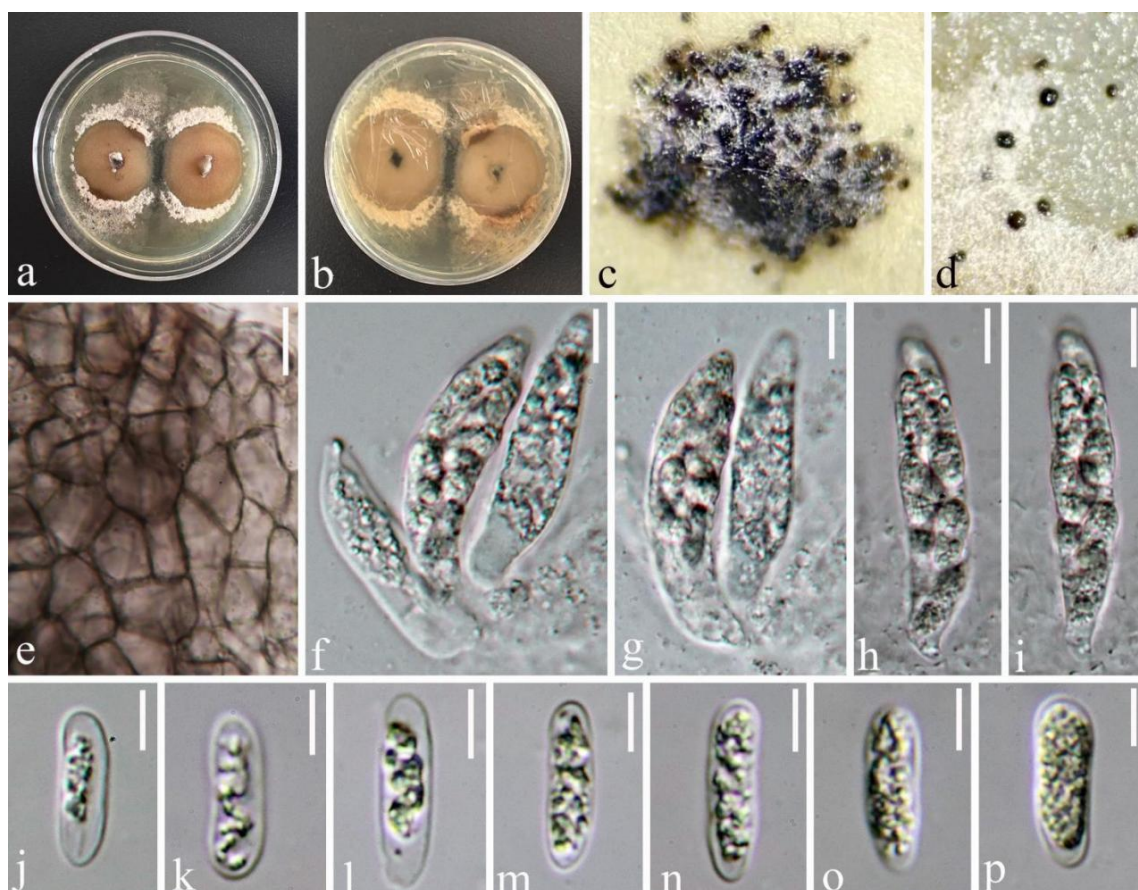


Figure 47 – *Colletotrichum guttulatisporum* (KUN-HKAS 136231, holotype). a, b. Obverse and reverse colony on PDA. c, d Ascomata on the PDA. e Ascomatal wall. f–i Asci. j–p Ascospores. Scale bars: e–i = 10 µm, j–p = 5 µm.

Colletotrichum simulanticitri Z.F. Yu, in Yu, Jiang, Zheng, Zhang & Qiao, Journal of Fungi 8 (2, no. 185): 24 (2022) Fig. 50
 = *Colletotrichum juglandis* Xin Wei & J.X. Deng, in Wei, Yang, Jiang, Cui, Deng & Zhang, Phytotaxa 556(3): 263 (2022)

Index Fungorum: IF 842560; Facesoffungi number: FoF 17874;

Endophytic in fresh leaves of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* dark brown to black, scattered or in groups. Setae $19\text{--}37.5 \times 2\text{--}3.5 \mu\text{m}$ ($\bar{x} = 28.4 \times 2.5 \mu\text{m}$, $n = 15$), cylindrical to subulate, obtuse at the apex, 0–1-septate, smooth-walled, dark brown, smooth-walled. *Conidiophores* cylindrical, branched, brown to dark brown, septate, smooth-walled. *Conidiogenous cells* $11\text{--}43 \times 2.5\text{--}4 \mu\text{m}$ ($\bar{x} = 24.8 \times 3.4 \mu\text{m}$, $n = 15$), cylindrical to clavate, brown, smooth-walled. *Conidia* $10\text{--}12 \times 2.5\text{--}4 \mu\text{m}$ ($\bar{x} = 11.2 \times 3.3 \mu\text{m}$, $n = 35$), hyaline, cylindrical to oblong, straight or slightly curved, hyaline, aseptate, dry, guttulate, smooth-walled. *Appressoria*: not observed.

Cultural characteristics – Colonies on PDA occupied the whole plate in 7 days at 25 °C, surface mycelium pink to pale brown at the centre, dense, felted, conidiomata erumpent at maturity, reverse dark brown in the center, white towards margin.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the fresh leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (130–1 = KUN-HKAS 136228), living culture (KUNCC 24–17934).

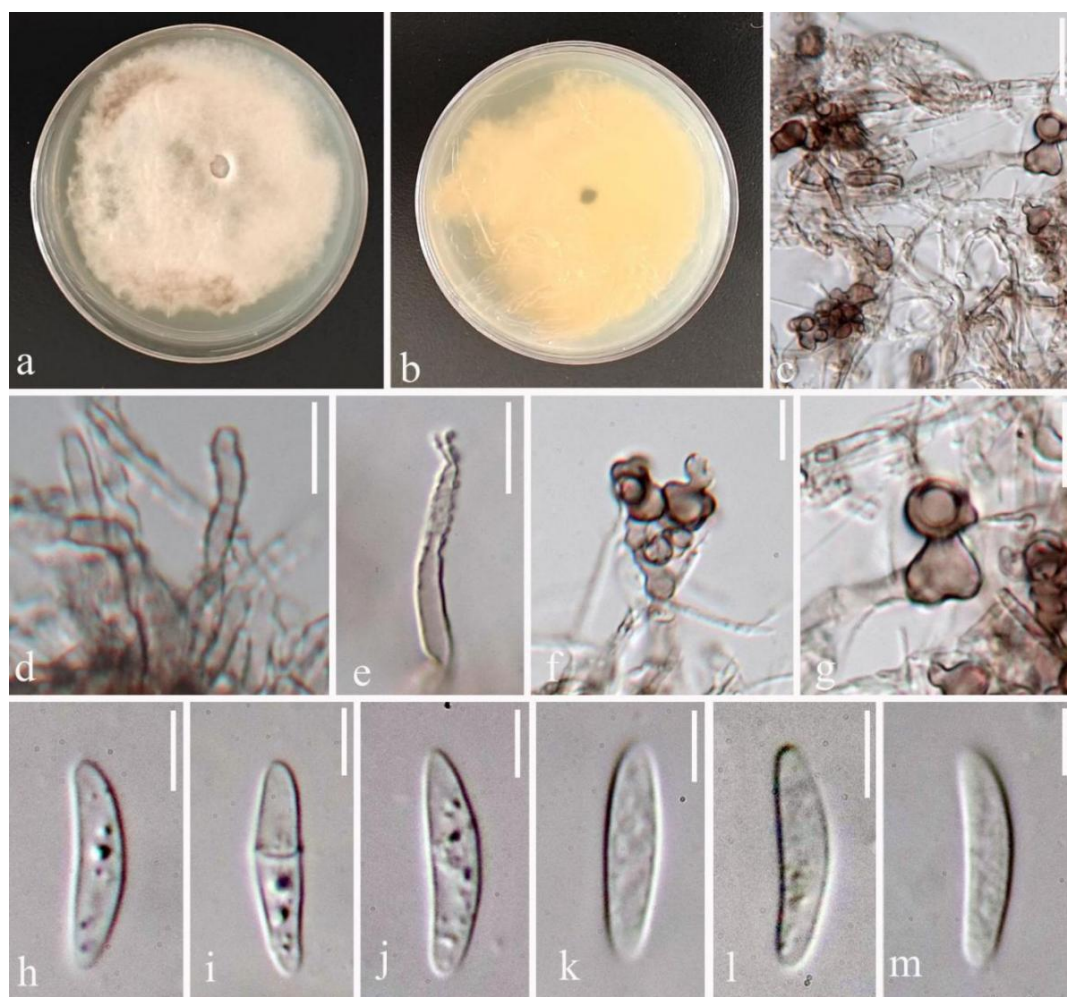


Figure 48 – *Colletotrichum jiangxiense* (KUN-HKAS 136232, new host record). a, b Obverse and reverse colony on PDA. c Mycelium with Appressoria. d, e Conidiophores. f, g Appressoria. h–m Conidia. Scale bars: c = 20 μm , d–g = 10 μm , f–m = 5 μm .

Table 3 Morphological comparisons of *C. nullisetosum*, *C. gracile* *C. jiangxiense* (CGMCC 3.17363 and KUNCC 24–17937), *C. oblongisporum* (YMF 1.06938), and *C. nullisetosum* (YMF 1.06946)

Species	Conidiomata	Conidiophores	Conidiogenous cells	Conidia	Appressoria	References
<i>C. gracile</i>	Not observed	Directly formed on hyphae, hyaline, smooth-walled, aseptate, unbranched	Hyaline, cylindrical to clavate, smooth-walled, collarette absent.	Cylindrical to clavate, aseptate, straight or slightly curved, both ends obtusely rounded or one end slightly acute, 13–18 × 4–6 μm	Dark brown, aseptate, unbranched, single and little, irregular but often sub-globose to ellipsoidal, margin sometimes lobed, 7–17.5 × 5–9 μm	Yu et al. (2022)
<i>C. nullisetosum</i>	Rudimentary, dark olivaceous brown.	Directly formed on hyphae, hyaline, smooth-walled, unbranched	Hyaline, cylindrical to clavate, smooth-walled, collarette absent	Unicellular, hyaline, dimorphic; (i) straight cylindrical, oblong to narrowly ovoid, obtuse at the base, rounded at the apex, contents 1–2-granular, (ii) sickle, aseptate, blunt at both ends, curved to one side, contents 1-granular, 14.8–19.3 × 5–6.5 13.5–19.5 × 4–6.5 μm	Dark brown, sometimes branched, always little and oval in outline, contents granular, 9–15 × 5–8 μm	Yu et al. (2022)

Species	Conidiomata	Conidiophores	Conidiogenous cells	Conidia	Appressoria	References
<i>C. oblongisporum</i>	Not observed	Directly formed on hyphae, hyaline, smooth-walled, septate, occasionally branched.	Hyaline, cylindrical, collarette not visible.	Oblong, unicellular, subtruncate at the base, biguttulate near the ends, hyaline, smooth-walled, 13–18.5 × 4–5.5 µm	Dark brown, sub-globose, cuneiform to irregular, sometimes with lobate margin, 8–15 × 4.5–7.5 µm.	Yu et al. (2022)
<i>C. jiangxiense</i> (CGMCC 3.17363)	Acervular, conidiophores formed on a cushion of roundish and medium brown cells. Setae not observed.	Hyaline to pale brown, branched	Hyaline to pale brown, cylindrical, 11.5–20 µm, apex 1–2.5 µm diam	Cylindrical, both ends bluntly rounded, or one end bluntly rounded and one end acutely rounded, hyaline, aseptate, smooth-walled, 13–19 × 4–6 µm	Not observed	Liu et al. (2015)
<i>C. jiangxiense</i> (KUNCC 24–17937)	Not observed	hyaline to pale brown, branched	Hyaline to pale brown, cylindrical	Cylindrical, both ends bluntly rounded, or one end bluntly rounded and one end acutely rounded, hyaline, aseptate, smooth-walled, 14–18 × 3–4 µm	brown to dark brown, smooth-walled, variable in shape, irregular unlobed or slightly lobed	This study

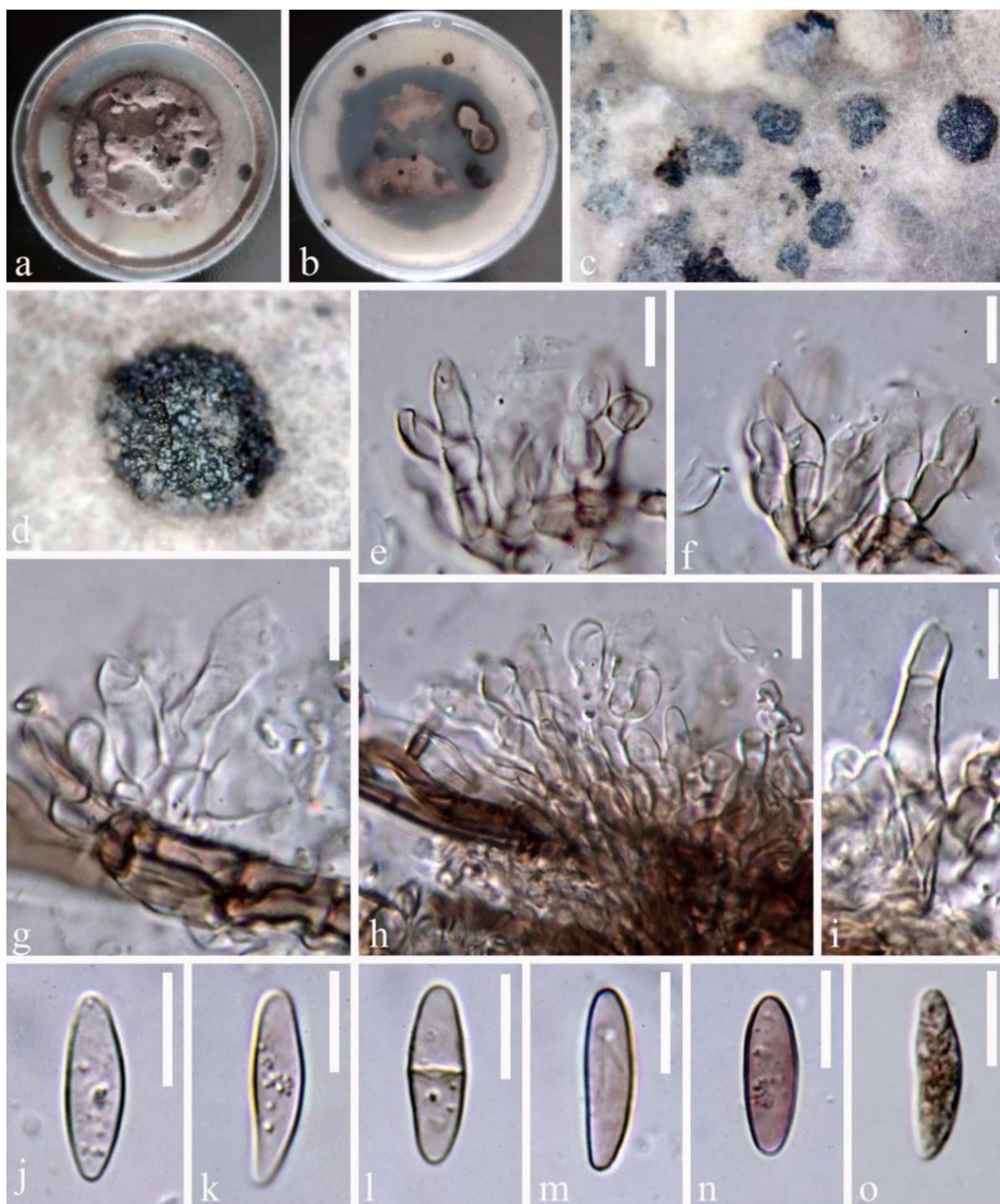


Figure 49 – *Colletotrichum plurivorum* (KUN-HKAS 136230, new host record). a, b Obverse and reverse colony on PDA. c, d Conidiomata on the PDA. e–i Conidiophores. j–o Conidia. Scale bars: e–o = 10 μ m.

GenBank numbers – ITS: PV138697, *tub2*: PV221987, *act*: PV188082, *gapdh*: PV221976.

Notes – In the phylogenetic analysis, the new isolate KUNCC 24–17934 clustered as sister to *C. simulanticitri* and *C. juglandis* (Fig. 45). The nucleotides of ITS and *act* sequence data of our new isolate (KUNCC 24–17934), *C. simulanticitri* (YMF1 07302) and *C. juglandis* (YZU 191277) are

completely identical. The comparison of nucleotide sequences of the *gapdh* gene revealed 0.21% (5/228 bp) and 0.25% (6/239 bp) differences between our isolate (KUNCC 24–17934) with *C. simulanticitri* and *C. juglandis* respectively. The nucleotide differences in *gapdh* between *C. simulanticitri* and *C. juglandis* are 0.93% (1/228 bp). This indicates no significant differences between our new isolate (KUNCC 24–17934), *C. simulanticitri*, and *C. juglandis* in the sequence data.

Morphologically, our isolate (KUNCC 24–17934), *C. simulanticitri*, and *C. juglandis* share similar characteristics, including hyaline, cylindrical to oblong, aseptate, guttulate conidia. The only notable difference is that both our isolate and *C. simulanticitri* have setae, which were not observed in the type of *C. juglandis* (Wei et al. 2022b). Damm et al. (2019) demonstrated that the presence or absence of setae can vary among strains of the same species. Therefore, this morphological variation is insufficient to distinguish our isolate, *C. simulanticitri*, and *C. juglandis* as separate species. This conclusion is further supported by nucleotide comparisons, where all three species exhibit less than 2% variation across all gene regions. Based on this evidence, we propose synonymizing *C. juglandis* under *C. simulanticitri*. Additionally, this study establishes a new host record for *C. simulanticitri* in association with *Dicranopteris pedata*.

***Hypocreales* Lindau**

Hypocreales is an ecologically highly diverse order with various lifestyles including bryophilous, endophytic, entomogenous, caulicolous, corticolous, foliicolous, fungicolous, herbicolous, lichenicolous, and algicolous to coprophilous. Some are associated with humans and animals; some occur with myxomycetes (Perera et al. 2023, Bao et al. 2023). *Hypocreales* species have a worldwide distribution and have been found on diverse substrates such as leaf litter, soil, water, and air in terrestrial, freshwater, and marine habitats (Hyde et al. 2020a, Perera et al. 2023, Bao et al. 2023). Perera et al. (2023) provided an up-to-date DNA sequence-based phylogenies (ITS, LSU, *rpb2*, *tef1-α*, and *tub2*) for *Hypocreales*, and accepted 17 families in the order.

***Hypocreaceae* De Not.**

The latest treatment of *Hypocreaceae* was provided by Perera et al. (2023) and Bao et al. (2023) with acceptance of 16 genera viz. *Arachnocrea*, *Dialhypocrea*, *Escovopsioides*, *Escovopsis*, *Hypocreopsis*, *Hypomyces*, *Kiflimonium*, *Lichenobarya*, *Mycogone*, *Protocrea*, *Rogersonia*, *Sepedonium*, *Sphaerostilbella*, *Sporophagomyces*, *Stephanoma*, and *Trichoderma*.

***Sphaerostilbella* (Henn.) Sacc. & D. Sacc.**

Sphaerostilbella, a fungicolous genus (Pöldmaa et al. 2000), was formally introduced by Seifert (1985) with *S. aurifila* as the type species. *Sphaerostilbella* is characterized by perithecial, superficial or semi-immersed in subiculum, solitary to gregarious, obpyriform, yellowish white to ochraceous, KOH- ascomata, 8-spored, cylindrical asci and fusiform to naviculate or ellipsoid, 1-septate, hyaline, finely spinulose or grossly warted-tuberculate ascospores (Pöldmaa et al. 2000; Perera et al. 2023). The asexual morphs of *Sphaerostilbella* are *Gliocladium* or gliocladium-like (Pöldmaa et al. 2000, Zare & Gams 2016). Currently, 13 species are listed in the Index Fungorum (2024), of which ten species are associated with sequence data.

***Sphaerostilbella dicranopteridis* J.Y. Zhang, D.F. Bao, K.D. Hyde & J.C. Kang, sp. nov. Fig. 51**

Index Fungorum: IF 903973; Facesoffungi number: FoF 17875.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from

which the type strain was isolated.

Holotype – KUN-HKAS 124930

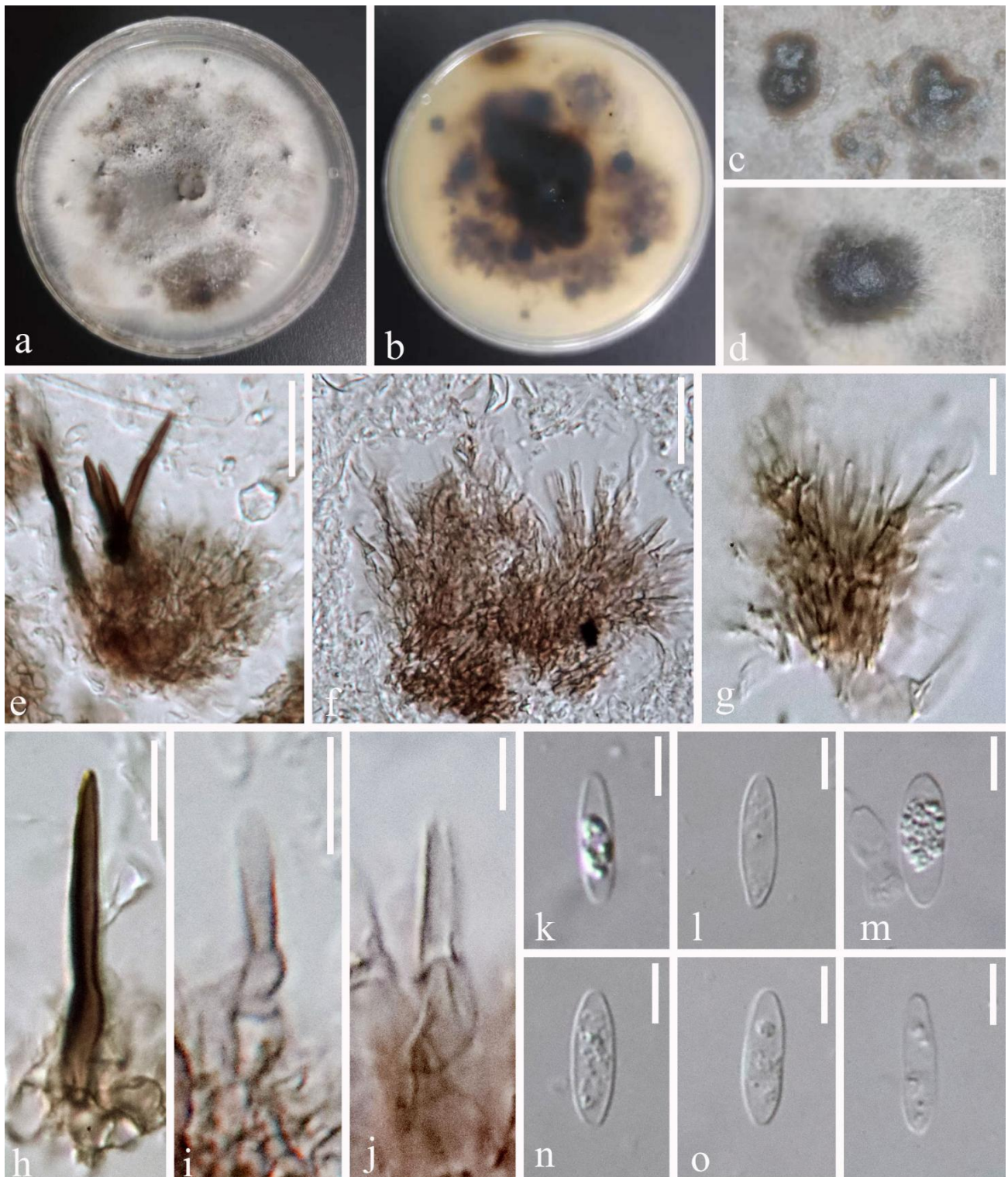


Figure 50 – *Colletotrichum simulanticitri* (KUN-HKAS 136228, new host record). a, b Obverse and reverse colony on PDA. c, d Conidiomata on the PDA. e Conidiophores with setae. f, g, i, j Conidiophores. h Setae. k–o Conidia. Scale bars: e, f = 20 µm, g–i = 10 µm, j–o = 5 µm.

Endophytic in the root of *Dicranopteris pedata*. Sexual morph: Undetermined. Asexual morph: *Mycelium* on agar media superficial and partly immersed, composed of septate, branched, hyaline, smooth, and thick-walled hyphae. *Conidiophores* formed laterally on aerial hyphae, semi-macronematous, mononematous, erect, straight, penicillate, septate, smooth-walled, hyaline, cylindrical, with 2–3 phialides at each level or branches, 13–29(–38) μm long, 2–4.5 μm wide near base, slightly tapering to 1.5–3 μm just below the phialides. *Conidiogenous cells* 5.5–13.5 $\times$ 2–3.5 μm ($\bar{x}$ = 9.6 $\times$ 2.9 μm , n = 15), holo- to polyblastic to phialidic, hyaline, cylindrical, in whorls of 2–3. *Conidia* 6–8(–10) $\times$ 3–5.5(–8) μm ($\bar{x}$ = 7.2 $\times$ 4.3 μm , n = 35), in slimy mass, aseptate, ellipsoidal, rounded at the apex, acute at the base, guttulate, hyaline, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h. and germ tubes produced from conidia. Colonies growing on PDA, slow growing, reaching 20 mm in diameter. in 20 days at 26 °C, circular, flat, velvety, with dense, white mycelium on the surface with undulate margin, from below olivaceous brown at the center, yellow at the edge and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Cheheng County, isolated from the healthy roots of *Dicranopteris pedata* in a disturbed forest near the roadside, 16 Mar. 2020, J.Y. Zhang, (NS155–2 = KUN-HKAS 124930, holotype), ex-type living culture (KUNCC 23–12693).

GenBank numbers – ITS: PV138727, LSU: PV138586, *tef1- α* : PV177126, *rpb1*: PV221981.

Notes – In the phylogenetic analysis, *Sphaerostilbella dicranopteridis* clustered sister to *Sphaerostilbella* sp. (NRRL 22971) (Fig. 52), which is an unidentified strain and lacks a morphological description and illustration. The nucleotide of ITS sequence data showed 13bp differences between our new isolate and *Sphaerostilbella* sp. (NRRL 22971); only ITS sequence data is available for this strain; it is insufficient to identify it. Thus, we introduce our new isolate as a novel species. However, morphological descriptions and more genetic data are necessary to clarify the placement of this strain (NRRL 22971). *Sphaerostilbella dicranopteridis* is phylogenetically closely related to *S. parabroomeana* (Fig. 52), but differs from *S. parabroomeana* in having aseptate, ellipsoidal conidia with round apex and acute base. While, the conidia of *S. parabroomeana* are cylindrical to short-cylindrical and 0–1-septate (Zare & Gams 2016).

***Nectriaceae* Tul. & C. Tul.**

Nectriaceae was introduced with *Nectria* as the type genus by Tulasne and Tulasne (1865). The family is characterized by orange, yellow, red to purple, uniloculate ascomata, reacting in KOH and lactic acid (LA); ascospores not disarticulating, globose, ellipsoid to long-fusiform (never truly filiform) (Lombard et al. 2015, Rossman et al. 1999); with phialidic asexual morphs. The taxonomy of *Nectriaceae* has been studied and reviewed by many authors with different conceptions (Rossman et al. 1999, Lumbsch & Huhndorf 2010, Lombard et al. 2015, Maharachchikumbura et al. 2016, Hyde et al. 2020a). Recently, Perera et al. (2023) accepted 77 genera in the family. Bao et al. (2023) accepted 78 genera, where *Varicosporella* has been synonymized under *Atractium*, *Neocalonectria* and *Sedecimiella* are accepted in the family, which were previously placed in *Hypocreales* genera *incertae sedis*. The latest treatment of *Nectriaceae* was provided by Hyde et al. (2024), with 83 genera accepted in the family.

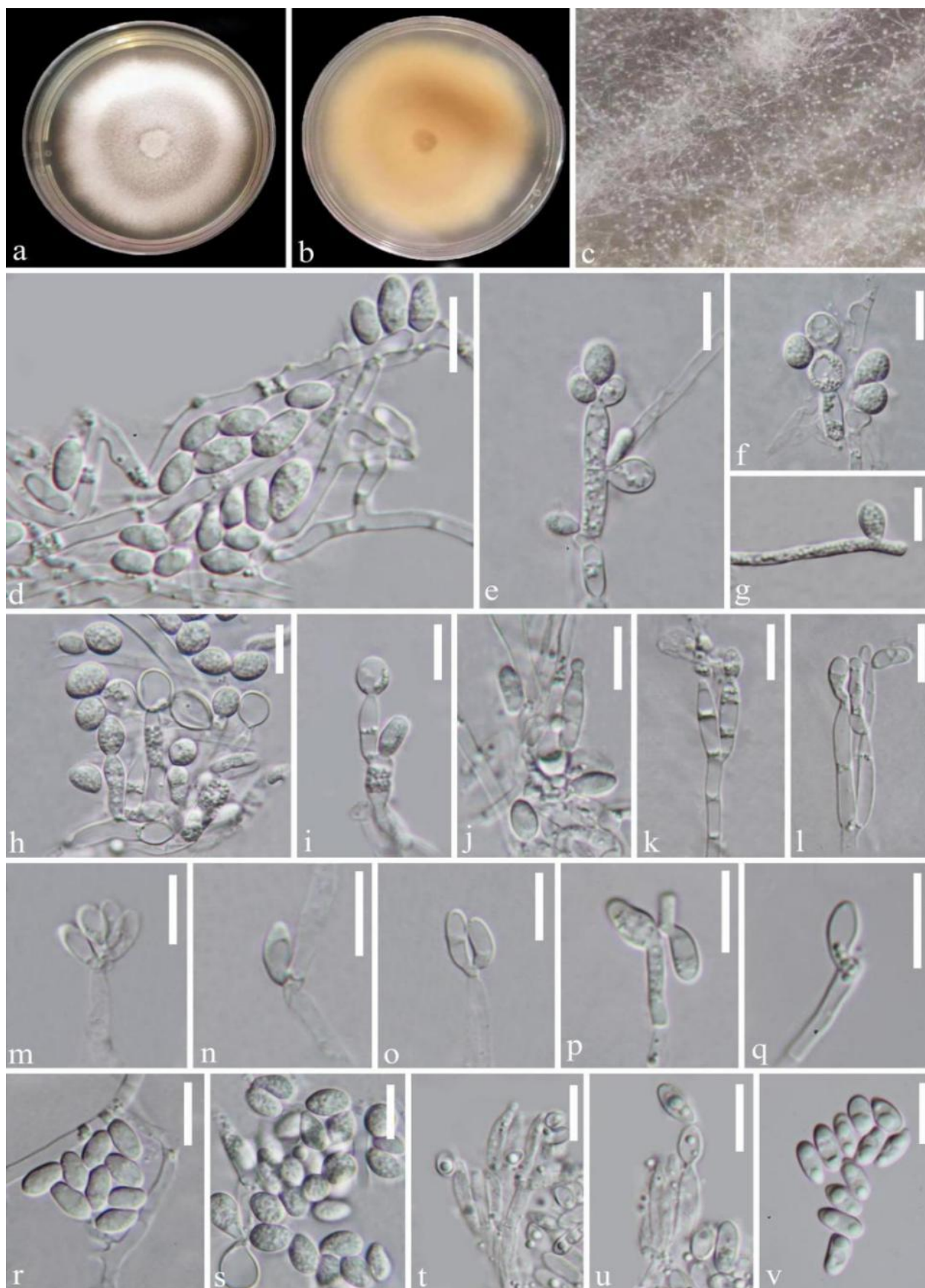


Figure 51 – *Sphaerostilbella dicranopteridis* (KUN-HKAS 124930, holotype). a–c Colonies on PDA. d–q Conidiophores, conidiogenous cells, and conidia. r–s Conidia. t–u Another mode of sporulation by conidiogenous cells. v Conidia. Scale bars: d–v = 10 μm.

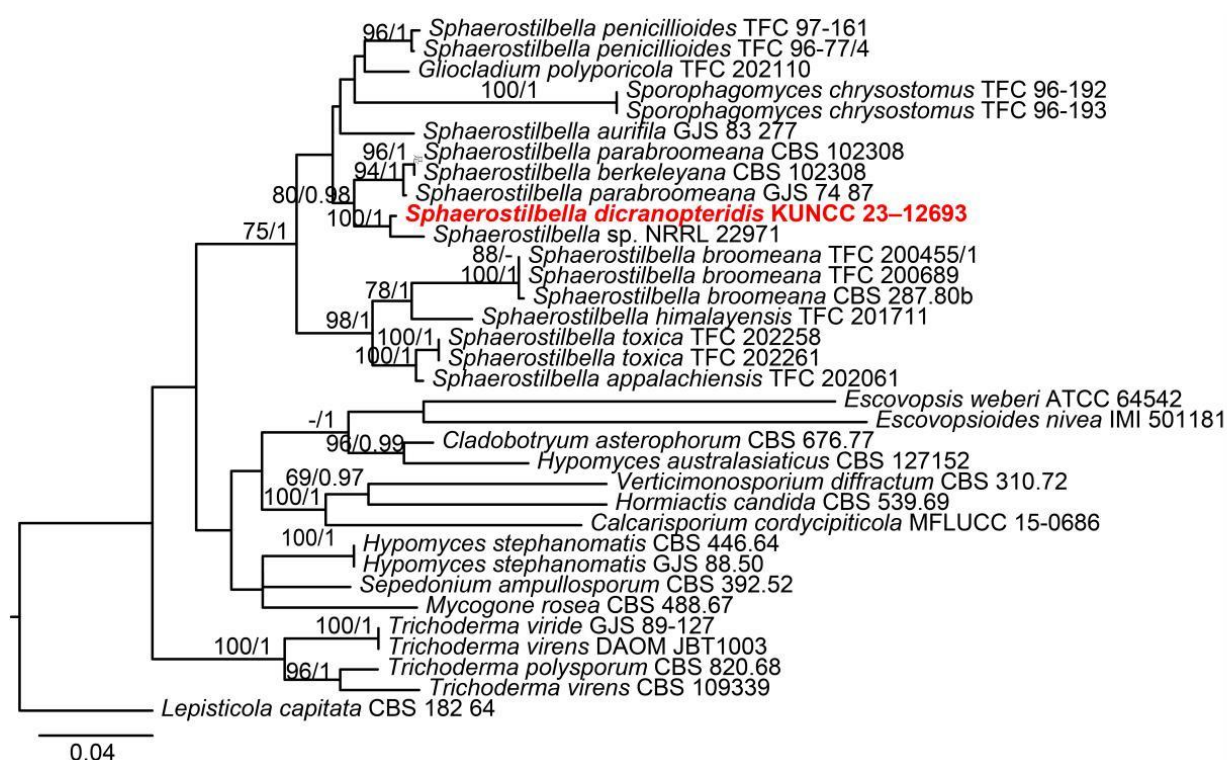


Figure 52 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. A total of 34 taxa were included in the combined analyses, which comprised 1526 characters after alignment. The best scoring RAxML tree with a final likelihood value of -8100.374701 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Lepisticola capitata* (CBS 182.64), the new strain is in red and bold.

***Dactylonectria* L. Lombard & Crous**

Dactylonectria was introduced by Lombard et al. (2014) with two new species and eight new combinations, most of which were previously placed in *Ilyonectria* except *D. pauciseptata* was treated in *Cylindrocarpon*. *Dactylonectria* differs from *Ilyonectria* and *Neonectria* in having ovoid to obpyriform, smooth to finely warted, dark-red perithecia with papillate ostiolar region at the apex and rarely produce chlamydospores in culture (Lombard et al. 2014). Later, seven new species were introduced to *Dactylonectria* (Gordillo et al. 2017, Mora-Sala et al. 2018). Presently, 17 species are included in the genus and all the species have been studied using sequence data. All members of *Dactylonectria* were associated with plant roots from various hosts such as grapevine, *Vitis vinifera*, *Piper* sp. (*Piperaceae*), and strawberry (Gordillo et al. 2017, Mora-Sala et al. 2018).

***Dactylonectria dicranopteridis* J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov.**

Fig. 53

Index Fungorum: IF 903974; Facesoffungi number: FoF 17876.

Etymology – The specific epithet *dicranopteridis* refers to the plant genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 23-0811

Endophytic in the healthy rhizome of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Mycelium* felty, white to pale buff, margin uneven, buff to amber; reverse buff to saffron,

zonation irregular concentric brown. *Conidiophores* solitary to loosely aggregated, arising laterally or terminally from aerial mycelium, unbranched or sparsely branched, hyaline, guttulate, smooth-walled. *Conidiogenous cells* $13\text{--}26.5 \times 2.5\text{--}4 \mu\text{m}$ ($\bar{x} = 19.8 \times 3 \mu\text{m}$, $n = 20$), phialidic, hyaline, cylindrical, slightly tapering towards the tip. *Microconidia* $6\text{--}9 \times 3\text{--}4 \mu\text{m}$ ($\bar{x} = 7.7 \times 3.5 \mu\text{m}$, $n = 34$), formed in heads, clavate, ellipsoid to short cylindrical, straight to faintly curved, rounded at both ends or sometimes rounded at the apex, tapering at the base, 0–1-septate, hyaline, smooth-walled. *Macroconidia* not observed.

Culture characteristics – Colonies on PDA medium circular, growly fast, reaching 40 mm diameter after 5 d at 28 °C in natural light, with sparse or no aerial mycelium, margin white, orange in sectors towards the center, the reverse brownish yellow to orange.

Material examined – China, Guizhou Province, Guiyang City, from the rhizome of *Dicranopteris pedata*, 2 August 2022, J.Y. Zhang, (S52–6 = GZAAS 23–0811, holotype), ex-type living culture (GZCC 23–0736).

GenBank numbers – ITS: PV138702, *tef1- α* : PV177098, *tub2*: PV221991, *his3*: PV188090.

Notes – *Dactylonectria* species have very similar morphologies, making it difficult to distinguish them based only on morphology. Thus, a multi-locus phylogenetic analysis was utilized to better understand the relationships and identify *Dactylonectria* species. Based on phylogenetic analysis of combined ITS, *tub2*, *his3*, and *tef1- α* sequence data, our new isolate formed a distinct lineage between *D. ecuadoriensis* and *D. valentina* (Fig. 54). The microconidia of both *D. ecuadoriensis* and *D. valentina* are subglobose to ovoid. Our new isolate has clavate, ellipsoid to short cylindrical, 0–1-septate microconidia, which are rounded at both ends or sometimes rounded at the apex, tapering at the base. Therefore, based on phylogenetic analysis and morphological characteristics, we introduce our new isolate as a new species.

Dactylonectria pauciseptata (Schroers & Crous) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Phytopath. Mediterr.* 53(3): 527 (2014) Fig. 55

Index Fungorum: IF 810151; Facesoffungi number: FoF 17877.

