

Taxonomy and diversity of woody litter microfungi associated with six phylogenetically related host species in Doi Tung national park, Chiang Rai, Thailand

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Abstract

Woody litter contributes to the high microbiological diversity of tropical forests, providing both habitat and nutrients. In forest environments, fungi are the most abundant microbial communities associated with woody litter, playing vital roles in the decomposition process. Diversity and abundance of fungal community are influenced by various factors, i.e., the decomposition stage, wood type, moisture content, and substrate size. This paper elaborates the study of morphology, phylogeny, host-recurrence, and diversity patterns across two seasons and three decomposition stages in saprobic microfungi associated with woody litter of *Nayariophyton zizyphifolium*, *Microcos paniculata* (Malvaceae), *Dipterocarpus alatus* (Dipterocarpaceae), *Azelia xylocarpa*, *Dalbergia cana*, and *D. cultrata* (Fabaceae) at Doi Tung national park, Chiang Rai, Thailand. Fungal communities of woody litter from these host species have not been well-investigated. Furthermore, the relationship of host

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phylogeny to wood-dwelling microfungal communities has not been established. Fungal isolates were obtained through single spore isolation, and their morphologies were characterized. Multilocus phylogenetic analyses using Maximum Likelihood (ML) and Bayesian Inference (BI), based on different gene regions specific to each taxon, were conducted to confirm species identify and taxonomic classifications. Host-recurrence of the identified fungi based on morphological and molecular data, and fungal diversity across seasons and decomposition stages were analyzed to evaluate fungal community composition. A total of 125 fungal collections were identified, representing three classes, 24 orders, 45 families, 63 genera, and 91 species (Table S1). Among these taxa, this study provides detailed taxonomic information and phylogenetic analyses for one new family, two new genera, 11 new species, five first reports of sexual or asexual morph connections, and 20 new host fungal records, additional fungal collections, habitat, and new geographical records. The newly introduced taxa are: *Chromolaenicola doitungensis*, *Colletotrichum nayariophyti*, *Corynespora Chiangraiensis*, *Cylindroconidiis doitungensis*, *Dictyoarthrinium doitungensis*, *Nemania doitungensis*, *Oxydothis dalbergiae*, *Palmiascoma Chiangraiense*, *Pisorisporium nayariophyti*, *Striaticonidium Chiangraiense*, and *Xylochrysis Chiangraiensis*. of these, *Novolignicolaceae* (*Novolignicola doitungensis*) is introduced as a new family, and *Doitungomyces* (*Doitungomyces dipterocarpi*) and *Sporicula* (*Sporicula Chiangraiensis*) as new genera. In addition, new sexual or asexual records for *Colletotrichum gigasporum*, *Cytospora heveae*, *Misturatosphaeria viridibrunnea*, *Paraconiothyrium archidendri*, and *Pseudofusicoccum kimberleyense* are described. In addition, fungal host-recurrence was also investigated. Hierarchical clustering revealed minor differences in fungal community composition across phylogenetically related hosts, with the highest specificity at the genus level. The early decomposition stage exhibited the highest diversity with distinct dominant genera. Additionally, fungal genus diversity showed distinct seasonal patterns, with more genera displaying high abundance during the dry season.

Keywords – 14 new taxa – fungal diversity – fungal community – host-recurrence – multilocus – taxonomy

INTRODUCTION

Woody litter decomposition, a vital process in forest ecosystems, is significantly influenced by fungal colonization (Blackwell 2011, Fukasawa et al. 2012, Niego et al. 2023a). Wood-inhabiting fungi, especially ascomycetes, play a crucial role in decomposing lignocellulosic material, driving nutrient cycling, and ecosystem functioning across in various habitats. Therefore, their diversity is essential to ecosystem dynamics (Treseder & Lennon 2015, Kahl et al. 2017, Sayer et al. 2020). The decomposition of forest litter represents one of the most diverse and vital functions within mycological communities (Hyde et al. 2007, 2016a). The natural structure of forests offers diverse microclimatic conditions such as differences in temperature, humidity, and substrate moisture and dynamics that support the needs of wood-decomposing fungi (Nordén et al. 2004). However, the fungal population is remarkably influenced by the diversity of plant communities, and the fungi affect plant growth through pathogenic and mutualistic behaviors, thus affecting nutrient availability and cycling (Abrego & Salcedo 2013, Tennakoon et al. 2021b, Niego et al. 2023b).

The composition of wood-inhabiting fungal communities is strongly influenced by tree (host) species (Purhonen et al. 2020), and plant species diversity has more significant impact on decomposition rates than climatic variations (Cornwell et al. 2008). The wood from diverse plant species possesses unique physical structures and chemical compositions, which vary according to the plant species, thus creating distinct microhabitats for various fungal species (Pioli et al. 2018). Rajala et al. (2010) found that the high species richness observed in broadleaved trees is primarily due to the higher diversity of Ascomycota. Although host-tree species clearly influence the composition of wood-inhabiting fungal communities, the impact of host identity on their functional composition remains largely unexplored

(Purhonen et al. 2020). The physical properties of the substrate significantly influence the diversity and abundance of woody litter fungi. For instance, woody litter consisting of individual pieces with a large diameter supports a higher abundance of species and fungal richness, whereas small-diameter twigs and branches provide suitable substrates for common fungal species (Bässler et al. 2010). Yang et al. (2022a) showed that fungal alpha diversity differed across tree species and stem compartments, with higher diversity in bark than wood. Also, Gymnosperms and angiosperms had distinct fungal communities, and stem chemistry and density were important factors shaping fungal community structure in decaying stems. Based on the capabilities of different fungal species to decompose lignocellulose, wood decomposition by fungi is categorized into three types of decay: white-rot, brown-rot, and soft-rot (Fukasawa 2012). Fungi change the wood during decomposition and cause changes in microscopic traits, decayed wood colour, and corresponding loss of acid unhydrolyzable residue (AUR) and holocellulose (Fukasawa et al. 2009). Fungal population varies with the progression of the decomposition process (Fukasawa & Matsukura 2021) due to changes in wood decay, such as fluctuations in lignin (Hoppe et al. 2016, Arnstadt et al. 2016), and other chemical content. The lignin content of woody substrates is influenced by both tree species and the degree of wood decomposition (Hoppe et al. 2016). High lignin content hinders the decay process by serving as a barrier that limits the penetration of enzyme molecules into the lignocellulose complex (Kahl et al. 2017). In addition to releasing energy and nutrients, wood dwelling fungi, in terrestrial and stream ecosystems fix significant amounts of nitrogen and significantly impact on carbon storage in forest ecosystems (Harmon et al. 1986).

“Host-specificity” is a concept initially adopted by plant pathologists (Rapilly 1998) that has frequently been applied in mycology to show a communal or unique fungal occurrence on a specific host compared to other hosts (Malvick et al. 1998, Augustin et al. 1999, Promputtha et al. 2017, Tennakoon et al. 2021a, b, Samaradiwakara et al. 2025). Zhou & Hyde (2001) proposed the terms “host-recurrence” and “host-exclusivity” for fungal use instead of using “host-preference”. Host-specificity may not be suitable for saprobes unless they have a symbiotic phase, such as endophytes, at some point in their life cycle. Therefore, they stated that host-recurrence is an appropriate term regarding the saprobe-plant interactions. Host-exclusivity, as defined by Zhou & Hyde (2001), refers to the occurrence of a strictly saprobic fungus on a specific host or a limited range of related host plants. They described host-recurrence as the frequent or predominant presence of a symbiotic, parasitic, or saprobic fungus on a particular host or a range of hosts while also being present on other host plants within the same habitat. Likewise, Mukwevho et al. (2020) referenced Zhou & Hyde (2001) in explaining host-exclusivity and recurrence in saprobic fungi. They also remarked that instead of being host-specific, these fungi are classified as either host-exclusive growing on material derived from a particular host or a limited range of related hosts- or host-recurrent. This refers to fungi that predominantly grow on material from a specific host but can also be found on material from other hosts within the same habitat (Mukwevho et al. 2020). Numerous saprobic fungal species exhibit strong preferences for decaying material originating from specific host plant species or families; however, it remains unconfirmed whether these fungi are exclusively linked to those particular hosts. Bhunjun et al. (2024) has suggested that most ascomycetes have an endophytic ancestor and this may be the reason the saprobic are host-specific or host-preferential. The recurrence of saprobic fungi associated with hosts has been investigated in leaf litter on forest floors (Lodge & Cantrell 1995, Ferrer & Gilbert 2003, Tennakoon et al. 2021a). Huhndorf & Lodge (1997) reported low host specificity of wood-inhabiting ascomycetes in a subtropical wet forest in Puerto Rico. This concept provides a framework for understanding fungal-host associations, however, studies on how phylogenetically related host species influence wood decomposer microfungi and the significance of such ‘preferences’ remain limited.

The term “biodiversity” was first introduced in the literature by Wilson (1988). It is a complex multidimensional concept. Biodiversity is a contraction of “biological diversity”, encompassing all of biotic variation from genetic differences to the entire ecosystems (Purvis & Hector 2000). Biodiversity

is frequently defined as “Biological diversity means the variability among living organisms from the ecological complexes of which organisms are part, and it is defined as species richness and relative species abundance in space and time” (Schloss & Handelsman 2006). Traditionally, community composition has been described by the number and abundance of species. In recent studies of biodiversity, trait and evolutionary (phylogenetic diversity) patterns as well as temporal analyses are providing deeper insights into the ecological and evolutionary mechanisms (Purvis & Hector 2000, Pavoine & Bonsall 2011). Diversity indices (Shannon-Weaver, Simpson, Fisher’s alpha) are mathematical tools that combine species richness and evenness into a single value. Shannon index being the most commonly used species diversity indices used in ecology (Colwell 2009). Beta diversity, defined as the difference in species composition (species presence/absence or abundance data) among different sites (Whittaker 1960, 1972). The concept of community resemblance is fundamental in ecology. It allows researchers to quantify changes in community composition over time (De Caceres et al. 2013).

This study investigates woody litter microfungi associated with six phylogenetically related host species in Doi Tung National Park, Chiang Rai, Thailand. It examines the host-recurrence and community composition of isolated fungi during wet and dry seasons and three different decomposition stages. A hierarchical selection of hosts is applied to evaluate whether closely related hosts have similar fungal communities, with the aim of understanding patterns of recurrence and ecological adaptation. The objectives of this study are: 1) to characterize and document new fungal taxa, update new host and geographical records associated with woody litter of six phylogenetically related hosts based on morphology and molecular phylogeny, 2) to address the existing knowledge gaps in the host-recurrence of woody litter microfungi, 3) to explore diversity patterns across two seasons and three decomposition stages. By integrating host phylogeny, seasonal variation, and decomposition stages, this study provides new insights into the ecological factors that shape fungal community and their roles in litter decomposition within a conserved tropical forest ecosystem.

MATERIALS AND METHODS

Study site, sample collection, fungal isolation, and morphological examination

Hanging or fallen dead branches of selected host plants were collected three times at three-month intervals during March 2022 (dry season) and June and September 2022 (wet season) in Doi Tung National Park, Chiang Rai Province, Thailand (temperature range: 25–33 °C). Doi Tung is a rehabilitated nature reserve in Mae Fah Luang and Mae Sai districts. This mountainous highland, with Permian limestone bedrock covers approximately 150 km² ranging from 400–1,500 m altitude (Maxwell 2007, Khamyong et al. 2014). A total of 10–30 samples per tree (30–90 per host, depending on tree size) were collected in each collection, with sample sizes ranging from 20–40 cm in length and 0.5–5 cm in diameter randomly and subsequently classified into three decomposition stages (recently fallen, middle, and late) based on their visual characteristics observed during examination. Six phylogenetically related host plant species were selected *Azelia xylocarpa* (Kurz) Craib (Fabaceae), *Dalbergia cana* Graham ex Kurz. (Fabaceae), *D. cultrata* T.S.Ralph (Fabaceae), *Dipterocarpus alatus* Roxb. ex G. Don (Dipterocarpaceae), *Microcos paniculata* L. (Malvaceae), and *Nayariophyton zizyphifolium* (Griff.) D.G.Long & A.G.Mill (Malvaceae) (Figs. 1, 2). Specimens from each tree were sorted into separate Ziploc bags and taken to the mycology laboratory at Mae Fah Luang University, Thailand. In the laboratory, all samples were transferred into paper envelopes to prevent contamination. The macro-morphological characteristics of fungi were examined using an Olympus SZX16 stereo microscope (Olympus Corporation, Tokyo, Japan). The micro-morphological features were observed with a Nikon ECLIPSE Ni (Nikon, Tokyo, Japan) and photographed using a mounted Canon EOS 600 D digital camera (Tokyo, Japan). Fungal structures were picked using a needle and mounted in distilled water on microscope slides for photomicrography.

All micro-morphological structures were measured using the Tarosoft^(R) v.09 Image Frame Work program and measurements are reported as the range minimum, maximum and the average value. Images were processed for creating photo plates using Adobe Photoshop CS6 software v.13 (Adobe Systems, San Jose, CA, USA). Axenic cultures were obtained through single spore isolation following the methods outlined by Senanayake et al. (2020). Germinating spores were photographed and individually transferred to potato dextrose agar (PDA) (39 g/L distilled water, Difco potato dextrose) or malt extract agar (MEA) (50 g/L distilled water) plates and incubated at room temperature (24–28 °C) in daylight for one week. Culture characteristics, such as growth rate and colony colour, texture and shape were determined from cultures on PDA. Herbarium materials were deposited in the Mae Fah Luang University Fungarium (MFLU), Chiang Rai, Thailand. Representative living cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC). Faces of Fungi numbers and Index Fungorum numbers were obtained for fungal novelties as described in Jayasiri et al. (2015) and Index Fungorum (2025). Data on the fungal taxa are deposited in the Greater Mekong Subregion fungal database (Chaiwan et al. 2021).

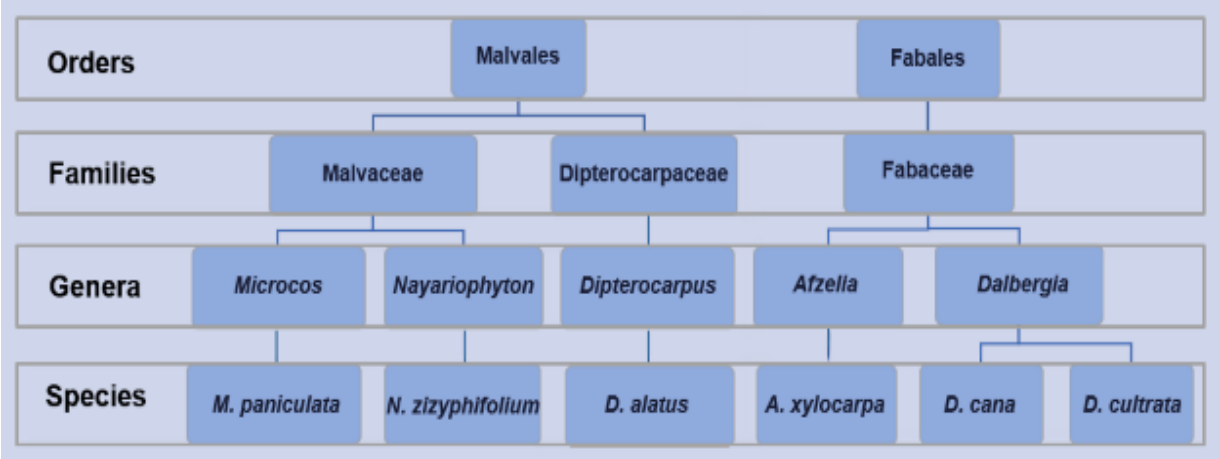


Figure 1 – Selected phylogenetically related host species in the experimental design.

DNA extraction, PCR amplification, and sequencing

Fresh mycelia were scraped from colonies grown on PDA plates and genomic DNA was extracted using the PureDirex Genomic DNA Isolation Kit (Bio-Helix Co., Keelung City) following the manufacturer’s instructions. Extracted DNA was kept at –20 °C for long-term storage. Polymerase chain reaction (PCR) was performed in a 25 µl reaction volume containing 12.5 µl of Mix2×QinKe PCR Master Mix, 2 µl (30–600 ng) DNA template, 1 µl of 20 picomolar for each forward and reverse primers and 8.5 µl double-sterilized water to amplify different gene regions. DNA purity was assessed by NanoDrop One^c spectrophotometer (Thermo Fisher Scientific, USA). The genes and primers utilized in this research are presented (Table 1). PCR amplification products were visualized on 1.5% agarose gel stained with DL5000 DNA Fluorescent Loading Dye (FluoroDyeTM Green, 6×, Hsinchu). The amplified PCR products were purified and sequenced by Biogenomed Co., (Seoul, Republic of Korea). All generated nucleotide sequences were deposited in GenBank and accession numbers are mentioned in this paper.

Alignments and phylogenetic analyses

The raw sequences were assembled using SeqMan Version 7.1.0 (DNASar Inc., Madison, WI, USA). They were compared against the NCBI nucleotide non-redundant GenBank database (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) and recent publications for selection of the most closely related

taxa. All sequences of representative taxa were downloaded and used for phylogenetic analysis. Individual gene sequence alignment used MAFFT v.7 online program (<http://mafft.cbrc.jp/alignment/server/>, Katoh et al. 2019) and were automatically trimmed using TrimAl v.1.3 with the *-gt* (0.3), *-gt* (0.5), *-gt* (0.7), or *gappyout* options (Capella-Gutierrez et al. 2009). Multigene datasets were concatenated using Sequence Matrix v.1.8 (Vaidya et al. 2011).

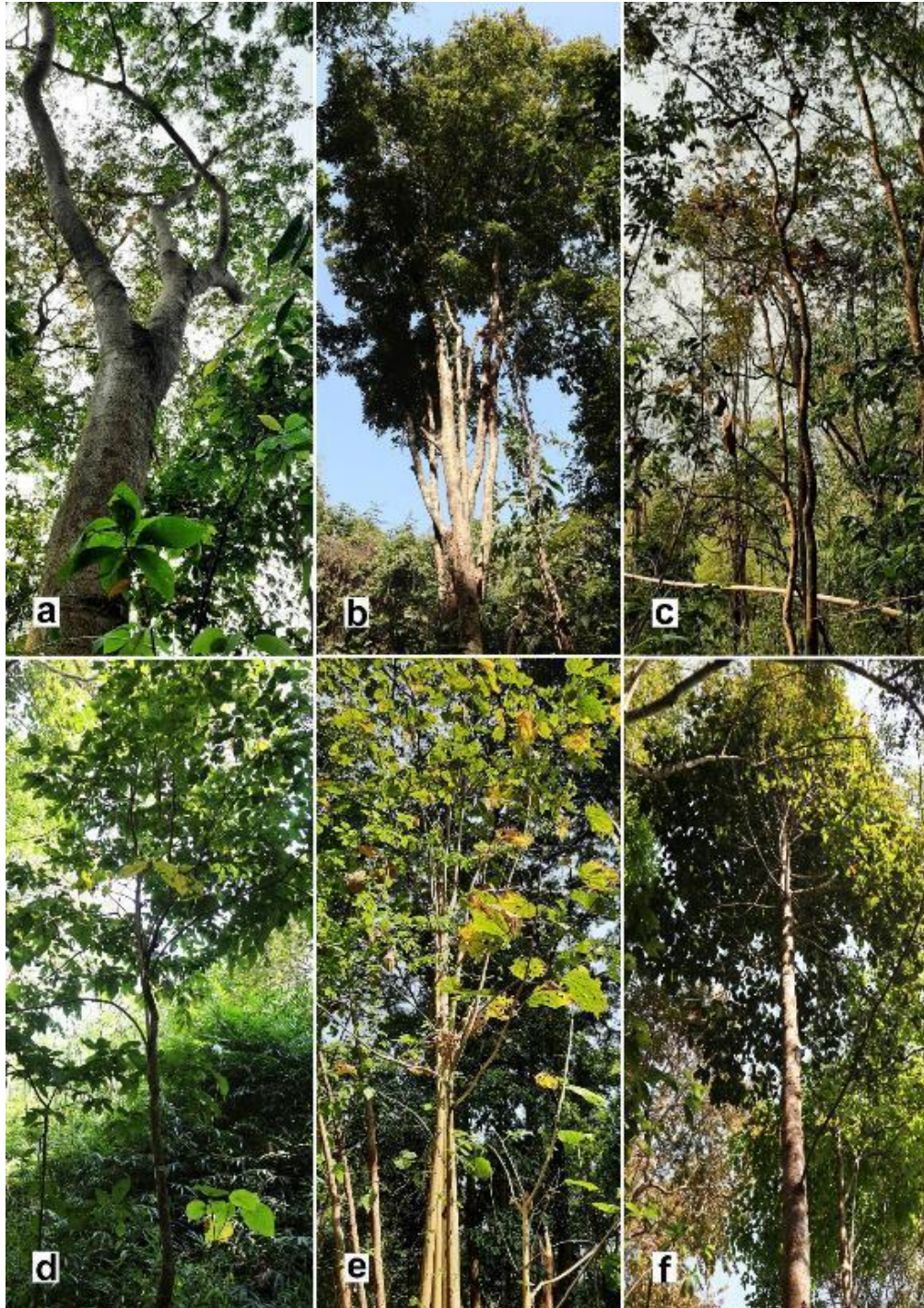


Figure 2 – Host plant species selected in this study. a *Afzelia xylocarpa*. b *Dalbergia cana*. c *Dalbergia cultrata*. d *Microcos paniculata*. e *Nayariophyton zizyphifolium*. f *Dipterocarpus alatus* at the Doi Tung National Park.

The combined sequences were subjected to maximum likelihood (ML) and Bayesian inference (BI) analyses. ML trees were constructed in the online CIPRES Science Gateway platform (<http://www.phylo.org/portal2/>, Miller et al. 2010), using RAXML-HPC2 on XSEDE (8.2.12) (Stamatakis 2014) with parameters set for 1,000 bootstrap replications and applying the GTRGAMMA substitution model, and also using the IQ-TREE v. 1.6.10 web server (Trifinopoulos et al. 2016) with branch supports reported as 1,000 Ultrafast Bootstraps (UFBoot). The most optimal model of nucleotide evolution was selected by ModelFinder within IQ-TREE (Kalyaanamoorthy et al. 2017). BI was generated using MrBayes v. 3.2.7a with four simultaneous Markov chain Monte Carlo (MCMC) chains and four runs (Ronquist et al. 2012). To determine Bayesian posterior probabilities the first 25% of trees were discarded as burn-in. The consensus tree was visualized with FigTree v.1.4.4 (Rambaut 2015) and edited using the open-source Inkscape v.1.3 (<https://inkscape.org/>).

Table 1 – Details of genes/loci and primers.

Gene/Locus	Primer (forward/reverse)	Reference
ITS	ITS5/ ITS4	White et al. (1990)
LSU	LR0R/ LR5	Vilgalys & Hester (1990)
SSU	NS1/ NS4	White et al. (1990)
<i>act</i>	ACT-512F/ ACT-783R	Carbone & Kohn (1999)
<i>chs-1</i>	CHS-79F/ CHS-345R	Carbone & Kohn (1999)
<i>gapdh</i>	GDF/ GDR	Templeton et al. (1992)
<i>rpb2</i>	fRPB2-5F/ fRPB2-7cR	Liu et al. (1999)
<i>tefl-α</i>	EF1-983F/ EF1-2218R	Rehner & Buckley (2005)
	EF1-728F/ EF1-986R	Carbone & Kohn (1999)
<i>tub2</i>	T1/ T22	O'Donnell et al. (2010)
	Bt2a/ Bt2b	Glass & Donaldson (1995)
	T1/ Bt2b	Glass & Donaldson (1995)

Genealogical concordance phylogenetic species recognition analysis

The pairwise homoplasy index (PHI) test was conducted for the combined sequence dataset of closely related species using Split Tree version 4.18.2 (Huson & Bryant 2006) to evaluate the recombination level within phylogenetically related species using multilocus genes including gaps. The results were demonstrated by constructing a split diagram using the splits decomposition and LogDet transformation possibility.

Diversity metrics and statistical analysis

The community diversity of isolated and identified fungi, based on molecular identification and morphological characteristics, was assessed using alpha and beta diversity indices. This was carried out as we could not accurately identify collections based on morphology alone. The Shannon diversity index was calculated to evaluate the alpha diversity of fungal genera and species associated with different phylogenetically related host tree species. This index quantifies species diversity by accounting for both the richness and evenness of taxa within each host tree. The analysis was performed using R Project for Statistical Computing (version 4.0.2, R Core Team 2020). The vegan package (version 2.6-4, Oksanen et al. 2024) was used to compute this analysis. The calculated diversity values were visualized as a heatmap using the *pheatmap* package (version 1.0.12, Kolde 2019) to provide a clear graphical representation of diversity patterns across host trees.

Beta diversity analysis was applied to explore fungal diversity patterns related to seasonal and decomposition level differences, as well as host-recurrence among phylogenetically related host trees. For beta diversity evaluation, the Bray-Curtis dissimilarity index was calculated using the *vegdist* function from the *vegan* package (Oksanen et al. 2024). This method captures variations in fungal composition by considering both the presence/absence and the relative abundance of isolated fungal species. To assess the similarity in fungal communities associated with different host trees, hierarchical cluster analysis (HCA) was conducted using the *hclust* function in R, implemented with the Bray-Curtis distance measure from the *vegan* package. Hierarchical clustering was visualized with dendrograms to illustrate patterns of similarity (Similarity = 1 – Dissimilarity) across fungal taxa.

To analyze fungal diversity patterns further, hierarchical clustering using Ward's D2 method was performed with the *gplots* (version 3.1.3, Warnes et al. 2020) packages. Heatmaps were generated using the *pheatmap* package (Kolde 2019) to present trends and clustering results visually. Heatmaps employed a colour gradient (green, yellow, and red) to indicate levels of diversity, corresponding to lower, moderate, and higher diversity, respectively.

For additional visualization, Venn diagrams were constructed using R to depict the overlap of fungal genera between two orders, three families, and five host genera. A Jaccard heatmap was also generated using the *vegan* package to assess pairwise similarities among groups based on the presence/absence of taxa. The heatmap complemented the insights from the Venn diagram, illustrating relationships and clustering among the groups.

Finally, a sunburst graph of fungal communities was created using Microsoft Excel (2010) to visualize relative abundance data.

RESULTS

Phylogenetic analyses and taxonomy

Based on polyphasic approaches that included isolation and molecular data, we identified one new family, two new genera, 11 new species, five first reports of sexual or asexual morphs, and 20 additional collection and new host and geographical records (Table 2). Phylogenetic trees, photo plates, and descriptions for all taxa are presented below, organized according to the classification outlined by Hyde et al. (2024a).

Ascomycota Caval. -Sm.

Dothideomycetes O.E. Erikss. & Winka

Acrospermales Minter, Peredo & A.T. Watson

Acrospermales was established by Minter et al. (2007) as an *incertae sedis* taxon. It was placed in an independent lineage that was closely related both *Dothideomycetes* and *Arthoniomycetes* (Stenroos et al. 2010). Later, Pang et al. (2013) assigned *Acrospermales* to *Dothideomycetes* based on phylogenetic analysis of partial SSU, LSU, and *tefl*- α sequences. *Acrospermales* represents one of the least studied orders of *Dothideomycetes* and includes epiphytic, saprotrophic, fungicolous, lichenicolous, and bryophilous species. The ordinal placement of *Acrospermaceae* has been disputed for a long time (Hudson et al. 2019, Darmostuk & Flakus 2024). In this study, we introduced a new family *Novolignincolaceae* to accommodate the new genus *Novolignincola* based on the specimens collected from dead wood in Thailand.

Novolignincolaceae N. Afshari, Lumyong & K.D. Hyde, fam. nov.

Index Fungorum number: IF904726; Facesoffungi number: FoF17215

Etymology – The name is derived from "*Novoligni*-" and "-*cola*", referring to the wood-dwelling fungus.

Type genus – *Novolignincola* N. Afshari, Lumyong & K.D. Hyde

Notes – *Novolignicolaceae* is established here to accommodate a monotypic genus, *Novolignincola*, which comprises two strains of *Novolignincola doitungensis*. Phylogenetic analysis, which included updated species of *Acrospermales*, as outlined by Hyde et al. (2024a), indicated that the new family formed a well-supported basal clade within *Acrospermales* (Fig. 4), with 98% ML and 1.0 PP values. *Novolignincola* is distinguished by its multilocular pycnidial conidiomata, and fusoid to falcate, curved conidia with an apical appendage at maturity.

Novolignincola N. Afshari, Lumyong & K.D. Hyde, gen. nov.

Index Fungorum number: IF904738; Facesoffungi number: FoF17216

Etymology – The generic name refers to the wood-dwelling fungus.

Holotype – MFLU 24-0456

Type species – *Novolignincola doitungensis* N. Afshari, Lumyong & K.D. Hyde

Saprobic on dead branches of *Afzelia xylocarpa*. Sexual morph: Undetermined. Asexual morph: *Coelomycetous*. Conidiomata multilocular, pycnidial, embedded in the stromatic tissue, dark brown to black, scattered, solitary or in clusters, immersed or semi-immersed, erumpent, sub-globose, coriaceous. Conidiomata wall composed of dark brown to hyaline towards the inner region, with cells of mostly *textura angularis* to *textura globulosa*, upper conidiomatal layer darkened and thickened, inner layers thin-walled. Paraphyses subcylindrical, hyaline, smooth-walled, septate, not branched or sparingly branched. Conidiophores reduced to conidiogenous cells. Conidiogenous cells sub-cylindrical to doliiform, monophialidic, smooth-walled, hyaline, percurrently proliferate or with periclinal thickening at apex. Conidia fusoid to falcate, curved, 10–15-septate with an apical appendage at maturity, hyaline, finely verruculose, thick-walled, rounded to truncate at base. Based on the description and phylogeny, herein we introduce *Novolignincola doitungensis* as a novel saprobic species from *Afzelia xylocarpa* woody litter from Thailand.

Novolignincola doitungensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 4

Index Fungorum number: IF904737; Facesoffungi number: FoF17217

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which it was collected.

Holotype – MFLU 24-0456

Saprobic on dead branches of *Afzelia xylocarpa*. Sexual morph: Undetermined. Asexual morph: *Coelomycetous*. Conidiomata $116\text{--}186 \times (154\text{--})181\text{--}240\text{ }\mu\text{m}$ ($\bar{x} = 150 \times 210\text{ }\mu\text{m}$, $n = 10$), pycnidial, multilocular, embedded in the stromatic tissue, scattered, solitary or in clusters, immersed or semi-immersed, erumpent, mainly sub-globose, dark brown to black, coriaceous. Conidiomatal wall (33–)37–56(–60) μm wide ($\bar{x} = 48\text{ }\mu\text{m}$, $n = 30$), composed of two to three layers, dark brown to hyaline towards the inner region, with cells of *textura angularis* to *textura globulosa*, upper conidiomatal layer darkened and thickened, inner layers thin-walled. Paraphyses subcylindrical, smooth-walled, hyaline, septate, not branched or sparingly branched. Conidiophores reduced to conidiogenous cells. Conidiogenous cells $6.6\text{--}11 \times 2.4\text{--}4\text{ }\mu\text{m}$ ($\bar{x} = 3.3 \times 8.6\text{ }\mu\text{m}$, $n = 30$), sub-cylindrical to doliiform, monophialidic, smooth-walled, hyaline, percurrently proliferate or with periclinal thickening at apex. Conidia $45\text{--}82 \times 8\text{--}12.5\text{ }\mu\text{m}$ ($\bar{x} = 70 \times 10\text{ }\mu\text{m}$, $n = 30$; L/W ratio = 7), fusoid to falcate, curved, 10–15-septate with an apical appendage at maturity, hyaline, finely verruculose, thick-walled, rounded to truncate at base.

Table 2 – Microfungi identified on woody litter from six different hosts.

Class	Order	Family	Species	Host species
<i>Dothideomycetes</i>	<i>Acrospermales</i>	<i>Novolignincolaceae</i>	<i>Novolignicola doitungensis</i>	<i>Afzelia xylocarpa</i>
		<i>Botryosphaeriaceae</i>	<i>Diplodia guttulata</i>	<i>Microcos paniculata</i>
			<i>Lasiodiplodia magnoliae</i>	<i>Dalbergia cultrata</i>
			<i>Pseudofusicoccum adansoniae</i>	<i>Dipterocarpus alatus</i>
		<i>Phyllostictaceae</i>	<i>Pseudofusicoccum kimberleyense</i>	<i>Dipterocarpus alatus</i>
	<i>Dyfrolomycetales</i>	<i>Pleurotremataceae</i>	<i>Melomastia thamplaensis</i>	<i>Nayariophyton zizyphifolium</i>
	<i>Pleosporales</i>	<i>Bambusicolaceae</i>	<i>Palmiascoma chiangraiense</i>	<i>Dipterocarpus alatus</i>
		<i>Corynesporascaceae</i>	<i>Corynespora chiangraiensis</i>	<i>Nayariophyton zizyphifolium</i>
		<i>Didymosphaeriaceae</i>	<i>Chromolaenicola doitungensis</i>	<i>Nayariophyton zizyphifolium</i>
			<i>Dictyoarthrinium doitungensis</i>	<i>Nayariophyton zizyphifolium</i>
			<i>Paraconiothyrium archidendri</i>	<i>Dipterocarpus alatus</i>
		<i>Fusculinaceae</i>	<i>Sporicula chiangraiensis</i>	<i>Microcos paniculata</i>
		<i>Hermatomycetaceae</i>	<i>Hermatomyces indicus</i>	<i>Dalbergia cana</i>
		<i>Massarinaceae</i>	<i>Helminthosporium chiangraiense</i>	<i>Afzelia xylocarpa</i>
			<i>Helminthosporium erythrinicola</i>	<i>Dalbergia cana</i>
		<i>Neomassariaceae</i>	<i>Neomassaria thailandica</i>	<i>Microcos paniculata</i>
		<i>Roussoellaceae</i>	<i>Pararoussoella lincangensis</i>	<i>Dalbergia cana</i>
		<i>Teichosporaceae</i>	<i>Misturatosphaeria viridibrunnea</i>	<i>Microcos paniculata/</i>
				<i>Dipterocarpus alatus</i>

Class	Order	Family	Species	Host species
<i>Eurotiomycetes</i>	<i>Sclerococcales</i>	<i>Dactylosporaceae</i>	<i>Cylindroconidiis doitungensis</i>	<i>Microcos paniculata</i>
<i>Sordariomycetes</i>	<i>Amphisphaeriales</i>	<i>Oxydothidaceae</i>	<i>Oxydothis dalbergiae</i>	<i>Dalbergia cana</i>
	<i>Barbatosphaeriales</i>	<i>Barbatosphaeriaceae</i>	<i>Barbatosphaeria lignicola</i>	<i>Dipterocarpus alatus</i>
	<i>Chaetosphaeriales</i>	<i>Linocarpaceae</i>	<i>Claviformispora phyllostachydis</i>	<i>Nayariophyton zizyphifolium</i>
	<i>Conioscyphales</i>	<i>Conioscyphaceae</i>	<i>Conioscypha Chiangmaiensis</i>	<i>Microcos paniculata</i>
	<i>Diaporthales</i>	<i>Cryphonectriaceae</i>	<i>Doitungomyces dipterocarpi</i>	<i>Dipterocarpus alatus</i>
		<i>Cytosporaceae</i>	<i>Cytospora heveae</i>	<i>Microcos paniculata</i>
	<i>Diaporthomycetidae</i>			
	families incertae sedis	<i>Woswasiaceae</i>	<i>Xylochrysis Chiangraiensis</i>	<i>Dipterocarpus alatus</i>
	<i>Glomerellales</i>	<i>Glomerellaceae</i>	<i>Colletotrichum durionigenum</i>	<i>Dalbergia cultrata</i>
			<i>Colletotrichum nayariophyti</i>	<i>Nayariophyton zizyphifolium</i>
			<i>Colletotrichum gigasporum</i>	<i>Dalbergia cultrata</i>
		<i>Trichosphaeriaceae</i>	<i>Chordomyces zizyphifolii</i>	<i>Nayariophyton zizyphifolium</i>
	<i>Hypocreales</i>	<i>Myrotheciomycetaceae</i>	<i>Trichothecium roseum</i>	<i>Dalbergia cultrata</i>
		<i>Stachybotryaceae</i>	<i>Striaticonidium Chiangraiense</i>	<i>Nayariophyton zizyphifolium</i>
	<i>Pisorisporiales</i>	<i>Pisorisporiaceae</i>	<i>Pisorisporium nayariophyti</i>	<i>Nayariophyton zizyphifolium</i>
	<i>Xylariales</i>	<i>Xylariaceae</i>	<i>Nemania doitungensis</i>	<i>Nayariophyton zizyphifolium</i>

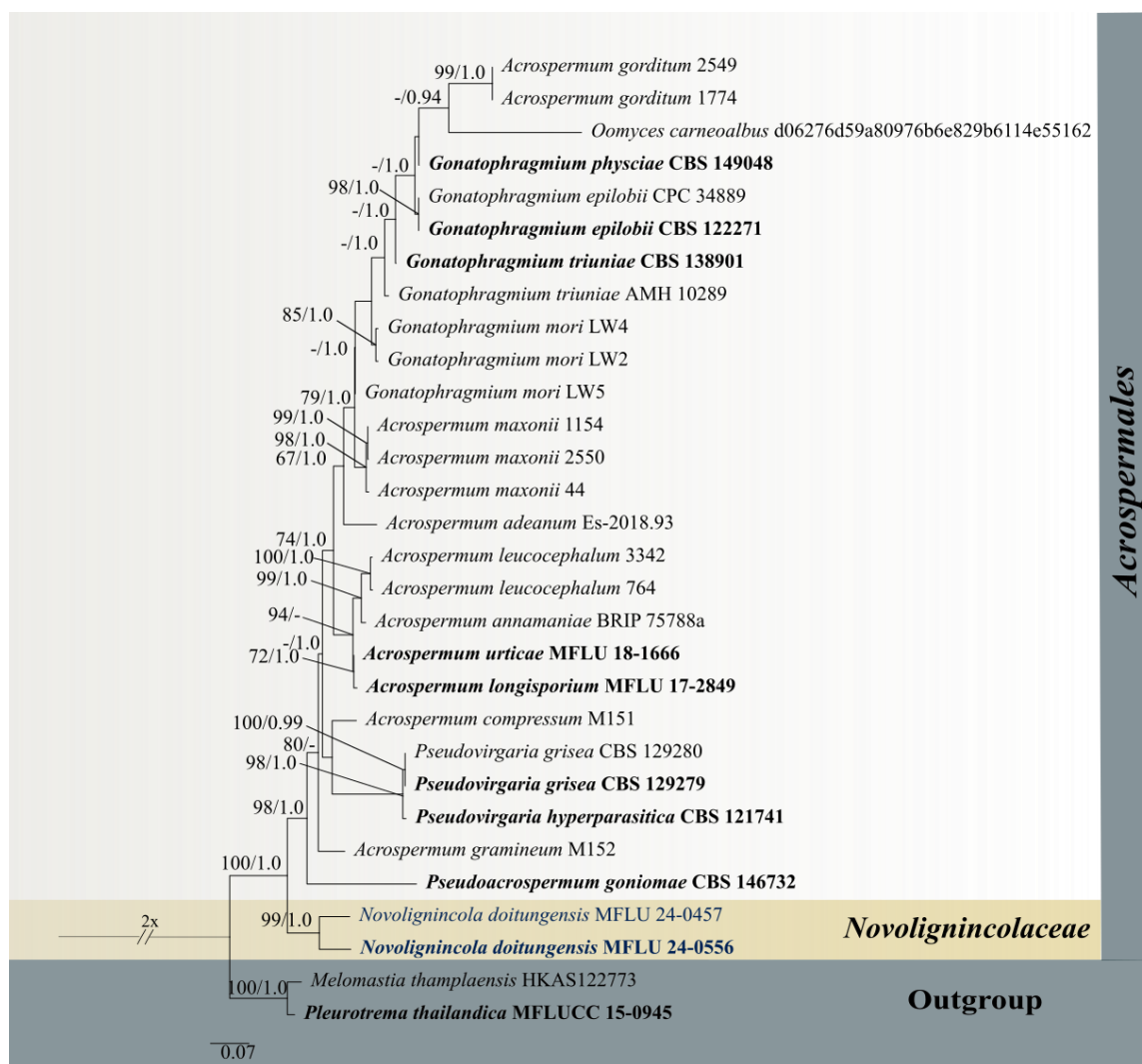


Figure 3 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, SSU, and *tefl*- α sequence data of *Acrospermales*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Thirty strains are included in the combined analyses which comprised 4,070 characters (ITS = 899, LSU = 819, SSU = 1,012, and *tefl*- α = 1,340). The best RAxML tree with a final optimization likelihood value of -16601.309265 is presented. The matrix had 1,121 distinct alignment patterns, with 55.18% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.235876, C = 0.251920, G = 0.297722, T = 0.214482; substitution rates AC = 1.363859, AG = 3.486811, AT = 1.678802, CG = 1.530311, CT = 4.831437, GT = 1.000000; gamma distribution shape parameter α = 0.358028. In the Bayesian analysis, average standard deviation of split frequencies at the end of 4,000,000 MCMC generations was calculated as 0.002586. The evolutionary models TIM1+I+G was applied to LSU, and TIM2+G were applied to ITS, SSU, and *tefl*- α sequence data. Bootstrap support values for ML greater than or equal to 60%, and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Melomastia thamplaensis* (HKAS122773), and *Pleurotrema thailandica* (MFLUCC 15-0945). Ex-type strains are in bold. The isolates generated in this study are indicated in blue.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerges from end cells. Colonies on PDA reaching 0.5–1 mm diam. after 14 days at room temperature (25–28 °C), irregular, raised, dense, felty or woolly, margin lobulated, grey at center, dark brown periphery, reverse: dark grey, dark brown at periphery, lobate margin.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Azelia xylocarpa* (Fabaceae), 26 March 2022, N. Afshari, 5C1T1R2 (MFLU 24-0456, holotype); ex-type living culture MFLUCC 24-0560; 4C1T1R3a (MFLU 24-0457, paratype).

GenBank numbers – MFLU 24-0456: ITS = PQ800246, LSU = PV072601, SSU = PV072694, *tefl-α* = PX739634. MFLU 24-0457: ITS = PQ800247, LSU = PV072602, SSU = PV072695, *tefl-α* = PX739635.

Notes – The phylogenetic tree of *Ascospermales* taxa based on combined ITS–LSU–SSU–*tefl-α* sequence data revealed two strains of *Novolignicola doitungensis* (MFLU 24-0457 and MFLU 24-0456) formed a distinct and basal clade to other taxa in the order (Fig. 3). We were not able to compare the morphological characters with *Acrospermum* and *Oomyces* genera as they are sexual taxa (Darmostuk & Flakus 2024). *Gonatophragmium* species have small, 1-septate conidia (Crous et al. 2014b), *Pseudoacrospermum* can be distinguished with multi-septate conidia (Crous et al. 2021), and *Pseudovirgaria* has aseptate, ovoid conidia (Braun et al. 2011). All reported asexual taxa are hyphomycetous and there is no morphological and molecular evidence to suggest that *Novolignicola* can be linked to the existing members of *Acrospermales*. Hence, based on unique morphological characteristics and multigene phylogeny, we established a new family (*Novolignicolaceae*) in *Acrospermales* and introduce *Novolignicola* as its type genus to accommodate the new species *N. doitungensis*.

***Botryosphaeriales* C.L. Schoch, Crous & Shoemaker**

***Botryosphaeriaceae* Theiss. & H. Syd. (= *Endomelanconiopsidaceae* Tao Yang & Crous)**

Theissen & Sydow (1918) introduced *Botryosphaeriaceae* to accommodate three genera, *Botryosphaeria*, *Dibotryon*, and *Phaeobotryon*. *Botryosphaeriaceae* is the largest monophyletic family, comprising 23 genera (Hyde et al. 2024a). SSU, ITS, LSU, *tefl-α*, and *tub2* sequence data are required for defining new species and genera in this family (Phillips et al. 2013). *Botryosphaeria* is the type genus in this family. Extensive hidden diversification within major genera in this family have been confirmed by proportional genomic analyses across *Botryosphaeriales*, which have increasingly clarified evolutionary affinities at genus and species levels (Deng et al. 2025). With numerous new host associations and geographic records reported for *Diplodia* and related genera, recent regional investigations based on multilocus phylogenetic analyses continue to expand the recognized diversity of *Botryosphaeriaceae* (Kurt et al. 2025). Members of this family have diverse lifestyles (saprobic, endophytic, and plant pathogenic) (Phillips et al. 2013, Hua et al. 2024), and are commonly associated with the decay of many woody plants with economic importance (Belair et al. 2022, Wang et al. 2024a).

***Diplodia* Fr.**

Index Fungorum number: IF8047; Facesoffungi number: FoF00147

Diplodia was erected by Montagne (1834), with *D. mutila* as the type species. *Diplodia* species exhibit pathogenic, saprobic, or endophytic lifestyles, affecting a wide variety of woody hosts, and are distributed worldwide (Crous et al. 2006, Slippers & Wingfield 2007, Jayawardena et al. 2019a). Both sexual and asexual morphs have been reported (Dissanayake et al. 2016). Two distinct conidial morphologies have been observed. In one type, conidia start as hyaline and

aseptate, later transitioning to pale to dark brown and one-septate. In the other type, conidia become pigmented in their development, sometimes remaining aseptate even while enclosed within the pycnidia (Phillips et al. 2005, 2012). There are approximately 600 species of *Diplodia* recorded in Species Fungorum (2025). In this study, we report an additional collection of *Diplodia guttulata* from woody litter of *Microcos paniculata*.

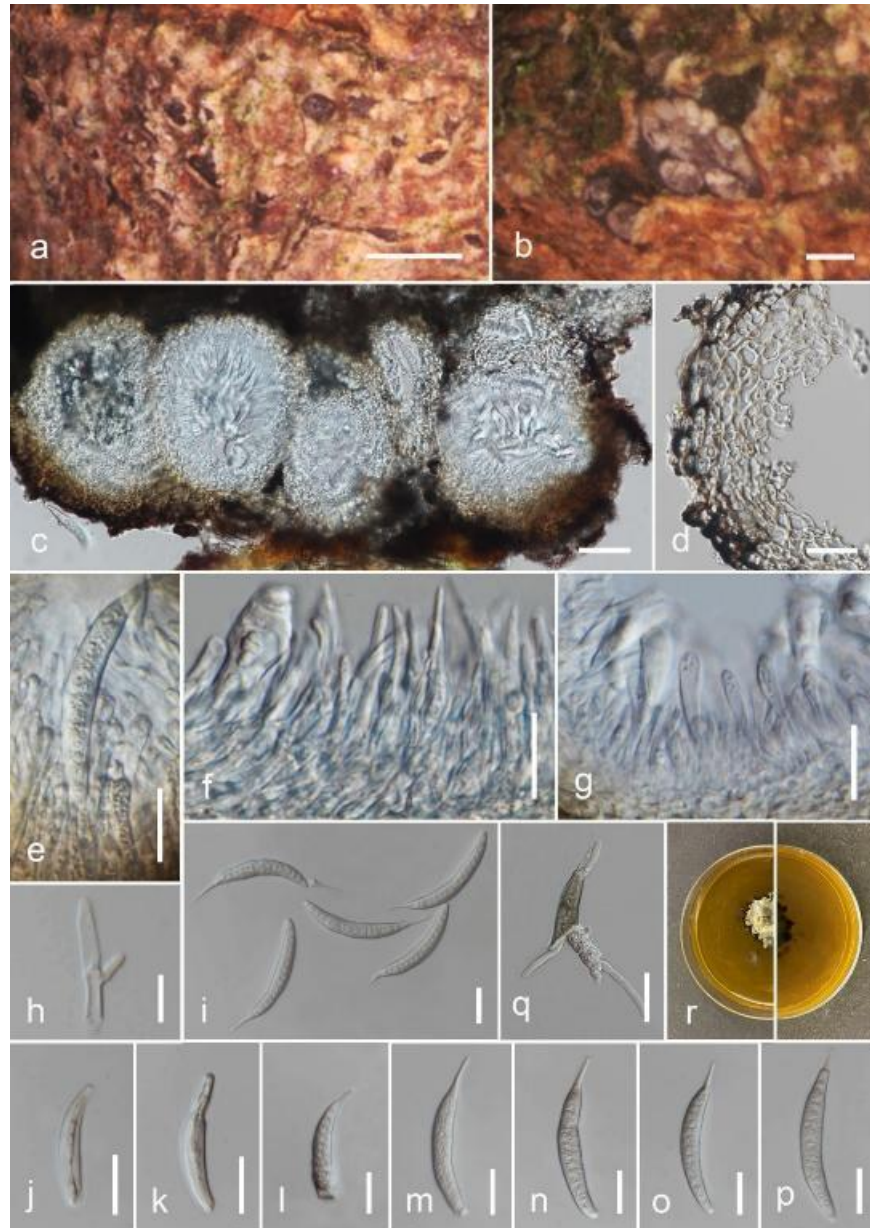


Figure 4 – *Novolignincola doitungensis* (MFLU 24-0456, holotype). a Conidiomata on *Afzelia xylocarpa* woody litter. b Longitudinal section of the conidiomata. c Vertical section through conidiomata. d Conidiomatal wall. e–g Conidia attached to conidiogenous cells. h Branched paraphyses. i–p Conidia. q A germinated conidium. r Colony on PDA from the above and reverse. Scale bars: a = 1 mm, b = 200 μ m, c = 50 μ m, d–q = 20 μ m.

Diplodia guttulata Samarad., Lumyong & K.D. Hyde, in Samaradiwakara et al. Fungal Diversity (2025). Fig. 6

Index Fungorum number: IF855731; Facesoffungi number: FoF16505

Saprobic on dead branches of *Microcos paniculata*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 130–300 µm diam., 120–235(–320) µm high ($\bar{x}$ = 213 × 200 µm, n = 5), pycnidial, embedded in stromatic tissue, mostly pyriform or sub-globose, brown to dark brown, multilocular, semi-immersed or immersed, becoming erumpent through the epidermis at maturity, appear as cracks on the host surface, scattered, mostly solitary or gregarious, glabrous, coriaceous, without conspicuous ostioles. *Conidiomata wall* (15–)17.5–35(–38) µm wide ($\bar{x}$ = 26.5 µm, n = 30), composed of thick-walled, brown to sub-hyaline towards the inner region cells of *textura angularis*. *Paraphyses* not observed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (3.8–)4.5–11.8(–13.5) × 2.5–4.4 µm ($\bar{x}$ = 6.3 × 3.4 µm, n = 25), monophialidic, hyaline, doliiform, slightly wider at the base, smooth-walled, proliferating percurrently or periclinal thickening at apex. *Conidia* 6.4–13.7 × 3.2–4.9 µm ($\bar{x}$ = 10.7 × 3.9 µm, n = 30), L/W ratio = 3.7, rounded at apex, truncate at base, smooth, thick-walled, straight, initially sub-hyaline, aseptate, ellipsoid or amygdaliform at immaturity, becoming pigmented, cylindrical, and 1–3-septate at maturity, not constricted at septa.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerges from one end cell. Colonies on PDA reaching 7 cm diam. after 7 days at room temperature (25–28 °C), irregular, dense, with umbonate elevation, and filiform margin, from surface pale grey in the first few days, and eventually becoming olivaceous grey at the center and black at margin after two weeks, from reverse dark grey.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 26 March 2022, N. Afshari, 3C1T3R5b (MFLU 24-0396); living culture MFLUCC 24-0525.

GenBank numbers – ITS = PQ800228, *tefl-α* = PV138145, *tub2* = PX739614.

Known hosts – *Microcos paniculata* (Samaradiwakara et al. 2025), *M. paniculata* (this study).

Known distribution – Thailand (Samaradiwakara et al. 2025, this study).

Notes – *Diplodia guttulata* (MFLUCC 24-0177) was introduced as a novel species from the leaf litter of *Microcos paniculata* in Doi Tung National Park, Chiang Rai Province, Thailand by Samaradiwakara et al. (2025). It was collected as a sexual morph from substrate and, while we observed only the asexual morph. We collected *D. guttulata* (MFLUCC 24-0525) from woody litter of same host and locality. The multigene phylogeny indicates that our strain (MFLUCC 24-0525) clustered together with *D. guttulata* (MFLUCC 24-0177), with 100% ML bootstrap support and 1.0 PP value (Fig. 5) based on the combined phylogeny of ITS, *tefl-α* and *tub2* sequence data. Taking into consideration the phylogenetic analyses, we report our saprobic strain (MFLUCC 24-0525) as a new collection of *D. guttulata* on woody litter of *Microcos paniculata*.

Lasiodiplodia Ellis & Everh.

Index Fungorum number: IF8708; Facesoffungi number: FoF00151

Lasiodiplodia was erected by Ellis & Everhart (1894) and typified by *L. theobromae*. Most species in this group are plant pathogens that can induce cankers, dieback, fruit or root decay, branch blight, or discolouration on various types of woody plants, primarily found in Wang et al. (2021a), tropical and subtropical climates (Slippers & Wingfield 2007, de Silva et al. 2019, Jayawardena et al. 2019a, Tian et al. 2024).