Endophytic in the healthy rhizome of *Dicranopteris linearis*. Sexual morph: unknown. Asexual morph: *Mycelium* felty, white to pale buff, margin uneven, buff to amber; reverse buff to saffron, zonation irregular concentric brown. *Conidiophores* arising laterally or terminally from aerial mycelium, solitary, unbranched or sparsely branched. *Conidiogenous cells* phialidic, hyaline, cylindrical. *Macroconidia* $20\text{--}38 \times 5\text{--}8 \mu\text{m}$ ($\bar{x} = 28 \times 6.5 \mu\text{m}$, $n = 20$), cylindrical, straight to faintly curved, with both ends rounded, 1–4-septate, hyaline, smooth-walled. *Microconidia* ellipsoid to short cylindrical, with obtuse ends, straight, aseptate, hyaline, smooth-walled, mostly with a visible, centrally located, or slightly laterally displaced hilum. *Chlamydospores* $9\text{--}13 \times 8\text{--}14 \mu\text{m}$, globose to ellipsoid, smooth, thick-walled, formed intercalary in chains or in clumps, hyaline to golden-brown.

Culture characteristics – Colonies on PDA medium circular, growly fast, reaching 55 mm diameter after 5 d at 28 °C in natural light, regular, convex, entire, dry, dark brown at center with light brown edges; reverse margin entire, light to dark brown.

Material examined – China, Guizhou Province, Ziyun Miao and Buyi Autonomous County, Anshun City, from the rhizome of *Dicranopteris linearis*, 2 August 2022, J.Y. Zhang, (S5–2 = GZAAS 23–0782), living culture (KUNCC 23–14211).

GenBank numbers – ITS: PV138701, *tef1- α* : PV177097, *tub2*: PV221990, *his3*: PV188089.

Notes – Our multi-locus phylogenetic analysis showed that the newly obtained strain (KUNCC 23–14211) clustered with four strains of *D. pauciseptata* with 93% ML statistical support (Fig. 54).

Morphologically, our new isolate is similar to *D. pauciseptata* in having solitary, unbranched or sparsely branched conidiophores that arise laterally or terminally from aerial mycelium, phialidic, hyaline, cylindrical conidiogenous cells and cylindrical macroconidia, with both ends rounded, 1–4-septate, hyaline, and smooth-walled. We, therefore, identified our new isolate as *D. pauciseptata* based on phylogenetic analysis and morphological characteristics. *Dactylonectria pauciseptata* (= *Cylindrocarpon pauciseptatum*) was isolated from partly decayed roots of *Vitis* in Slovenia (Schroers et al. 2008, Lombard et al. 2014). Our new strain was isolated from the rhizome of *Dicranopteris linearis*.

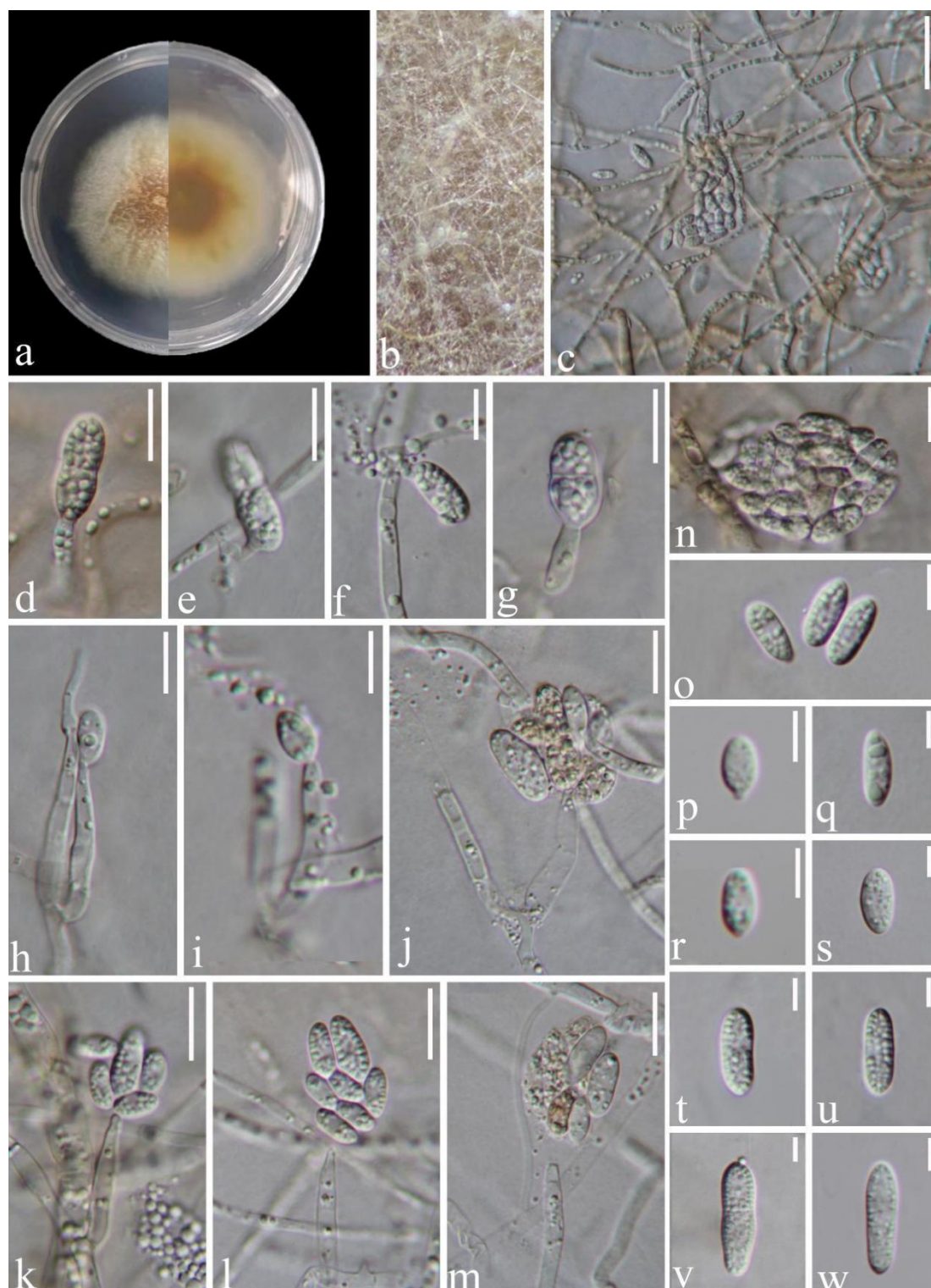


Figure 53 – *Dactylonectria dicranopteris* (GZAAS 23–0811, holotype). a Culture on PDA from above and below. b Mycelium. c Mycelium and conidia d–m Conidiophores, conidiogenous cells, and conidia. n–w Conidia. Scale bar: c = 20 μ m; d–h, j–n = 10 μ m, i, o–w = 5 μ m.

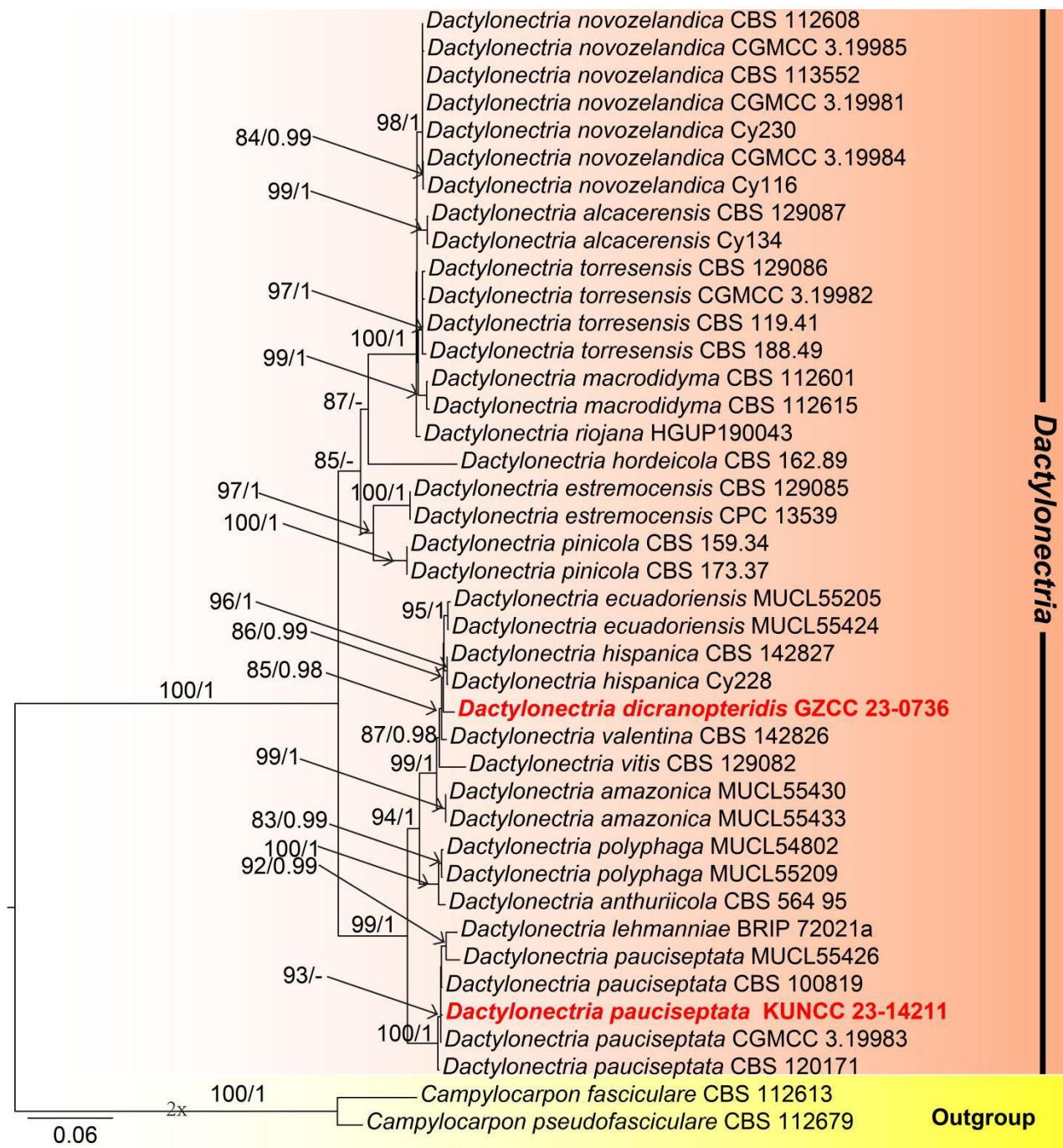


Figure 54 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tub2*, *his3*, and *tef1- α* sequence data. 41 taxa were included in the combined analyses, which comprised 2381 characters after alignment. The best scoring RAxML tree with a final likelihood value of -9219.574186 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Campylocarpon fasciculare* (CBS 112613) and *C. pseudofasciculare* (CBS 112679); the new strains are in red and bold.

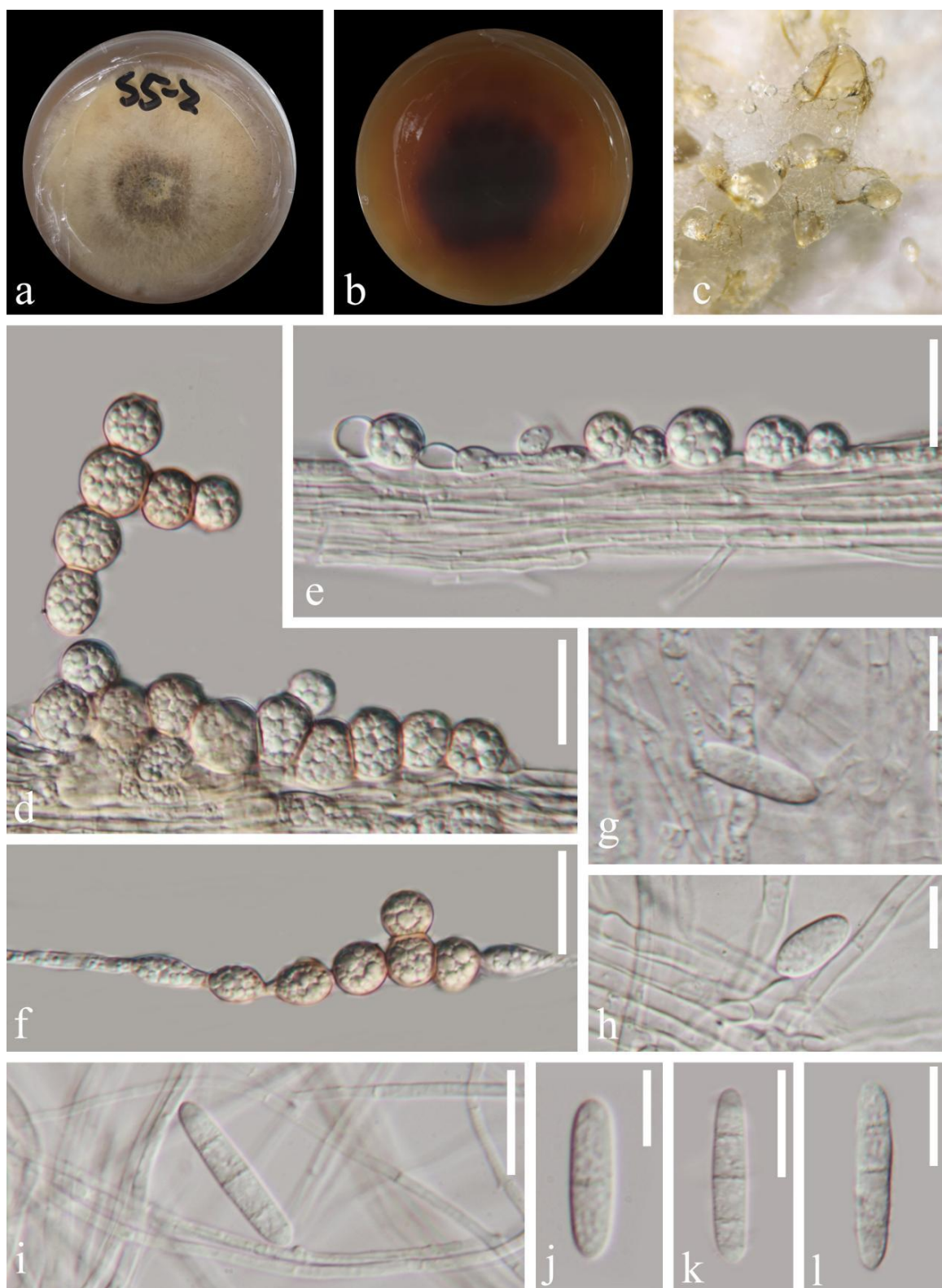


Figure 55 – *Dactylonectria pauciseptata* (GZAAS 23–0782, new host record). a, b Culture on PDA from above and below. c Colonies on PDA. d–f: Chlamydospore. g, i–l Macroconidia. h Microconidia. Scale bars: d–i, k–l = 20 μ m, j = 10 μ m.

Ilyonectria P. Chaverri & Salgado

Ilyonectria, one of several genera that are segregated from *Cylindrocarpon*, was introduced by

Chaverri et al. (2011) with *I. radicola* as the type species. Since the genus was established, several new species have been consequently introduced in *Ilyonectria* based on phylogenetic analysis and morphological characters (Cabral et al. 2012a, b, Aiello et al. 2013, 2017, Zeng et al. 2013, Lombard et al. 2013, Lu et al. 2020a, Zhang et al. 2024c). Currently, 38 species are listed in the (<http://www.indexfungorum.org/>) (accessed on July 10, 2024), of which eight have been transferred to *Dactylonectria* and *Cylindrodendrum*. *Ilyonectria* is characterized by red, globose to subglobose perithecia with scaly or slightly warted perithecial walls, and producing ellipsoidal, 1-septate ascospores. The asexual morphs of this genus are cylindrocarpon-like and produce abundant ellipsoidal to ovoid, 0–1-septate microconidia, almost straight, 1–3-septate macroconidia and intercalary, globose chlamydospores (Chaverri et al. 2011). Members of *Ilyonectria* are reported as plant pathogens associated with various hosts, such as grapevines (Cabral et al. 2012a, b, Reis et al. 2013, Probst et al. 2019), *Proteaceae* (Lombard et al. 2013), *American ginseng* (Zhang et al. 2019b), and *Aceraceae* (Aiello et al. 2017). While *I. radicina* has been reported as endophytes (Zhang et al. 2024c). In this study, a new endophytic species, *I. dicranopteridis*, was isolated from *Dicranopteris*.

Ilyonectria dicranopteridis J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov.

Fig. 56

Index Fungorum: IF 903975; Facesoffungi number: FoF 17878.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 25–0516

Endophytic in the root of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Conidiophores* simple or complex. *Simple conidiophores* arising laterally or terminally from aerial mycelium, unbranched or sparsely branched, solitary to loosely aggregated, one to three phialides, one- to two-septate, $24\text{--}38 \times 2.5\text{--}3.5 \mu\text{m}$ ($\bar{x} = 31.1 \times 3.1 \mu\text{m}$, $n = 15$). *Densely aggregated conidiophores* cylindrical, irregularly branched, tapering towards the apex, with flared collarete. *Phialides* $12.5\text{--}15 \times 2.5\text{--}3.5 \mu\text{m}$ ($\bar{x} = 13.9 \times 3.2 \mu\text{m}$, $n = 15$), monophialidic, straight or slightly curved, cylindrical to subcylindrical, slightly tapering towards the apex at the top, with a small flared collarete. *Densely aggregated conidiophores* cylindrical, richly and irregularly branched; mostly widest near the base; tapering towards the apex, with flared collarete. *Macroconidia* predominant, formed in flat domes of slimy masses, (1-)3-septate, mostly 3-septate, straight or slightly curved, cylindrical or minutely widening towards the tip, appearing somewhat clavate, particularly when still attached to the phialide; apex or apical cell typically slightly bent to one side and minutely beaked; base mostly with a visible, centrally located or laterally displaced hilum; one-septate conidia $(11\text{--})13.5\text{--}20.5\text{--}(23) \times 4.5\text{--}6.5 \mu\text{m}$ ($\bar{x} = 17 \times 5.4 \mu\text{m}$, $n = 30$); two-septate conidia $21\text{--}27.5 \times 6\text{--}8 \mu\text{m}$ ($\bar{x} = 24.3 \times 6.9 \mu\text{m}$, $n = 30$), and three-septate conidia $24.5\text{--}29 \times 7\text{--}8 \mu\text{m}$ ($\bar{x} = 26.8 \times 7.4 \mu\text{m}$, $n = 30$). *Microconidia* $5\text{--}8 \times 2\text{--}3 \mu\text{m}$ ($\bar{x} = 6.6 \times 2.3 \mu\text{m}$, $n = 40$), various in shape, ellipsoid to ovoid, cylindrical, oval, aseptate, straight or slightly curved, with or without an aminutely or clearly laterally displaced hilum, hyaline to medium brown, guttulate, smooth-walled. *Chlamydospores* $9\text{--}12 \times 8.5\text{--}10 \mu\text{m}$ ($\bar{x} = 10.4 \times 9.3 \mu\text{m}$, $n = 30$), abundant, globose, subglobose, ellipsoidal, hyaline to golden brown with age, thick walled, sometimes intercalary in chains, solitary, in short or chains or aggregated, uni- or multicellular, smooth but often appearing rough due to deposits.

Culture characteristics – Colonies on PDA medium occupied the whole plate in 15 days at 25 °C; from above: round, cream to pale yellow, slightly low, irregular to rhizoid and aerial mycelium scarce near the center, cottony, dense and raised towards the periphery, with abundant aerial mycelium, regular margins; reverse: buff.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the roots of *Dicranopteris ampla*, 20 February 2022, J.Y. Zhang, (NS251–2 = GZAAS 25–0516, holotype), ex-type living culture GZCC 25–0506. *ibid.* (NS251–6 = GZAAS25–0517, paratype).

GenBank numbers – GZCC 25–0506: ITS: PV138707, *tef1*- α : PV177103, *tub2*: PV221996, *his3*: PV188094. GZAAS25–0517: ITS: PV138708, *tef1*- α : PV177104, *tub2*: PV221997, *his3*: PV188095.

Notes – Phylogenetic analysis showed that our two new isolates grouped together and were sister to *Ilyonectria radicigena* (Fig. 57). However, *I. dicranopteridis* is different from *I. radicigena* in having (1–)3-septate, mostly 3-septate macroconidia and aseptate microconidia, which are various in shape, ellipsoid to ovoid, cylindrical, oval. While *I. radicigena* has one- to three septate (mostly one) macroconidia and zero- to one septate, oval to ellipsoidal to subcylindrical microconidia (Zhang et al. 2024c).

***Chaetosphaeriales* Huhndorf, A.N. Mill. & F.A. Fernández**

Chaetosphaeriales was established by Huhndorf et al. (2004) for *Chaetosphaeriaceae*. Currently, the order comprises four families, viz. *Chaetosphaeriaceae*, *Helminthosphaeriaceae*, *Leptosporaceae* and *Linocarpaceae* (Wijayawardene et al. 2022).

***Chaetosphaeriaceae* Réblová, M.E. Barr & Samuels**

Chaetosphaeriaceae, the largest family in *Chaetosphaeriales*, was invalidated and introduced by Locquin (1984) to accommodate *Chaetosphaeria*. It was formally established by Réblová et al. (1999) with seven genera *Ascocodinaea*, *Chaetosphaeria*, *Melanopsammella*, *Porosphaerella*, *Porosphaerellopsis*, and *Striatosphaeria* based on LSU sequence data. The taxonomy of this family has long been problematic and has been reviewed by various authors; for example, Lin et al. (2019a) expanded the family to accommodate 49 genera. While Hyde et al. (2020) accepted 39 genera in the family. Réblová et al. (2020, 2021a, b, c, d, e) systematically reviewed several polyphyletic genera and established several new genera under the family. The latest treatment of the family was provided by Wu & Diao (2022), who conducted a systematic study on diversity, taxonomy, and phylogeny of anamorphic *Chaetosphaeriaceae* in China using an integrated approach of morphological observation and phylogenetic analysis, which expanded the family to include 89 accepted genera. In addition, several polyphyletic genera, e.g., *Codinaea*, *Dictyochaeta* and *Tainosphaeria* complex, have been resolved by re-delimiting *Codinaea* and *Dictyochaeta* with a narrower concept (Réblová et al. 2020b, 2021a, b, c, d, e, Wu & Diao 2022). Hyde et al. (2024) accepted 109 genera in the family.

***Geniculoseta* Réblová**

The monotypic genus *Geniculoseta* was recently established by Réblová et al. (2023) with a single species *G. preussii*, which was previously introduced as *Chaetosphaeria preussii*. Réblová et al. (2023) showed that *C. preussii* is morphologically different and distantly related to its presumed asexual morph, *Chloridium preussii*. They, therefore, introduced a new genus *Geniculoseta*, to accommodate this species. In this study, a new endophytic fungus, *G. dicranopteridis* is introduced based on morphological and phylogenetic analyses.

***Geniculoseta dicranopteridis* J.Y. Zhang, D.F. Bao, K.D. Hyde & J.C. Kang, sp. nov. Fig. 58**

Index Fungorum: IF 903976; Facesoffungi number: FoF 17879.

Etymology – The specific epithet *dicranopteridis* refers to the plant genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 23–0791

Endophytic in the healthy roots of *Dicranopteris amplax*. Sexual morph: unknown. Asexual morph: *Conidiophores* 160–170 × 3–4.1 μm, macronematous, solitary, scattered, crowded or caespitose, erect, straight or slightly flexuous, subulately tapering, unbranched, brown to greenish-brown, with 1–3 percurrent proliferations assuming a geniculate appearance. *Conidiogenous cells* 2.5–8 × 1.8–3.5 μm ($\bar{x}$ = 4.8 × 2.5 μm, n = 7) monophialidic with a single conidiogenous locus, integrated, terminal, rarely discrete, lateral, extending percurrently, subulate or narrowly lageniform, pale greenish-brown, smooth, with a collarete. *Conidia* 2–3.5 × 1.5–2.5 μm ($\bar{x}$ = 2.7 × 2.1 μm, n = 33), acrogenous, aseptate, globose to ellipsoidal, cuneiform, sub-triangular, hyaline, smooth, guttulate.

Culture characteristics – Colonies on PDA medium reach 25–30 mm in diameter within 14 days when incubated at 25°C. They are irregular in shape, dry, convex, with entire margins. The surface exhibits a dark brown center grading to white-to-cream at the edges; the reverse side displays entire margins and a white-to-cream coloration.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the roots of *Dicranopteris amplax*, 20 February 2022, J.Y. Zhang (SN203–1 = GZAAS 23–0791, holotype), living culture (KUNCC 23–14189 = GZCC 23–0705).

GenBank numbers – ITS: PV138686, LSU: PV138583

Notes – In our phylogenetic analysis, the new isolate (KUNCC 23–14189) forms a distinct clade close to *Geniculoseta preussii* (Fig. 59). However, it can be differentiated from *G. preussii* by its brown to greenish-brown conidiophores with 1–3 percurrent proliferations, which assume a geniculate appearance and are not bulbous at the base. The conidia are aseptate, globose to ellipsoidal, cuneiform, or sub-triangular. In contrast, the conidiophores of *G. preussii* are bulbous at the base, brown to dark reddish-brown, and have 1–5 percurrent proliferations with a geniculate appearance, and the conidia are ellipsoidal to oblong (Réblová et al. 2023).

Although the phylogenetic analysis showed that our new isolate did not cluster within the genus *Geniculoseta*, morphologically, it aligns with the generic characteristics of *Geniculoseta*. It exhibits macronematous, mononematous, erect, solitary, scattered, crowded, or caespitose unbranched conidiophores with several percurrent proliferations; conidiogenous cells are monophialidic with a single conidiogenous locus, terminal, and extend percurrently, with flaring, funnel-shaped collarettes, and conidia are hyaline, aseptate, smooth conidia, which accumulate in slimy heads. Currently, only a single species is recognized in *Geniculoseta*, making it challenging to accurately determine the status and placement of this genus. Additionally, *Geniculoseta* is phylogenetically close to *Gongromeriza*, and morphologically, these two genera are quite similar, with a close phylogenetic affinity. Therefore, the status of these two genera may need to be re-evaluated with more collections (Réblová et al. 2023). Considering these factors, we tentatively place our new isolate within *Geniculoseta*. However, further sampling and additional sequence data are necessary to confirm the status of the genus and the precise placement of our new species.

Tainosphaeria F.A. Fernández & Huhndorf

Tainosphaeria was established by Fernández and Huhndorf (2005) with *T. crassiparves* as the type, which was introduced based on both sexual and asexual morphs. Subsequently, several new species have been consequently added to the genus (Lu et al. 2016, Luo et al. 2019, Lin et al. 2019a, Wu & Diao 2022). However, the phylogenetic analysis of Réblová et al. (2021b) showed that *Tainosphaeria* is polyphyletic, and they separated the genus into three genera (*Tainosphaeria*, *Phialoturbella* and *Flectospora*) with acceptance of five species in *Tainosphaeria*, this was also

supported by morphological characteristics. Recently, Wu & Diao (2022) accepted this treatment and provided a key to species of *Tainosphaeria*, accepting 12 species (including five new species) in this genus. Members of *Tainosphaeria* are saprobes on decaying or submerged wood; it is characterized by macronematous, solitary, simple conidiophores, usually monophialidic conidiogenous cells, and falcate, setulate conidia (Fernández and Huhndorf 2005, Luo et al. 2019, Réblová et al. 2021b, Wu & Diao 2022). In this study, *Tainosphaeria phialogeniculata* is reported as an endophyte from *Dicranopteris ampla*; this is the first species of *Tainosphaeria* reported as an endophyte.

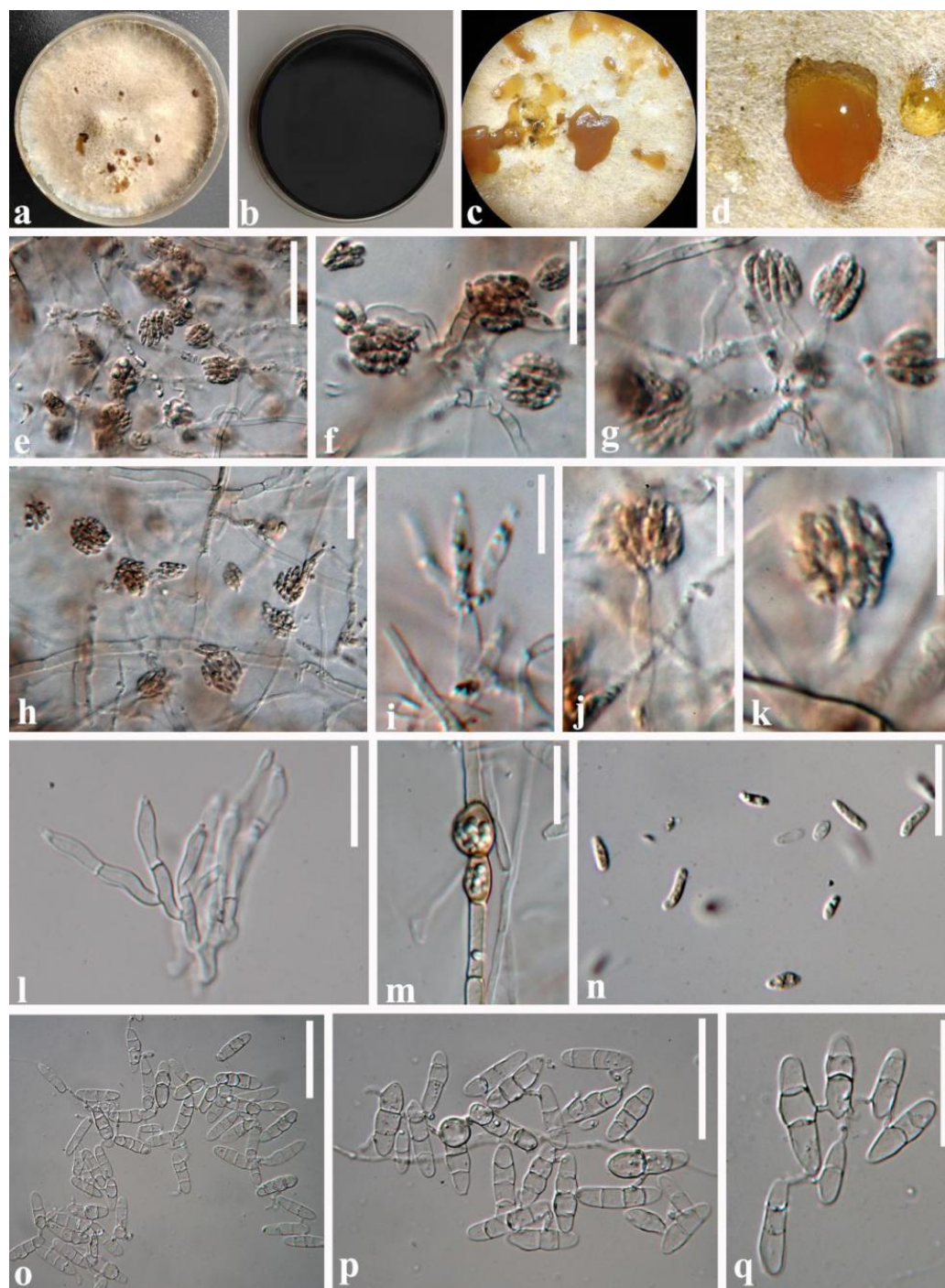


Figure 56 – *Ilyonectria dicranopteridis* (GZAAS 25–0516, holotype). a, b Culture on PDA from obverse and reverse. c, d Colonies on MEA. e–k Mycelium, conidiophores and conidia. l Conidiophores. m Chlamydospores. n Microconidia. o–q Macroconidia. Scale bar: e, p, q = 30 μ m;

f–h = 20 μ m, i–k = 10 μ m, l–n = 20 μ m, o = 50 μ m.

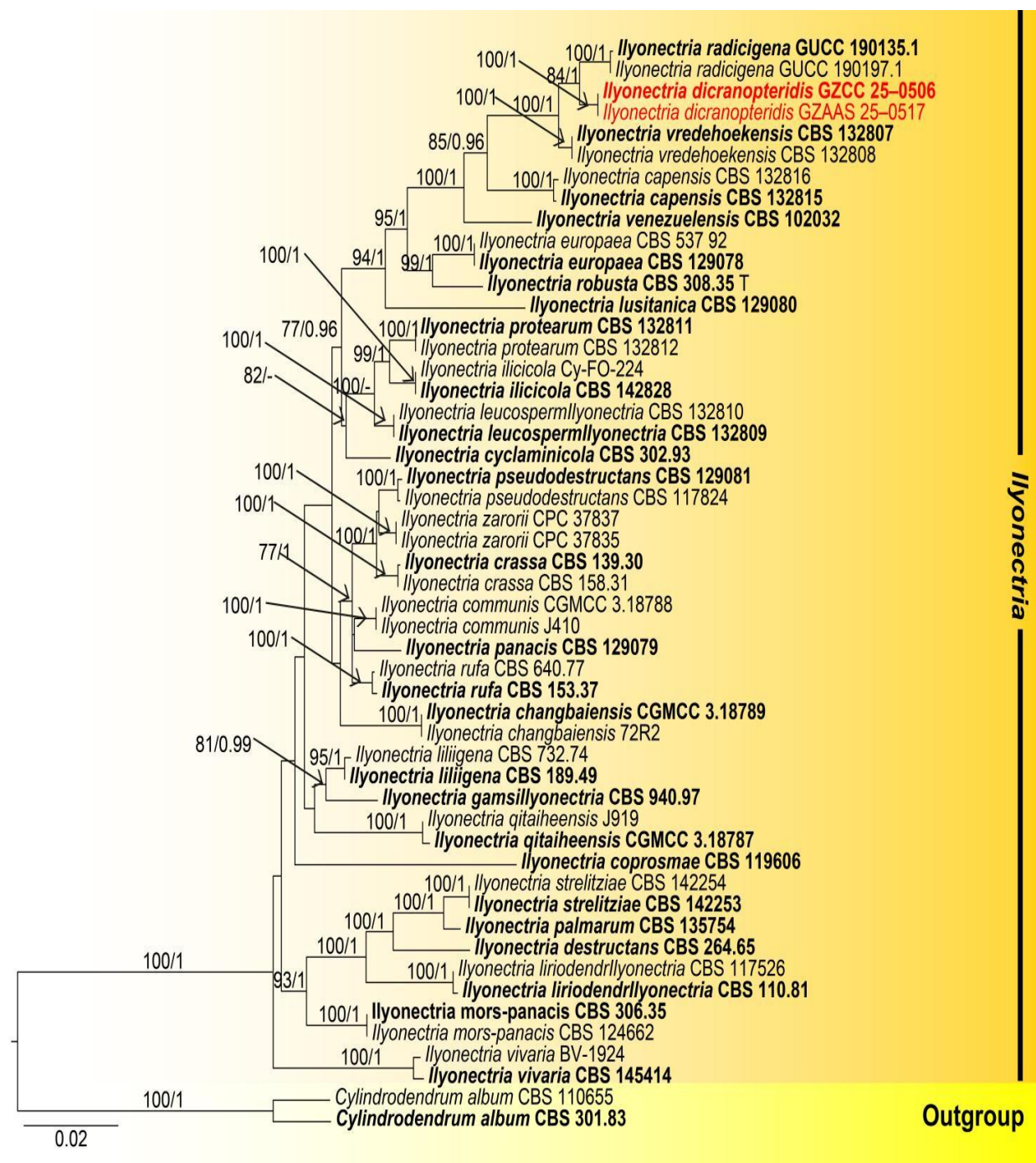


Figure 57 – Phylogram generated from maximum likelihood analysis based on combined ITS, *his3*, *tef1- α* , and *tub2*, sequence data. 51 taxa were included in the combined analyses, which comprised 2527 characters after alignment. The best scoring RAxML tree with a final likelihood value of -10247.337190 is presented. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Cylindrodendrum album* (CBS 110655 and CBS 301.83); the type strains are in bold and new strains are in red.



Figure 58 – *Geniculoseta dicranopteridis* (GZAAS 23–0791, holotype). a, b Culture on PDA from above and below. c Colonies on PDA. d–i Conidiophores, conidiogenous cells, and conidia. j–l Conidia. Scale bar: d–f = 50 μ m, g–i = 10 μ m, j–l = 5 μ m.

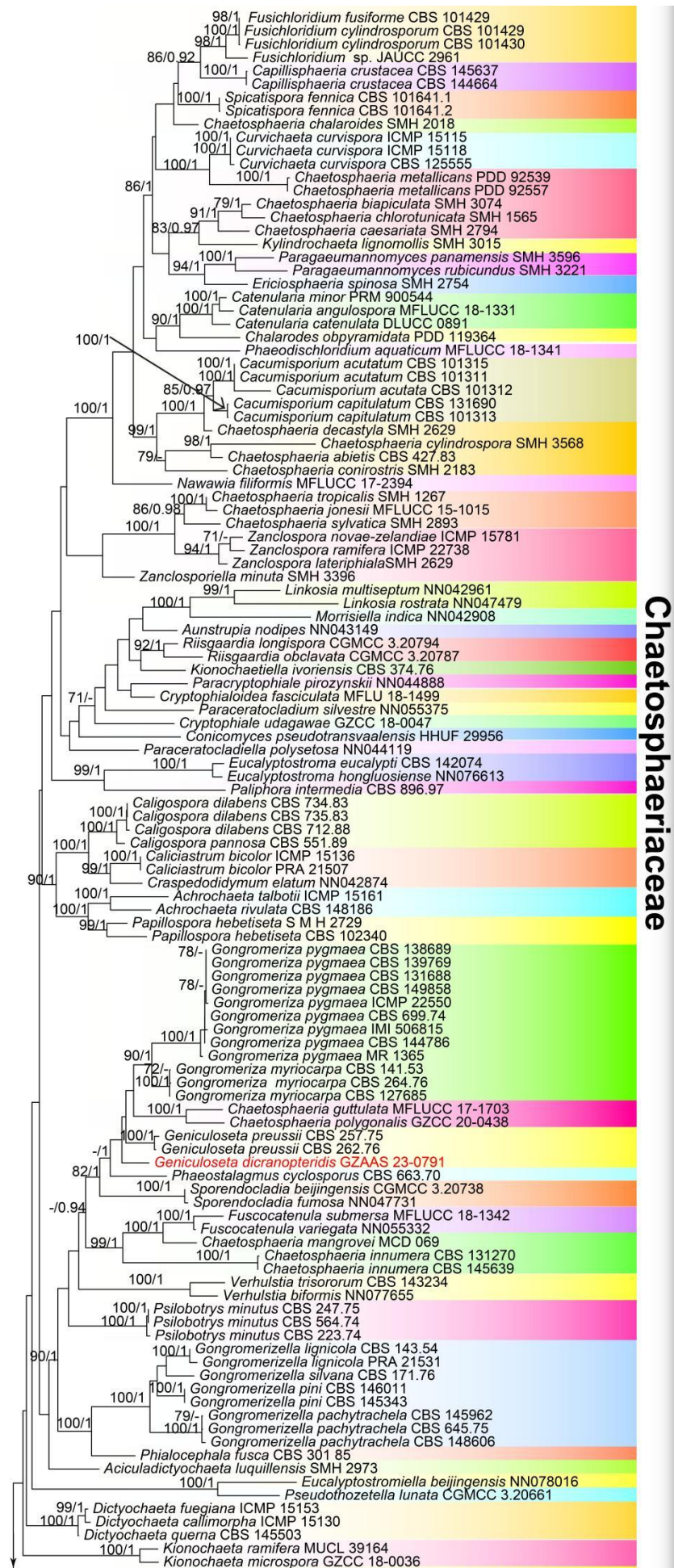


Figure 59 – Phylogram generated from maximum likelihood analysis based on combined ITS, *his3*, and *tef1- α* sequence data. A total of 201 taxa were included in the combined analyses, which comprised 2853 characters after alignment. The best scoring RAxML tree with a final likelihood value of -50527.827145 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Tracylla aristata* (CBS 141404) and *T. eucalypti* (CBS 144429); the new strains are in red.