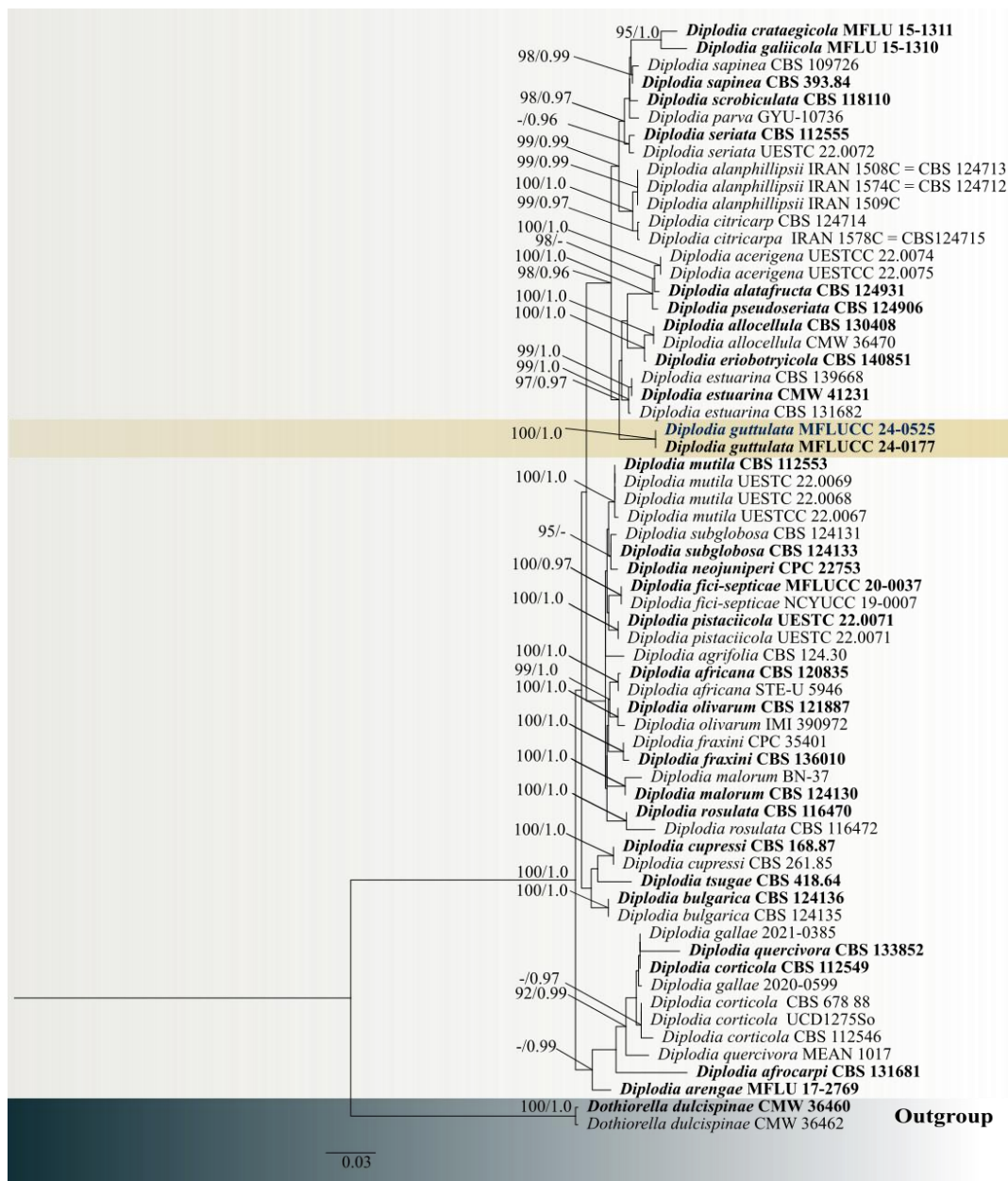


Figure 5 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, *tefl-α*, and *tub2* sequence data of *Diplodia*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Sixty-four strains are included in the combined analyses which comprised 1,212 characters (ITS = 515, *tefl-α* = 267, and *tub2* = 430). The best score for log-likelihood of consensus tree is -5328.152. The matrix had 38 distinct patterns 285 parsimony-informative, 65 singleton sites, and 862 constant sites. Selecting individual models K2P+I+G4, TN+F+G4, and TN+F+I+G4 were applied to ITS, *tefl-α*, and *tub2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 4,000,000 MCMC generations was calculated as 0.007997. Bootstrap support values for ML greater than or equal to 90% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Dothiorella*

dulcispinae (CMW 36460 and CMW 36462). Ex-type strains are in bold. The isolate of the current study is indicated in bold and blue.

The latest phylogenetic tree of *Lasiodiplodia* spp. by Tian et al. (2025) used a combination of ITS, *rpb2*, *tefl-α*, and *tub2* sequence data. Currently, 96 epithets of *Lasiodiplodia* are recorded in Index Fungorum (2025). Both sexual and asexual morphs have been recorded in this genus. The sexual morph exhibits globose to subglobose ascomata, and clavate, stipitate asci with hyaline to dark brown, aseptate ascospores. The asexual morph features stromatic, immersed, or superficial, globose-shaped, uni- or multi-loculate conidiomata with a central, single, papillate ostiole. Conidiophores are usually reduced to conidiogenous cells, which are cylindrical to conical, holoblastic, producing subglobose or oval, smooth, thick-walled conidia that are hyaline when immature and turn dark brown and striate when mature (Rathnayaka et al. 2023). In this study, we found *Lasiodiplodia magnoliae* as a new geographical record and a new host record on *Dalbergia cultrata* from Doi Tung National Park, Chiang Rai, Thailand. An updated phylogeny for the genus is shown in Fig. 7.

Lasiodiplodia magnoliae N.I. de Silva, A.J.L. Phillips & K.D. Hyde, in de Silva et al. Sci. Rep. 9 (no. 14355), 2 (2019). Fig. 8

Index Fungorum number: IF556217; Facesoffungi number: FoF05797

Saprobic on dead branches of *Dalbergia cultrata*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 245–285 µm diam., 230–325 µm high ($\bar{x}$ = 260 × 290 µm, n = 5), pycnidial, uniloculate, globose to mostly subglobose, black, scattered, solitary immersed, visible as black dots on the host surface, coriaceous, without a conspicuous ostiole. *Conidiomatal wall* (29–)33–50.5(–53) µm wide ($\bar{x}$ = 41 µm, n = 30), composed of two layers of thick-walled, black to dark brown cells of *textura angularis*, hyaline towards the inner region. *Paraphyses* 2.3–4.7 µm wide, hyaline, cylindrical to ampulliform, wider at base, and narrow towards apex, smooth-walled, septate, not branched. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.8–7 × 8.7–18 µm ($\bar{x}$ = 5.2 × 13.9 µm, n = 25), hyaline, sub-cylindrical to doliiform, monophialidic, smooth-walled, discrete, percurrently proliferate. *Conidia* (17.6–)20.5–31 × 11.2–16.5 µm ($\bar{x}$ = 26.8 × 14.6 µm, n = 30; L/W ratio = 1.8), hyaline, ellipsoid-ovoid, straight, aseptate, thick-walled, broadly rounded at apex rounded to truncate at the base, with vivid granular content, base round or truncate, wall 1.4–2.5 µm thick.

Culture characteristics – Conidia germinated on PDA within 24 h and a germ tube emerged from one end. Colonies on PDA reaching 7–8 cm diam. after one week at room temperature (25–28 °C), circular, flat, medium dense, entire margin, cottony to fairly fluffy, from surface greyish-green, from reverse black.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cultrata* (Fabaceae), 27 September 2022, N. Afshari, 6C3T1R3 (MFLU 24-0458); living culture MFLUCC 24-0559.

GenBank numbers – ITS = PQ800248, *tefl-α* = PV138148, *tub2* = PX739611.

Known hosts – *Magnolia candolii* (de Silva et al. 2019), *Dalbergia cultrata* (this study).

Known distribution – China (de Silva et al. 2019), Thailand (this study).

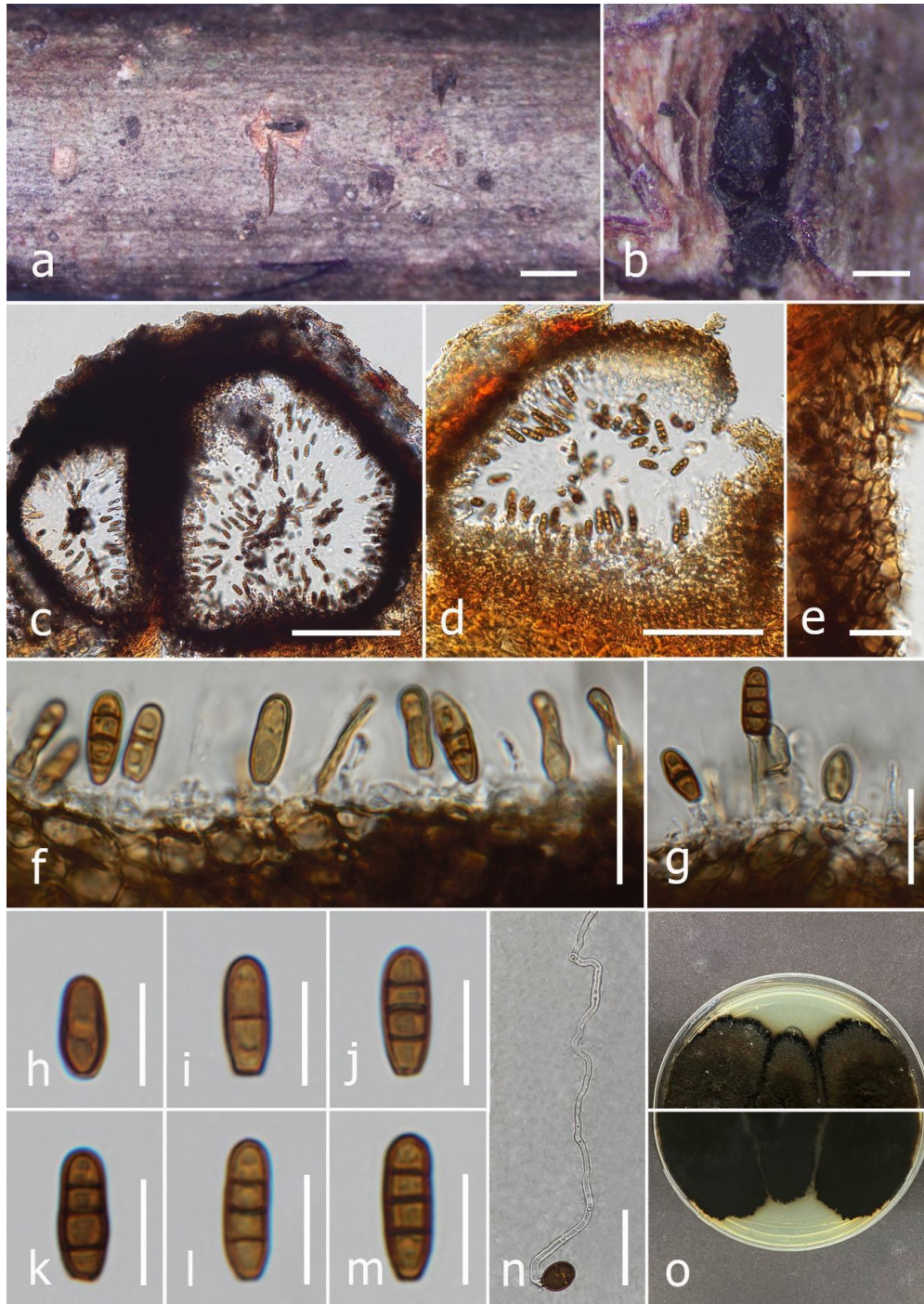


Figure 6 – *Diplodia guttulata* (MFLU 24-0396, additional collection from dead wood). a Conidiomata on *Microcos paniculata* woody litter. b Longitudinal section of a conidioma. c, d Vertical section through conidiomata. e Conidiomatal wall. f, g Conidia attached to conidiogenous cells. h–m Conidia. n A germinated conidium. o Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d, n = 50 μ m, e–g = 20 μ m, h–m = 10 μ m.

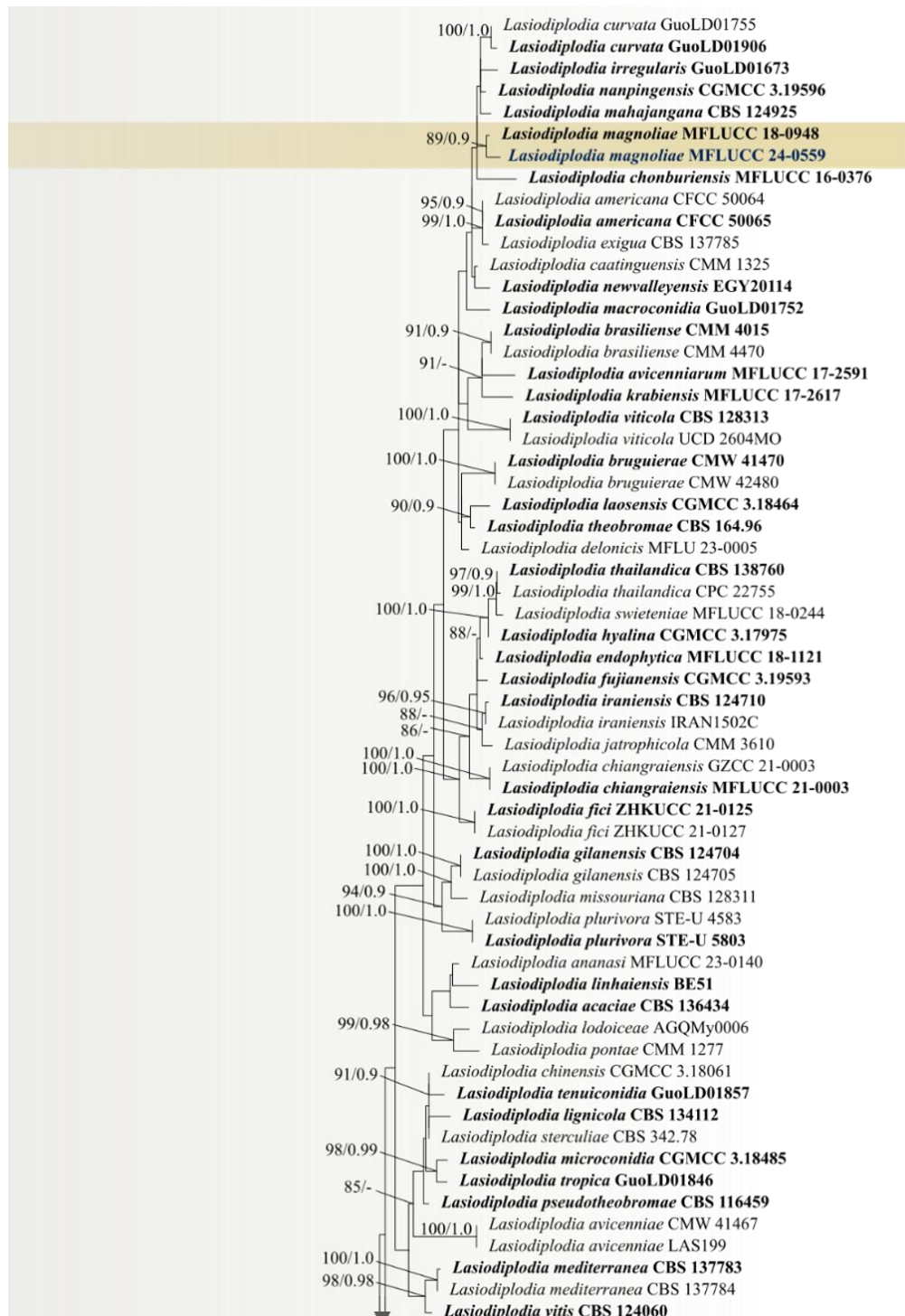


Figure 7 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, *tefl-α*, and *tub2* sequence data of *Lasiodiplodia*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. One hundred and nine strains are included in the combined analyses which comprised 1,446 characters (ITS = 531, *tefl-α* = 456, and *tub2* = 459). The best score for log-likelihood of consensus tree is -6147.883. The matrix had 431 distinct alignment patterns, 218 parsimony-informative, 103 singleton sites, and 907 constant

sites. Selecting individual models K2P+I+G4, K2P+I+G4, and TN+F+I+G4 were applied to ITS, *tefl-α*, and *tub2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.011240. Bootstrap support values for maximum likelihood greater than or equal to 85% and Bayesian posterior probabilities greater than or equal to 0.9 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Diplodia seriata* (CBS 112555) and *D. mutila* (CMW 7060). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

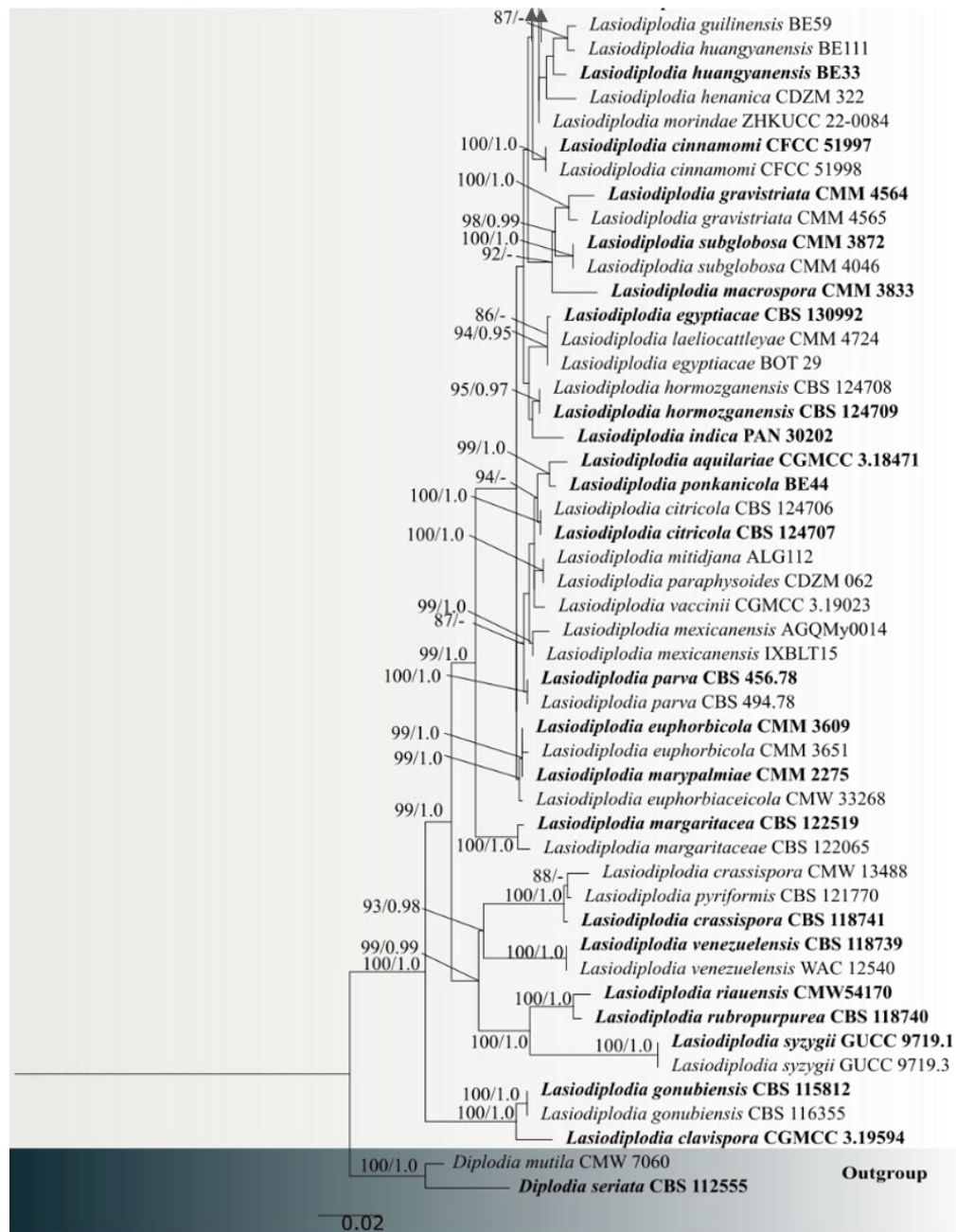


Figure 7 – Continued.

Notes – In the combined ITS, *tef1-α*, and *tub2* phylogenetic tree, *Lasiodiplodia magnoliae* (MFLUCC 24-0559) constituted a lineage (with 89% ML, 0.9 PP values) between *L. magnoliae* and *L. macroconidia* (Fig. 7). Our collection of *L. magnoliae* (MFLU 24-0458) is similar to *L. magnoliae* (MFLU 18-1030) in shape of the conidiomata, the structure of the conidiomatal wall, the absence of conidiophores, and the size of paraphyses. However, our collection has larger conidiomata (245–285 μm diam., 230–325 μm high ($\bar{x}$ = 260 × 290 μm) vs. 180–200 μm diam., 200–250 μm high), and conidiogenous cells (3.8–7 μm vs. 2–5 μm diam.) than *L. magnoliae* (MFLUCC 18-0948) (de Silva et al. 2019). The differences in host species, geographic distribution, and substrate may explain the observed size differences between the two collections. However, ITS showed no difference, while *tef1-α* and *tub2* differed by 0.8% and 0.5%, respectively, compared with *L. magnoliae* (MFLUCC 18-0948). *Lasiodiplodia magnoliae* (MFLUCC 18-0948) was isolated from *Magnolia candolii* in Yunnan, China, whereas our strain was obtained from dead wood of *Dalbergia cultrata* in northern Thailand. Therefore, we consider this as a new host and geographical record of *L. magnoliae*.

***Phyllostictaceae* Fr.**

Wikee et al. (2013) reinstated *Phyllostictaceae* as a distinct family in *Botryosphaeriales* to place *Phyllosticta* (= *Guignardia*) based on comprehensive morphology and phylogenetic analyses. Taxa of *Phyllostictaceae* have been reported as foliicolous plant pathogens, endophytes, or saprobes (Jayawardena et al. 2019b, Phillips et al. 2019, Hosanna et al. 2020b). Recent taxonomic revisions and regional surveys have increased the known host range, ecological roles, and geographic distribution of members of this family (Hongsanant et al. 2020b). Hyde et al. (2024a) reported *Phyllosticta* and *Pseudofusicoccum* genera in this family.

***Pseudofusicoccum* Mohali, Slippers & M.J. Wingf.**

Index Fungorum number: IF500884; Facesoffungi number: FoF05299

Crous et al. (2006) erected *Pseudofusicoccum* based on asexual morph characteristics and multigene phylogeny, typified by *P. stromaticum* within *Botryosphaeriaceae*. Most species of this genus were described by their asexual morph (Chethana et al. 2023), but Senwanna et al. (2020) described a sexual morph. Yang et al. (2016) transferred *Pseudofusicoccum* from *Botryosphaeriaceae* to *Pseudofusicoccumaceae* based on morphology and phylogenetic results. The asexual morph is similar to *Fusicoccum* asexual morphs of *Botryosphaeria* (*Botryosphaeriaceae*), having corticolous, coriaceous, uni- to multilocular, immersed to superficial, large pycnidial conidiomata, along with hyaline, thin- to moderately thick-walled, aseptate, cylindrical to ellipsoid conidia surrounded by a mucilaginous sheath (Senwanna et al. 2020). The sexual morph is distinguished by scattered to clustered, uniloculate ascomata; bitunicate, cylindro-clavate asci with ocular chambers; and, hyaline uni- to bi-seriate, aseptate, short clavate, ascospores with fine granules, covered by a mucilaginous sheath (Senwanna et al. 2020). *Pseudofusicoccum* has been reported as an endophyte, saprobe, and plant pathogen. It comprises nine species (Senwanna et al. 2020, Sharma et al. 2022, Chethana et al. 2023, Li et al. 2023b, Hyde et al. 2024a). In this study, we report *Pseudofusicoccum adansoniae* as a new host record from dead wood of *Dipterocarpus alatus*, and also, we document the first sexual morph and new host record of *P. kimberleyensespecies* from *D. alatus* in Thailand.

Pseudofusicoccum adansoniae Pavlic, T.I. Burgess & M.J. Wingf., *Mycologia* 100(6), 855 (2008). Fig. 10

Index Fungorum number: IF512048; Facesoffungi number: FoF00168

Saprobic on Dipterocarpus alatus woody litter. Sexual morph: *Ascomata* 150–192 μm diam., 155–193 μm high ($\bar{x} = 176 \times 178 \mu\text{m}$, $n = 5$), uniloculate, subglobose to globose, scattered to clustered, coriaceous, immersed to semi-immersed, ostiolate. *Ostiole canal*, central, in horizontal section locular contents look brilliant white. *Peridium* 16–34 μm diam ($\bar{x} = 26 \mu\text{m}$, $n = 30$), outer layers thick-walled, brown cells and inner layers thin-walled, hyaline, composed of cells of *textura angularis*.

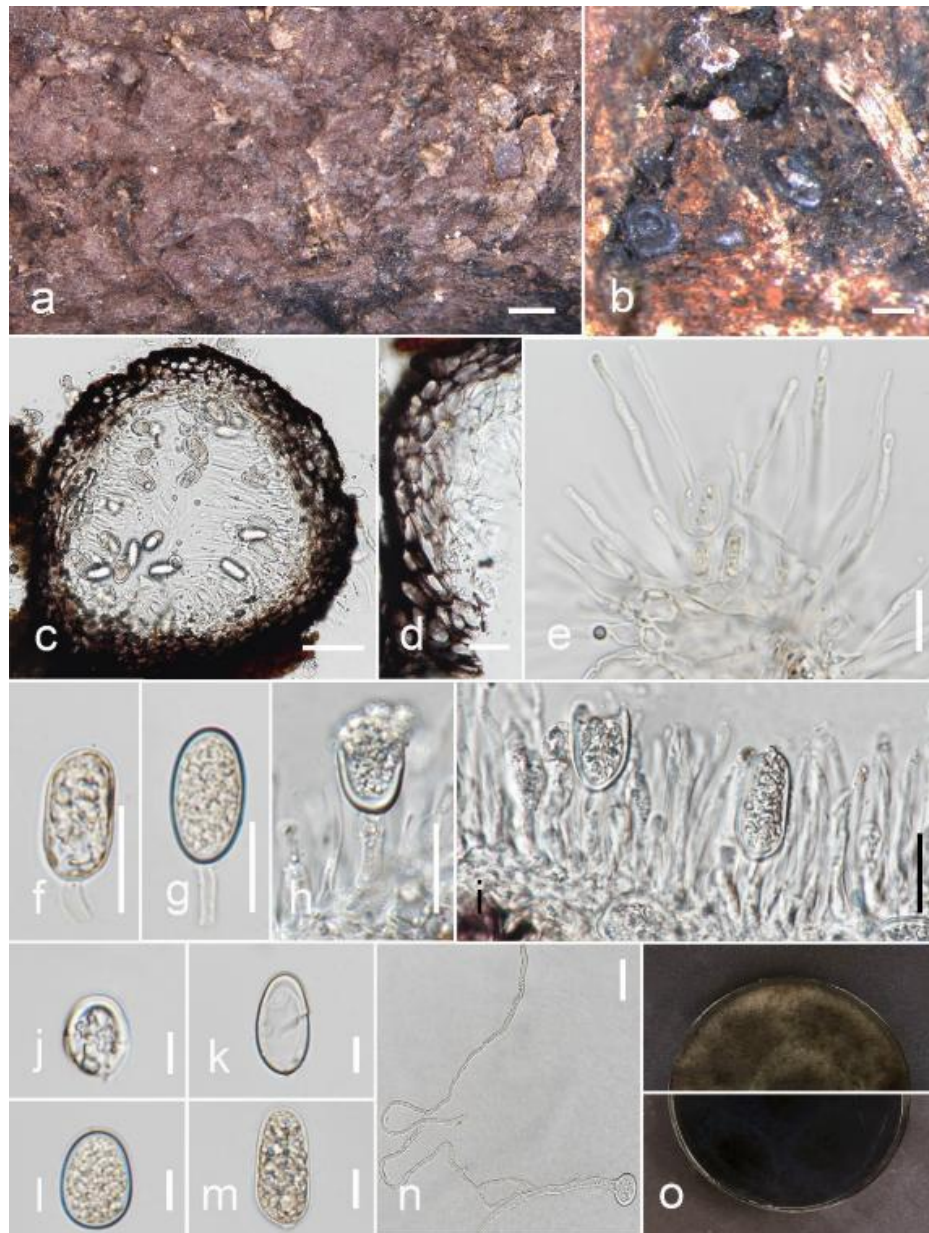


Figure 8 – *Lasiodiplodia magnoliae* (MFLU 24-0458, new host and geographical record). a Appearance of conidiomata on *Dalbergia cultrata* woody litter. b Longitudinal section of the conidiomata. c Vertical section through conidioma. d Conidiomatal wall. e Paraphyses. f–i Conidiogenous cells and developing conidia. j–m Conidia. n A germinated conidium. o Colony on

PDA (front and reverse). Scale bars: a = 2.5 mm, b = 500 μm , c = 50 μm , d–i, n = 20 μm , j–m = 10 μm .

Hamathecium comprises hyaline, septate pseudoparaphyses arising from a basal stromatal tissue, intermixed with asci. *Asci* 76–130(–138) $\times$ 14–21 μm ($\bar{x}$ = 99 $\times$ 18 μm , n = 15), 8-spored, bitunicate, fissitunicate, inner wall raised in the center, clavate to cylindric-clavate, relatively short pedicel, apically rounded with a wide ocular chamber. *Ascospores* 16–24 $\times$ 8.5–13 μm ($\bar{x}$ = 20 $\times$ 11.7 μm , n = 35), hyaline, overlapping, 1–2-seriate, ovoid to clavate, aseptate, straight, wide and rounded at apex, smooth-walled, straight, or slightly curved, finely guttulate, surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h. Colonies reached 90 mm diam. after 10 days at room temperature (25–28 $^{\circ}\text{C}$), round, with umbonate elevation, thinner towards the periphery, with fluffy appearance. The upper surface is dark brown after one month, while reverse is opaque black. Pigmentation produced on PDA medium with age.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T3R3b (MFLU 24-0397); living culture MFLUCC 24-0526.

GenBank numbers – ITS = PQ800229, *tub2* = PX739615.

Known hosts – *Acacia synchronica*, *Adansonia gibbosa*, *Eucalyptus* sp., *Ficus opposita*, (Pavlic et al. 2008), *Jatropha podagrica* (Sharma et al. 2013), *Tectona grandis* (Doilom et al. 2015), *Hevea brasiliensis* (Senwanna et al. 2020), *Dipterocarpus alatus* (this study).

Known distribution – Australia (Pavlic et al. 2008), India (Sharma et al. 2013), Thailand (Doilom et al. 2015, Senwanna et al. 2020, this study).

Notes – *Pseudofusicoccum adansoniae* was isolated from branches of *Adansonia gibbosa* and *Eucalyptus* sp. in Western Australia and introduced by Pavlic et al. (2008) based on morphology and phylogenetic analyses. Subsequently, it was also reported as an endophyte from the leaf midrib of *Jatropha podagrica* in Maharashtra State, India, by Sharma et al. (2013). Later Senwanna et al. (2020) described the sexual morph of *P. adansoniae* for the first time. Based on our phylogenetic tree of combined ITS, *tef1- α* , and *tub2* sequence data, our collection (MFLUCC 24-0526.) clustered with *P. adansoniae* (CBS 122055; type species), and *P. adansoniae* (CBS 122054) with 100% ML, 1.00 PP bootstrap support (Fig. 9). Our isolation (MFLU 24-0397) mostly shares similar morphological characteristics to *P. adansoniae* (CBS 122055), but some features, such as the size of asci and ascospores, are larger than described for *P. adansoniae* (MFLU 19-0239). However, combined ITS–*tef1- α* –*tub2* phylogeny and morphological features support *P. adansoniae* (MFLU 24-0397) as a new host record from decaying wood of *Dipterocarpus alatus* in Thailand.

Pseudofusicoccum kimberleyense Pavlic, T.I. Burgess & M.J. Wingf., Mycologia 100(6), 857 (2008). Fig. 11

Index Fungorum number: IF512049; Facesoffungi number: FoF16088

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 218–279 μm diam., 160–320 μm high ($\bar{x}$ = 250 $\times$ 227 μm , n = 5), uniloculate, appearing as black spots on host bark surface, subglobose to globose, solitary or scattered, immersed to semi-immersed, coriaceous. *Peridium* 35.5–60(–62) μm wide ($\bar{x}$ = 47 μm , n = 35), two strata composed of cells of *textura angularis*, outer stratum of dark brown to black thick-walled cells combining at the outside with the host tissues, inner stratum lightly pigmented to hyaline. *Hamathecium* comprises hyaline

pseudoparaphyses arising from a basal stromatal tissue and shorter than asci. *Asci* (70–)80–140(–155) × 19–25(–28) μm ($\bar{x}$ = 105 × 22 μm , n = 30), 8-spored, bitunicate, fissitunicate, with thick outer wall, inner wall raised in center, clavate to cylindric-clavate, straight to curved, with short, knob-like pedicel, apically rounded with a moderately distinct ocular chamber. *Ascospores* 19.5–30 × 10.5–14.5 μm ($\bar{x}$ = 24 × 12 μm , n = 35), biseriata, overlapping, ovoid to clavate, wide and rounded at apex, hyaline, aseptate, smooth-walled, straight, finely guttulate surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

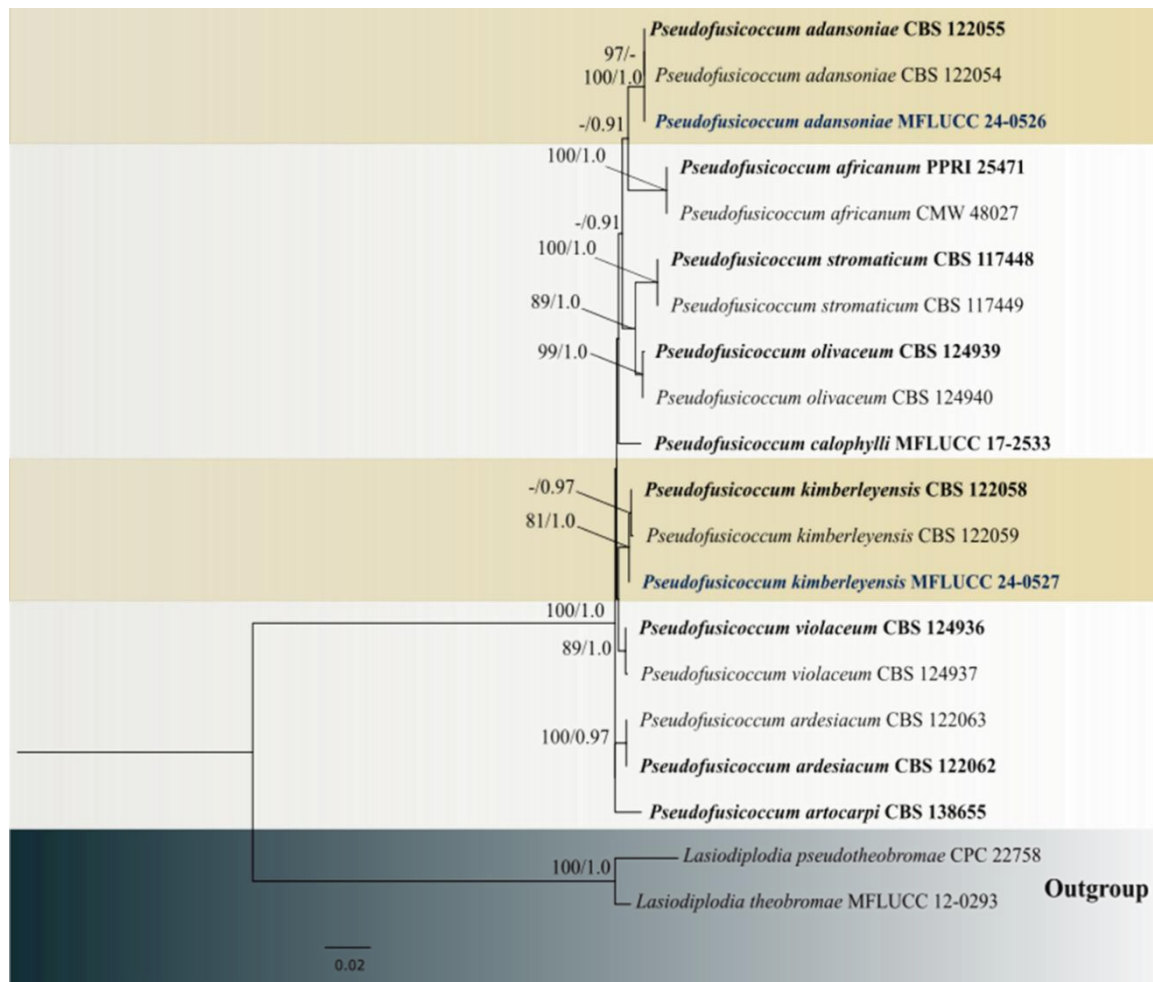


Figure 9 – Phylogram generated from maximum likelihood analysis based on the combined ITS, *tef1- α* , and *tub2* sequence data of *Pseudofusicoccum*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Twenty-one strains are included in the combined analyses which comprised 1,270 characters (ITS = 520, *tef1- α* = 298, and *tub2* = 452) in the combined dataset. The best RAxML tree with a final optimization likelihood value of -3124.719755 is presented. The matrix had 215 distinct alignment patterns, with 12.38% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.197834, C = 0.311332, G = 0.265322, T = 0.225512; substitution rates AC = 0.615930, AG = 2.767036, AT = 0.769769, CG = 0.593671, CT = 5.579173, GT = 1.000000; gamma distribution shape parameter α = 0.210720. In the Bayesian analysis, average standard deviation of split frequencies at the end of 2,000,000 MCMC generations was calculated as 0.004506. The evolutionary models TIM3ef+I,

TrN+G, and TIM3+I were applied to ITS, *tefl-α*, and *tub2* sequence data respectively in BI analysis. Bootstrap support values for maximum likelihood greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Lasiodiplodia pseudotheobromae* (CPC 22758) and *L. theobromae* (MFLUCC 12-0293). Ex-type strains are in bold. The isolates generated in this study are indicated in bold and blue.

Culture characteristics – Ascospores germinated on PDA within 24 h and a germ tube emerged from one end cell. Colonies reached 90 mm diam. after 10 days at room temperature (25–28 °C), curled, with umbonate elevation, dense, fluffy appearance, narrow towards margin, non-pigmented, at upper surface radiating from brown to grey outwardly, from reverse opaque black.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T1R2a (MFLU 24-0398); living culture MFLUCC 24-0527.

GenBank numbers – ITS = PQ800230, *tefl-α* = PV138146, *tub2* = PX753045.

Known hosts – *Adansonia gibbosa*, *Acacia synchronica*, *Eucalyptus* sp., and *Ficus opposita* (Pavlic et al. 2008), *Carya illinoensis* (Rolim et al. 2020), *Acacia mangium*, *Pinus massoniana*, and *Eucalyptus* sp. (Li et al. 2023b), *Dipterocarpus alatus* (this study).

Known distribution – Australia (Pavlic et al. 2008), Brazil (Rolim et al. 2020), China (Li et al. 2023b), Thailand (this study).

Notes – Based on BLASTn search of ITS–*tefl-α*–*tub2* sequences in GenBank, it was found that our isolate shows high similarity to *P. kimberleyense* (ex-type strain, CBS 122058) with 99.52%, 100%, and 100% similarity, respectively. Additionally, in the phylogenetic tree, *P. kimberleyense* (MFLUCC 24-0527) is closely related to CBS 122058 and CBS 122059 strains, showing 81% ML/ 1.0 PP support values (Fig. 9). Our strain was isolated from decaying wood of *Dipterocarpus alatus* in Thailand, while the ex-type strain was collected on dying branches of *Adansonia gibbosa*, *Acacia synchronica*, *Eucalyptus* sp., and *Ficus opposita* in Western Australia (Pavlic et al. 2008). It has also been isolated in Brazil and China (Rolim et al. 2020, Li et al. 2023b). According to the multilocus phylogenetic results of ITS, *tefl-α*, and *tub2* DNA matrix, we report our strain as the first recorded sexual morph of *P. kimberleyense*. This is also the first report of *P. kimberleyense* from *Dipterocarpus alatus* in Thailand.

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

Pleurotremataceae Walt. Watson

Pleurotremataceae was established by Watson et al. (1929) for a monotypic genus, *Pleurotrema* which typified by *P. polysemum*. This family was placed under *Chaetosphaeriales*, *Sordariomycetes* by Maharachchikumbura et al. (2015). Maharachchikumbura et al. (2016) examined the isotype of *P. polysemum* and found that *Dyfrulomycetaceae* is a synonym of *Pleurotremataceae*, therefore removed *Pleurotremataceae* from *Sordariomycetes* to be a single family of *Dyfrulomycetales*. Currently, this family includes four genera viz. *Dyfrulomyces*, *Longiascospora*, *Melomastia* and *Pleurotrema* (Hyde et al. 2024a, Wanasinghe et al. 2025). *Pleurotremataceae* has perithecial, ostiolate, ovoid to subglobose ascomata, clavate to cylindrical, short pedicellate asci, with a J- apical ring along with hyaline, ellipsoidal to cylindrical, multi-distoseptate ascospores (Hongsanant et al. 2020b). Species of this family are saprobes on wood in terrestrial and aquatic habitats (Hongsanant et al. 2020b).

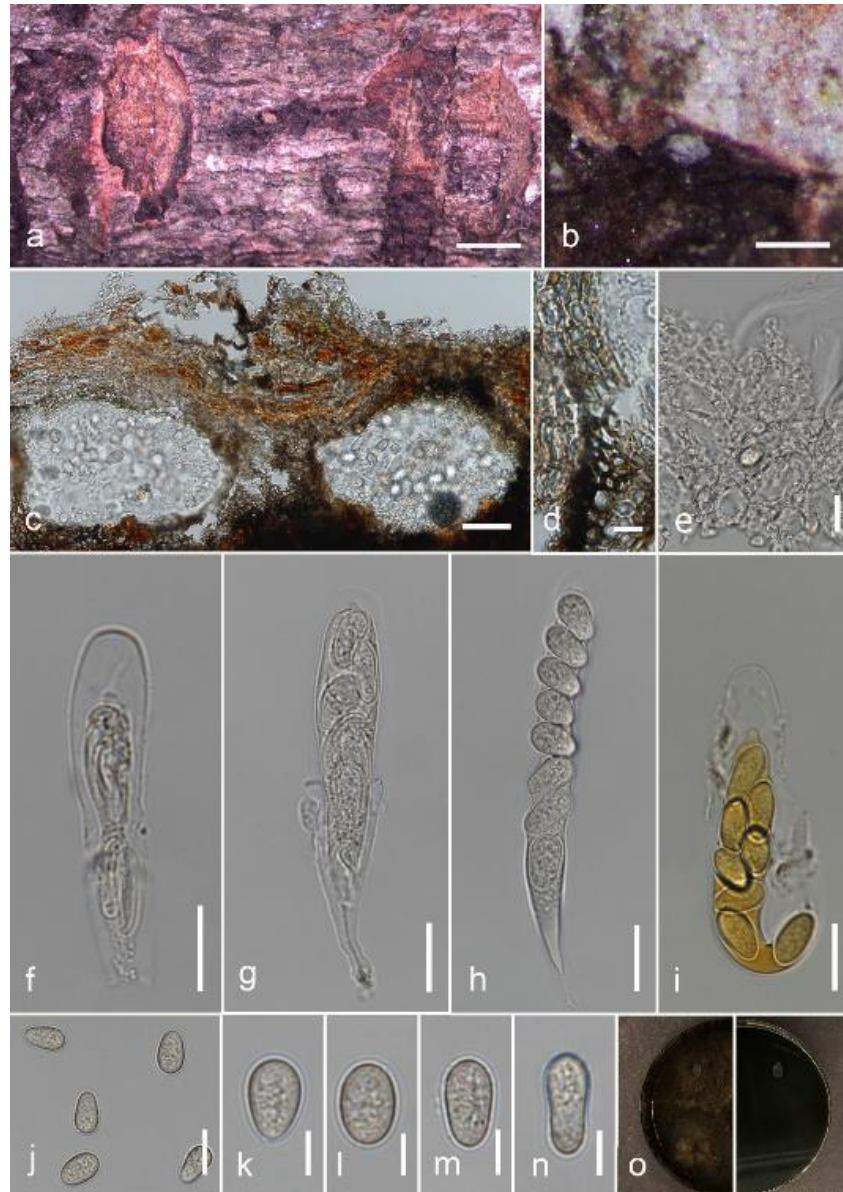


Figure 10 – *Pseudofusicoccum adansoniae* (MFLU 24-0397, a new host record). a Close-up of ascomata on *Dipterocarpus alatus* woody litter. b Longitudinal section of ascoma. c Vertical section through ascomata. d Section of peridium. e Pseudoparaphyses. f–h Asci. i Ascus in Melzer's reagent. j–n Ascospores. o Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 µm, c = 50 µm, e–j = 20 µm, d, k–n = 10 µm.

***Melomastia* Nitschke ex Sacc.**

Index Fungorum number: IF3118; Facesoffungi number: FoF07673

Melomastia was erected by Saccardo (1875) with the type species *M. mastoidea* (= *M. friesii*), which was isolated from *Viburnum opulus* (Adoxaceae) in Germany. The taxonomic placement of this genus has been widely discussed (Lumbsch & Huhndorf 2010, Maharachchikumbura et al. 2016). Norphanphoun et al. (2017), verified *Melomastia* in *Pleurotremataceae* based on morphology and multigene phylogeny. According to morpho-

molecular studies, 11 species of *Dyfrlomycetes* were synonymized under *Melomastia* (Li et al. 2022). Kularathnage et al. (2023) demonstrated that two species (*M. chromolaenae* and *M. tiomanensis*) form a distinct basal clade with other *Melomastia* species. Most *Melomastia* species are saprobes in terrestrial, freshwater, marine, and mangrove ecosystems in both temperate and tropical regions (Norphanphoun et al. 2017, Phukhamsakda et al. 2020, Li et al. 2022, Kularathnage et al. 2023). *Melomastia* species have immersed, globose, ascomata, uniseriate asci with a J-, subapical ring, and ovoid, 2-septate ascospores which are constricted at the septum, with or without a gelatinous sheath (Norphanphoun et al. 2017, Li et al. 2022). Currently, 53 accepted species are listed under *Melomastia* in Index Fungorum (2025). In this study we report *Melomastia thamplaensis* as a new record on dead wood of *Nayariophyton zizyphifolium* from Doi Tung National Park, Thailand. An updated phylogeny for the genus is shown in Fig. 12.

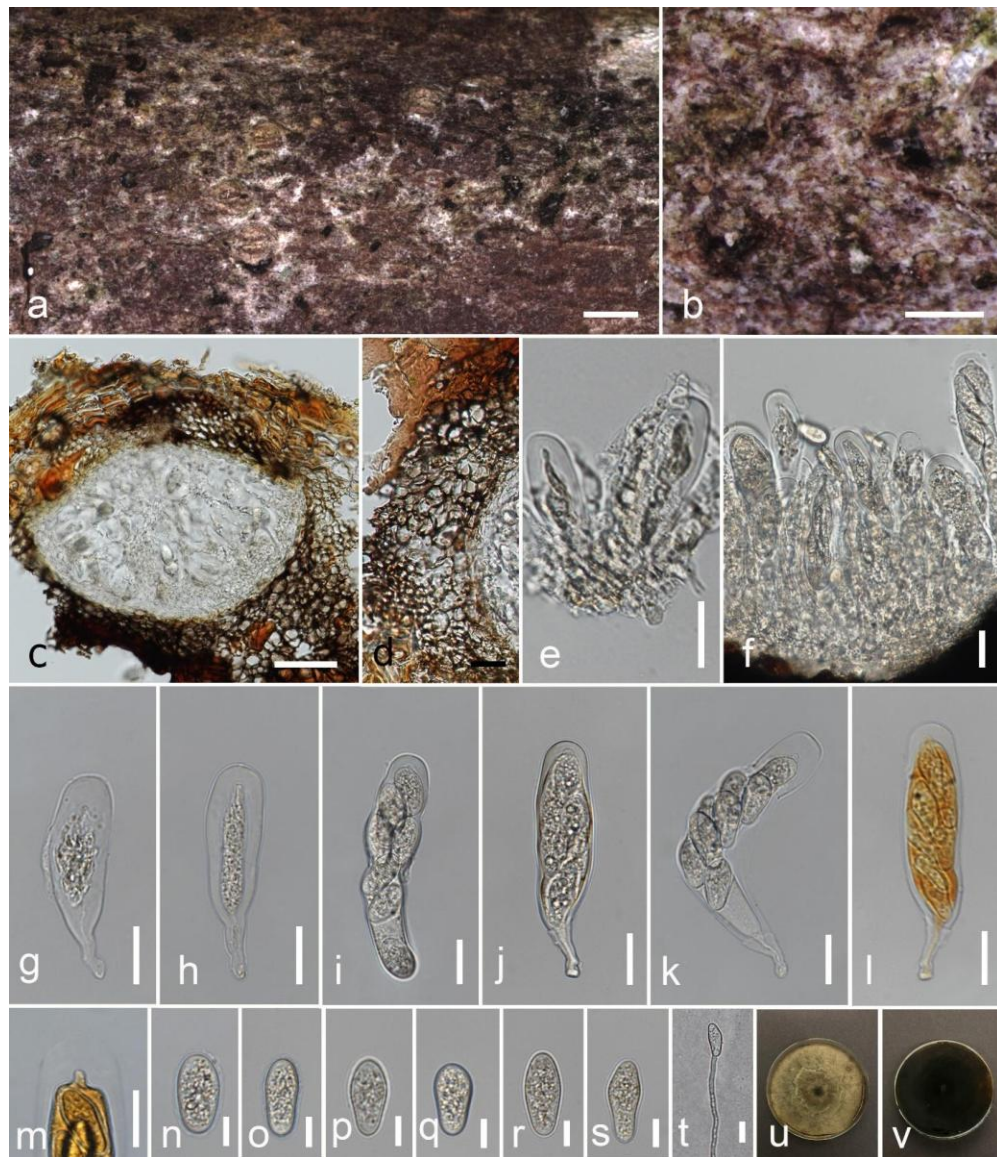


Figure 11 – *Pseudofusicoccum kimberleyense* (MFLU 24-0398, first report of the sexual morph, and new host and geographical record). a, b Close-up of ascomata on *Dipterocarpus alatus* woody

litter. c Vertical section through ascoma. d Peridium. e, f Pseudoparaphyses and asci. g–k Asci. l Ascus in Melzer’s reagent. m Ocular chamber in Melzer’s reagent. n–s Ascospores. t A germinated ascospore. u, v Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 500 μ m, c = 50 μ m, d–m, t = 20 μ m, n–s = 10 μ m.

Melomastia thamplaensis (J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu) W.L. Li, Maharachch. & J.K. Liu, *Journal of Fungi* 8(76), 16 (2022) Fig. 13

Index Fungorum number: IF552496; Facesoffungi number: FoF02612

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: *Ascomata* (excluding neck) 300–375 μ m wide, 230–315 μ m high ($\bar{x}$ = 320 $\times$ 285 μ m, n = 5), scattered, visible on the substrate surface as black, raised spots, immersed to semi-immersed, subglobose to pyriform, mostly with flattened base, coriaceous to carbonaceous, ostiolate, papillate, clypeate. *Clypeus* 16.5–53 μ m thick, radiating outward around the ascomata, thicker in middle, composed of dense, dark thick-walled cells. *Papilla* conical, ostiole periphysate. *Peridium* 25–51 μ m wide ($\bar{x}$ = 38 μ m, n = 30), composed of two layers, an outer layer of brown, dense, thick-walled cells of *textura angularis*, and an inner layer of thin-walled sub-hyaline cells of *textura angularis*. *Hamathecium* comprises 1–2.5 μ m wide, composed of abundant, septate, unbranched pseudoparaphyses, attached at the base of ascomata, embedded in a gelatinous matrix. *Asci* 127–198 $\times$ 6.9–10.6 μ m ($\bar{x}$ = 171 $\times$ 8.6 μ m, n = 25), 8-spored, cylindrical, with short pedicel, apically rounded to truncate with an obvious apical ring. *Ascospores* (8–)19–32.5(–35.5) $\times$ 4.5–8.5 μ m ($\bar{x}$ = 27 $\times$ 6.5 μ m, n = 50), uniseriate, fusiform, mostly sharp angular ends, 1–3-septate, constricted at septa, straight, hyaline, smooth-walled, mostly containing 1–5 guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h and germ tubes emerge from both end cells. Colonies on PDA reached 1.7–2 cm diam. after 20 days at room temperature (25–28 $^{\circ}$ C), circular, medium sparse, flat, fluffy at margin, upper surface white, reverse brown in center to yellow outwardly.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T3R2a (MFLU 24-0411); living culture MFLUCC 24-0538.

GenBank numbers – ITS = PQ800243, SSU = PV072703, *tef1*- α = PX739627.

Known hosts – on dead branch of an unidentified host (Zhang et al. 2017), *Millettia leptobotrya* (Ren et al. 2024), *Nayariophyton zizyphifolium* (this study).

Known distribution – Thailand (Zhang et al. 2017, this study), China (Ren et al. 2024).

Notes – In the multigene phylogeny, our strain (MFLUCC 24-0538) clustered together with strains of *Melomastia thamplaensis* (MFLUCC 15-0635, and KUMCC 21-0671) with 77% ML bootstrap support and 0.95 PP value (Fig. 12). Sequence comparison for the SSU region between our isolate and the *M. thamplaensis* isolate showed no significant base pair differences, but there are 1.5%, 1.6% (without gaps) base pair differences in the *tef1*- α region. These three strains of *M. thamplaensis* are similar in having globose to subglobose, coriaceous to carbonaceous ascomata, papillate ostioles, size and shapes of peridium and paraphyses, short-pedicellate, long cylindrical asci with conspicuous apical ring, and ascospores that are fusiform, hyaline, slightly constricted at the septa, with guttules in each cell. However, our isolate has larger asci and ascospores compared to the ex-type ($\bar{x}$ = 171 $\times$ 8.6 μ m, vs. $\bar{x}$ = 137 $\times$ 7 μ m; $\bar{x}$ = 27 $\times$ 6.5 μ m, vs. $\bar{x}$ = 22 $\times$ 5.5 μ m), respectively (Zhang et al. 2017, Ren et al. 2024). *Dyfirolomyces thamplaensis* was introduced based on the combined phylogeny of SSU, LSU, and *tef1*- α sequence data from dead wood in China and

Thailand (Zhang et al. 2017). Subsequently, based on morphological features and phylogenetic analyses, it was synonymized under *M. thamplaensis* (Li et al. 2022). Based on morphological similarity and less genetic differences, we report our saprobic fungus as the first record of *M. thamplaensis* isolated on dead wood of *Nayariophyton zizyphifolium*.