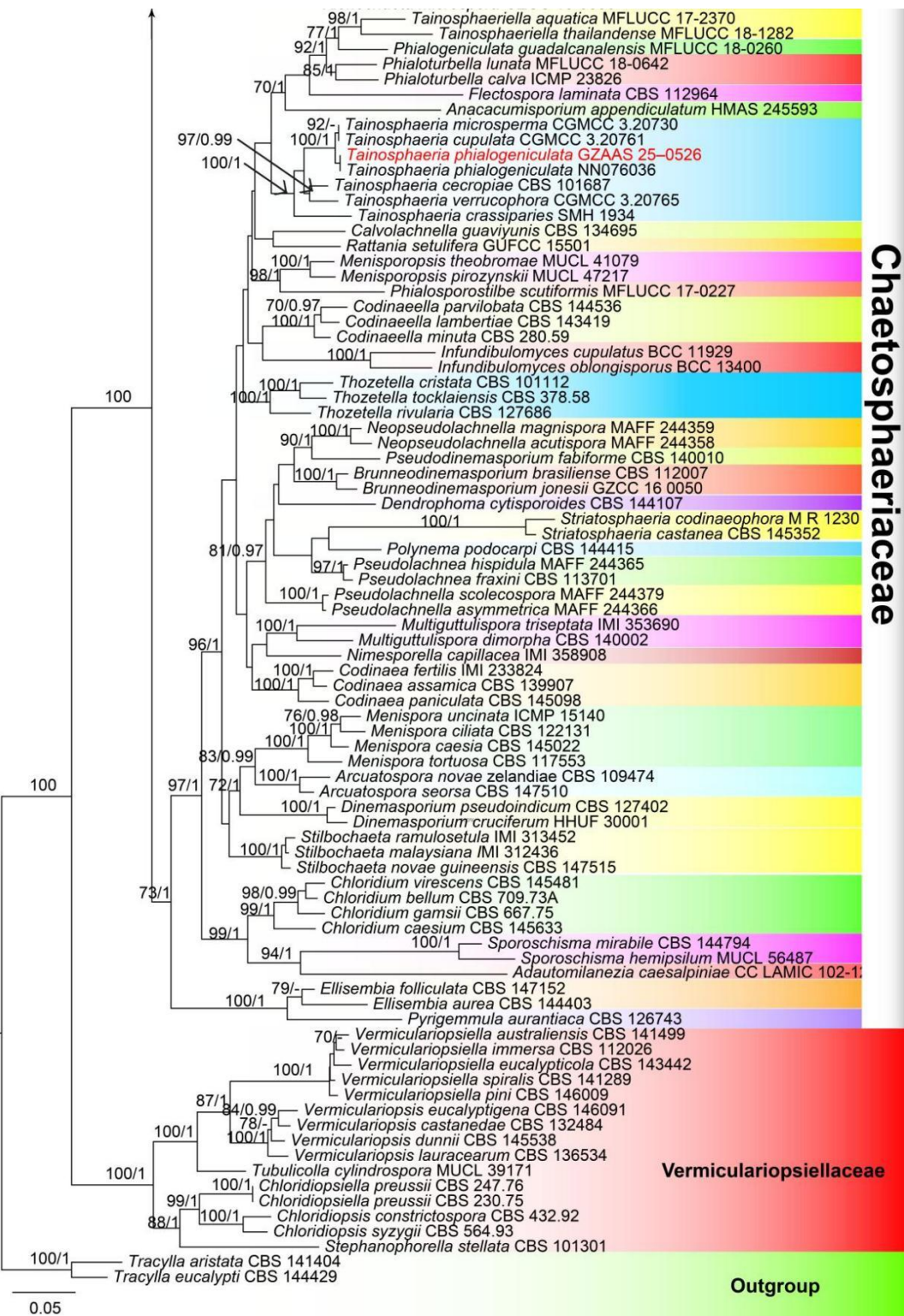


Figure 59 – Continued

Tainosphaeria phialogeniculata W.P. Wu & Y.Z. Diao, Fungal Diversity: 116(1):216 (2022) Fig. 60

Index Fungorum: IF 841592; Facesoffungi number: FoF 17880.

See the description in Wu and Diao (2022)

Culture characteristics – Colonies on MEA reaching 55 mm diameter after 20 days at 25°C, colonies circular, margin wavy, flat, velvety appearance with brown aerial mycelia in the middle, colony from above brown to dark brown; reverse: dark brown to black.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the rhizome of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (NS317–1 = GZAAS 25–0526).

GenBank numbers – ITS: PV138687, LSU: PV138584

Notes – Based on the combined ITS and LSU phylogeny, this new isolate (GZAAS 25–0526) clustered with *Tainosphaeria phialogeniculata* (NN076036) with 79% ML, xx MP, and xxx BYPP support (Fig. 59). We were unable to observe asexual or sexual morph characters in the culture. However, the nucleotides of ITS and LSU sequences data of our new isolate are identical to those of *T. phialogeniculata* (NN076036). Thus, we identified our new isolate as *T. phialogeniculata*. *Tainosphaeria phialogeniculata* was introduced by Wu & Diao (2022), which is a saprobe found on dead leaves of an unidentified tree in Yunnan, China. Here, we record the endophytic lifestyle of *T. phialogeniculata* from the rhizome of *Dicranopteris ampla* in Guizhou Province, China.

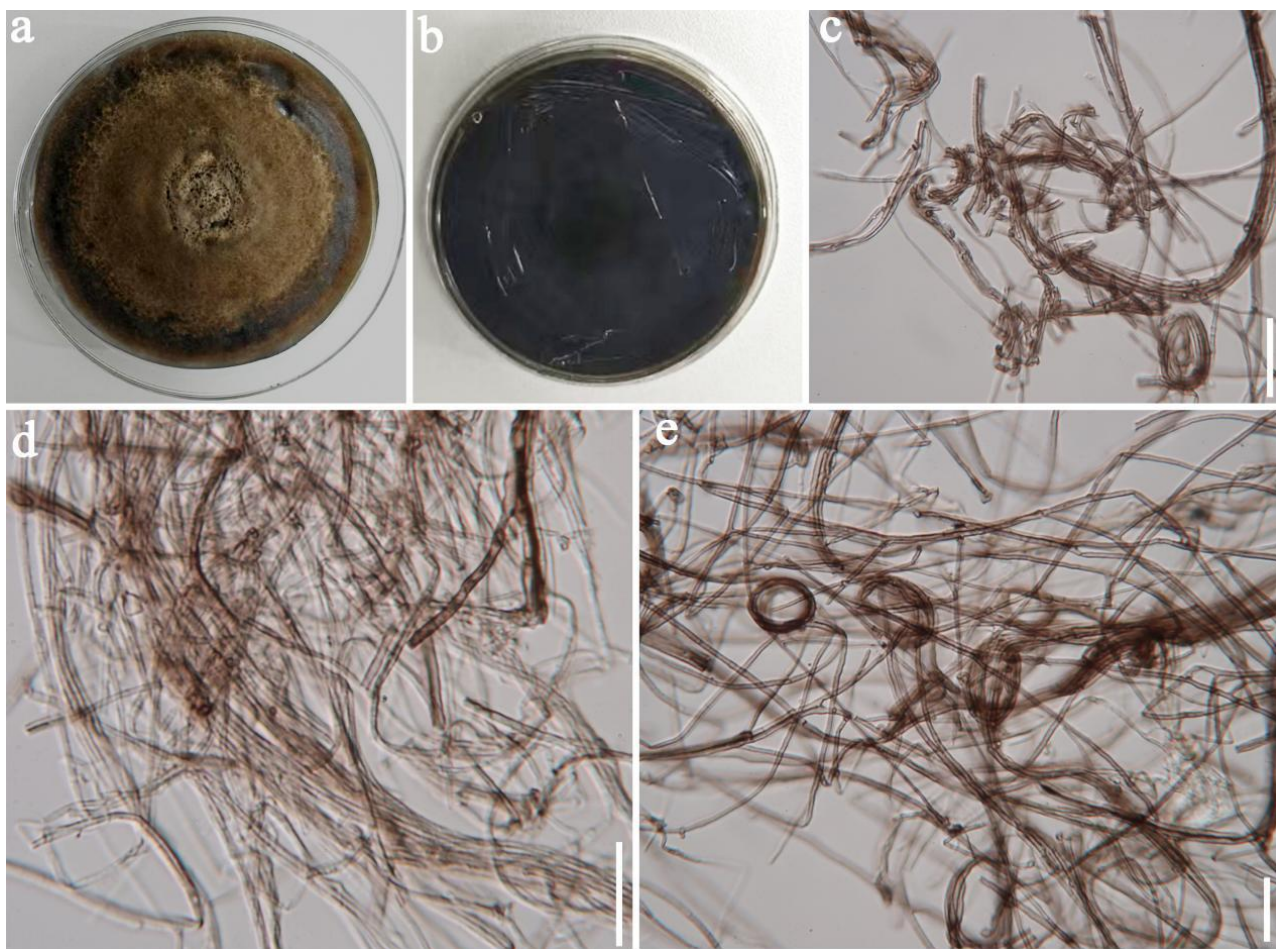


Figure 60 – *Tainosphaeria phialogeniculata* (GZAAS 25–0526, new host record). a, b Culture on PDA from above and below. c–e Mycelium. Scale bar: c = 30 μ m, d, e = 20 μ m.

Magnaporthales Thongk., Vijaykr. & K.D. Hyde

In this study, we follow the latest treatment and updated accounts of *Magnaporthales* by Feng et al. (2024), who accepted six families, viz. *Ceratosphaeriaceae*, *Magnaporthaceae*, *Ophiocercaceae*, *Plagiosphaeraceae*, *Pseudohalonectriaceae*, and *Pyriculariaceae* in this order.

Magnaporthaceae P.F. Cannon

Magnaporthaceae was established by Cannon (1994), and placed in *Magnaporthales*, *Sordariomycetes*. The latest treatment of this family was provided by Feng et al. (2024), they transferred *Plagiosphaera*, *Muraeriata*, and *Aquafiliformis* to a newly introduced family *Plagiosphaeraceae*, accepting 28 genera in *Magnaporthaceae*, including 10 new genera.

Omnidemptus P.F. Cannon & Alcorn, Mycotaxon 51: 483

Omnidemptus was introduced as the sexual morph of *Mycoleptodiscus* by Cannon (1994). Hernández-Restrepo et al. (2019) showed that *Omnidemptus* formed an independent lineage within *Magnaporthaceae*, thus, they formally treated *Omnidemptus* as a distinct genus, as well as introduced two new species *O. graminis* and *O. lunatus* into the genus. Recently, Feng et al. (2024) introduced four new species to the genus. Thus, seven species are included in this genus. *Omnidemptus* is characterized by superficial, perithecial, ostiolate, pyriform ascomata with a long neck, bitunicate, 8-spored, cylindric-clavate short-stalked asci with an obtuse apex, apical pore and biseriate, fusiform, centrally swollen, 1–3-septate, hyaline ascospore; phialidic, ampulliform or elongated, cylindrical, clavate or ellipsoid, dark brown conidiogenous cells with a circular aperture enclosed by a cylindrical to flared collarette, and falcate, hyaline, 1–2(–3)-septate conidia (Feng et al. 2024).

Omnidemptus dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov.

Fig. 61

Index Fungorum: IF 903977; Facesoffungi number: FoF 17881.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – KUN-HKAS 129909

Endophytic in the stem of *Dicranopteris ampla*. *Mycelium* mostly immersed composed of septate, branched, hyaline to pale brown, with smooth and thick-walled hyphae. Sexual morph: Undetermined. Asexual morph: *Conidiophores* 10–57 × 5–7.5 µm (*n* = 20), macronematous, mononematous, unbranched, swollen at the apex, pale brown, septate, smooth-walled. *Conidiogenous cells* 10–19 × 6.5–10 µm (*n* = 20), phialidic, terminal or intercalary, cylindrical to lageniform, subhyaline to pale brown. *Conidia* 45–63 × 4–6 µm (*n* = 30), lunate, fusiform to filiform, tapering towards the ends, slightly curved, hyaline, septate, smooth.

Culture characteristics – Colonies on PDA reaching 15 mm diameter after 7 days at 25 °C circular with entire margin, cottony to fluffy, white and not sporulate in culture; Colonies on medium of WA-carrot mixture sporiferous, irregular, with several white to brown spots, thin, flat, hyaline to white, and does not produce pigmentation in culture.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi and Miao Autonomous Prefecture, Zhenfeng County, isolated from the healthy stem of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (NS299–3 = KUN-HKAS 129909, holotype), ex-type culture (KUNCC 23–14201).

GenBank number: ITS: PV138746, LSU: PV138601, rpb1: PV221980.

Notes – In a BLASTn search of NCBI GenBank, the closest match of the ITS sequence of *Omnidemptus dicranopteridis* (KUNCC 23–14201, ex-type) with 93.57% similarity was *O. graminis* FMR 12415. The closest match with the LSU sequences with 99.32% similarity was *O. affinis* strain

BRIP 17195b, but there are 39bp differences in ITS gene region between them. Phylogenetic analyses showed that *O. dicranopteridis* (KUNCC 23–1420) formed a distinct lineage in the genus (Fig. 62). Morphologically, *O. dicranopteridis* fits well with the generic concept of having phialidic, ampulliform or elongated, brown conidiogenous cells with a circular aperture enclosed by a cylindrical to flared collarette and falcate, hyaline, septate conidia. It is phylogenetically close to *Omnidemtus* sp. (YNE00826). *Omnidemtus* sp. (YNE00826) was introduced by Feng et al. (2024) without description and illustration, but they are phylogenetically distinct, the nucleotide comparisons revealed that *O. dicranopteridis* is different from *Omnidemtus* sp. (YNE00826) in 44/446 bp (9.86%) of the ITS, which strongly supports *O. dicranopteridis* as a new species.

***Pseudodactylariales* Crous**

Pseudodactylariales was established by Crous et al. (2017) with a single family *Pseudodactylariaceae*. The status of this order is well-supported by phylogenetic analysis and divergence time estimates (Hyde et al. 2020a).

***Pseudodactylariaceae* Crous**

Crous et al. (2017) introduced *Pseudodactylariaceae* to accommodate a single genus, *Pseudodactylaria*. Currently, *Pseudodactylariaceae* includes one genus with 10 species, all of which are saprobes from terrestrial and freshwater habitats (Crous et al. 2017, Lin et al. 2018b, Hyde et al. 2020b, Lu et al. 2020b, Bao et al. 2021, Boonmee et al. 2021, Yang et al. 2023b).

***Pseudodactylaria* Crous**

Pseudodactylaria, a well-studied genus with all species has sequence data available in the GenBank (Crous et al. 2017, Lin et al. 2018b, Hyde et al. 2020b, Lu et al. 2020b, Bao et al. 2021, Boonmee et al. 2021, Yang et al. 2023b). The genus was introduced by Crous et al. (2017) to accommodate the type species *P. xanthorrhoeae*, which was reported isolated from *Xanthorrhoea* sp. in Australia. To date, ten species are accepted in *Pseudodactylaria*, characterized by single, unbranched, septate conidiophores, polyblastic, denticulate conidiogenous cells, and solitary, fusoid-ellipsoid, hyaline conidia (Crous et al. 2017, Hyde et al. 2020b, Bao et al. 2021, Yang et al. 2023b).

***Pseudodactylaria dicranopteridis* J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 63**

Index Fungorum: IF 903978; Facesoffungi number: FoF 17882.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 23–0788

Endophytic in the rhizome of *Dicranopteris pedate*. *Mycelium* superficial and immersed composed of septate, branched, hyaline to pale brown, with smooth and thick-walled hyphae. *Chlamydospores* 10–19 × 8–14 µm ($\bar{x}$ = 13.5 × 9.5 µm, n = 30), solitary, subglobose, coiled, irregular, hyaline to subhyaline when young, brown when mature, septate, guttulate.

Culture characteristics – *Colonies* on PDA medium under natural light, circular, with a flat surface, edge undulate, reaching 38 mm in 20 days at 26°C, spread, without veined and wrinkle, taupe to grey to brown from center to margin from above; dark brown to brown towards the edge in reverse, and not producing pigmentation in culture.

Material examined – China, Guizhou Province, Southwest Guizhou Buyi and Miao Autonomous County, Libo County, isolated from the healthy rhizome of *Dicranopteris pedata*, 8 April 2022, J.Y. Zhang, (378–1 = GZAAS 23–0788, holotype), ex-type living culture (KUNCC 23–14205).

GenBank numbers – ITS: PV138737, LSU: PV138592

Notes – The genus has ten identified species, all of which are saprobes, with the majority from freshwater habitats. (Crous et al. 2017, Lin et al. 2018b, Hyde et al. 2020b, Lu et al. 2020b, Bao et al. 2021, Boonmee et al. 2021, Yang et al. 2023b). Our collection is the only endophytic species in *Pseudodactylaria*; only chlamydospores have been found in the culture. The conidia and denticulate conidiogenous cells were not observed from our culture. In the phylogenetic analyses, our new strain KUNCC 23–14205 formed a distinct clade within the *Pseudodactylaria* group, which supports our species as a new species (Fig. 64). Therefore, we introduce *P. dicranopteridis* as a new species based on phylogenetic analysis.

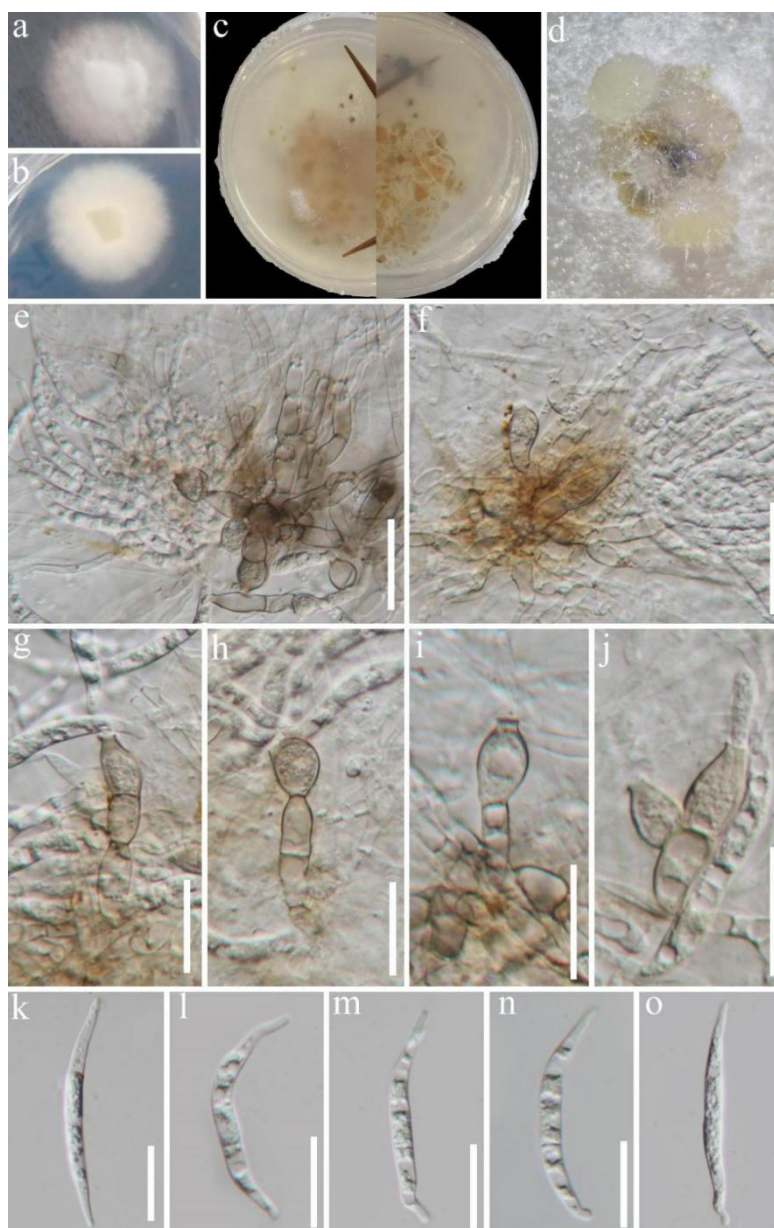


Figure 61 – *Omnidemptus dicranopteridis* (KUN-HKAS 129909, holotype) a, b Cultures on PDA from obverse and reverse. c Cultures on WA-carrot mixture. d Colonies on the media of WA-carrot mixture. e–j Conidiophores, conidiogenous cells and conidia. k–o Conidia. Scale bars: e, f = 30 µm, g–o = 20 µm.

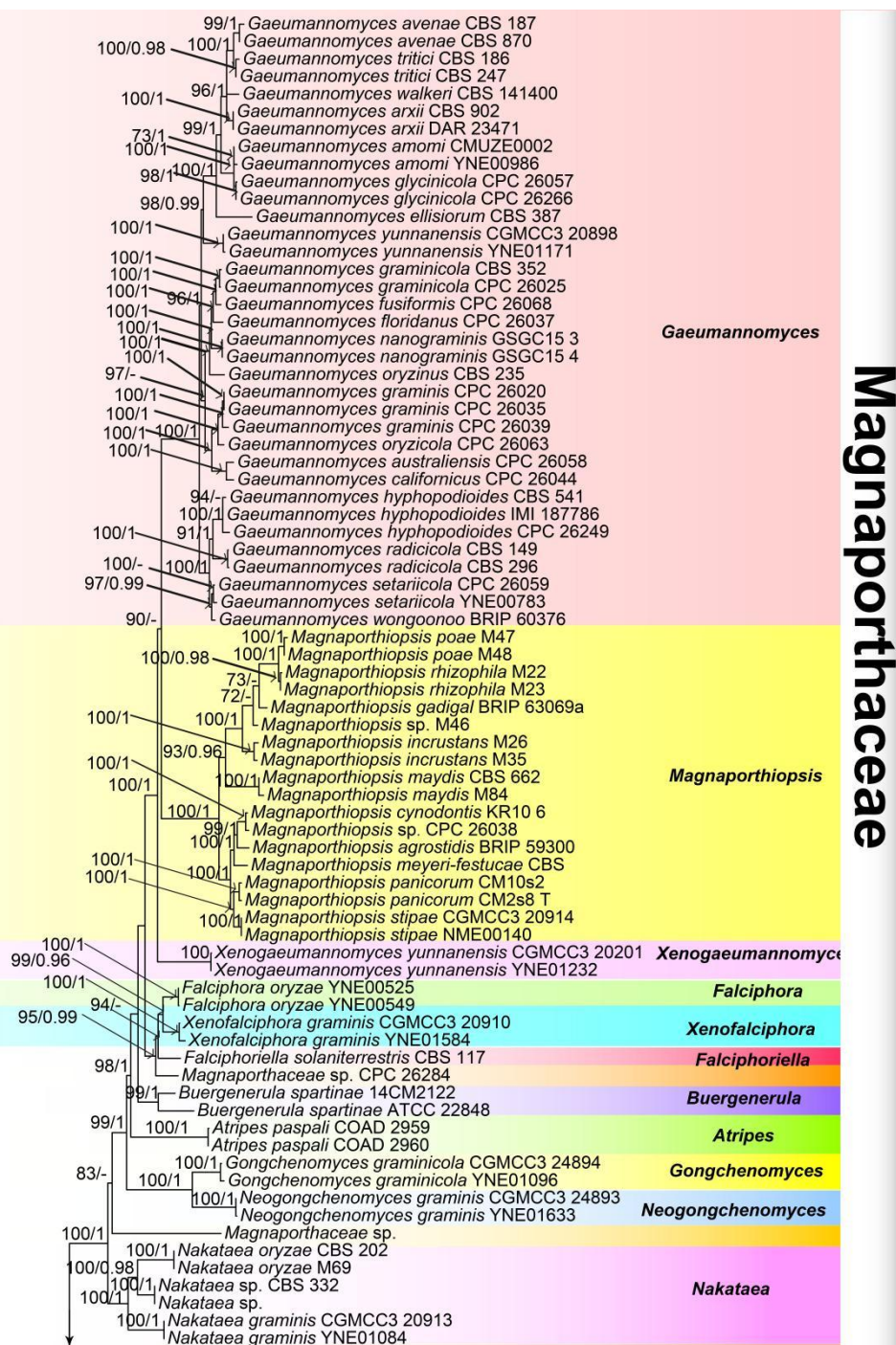


Figure 62 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *mcm7* and *rpb1* sequence data. 159 taxa were included in the combined analyses, which comprised 2793 characters after alignment. The best scoring RAXML tree with a final likelihood value of -14189.447665 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Ophioceras graminis* (YNE00713 and YNE00717). The newly obtained strains are in red.

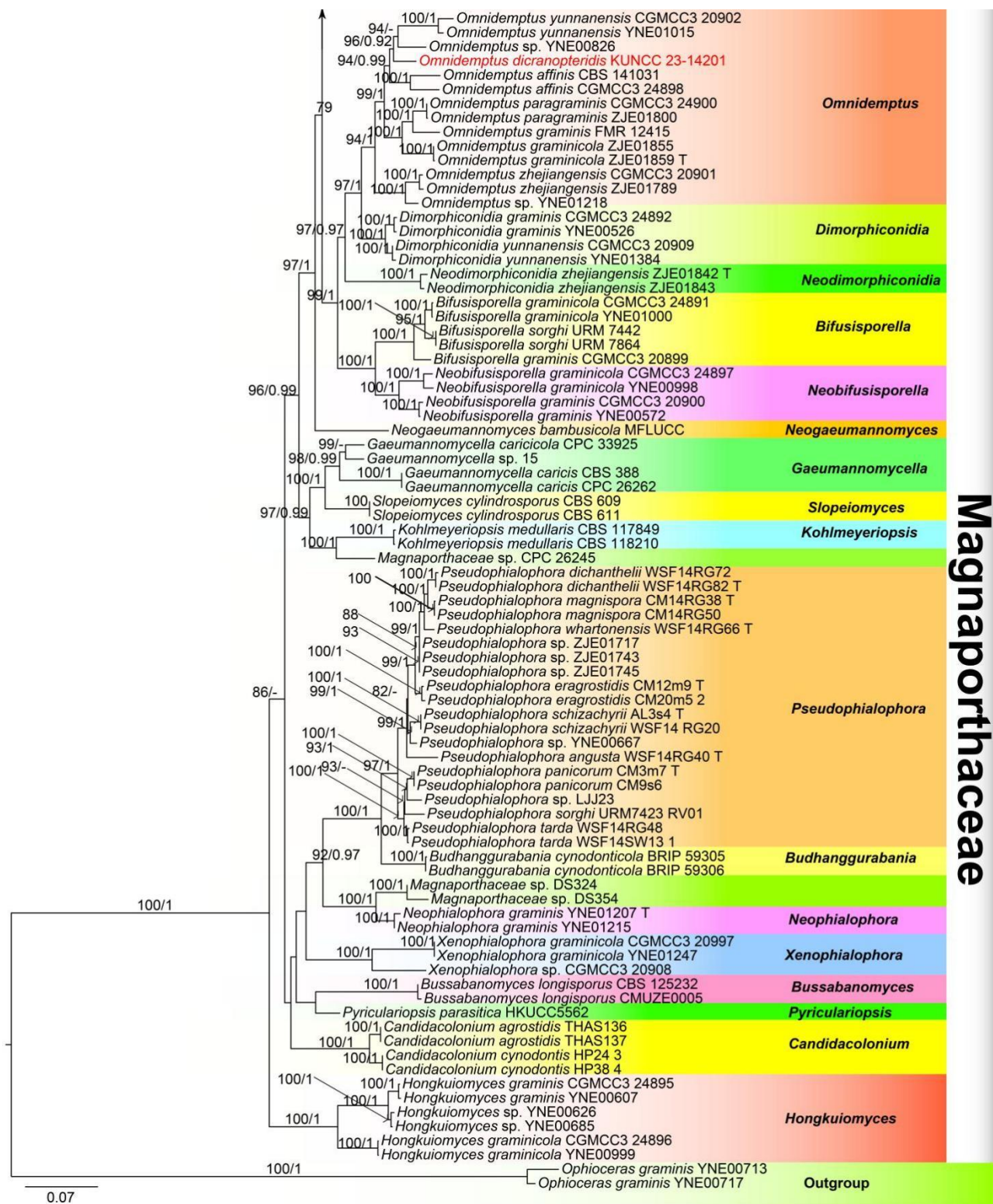


Figure 62 – Continued

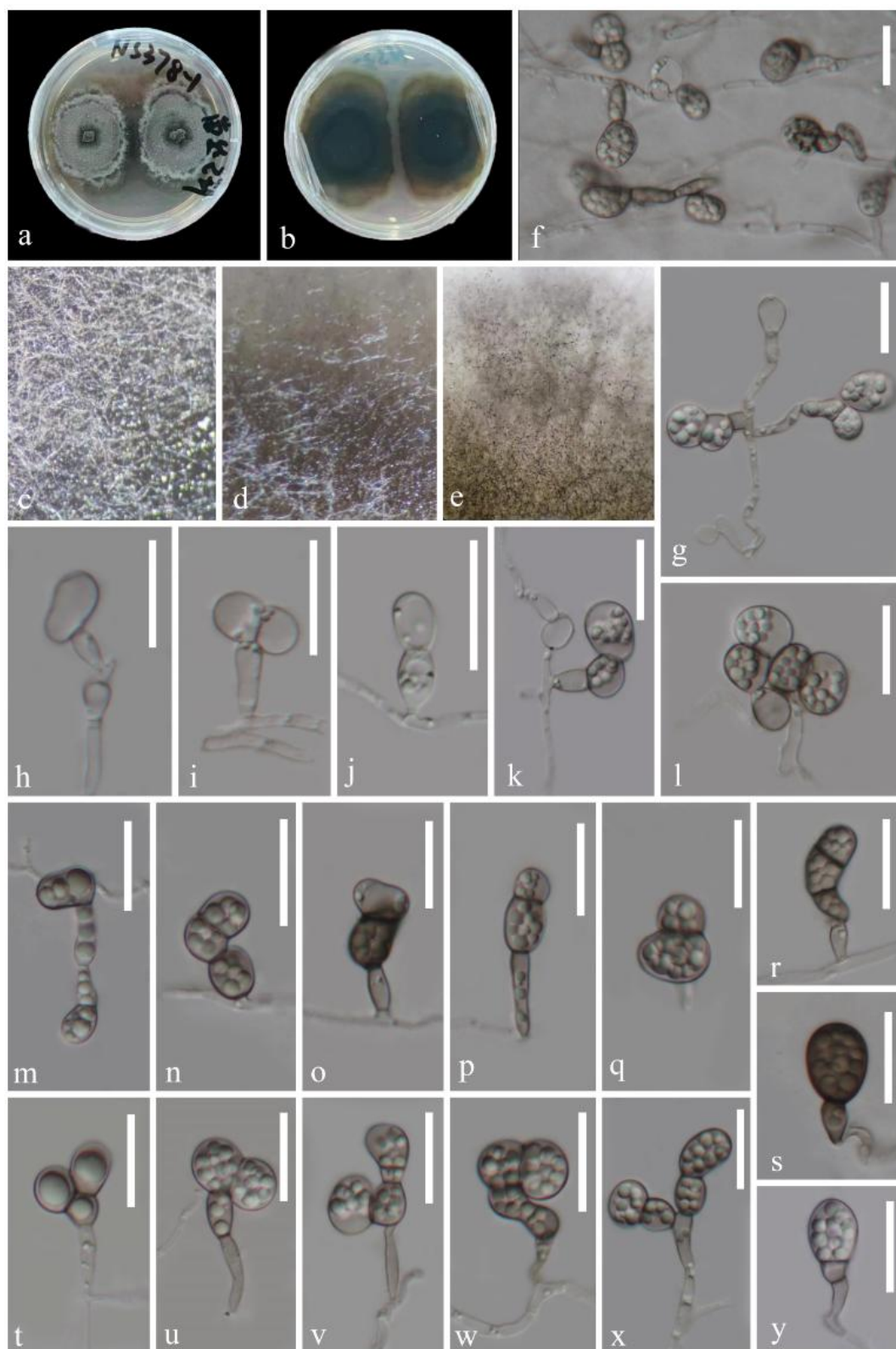


Figure 63 – *Pseudodactylaria dicranopteridis* (GZAAS 23–0788, holotype). a, b Cultures on PDA from above and below. c–e Colonies on the PDA. f–y Hyphae with chlamydospores. Scale bars: f–y = 20 µm.

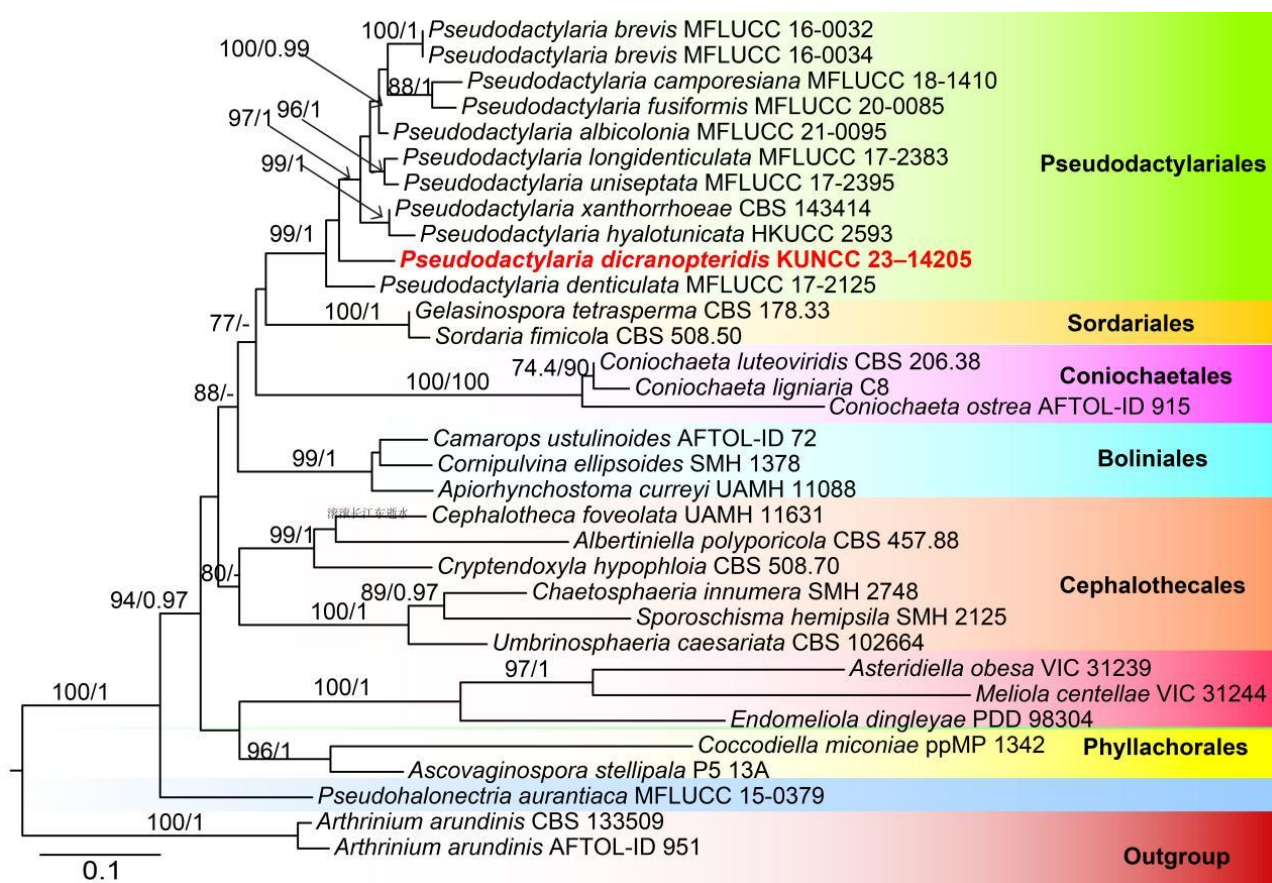


Figure 64 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. 33 taxa were included in the combined analyses, which comprised 1392 characters after alignment. The best scoring RAxML tree with a final likelihood value of -11439.250915 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Arthriniium arundinis* (CBS 133509 and AFTOL-ID 951). The new strain is in red and bold.

Sordariales Chadev. ex D. Hawksw. & O.E. Erikss.

Sordariales was introduced by Hawksworth & Eriksson (1986) and further clarified by Huhndorf et al. (2004) based on an analysis of LSU sequence data. In this study, we follow the latest treatment of *Sordariales* provided by Wijayawardene et al. (2022).

Chaetomiaceae G. Winter

Chaetomiaceae species are important human and animal pathogens, such as severe opportunistic infections in immunocompromised individuals and equine mycotic encephalitis (Ahmed et al. 2016, Plumlee et al. 2017). Species of this genus are medically and commercially important; they have proven an immense potential for use in biological control and the development of beneficial secondary metabolites (Berka et al. 2011, Yang et al. 2014, Singh 2016, Ahmed et al. 2016, Plumlee et al. 2017, Vivi et al. 2019, Wang et al. 2022). The family was described by Winter (1885) and the members of this family are globally dispersed, with the majority being saprobes, and have been found in soil, feces, air, seed, compost, decaying plant materials, and indoor habitats (Cooney & Emerson 1964, Tiscornia et al. 2009, Betancourt et al. 2013, Wang et al. 2016a, b). Many authors have studied

the taxonomy of this family; Maharachchikumbura et al. (2016) accepted 20 genera in the family, as well as a key to genera of *Chaetomiaceae* was provided and Wijayawardene et al. (2018) included 26 genera in this family. While Hyde et al. (2020a) accepted 25 genera. Recently, Wang et al. (2022) provided an up-to-date overview of the taxonomy and phylogeny of *Chaetomiaceae*, based on the phylogeny and molecular dating analyses; together with morphological characteristics and temperature-growth characteristics, 50 genera and 275 species are accepted in *Chaetomiaceae*.

***Arcopilus* X. Wei Wang, Samson & Crous**

Arcopilus was proposed by Wang et al. (2016b) to accommodate five new combinations, with *A. aureus* as the type species based on morphological characteristics and multi-locus phylogenetic analysis. Since then, several new species have been described. Index Fungorum listed 14 species of *Arcopilus*. However, based on sequence data, Wang et al. (2022) considered *A. globulus* as a synonym of *A. aureus*. Therefore, 13 species are currently accepted in the genus (Wang et al. 2016b, Sousa et al. 2020, Raza et al. 2019, Tavares et al. 2022, Wang et al. 2022, Crous et al. 2021a, Yang et al. 2023c). The typical morphological characteristics of this genus are the ascomata hairs are usually arcuate, with apices incurved and circinate to coiled and the ascospores are relatively diverse in shape, such as fusiform, navicular, reniform, lunate or limoniform, and exudate production that result in colony coloration, ranging from yellow, orange, or red to rust (Wang et al. 2016b, Tavares et al. 2022). *Arcopilus* species have been used to control phytopathogens, with potential antifungal, anticancer, antiviral, and antibacterial properties (Kanokmedhakul et al. 2006, Kabbaj et al. 2015, Vilavong & Soyong 2016, Tann & Soyong 2017, Liu & Chang 2018). We are investigating endophytic fungi in *Dicranopteris*, *A. aureus* was isolated and identified based on phylogeny and morphology. It is the first report of *Arcopilus* isolated from *Dicranopteris*.