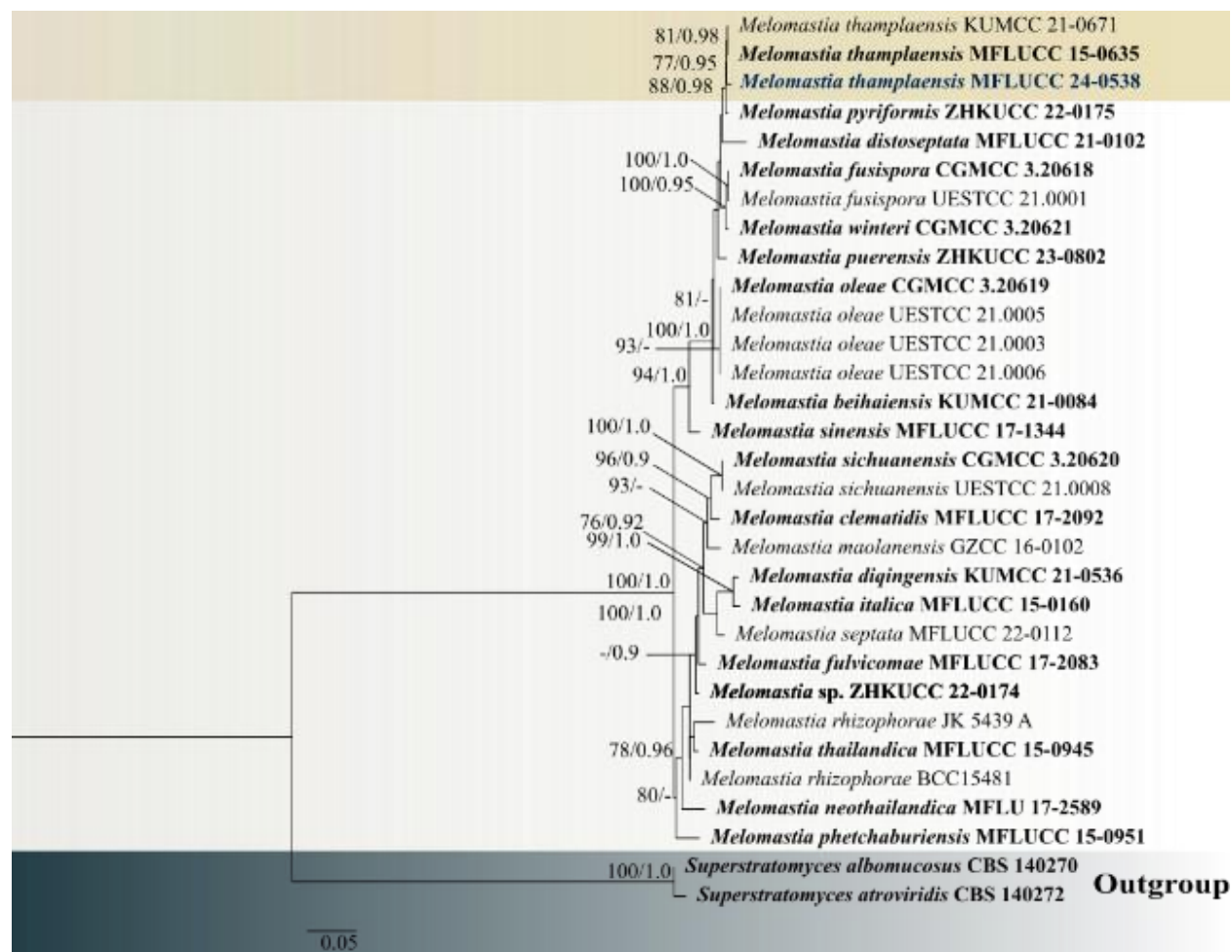


Figure 12 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined SSU, LSU, and *tef1*- α sequence data of *Melomastia*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Thirty-one strains are included in the combined analyses which comprised 2,677 characters (SSU = 980, LSU = 827, and *tef1*- α = 870). The best score for log-likelihood of consensus tree is -8761.513. The matrix had 479 distinct patterns 657 parsimony-informative, 111 singleton sites, 1,909 constant sites. Selecting individual models K2P+G4, TIM2+F+G4, and TN+F+G4 were applied to SSU, LSU, and *tef1*- α using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 2,000,000 MCMC generations was calculated as 0.009333. Bootstrap support values for ML greater than or equal to 75% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Superstratomyces albomucosus* (CBS 140270) and *S. atroviridis* (CBS 140272). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

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

Pleosporales, the largest order within class *Dothideomycetes*, encompasses a significant proportion of its species, with the type species being *Pleospora herbarum* (Barr 1987). The order was initially proposed by Luttrell (1955) and later formally established by Barr (1987). It includes a diverse array of species with a global distribution, fulfilling various ecological roles such as epiphytes, saprobes, endophytes, parasites, and lichenized fungi (Bhunjun et al. 2021b, Su et al. 2022, Xu et al. 2022). Members of *Pleosporales* have primarily perithecioid ascomata with a bitunicate, and fissitunicate asci that contain predominantly septate ascospores (Madagammana et al. 2024, Mekala et al. 2024, Mukhopadhyay et al. 2024, Tun et al. 2024). They often exhibit coelomycetous or hyphomycetous asexual morphs (Tennakoon et al. 2021b).

***Bambusicolaceae* D.Q. Dai & K.D. Hyde**

Hyde et al. (2013) introduced *Bambusicolaceae* to accommodate *Bambusicola*. Subsequent research placed *Leucaenicola*, *Longipedicellata*, *Neobambusicola*, and *Palmiascoma* in this family (Crous et al. 2014b, Liu et al. 2015, Jayasiri et al. 2019). However, *Neobambusicola* and *Longipedicellata* were transferred to *Sulcatissporaceae* and *Longipedicellataceae*, respectively (Tanaka et al. 2015, Phukhamsakda et al. 2016). Wijesinghe et al. (2020) introduced *Corylicola* in this family. *Bambusicolaceae* has hyaline, fusiform ascospores encased in a gelatinous sheath, cylindrical to clavate asci, and superficial, globose to subglobose ascomata (Hyde et al. 2013). Currently five genera are placed in this family including (Hyde et al. 2024a).

***Palmiascoma* Phook. & K.D. Hyde**

Index Fungorum number: IF550926; Facesoffungi number: FoF00428

Liu et al. (2015) described *Palmiascoma* with *P. gregariascomum* as the type species, including both asexual and sexual morphs isolated from palm. Currently, it contains three species. Members of this genus are also distinguished based on molecular data from LSU, SSU, and *rpb2* datasets (Liu et al. 2015, Monkai et al. 2021a, Li et al. 2023a, Pem et al. 2024). *Palmiascoma* is similar to *Didymosphaeria* and *Verruculina* with producing echinulate, didymospores (Zhang et al. 2012). The sexual morph has gregarious, uniloculate ascomata, clavate, short pedicellate asci, clavate to ellipsoidal, 1-septate ascospores surrounded by a mucilaginous sheath. The asexual morph has pycnidial conidiomata with conidiophores arising from the basal cavity, but mostly reduced to conidiogenous cells, holoblastic, phialidic, discrete, ampulliform to cylindrical, aseptate conidiogenous cells, and solitary, aseptate, oblong to ellipsoidal, initially hyaline, becoming brown at maturity conidia (Liu et al. 2015, Pem et al. 2024). In this study, we introduce *Palmiascoma chiangraiense* as a novel species found on decaying wood of *Dipterocarpus alatus* from Doi Tung National Park, Thailand.

***Palmiascoma chiangraiense* N. Afshari, Lumyong & K.D. Hyde, sp. nov.**

Fig. 15

Index Fungorum number: IF904739; Facesoffungi number: FoF17219

Etymology – The specific epithet is derived from Chiang Rai, location where the holotype was collected.

Holotype – MFLU 24-0459

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* (excluding necks) 200–300 µm high, 240–300 µm diam. ($\bar{x}$ = 269 × 268 µm, n = 10), immersed, erumpent, gregarious, clustered, unilocular, mostly globose, dark brown to black, ostiolate. *Ostiole* 58–86 µm wide, centric, or eccentric, cylindrical, with hyaline periphyses in the canal. *Peridium* 36–55

μm wide, 2-layered, composed of *textura angularis* cells, outer layer brown and thick-walled cells, inner layer hyaline, thin-walled cells. *Hamathecium* comprises 1–2.8 μm wide, dense, aseptate pseudoparaphyses longer than asci, branched, and hyaline. *Asci* 49–72 $\times$ 7–11.5 μm ($\bar{x}$ = 58 $\times$ 9 μm , n = 25), 8-spored, bitunicate, fissitunicate, pedicellate, cylindric-clavate, slightly curved, shallow ocular chamber at the rounded apex. *Ascospores* 7.6–12 $\times$ 3.3–5 μm ($\bar{x}$ = 9.8 $\times$ 4.1 μm , n = 30), biserial, overlapping, 1-septate, mainly fusiform to ellipsoid, with obtuse ends, constricted at the septum, moderately wider upper cell, straight or slightly curved, pale brown to brown, rough-walled, guttulate. Asexual morph: Undetermined.

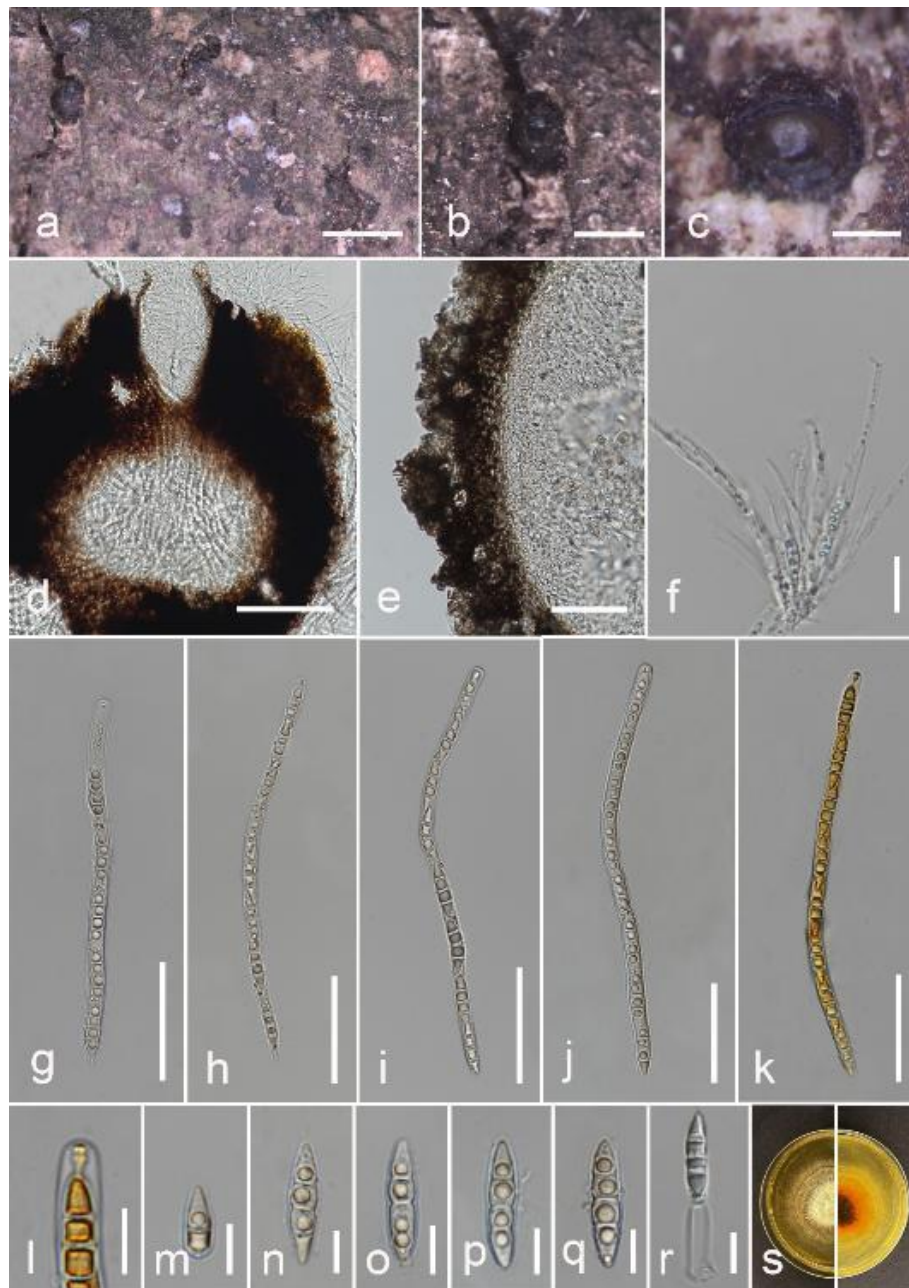


Figure 13 – *Melomastia thamplaensis* (MFLU 24-0411, a new host record). a, b Appearance of ascomata on *Nayariophyton zizyphifolium* woody litter. c Longitudinal section of ascoma. d Vertical section of ascoma. e Section of peridium. f Pseudoparaphyses. g–j Asci. k Ascus in Melzer’s reagent. l Apical ring in Melzer’s reagent. m–r Ascospores. s Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 500 μ m, c = 200 μ m, d = 100 μ m, e, g–k = 50 μ m, f = 20 μ m, l–r = 10 μ m.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes emerged from both cells. Colonies reached 50 mm diam. after 10 days at room temperature (25–28 °C), after one month irregular, flattened, dense, with two distinct layers, undulate edge, upper surface white in the center and creamy white at the margin, from reverse pale brown in the center and yellow at the margin

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T3R1a (MFLU 24-0459, holotype); ex-type living culture MFLUCC 24-0546.

GenBank numbers – ITS = PQ800249, LSU = PV072603, *rpb2* = PV138139, SSU = PV072696.

Notes – In the multigene phylogenetic analysis, our strain (MFLUCC 24-0546) formed a separate lineage sister to other *Palmiascoma* taxa, with 96% ML/ 1.0 PP support values (Fig. 14). Sequence comparison among *P. chiangraiense* (MFLUCC 24-0546) and ex-type species of *P. gregariascomum* (MFLUCC 11-0175), *P. qujingense* (KUMCC 19-0201), and *P. acericola* (CGMCC 3.24963) revealed 4.7%, 4.5%, and 8% base pair differences (excluding gaps) for the ITS region, 14.1%, 12.5%, and 16.2% base pair differences (excluding gaps) for *rpb2* sequence, which aligns with the new species concept proposed by Jeewon & Hyde (2016). Base pair differences in LSU (1.8–1.1–0.9%) and SSU (1.7–0.3–0.3%) were low, showing minor genetic variation among the studied taxa. This result aligns with Li et al. (2023a), which reported zero base pair differences in the LSU and SSU of closely related species. Morphologically, *P. chiangraiense* is most similar to the other three species in the shape and size of asci. However, *P. chiangraiense* has the widest peridium (36–55 μ m) compared with *P. gregariascomum* (10–50 μ m) and *P. acericola* (26–38 μ m), and its ascomata are larger (200–300 $\times$ 240–300 μ m) than those of *P. gregariascomum* (130–180 $\times$ 130–250 μ m) and *P. acericola* (170–240 $\times$ 180–210 μ m), but smaller than those of *P. qujingense* (280–400 $\times$ 200–300 μ m). Additionally, ascospores of *P. chiangraiense* are smaller than those of the other described species (7.6–12 $\times$ 3.3–5 μ m ($\bar{x}$ = 9.8 $\times$ 4.1 μ m), compared with *P. gregariascomum* (11–13 $\times$ 3–4 μ m, $\bar{x}$ = 11.9 $\times$ 3.9 μ m), *P. acericola* (12–14 $\times$ 3.5–4.5 μ m, $\bar{x}$ = 13 $\times$ 4 μ m), and *P. qujingense* (12–16 $\times$ 4.5–5.5 μ m, $\bar{x}$ = 14.1 $\pm$ 1.1 $\times$ 4.6 $\pm$ 0.5 μ m). Thus, based on morphology and phylogenetic evidence we introduce *P. chiangraiense* as a new species.

***Corynesporascaceae* Sivan.**

Corynesporascaceae, established by Sivanesan (1996), was initially associated with *Melanommatales* based on morphological characteristics. Hyde et al. (2013) reclassified it within *Pleosporales* in *Dothideomycetes*, a classification subsequently confirmed by Wijayawardene et al. (2014). A comprehensive study by Liu et al. (2017) revealed that *Corynesporascaceae* is closely related to suborders *Massarineae* and *Pleosporineae* within *Pleosporales*. Species within *Corynesporascaceae* are notable for causing foliar diseases in plants, particularly in tropical and subtropical regions (Hyde et al. 2013). Only hyphomycetous asexual morph is known while, the

sexual morph is unknown. They are distinguished by large, pale olivaceous, multi-distoseptate conidia that may exhibit percurrent proliferation, terminal monotretic conidiogenous cells, and dark, unbranched conidiophores. (Li et al. 2023a). This family includes two genera (*Corynespora*, and *Corynesporasca*) (Hyde et al. 2024a).

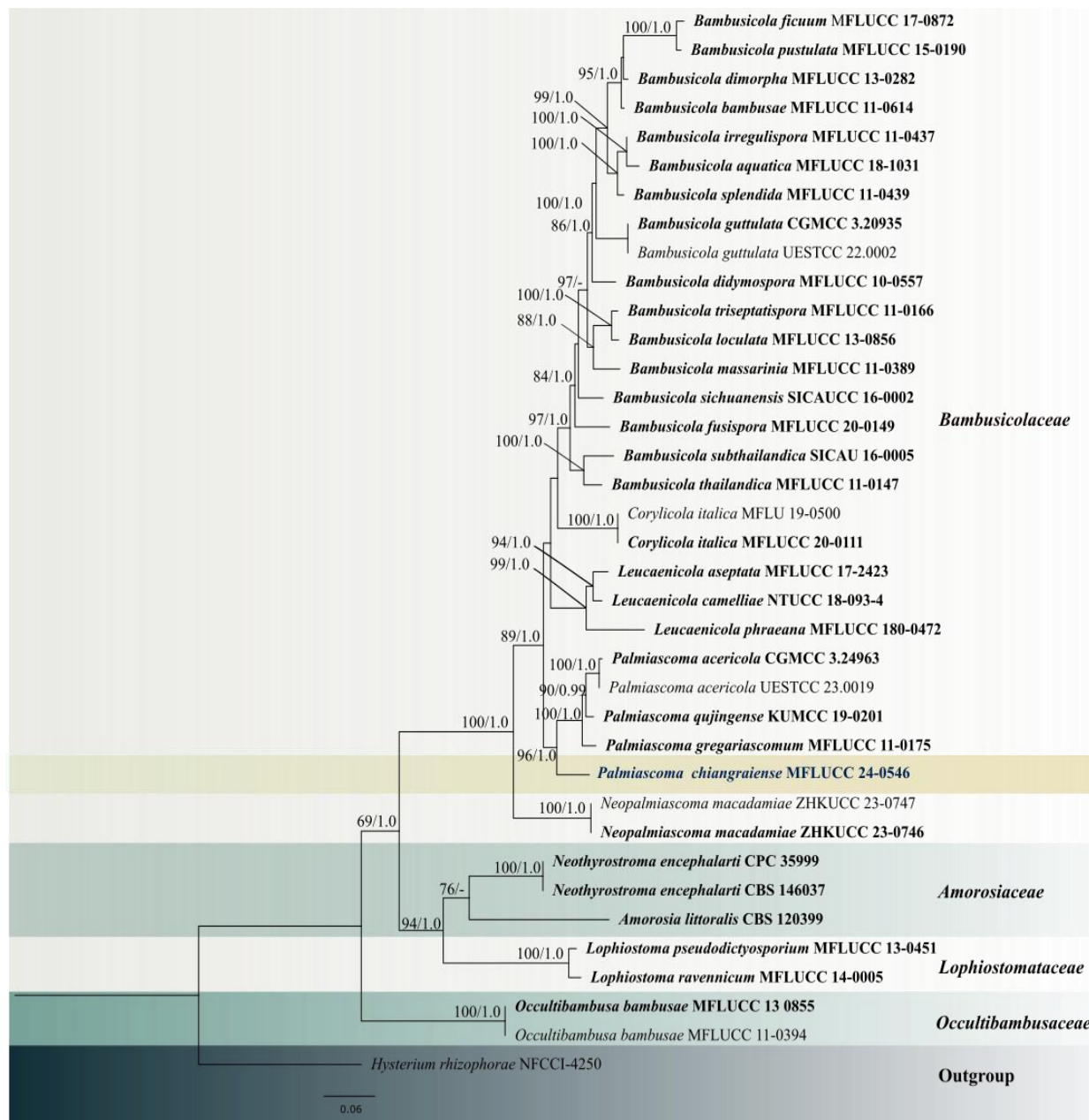


Figure 14 – Phylogram generated from maximum likelihood analysis based on the combined ITS, LSU, *rpb2*, SSU, and *tefl-α* sequence data of taxa in *Bambusicolaceae* and some closely related families. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Thirty-seven strains are included in the combined analyses which comprised 4,594 characters (ITS = 746, LSU = 842, *rpb2* = 1,044, SSU = 1,009, and *tefl-α* = 953). The best RAXML tree with a final optimization likelihood value of -25969.117748 is presented. The matrix had 1,638 distinct

alignment patterns, with 22.40% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244225, C = 0.253263, G = 0.272221, T = 0.230290; substitution rates AC = 1.172257, AG = 2.558523, AT = 1.017371, CG = 0.976434, CT = 6.204100, GT = 1.000000; gamma distribution shape parameter α = 0.202896. In the Bayesian analysis, average standard deviation of split frequencies at the end of 5,000,000 MCMC generations was calculated as 0.001347. The evolutionary models TIM2+I+G were applied for ITS and *tefl*- α , TrN+I+G were applied for LSU and *rpb2*, and TIM2+I was applied for SSU sequence data in BI analysis. Bootstrap support values for maximum likelihood greater than or equal to 65% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Hysterium rhizophorae* (NFCCI-4250). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

***Corynespora* Güssow**

Index Fungorum number: IF7795; Facesoffungi number: FoF06663

Corynespora was described by Güssow (1905), with *C. mazei* as the type species. Wei (1950) proposed that *C. mazei* should be regarded as synonymous with *Helminthosporium cassicola*, leading to the new combination, *C. cassicola*. The defining characteristics of this genus include distinctive conidiophores that are determinate or percurrent, along with integrated conidiogenous cells that produce single or occasionally catenate, distoseptate conidia (Ellis 1971, Pem et al. 2024). *Corynespora* comprises 182 recognized species, mostly distinguished by their physical characteristics (Hongsanant et al. 2025). Leaf spots, fruit rots, and root rots are symptoms of disease caused by *Corynespora*. The most prevalent symptom is leaf spots, which are brown to black, irregular to circular lesions that eventually grow into larger spots (Jayawardena et al. 2025). In this study, we describe *Corynespora chiangraiensis* as a novel species on dead wood of *Nayariophyton zizyphifolium* from Doi Tung National Park, Thailand.

***Corynespora chiangraiensis* N. Afshari, Lumyong & K.D. Hyde, sp. nov.**

Fig. 17

Index Fungorum number: IF904740; Facesoffungi number: FoF17220

Etymology – The specific epithet is derived from Chiang Rai, location where the holotype was collected.

Holotype – MFLU 24-0460

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate, effuse, hairy, scattered or in small groups, glistening, dark brown to black. *Mycelium* superficial and immersed in the substratum, composed of septate, branched, pale brown to hyaline, smooth-walled hyphae. *Conidiophores* 220–370 $\times$ 8–13 μ m ($\bar{x}$ = 255 $\times$ 11.5 μ m, n = 10), macronematous, mononematous, solitary, unbranched, straight or slightly flexuous, cylindrical, smooth, thick-walled, brown to dark brown, rounded and paler at apex, 6–10-septate. *Conidiogenous cells* 23.5–28 $\times$ 10–13 μ m ($\bar{x}$ = 25.7 $\times$ 12 μ m, n = 5), terminal, integrated, monotretic, monoblastic, cylindrical, pale brown. *Conidia* 100–150 $\times$ 12–14 μ m ($\bar{x}$ = 128 $\times$ 25 μ m, n = 15; L/W ratio = 5.1), solitary, acrogenous, obclavate, rostrate, straight or slightly curved, thick-walled, brown, 11–20-distoseptate, guttulate, thick-walled, smooth-walled, golden brown, truncate at base, hila darkened.

Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes emerge from both end cells. Colonies on PDA reached 4.5 cm diam. after 3 weeks at room temperature (25–28 °C), after one month irregular, flattened, medium dense, wavy margin, pigment diffusing

in the agar after one-month, upper surface initially white, becoming dirty-white in the center and creamy white at outer zone with age, from reverse dark brown in the center and brown at margin.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T2R7a (MFLU 24-0460, holotype); ex-type living culture MFLUCC 24-0548.

GenBank numbers – ITS = PQ800250, LSU = PV072604, *rpb2* = PV138140, SSU = PV072697.

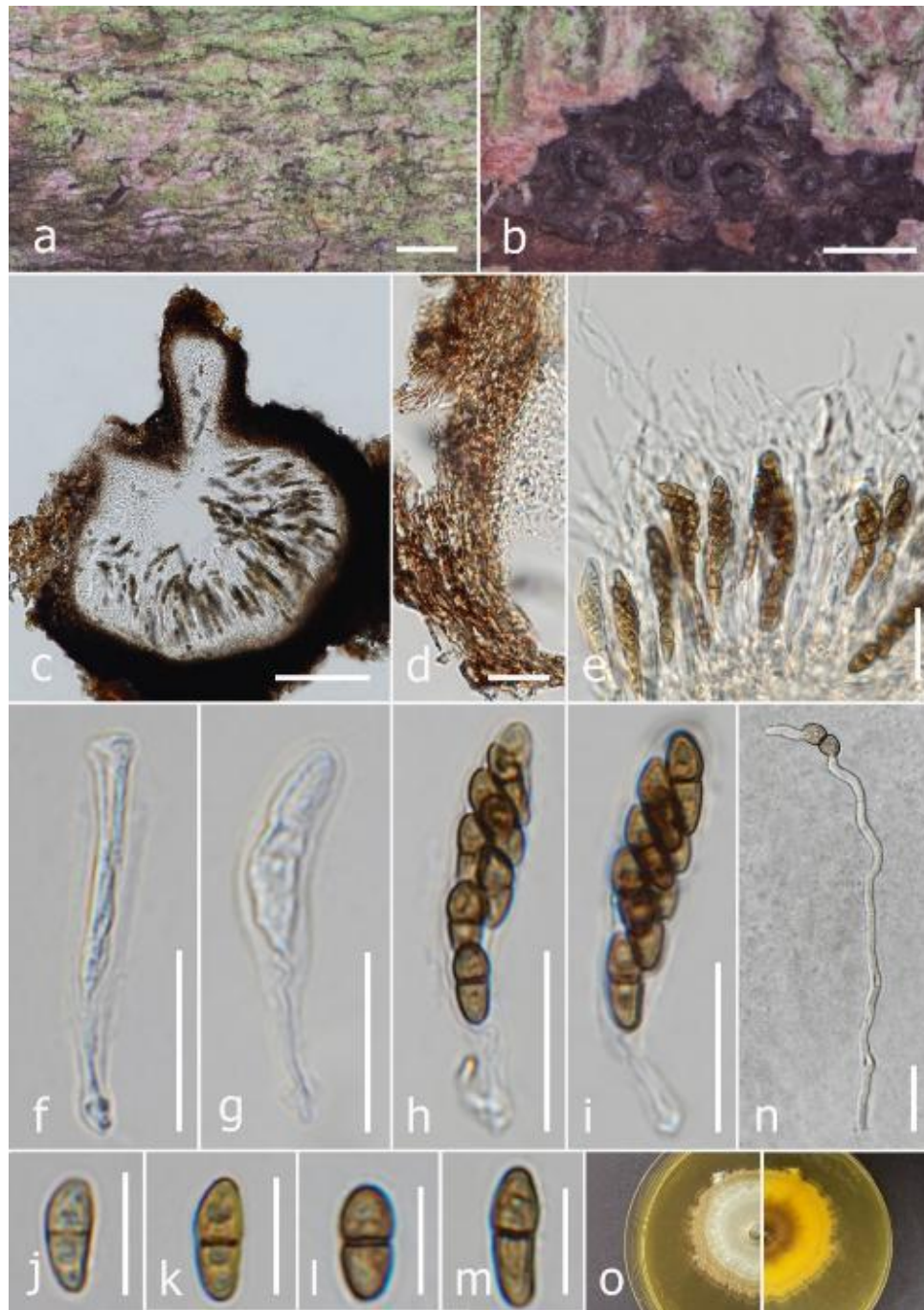


Figure 15 – *Palmiascoma chiangraiense* (MFLU 24-0459, holotype). a Appearance of ascomata on *Dipterocarpus alatus* woody litter. b Longitudinal section of ascomata. c Vertical section through ascoma. d Section of peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n A germinated ascospore. o Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 500 μ m, c, j–m = 100 μ m, d–i, n = 20 μ m.

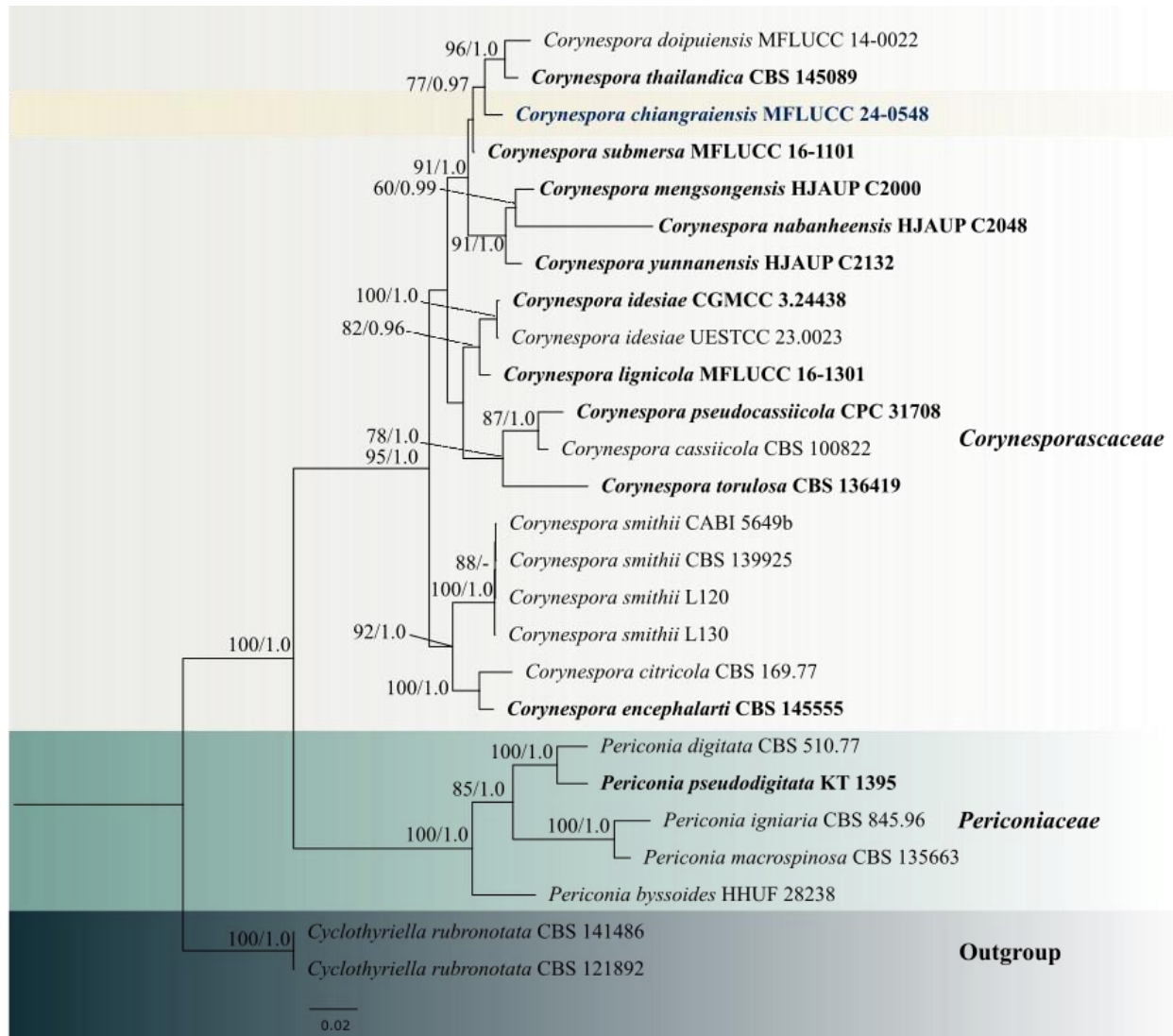


Figure 16 – Phylogram generated from Bayesian Inference (BI) analysis based on the combined ITS, LSU, *rpb2*, SSU, and *tef1- α* sequence data of *Corynesporascaceae* and *Periconiaceae*. Tree topology of Bayesian analysis is similar to the maximum likelihood analysis. Twenty-six strains are included in the combined analyses which comprised 4,347 characters (ITS = 553, LSU = 859, *rpb2* = 1,055, SSU = 1,032, and *tef1- α* = 848). The best RAXML tree with a final optimization likelihood value of -13512.755957 is presented. The matrix had 833 distinct alignment patterns, with 46.72% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251343, C = 0.242038, G = 0.274840, T = 0.231780; substitution rates AC = 2.635320, AG = 3.533685, AT = 1.523914, CG = 1.719781, CT = 9.802443, GT = 1.000000; gamma distribution shape parameter α = 0.164397. In the Bayesian analysis, average standard deviation of split

frequencies at the end of 3,000,000 MCMC generations was calculated as 0.003907. The evolutionary models SYM+G, TIM2+I, TIM3+I+G, were applied for ITS, LSU, *rpb2*, and TrN+I+G, were applied for SSU, and *tefl*- α sequence data, respectively in BI analysis. Bootstrap support values for ML greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Cylothyriella rubronotata* (CBS 141486) and *C. rubronotata* (CBS 121892). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Notes – In the combined ITS, LSU, *rpb2*, SSU, and *tefl*- α phylogenetic analysis (Fig. 16), our strain (MFLUCC 24-0548) forms a sister clade to *C. thailandica* (CBS 145089) and *C. doipuiensis* (MFLUCC 14-0022) with 77% ML/ 0.97 PP bootstrap support. The nucleotide differences between ITS of our collection and *C. thailandica* (CBS 145089) and *C. doipuiensis* (MFLUCC 14-0022) are 1.3% and 4.6% (excluding gaps), respectively. *Corynespora chiangraiensis* (MFLU 24-0460) resembles *C. thailandica* (CBS 145089), and *C. doipuiensis* (MFLUCC 14-0022) in having macronematous, thick-walled conidiophores and conidia. However, *C. chiangraiensis* differs from *C. thailandica* in having wider conidia ($100\text{--}150 \times 12\text{--}14\text{ }\mu\text{m}$, L/W ratio = 5.1, vs. $(50\text{--})80\text{--}110\text{--}200 \times (9\text{--})10\text{--}12\text{--}13\text{ }\mu\text{m}$, L/W ratio = 8.5). with more septa (11–20 vs. 4–8). *Corynespora doipuiensis* (MFLUCC 14-0022) has larger conidiophores ($212\text{--}426 \times 10\text{--}15\text{ }\mu\text{m}$ ($\bar{x} = 313.45 \times 13.89\text{ }\mu\text{m}$, $n = 40$)), larger conidiogenous cells ($27\text{--}5(?) \times 10\text{--}16\text{ }\mu\text{m}$ ($\bar{x} = 33.71 \times 13.34\text{ }\mu\text{m}$)), larger conidia ($136\text{--}165 \times 5\text{--}25.5\text{ }\mu\text{m}$ ($\bar{x} = 143.7 \times 21.31$)). These three species were collected from dead wood in Thailand (Crous et al. 2018a, Hyde et al. 2020a). Based on the morphological evidence coupled with multigene phylogeny, the current study presents *C. chiangraiensis* as a new species.

***Didymosphaeriaceae* Munk**

Munk (1953) introduced *Didymosphaeriaceae* and typified the family by *Didymosphaeria*, with *D. epidermidis* as the type species, in *Pleosporales*. The family contains morphologically diverse taxa, with most having uni-septate, brown ascospores. The asexual morphs can be coelomycetes or hyphomycetes, and can be camarosporium-like, *Diplodia*, *Fusicladium*, *Pithomyces*, *Phoma*, and spigazzinia-like (Boonmee et al. 2021, Wijayawardene et al. 2021). These fungi are found worldwide and are mostly saprobes, but some are pathogens or endophytes (Tennakoon et al. 2022a). According to Hyde et. al. (2024a) this family comprises 39 genera. Members of this group can be found on woody and herbaceous hosts as saprobes, endophytes, or pathogens, and they can even occasionally infect humans. They are distinguished by bitunicate asci, brown, septate to muriform ascospores, and globose to subglobose, immersed to semi-immersed ascomata with a central ostiole. The asexual forms resemble *Phoma* or *Fusicladium* (Hyde et al. 2013).

***Chromolaenicola* Mapook & K.D. Hyde**

Index Fungorum number: IF557279; Facesoffungi number: FoF07783

Chromolaenicola was erected by Mapook et al. (2020) to accommodate *C. nanensis* that was isolated from dead stems of *Chromolaena odorata* in Thailand. Multigene phylogenetic analyses incorporating LSU, ITS, SSU, and *tefl*- α sequence data revealed that *Chromolaenicola* species form a monophyletic clade within *Didymosphaeriaceae*. The sexual morph has immersed to semi-immersed ascomata with bitunicate asci. The asexual morph forms pycnidial conidiomata

(Mapook et al. 2020). In this study, we describe *Chromolaenicola doitungensis* and as a novel taxon on dead wood of *Nayariophyton zizyphifolium* from Thailand.

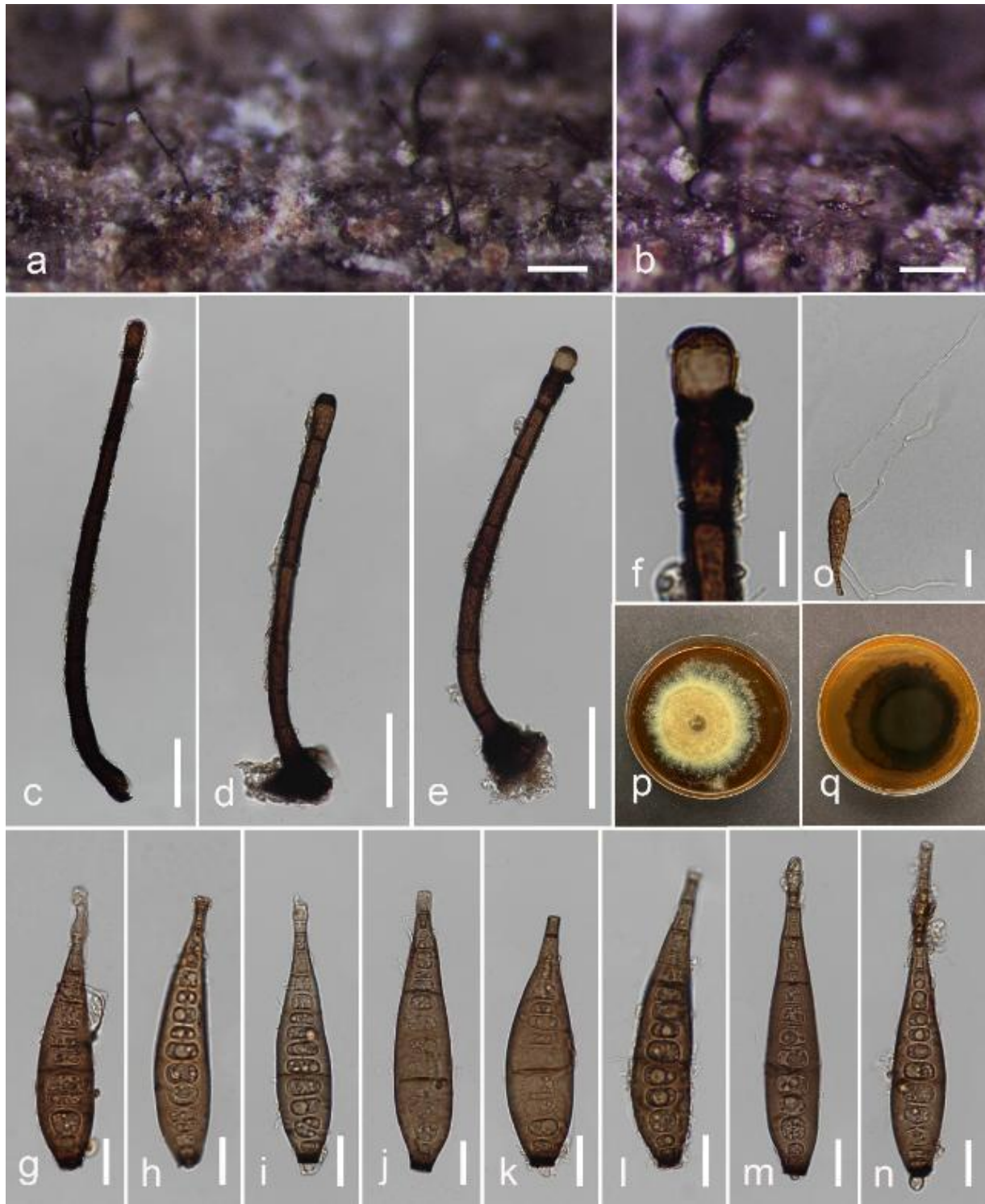


Figure 17 – *Corynespora chiangraiensis* (MFLU 24-0460, holotype). a, b Colonies on *Nayariophyton zizyphifolium* woody litter. c–e Conidiophores and conidiogenous cells. f Apical

conidiophores and conidiogenesis. g–n Conidia. o A germinated conidium. p, q Colony on PDA (front and reverse). Scale bars: a, b = 200 μ m, c–e, o = 50 μ m, g–n = 20 μ m, f = 10 μ m.

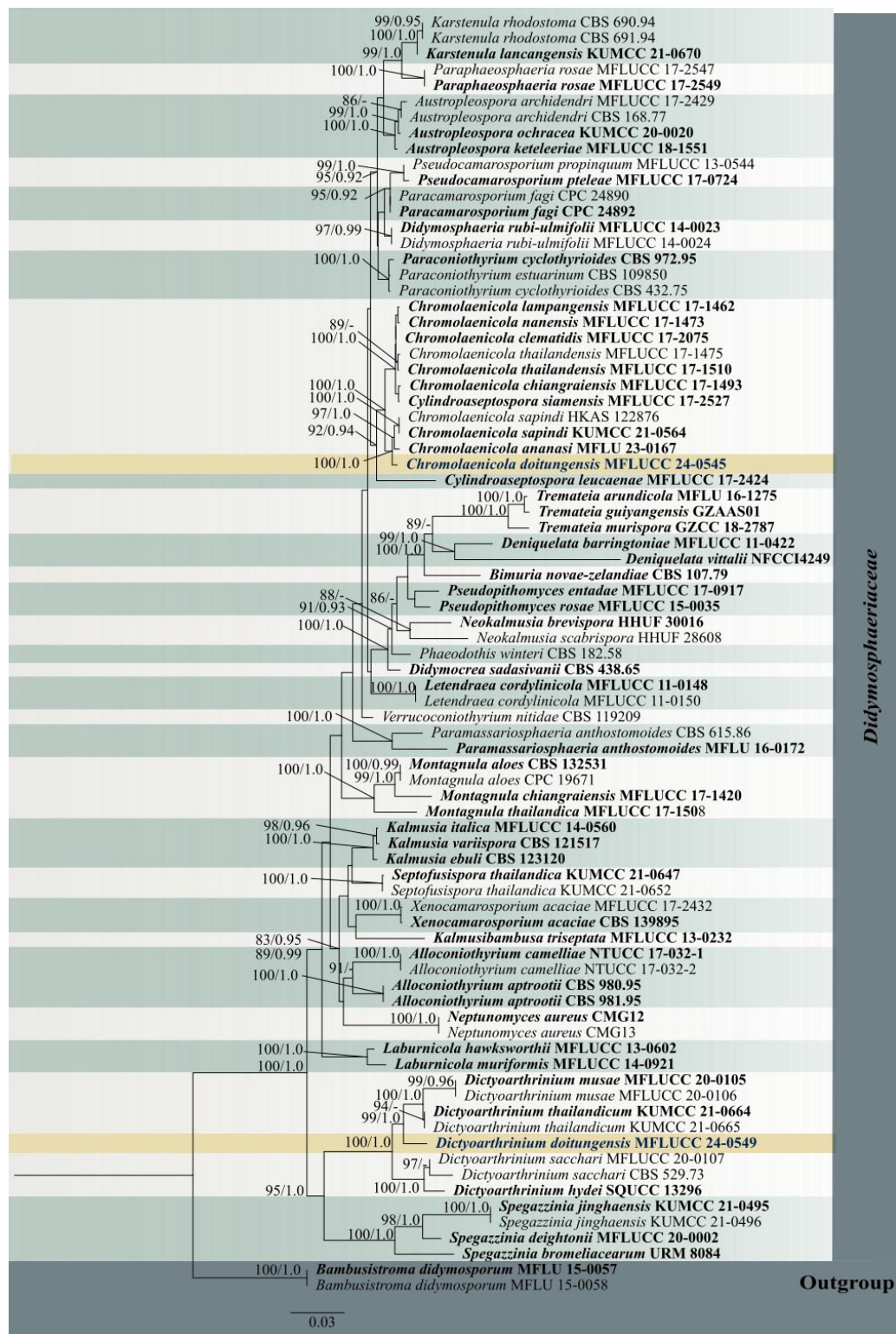


Figure 18 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, SSU, and *tefl-α* sequence data of *Didymosphaeriaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Eighty-one strains are included in the combined analyses which comprised 2,801 characters (SSU = 733, LSU = 779, ITS = 422 and *tefl-α* = 867). The best score for log-likelihood of consensus tree is -15824.137. The matrix had 762 distinct alignment patterns, 555 parsimony-informative, 174 singleton sites, 2072 constant sites. Individual models K2P+G4, TNe+I+G4, TIM2+F+I+G4 and TN+F+I+G4 were applied SSU, LSU, ITS, and *tefl-α* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.005775. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Bambusistroma didymosporum* (MFLU 15-0057) and *B. didymosporum* (MFLU 15-0058). Ex-type strains are in bold. The isolates generated in this study are indicated in bold and blue.

Chromolaenicola doitungensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 19

Index Fungorum number: IF904741; Facesoffungi number: FoF17221

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which the fungus was collected.

Holotype – MFLU 24-0461

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 105–270 µm diam, 140–205 µm high ($\bar{x}$ = 200 × 175 µm, n = 5), pycnidial, unilocular, mostly solitary or in small groups, mostly subglobose or conical, immersed, coriaceous, brown to dark brown, ostiolate. *Conidiomatal wall* 15–25 µm wide, composed of two layers, outer brown thick-walled *textura angularis* cells linked with hyaline and loosely packed *textura angularis* cells bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.7–8.3 × 2.5–4 µm ($\bar{x}$ = 6.5 × 3.4 µm, n = 20), phialidic, enteroblastic, discrete, determinate, hyaline, cylindrical and moderately truncate towards apex, smooth-walled, arising from the inner layer of pycnidial wall. *Conidia* 5–7 × 3.5–5.4 µm ($\bar{x}$ = 6.1 × 4.2 µm, n = 50), L/W ratio = 1.5, oblong or oval, rounded at both ends, hyaline to pale brown when immature, brown at maturity, mostly aseptate, rarely 1-septate, verrucose, rough-walled.

Culture characteristics – Colonies on PDA reaching 3–3.5 cm diam. after 2 weeks at room temperature (25–28 °C), circular, dense, undulate edge, umbonate, fluffy upper surface covered with cream to salmon aerial mycelium, reverse dark brown at the center, light brown radiating outwardly.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T3R7a (MFLU 24-0461, holotype); ex-type living culture MFLUCC 24-0545.

GenBank numbers – ITS = PQ800251, LSU = PV072605, SSU = PV072698, *tefl-α* = PX739629.

Notes – In the phylogenetic analysis, the isolates of *Chromolaenicola doitungensis* (MFLUCC 24-0545), *C. sapindi* (HKAS 122789, HKAS 122876), and *C. ananasi* (MFLU 23-0167) form an independent clade. Among these close relatives, *C. doitungensis* forms a separate branch with 100% ML and 1.00 PP bootstrap support (Fig. 18). Comparison of ITS and *tefl-α* gene regions between *C. doitungensis* (MFLUCC 24-0545) and *C. ananasi* indicated 1.4% (6/426), and 1.2% (11/4902) base pair differences (excluding gaps), respectively. *Chromolaenicola sapindi*

was described by Ren et al. (2022) from sexual morph characters. *Chromolaenicola doitungensis* differs from *C. ananasi* in having smaller conidia ($5\text{--}7 \times 3.5\text{--}5.4\text{ }\mu\text{m}$, $\bar{x} = 6.1 \times 4.2\text{ }\mu\text{m}$ vs. $7\text{--}8 \times 4\text{--}5\text{ }\mu\text{m}$, $\bar{x} = 8 \times 5\text{ }\mu\text{m}$). *Chromolaenicola ananasi* was isolated from dead leaves of *Ananas comosus* in Thailand (Tian et al. 2024). In addition, in our strain, conidiophores are reduced to conidiogenous cells. Also, it has smaller conidia ($3.5\text{--}5.4 \times 5\text{--}7\text{ }\mu\text{m}$ ($\bar{x} = 4.2 \times 6.1\text{ }\mu\text{m}$, $n = 50$) vs. $7\text{--}8 \times 4\text{--}5\text{ }\mu\text{m}$ ($\bar{x} = 8 \times 5\text{ }\mu\text{m}$)) mostly aseptate at maturity, compared to *C. ananasi* (Tian et al. 2024). *Chromolaenicola doitungensis* (MFLU 24-0461) is introduced as a novel species based on its morphology and phylogenetic analysis of a combined ITS, LSU, SSU, and *tef1*- α dataset.

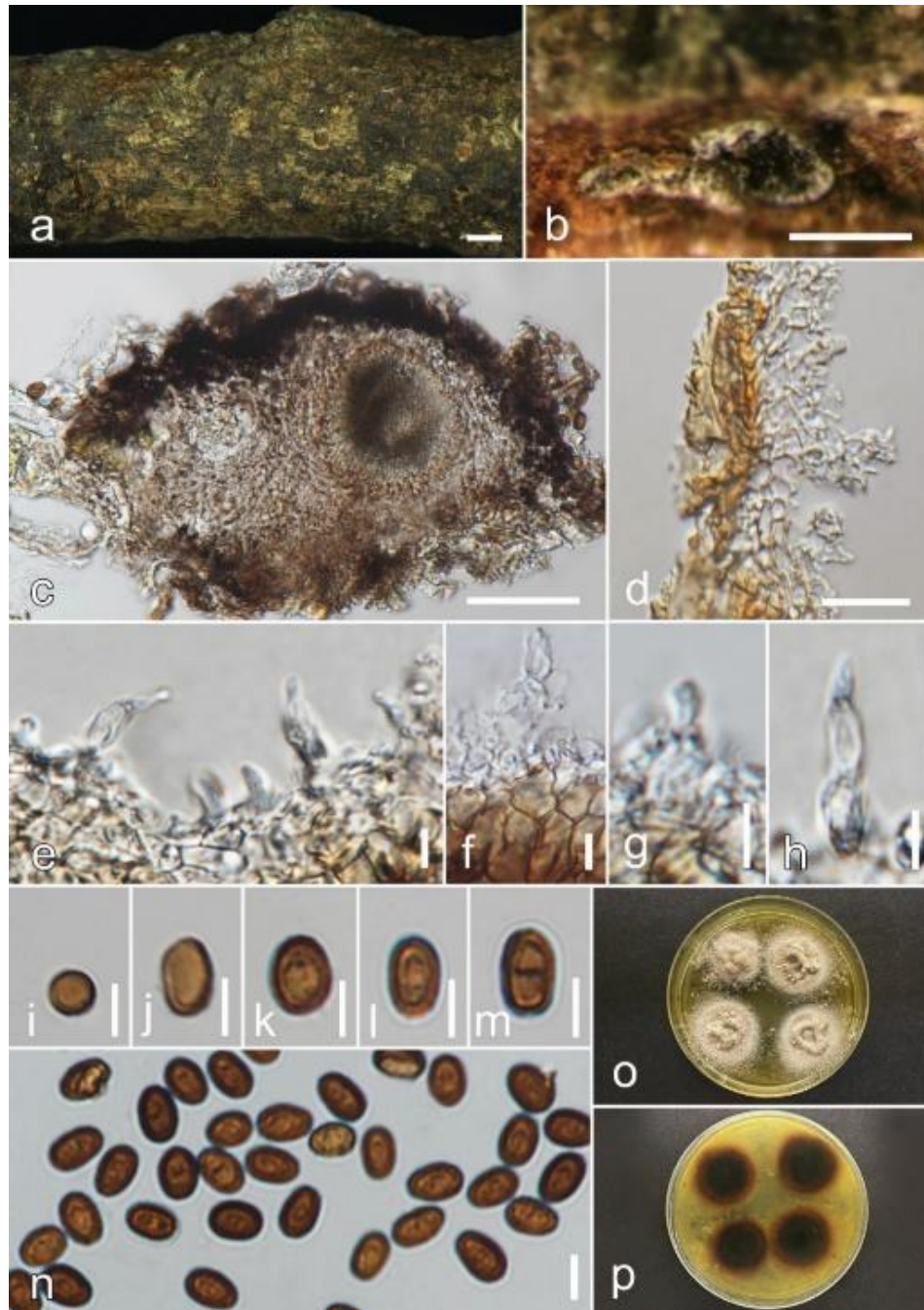


Figure 19 – *Chromolaenicola doitungensis* (MFLU 24-0461, holotype). a Conidiomata on *Nayariophyton zizyphifolium* woody litter. b Longitudinal section of the conidiomata c Vertical section through a conidioma. d Section through conidiomatal wall. e–h Conidiogenous cells. i–n Conidia. o, p Colonies on PDA (front and reverse). Scale bars: a = 2.5 mm, b = 500 μ m, c = 100 μ m, c = 50 μ m, d = 20 μ m, e–n = 5 μ m.

***Dictyoarthrinium* S. Hughes**

Index Fungorum number: IF7993; Facesoffungi number: FoF12991

Dictyoarthrinium was erected by Hughes (1952), and is typified by *D. quadratum*. This genus has unique basauxic conidiogenous cell development; conidiophores are minutely verruculose, subhyaline and transversely septate. Conidiophore mother cells are often hyaline or pale brown and cup-shaped or subspherical. Moreover, conidia are square to spherical, subspherical or oblong, pale to dark brown, often 4-celled, and sometimes 16-celled. The surface of conidia is verruculose, and in most species have warts. The sexual morph of *Dictyoarthrinium* is currently unknown (Hughes 1952, Ellis 1971, Matsushima 1971, Samarakoon et al. 2020). All *Dictyoarthrinium* species were documented based only on morphological characters. Hyde et al. (1998) accommodated *Dictyoarthrinium* in *Apiosporaceae* (*Xylariales*, *Sordariomycetes*) based on morphological characteristics. LSU data of *D. sacchari* (CBS 529.73) were submitted to GenBank as the first authentic molecular record for the genus by Vu et al. (2019). Samarakoon et al. (2020) transferred *Dictyoarthrinium* from *Apiosporaceae* to *Didymosphaeriaceae* (*Pleosporales*, *Dothideomycetes*) according to phylogenetic analyses of combined SSU, LSU, ITS, and *tef1- α* sequence data. Ten species are known in this genus in Index Fungorum (2025). In this study, we introduce *Dictyoarthrinium doitungensis* as a novel species on woody litter of *Nayariophyton zizyphifolium* from Doi Tung National Park, Thailand.

***Dictyoarthrinium doitungensis* N. Afshari, Lumyong & K.D. Hyde, sp. nov.**

Fig. 20

Index Fungorum number: IF904742; Facesoffungi number: FoF17222

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which the fungus was collected.