***Arcopilus globulus* Raza & L. Cai, in Raza, Zhang, Hyde, Diao & Cai, Fungal Diversity 99: 75 (2019)** Fig. 65

Index Fungorum: IF 556674; Facesoffungi number: FoF 06163.

Endophytic in roots of *Dicranopteris pedata*. Sexual morph: *Ascomata* 130–210 × 30–70 µm ($\bar{x}$ = 170 × 50 µm, n = 10), superficial, ostiolate, with ascomatal hairs, ellipsoid. *Ascomatal wall* brown, membranaceous, comprised of dark brown. *Terminal hairs* 2–5 µm wide at the base, verrucose, brown to dark in reflected light, septate, fading and tapering towards the tips, lateral hairs apically incurved. *Asci* appeared quickly when the culture matured; they could not be seen during observation. *Ascospores* 9–12 × 5–7 µm ($\bar{x}$ = 10.5 × 6 µm, n = 30), brown when mature, limoniform or broadly fusiform, usually biapiculate at both ends, with a germ pore, guttulate, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA medium circular, growly fast, reaching 55 mm diameter after 6 d at 25 °C in natural light, cottony, velvety, dense, light to dark brown with grayish-white margins from above; dull dark in reverse. Forming a few dark-brown fruiting bodies after two months in PDA, also produced reddish brown pigments in PDA.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, isolated from healthy roots of *Dicranopteris pedata* (*Gleicheniaceae*) collected from the rock crevices, 16 March 2022, J.Y. Zhang (173–4 = KUN-HKAS 129885), living culture (KUNCC 23–14182).

GenBank numbers – ITS: PV138682, LSU: PV138581, *tub2*: PV221983, *rpb2*: PV188066

Notes – The morphology of our new isolate (KUNCC23–14182) matches with *Arcopilus globulus* based on the morphology of the holotype given by Raza et al. (2019), and the size of

ascomata and ascospores overlap with the holotype. Based on phylogenetic evidence, our new isolate clusters with *A. globulus* (CGMCC3.19359) (Fig. 66) and compares the nucleotide base pairs between *A. globulus* CGMCC3.19359 and our new isolate (KUNCC23–14182); there were essentially no significant nucleotide differences in the ITS, LSU, *tub2*, and *rpb2* gene regions. We, therefore, identified our new isolate as *A. globulus*. *Arcopilus globulus* was introduced by Raza et al. (2019) which is a pathogenic fungus isolated from *Saccharum officinarum* in China. This species is found in *Dicranopteris pedata* for the first time.

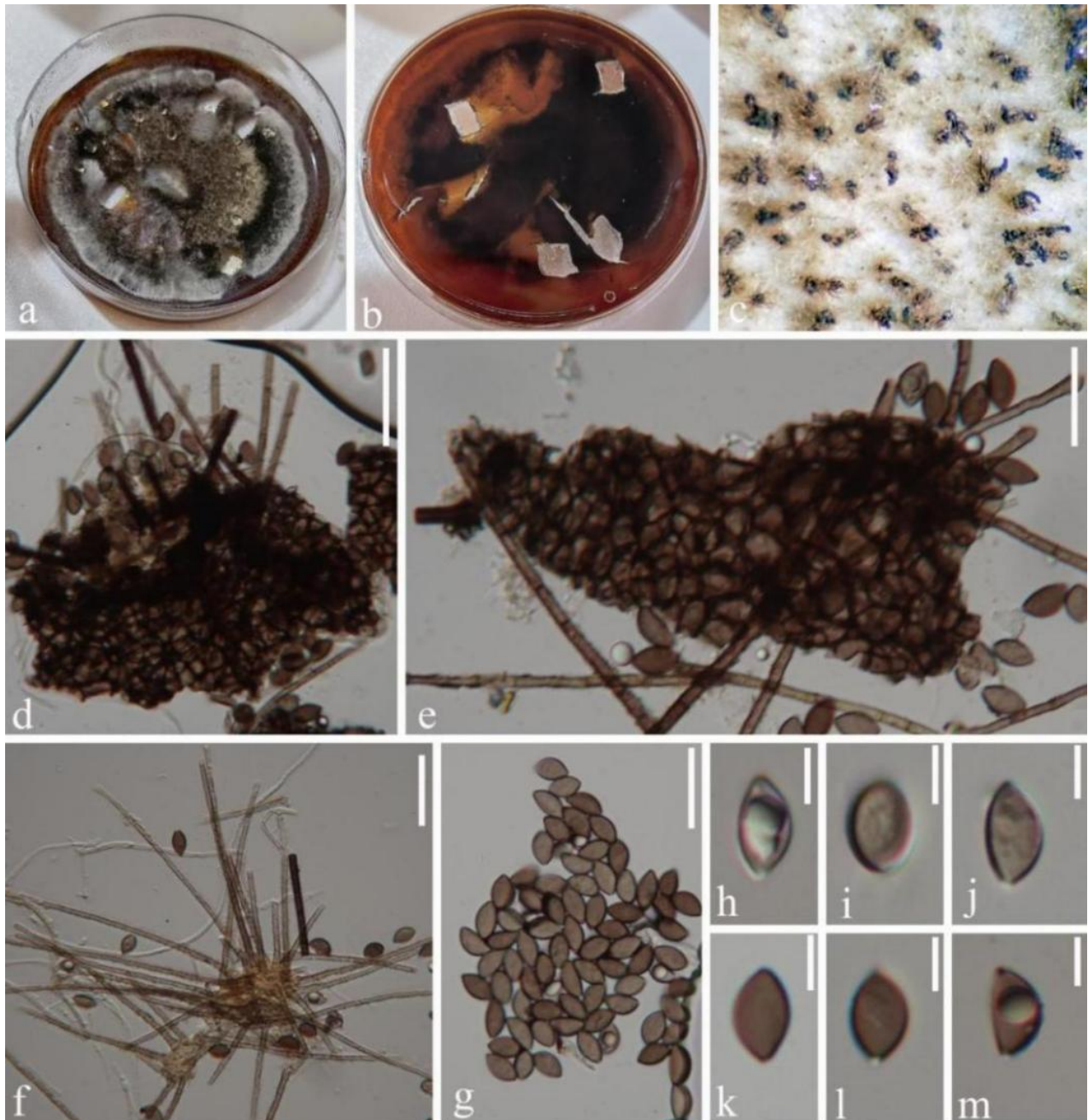


Figure 65 – *Arcopilus globulus* (KUN-HKAS 129885, new host record). **a, b** Colonies on PDA medium. **c** Ascomata on PDA. **d, e** Ascomatal wall with terminal ascomatal hairs. **f** Terminal ascomatal hairs. **g–m** Ascospores. Scale bars: **d, f** = 30 μ m, **e, g** = 20 μ m, **h–m** = 5 μ m.

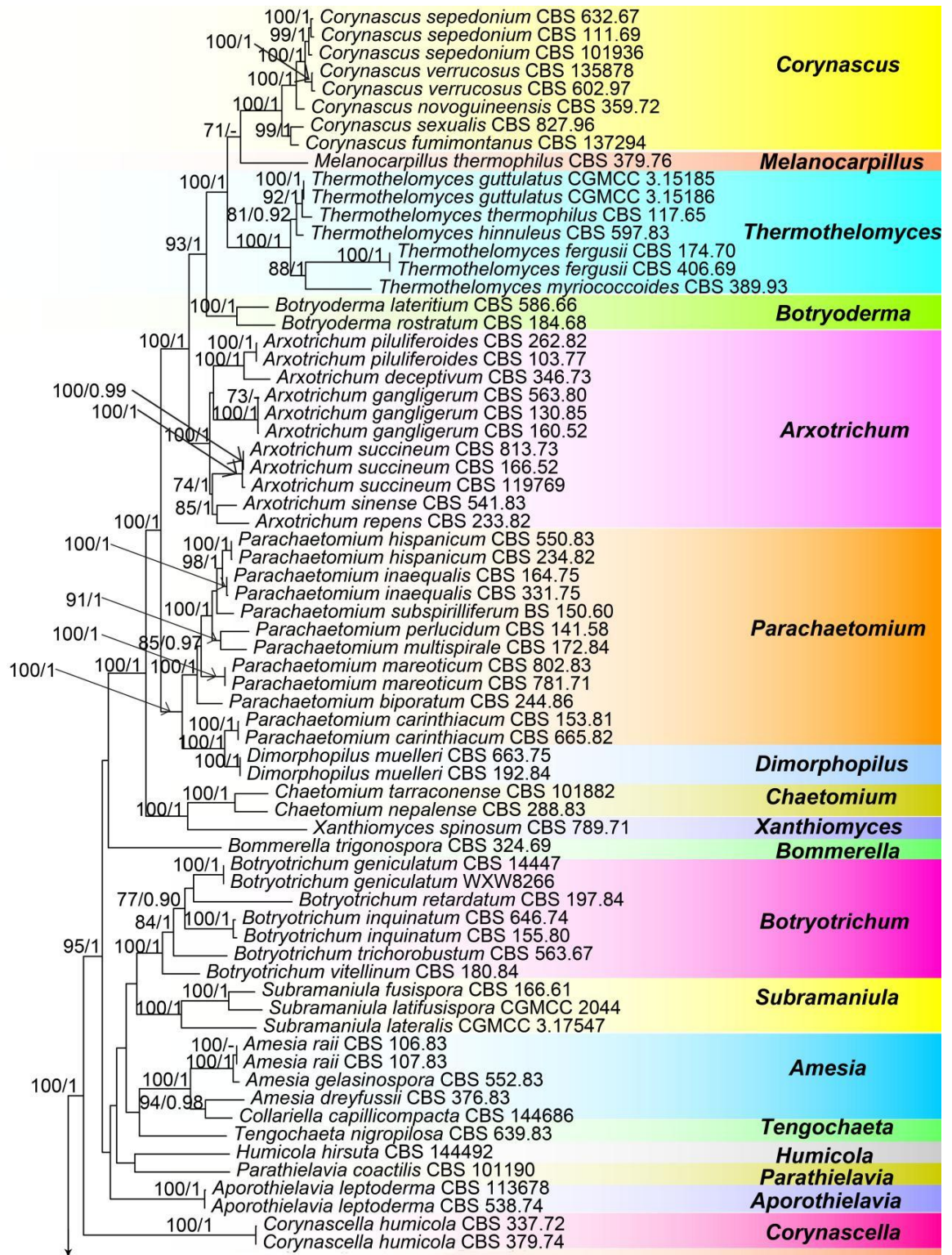


Figure 66 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, and *tub2* sequence data. 129 taxa were included in the combined analyses, which comprised 2638 characters after alignment. The best-scoring RAxML tree with a final likelihood value of -47350.996715 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Diplogelasinospora princeps* (FMR 13414) and *D. moalensis* (CBS 136018). The new strains are in red and bold.

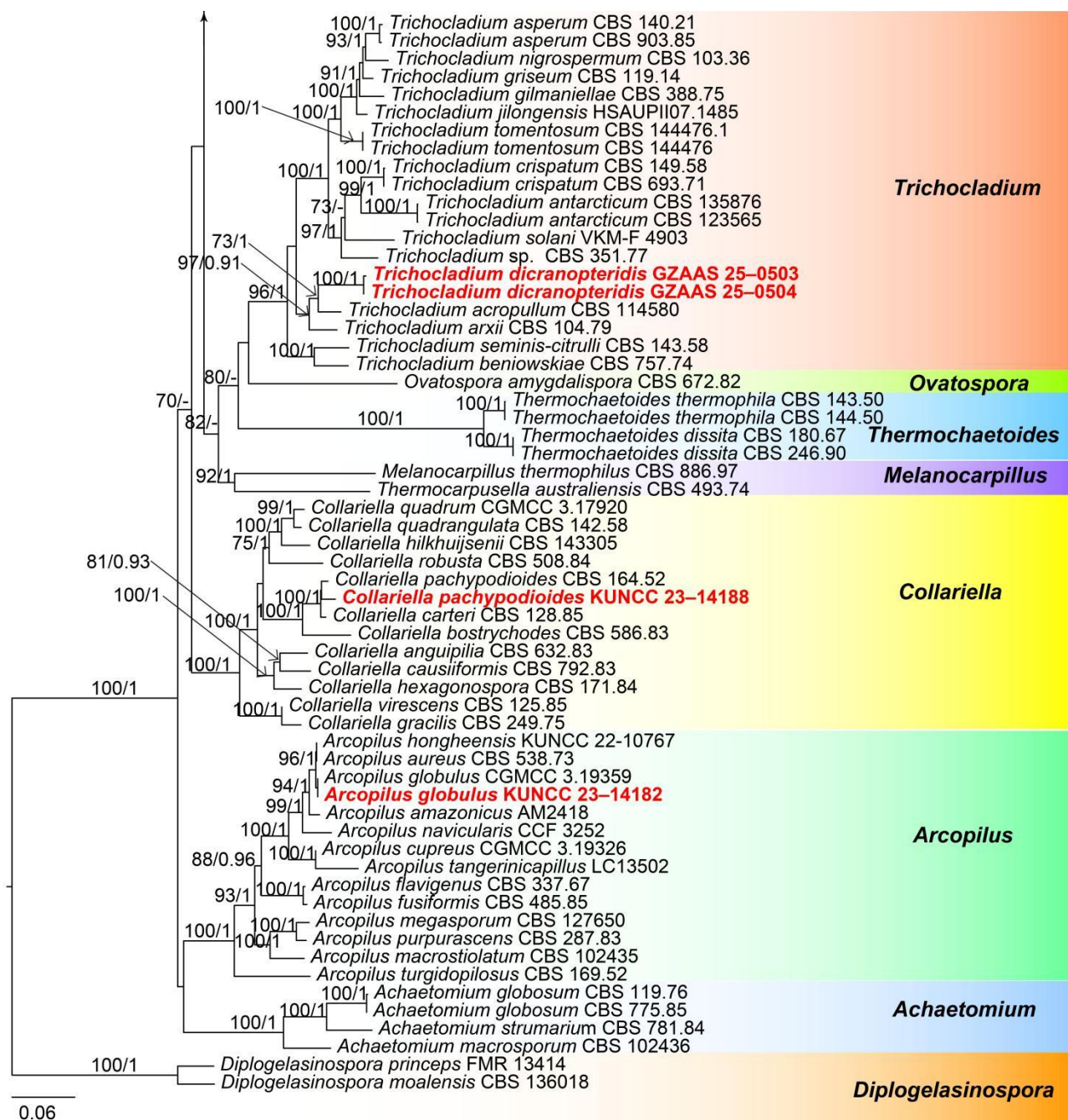


Figure 66 – Continued

Collariella X.Wei Wang, Samson & Crous

Collariella, typified by *C. bostrychodes*, was introduced by Wang et al. (2016b) to accommodate seven species previously referred to *Chaetomium*. Zhang et al. (2017) introduced two new species *C. quadrum*, which were collected from karst caves in China. Crous et al. (2017) introduced *C. hilkhuijsenii*, and Aghyl et al. (2021) described a new species *C. capillicompacta*. Wang et al. (2022) transferred two *Chaetomium* species to the genus as *C. bostrychodes* and *C. pachypodioides*. Presently, 13 species are included in the genus. *Collariella* is characterized by superficial, ampulliform or cylindrical, ovate, obovate, subglobose, ostiolate ascomata, fusiform or clavate, pedicellate, evanescent asci and broadly limoniform to quadrangular, fasciculate olivaceous brown, bilaterally flattened ascospores with one or two apical or subapical germ pores (Wang et al. 2016b). *Collariella* species are commonly reported from soil and dung; a few have been isolated from the air

(e.g., *C. carteri*) worldwide (Wang et al. 2016b, 2022, Zhang et al. 2017). We reported an endophytic species, *C. carteri* from *Dicranopteris*.

Collariella pachypodioides (L.M. Ames) X. Wei Wang & Houbraken, in Wang et al., Stud. Mycol. 101: 167 (2022) Fig. 67

Index Fungorum: IF 840147; Facesoffungi number: FoF 17883.

Endophytic in the healthy roots of *Dicranopteris ampla*. Sexual morph: *Ascomata* 220–270 × 140–200 µm ($\bar{x}$ = 245 × 170 µm, n = 10) superficial, often covered by sparse white aerial hyphae, sepia, globose or subglobose. *Ascomatal wall* brown, *textura intricata* mixed with angularis or epidermoidea in surface view. *Terminal hairs* arising from the apical collar, seta-like or flexuous, 90–200 × 3–6 µm ($\bar{x}$ = 145 × 4.5 µm, n = 30), smooth, dark brown, distinctly septate, tapering and fading towards. Lateral hairs similar but quite sparse. *Asci* appeared soon after the cultures matured; no asci were seen during the observations. *Ascospores* globose or subglobose, 5.5–7.0 × 4.0–6.0 µm ($\bar{x}$ = 6.2 × 5 µm, n = 30). Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA medium circular, entirely to slightly filamentous, growly fast, reaching 50 mm diameter after 5 days at 25 °C in natural light, cottony, velvety, loose, dull green from above; pale luteous in reverse.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Cheheng County, isolated from the healthy roots of *Dicranopteris ampla* collected from the rock crevices, 16 March 2022, J.Y. Zhang, (NS198–2 = KUN-HKAS 129892), living culture (KUNCC 23–14188).

GenBank numbers – ITS: PV138683, LSU: PV138582, *tub2*: PV221984, *rpb2*: PV188067

Notes – Phylogenetic analyses of ITS, LSU, *tef1-α* and *tub2* showed that the new isolate clustered with *Collariella pachypodioides* (CBS 164.52) (Fig. 66). *Collariella pachypodioides* was initially introduced by Greathouse and Ames (1945) as *Chaetomium pachypodioides*, von Arx et al. (1986) treated it as a synonym of *Col. bostrychodes*. However, Wang et al. (2022) showed that this species is phylogenetically distinct from *Col. bostrychodes*, they therefore identified it as a distinct species and synonymized it as *Col. pachypodioides*. Morphologically, our new isolate matches the original description of *Col. pachypodioides* as provided by Greathouse & Ames (1945). Therefore, we identified our new as *Col. pachypodioides* based on both phylogeny and morphology.

***Trichocladium* Harz**

Trichocladium was introduced by Harz (1871) with *T. asperum* as the type species. The genus is a morphologically highly diverse group; Wang et al. (2019) showed that it includes four closely related subclades; however, these subclades no distinctive phenotypic characteristics are linked to any of them, they accepted 14 species in this genus based on both phylogeny and morphology. Subsequently, four new species, viz. *T. aquaticum*, *T. microsporium*, *T. solani* and *T. tomentosum* were added to the genus. Species of this genus are commonly found in submerged decomposing wood in tropical regions, or from dead plant material and associated substrata, and a few species are thermophilic and plant pathogens (Goh et al. 1999, Wang et al. 2019, Belosokhov 2022). This study introduces a new species *T. dicranopteridis*, which is an endophytic fungus isolated from the roots of *Dicranopteris pedata*.

Trichocladium dicranopteridis J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov. Fig. 68

Index Fungorum: IF 903979; Facesoffungi number: FoF 17884.

Etymology – The specific epithet *dicranopteridis* refers to the plant genus *Dicranopteris*, from

which the type strain was isolated.

Holotype – GZAAS 25–0504

Endophytic in the healthy roots of *Dicranopteris pedata*. Sexual morph: *Ascomata* 230–290 × 204–230 μm ($\bar{x}$ = 258 × 216 μm, n = 10) superficial, often covered by sparse white aerial hyphae, sepia, globose or subglobose. *Ascomatal wall* brown, *textura intricata* mixed with *angularis* or *epidermoidea* in surface view. *Terminal hairs* 5–6 μm wide, arising from around the ostiole, flexuous and regularly spirally coiled along their entire length, not changing direction (usually a right-hand spiral), dark brown, thick-walled, unbranched, punctulate or verrucose, filament. *Asci* appeared soon after the cultures matured; asci were not observed. *Ascospores* 5–6 × 4–5 μm ($\bar{x}$ = 5.7 × 4.7 μm, n = 40), 1-celled, globose or subglobose, ovoid, brown to olivaceous-brown, smooth-walled, with an apical germ pore at the attenuated end. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA medium circular, entirely to slightly filamentous, growly fast, reaching 50 mm diameter after one week at 25 °C in natural light, cottony, velvety, loose, dull green from above; pale luteous in reverse.

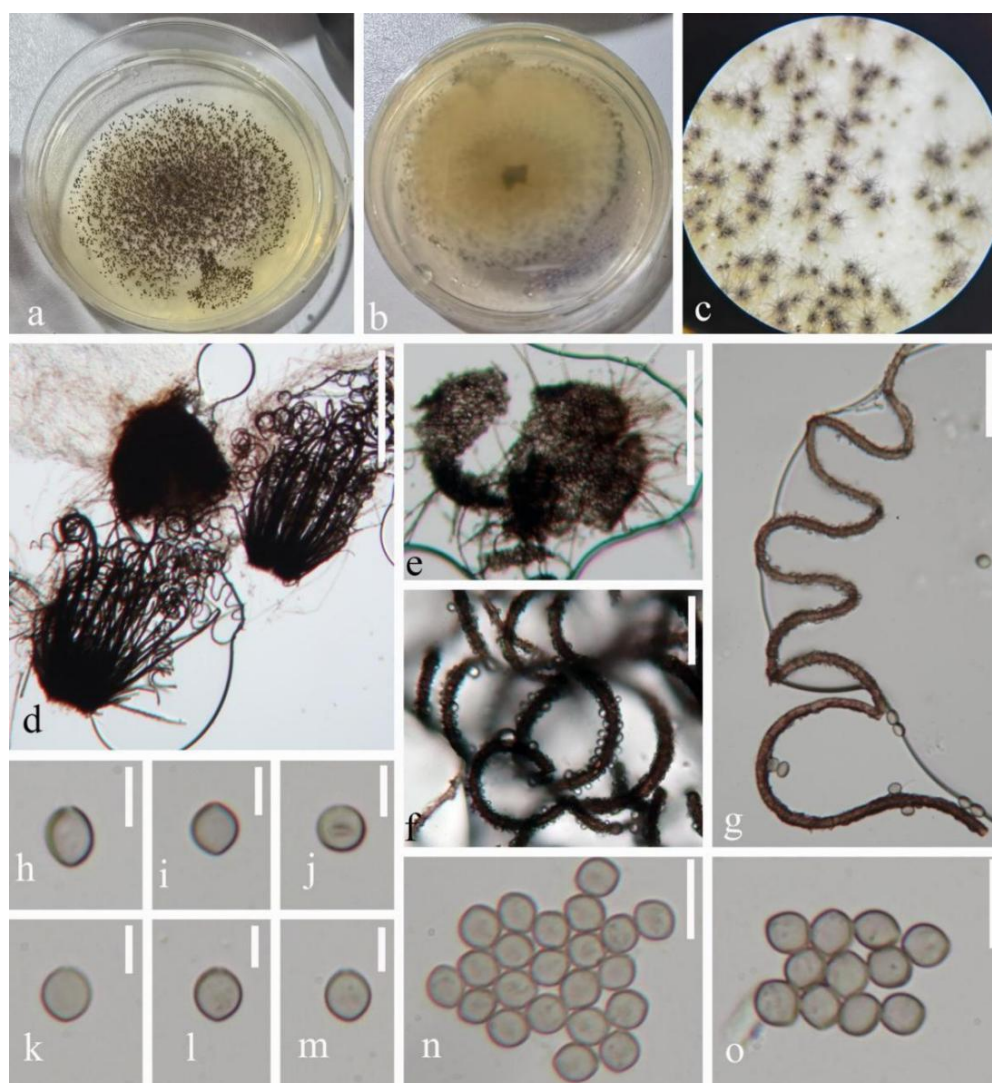


Figure 67 – *Collariella pachypodioides* (HKAS-KUNCC 129892, new host record). a, b Colonies on PDA. c Ascomata on PDA. d, e Ascomata. f–g Terminal ascomatal hairs. h–o Ascospores. Scale bars: d = 200 μm, e = 150 μm, f, g = 30 μm, h–m = 5 μm, n, o = 10 μm.

Material examined – China, Guizhou Province, Qianxinan Buyi and Miao Autonomous Prefecture, Cheheng County, isolated from the healthy roots of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS132–2 = GZAAS 25–0504, holotype). *ibid* (NS132–1 = GZAAS 25–0503).

GenBank numbers – GZAAS 25–0504: ITS: PV138684, LSU: PV138579, *rpb2*: PV188068. GZAAS 25–0503: ITS: PV138685, LSU: PV138580, *tub2*: PV221985

Notes – In our phylogenetic analysis, *Trichocladium dicranopteridis* clustered as a sister taxon to *T. acropullum*, with 73% ML and 1.00 PP statical support (Fig. 66). The ITS, *tub2*, and *rpb2* sequences of *T. dicranopteridis* (GZAAS 25–0504) revealed 14 bp (including gaps), 41 bp (without gaps), and 45 bp (without gaps) differences, respectively, when compared to the type material of *T. acropullum* (CBS 114580). These genetic differences strongly support the recognition of our isolate as a new species. Morphologically, *T. dicranopteridis* is distinguishable from *T. acropullum* by its wider terminal hairs, which are regularly spirally coiled along their entire length (5–6 μm vs. 3–4.5 μm). In contrast, the terminal hairs of *T. acropullum* are coiled only in the upper half to three-quarters of their length (Wang and Zheng 2005). Additionally, the ascospores of *T. dicranopteridis* are slightly shorter and narrower compared to those of *T. acropullum* (5–6 $\times$ 4–5 μm vs. 5.5–9(–10.5) $\times$ 5–7.5 $\times$ 4.5–5.5 μm). Therefore, *T. dicranopteridis* is introduced as a new species in this study.

Xylariomycetidae O.E. Erikss & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

The status of *Amphisphaeriales* has long been controversial, and the placement of this order has been changed and revised by different studies (Eriksson 1983, Kang et al. 1998), several studies treated it as a distinct order in *Xylariomycetidae*, while several studies placed it in *Xylariales* (Barr 1990, Kang et al. 2002). Senanayake et al. (2015) revised the subclass *Xylariomycetidae* based on the additional collections and the morpho-phylogenetic analyses, *Amphisphaeriales* with six families *Amphisphaeriaceae*, *Bartaliniaceae*, *Clypeosphaeriaceae*, *Discosiaceae*, *Pestalotiopsidaceae* and *Phlogicylindriaceae*, and *Xylariales* have been confirmed to the subclass. While Maharachchikumbura et al. (2016) treated *Amphisphaeriales* as a synonym of *Xylariales*. Samarakoon et al. (2016) and Hongsanan et al. (2017) accepted *Amphisphaeriales* as a distinct order based on phylogenetic analysis and divergence time estimates. Hyde et al. (2020a) accepted 17 families and 88 genera in this order. Recently, Samarakoon et al. (2022) revised the classification of *Xylariomycetidae* and accepted 22 families in the order based on a multi-locus phylogenetic analysis along with divergence time estimates.

Sporocadaceae Corda

Sporocadaceae was introduced by Corda (1842), and the processes appendage-bearing conidia are the typical morphological characteristics of this family. This family includes endophytes, plant pathogens, and saprobes that are associated with a variety of host plants with a global distribution (Liu et al. 2019, Hyde et al. 2020a, Samarakoon et al. 2022, Tian et al. 2024). Liu et al. (2019) provide a natural classification for the *Sporocadaceae* based on multi-locus (LSU, ITS, *tef-1 α* , *tub2*, and *rpb2*) and 30 genera were accepted in the family. Hyde et al. (2020a) accepted *Annellolacinia* and *Doliomyces* in the family, however, due to the lack of sequence data or cultures for these two genera, the placements for the two genera need to be validated in the future. Wijayawardene (2022) accepted 35 genera, including *Dilophospora*, *Millesimomyces* and *Nothoseiridium*. *Millesimomyces* and *Nothoseiridium* were newly established genera introduced by Crous et al. (2019b) and Crous et al. (2020), respectively. Recently, Razaghi et al. (2024) revisited *Sporocadaceae*, and introduced a new genus *Cavernicola*. Currently, 35 genera are accepted in this family (Hyde et al. 2024)

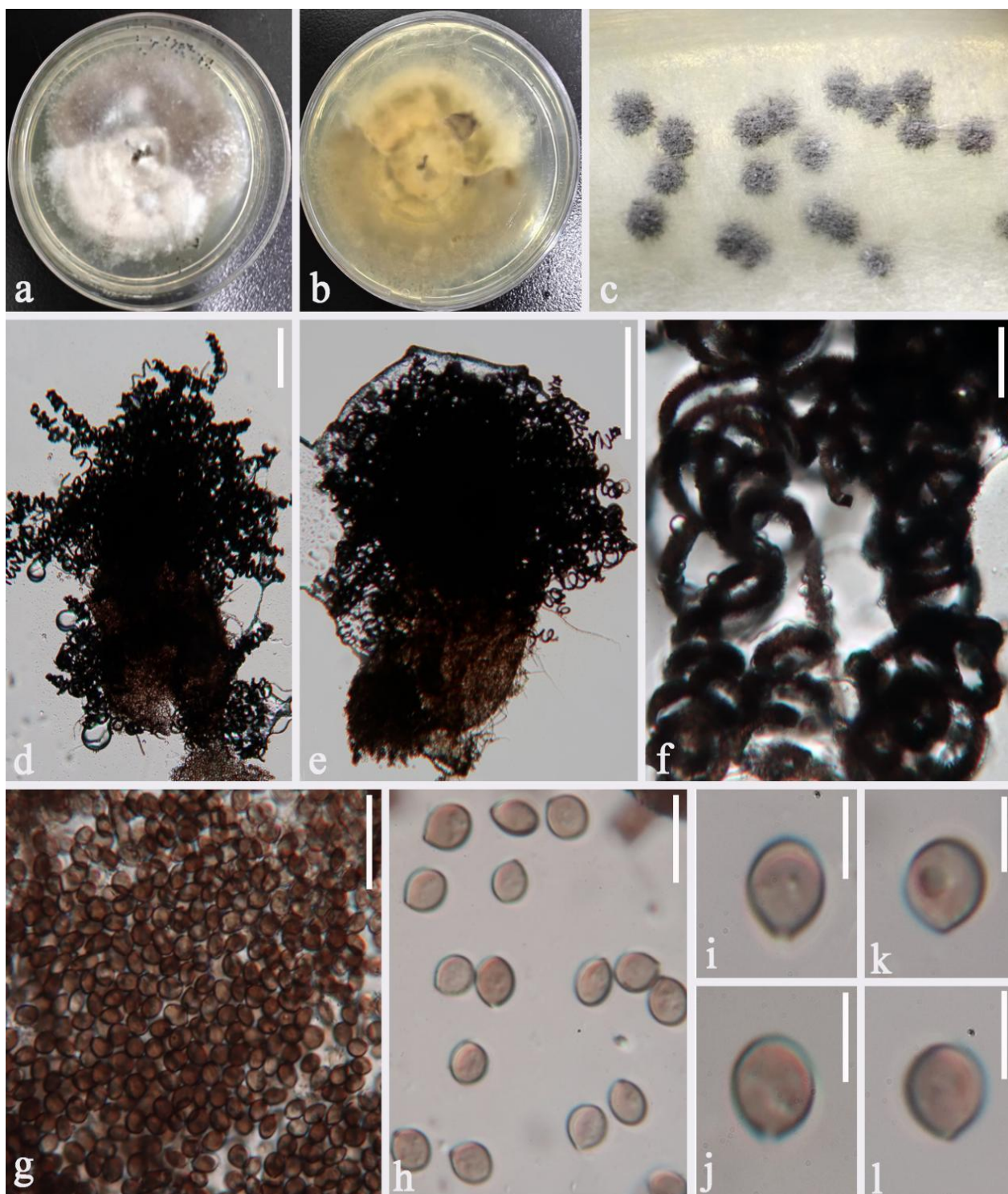


Figure 68 – *Trichocladium dicranopteridis* (GZAAS 25–0504, holotype). a, b Colonies on PDA medium. c Ascomata on PDA. d, e Ascomata. f Terminal ascomatal hairs. g–l Ascospores. Scale bars: d, e = 100 μm , f, g = 20 μm , h = 10 μm , i–l = 5 μm .

***Pestalotiopsis* Steyaert**

Pestalotiopsis is a species-rich asexual genus with appendage-bearing conidia (Barr 1975, Kang et al. 1999, Lee et al. 2006). It was introduced by Steyaert (1949) with *P. maculans* as the type, characterized by acervuli, fusiform conidia that are usually 5-celled, with 3 colored median cells and 2 colourless end cells with two or more apical appendages and annellidic conidiogenous cells (Sutton 1980). Species in this genus were mainly distinguished on the basis of conidial form, colour, and size, number and length of apical appendages, number and length of basal appendages (Jeewon et al. 2003, Liu et al. 2010, Maharachchikumbura et al. 2014). However, due to the overlapping morphological characters, thus it is insufficient to identify them. Hence, a multi-locus (ITS, *tefl-α*, and *tub2*) phylogenetic analysis was proposed to resolve and define species diversity within the genus, which has greatly promoted the development of taxonomy (Hu et al. 2007, Liu et al. 2010, Maharachchikumbura et al. 2014, 2015). *Pestalotiopsis* currently contains 414 names in the Index Fungorum (2024), however the majority of these lack sequence data and will need to be clarified in the future.

Pestalotiopsis species are widely distributed and associated with a variety of hosts as endophytes, pathogens, and saprobes. They can exist as both pathogenic and endophytic fungi due to their diverse ways of living (Ellis & Ellis 1997, Maharachchikumbura et al. 2014, Zhou et al. 2023). However, some species have also been found in non-plant substrates (Guba 1961, Strobel et al. 1996, Tejesvi et al. 2009). In this study, an endophyte, *Pestalotiopsis chamaeropsis* was isolated from *Dicranopteris pedata*; it is the first report of *Pestalotiopsis* species reported on *D. pedata*.

Pestalotiopsis chamaeropsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 158 (2014) Fig. 69

Index Fungorum: IF 809735; Facesoffungi number: FoF 11691.

Endophytic in the stem of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial in culture on PDA, globose, semi-immersed or partly erumpent, aggregated or scattered, exuding globose, dark brown to black conidial masses. *Conidiophores* 1–3-septate, branched, subcylindrical, hyaline, smooth-walled. *Conidiogenous cells* discrete, cylindrical, hyaline, smooth-walled, proliferating percurrently, 10–20 × 3–5 μm ($\bar{x}$ = 14.9 × 3.7 μm, n = 30), collarette present and not flared, with prominent periclinal thickening. *Conidia* 20–23 × 5–7 μm ($\bar{x}$ = 21.6 × 6 μm, n = 30), fusoid, ellipsoid, straight to slightly curved, 4-septate; basal cell 4–5 μm long, obconic with a truncate base, hyaline, minutely verruculose and thin-walled, 5–6.5 μm long; three median cells doliiform to subcylindrical, 13–16 μm long ($\bar{x}$ = 14.3 μm, n = 30), smooth-walled, concolourous, but occasionally the two upper median cells are slightly darker than the lower median cell, brown, septa darker than the rest of the cell (second cell from the base 4–5 μm long; third cell 4–6 μm long; fourth cell 4–5 μm long); apical cell 3–5 μm long, hyaline, subcylindrical, thin- and smooth walled; with 2–3 tubular apical appendages, arising from the apical crest, unbranched, filiform 11–20 μm long ($\bar{x}$ = 15.5 μm, n = 30); basal appendage 6–10 μm long ($\bar{x}$ = 8.2 μm, n = 30), single, tubular, unbranched, centric.

Culture characteristics – Colonies on PDA attaining 35–45 mm diameter after 7 days at 25 °C, with smooth edge, whitish, with sparse aerial mycelium on the surface with black, gregarious conidiomata; reverse similar in colour.

Material examined – China, Guizhou Province, Zhenfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stem of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (257–2 = KUN-HKAS 129901), living culture (GZCC 23–0707).

GenBank numbers – ITS: PV138732, *tefl-α*: PV177120, *tub2*: PV222017

Notes – In our phylogenetic analysis, our new isolate clustered with *Pestalotiopsis chamaeropsis* with 97% bootstrap support (Fig. 70). *Pestalotiopsis chamaeropsis* was introduced by Maharachchikumbura et al. (2014), and the morphological characteristics of *P. chamaeropsis* well-matched by our new isolate (GZCC 23–0707), including 1–3-septate, branched, subcylindrical, hyaline conidiophores, discrete, hyaline, proliferating percurrently conidiogenous cells and fusoid, ellipsoid, 4-septate conidia with 1 appendage at the base and 2–3 tubular appendages at apex. Thus, we identify it as *P. chamaeropsis* based on phylogenetic and morphological investigations and report our isolate GZCC 23–0707 as a new host record on *Dicranopteris pedata*.

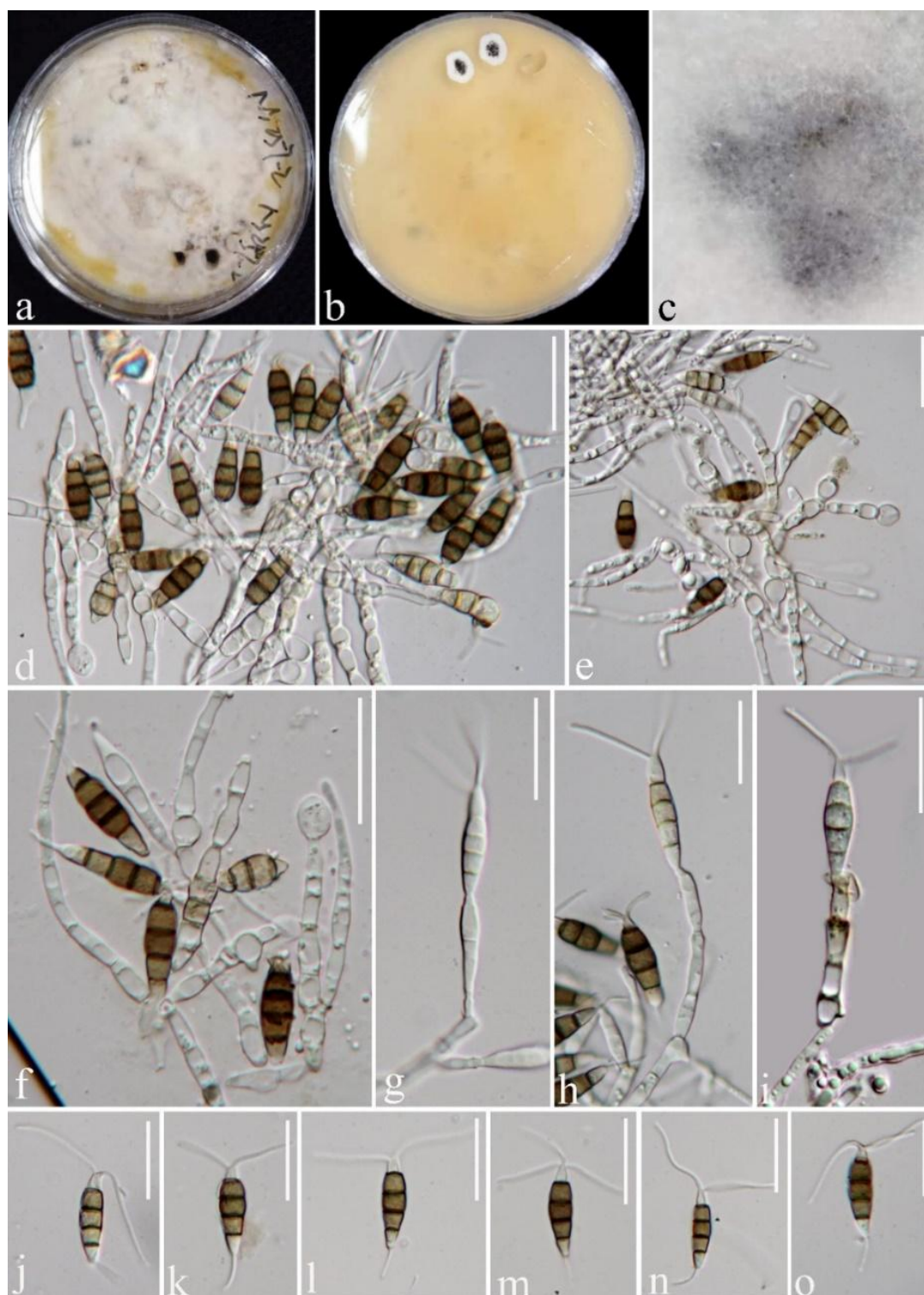


Figure 69 – *Pestalotiopsis chamaeropsis* (KUN-HKAS 129901, new host record) a, b Colonies on PDA from surface and reverse. c Conidiomata on the PDA. d–i Conidiogenous cells and conidia. j–o Conidia. Scale bars: d–f = 25 μ m, g–o = 20 μ m.