Holotype – MFLU 24-0462

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, irregular, pulvinate, dark brown to black. *Mycelium* superficial, branched anastomosing hyphae. *Conidiophores* 140–285(–300) $\times$ 5.5–9.3 μ m ($\bar{x}$ = 215 $\times$ 7 μ m, n = 20), macronematous, basauxic, branched, brown, cylindrical, slightly tapering and paler toward apex, erect, straight or flexuous, brown (mostly same colour as conidiophore) transverse septa 3.2–11(–13) μ m apart, smooth-walled. *Conidiogenous cells* 8–16.3 $\times$ 4.7–8 μ m ($\bar{x}$ = 12 $\times$ 6.5 μ m, n = 10), blastic, integrated, terminal, frequently becoming intercalary, denticles absent, cylindrical, brown. *Conidia* (4.6–)6.7–9 $\times$ 5.2–9 μ m ($\bar{x}$ = 7.8 $\times$ 6.7 μ m, n = 20; L/W ratio = 1.2), solitary, spherical to ellipsoid, holoblastic, 1-celled, subhyaline to greyish-brown when immature, cruciate-septate, 4-cells, constricted at septa, rounded at the corners, spherical or subspherical, verruculose, greyish-brown at maturity, occasionally mature conidium splits along one line of the septa.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerged from each cell. Colonies on PDA reached 5–5.5 cm diam. after 3 weeks at room temperature (25–28 $^{\circ}$ C), circular, with umbonate elevation, velvety, dense in the middle, mycelia

radiating outwards, entire edge, upper surface white, from reverse pale brown at center becoming radiantly yellow to the edge.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T3R6a (MFLU 24-0462, holotype); ex-type living culture MFLUCC 24-0549.

GenBank numbers – ITS = PQ800252, LSU = PV072606, SSU = PV072699, *tefl-α* = PX739630.

Notes – Our isolate (MFLUCC 24-0549) clustered within other *Dictyoarthrinium* species, sister to *D. musae* and *D. thailandicum* with 99% ML bootstrap and 1.0 PP support (Fig. 18). The nucleotide differences between ITS of our collection and *D. musae* (MFLUCC 20-0105) and *D. thailandicum* (KUMCC 21-0664) are 4% and 4.5% (excluding gaps), respectively. Morphologically, *D. doitungensis* is similar to the holotype of closely related species, *D. musae* and *D. thailandicum*, by having macronematous, basauxic conidiophores, cylindrical conidiogenous cells, and shape of conidia (Samarakoon et al. 2020, Ren et al. 2022). Conidiogenous cells of *D. doitungensis* are integrated, terminal like other species but frequently become intercalary, and brown. The colour of the transverse septa in *D. doitungensis* does not significantly contrast with the other parts of the conidiophore, unlike in the two other species. The conidiophores and conidiogenous cells of *D. doitungensis* ($140\text{--}285\text{--}(300) \times 5.5\text{--}9.3 \mu\text{m}$; $8\text{--}16.3 \times 4.7\text{--}8 \mu\text{m}$) are larger than those of *D. musae* ($30\text{--}140 \times 1\text{--}2 \mu\text{m}$; $4.1\text{--}4.5 \times 4.3\text{--}4.7 \mu\text{m}$) and *D. thailandicum* ($130\text{--}220 \times 4\text{--}5 \mu\text{m}$; $3\text{--}7 \times 3\text{--}5 \mu\text{m}$), respectively. However, the conidia of *D. doitungensis* ($(4.6\text{--})6.7\text{--}9 \times 5.2\text{--}9 \mu\text{m}$) are smaller than those of *D. musae* ($7\text{--}11.5 \times 6.5\text{--}9 \mu\text{m}$) and *D. thailandicum* ($9\text{--}11 \times 8.5\text{--}10.5 \mu\text{m}$) (Samarakoon et al. 2020, Ren et al. 2022). *Dictyoarthrinium doitungensis* is described as a new species due to its distinct morphology and molecular differences from other *Dictyoarthrinium* sequences in the combined SSU, LSU, ITS, *tefl-α* dataset.

***Paraconiothyrium* Verkley**

Index Fungorum number: IF500080; Facesoffungi number: FoF00053

Paraconiothyrium was erected by Verkley et al. (2004) to accommodate four species based on morphology and phylogeny (ITS and SSU gene regions). Currently 32 species of *Paraconiothyrium* have been listed in Index Fungorum (2025). Conidiomata are typically estromatic or pycnidial, solitary, subglobose to globose, and have relatively thick walls. Conidiophores are reduced to conidiogenous cells that are phialidic, conical to subulate or subcylindrical, doliiform or elongated ampulliform shapes. Conidia are variously-shaped, initially hyaline, 0–1-septate, either smooth-walled or minutely verrucose, and range from hyaline to brown. *Paraconiothyrium fuckelii*, *P. magnoliae*, *P. thysanolaenae*, and *P. iridis* were documented for their sexual morphology, with only *P. fuckelii* displaying both sexual and asexual forms (Wang et al. 2021b). DNA-based comparative studies have proven valuable in phylogenetics and have been employed to assess the genetic diversity of *Paraconiothyrium*. For instance, *Paraconiothyrium* shares similarities with *Coniothyrium sensu stricto* and *Alloconiothyrium* from two different families. Therefore, phylogenetic analysis is necessary to determine the appropriate generic classification of *Paraconiothyrium*-like species (Wijayawardene et al. 2016). In this study, we document *Paraconiothyrium archidendri* as the first sexual morph and a new host record on *Dipterocarpus alatus* from Doi Tung National Park, Thailand. An updated phylogenetic tree for the genus *Paraconiothyrium* is shown in Fig. 21.



Figure 20 – *Dictyoarthrinium doitungensis* (MFLU 24-0462, holotype). a, b Colonies on *Nayariophyton zizyphifolium* woody litter. c–f Conidiophores. g–i Developing stage of immature lateral conidia. j–o Conidia. p A germinated conidium. q, r Colonies on PDA (front and reverse). Scale bars: a = 200 μ m, b = 100 μ m, c–f, p = 50 μ m, g–i = 20 μ m, j–o = 10 μ m.

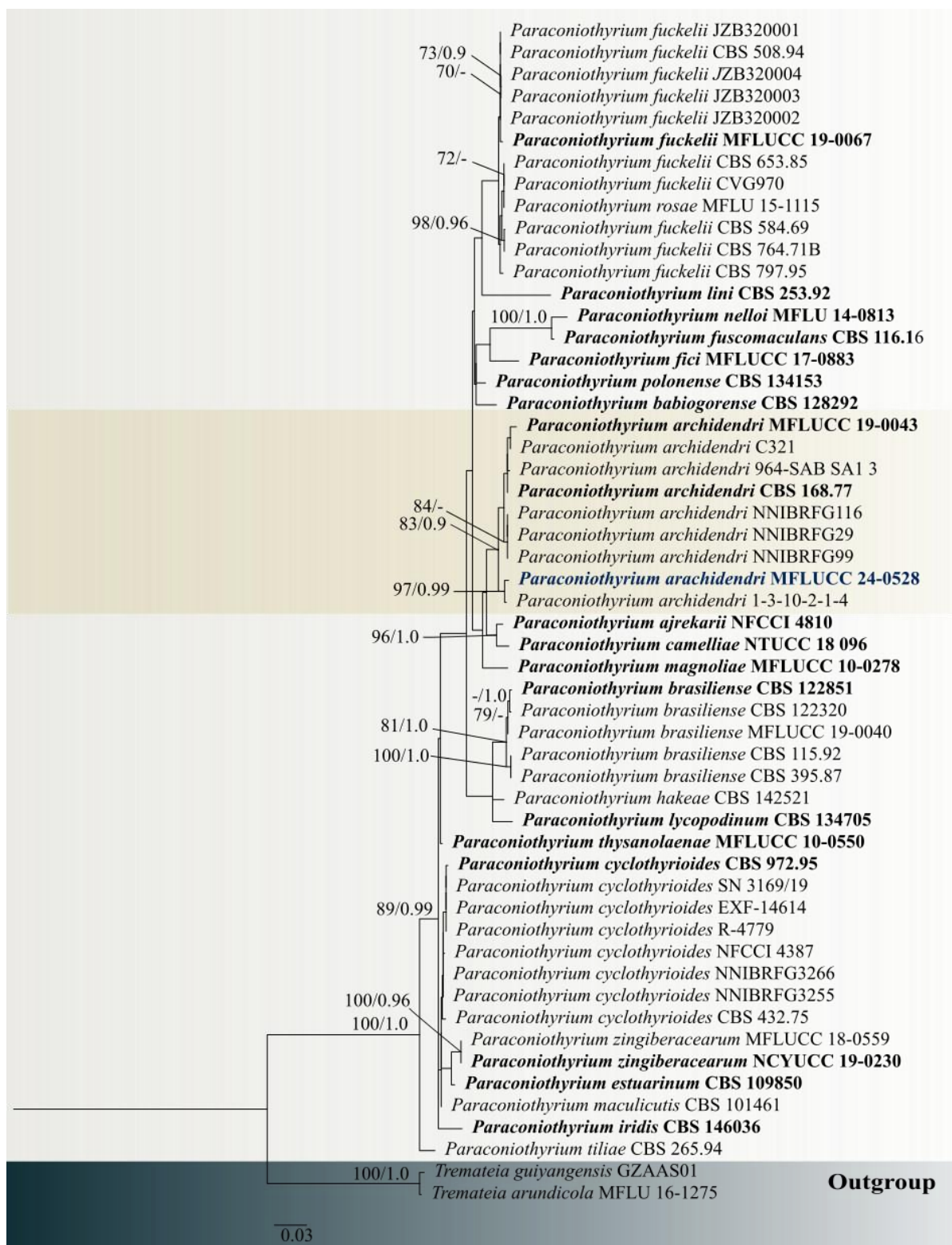


Figure 21 – Phylogram generated from maximum likelihood analysis based on the combined ITS, LSU, and *tub2* sequence data of *Paraconiothyrium*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Fifty-four strains are included in the combined analyses

which comprised 2,307 characters (ITS = 504, LSU = 1,358, and *tub2* = 445). The best RAxML tree with a final optimization likelihood value of -7497.531186 is presented. The matrix had 580 distinct alignment patterns, with 40.45% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231688, C = 0.247955, G = 0.281583, T = 0.238774; substitution rates AC = 1.488240, AG = 3.323098, AT = 1.440713, CG = 0.961639, CT = 6.911311, GT = 1.000000; gamma distribution shape parameter α = 0.136352. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.012683. The evolutionary models TrN+I+G, were applied for ITS, and LSU, and TPM2uf+G were applied for *tub2* sequence data. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Tremateia guiyangensis* (GZAAS01) and *T. arundicola* (MFLU 16-1275). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Paraconiothyrium archidendri Verkley, Göker & Stielow, in Verkley et al. Persoonia 32, 37 (2014). 22

Index Fungorum number: IF800761; Facesoffungi number: FoF 05243.

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 174–232 μ m high $\times$ 211–288 μ m diam. ($\bar{x}$ = 212 $\times$ 242 μ m, n = 5), less commonly solitary or 2–4-clustered, semi-immersed, erumpent, unilocular, compressed globose, coriaceous, dark brown to black. *Peridium* 15.5–27 μ m wide ($\bar{x}$ = 20 μ m, n = 35), outer layer comprises dark brown, thick-walled, tightly packed cells of *textura angularis*, inner layer comprises hyaline, thin-walled, loosely packed cells of *textura angularis*. *Hamathecium* comprises 1.6–3 μ m wide ($\bar{x}$ = 2.0 μ m, n = 25), filiform to cylindrical, aseptate, branched, cellular pseudoparaphyses. *Asci* 60–95(–120) $\times$ 6.5–8.5 μ m ($\bar{x}$ = 76 $\times$ 7.8 μ m, n = 20), bitunicate, fissitunicate, 8-spored, mostly clavate to cylindric-clavate, moderately curved, shallow ocular chamber at the rounded apex. *Ascospores* 10–14.5 $\times$ 3.5–6 μ m ($\bar{x}$ = 12.5 $\times$ 4.5 μ m, n = 30), overlapping 1–2-seriate, light brown, oblong to fusiform, straight or sometimes curved, 1-septate at middle, constricted at septum, slightly pointed at ends, thick-walled, guttulate, without a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h. Colonies reaching 35 mm diam. after 10 days on PDA at room temperature (25–28 °C), circular, umbonate, wrinkled folded in the middle, velvety, dense, non-pigmented, with two distinct layers, narrow towards fringe, at upper surface white, from reverse white at the margin, yellowish-brown in the center.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T1R4a (MFLU 24-0399); living culture MFLUCC 24-0528.

GenBank numbers – ITS = PQ800231, LSU = PV072589, *tub2* = PX739616.

Known hosts – *Pithecellobium bigeminum* (Verkley et al. 2014), on unidentified from plant litter (Goh et al. 2016), *Leucaena* sp. (Jayasiri et al. 2019), *Magnolia* sp. (Tennakoon et al. 2022a), *Dipterocarpus alatus* (this study).

Known distribution – Myanmar (Verkley et al. 2014), Korea (Goh et al. 2016), Thailand (Jayasiri et al. 2019, this study), China (Tennakoon et al. 2022a)

Notes – Phylogenetic analyses demonstrated that our strain (MFLUCC 24-0528) formed a clade with eight other isolates of *P. archidendri*, specifically grouping with *P. archidendri* (1-3-10-2-1-4) (97% ML/ 0.99 PP bootstrap support) (Fig. 21). *Paraconiothyrium archidendri* was isolated from leaf spots of *Pithecellobium bigeminum* in Myanmar (Verkley et al. 2014). In

previous collections of *P. archidendri*, the sexual morph was not reported. Most species have been found in asexual morph, and only *P. fuckelii* exhibited both sexual and asexual forms (Wang et al. 2021b). Based on multigene phylogeny, our new collection represents the first report of the sexual morph of *P. archidendri* and is reported as a new host record from *Dipterocarpus alatus*.

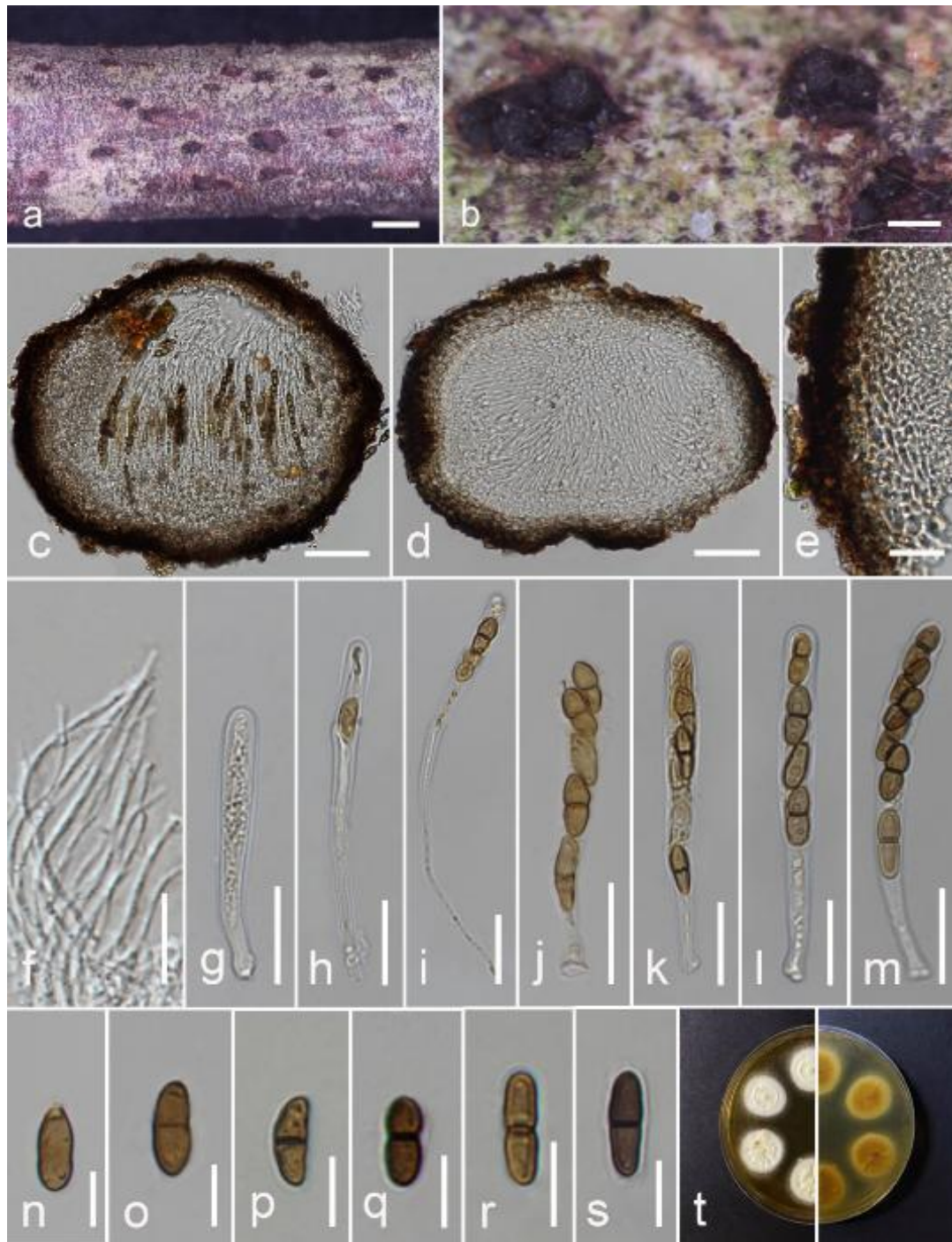


Figure 22 – *Paraconiothyrium archidendri* (MFLU 24-0399, a new host record and first report of the sexual morph). a, b Appearance of ascomata on *Dipterocarpus alatus* woody litter. c, d Vertical

sections of ascomata. e Section of peridium. f Pseudoparaphyses. g–m Asci. n–s Ascospores. t Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 µm, c, d = 50 µm, e–m = 20 µm, n–s = 10 µm.

***Fusculinaceae* Crous**

Fusculinaceae was established by Crous et al. (2018a) to accommodate *Fusculina* and *Gordonomyces*. *Fusculina* and *Gordonomyces* formed a distinct clade within *Pleoporales* supported by ITS and LSU sequence data. This family is typified with *Fusculina eucalypti*, isolated as a saprobe on the leaves of *Eucalyptus* in New South Wales. The sexual morph has not been observed. The asexual morph is coelomycetous, characterized by globose, single, erumpent conidiomata. Conidiophores lining the cavity are hyaline cells that are subcylindrical, Conidiogenous cells are terminal and intercalary. Conidia are solitary, hyaline, aseptate, guttulate, smooth-walled, fusoid with a sub-obtuse apex (Crous et al. 2018a). Herein, we introduce a genus *Sporicula* to accommodate *Sporicula Chiangraiensis* (MFLUCC 24-0551) based on multigene phylogeny and morphological identification.

Sporicula N. Afshari, Lumyong & K.D. Hyde, gen. nov.

Fig. 24

Index Fungorum number: IF904744; Facesoffungi number: FoF17223

Etymology – The genus name is derived from the Latin word “-ula” meaning ‘small’, in reference to the small spores.

Type species – *Sporicula Chiangraiensis* N. Afshari, Lumyong & K.D. Hyde

Holotype – MFLU 24-0463

Saprobic on dead branches of *Microcos paniculata*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, embedded in stromatic tissue, brown to pale brown, scattered, solitary, immersed, erumpent, globose to sub-globose, coriaceous. *Conidiomatal wall* composed of brown, loosely arranged cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* sub-cylindrical, tapering towards apex, hyaline, smooth-walled, monophialidic, mostly percurrent proliferations in apical part. *Conidia* fusiform, straight, hyaline, aseptate, verruculose, smooth-walled, rounded to truncate at base.

Notes – *Sporicula* has a single species, *S. Chiangraiensis* (MFLUCC 24-0551), formed a basal clade to other members in *Fusculinaceae* (*Fusculina eucalypti* (CBS 120083), *F. eucalyptorum* (CBS 145083), *F. regnans* (CBS 143428), and *Gordonomyces mucovaginat* (CMW 22212)) with 98% ML support in the combined LSU, ITS, SSU, and *tefl-α* sequence data of *Pleosporales* (Fig. 23). Based on BLAST search results LSU, ITS, SSU, and 93.69% sequences, *S. Chiangraiensis* (MFLUCC 24-0551), demonstrates 97.91%, 88.27%, 89.47% and 91.83% similarities to the closest related taxa available in GenBank. The genus is similar to the members of *Fusculinaceae* in having brown, immersed pycnidial conidiomata, conidiomatal wall consisting of brown cells of *textura angularis*, and conidiophores reduced to conidiogenous cells. However, this genus has only one type of conidiogenous cells and conidia (Table 3) (Crous et al. 2018). In *Fusculinaceae*, *Sporicula Chiangraiensis* is a saprobic species, whereas *Gordonomyces mucovaginat* is a pathogen (Crous et al. 2011), also both *Fusculina eucalypti* and *F. regnans* are pathogenic, while *F. eucalyptorum* has been isolated as an endophyte (Crous et al. 2019a). Hence, based on these morphological and phylogenetic differences, we establish a new genus to accommodate *S. Chiangraiensis*. Additional collections and molecular characterization are essential to further validate the placement of this genus.

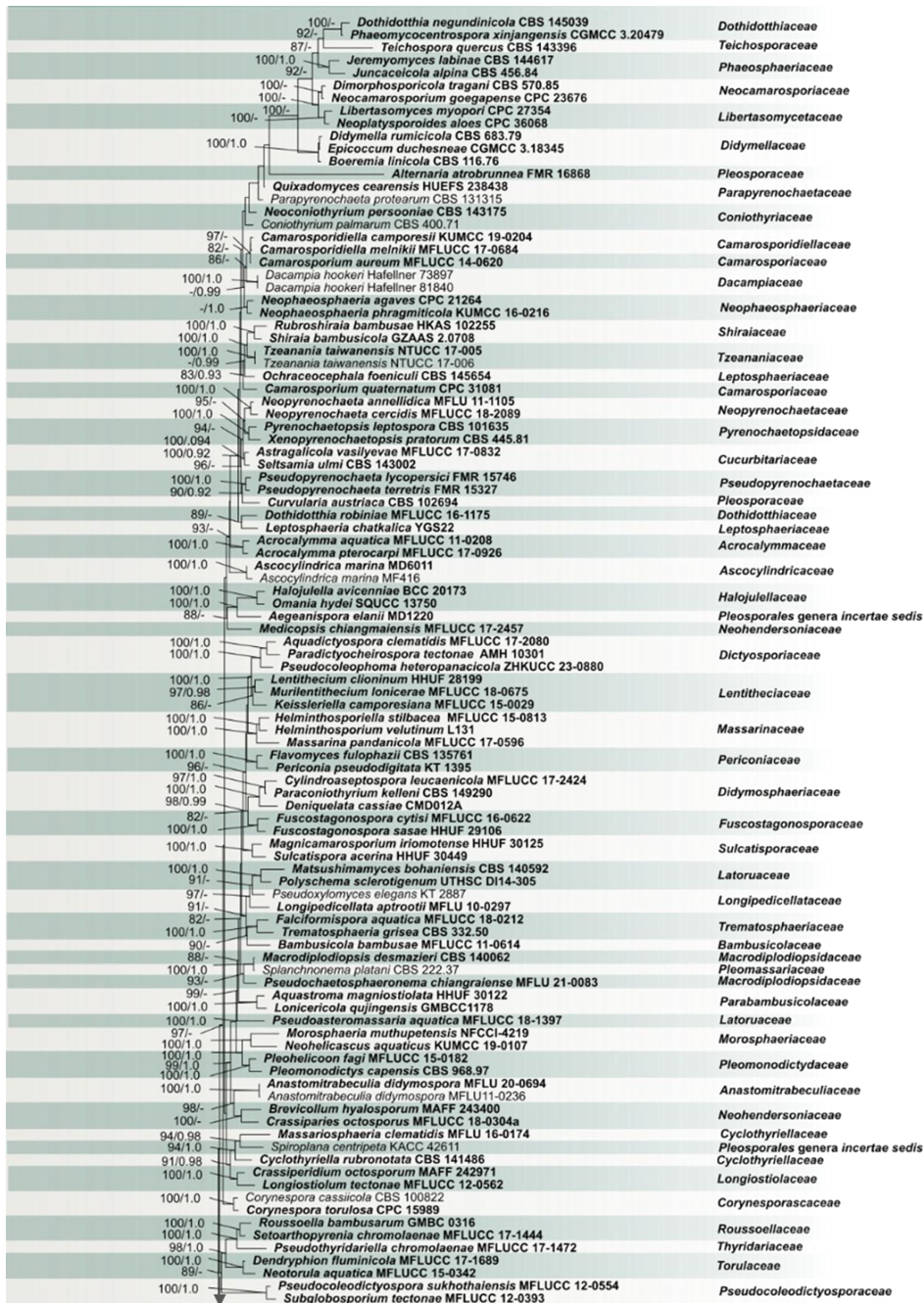


Figure 23 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined LSU, ITS, SSU, and *tefl*- α sequence data of *Pleosporales*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. One hundred ninety strains

are included in the combined analyses which comprised 3,326 characters (LSU = 866, ITS = 527, SSU = 1,017, and *tefl-α* = 916). The best score for log-likelihood of consensus tree is -80871.863. The matrix had 2,254 distinct patterns, 1,405 parsimony-informative, 506 singleton sites, 1,415 constant sites. Selecting individual models GTR+F+I+G4, TIM2+F+I+G4, K2P+G4, and GTR+F+I+G4 were applied to LSU, ITS, SSU, and *tefl-α* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 100,000,000 MCMC generations was calculated as 0.011347. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Hysterobrevium karsti* (MFLU 18-2251) and *H. baoshanense* (MFLUCC 16-2162). Ex-type strains are in bold. The isolates generated in this study are indicated in blue.

Sporicula chiangraiensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 24

Index Fungorum number: IF904743; Facesoffungi number: FoF17224

Etymology – The specific epithet is derived from Chiang Rai, location where the holotype was collected.

Holotype – MFLU 24-0463

Saprobic on dead branches of *Microcos paniculata*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* (52–)81.5–153 µm diam., (67.5–)73–139 µm high ($\bar{x}$ = 118 × 115 µm, n = 10), pycnidial, embedded in stromatic tissue, brown to pale brown, scattered, solitary, immersed, erumpent, globose to sub-globose, coriaceous. *Conidiomata wall* (12–)13.5–21(–23) µm wide ($\bar{x}$ = 17.6 µm, n = 35), composed of brown, loosely arranged cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (1.8–)2.2–3(–3.5) × (5.5–)6.2–11.5(–12.2) µm ($\bar{x}$ = 2.7 × 8.6 µm, n = 35), monophialidic, sub-cylindrical, tapering towards apex, hyaline, smooth-walled, mostly percurrent proliferations in apical part. *Conidia* 1.9–3.6 × 0.8–1.6 µm ($\bar{x}$ = 2.7 × 1.3 µm, n = 50; L/W ratio = 2.0), fusiform, straight, hyaline, aseptate, verruculose, smooth-walled, rounded to truncate at base.

Culture characteristics – Conidia germinated on PDA and a germ tube emerged from end cells. Colonies on PDA reaching 2–2.5 mm diam. after 2 weeks at room temperature (25–28 °C), irregular, raised, rugose, dense, cerebriform, membranous, granulose, margin undulate, buff at center, pale brown periphery, reverse pale brown, producing yellow pigment in culture with age.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 26 March 2022, N. Afshari, 3C1T3R5c (MFLU 24-0463, holotype); ex-type living culture MFLUCC 24-0551, (3C1T3R5a = MFLU 24-0481, isotype).

GenBank numbers – MFLU 24-0463: LSU = PV072607, ITS = PQ800253, SSU = PV072700, *tefl-α* = PX739632; MFLU 24-0481: LSU = PV072608, ITS = PQ800254, SSU = PV072701, *tefl-α* = PX739633.