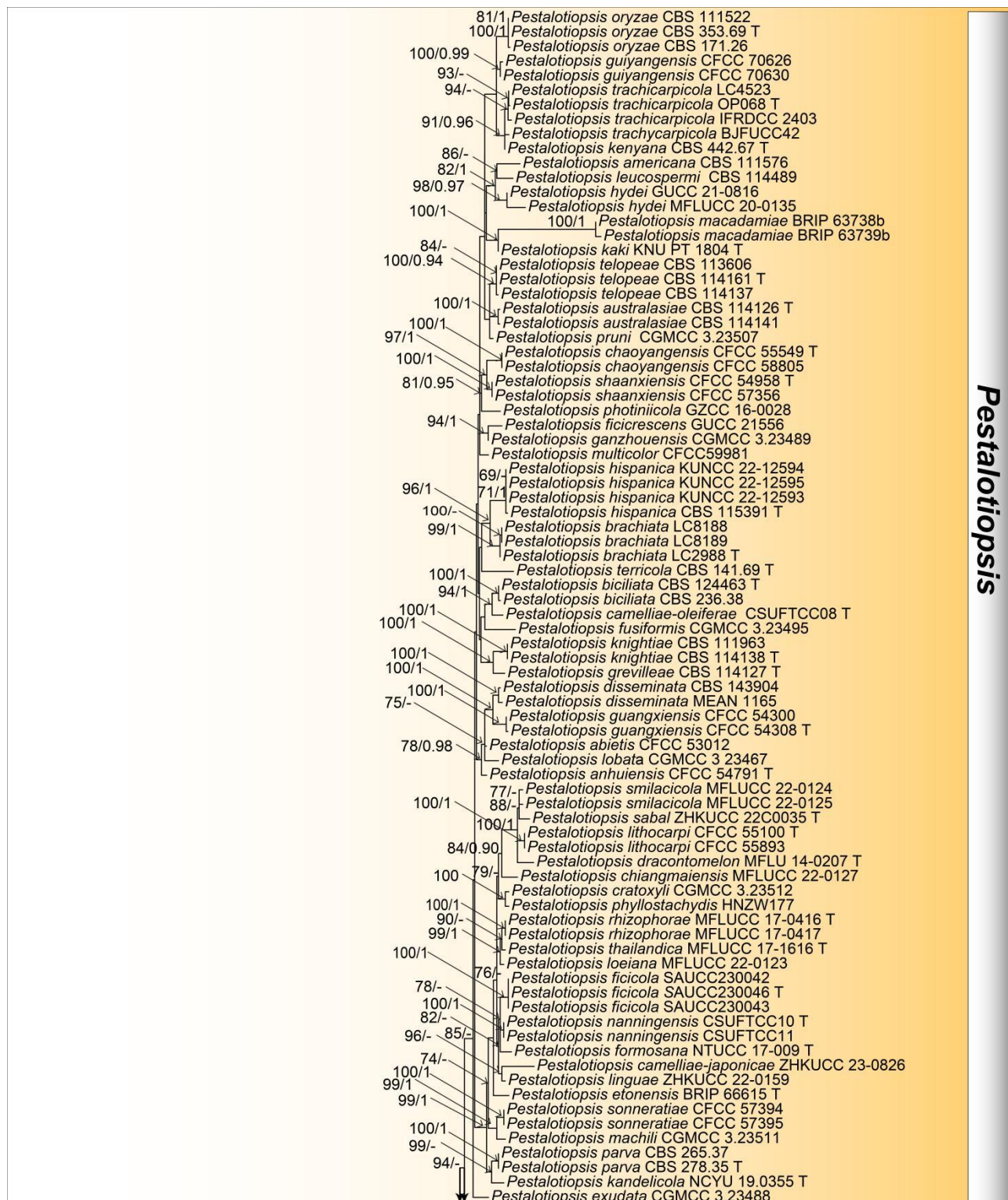


Figure 70 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1*- α , and *tub2* sequence data. A total of 111 taxa were included in the combined analyses, which comprised 1809 characters after alignment. The best scoring RAxML tree with a final likelihood

value of -14224.313761 is presented. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near branches as ML/PP. The tree is rooted to *Neopestalotiopsis cubana* (CBS 600.96). The newly generated sequences are shown in red and bold.

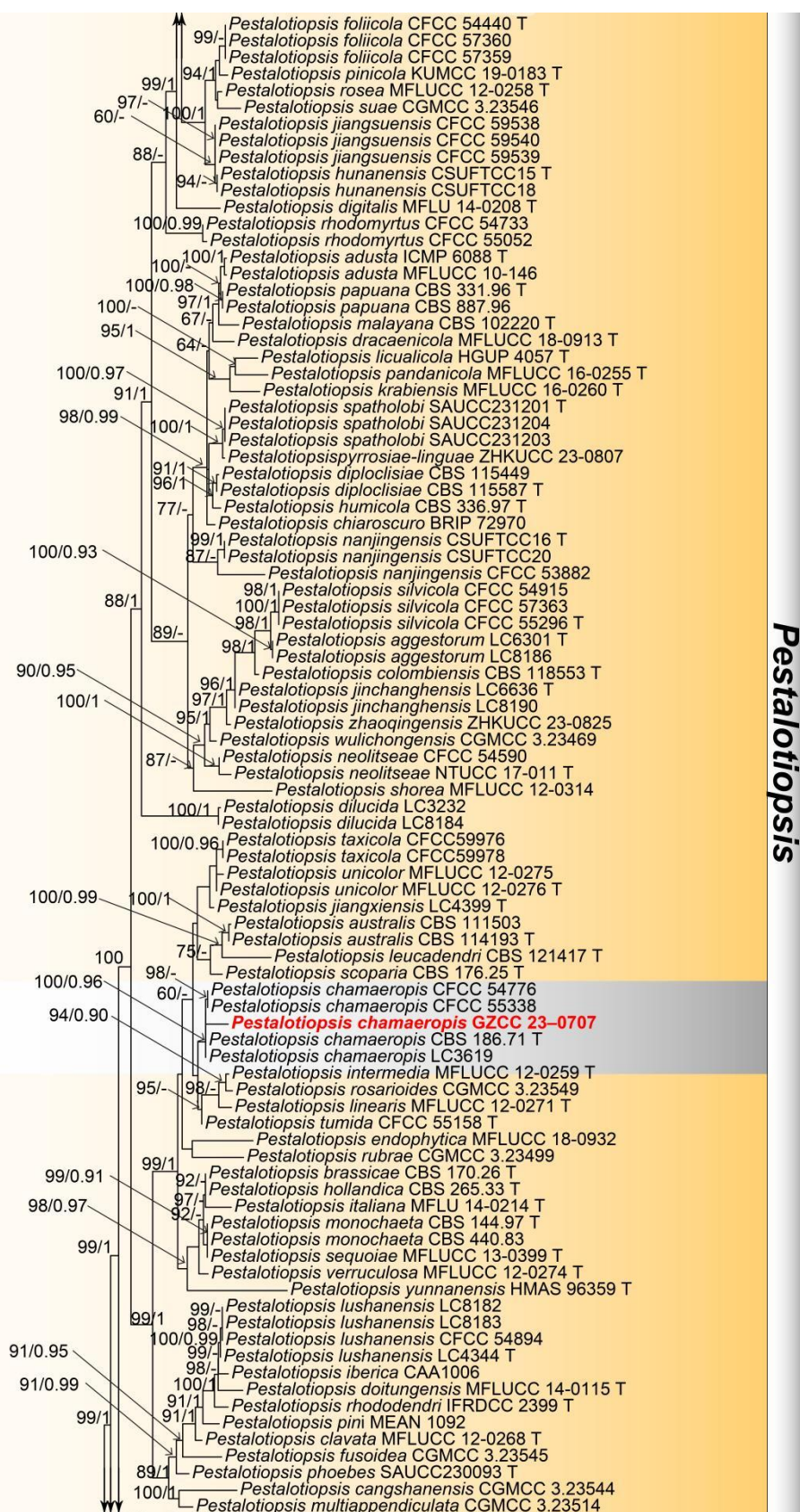


Figure 70 – Continued

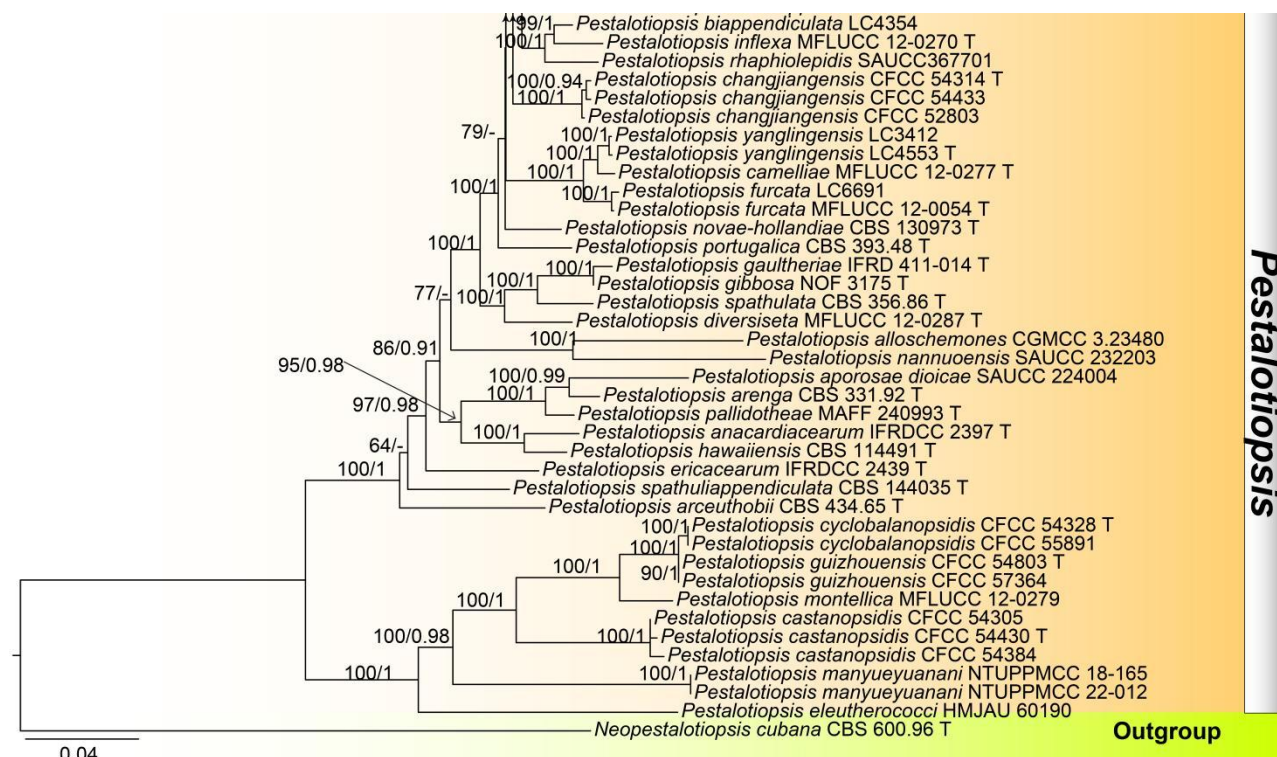


Figure 70 – Continued

Neopestalotiopsis Maharachch., K.D. Hyde & Crous

Neopestalotiopsis typified by *N. protearum* (Crous & L. Swart) Maharachch., K.D. Hyde & Crous, was introduced by Maharachchikumbura et al. (2014). The genus is distinct from other pestaloid genera (*Pestalotiopsis* and *Pseudopestalotiopsis*) in having varicolored median cells and indistinct conidiophores, which are often reduced to conidiogenous cells (Maharachchikumbura et al. 2014). *Neopestalotiopsis* species are commonly reported as endophytic and pathogenic on a wide range of plants; they can cause leaf spots, trunk diseases, post-harvest fruit rots, and root rots worldwide (Maharachchikumbura et al. 2014, Jayawardena et al. 2019). A total of 119 records of *Neopestalotiopsis* are listed in the Index Fungorum (2024), while none of them have been found from *Dicranopteris* spp. During our investigation of the diversity of endophytic fungi associated with *Dicranopteris*, five known species of *Neopestalotiopsis* viz. *N. concentrica*, *N. ellipsospora*, *N. keteleeria*, and *N. saprophytica*, with a new species, *N. dicranopteridis*, have been described, which indicates the *Neopestalotiopsis* are highly diverse in *Dicranopteris* plants.

Neopestalotiopsis dicranopteridis J.Y. Zhang, D.F. Bao & J.C. Kang, sp. nov.

Fig.71

Index Fungorum: IF 903980; Facesoffungi number: FoF 17885.

Etymology – Refers to the host plant *Dicranopteris*, on which the fungus was collected.

Holotype – KUN-HKAS 129874

Endophytic in the rhizome of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* variable in shape and size, mostly globose to subglobose, glabrous, solitary or aggregated in clusters, semi-immersed, black; exuding globose, black, glistening, conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–10 × 1–4 µm ($\bar{x}$ = 6.19 × 2.41 µm, n = 30), holoblastic, discrete or integrated, lageniform, globose to subglobose, hyaline to pale brown. *Conidia* 18–24 × 5–12 µm ($\bar{x}$ = 21.3 × 6.3 µm, n = 30), ellipsoid to fusiform, straight to

slightly curved, 4-septate, constricted at the septa, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 2–4 μm long ($\bar{x}$ = 3 μm , n = 35); three median cells dolioform, 13–17 μm long ($\bar{x}$ = 15.4 μm , n = 35), smooth-walled, yellow-brown to brown, septa darker than the rest of the cell (second cell from the base pale brown, 4–5 μm long; third cell yellow-brown, 4–6 μm long; fourth cell brown, 5–6 μm long); apical cell 2–4 μm long ($\bar{x}$ = 2.9 μm , n = 35), hyaline, cylindric to subcylindric, thin- and smooth-walled; appendages not observed.

Culture characteristics – Colonies on PDA with dense mycelium, white to pale brown with distinct black fruiting bodies on the surface, and colonies appeared yellow from the below.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the rhizome of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS133–1 = KUN-HKAS 129874, holotype), ex-type living culture (KUNCC 23–14168).

GenBank numbers – ITS: PV138712, *tef1*- α : PV177106, *tub2*: PV222001

Notes: *Neopestalotiopsis dicranopteridis* is a distinct species in terms of its morphology and DNA phylogeny. This species is characterized by its conidia lacking appendages, which is distinct in the genus. *Neopestalotiopsis dicranopteridis* and *N. steyaertii* form a sister clade. Morphologically, *N. dicranopteridis* can be differentiated from *N. steyaertii* in having pale brown to brown conidia and lacking appendages (Maharachchikumbura et al. 2014). Phylogenetically, *N. dicranopteridis* is sister to *N. steyaerti* (Fig. 72), but *N. dicranopteridis* differs from *N. steyaerti* in 9/481 bp (1.87%), 7/450 bp (1.56%), 7/481 bp (1.45%) of the ITS, *tub2*, and *tef1*- α sequences respectively. Thus, we treated *N. dicranopteridis* as a new species.

Neopestalotiopsis piceana Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 146 (2014) Fig. 73

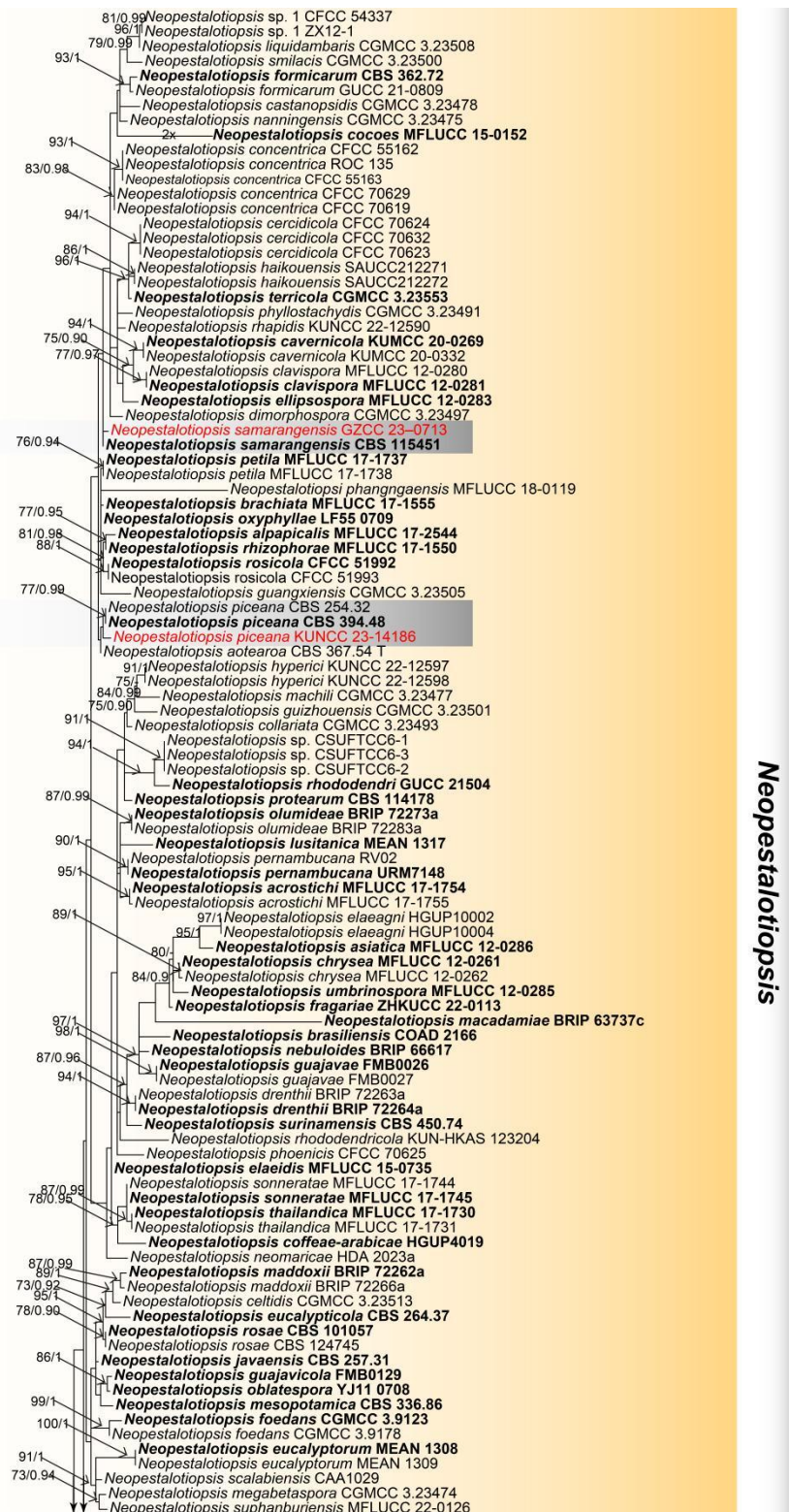
Index Fungorum: IF 809775; Facesoffungi number: FoF 17886.

Endophytic in the fresh leaves of *Dicranopteris pedata*. Colonies on PDA, fluffy appearance, white aerial mycelia. *Mycelia* superficial and immersed composed of septate, branched, 2–3 μm wide, hyaline and brown with smooth and thick-walled hyphae. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial on pine needles, globose, solitary or aggregated, embedded or semi-immersed, exuding black conidial masses. *Conidiomatal wall* brown to dark brown, composed several layers of brown to dark brown cells of *textura angularis*. *Conidiophores* cylindrical, branched, septate, hyaline, smooth-walled. *Conidiogenous cells* 6.5–14 $\times$ 2–3 μm ($\bar{x}$ = 10.3 $\times$ 2.5 μm , n = 30), holoblastic, polyblastic, discrete or integrated, lageniform, globose to subglobose, hyaline to pale brown. *Conidia* 16–20 $\times$ 5–7 μm ($\bar{x}$ = 18.1 $\times$ 6.1 μm , n = 45), ellipsoid, fusoid, straight to slightly curved, 4-septate; basal cell 2.5–4 μm long ($\bar{x}$ = 12.4 μm , n = 45), hyaline to pale brown, obconic, smooth- and thin-walled; three median cells 11–14 μm ($\bar{x}$ = 12.4 μm , n = 45), brown, doliiform, (the second cell from base 4–5.5 μm long, third cell 4–5 μm long, fourth cell 4–5 μm long); apical cell 3–4 μm long, cylindrical to subcylindrical, conic to bell-shaped, hyaline, smooth- and thin-walled, with 3 tubular apical appendages, 9–14 μm long ($\bar{x}$ = 9.3 μm , n = 45), arising from the apical crest, filiform, basal appendage 3–4.5 μm long ($\bar{x}$ = 3 μm , n = 45), single, tubular, unbranched, straight and centric.

Culture characteristics: Colonies on PDA reaching 40mm diameter after 7 days at 25°C, colonies margin entire, circular, fluffy appearance, white at above with black, gregarious fruiting bodies, reverse white to cream.



Figure 71 – *Neopestalotiopsis dicranopteridis* (KUN-HKAS 129874, holotype) a, b Colonies on PDA from surface and reverse. c Conidiomata on the PDA. d–h Conidiogenous cells and conidia. j–n Conidia. Scale bars: d–g, j–n = 10 µm, h = 5 µm, i = 20 µm.



Neopestalotiopsis

Figure 72 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1*- α , and *tub2* sequence data. A total of 177 taxa were included in the combined analyses, which comprised 1806 characters after alignment. The best scoring RAXML tree with a final likelihood value of -11455.7127 is presented. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree is rooted to *Pestalotiopsis colombiensis* (CBS 118553) and *P. diversiseta* (MFLUCC 12-0287). The newly generated sequences are shown in red and the type strains are in bold.

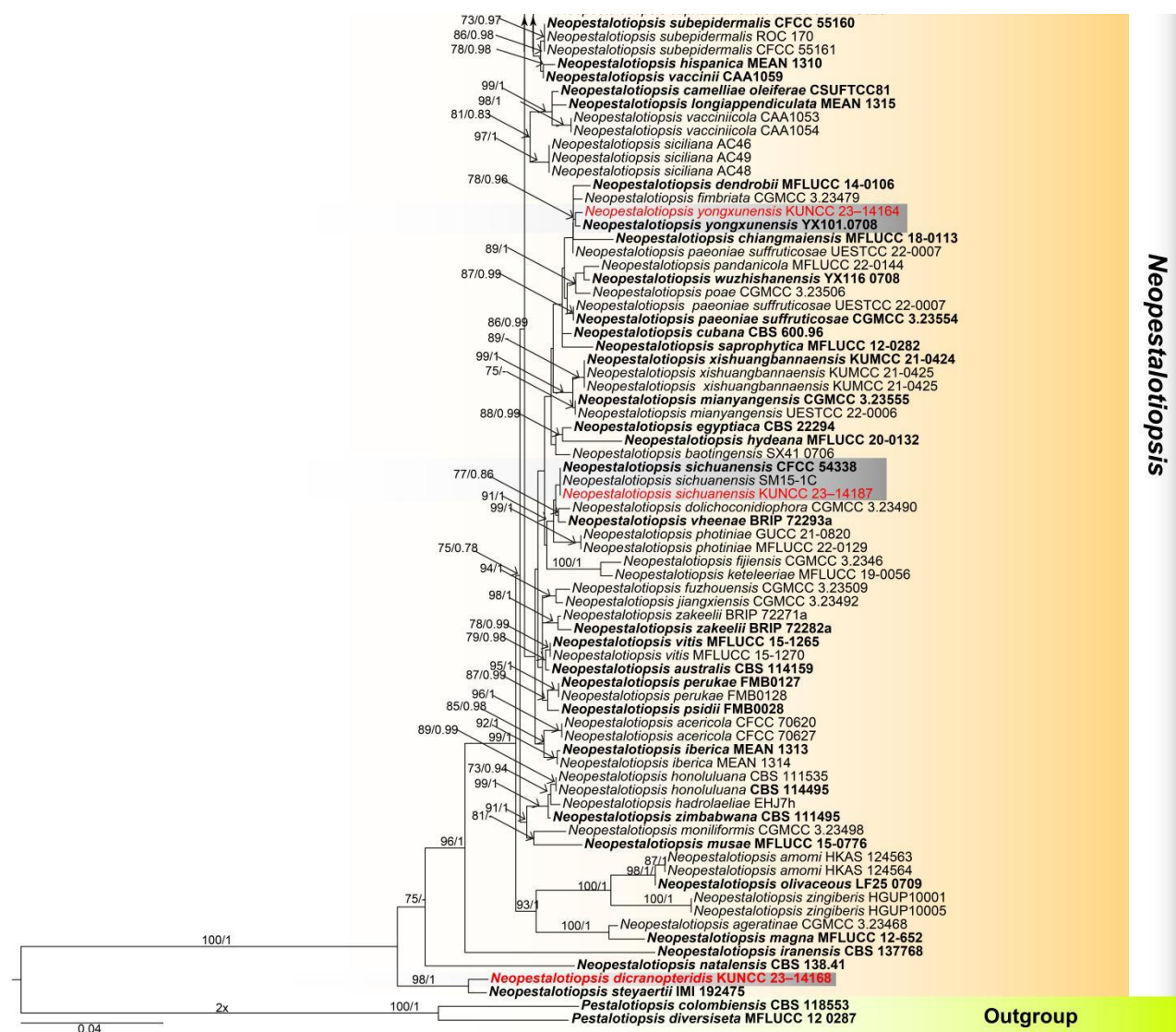


Figure 72 – Continued

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (195–1 = KUN-HKAS 129890), living culture (KUNCC 23–14186).

GenBank numbers – ITS: PV138711, *tef1-α*: PV177107, *tub2*: PV222000

Notes – The new isolate (KUNCC 23–14186) clustered with *Neopestalotiopsis piceana* (CBS 394.48 and CBS 254.32) in the combined ITS, *tub2*, and *tef1-α* phylogenetic analysis (Fig. 72). The *tub2* and *tef1-α* gene regions of the new isolate (KUNCC23–14186) are similar to those of the ex-type strain of *N. piceana* (CBS 394.48). Morphologically, the new isolate is nearly identical to the holotype of *N. piceana*, first described by Maharachchikumbura et al. (2014). Based on these findings, we identify the new isolate as *N. piceana*. This species was originally isolated from *Picea* wood by Maharachchikumbura et al. (2014) and was later reported as an endophyte in *Ananas comosus* (Bhattacharya et al. 2019) and as a pathogen that causes gray blight in *Camellia sinensis* in China (Wang et al. 2023b). Our new isolate, however, was obtained from the rhizome of *Dicranopteris pedata*, and we report it as a new host record for *D. dichotoma*.

Neopestalotiopsis samarangensis (Maharachch. & K.D. Hyde) Maharachch., K.D. Hyde & Crous,

in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 147 (2014) Fig. 74
Index Fungorum: IF 809778; Facesoffungi number: FoF 17887.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Acervular conidiomata* globose or irregular, superficial to semi-immersed, scattered or aggregated. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–8.5 × 4.5–7 µm ($\bar{x}$ = 7.3 ± 1.1 × 5.8 ± 1.2 µm), discrete, ampulliform or irregular, lageniform, globose to subglobose, hyaline to pale brown. *Conidia* 17–21(–14) × (3–) 5–6 µm ($\bar{x}$ = 19.1 ± 2.2 × 5.5 ± 0.6 µm) fusoid, ellipsoid, straight or slightly curved, 4-septate; basal cell conic to obconic with a truncate base, hyaline to subhyaline, thin-walled, 2.5–4.0 µm ($\bar{x}$ = 3.5 ± 0.7 µm) long; three median cells doliform, 10.5–14(–11) µm ($\bar{x}$ = 12.2 ± 1.6 µm) long, versicoloured, septa darker than the rest of the cell, second cell from the base pale brown, 3.5–5 µm ($\bar{x}$ = 4.3 ± 0.7 µm) long; third cell honey brown, 3–5 µm ($\bar{x}$ = 4.1 ± 1.1 µm) long; fourth cell brown, 3–5 µm ($\bar{x}$ = 4.0 ± 0.7 µm) long; apical cell 2.5–5 µm ($\bar{x}$ = 3.8 ± 1.1 µm) long, hyaline to subhyaline, cylindrical, smooth-walled; with 2–3 tubular apical appendages (mostly three), branched or unbranched, filiform, 6.5–14(–18) µm ($\bar{x}$ = 10.3 ± 3.8 µm) long; basal appendage single, tubular, unbranched, centric, (3–)2.5–6 µm ($\bar{x}$ = 4.3 ± 1.7 µm) long.

Culture characteristics – Colony on PDA with flattened mycelium, white, smoke grey in the center, reverse with smoke grey pigments formed a concentric ring pattern, reaching at 58–62 mm diameter in 15 days at 28 °C. Conidiomata globose, irregularly distributed on the medium surface, exuding globose, dark brown to black conidial masses.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi and Miao Autonomous County, from the leave of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (201–1 = KUN-HKAS 129893), living culture (GZCC 23–0713)

GenBank numbers – ITS: PV138714, *tef1-α*: PV177108, *tub2*: PV222003

Notes – During our investigation of endophytic fungi associated with *Dicranopteris*, a pestalotiopsis-like taxon was collected and identified as *Neopestalotiopsis samarangensis* based on phylogenetic analysis and morphological characters. Although Maharachchikumbura et al. (2014) initially introduced it as *P. samarangensis*, it was later synonymized as *N. samarangensis* based on phylogenetic analysis and morphological characteristics.

Morphologically, our new isolate (GZCC 23–0713) matches with *N. samarangensis* in having discrete, ampulliform, or irregular conidiogenous cells and fusoid, ellipsoid, 4-septate conidia with 2–3 tubular apical appendages and a single basal appendage. Phylogenetically, our new isolate (GZCC 23–0713) clustered with the ex-type of *N. samarangensis* (CBS 115451) as the same species (Fig. 72). Thus, we identified our new isolate *N. samarangensis* and reported it as a new host record from *Dicranopteris pedata*.

Neopestalotiopsis sichuanensis C.M. Tian & N. Jiang, in Jiang, Fan & Tian, Journal of Fungi 7(1, no. 64): 22 (2021) Fig. 75

Index Fungorum: IF 837792; Facesoffungi number: FoF 15550.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: Not observed. Asexual morph: *Conidiomata* variable in shape and size, mostly globose to subglobose, glabrous, solitary or aggregated in clusters, semi-immersed, black; exuding globose, black, glistening, conidial masses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–16.5 × 2.5–4 µm ($\bar{x}$ = 10.8 × 3.41 µm, *n* = 20), holoblastic, discrete or integrated, lageniform, globose to subglobose, hyaline to pale brown. *Conidia* 18–23 × 5–7 µm ($\bar{x}$ = 20.2 × 5.9 µm, *n* = 30), fusiform, straight to slightly curved, 4-septate; with basal cell conical with obtuse end, hyaline, thin and smooth-walled, 3.5–6 µm long ($\bar{x}$ = 4.7 µm, *n* = 30); with three median cells 11–15 µm long ($\bar{x}$ = 13.5 µm, *n* = 30), dark brown,

septa and periclinal walls darker than the rest of the cell, versicoloured, second cell from base pale brown, 4–6 μm ($\bar{x}$ = 5.0 μm , n = 30); third cell darker brown, 4–5 μm ($\bar{x}$ = 4.6 μm , n = 30); fourth cell darker, 4–6 μm ($\bar{x}$ = 4.9 μm , n = 30); apical cell 3–4.5 μm long ($\bar{x}$ = 3.9 μm , n = 30), hyaline, conical; with apical appendages 10–20 μm long ($\bar{x}$ = 15.4 μm , n = 30), tubular, 1–3, arising from the apex of the apical cell; basal appendage small or absent, 2.5–4 μm long ($\bar{x}$ = 3.3 μm , n = 30), filiform.

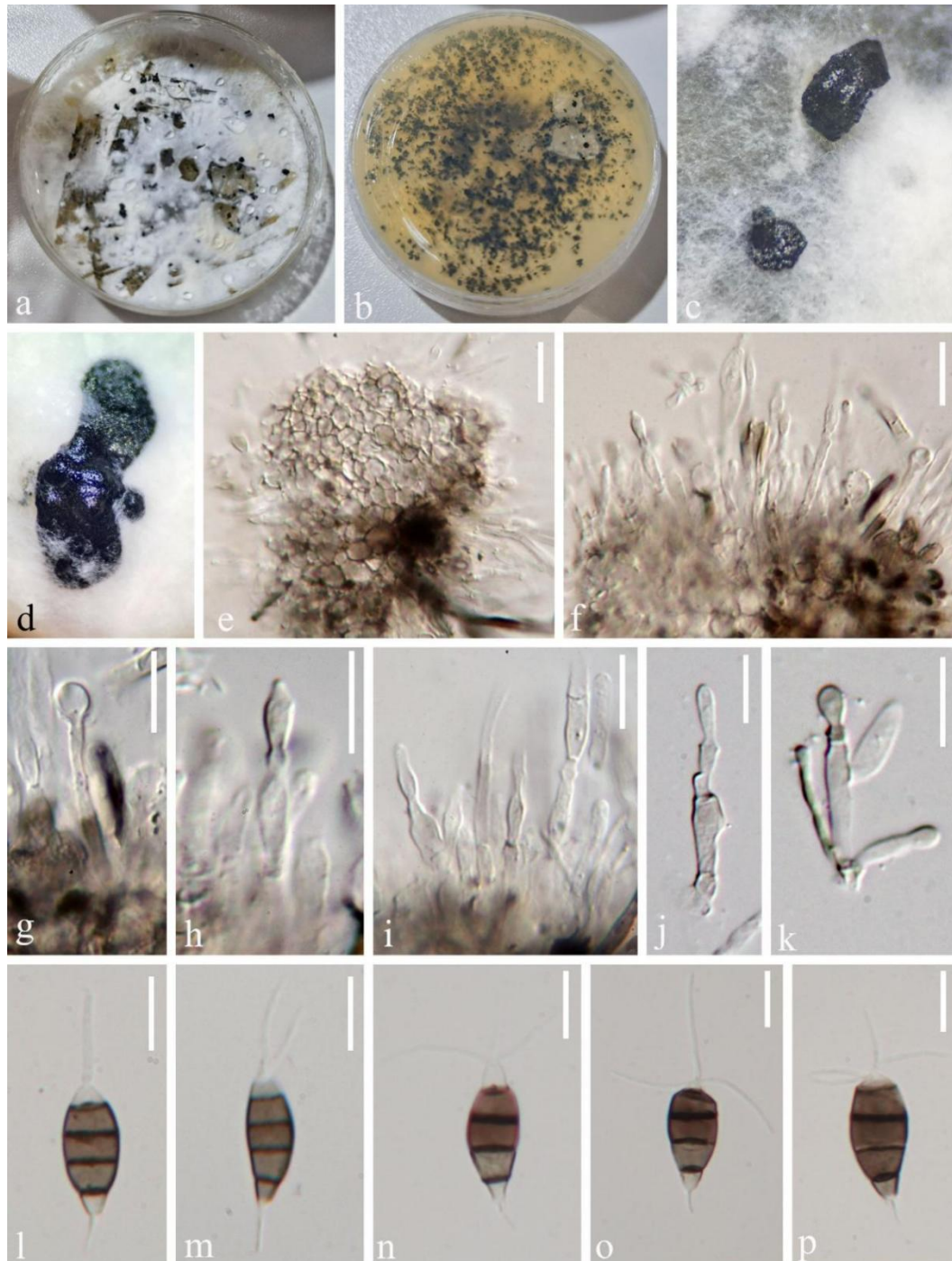


Figure 73 – *Neopestalotiopsis piceana* (KUN-HKAS 129890, new host record). a, b Colonies on PDA from surface and reverse. c, d Conidiomata on the PDA. e Conidiomatal wall. f–k Conidiophores, conidiogenous cells, and immature conidia. l–p Conidia. Scale bars: e, f = 15 μm , g–p = 10 μm .

Culture characteristics – Colonies on PDA reaching 6 cm diameter after 7 days at 25 °C, edge crenate, whitish, with aerial mycelium on the surface, with black, gregarious fruiting bodies; reverse of the culture white.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leave of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (195–2 = KUN-HKAS 129891), living culture (KUNCC 23–14187).

GenBank numbers – ITS: PV138710, *tub2*: PV221999

Notes – *Neopestalotiopsis sichuanensis* was introduced by Jiang et al. (2021), isolated from leaf spots of *Castanea mollissima*. *Neopestalotiopsis sichuanensis* is characterized by fusiform, 4-septate, conidia with hyaline, conical basal cell, dark brown, septate three median cells, which are darker than the apical and basal cells, and hyaline, a conical apical cell with 1–3 apical appendages and a small or absent basal appendage. Our new isolate (KUNCC 23–14187) fits well with the description of *N. sichuanensis* except the size of conidia ($18\text{--}23 \times 5\text{--}7$ vs. $(23.2\text{--})24.3\text{--}30.4\text{--}(32.8) \times (5.7\text{--})6.3\text{--}7.1\text{--}(7.5)$). Phylogenetically, our new isolate clustered with two strains of *N. sichuanensis*, which were not significantly different from our new isolate (Fig. 72). Thus, based on both phylogeny and morphology, we identified our new isolate as *N. sichuanensis*. Our strain *N. sichuanensis* (KUNCC 23–14187) is reported as a new host record on *Dicranopteris pedata*.

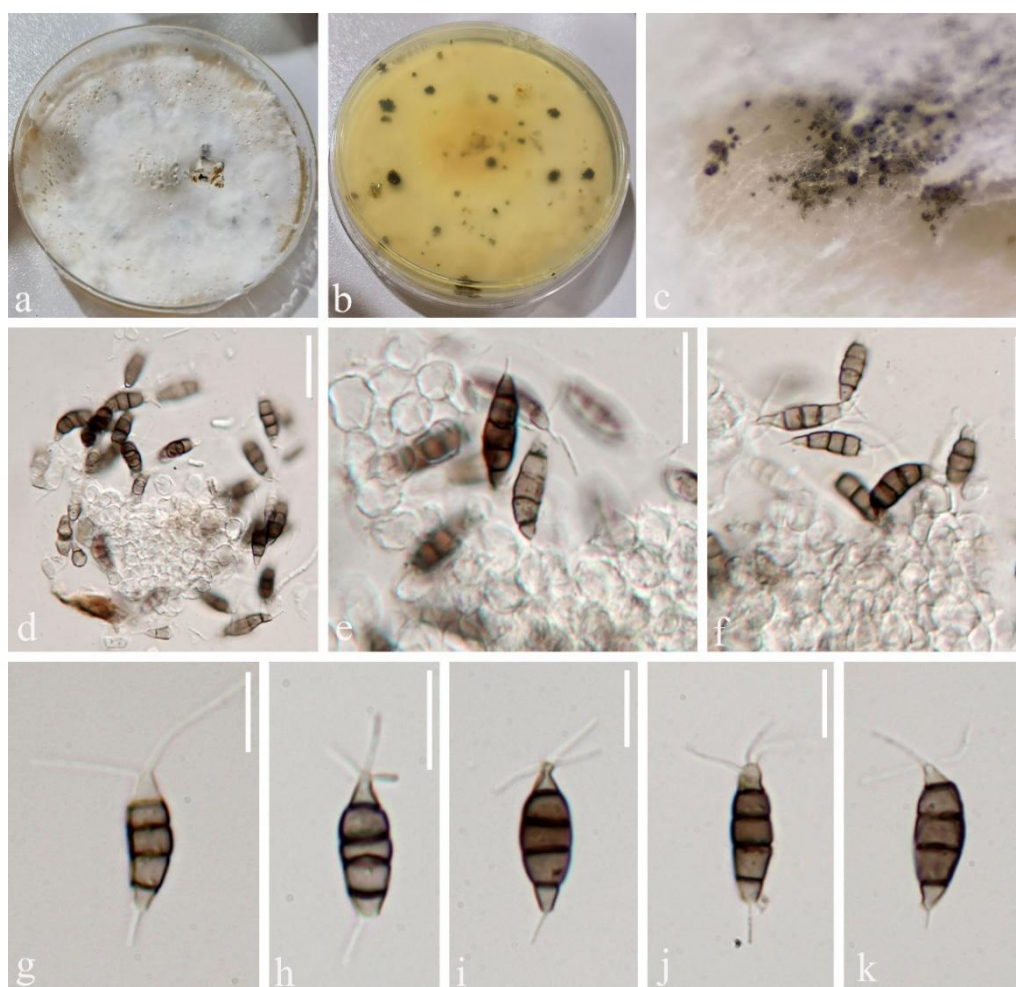


Figure 74 – *Neopestalotiopsis samarangensis* (KUN-HKAS 129893, new host record) a, b Colonies on PDA from surface and reverse. c Conidiomata on the PDA. d–f Conidiogenous cells and conidia. g–k Conidia. Scale bars: d–f = 20 µm, g–k = 10 µm.

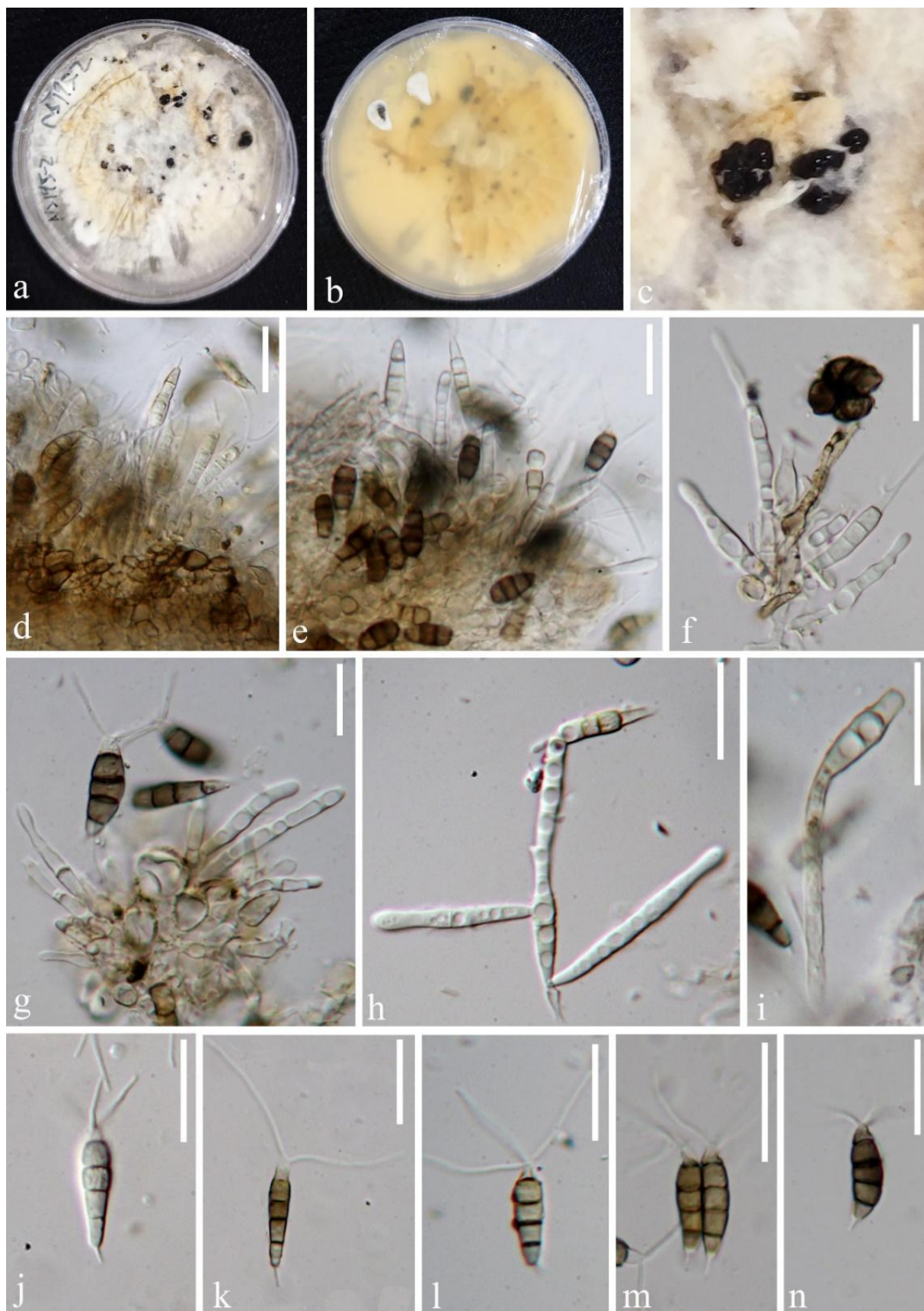


Figure 75 – *Neopestalotiopsis sichuanensis* (KUN-HKAS 129891, new host record). a, b Colonies on PDA from surface and reverse. c Conidiomata on the PDA. d, e Conidia mass with conidiophores. f–i Conidiophores, conidiogenous cells, and immature conidia. j–n Conidia. Scale bars: d–n = 20 μm.

Neopestalotiopsis yongxunensis X.F. Cui & Z.G. Hao, in Cui, Hao, Chen, Song, Zhang, Li, Li, Liu & Luo, Journal of Fungi 10(6, no. 371): 22 (2024) Fig. 76

Index Fungorum: IF 854055; Facesoffungi number: FoF 17888.

Endophytic in the stem of *Dicranopteris pedata*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, solitary, black, semi-immersed on PDA, exuding dark brown mass of conidia. *Conidiophores* often reduced to conidiogenous cells, branched or unbranched, hyaline to brown, thin-walled. *Conidiogenous cells* discrete, ampulliform to lageniform, hyaline, thin-walled, smooth. *Conidia* $15.0\text{--}20.9 \times 2.1\text{--}10.8\mu\text{m}$ ($\bar{x} = 17.7 \times 7.8\mu\text{m}$, $n = 32$), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic, hyaline or brown, thin-walled, smooth. *Apical cell* triangular, hyaline; 1–3 tubular apical appendages, arising from the apex of the apical cell each at different point, flexuous; basal appendage presents most of the time, single, tubular, unbranched.

Culture characteristics – colonies on PDA were circular with a rough, black fruiting bodies on the surface and appeared white from above and pale yellow from below with black spots.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stem of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS112–1 = KUN-HKAS 129871), living culture (KUNCC 23–14164).

GenBank numbers – ITS: PV138713, *tef1- α* : PV177105, *tub2*: PV222002

Notes – *Neopestalotiopsis yongxunensis*, was recently described by Cui et al. (2024), isolated from leaves of *Alpinia oxyphylla* in Hainan Province, China. In our phylogenetic analysis, our new isolate clustered with *N. yongxunensis* with strong statistical support (Fig. 72). Morphology of our new isolate fits well with the holotype of *N. yongxunensis* (Cui et al. 2024). We therefore reported this new isolate as a new host record of *N. yongxunensis* isolated from *Dicranopteris pedata*.

***Xylariales* Nannf.**

Xylariales is an order of fungi within the class *Sordariomycetes*, known for its ecological diversity and importance. Members of *Xylariales* are typically saprobic, breaking down organic matter such as wood, but many are also plant endophytes or pathogens (Zhang et al. 2006; U'Ren et al. 2016, Rashmi et al. 2019, Daranagama et al. 2018). The taxonomy of *Xylariales* has been continuously refined with advancements in molecular phylogenetic techniques, leading to the discovery of new species and reclassification of known ones (Maharachchikumbura et al. 2016, Wendt et al. 2018, Konta et al. 2020, Hyde et al. 2020a, Samarakoon et al. 2022). The order is large and diverse, with many genera still requiring detailed study for proper classification (Samarakoon et al. 2022). Currently, the order comprises 20 families (Wijayawardene et al. 2022).

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

Apiosporaceae was introduced by Hyde et al. (1998) to accommodate taxa that produce apiospores and a basauxic, arthrinium-like conidiogenesis (Hyde et al. 2020a). Hyde et al. (2020a) accepted five genera *Appendicospora*, *Arthrinium*, *Dictyoarthrinium*, *Endocalyx*, and *Nigrospora* in the family. However, *Dictyoarthrinium*, *Endocalyx*, and *Appendicospora* have been transferred to *Didymosphaeriaceae*, *Cainiaceae* and *Appendicosporaceae*, respectively (Konta et al. 2020, Samarakoon et al. 2022). Pintos & Alvarado (2021) re-evaluated the multigene phylogeny and the morphology of *Arthrinium* and accepted *Apiospora* as a distinct genus within *Apiosporaceae*. Hence, only *Apiospora*, *Arthrinium*, and *Nigrospora* are accepted in *Apiosporaceae* (Wijayawardene et al. 2022).

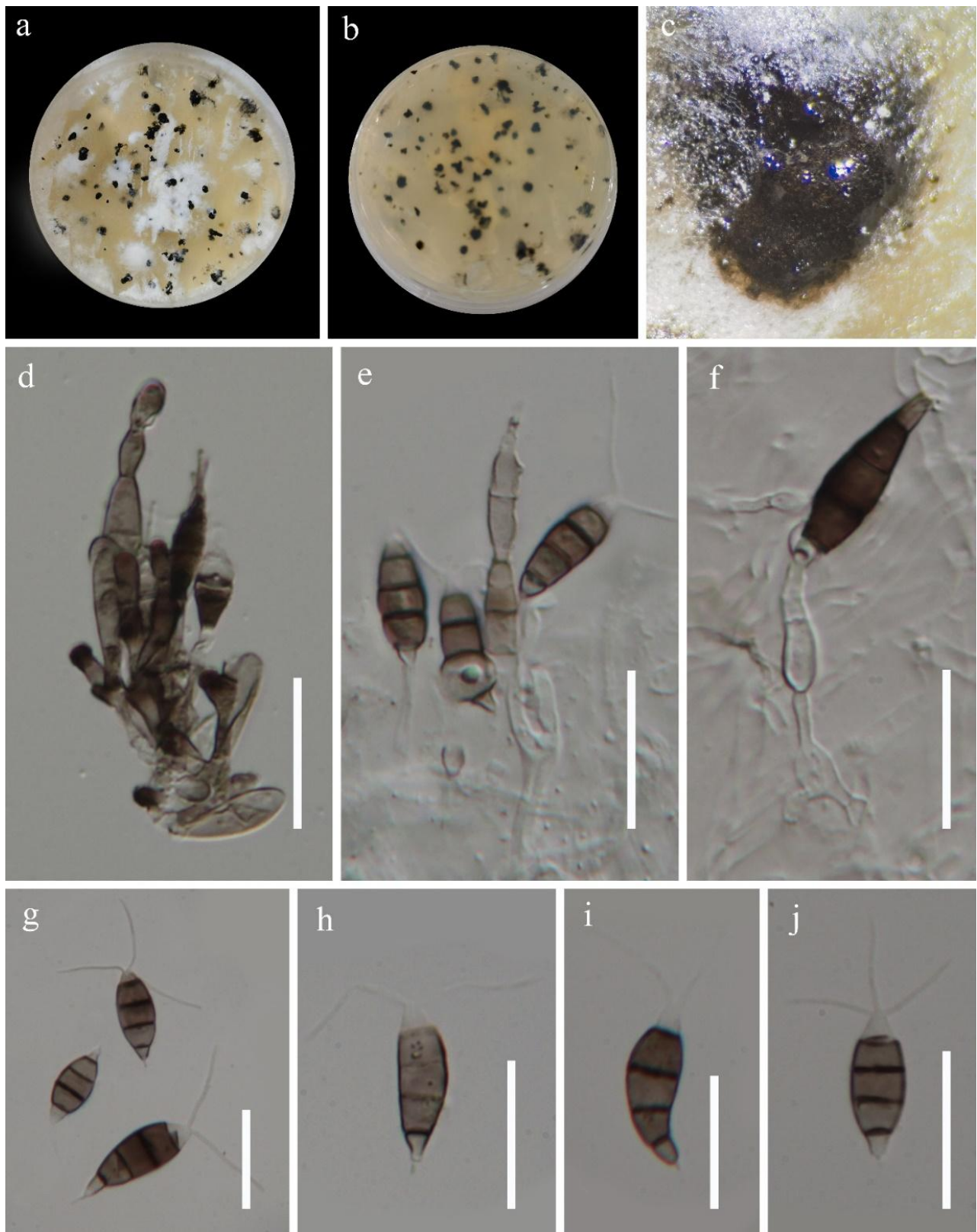


Figure 76 – *Neopestalotiopsis yongxunensis* (KUN-HKAS 129871, New host record) a, b Culture on PDA from above and below. c Colonies on PDA. d–f Conidiogenous cells and Conidia. g–j Conidia. Scale bar: d–j = 20 μm.

Nigrospora Zimm.

Nigrospora is an ecologically highly diverse genus with species found as pathogens, endophytes,

and saprobes from a diverse host range around the world (Mason 1927, Wu et al. 2009, Thalavaipandian et al. 2011, Uzor et al. 2015, Wang et al. 2017, Rashmi et al. 2019). The taxonomy of *Nigrospora* is controversial and has been successively placed in *Dematiaceae* (*Moniliales*) and *Trichosphaeriaceae* (*Trichosphaeriales*) by Barnett and Hunter (1998) and Kirk et al. (2008), respectively, based on morphology. Wang et al. (2017) reassessed the genus based on a multi-locus (ITS, *tef1-α*, and *tub2*) phylogeny which significantly stabilized the taxonomy of the genus overlapping morphological characteristics of *Nigrospora* species and they confirmed the genus belongs to *Apiosporaceae* (*Xylariales*, *Sordariomycetes*), as well as 27 species have been accepted in the genus. Afterwards, several new species have been introduced (Raza et al. 2019, Tennakoon et al. 2021, Tan et al. 2022, Brito et al. 2023, Zhang et al. 2024d). Currently, 49 *Nigrospora* species have been recorded in the Index Fungorum 2024. *Nigrospora* is characterized by spherical to subspherical conidiogenous cells and black and globose to subglobose conidia (Wang et al. 2017). In this study, we reported seven endophytic *Nigrospora* species from *Dicranopteris*, which is the first report of *Nigrospora* isolated from *Dicranopteris*

***Nigrospora aurantiaca* Mei Wang & L. Cai, (2017)**

Fig. 77

Index Fungorum: IF 820730; Facesoffungi number: FoF 17889.

Endophytic in the root of *Dicranopteris linearis*. Sexual morph: unknown. Asexual morph: *Hyphae* superficial, hyaline to brown, septate, branched, aerial mycelium. *Conidiophores* reduced to conidiogenous cells, hyaline to slightly brownish, branched, smooth. *Conidiogenous cells* 5.7–13.8 × 4.2–14.3 μm ($\bar{x}$ = 5.2 × 12.5 μm, n = 20), monoblastic, discrete, doliiform, smooth, hyaline to pale brown, cylindrical to subcylindrical, aggregated in clusters on hyphae. *Conidia* 9.8–16.4 × 10.8–16.3 μm ($\bar{x}$ = 12.6 × 13.7 μm, n = 30), solitary, globose to ellipsoidal, aseptate, light brown to black, smooth-walled.

Culture characteristics – Colonies on PDA medium, low, with aerial mycelium, cottony, brown with white; reverse black, with red pigments.

Material examined – China, Guizhou Province, Tongren City, from the leaves of *D. pedata*, 21 February 2022, J.Y. Zhang, (NS76–2 = KUN-HKAS 129919). China, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the root of *D. linearis*, 16 March 2022, J.Y. Zhang, (276–2 = KUN-HKAS 129907), living culture (KUNCC 24–17930).

GenBank numbers – KUN-HKAS:129919: ITS: PV138715, *tef1-α*: PV177109, *tub2*: PV222004. KUNCC:24-17930: ITS: PV138723, *tub2*: PV222010.

Notes – *Nigrospora aurantiaca* was introduced by Wang et al. (2017) based on phylogenetic and morphological characteristics (Wang et al. 2017). Our new isolates (KUN-HKAS 129919 and KUNCC 24–17930) are similar to the holotype of *N. aurantiaca* in having monoblastic, discrete, doliiform, hyaline to pale brown, cylindrical conidiogenous cells and globose to ellipsoidal, aseptate, light brown to black, smooth-walled conidia. In our phylogenetic analysis, the new isolates (KUN-HKAS 129919 and KUNCC 24–17930) clustered with *N. aurantiaca* (Fig. 78). Both phylogeny and morphology of our isolates are not significantly different from *N. aurantiaca*. We, therefore, identified our new isolates as *N. aurantiaca*. *Nigrospora aurantiaca* is reported here from *Dicranopteris pedata* for the first time.

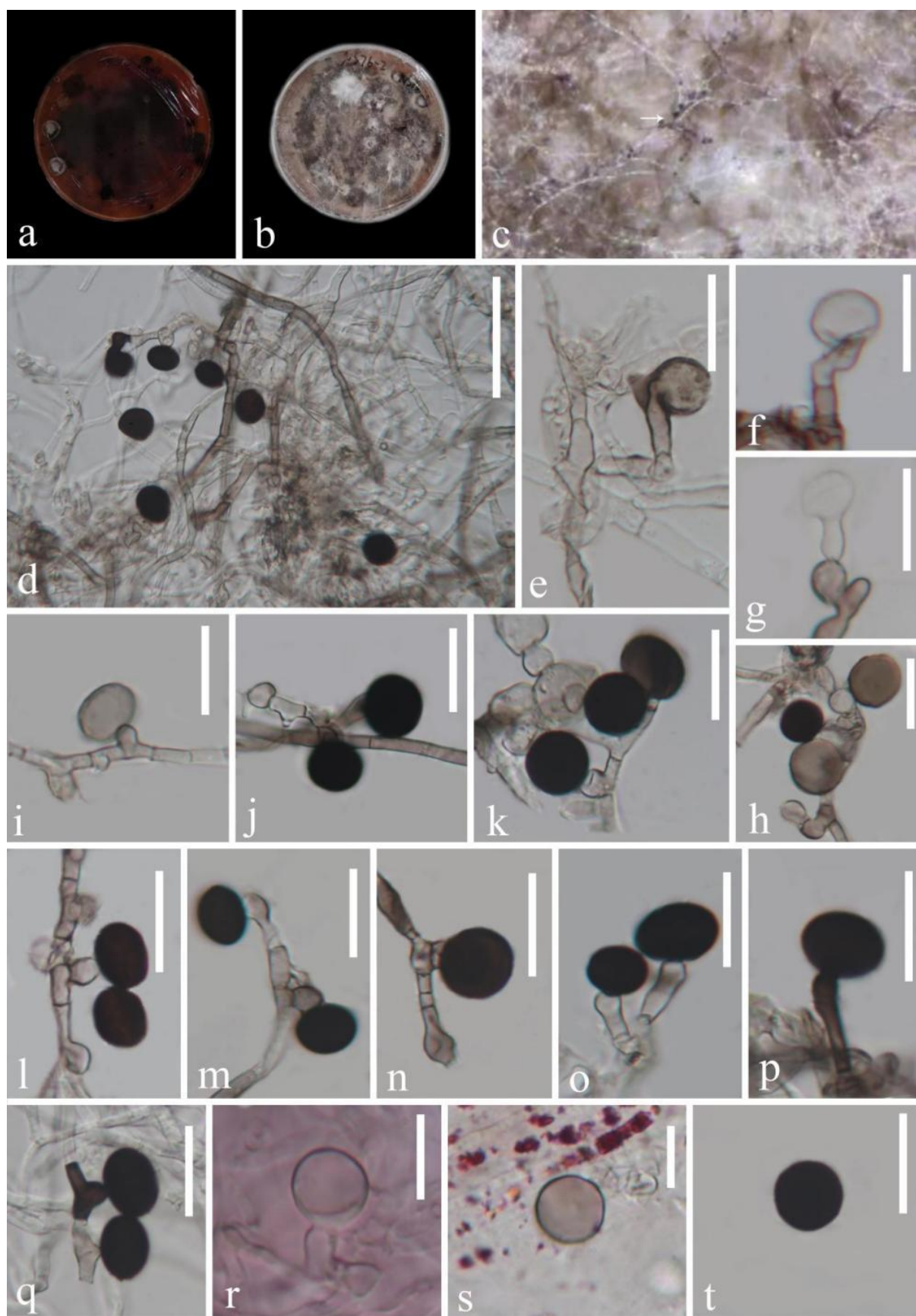


Figure 77 – *Nigrospora aurantiaca* (KUN-HKAS 129919, New host record). a, b Culture on PDA from above and below. c Colonies on PDA. d–r Conidiogenous cells and conidia. s, t Conidia. Scale bar: d = 50 μm, e–q = 20 μm, r, s = 10 μm, t = 20 μm.

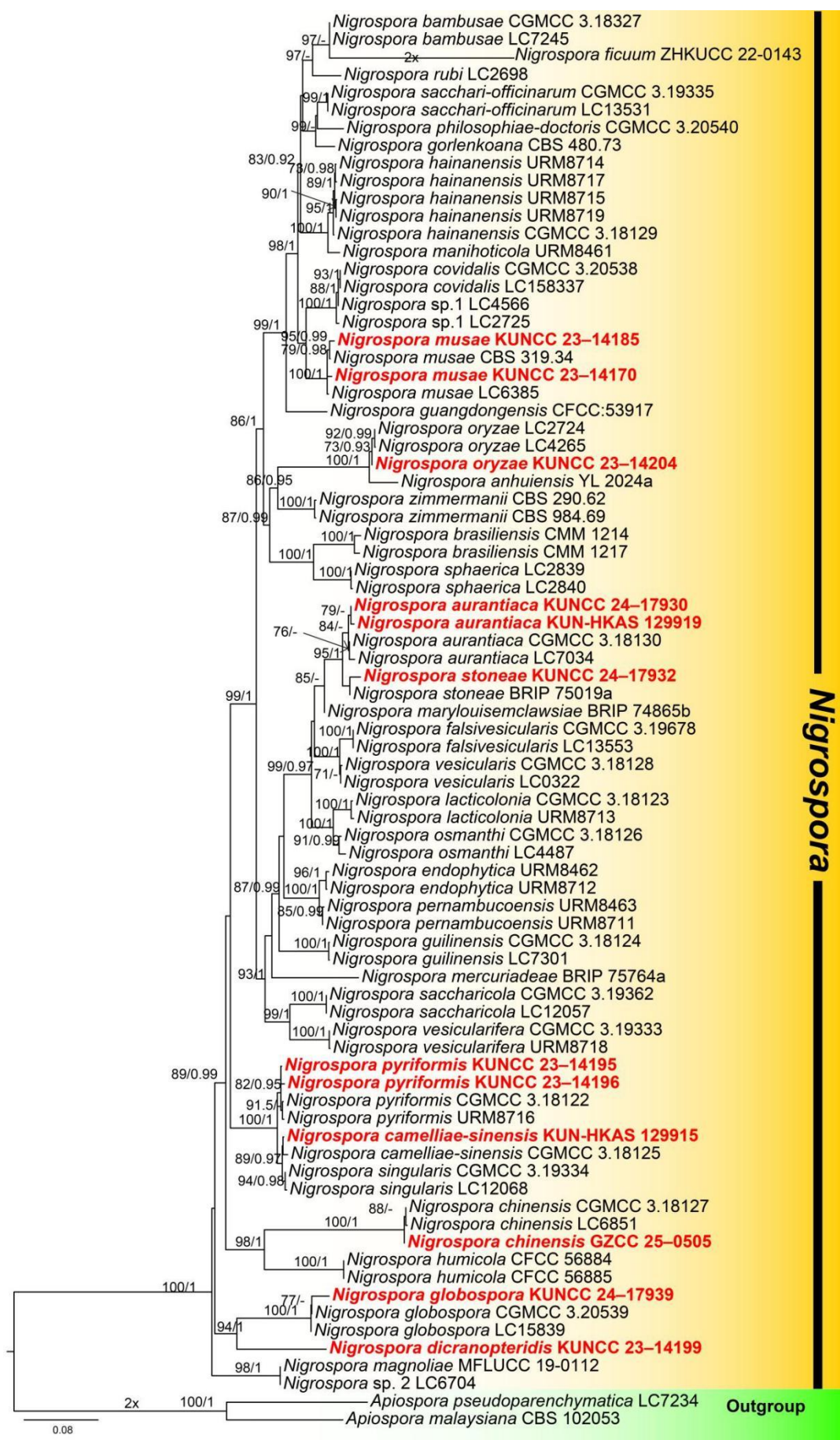


Figure 78 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1*-

α , and *tub2* sequence data. 80 taxa were included in the combined analyses, which comprised 1438 characters after alignment. The best scoring RAxML tree with a final likelihood value of -13747.020 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Apiospora malaysiana* (CBS 102053) and *A. pseudoparenchymatica* (LC7234). The newly obtained strains are in red and bold.

Nigrospora camelliae-sinensis Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39: 127 (2017) Fig. 79

Index Fungorum: IF 820731; Facesoffungi number: FoF 09396.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* superficial, hyaline to brown, septate, branched, aerial mycelium, smooth. *Conidiogenous* reduced to conidiogenous cells. *Conidiogenous cells* 7.5–14.5 × 4.5–8.5 µm, smooth, brown, cylindrical to subcylindrical. *Conidia* 10.5–17.0 × 9.5–17.5 µm ($\bar{x}$ = 13.5 × 13.5 µm, n = 18), aseptate, globose to ellipsoidal, brown to black, smooth-walled.

Culture characteristics – Colonies on PDA medium, white to grey, with aerial mycelium, cottony; reverse black, with black spots.

Material examined – China, Guizhou Province, Yaoshan Yao Township, Libo County, Qiannan Buyi and Miao Autonomous Prefecture, from the healthy leaves of *Dicranopteris pedata*, 8 April 2022, J.Y. Zhang, (NS361–1 = KUN-HKAS 129915).

GenBank numbers – ITS: PV138725, *tef1*- α : PV177117, *tub2*: PV222012

Notes – *Nigrospora camelliae-sinensis* was introduced by Wang et al. (2017), isolated from *Camellia sinensis* in China. Later, *N. camelliae-sinensis* was reported on mangrove plant (*Lumnitzera littorea*). Our isolate and the holotype of *N. camelliae-sinensis* are morphologically indistinguishable. The multi-locus phylogenetic analysis of ITS, LSU, *tef1*- α , and *tub2* showed that the new isolate clustered with *N. camelliae-sinensis* with strong statistical support (Fig. 78). We therefore reported this newly obtained strain as a new host record of *N. camelliae-sinensis* isolated from *Dicranopteris pedata* in China.

Nigrospora chinensis Mei Wang & L. Cai (2017) Fig. 80

Index Fungorum: IF 820732; Facesoffungi number: FoF 09446.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* dense, hyaline to light brown, branched. *Conidiophores* reduced to conidiogenous cells, hyaline to pale brown, smooth, branched. *Conidiogenous cells* 1.7 × 3.0–5.5 µm ($\bar{x}$ = 1.3 × 4.4, n = 20), monoblastic, discrete, solitary, ampulliform, smooth, hyaline to pale brown, ellipsoidal, subcylindrical. *Conidia* 8.9–12.4 × 10.5–13.4 µm ($\bar{x}$ = 10.6 × 11.7 µm, n = 30), aseptate, globose to ellipsoidal, pale brown to black, shiny, smooth-walled.

Culture characteristics – Colonies on PDA medium, cottony, spreading, with aerial mycelium, surface white; reverse orange with black spots.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS193–2 = GZAAS 25–0513), living culture (GZCC 25–0505).

GenBank numbers – ITS: PV138720, *tef1*- α : PV177113, *tub2*: PV222008

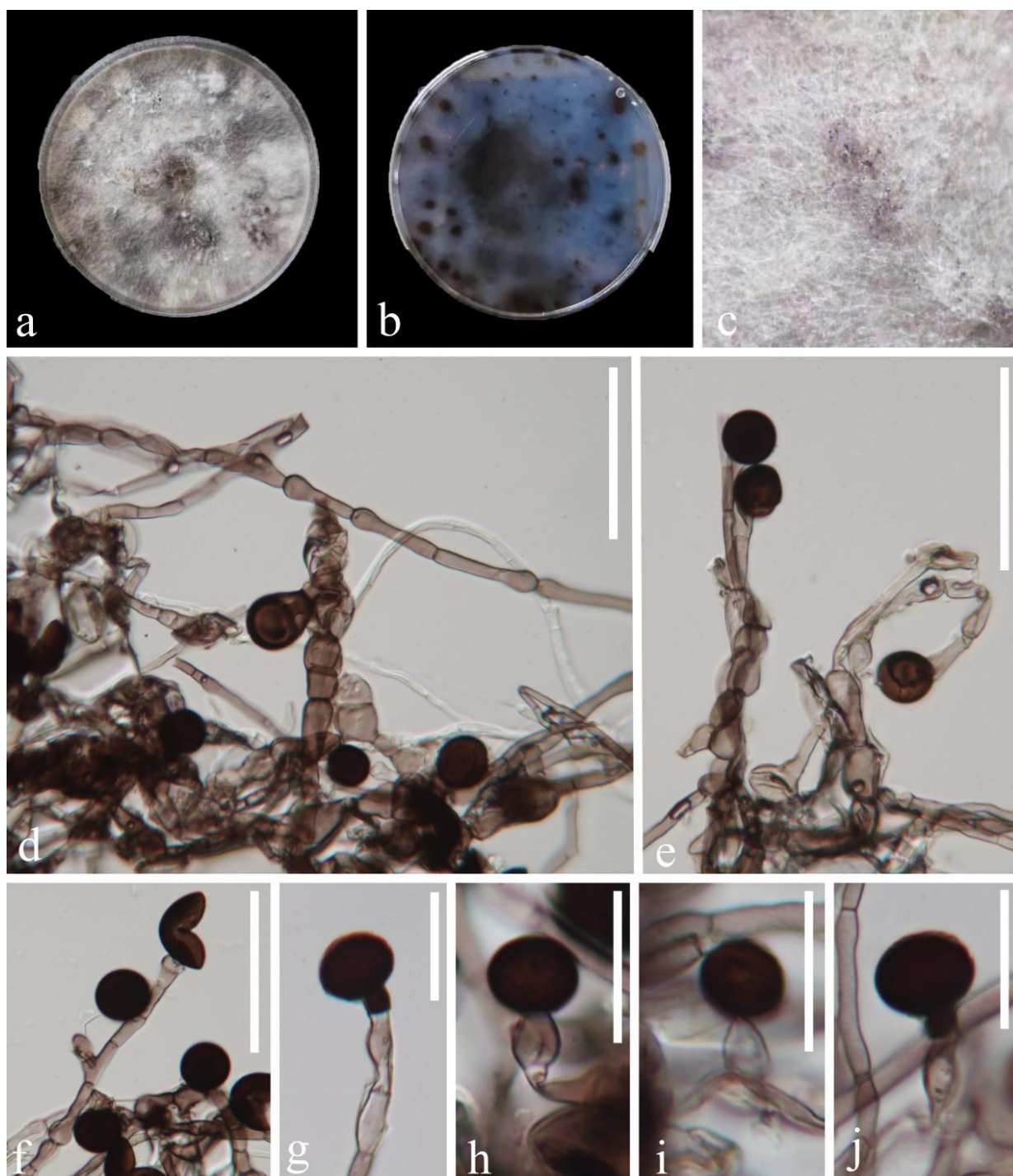


Figure 79 – *Nigrospora camelliae-sinensis* (KUN-HKAS 129915, New host record). a, b Culture on PDA from obverse and reverse. c Colonies on PDA. d–j Conidiogenous cells and conidia. Scale bar: d–f = 50 μ m; g–j = 20 μ m.

Notes – Phylogenetic analysis showed that the newly obtained strain (GZCC 25–0505) clustered with two strains of *N. chinensis* (CGMCC 3.18127 and LC6851) with 100%ML/1.00 PP statistical support (Fig.78). *Nigrospora chinensis* was introduced by Wang et al. (2017), and it is characterized by monoblastic, discrete, determinate, ampulliform, or subspherical conidiogenous cells and solitary, globose or subglobose, black, smooth, aseptate conidia. Our new isolate is morphologically indistinguishable from the type specimen of *N. chinensis* (CGMCC 3.18127) (Wang et al. 2017). The

phylogeny and morphology of our new isolates are not significantly different from *N. chinensis*; thus, we identified our new isolates as *N. chinensis*. Since the new isolate was first found on *Dicranopteris pedata*, we identified it as a new record of an endophytic fungus in *D. pedata*.

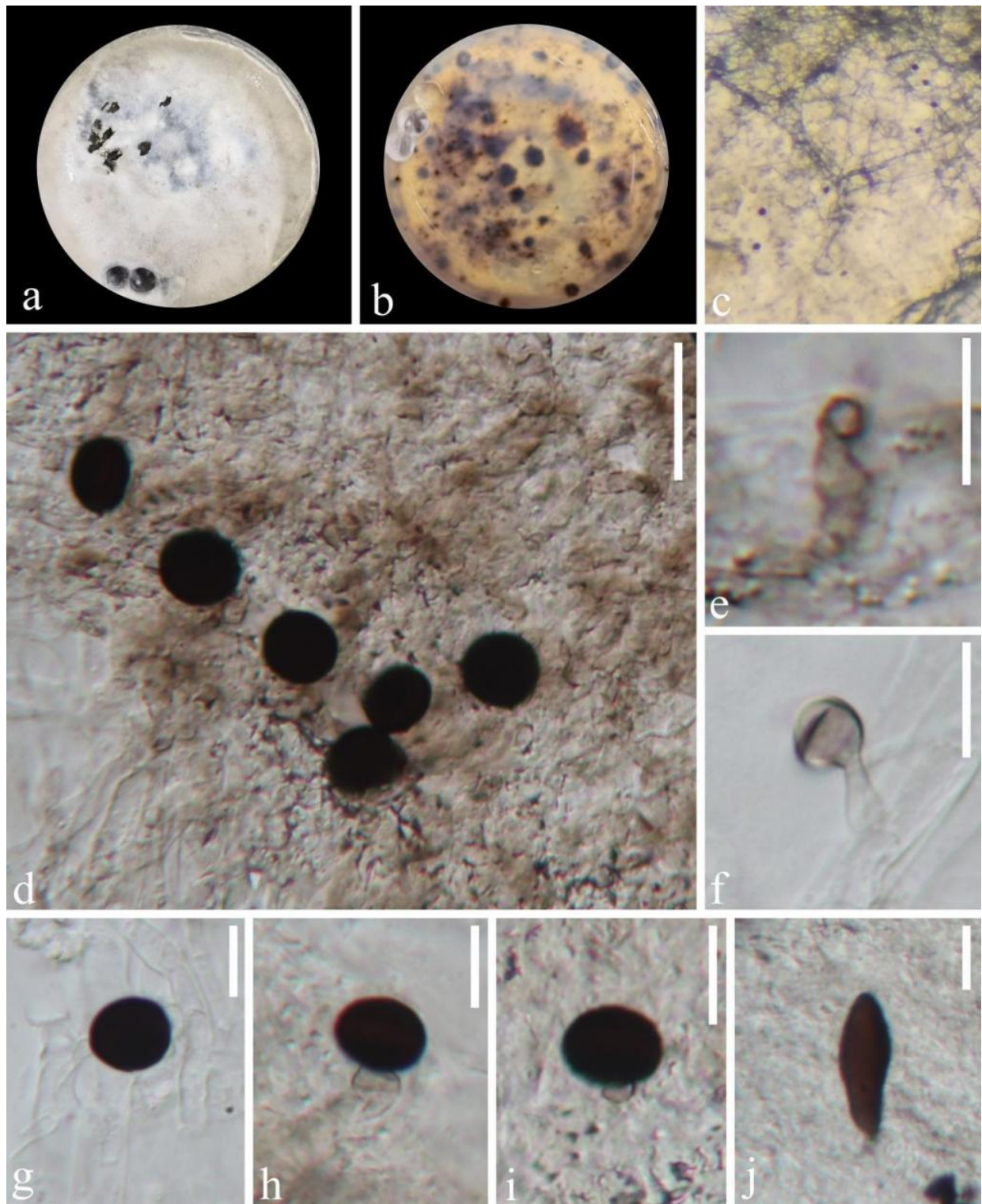


Figure 80 – *Nigrospora chinensis* (GZAAS25–0513, New host record). a, b Culture on PDA from obverse and below. c Colonies on PDA. d–i Conidiogenous cells and conidia. j Conidia. Scale bar: d = 20 μ m; e–j = 10 μ m.

Nigrospora dicranopteridis J.Y. Zhang, D.F. Bao & K.D. Hyde, sp. nov

Fig. 81

Index Fungorum: IF 903981; Facesoffungi number: FoF 17890.

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 25–0525

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* smooth, septate, branched, hyaline to dark brown. *Conidiophores* reduced to conidiogenous cells, hyaline to dark brown, smooth. *Conidiogenous cells* monoblastic, solitary, discrete, sub-spherical or ampulliform, smooth, hyaline to dark brown. *Conidia* $10\text{--}13 \times 10\text{--}11\ \mu\text{m}$ ($\bar{x} = 12 \times 10.8\ \mu\text{m}$, $n = 20$), aseptate, sparse, shiny, globose to subglobose, hyaline when young, becoming dark brown at maturity, smooth-walled. *Chlamydospore* $16\text{--}23 \times 7\text{--}10\ \mu\text{m}$ ($\bar{x} = 19.5 \times 8.3\ \mu\text{m}$, $n = 20$), clavate, obclavate, truncate at the base, pale brown to dark brown, thick and smooth-walled.

Culture characteristics – Colonies on PDA medium circular, flat with entire edge, reaching 50 mm diameter after 14 days at 25 °C, cottony, velvety, grey to greyish pink or slight pale brown from above, dark brown to pink reverse.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi and Miao Autonomous County, from the leaves of *Dicranopteris ampla*, 17 March 2022, J.Y. Zhang, (NS294–2 = GZAAS 25–0525, holotype), ex-type culture (KUNCC 23–14199).

GenBank numbers – ITS: PV138724, *tef1- α* : PV177116, *tub2*: PV222011

Notes – Morphologically, *Nigrospora* species are quite similar, making it difficult to identify species based solely on morphological characteristics. Therefore, species delimitation in this genus relies on multi-gene phylogenetic analysis. Our new isolate, *N. dicranopteridis*, aligns with the genus's morphological traits, having spherical to subspherical conidiogenous cells and black, globose to subglobose conidia. Phylogenetic analysis showed that *N. dicranopteridis* formed a sister clade to *N. globospora*, with 94% ML/1.00 BYPP statistical support (Fig. 78). However, *N. dicranopteridis* differs from *N. globospora* in the color of its culture (initially grey to greyish pink in *N. dicranopteridis* vs. whitish black in *N. lacticolonia*) and in its globose to subglobose, hyaline to dark brown conidia and chlamydospores. In contrast, *N. globospora* has black, mostly ellipsoidal conidia, and no chlamydospores were observed (Chen et al. 2022). Based on both phylogenetic and morphological evidence, we introduce *N. dicranopteridis* as a new species.

Nigrospora globospora M. Raza, Qian Chen & L. Cai, (2022)

Fig. 82

Index Fungorum: IF 840805; Facesoffungi number: FoF 17891.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* smooth, septate, branched, hyaline to pale brown. *Conidiophores* reduced to conidiogenous cells, hyaline to pale brown, smooth. *Conidiogenous cells* $6.5\text{--}9.9 \times 3.8\text{--}7.3\ \mu\text{m}$ ($\bar{x} = 7.8 \times 6.0\ \mu\text{m}$, $n = 7$), monoblastic, solitary, discrete, sub-spherical or ampulliform, smooth, hyaline to pale brown. *Conidia* $10.7\text{--}15.8 \times 11.7\text{--}16.3\ \mu\text{m}$ ($\bar{x} = 12.6 \times 14.2\ \mu\text{m}$, $n = 24$), aseptate, sparse, shiny, globose to ellipsoidal, pale brown to black, smooth.

Culture characteristics – Colonies on PDA medium circular, flat with entire edge, reaching 50 mm diameter after 14 days at 25 °C, cottony, velvety, white from above, yellow brown reverse. Vegetative hypha septate, branched, hyaline to brown.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS165–2 = KUN-HKAS 129881), living culture KUNCC 24–17939.

GenBank numbers – ITS: PV138717

Notes – *Nigrospora globospora* was introduced on *Petasites hybridus* by Chen et al. (2022). Phylogenetic analysis showed that the new isolate clustered with two strains of *N. globospora* (Fig. 78). The morphological characteristics are similar to the type specimen of *N. globospora* (CGMCC 3.20539), and the difference in DNA molecular data between our new isolate and the ex-type of *N. globospora* (CGMCC 3.20539) are not significant. Therefore, we identified the new isolate as *N. globospora*. This species is a new endophytic fungus reported in *Dicranopteris pedata*.

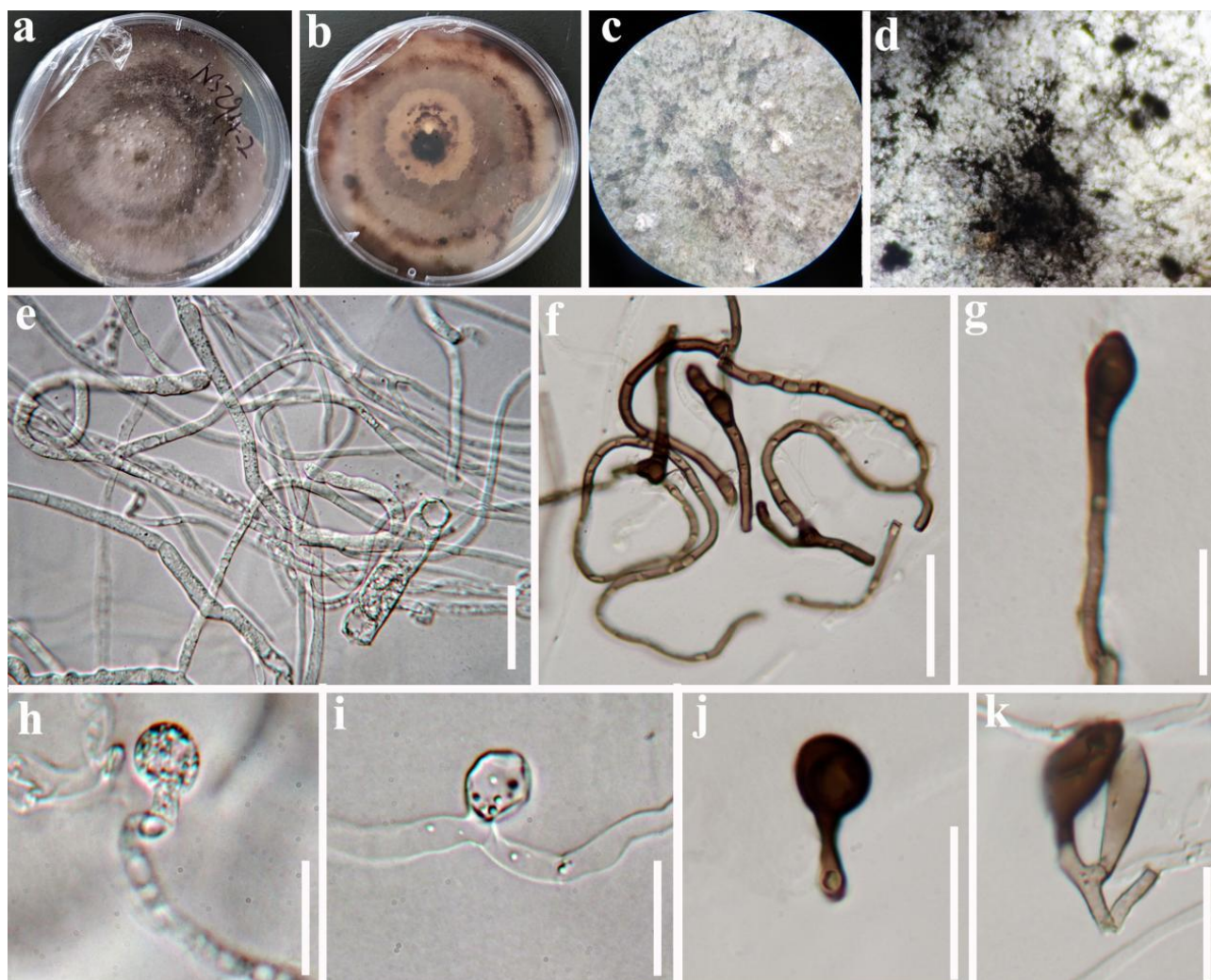


Figure 81 – *Nigrospora dicranopteridis* (GZAAS 25–0525, holotype). a, b Culture on SNA from above and below. c, d Colonies on SNA. e, f mycelium. h–j Conidiogenous cells and Conidia. g, k Chlamydospore. Scale bar: d = 50 μ m, e–m = 20 μ m.

***Nigrospora musae* McLennan & Hoëtte (1933)**

Fig. 83

Index Fungorum: IF 271866; Facesoffungi number: FoF 09447.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* dense, hyaline to light brown, branched. *Conidiophores* aggregated in black sporodochia, micronematous or semi-macronematous, basauxic, hyaline to pale brown, smooth, branched. *Conidiogenous cells* 5.6–11.5 $\times$ 5.6–7.2 μ m ($\bar{x}$ = 7.4 $\times$ 6.5 μ m, n = 7), smooth, hyaline to pale brown, aggregated, monoblastic, subglobose to ampulliform. *Conidia* 10.3–16.1 $\times$ 13.4–17.2 μ m ($\bar{x}$ = 13.3 $\times$ 15.6 μ m, n = 20), sparse, solitary, globose or subglobose, black, shiny, aseptate, hyaline to black, smooth-walled.

Culture characteristics – Colonies on PDA medium are cottony, rough-textured, and spreading, with prominent aerial mycelium. The surface appears ivory-white; the reverse exhibits alternating brown and white patches with red pigmentation.

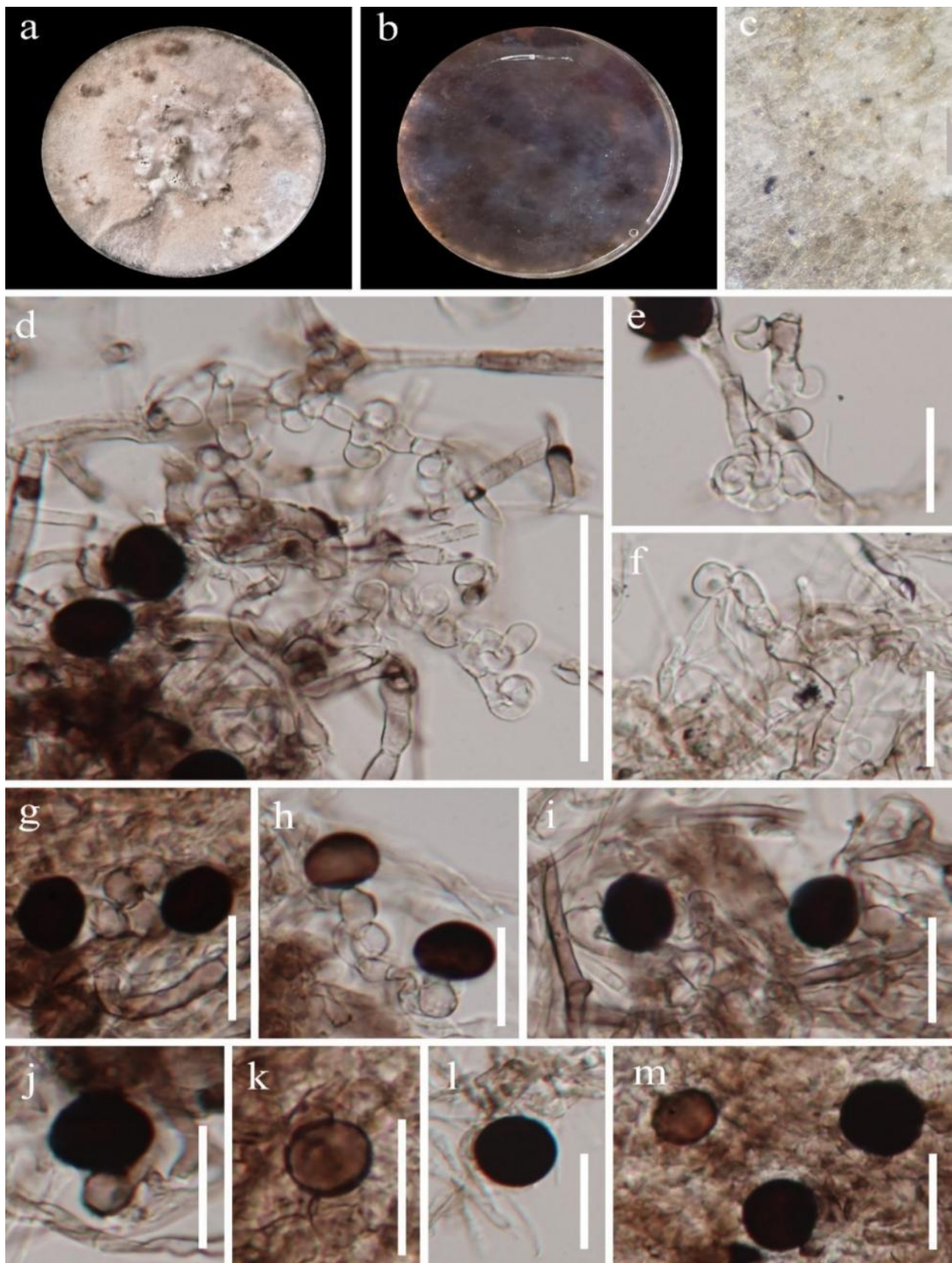


Figure 82 – *Nigrospora globospora* (KUN-HKAS 129881, New host record). a, b Culture on PDA from above and below. c Colonies on PDA. d–j Conidiogenous cells and Conidia. k–m Conidia. Scale bar d = 50 μ m; e–m = 20 μ m.

Material examined – China, Guizhou Province, Ceheng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 16 March 2022, J.Y. Zhang, (NS138–4 = KUN-HKAS 129876), living culture (KUNCC 23–14170). China, Zhenfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *D. pedata*, 17 March 2022, J.Y. Zhang, (189–2 = KUN-HKAS, 129889), living culture (KUNCC 23–14185).

GenBank numbers – KUNCC:23–14170: ITS: PV138716, *tef1*- α : PV177110, *tub2*: PV222005. KUNCC:23–14185: ITS: PV138719, *tef1*- α : PV177112, *tub2*: PV222007

Notes – *Nigrospora musae* isolated from banana leaves in Australia, was introduced by McLennan et al. (1933). *Nigrospora musae* have been reported on various hosts, such as *Camellia sinensis*, *Musa paradisiaca*, and the leaves of *Basella alba*. The morphological features indicated that our isolates (KUNCC23–14170 and KUNCC23–14185) were identical to *N. musae*. Phylogenetically, the newly obtained strains (KUNCC23–14170 and KUNCC23–14185) clustered with two strains of *N. musae* (CBS 319.34 and LC6385) with 100%ML/1.00 PP statistical support (Fig. 78). As a result, we reported our new isolates as a new host record for *N. musae* from *Dicranopteris pedata* in China.

***Nigrospora oryzae* (Berk. & Broome) Petch (1924)**

Fig. 84

Index Fungorum: IF 253729; Facesoffungi number: FoF 06596.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* dense, hyaline to brown, branched. *Conidiophores* basauxic, hyaline to pale brown, smooth, branched. *Conidiogenous cells* 5.2–9.9 $\times$ 4.1–6 μ m ($\bar{x}$ = 7.8 $\times$ 5.3 μ m, n = 20), smooth, hyaline to pale brown, elliptical to subcylindrical. *Conidia* 9.2–13.7 $\times$ 9.6–15.4 μ m ($\bar{x}$ = 12 $\times$ 13 μ m, n = 30), aseptate, globose to ellipsoidal, hyaline to black, smooth.

Culture characteristics – Colonies on PDA medium, flat, with aerial mycelium, grey, cottony; reverse black with red pigmentation.

Material examined – China, Guizhou Province, Yaoshan Yao Township, Libo County, Qiannan Buyi and Miao Autonomous Prefecture, from the healthy leaves of *Dicranopteris pedata*, 11 April 2022, J.Y. Zhang, (NS376–2 = KUN-HKAS 129917), living culture (KUNCC 23–14204).

GenBank numbers – ITS: PV138726, *tef1*- α : PV177118

Notes – The multigene phylogenetic analysis showed that our new isolate (KUNCC 23–14204) with *Nigrospora oryzae* with 100%ML/1.00 PP support (Fig. 78). The Morphology of our new isolate is similar to *N. oryzae* in having micronematous or semi-macronematous, septate, flexuous or straight, pale brown, smooth-walled conidiophores, monoblastic, determinate conidiogenous cells, and globose or subglobose, black, smooth, aseptate conidia, and there was no significant difference in DNA molecular data between the two strains. Therefore, the new isolate was identified as *Nigrospora oryzae*. *Nigrospora oryzae* has been found on a wide range of hosts with a worldwide distribution (Tian et al. 2024). However, this is the first time, *N. oryzae* is reported from *Dicranopteris pedata*.

***Nigrospora pyriformis* Mei Wang & L. Cai (2017)**

Fig. 85

Index Fungorum: IF 820737; Facesoffungi number: FoF 14212.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* sparse, light brown, branched. *Conidiophores* basauxic, brown, smooth, branched, thin-

walled, short, septate. *Conidiogenous cells* $4.4\text{--}10.6 \times 2.7\text{--}6.5 \mu\text{m}$ ($\bar{x} = 8.5 \times 5.4 \mu\text{m}$, $n = 15$) polyblastic, smooth, brown, subcylindrical. *Conidia* $8.0\text{--}15.9 \times 8.8\text{--}16.6 \mu\text{m}$ ($\bar{x} = 13.1 \times 13.6 \mu\text{m}$, $n = 30$), pleuroacrogenous, aseptate, globose to ellipsoidal, hyaline to black, smooth, guttulate.

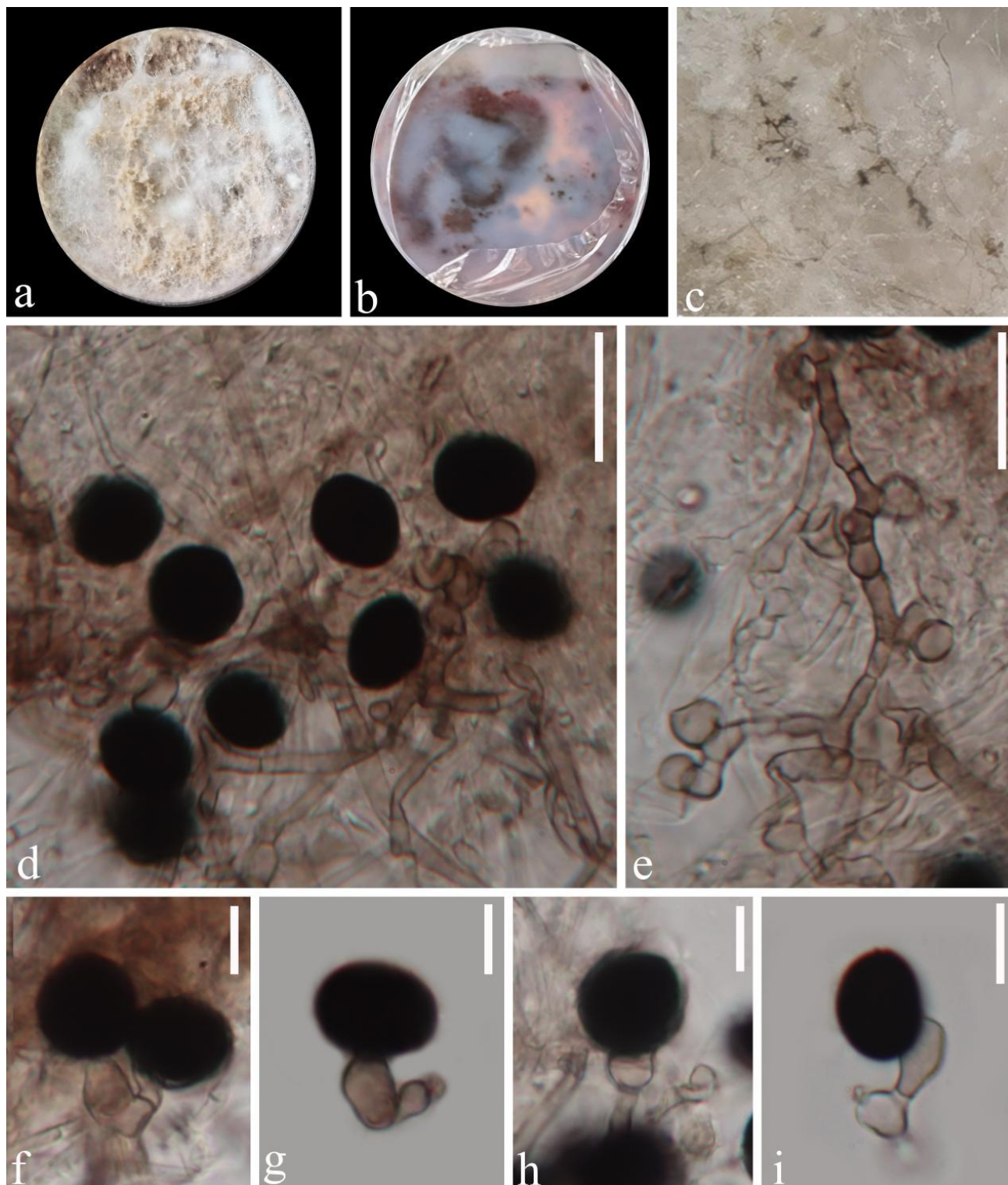


Figure 83 – *Nigrospora musae* (KUN-HKAS 129876, New host record) a, b Culture on PDA from above and below. c Colonies on PDA. d–i Conidiogenous cells and conidia. Scale bar: d, e = $20 \mu\text{m}$, f–i = $10 \mu\text{m}$.

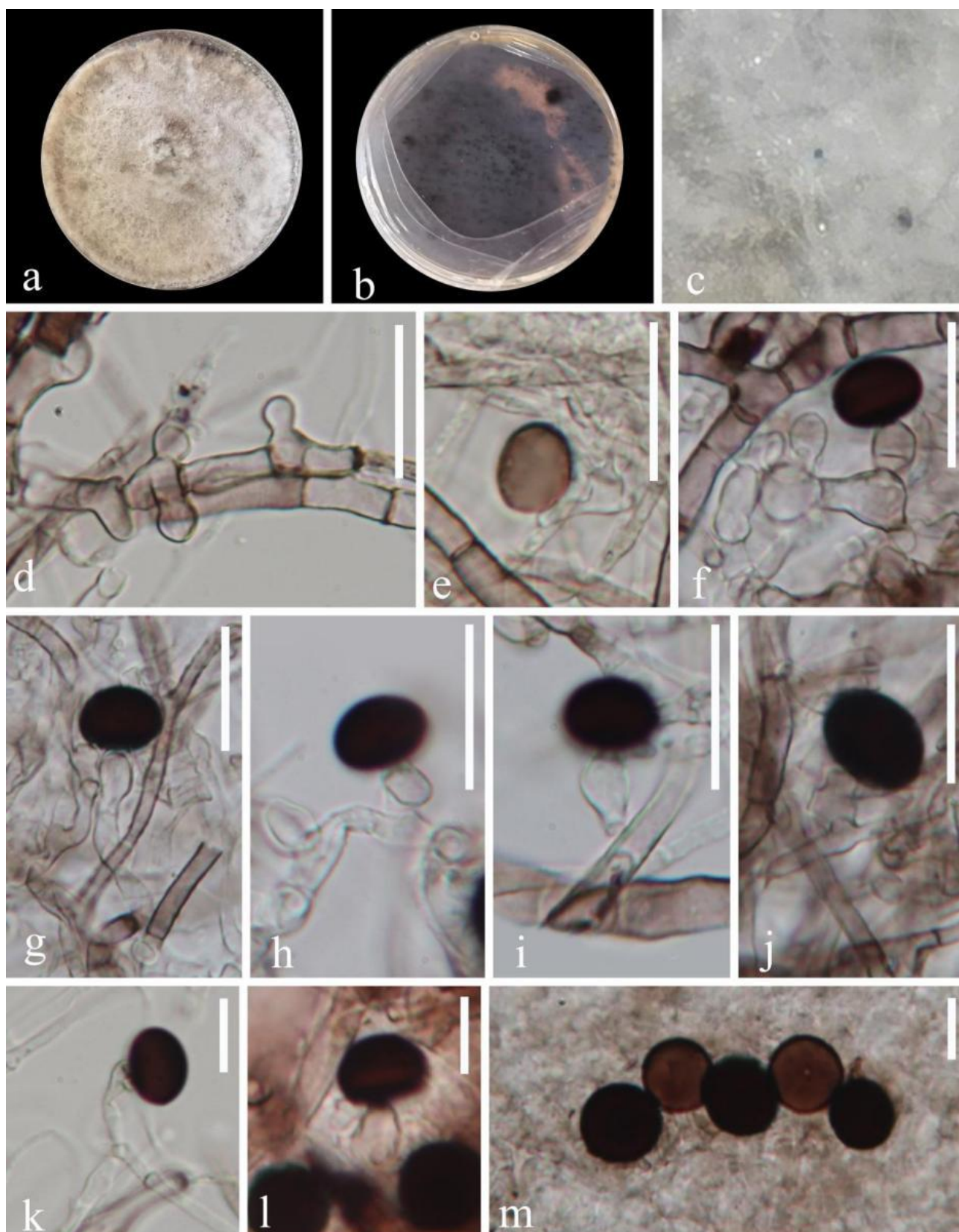


Figure 84 – *Nigrospora oryzae* (KUN-HKAS 129917, New host record) a, b Culture on PDA from above and below. c Colonies on PDA. d–l Conidiogenous cells and conidia. m Conidia. Scale bar: d–j = 20 µm; k–m = 10 µm.

Culture characteristics – Colonies on WA medium are flat, rhizoid (root-like), and filiform

(thread-like), with an overall brown coloration. The reverse side is brown and bears black, filiform mycelium. No pigments are produced.

Material examined – China, Guizhou Province, Zhenfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the leaves of *Dicranopteris pedata*, 17 March 2022, J.Y. Zhang, (NS273–2 = KUN-HKAS 129903), living culture (KUNCC 23–14195). *ibid* (NS275–2 = KUN-HKAS 129904), living culture (KUNCC 23–14196)

GenBank numbers – KUNCC 23–14195: ITS: PV138721, *tef1*- α : PV177114, *tub2*: PV222009. KUNCC 23–14196: ITS: PV138722, *tef1*- α : PV177115, *tub2*: PV222013

Notes – Wang et al. (2017) introduced *Nigrospora pyriformis*, isolated from *Citrus reticulata* in China. Phylogenetic analysis of multiple genes showed that our new isolates (KUNCC 23–14195 and KUNCC 23–14196) and *N. pyriformis* clustered together with 91%ML/1.00 support (Fig. 78). The morphological characteristics of the new isolates are similar to those of *N. pyriformis* (Wang et al. 2017), and the differences of the molecular data between our new isolates and ex-type strain of *N. pyriformis* (CGMCC 3.18122) are not significant. Therefore, we identified the new isolates as *N. pyriformis*. *Nigrospora pyriformis* is a new record for *Dicranopteris pedata*.

Nigrospora stoneae Y.P. Tan, Bishop-Hurley & R.G. Shivas, in Tan & Shivas, Index of Australian Fungi 17: 5 (2023) Fig. 86

Index Fungorum: IF 901169; Facesoffungi number: FoF 17892.

Endophytic in the leaves of *Dicranopteris pedata*. Sexual morph: unknown. Asexual morph: *Hyphae* sparse, brown to dark brown or greyish brown, branched, smooth-walled. *Conidiophores* basauxic, smooth, branched, thin-walled, short, septate, brown to dark brown. *Conidiogenous cells* 8.5–16 $\times$ 5–8 μm ($\bar{x}$ = 12.4 $\times$ 6.4 μm , n = 15) polyblastic, brown, smooth, subcylindrical, oval. *Conidia* 10–15 $\times$ 11–15 μm ($\bar{x}$ = 12.8 $\times$ 13.2 μm , n = 30), pleuroacrogenous, aseptate, globose to ellipsoidal, Hyaline when young, dark brown to black at maturity, smooth-walled.

Culture characteristics – Colonies on WA medium, circular, margin entire, flat, white mycelia, colony from above: white; reverse: cream. Produces pink or lavender pigment in the medium plate.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the stem of *D. pedata*, 16 March 2022, J.Y. Zhang (187–1 = KUN-HKAS 129887), living culture (KUNCC 24–17932).

GenBank numbers – ITS: PV138718

Notes – *Nigrospora stoneae* was recently introduced by Tan et al. (2023) based on phylogenetic analysis, it was showing 99% identity (455/456) and 95% identity (401/420) to its phylogenetically close species, *N. aurantiaca*. Our phylogenetic analysis revealed that the new isolate KUNCC 24–17932 clustered with the ex-type strain of *N. stoneae* (BRIP 75019a) and was sister to *N. aurantiaca* (Fig. 78). No morphological description was provided for this species in the original study. In this study, we provide a detailed morphological description and illustration of *N. stoneae*. This species was previously collected from leaf spots on *Cyperus aromaticus* in Queensland, we herein report it as a new host and country record for *D. pedata* in China.

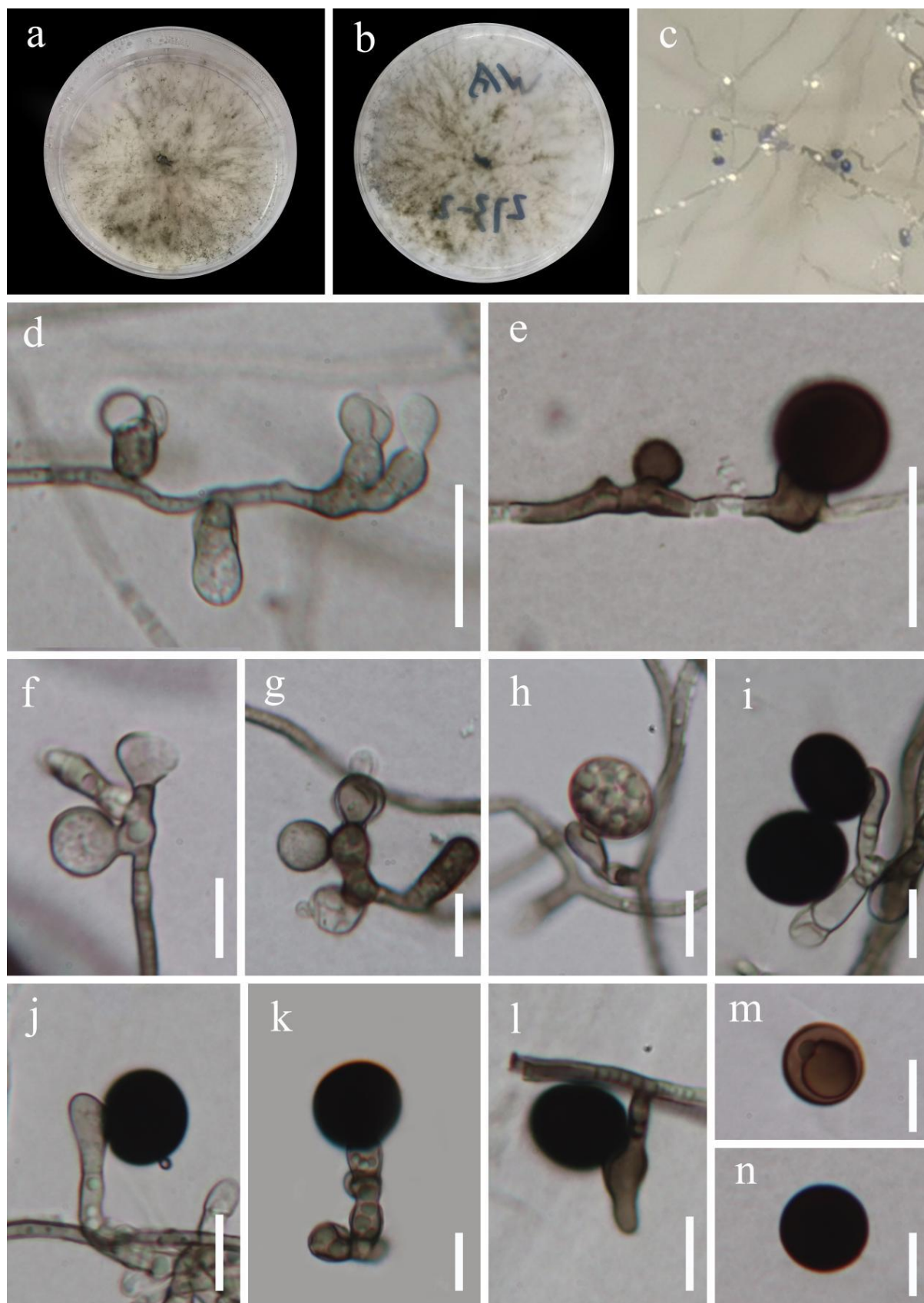


Figure 85 – *Nigrospora pyriformis* (KUN-HKAS 129903, New host record) a, b Culture on WA from above and below. c Colonies on WA. d–l Conidiogenous cells and conidia. m, n Conidia. Scale bar: d, e = 20 μm; f–n = 10 μm.

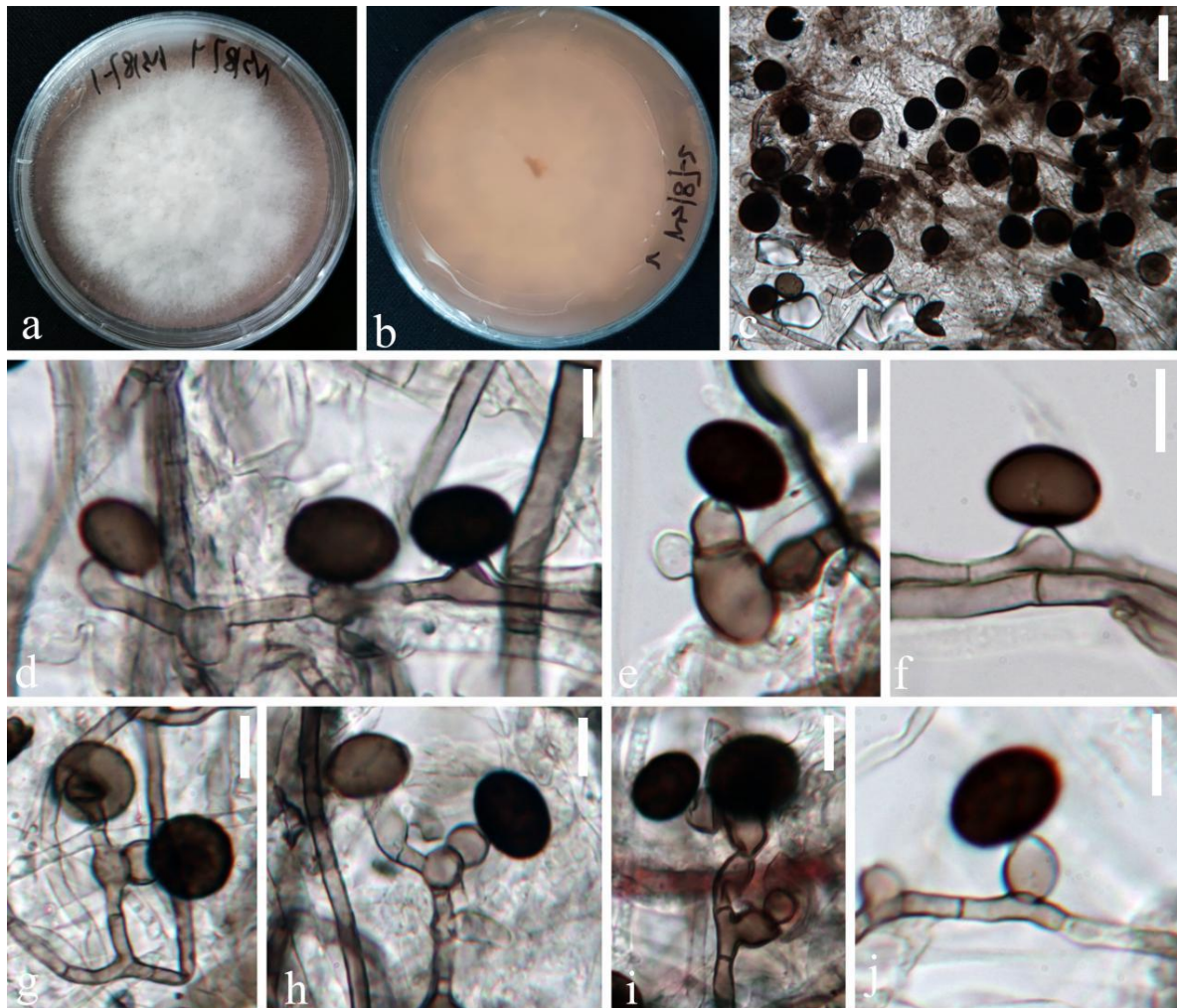


Figure 86 – *Nigrospora stoneae* (KUN-HKAS 129887, New host record) a, b Culture on WA from above and below. c Conidia with mycelium. d–j Conidiogenous cells and conidia. Scale bar: c = 30 μ m; d–j = 10 μ m.

Castanediellaceae Hern.-Restr., Guarro & Crous

Castanediellaceae was established by Hernández-Restrepo et al. (2017) to accommodate *Castanediella* within *Xylariales*. Currently, the family contains a single genus with 19 species (Hernández-Restrepo et al. 2017, Costa et al. 2018; Wanasinghe et al. 2018, Lin et al. 2019b, Crous et al. 2021c).

Castanediella Hern.-Restr., Crous & M.J. Wingf.

Castanediella was introduced by Crous et al. (2015b) with three species *C. acaciae* (type), *C. cagnizarii* and *C. ramosa*. Subsequently, several new species were added to the genus, up to now, 19 species are accepted in this genus (Crous et al. 2016, 2021c, Costa et al. 2018; Wanasinghe et al. 2018, Hernández-Restrepo et al. 2016, Lin et al. 2019b). *Castanediella* is characterized by branched, hyaline to pale brown conidiophores, holoblastic, sympodial conidiogenous cells and falcate, cylindrical or fusiform, 0–3-sepate, hyaline conidia (Crous et al. 2015b).

Castanediella dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. Nov.
Index Fungorum: IF 903982; Facesoffungi number: FoF 17893.

Fig. 87

Etymology – The specific epithet *dicranopteridis* refers to the fern genus *Dicranopteris*, from which the type strain was isolated.

Holotype – GZAAS 25–0506

Endophytic in the rhizome of *Dicranopteris ampla*. *Mycelium* superficial and immersed composed of septate, branched, hyaline to pale brown, with smooth and thick-walled hyphae. Chlamydospores $9\text{--}12 \times 7\text{--}8.5\ \mu\text{m}$ ($\bar{x} = 10.3 \times 7.2\ \mu\text{m}$, $n = 30$), in chains, globose, subglobose, clavate, irregular, brown to dark brown, septate, guttulate.

Culture characteristics – Colonies on PDA, 55–60 mm diameter After one month, colonies from above, medium dense, flat, circular, entire edge, margin well-defined, cottony to fairly fluffy with sparse aspects, light brown to dark brown; reverse dark brown.

Material examined – China, Guizhou Province, Zhengfeng County, Southwest Guizhou Buyi, and Miao Autonomous County, from the rhizome of *Dicranopteris ampla*, 17 March 2022, Y. Yang, (147–1 = GZAAS 25–0506, holotype).

GenBank numbers – ITS: PV138745, LSU: PV138600

Notes – Based on a sequence similarity search against in the NCBI's GenBank nucleotide database using the ITS sequence of our new strain *Castanediella dicranopteridis* (GZAAS 25–0506), the closest hits include *Menispora cobaltina* (98.47% similarity) and *Castanediella brevis* (98.08% similarity). The closest match with the LSU sequences with 98.51% similarity was *Castanediella neomalaysiana* (CPC:39275). Phylogenetic analysis showed that *C. dicranopteridis* clustered with *C. communis*, *C. eucalypti* and *C. eucalypticola*, but in a distinct basal clade (Fig. 88). Morphologically, unlike other *Castanediella* species, *C. dicranopteridis* does not produce conidiophores, or conidia and only Chlamydospores was observed. Thus, based on both phylogeny and morphology, *Castanediella dicranopteridis* is introduced as a new species.

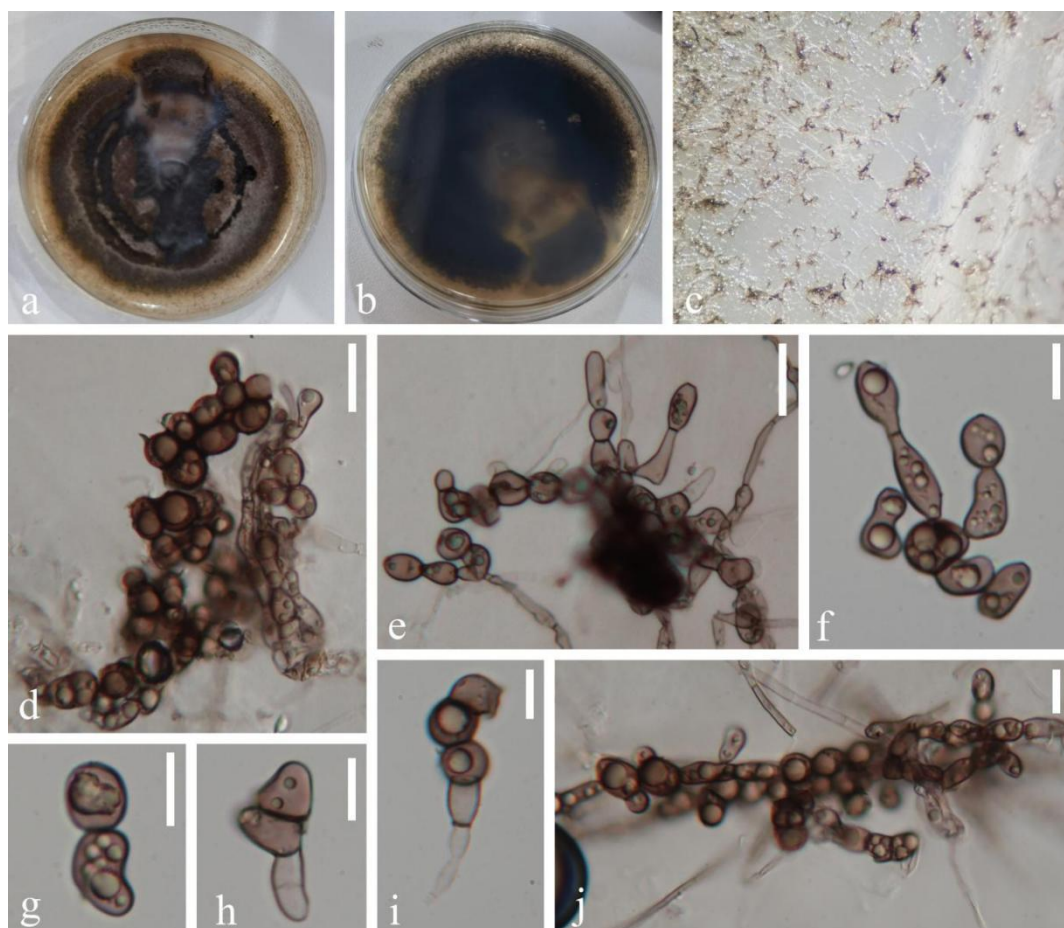


Figure 87 – *Castanediella dicranopteridis* (GZAAS 25–0506, holotype). a, b Cultures on PDA from above and below. C Colonies on the PDA. d–j Hyphae with chlamydospores. Scale bars: d = 20 µm, e–j = 10 µm.

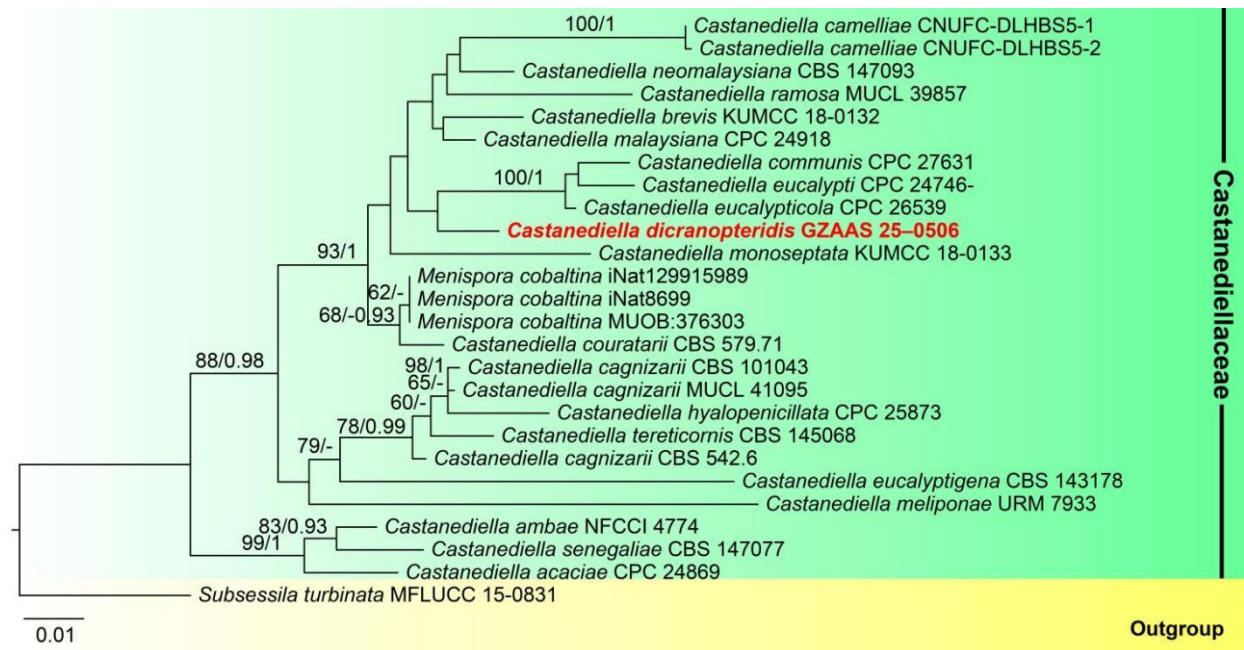


Figure 88 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. A total of 26 taxa were included in the combined analyses, which comprised 1405 characters after alignment. The best scoring RAxML tree with a final likelihood value of -4535.505314 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Subsessila turbinata* (MFLUCC 15-0831). The newly generated sequences are shown in red and bold.

Hypoxylaceae DC.

Hypoxylaceae belongs to *Xylariales*, which was formally introduced by Wendt et al. (2018) to accommodate *Annulohypoxylon*, *Hypoxylon*, *Daldinia*, and several related genera that have stomatal pigments and a nodulisporium-like anamorph, and they accepted 13 genera in the family based on a multi-locus phylogeny and morphology. Subsequently, several studies have constantly revised and updated the classification of the family (Daranagama et al. 2018, Hyde et al. 2020a, Cedeño-Sanchez et al. 2024, Karimi et al. 2024). To date, 18 genera have been accepted in this family (Wijayawardene et al. 2022).

Hypoxylon Bull.

Hypoxylon species are primarily saprobes and endophytes with a global distribution, however, they exhibit higher diversity in the tropics and subtropics (Ju & Rogers 1996, Daranagama et al. 2018, Ma et al. 2022, Song et al. 2022, Fournier et al. 2024). This species-rich genus was established by Bulliard (1791) with 1218 epithets in the Index Fungorum (<http://www.indexfungorum.org/names/names.asp>, accessed on 11 October 2024). Previously, the identification of *Hypoxylon* based on only morphological characteristics, however, which is not sufficient to distinguish *Hypoxylon* species (Ju and Rogers 1996, Daranagama et al. 2018, Ma et al.

2022, Song et al. 2022). The use of a multi-locus phylogenetic analysis has been a major advantage to obtain a greater resolution in *Hypoxyton* (Daranagama et al. 2018). Recent studies showed that *Hypoxyton* is polyphyletic and species of *Hypoxyton* clustered into eight clades (Song et al. 2022). Hence, the taxonomy of this group needs further studies to resolve the taxonomic problems of this group.

Hypoxyton dicranopteridis J.Y. Zhang, D.F. Bao, K.D. Hyde & Y.Z. Lu, sp. nov.

Fig. 89

Index Fungorum: IF 903983; Facesoffungi number: FoF 17894.

Etymology – Refers to the host fern genus *Dicranopteris*, on which the holotype was collected.

Holotype – GZAAS 25–0512

Endophytic in the rhizome of *Dicranopteris linearis*. Sexual morph: not observed. Asexual morph: *Hyphae* hyaline to brown, septate, branched, aerial mycelium, thin-walled. *Conidiophores* immersed or semi-immersed, macronematous, mononematous, hyaline to brownish, septate, branched, slightly flexuous, with conidiogenous cells arising terminally or laterally. *Conidiogenous cells* $7.8\text{--}21.1 \times 1.7\text{--}5.0 \mu\text{m}$ ($\bar{x} = 11.8 \times 2.8 \mu\text{m}$, $n = 13$), hyaline to light brownish, rough-walled, cylindrical to oblong. *Conidia* $3.6\text{--}6.2 \times 1.8\text{--}2.7 \mu\text{m}$ ($\bar{x} = 4.2 \times 2.4 \mu\text{m}$, $n = 30$), hyaline, 0-septate, thin-walled, smooth, obovoid to clavate.

Culture characters – Colonies on PDA medium, growing fast, dense, covered with abundant, at center white with dark brown edges, cottony to woolly aerial mycelia; reverse black.

Material examined – China, Guizhou Province, Ziyun Miao and Buyi Autonomous County, Anshun City, from the rhizome of *Dicranopteris linearis*, 2 August 2022, J.Y. Zhang, (S19–3 = GZAAS 25–0512, holotype), ex-type living culture (KUNCC 23–14209).

GenBank numbers – ITS: PV138738, LSU: PV138593, *tub2*: PV222018, *rpb2*: PV188069.

Notes – Our phylogenetic analysis showed that *Hypoxyton* is polyphyletic and formed eight clades, which is consistent with the recent phylogenetic study of Cedeño-Sánchez et al. (2024). *Hypoxyton dicranopteridis* nested within the clade of *Hypoxyton* 1 and sister to *H. investiens* (Fig. 90). Due to the lack of an asexual morph of *H. investiens* (Curtis et al. 1867), we were unable to compare the morphology between *H. dicranopteridis* and *H. investiens*. Phylogenetically, they are distinct, and the comparisons of nucleosides of *rpb2* and *tub2* gene regions between *H. dicranopteridis* and *H. investiens* showed 41 bp and 31 bp differences, which strongly support our new isolate as a new species.

DISCUSSION AND CONCLUSION

The fungi associated with *Dicranopteris* have been a relatively unexplored area of research, with only a handful of species documented so far (Kirschner & Liu 2014, Kirschner & Wang 2015, Guatimosim et al. 2016, Zhang et al. 2023a, 2025, Chen et al. 2024). In this study, we present a comprehensive checklist of fungi associated with *Dicranopteris*, unveiling a total of 23 species from 17 genera (Table 4). Our research systematically investigated endophytic fungi associated with *Dicranopteris* in Guizhou Province, China, and has led to the isolation of 84 fungal strains from *D. ampla*, *D. pedata*, and *D. linearis*. Through meticulous analysis of their morphological characteristics and phylogenetic relationships, we have identified 59 species belonging to 34 genera, 28 families, 18 orders, and four classes within the *Ascomycota*. Notably, 24 of these species are entirely new to science, as are two genera, one family, and 25 are new host records for *Dicranopteris*. This study unveils a remarkably high species diversity of endophytic fungi in *Dicranopteris*, with approximately half of the identified species being previously unknown. These findings not only underscore the vast and underexplored diversity of endophytic fungi but also significantly enhance our understanding of

fungus biodiversity. Moreover, they highlight the potential of these fungi to contribute to their host plants' medicinal properties, offering promising new directions for research in medicinal and environmental mycology.

Our identification of 59 species from various ascomycete classes (*Dothideomycetes*, *Leotiomycetes*, and *Sordariomycetes*) as endophytes further supports the idea that most ascomycetes have an endophytic phase in their life cycle. Bhunjun et al. (2024) discussed this in detail, suggesting that many ascomycetes, whether saprobes or pathogens, likely evolved from endophytic lifestyles. Similarly, Rathnayaka et al. (2023) and Wang et al. (2024) proposed that *Botryosphaeriaceae* ancestors may have originated as endophytes and then switched into saprobes or pathogens. Promputtha et al. (2007) found that fungal species like *Colletotrichum*, *Fusarium*, *Phyllosticta* (as *Guignardia*), and *Phomopsis*, which are common endophytes, share genetic similarities with saprotrophic fungi. This indicates that these endophytes may transition to a saprotrophic lifestyle under certain conditions. Further supporting this idea, Demir et al. (2024) demonstrated that *Lachnum* species, once thought to be exclusively saprobes, also exhibit multiple life cycle phases, including appressoria formation. Appressoria are specialized cells or adhesion structures from which a penetration peg emerges to pierce the host tissues and function in pathogen and endophyte infection of their hosts (Chethana et al. 2021b, Konta et al. 2023). This reinforces the concept that endophytes can switch lifestyles, becoming pathogens or saprobes. The potential of endophytes to switch lifestyles is truly impressive, and numerous studies have documented such shifts, including in genera like *Diaporthe* and *Colletotrichum*, which include both endophytes and pathogens across a wide range of plant hosts. For example, *Colletotrichum coccodes*, identified as an endophyte in symptomless plants of potato, cabbage, white mustard, lettuce, and chrysanthemum (Chesters & Hornby 1965, Chang et al. 2014), causes black dot disease on potato tubers.

However, Chang et al. (2014) observed no symptoms in potato leaves inoculated with *C. coccodes* from infected tubers despite appressoria and infection hyphae. A similar phenomenon was observed in our study with *Diaporthe arecae*, identified as an endophyte and a pathogen causing dieback in Chinese Olive (*Canarium album*) (Lai et al. 2024). Likewise, *Colletotrichum fiorinae*, another endophyte, has been reported to cause postharvest bitter rot of apples in South Tyrol (Carneiro and Baric 2021). In addition to these examples, our study identified several other endophytic species that are significant pathogens infecting various plants, including *Alternaria longipes*, *Phyllosticta capitalensis*, and *Stagonospora tainanensis*. Additionally, *Tainosphaeria phialogeniculata* and *Cladosporium benschiae*, both reported as endophytes in our study, are also known as saprobes (Wu and Diao 2022, Costa et al. 2022). Furthermore, the genus *Pseudodactylaria* has been recognized exclusively as saprobes from freshwater habitats (Crous et al. 2017, Lin et al. 2018b, Hyde et al. 2020b, Lu et al. 2020b, Bao et al. 2021, Boonmee et al. 2021, Yang et al. 2023b). Our study discovered a new species of *Pseudodactylaria* as an endophyte in the healthy rhizome of *Dicranopteris pedata*. Thus, our study provides strong evidence that many saprobes have an endophytic phase and that endophytes can switch between lifestyles, adapting to various ecological niches.

In this study, the analysis of the fungal genera associated with *Dicranopteris* reveals a significant pattern of dominance and habitat-specific distribution. The dominant genera, *Nigrospora* (nine species), *Colletotrichum* (six species), *Neopestalotiopsis* (five species), *Cladosporium* (four species), and *Diaporthe* (four species) (Fig. 91), suggest a strong association with *Dicranopteris*. This dominance could indicate a potential symbiotic relationship or a specific adaptation to the *Dicranopteris*'s environment. In contrast, other genera were represented by only one species (Fig. 90), indicating that some fungi may have a more specialized or limited occurrence.

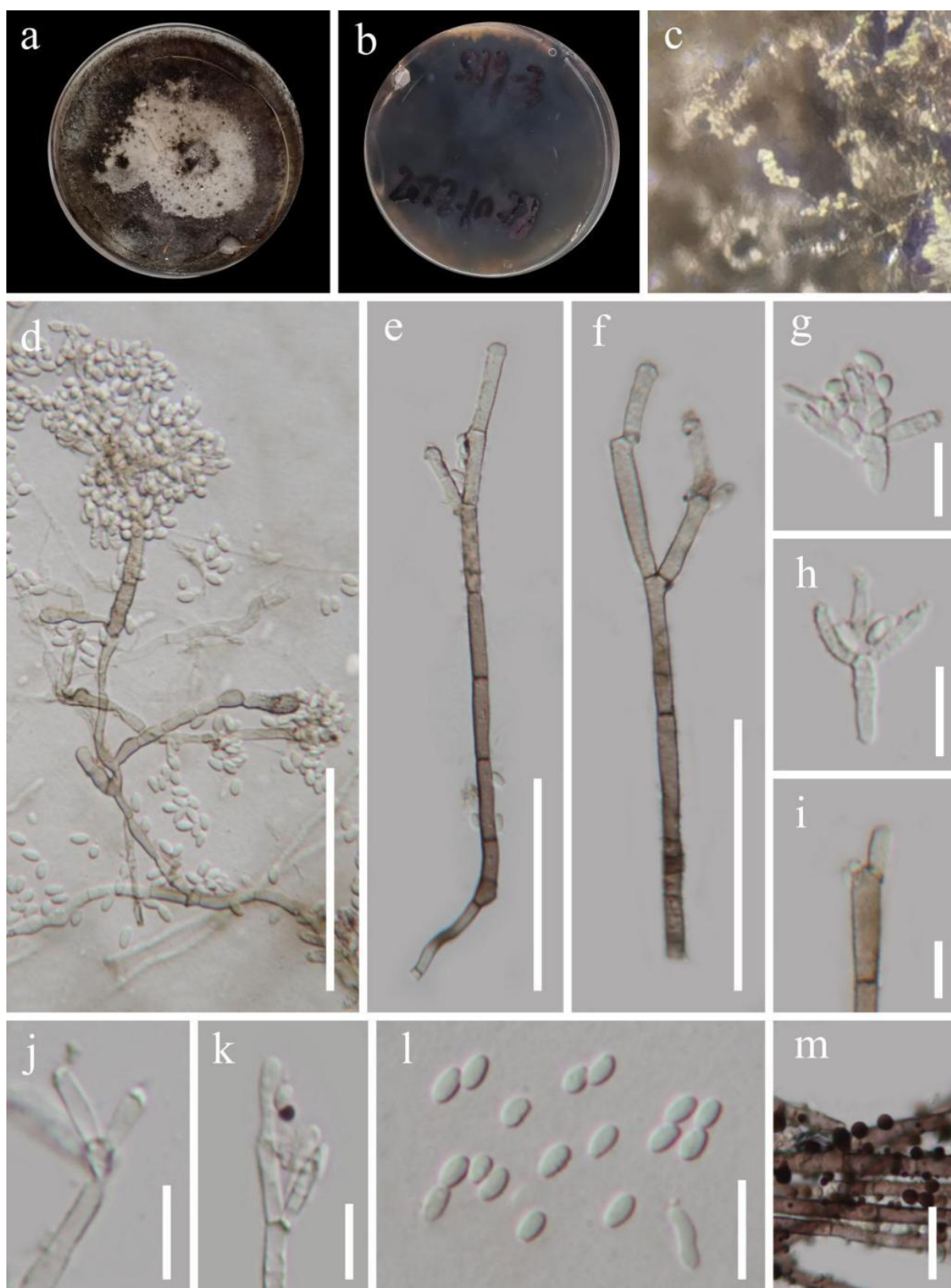


Figure 89 – *Hypoxylon dicranopteridis* (GZAAS 25–0512, new host record). a, b Culture on PDA from above and below. c Colonies on PDA. d–k Conidiophores, conidiogenous cells, and conidia. l Conidia. m Pigmentation. Scale bars: d–f = 50 μ m, g–l = 10 μ m, m = 20 μ m.

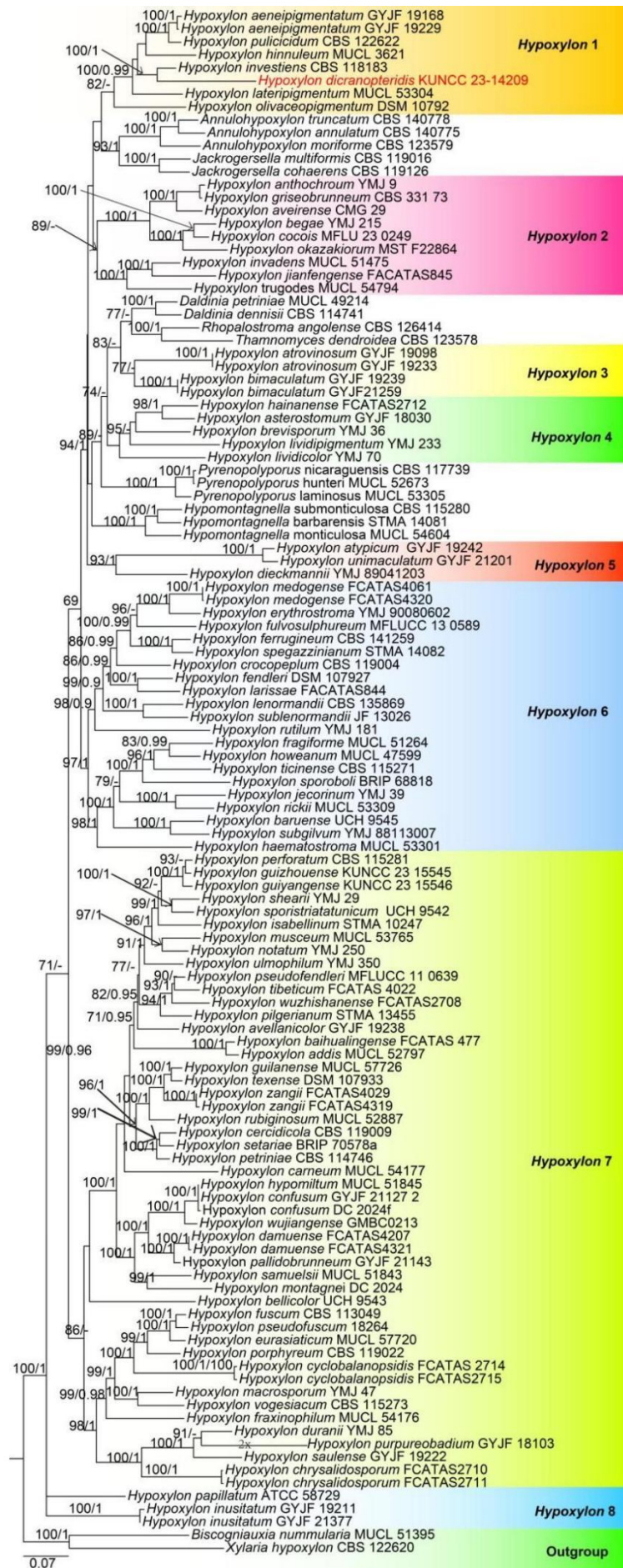


Figure 90 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tub2*, and *rpb2* sequence data. A total of 4280 taxa were included in the combined analyses, which comprised 1981 characters after alignment. The best scoring RAxML tree with a final likelihood value of -86424.379482 is presented. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated above branches as ML BS/PP. The tree was rooted to *Xylaria hypoxylon* (CBS 122620) and *Biscogniauxia nummularia* (MUCL 51395). The newly generated sequences are shown in red.

Fungal distribution varied across the plant tissues (roots, stems, rhizomes, and leaves). *Colletotrichum*, *Neopestalotiopsis*, and *Nigrospora* were predominantly found in the leaves (Table 5), highlighting their potential specialization or preference for leaf tissue. Conversely, several genera with only one species, such as *Periconia dicranopterisis*, *Amorocoelophoma dicranopterisis*, and *Massicellispora globosa*, were isolated exclusively from roots (Table 5), suggesting a unique relationship with root structures. Additionally, some species were distributed across leaves, stems, and roots (e.g., *Phyllosticta capitalensis*), although these plant tissues appeared to harbor fewer diverse fungi compared to leaves and roots. Interestingly, most of the newly discovered species were found in the root (nine new species) and rhizome (seven new species), indicating these parts are under-explored fungal niches with high potential for discovering novel species. In contrast, only two and one new species were identified from the leaves and stems, respectively, and a new species occur in both leaves and stems (Fig. 92), suggesting that the leaves and stems may be more commonly studied or may have less fungal diversity than the subterranean parts. This pattern reinforces those roots and rhizomes might be reservoirs for previously unknown fungal diversity, underscoring the urgent need for further investigation.

In this study, we emphasize a morpho-molecular taxonomic approach to investigate culturable endophytic fungi, leading to the identification of 59 species based on phylogenetic analysis and morphological characteristics. However, we encountered challenges in species definition, a common issue in taxonomic studies. For example, *Colletotrichum gracile*, *C. oblongisporum*, and *C. nullisetosum* were introduced as new species by Yu et al. (2022) based on minor morphological differences. Their phylogenetic analysis indicated that these three species clustered closely with *C. jiangxiense*, showing no significant sequence variation among them. Our re-evaluation suggests that these four taxa are not distinct species but rather represent the same species due to the lack of significant differences in their sequence data. These findings highlight the need for integrative taxonomic approaches and underscore the complexity of species delimitation in endophytic fungi.

Future research directions

We initiated a significant and systematic study of endophytic fungi associated with medicinal ferns from Guizhou Province, China. This pioneering study, the first in a series, is a crucial step toward understanding the role of endophytic fungi in medicinal ferns, with a specific focus on *Dicranopteris*. Our findings not only contribute to the existing body of knowledge but also pave the way for several important future research directions in this field.

(1) Expand to other medicinal fern species: Our study, which focused on *Dicranopteris* in Guizhou Province, revealed a high diversity of endophytic fungi, including more than 20 new species. The potential for future discoveries is vast, as we plan to extend our research to other medicinal fern species in this region. With the rich fern biodiversity in Guizhou, we anticipate that investigating different medicinal fern hosts will uncover additional fungal species, providing a more comprehensive understanding of the fungal diversity of medicinal ferns in this area.

(2) Influence of karst ecosystems: Guizhou's unique karst formations create distinct and unparalleled ecological conditions that likely influence the distribution and diversity of endophytic fungi. Our future research will delve into how these karst landscapes impact the fungal communities in *Dicranopteris* and other ferns, potentially leading to insights into how environmental factors shape fungal diversity and distribution patterns.

(3) Exploration of novel metabolites: Endophytic fungi are known to produce bioactive metabolites with medicinal potential. Given that this study isolated 55 species, future research should focus on exploring the metabolic profiles of these fungi, particularly in medicinal plants like *Dicranopteris*. This could lead to the discovery of novel compounds with pharmaceutical applications, further emphasizing the importance of fungal diversity in drug discovery and medicinal research.

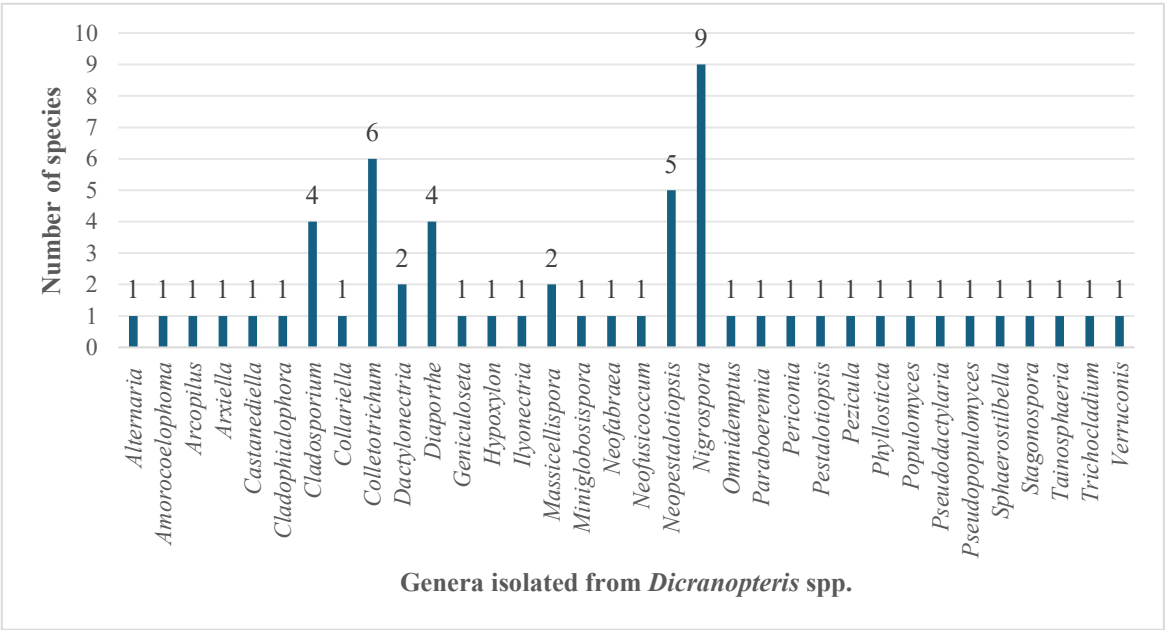


Figure 91 – The number of species in each fungal genus isolated from *Dicranopteris*

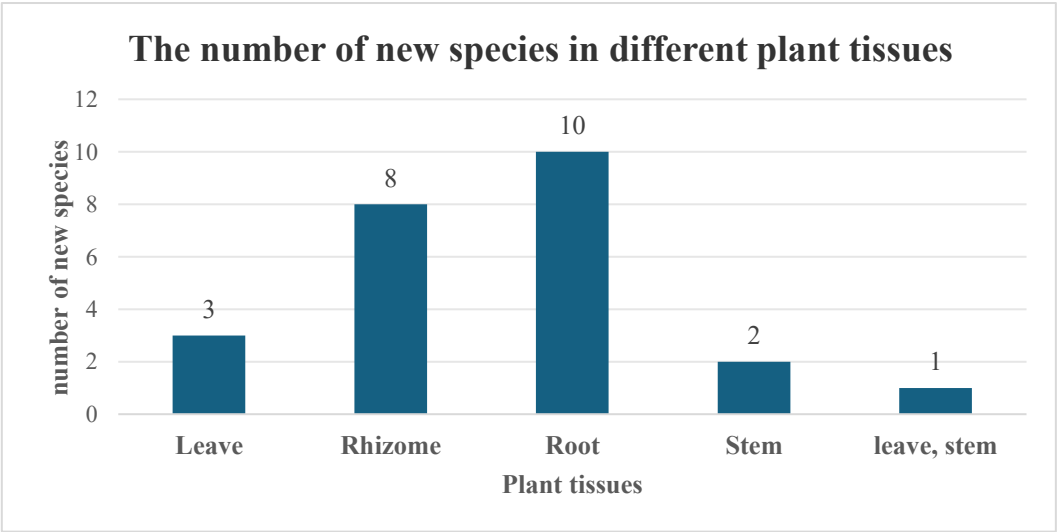


Figure 92 – The number of new species isolated from different plant tissues of *Dicranopteris*

Table 4 Checklist of fungi reported on *Dicranopteris* spp.

Species	Host	Location	References
<i>Apiospora aseptata</i>	<i>D. pedata</i>	China	Zhang et al. (2023b)
<i>A. dematiacea</i>	<i>D. ampla</i>	China	Zhang et al. (2023b)
<i>A. dicranopteridi</i>	<i>D. pedata</i>	China	Zhang et al. (2023b)
<i>A. globosa</i>	<i>D. linearis</i>	China	Zhang et al. (2023b)
<i>Bifusella anomala</i>	<i>D. dichotoma</i>	China	Lin (1994)
<i>Biscogniauxia dicranopteridis</i>	<i>D. dichotoma</i>	China	Chen et al. (2024)
<i>B. petrensis</i>	<i>D. dichotoma</i>	China	Chen et al. (2024)
<i>Dothidella portoricensis</i>	<i>D. flexuosa</i>	Colombia	Dennis (1970)
<i>Helminthosporium gleicheniae</i>	<i>D. linearis</i>	United States	Raabe (1981)
<i>Lachnella gleicheniae</i>	<i>Dicranopteris</i> sp.	United States	Haines (1980), Raabe (1981)
<i>Lachnum ulei</i>	<i>Dicranopteris</i> sp.	United States	Raabe (1981)
<i>Lanzia cremea</i>	<i>Dicranopteris</i> sp.	United States	Raabe (1981)
<i>Leptothyrium gleicheniae</i>	<i>Dicranopteris</i> sp.	United States	Raabe (1981)
<i>Lophodermium dicranopteris</i>	<i>D. dichotoma</i>	China	Liu et al. (1995)
<i>Mycosphaerella gleicheniae</i>	<i>D. linearis</i>	China (Taiwan province)	Kirschner and Liu (2014)
<i>Oberwinklerozyma dicranopteridis</i>	<i>D. dichotoma</i>	China	Li et al. (2020b)
<i>Paramycosphaerella dicranopteridis</i>	<i>D. linearis</i>	China (Fujian, Taiwan, Wuyishan)	Kirschner and Wang. (2015), Kirschner and Liu (2014), Guatimosim et al. (2016)
<i>P. dicranopteridis-flexuosae</i>	<i>D. flexuosa</i>	Brazil China (Fujian, Wuyishan, Taiwan),	Guatimosim et al. (2016)
<i>P. gleicheniae</i>	<i>D. linearis</i>	India, Malaysia	Kirschner and Liu 2014, Guatimosim et al. 2016
<i>Phytophthora cinnamomi</i>	<i>D. linearis</i>	United States	Raabe (1981)
<i>Pseudocercospora gleicheniae</i>	<i>D. linearis</i>	Gabon China	Braun et al. (2013)
<i>Teratosperma dicranopteridis</i>	<i>D. linearis</i>	(Taiwan province) China	Kirschne et al. (2019)
<i>Zasmidium dicranopteridis</i>	<i>D. linearis</i>	(Taiwan province)	Kirschner and Liu (2014)

Table 5 Endophytic fungi isolated from *Dicranopteris* in this study

Species	Host	Plant tissue	Note
<i>Alternaria longipes</i>	<i>D. pedata</i>	Leaves	
<i>Amorocoelophoma dicranopteridis</i>	<i>D. linearis</i>	Root	New species
<i>Arcopilus globulus</i>	<i>D. pedata</i>	Root	
<i>Arxiella ellipsoidea</i>	<i>D. pedata</i>	Rhizome	New species
<i>Castanediella dicranopteridis</i>	<i>D. ampla</i>	Rhizome	New species
<i>Cladophialophora globosa</i>	<i>D. ampla</i>	Rhizome	New species
<i>Cladosporium angulosum</i>	<i>D. ampla</i>	Stem	
<i>C. benschiae</i>	<i>D. pedata</i>	Leaves	
<i>C. chlamydosporiformans</i>	<i>D. ampla</i>	Stem	
<i>C. punicae</i>	<i>D. pedata</i>	Stem and leaves	
<i>Collariella pachypodioides</i>	<i>D. ampla</i>	Root	
<i>Colletotrichum dicranopteridis</i>	<i>D. ampla</i>	Leaves	New species
<i>C. fiorinae</i>	<i>D. ampla</i>	Stem	
<i>C. guttulaspore</i>	<i>D. padata</i>	Leaves	New species
<i>C. jiangxiense</i>	<i>D. ampla</i>	Leaves	
<i>C. plurivorum</i>	<i>D. ampla</i>	Leaves	
<i>C. simulanticitri</i>	<i>D. pedata</i>	Leaves	
<i>Dactylonectria dicranopteridis</i>	<i>D. pedata</i>	Rhizome	New species
<i>D. pauciseptata</i>	<i>D. linearis</i>	Rhizome	
<i>Diaporthe arecae</i>	<i>D. pedata</i>	Stem	
<i>D. dicranopteridis</i>	<i>D. pedata</i>	Stem	New species
<i>D. tulliensis</i>	<i>D. pedata</i>	Stem	
<i>D. xishuangbanica</i>	<i>D. pedata</i>	Rhizome	
<i>Geniculoseta dicranopteridis</i>	<i>D. ampla</i>	Root	New species
<i>Hypoxylon dicranopteridis</i>	<i>D. linearis</i>	Rhizome	New species
<i>Ilyonectria dicranopteridis</i>	<i>D. ampla</i>	Root	New species
<i>Massicellispora dicranopteridis</i>	<i>D. pedata</i>	Root	New species
<i>M. globosa</i>	<i>D. ampla</i>	Root	New species
<i>Miniglobosispora guizhounises</i>	<i>D. ampla</i>	Root	New species
<i>Neofabraea actinidiae</i>	<i>D. ampla</i>	Stem	
<i>Neofusicoccum sichuanense</i>	<i>D. pedata</i>	Stem	
<i>Neopestalotiopsis dicranopteridis</i>	<i>D. pedata</i>	Rhizome	New species
<i>N. piceana</i>	<i>D. pedata</i>	Leaves	
<i>N. samarangensis</i>	<i>D. pedata</i>	Leaves	
<i>N. sichuanensis</i>	<i>D. pedata</i>	Leaves	
<i>N. yongxunensis</i>	<i>D. pedata</i>	Stem	
<i>Nigrospora aurantiaca</i>	<i>D. pedata</i> , <i>D. linearis</i>	Leaves and stem	
<i>N. camelliae-sinensis</i>	<i>D. pedata</i>	Leaves	
<i>N. chinensis</i>	<i>D. pedata</i>	Leaves	

<i>N. dicranopteridis</i>	<i>D. ampla</i>	Leaves	New species
<i>N. globospora</i>	<i>D. pedata</i>	Leaves	
<i>N. musae</i>	<i>D. pedata</i>	Leaves	
<i>N. oryzae</i>	<i>D. pedata</i>	Leaves	
<i>N. pyriformis</i>	<i>D. pedata</i>	Leaves	
<i>N. stoneae</i>	<i>D. pedata</i>	Stem	
<i>Omnidemptus dicranopteridis</i>	<i>D. ampla</i>	Stem	New species
<i>Paraboeremia litseae</i>	<i>D. pedata</i>	Rhizome	
<i>Periconia dicranopteridis</i>	<i>D. pedata</i>	Root	New species
<i>Pestalotiopsis chamaeropis</i>	<i>D. pedata</i>	Stem	
<i>Pezicula dicranopteridis</i>	<i>D. pedata</i>	Stem and leaves	New species
<i>Phyllosticta capitalensis</i>	<i>D. pedata</i>	Rhizome, stem, and leaves	
<i>Populomyces barnardiae</i>	<i>D. pedata</i>	Root	
<i>Pseudodactylaria dicranopteridis</i>	<i>D. pedata</i>	Rhizome	New species
<i>Pseudopopulomyces dicranopteridis</i>	<i>D. pedata</i>	Root	New species
<i>Sphaerostilbella dicranopteridis</i>	<i>D. pedata</i>	Root	New species
<i>Stagonospora tainanensis</i>	<i>D. ampla</i>	Root, rhizome, and stem	
<i>Tainosphaeria phialogeniculata</i>	<i>D. ampla</i>	Rhizome	
<i>Trichocladium dicranopteridis</i>	<i>D. pedata</i>	Root	New species
<i>Verruconis hyalinus</i>	<i>D. pedata</i>	Rhizome	New species

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