Notes – In the multigene phylogenetic analyses, our strains formed a basal lineage with other members of two genera (*Fusculina* and *Gordonomyces*) in *Fusculinaceae* (Fig. 23) with 98% ML support value. In *Fusculinaceae*, *Sporicula chiangraiensis* is a saprobic species, whereas *Gordonomyces mucovaginat* is a pathogen (Crous et al. 2011), also both *Fusculina eucalypti* and *F. regnans* are pathogenic, while *F. eucalyptorum* has been isolated as an endophyte (Crous et al. 2019a). We therefore, introduce a new genus *Sporicula* based on morphological (Table 3) and phylogenetic evidence for a fungus collected on *Microcos paniculata*. Herein we introduce

Sporicula chiangraiensis (MFLUCC 24-0551) as a new species on dead wood of *Microcos paniculata*.

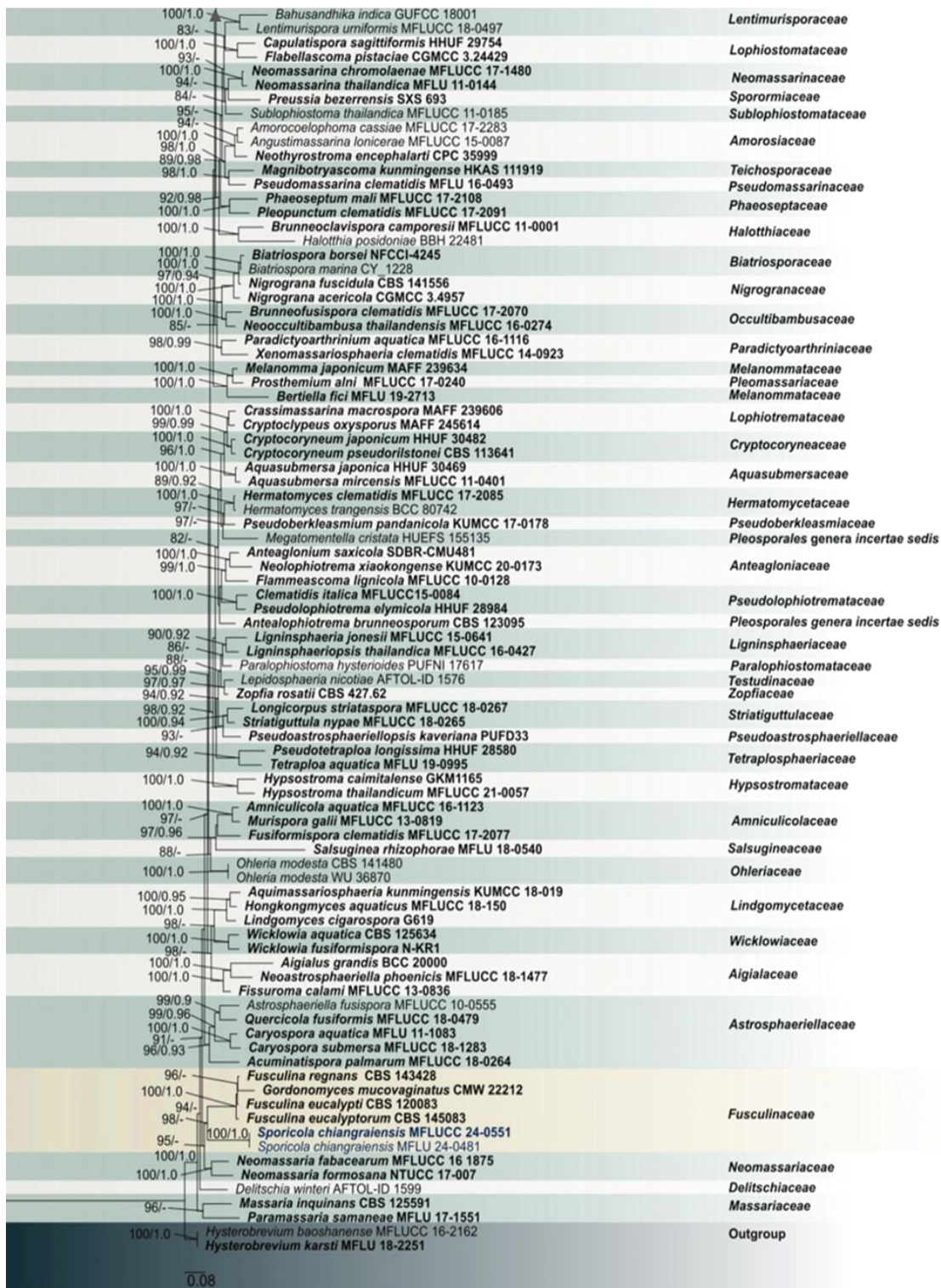


Figure 23 – Continued.

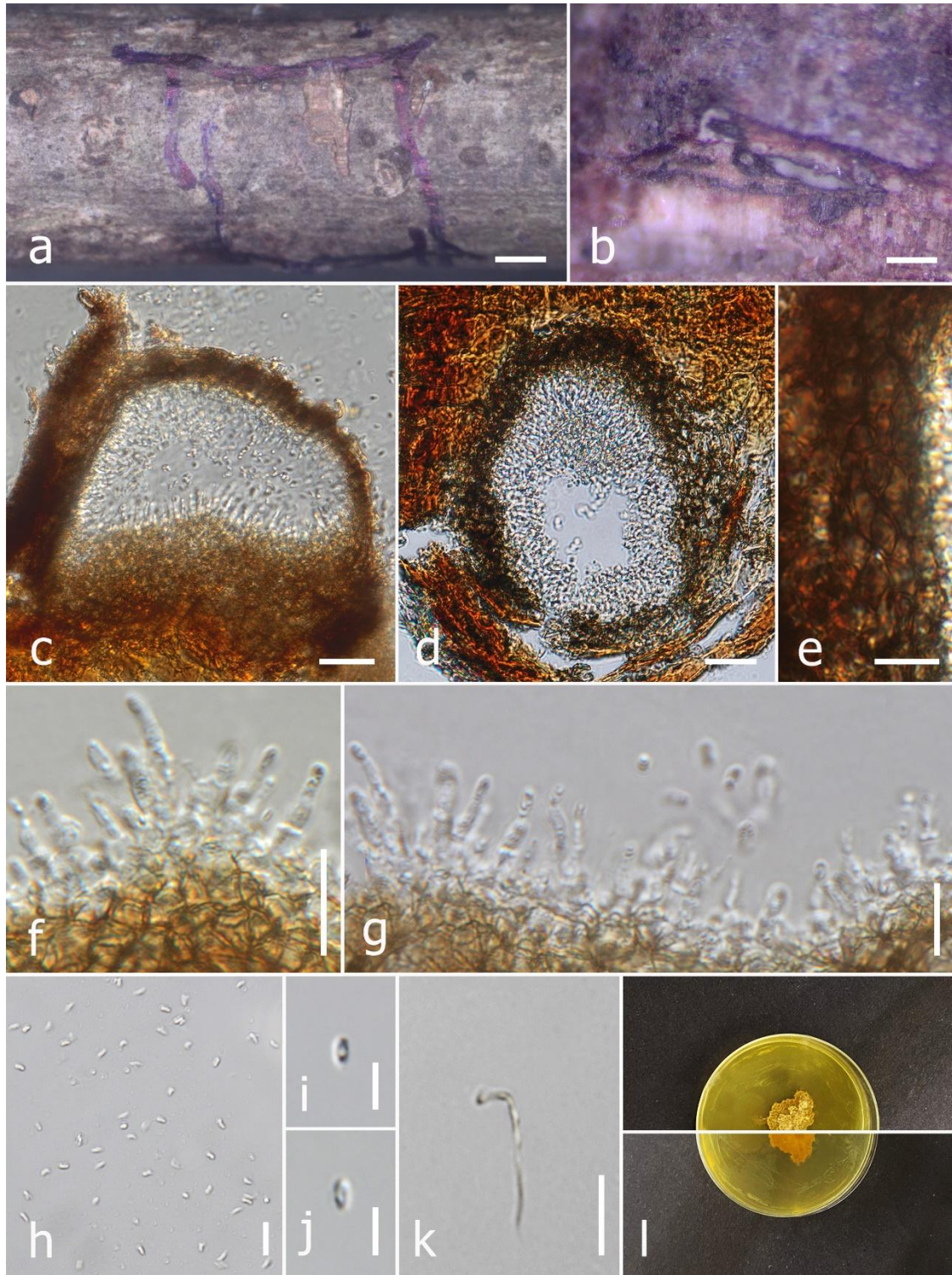


Figure 24 – *Sporicula chiangraiensis* (MFLU 24-0463, holotype). a Conidiomata on *Microcos paniculata* woody litter. b Longitudinal section of conidiomata. c, d Vertical section through conidiomata. e Conidiomatal wall. f, g Conidiophores with conidia. h–j Conidia. k A germinated conidium. l Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 µm, c, d = 20 µm, e–h, k = 10 µm, i, j = 5 µm.

Table 3 – Morphology of *Fusculinaceae* species.

Species	Conidiomata	Conidiomatal wall	Paraphyses	Conidiophores	Conidiogenous cells	Conidia	Distribution and hosts	References
<i>Fusculina eucalyptorum</i>	Solitary, erumpent, pycnidial, globose, brown, 200–250 µm diam., exuding a creamy conidial mass. On OA surrounded by chains of chlamydospore-like cells, prominently constricted at septa, hyaline to brown, 0–1-septate, up to 8 µm diam.	6–8 layers of brown <i>textura angularis</i>	among conidiophores, hyaline, smooth, septate, hyphae-like, 2–3 µm diam.	lining the inner cavity, subcylindrical, 15–25 × 4–5 µm, smooth, hyaline, with 1–2 conidiogenous cells	hyaline, smooth, terminal and intercalary, 7–15 × 3–4 µm, proliferating percurrently.	solitary, hyaline, smooth, guttulate, aseptate, fusoid, apex subobtuse, base truncate, 2–2.5 µm diam, (10–)13–15(–17) × (3.5–)4 µm., L/W ratio = 3.7	Australia, endophyte in leaves of <i>Eucalyptus socialis</i>	Crous et al. (2018a)
<i>F. regnans</i>	immersed, becoming erumpent, black, On OA eustromatic, opening via irregular split, grey-black, in clusters, 150–300 µm diam.	6–8 layers of brown <i>textura angularis</i>	intermingled among conidiophores, hyaline, smooth, septate, 25–40 × 4–5 µm.	lining the inner cavity, hyaline, smooth, 0–2-septate, subcylindrical, 15–25 × 5–7 µm	terminal, integrated, subcylindrical to ampulliform, hyaline, smooth, with numerous prominent percurrent proliferations in	solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate to bluntly rounded, (14–)17–20(–23) × (3.5–)4–5(–6) µm, L/W ratio = 4.1	Australia, pathogen on <i>E. regnans</i>	Crous et al. (2019a)

Species	Conidiomata	Conidiomatal wall	Paraphyses	Conidiophores	Conidiogenous cells	Conidia	Distribution and hosts	References
<i>F. eucalypti</i>	black on leaves, pycnidial, immersed, becoming slightly erumpent, up to 250 µm diam., brown under light microscope, upper region appearing crust-like, dark-brown; opening by irregular rupture;	consisting of 2–4 layers of brown cells of <i>textura angularis</i> that give rise to 2–4 layers of hyaline cells	N/A	N/A	apical region, 5–20 × 5–7 µm Primary: hyaline, smooth, ampulliform to subcylindrical, proliferating several times percurrently near apex, 5–15 × 4–8 µm, giving rise to subcylindrical primary conidia. Secondary: integrated among primary conidiogenous cells, hyaline, smooth, proliferating sympodially, 5–10 µm long and 3–4 µm wide.	Primary: hyaline, granular, smooth, straight to somewhat irregular, subcylindrical, apex obtuse, base truncate, (16–)18–20(–22) × 3–4 µm, L/W ratio = 5.4 Secondary: hyaline, smooth, granular, ellipsoid with rounded ends, or subcylindrical with obtuse apex and truncate base, 5–8 × 3–4 µm, L/W ratio = 1.8	Australia, pathogen on <i>Eucalyptus</i> sp.	Summerbell et al. (2006)
<i>Gordonomyces mucovaginatus</i>	up to 600 µm diam., globose, erumpent on agar, separate or aggregated, black, outer wall smooth;	<i>textura angularis</i> , up to 60 µm thick, outer region of 3–8 layers of dark brown cells,	intermingled among conidiogenous cells, cylindrical, branched below, 1–6-	N/A	Subcylindrical to ampulliform, mostly reduced to single cells, with apical percurrent	golden-brown, verruculose, obovoid to semi-clavate, 1-euseptate, apex obtuse, base subtruncate,	South Africa, on leaf litter of <i>Leucadendron laureolum</i> ,	Crous et al. (2011)

Species	Conidiomata	Conidiomatal wall	Paraphyses	Conidiophores	Conidiogenous cells	Conidia	Distribution and hosts	References
	filled with a brown-black mucoid mass containing numerous conidia	inner region of 3–7 layers of thick-walled, hyaline cells.	septate, 30–70 × 3–4 µm, with obtuse ends, at times becoming fertile.		proliferation, 5–15 × 3.5–4 µm.	covered in mucoid sheath, 2–3 µm wide, (12–)13–15(–17) × (4–)4.5–5 µm, L/W ratio = 3.0		
<i>Sporicula Chiangraiensis</i>	(–52)81.5–153 µm diam., (67.5–)73–139 µm high ($\bar{x}$ = 118 × 115 µm), pycnidial, embedded in stromatic tissue, brown to pale brown, scattered, solitary, immersed, erumpent, globose to sub-globose, coriaceous.	(12–)13.5–21(–23) µm wide ($\bar{x}$ = 17.6 µm), composed of brown, loosely arranged cells of <i>textura angularis</i> .	N/A	reduced to conidiogenous cells.	(1.8–)2.2–3(–3.5) × (5.5–)6.2–11.5(–12.2) µm ($\bar{x}$ = 2.7 × 8.6 µm), hyaline, sub-cylindrical, tapering towards apex, smooth-walled, monophialidic, mostly percurrent proliferations in apical part.	1.9–3.6 × 0.8–1.6 µm ($\bar{x}$ = 2.7 × 1.3 µm), L/W ratio = 2.0, hyaline, fusiform, straight, aseptate, verruculose, smooth-walled, rounded to truncate at base.	Thailand, on wood litter of <i>Microcos paniculata</i>	This study

The symbol “N/A” denotes no data available or not mentioned in references.

***Hermatomycetaceae* Locq.**

Hermatomycetaceae was validated and reintroduced by Hashimoto et al. (2017) to accommodate the single genus *Hermatomyces* with the type species *Hermatomyces tucumanensis* isolated from as a saprobic fallen rotten branches of *Smilax campestris* and *Celtis* sp. in Tucumán (Hashimoto et al. 2017). In the phylogeny presented by Hashimoto et al. (2017), *Hermatomycetaceae* clade is rooted separately from the closely related *Anteagloniaceae* and *Lophiotremataceae* families, suggesting similar divergence times.

***Hermatomyces* Speg. (= *Subicularium* M.L. Farr & Goos)**

Index Fungorum number: IF8517; Facesoffungi number: FoF08252

Hermatomyces was introduced by Spegazzini (1910), with *H. tucumanensis* as the type species. Doilom et al. (2017) placed this genus within *Lophiotremataceae* based on combined sequence data from LSU, SSU, *tefl-α*, and *rpb2* genes. Subsequently, Hashimoto et al. (2017) validated *Hermatomycetaceae* to accommodate *Hermatomyces*. The earlier attempt by Locquin (1984) to establish *Hermatomycetaceae* was not validly published according to Article 39.1 of the International Code of Nomenclature. *Hermatomyces* is distinguished by sporodochial conidiomata and dimorphic conidia, lenticular conidia are globose to subglobose, with hyaline to pale brown peripheral cells and dark brown central cells, cylindrical conidia are hyaline, cylindrical to subcylindrical or turbinate, and composed of 1–4 columns of 2–12 cells (Spegazzini 1910, Tibpromma et al. 2016, Hashimoto et al. 2017, Hyde et al. 2019, Pem et al. 2019, Phukhamsakda et al. 2020). In the current study we report *Hermatomyces indicus* as a new host record on dead wood of *Dalbergia cana* from Thailand. An updated phylogenetic tree for this genus is shown in Fig. 25.

***Hermatomyces indicus* Prasher & Sushma, Nova Hedwigia 94, 552 (2014).**

Fig. 26

Synonym: *Hermatomyces thailandicus* Doilom et al. Fungal Div. 82: 121 (2016) as “*thailandica*”

Index Fungorum number: IF805645; Facesoffungi number: FoF17236

Saprobic on *Dalbergia cana* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate sporodochial, scattered, effuse, superficial, mostly circular to subcircular, glistening, dark brown to black, comprising a dark brown sterile mycelial outer section and abundant sporulation, conidia promptly liberated. *Mycelium* mostly superficial, composed of a loose network of branched, septate, thick-walled, pale brown hyphae. *Subicular hyphae* brown and short, irregularly straight or mostly flexuous. *Conidiophores* 17–36 × 2.4–5 μm ($\bar{x}$ = 25 × 3.7 μm, n = 20), micronematous to semi-macronematous, mononematous, unequally cylindrical, geniculate, pale brown to brown, septate, branched, thick-walled. *Conidiogenous cells* 4–9.5 × 2.2–5 μm ($\bar{x}$ = 6.6 × 3.7 μm, n = 30), solitary, holoblastic, monoblastic, integrated, terminal, determinate, subcylindrical or subsphaerical, pale brown. *Conidia* 25–35 × 16–25 μm ($\bar{x}$ = 30.4 × 22.5 μm, n = 15), L/W ratio = 1.4, lenticular, muriform, solitary, mainly ellipsoidal or rarely circular in front view, central cells blackish brown, peripheral cells subhyaline to pale brown, creating a distinct ring, usually carrying remains of conidiogenous cell at base, smooth-walled, slightly constricted at the septa, side view not observed.

Culture characteristics – Conidium germinated on PDA within 24 h and germ tubes emerged from each cell. Colonies on PDA reaching 2 cm diam. after 10 days at room temperature (25–28 °C), circular, entire edge, raised, dense, velvety, radially furrowed into agar, with smooth aspect, upper surface white-grey, reverse grey to beige at center with buff ring.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cana* (Fabaceae), 27 September 2022, N. Afshari, 4C3T2R4 (MFLU 24-0400); living culture MFLUCC 24-0529.

GenBank numbers – LSU = PV072590, ITS = PQ800232, *tefl-α* = PX739621, *rpb2* = PV138134.

Known hosts – *Phoenix rupicola* (Prasher & Prasher 2014), *Tectona grandis* (Doilom et al. 2017), *Dalbergia cana* (this study).

Known distribution – India (Prasher & Prasher 2014), Thailand (Doilom et al. 2017, this study).

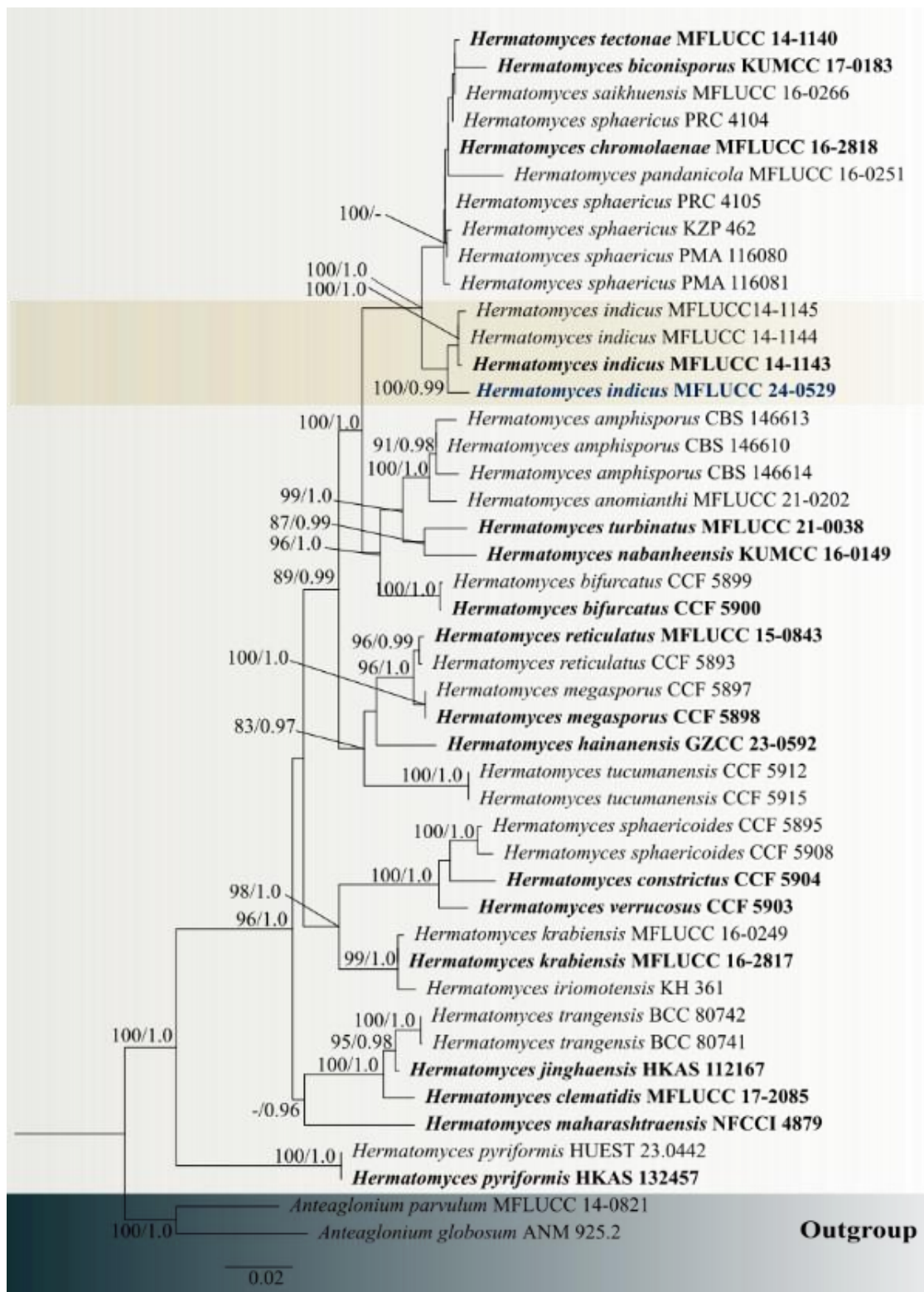


Figure 25 – Phylogram generated from maximum likelihood analysis based on the combined LSU, ITS, *tef1-α*, and *rpb2* sequence data of *Hermatomyces*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Forty-five strains are included in the combined analyses which comprised 3,370 characters (LSU = 879, ITS = 530, *tef1-α* = 935, and *rpb2* = 1,026). The best RAXML tree with a final optimization likelihood value of -12687.472352 is presented. The matrix had 941 distinct alignment patterns, with 22.33% of undetermined characters or gaps. Estimated base

frequencies were as follows: A = 0.246736, C = 0.262471, G = 0.262629, T = 0.228164; substitution rates AC = 1.131580, AG = 5.042697, AT = 1.294458, CG = 0.832285, CT = 11.918437, GT = 1.000000; gamma distribution shape parameter α = 0.149339. In the Bayesian analysis, average standard deviation of split frequencies at the end of 5,000,000 MCMC generations was calculated as 0.005509. The evolutionary models TIM2+I+G, TIM2ef+I+G, TIM2+I+G, TrN+G were applied for LSU, ITS, *tefl*- α , and *rpb2* sequence data. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Anteaglonium parvulum* (MFLUCC 14-0821) and *A. globosum* (ANM 925.2). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Notes – In the phylogenetic analysis, *Hermatomyces indicus* (MFLUCC 24-0529) formed a separate lineage with *H. indicus* strains (MFLUCC 14-1143, MFLUCC 14-1144, MFLUCC 14-1145), with 100% ML and 0.99 PP values (Fig. 25). Koukol et al. (2018), synonymized *H. thailandicus* under *H. indicus*. Hyde et al. (2019) introduced a new species *H. bauhiniae*, which clustered with *H. indicus*, but subsequently Koukol & Delgado (2021) synonymized it under *Pleopunctum bauhiniae*. Therefore, we compared the phylogeny and morphology of our isolate with the holotype of *H. indicus*. *Hermatomyces indicus* (MFLU 24-0400) has slightly wider conidiophores than *H. indicus* (MFLUCC 14-1143) (2.4–5 μ m vs. 2–3.5 μ m) and larger lenticular conidia (25–35 $\times$ 16–25 μ m vs. (23–)28–29(–31) $\times$ (14–)17–18(–20) μ m) (Doilom et al. 2017). Most species of *Hermatomyces*, including *H. indicus*, are characterized by dimorphic conidia; in contrast, our collection together with *H. reticulatus* and *H. pyriformis* possess only a single conidial type (Prasher & Prasher 2014, Koukol et al. 2018, Du et al. 2024). Comparisons of ITS, LSU and *tefl*- α sequences between *H. indicus* (MFLUCC 24-0529) and *H. indicus* (MFLUCC 14-1143) did not indicate a significant difference and only 2.5% differences in *rpb2* sequences. *Hermatomyces indicus* was isolated from *Phoenix rupicola* in India (Prasher & Prasher 2014) and *Tectona grandis* in Thailand (Doilom et al. 2017). The current study reports *H. indicus* for the first time on dead wood of *Dalbergia cana*.

Massarinaceae Munk

Massarinaceae was introduced by Munk (1956) to accommodate *Massarina*, with *M. eburnea* as the type species and it was described based on the sexual morph (Saccardo 1883). Currently 12 genera are accepted in this family (Hyde et al. 2024a). The members of this family are known as saprobes, or hemibiotrophic and pathogenic fungi on living leaves. The sexual form of these fungi has ascomata that are either sunk into the surface or half-sunk, and they can be alone or grouped together (Tanaka et al. 2015). The asexual forms of these fungi can have different types of structures, either coelomycetous or hyphomycetous (Hyde et al. 2013, Crous et al. 2019b).

Helminthosporium Link (= *Helminthosporiella* Hern. -Restr.)

Index Fungorum number: IF8495; Facesoffungi number: FoF06499

Helminthosporium is a hyphomycetous genus that was erected by Link (1809), and typified by *H. velutinum*. *Helminthosporium* species are frequently saprobes and endophytes (Konta et al. 2021, Chen et al. 2022). However, *H. solani* is a significant global pathogen causing silver scurf disease in potatoes (Liu et al. 2022a). Currently, 327 species of this genus are accepted in Index Fungorum (2025), but only nearly 30 species have sequence data. Most *Helminthosporium* species are not congeneric with the generic type (Hu et al. 2023). By analysis of multiple loci of genes (combined ITS, LSU, SSU, and *tefl*- α sequence data), Konta et al. (2021) showed that *Helminthosporium* is polyphyletic. This was confirmed by Hu et al. (2023). The genus produces macronematous, cylindrical, septate, erect conidiophores with tretic conidiogenous cells and clavate or obclavate, distoseptate conidia with a flat, ringed pore at the base (Chen et al. 2022). In this study, we report *Helminthosporium Chiangraiense* and *H. erythrinicola* as new records on *Azadirachta indica*.

and *Dalbergia cana*, respectively, from Thailand. An updated phylogenetic tree for *Helminthosporium* is presented in Fig. 27.



Figure 26 – *Hermatomyces indicus* (MFLU 24-0400, a new host record). a Sporodochia on *Dalbergia cana* woody litter. b Subicular hyphae. c–e Conidiophores, conidiogenous cells and conidia. f–h Conidiophores. i, j Lateral view of lenticular conidia. k A germinated conidium. l, m Colonies on PDA (front and reverse). Scale bars: a = 100 μ m, b–e = 20 μ m, f–k = 10 μ m.

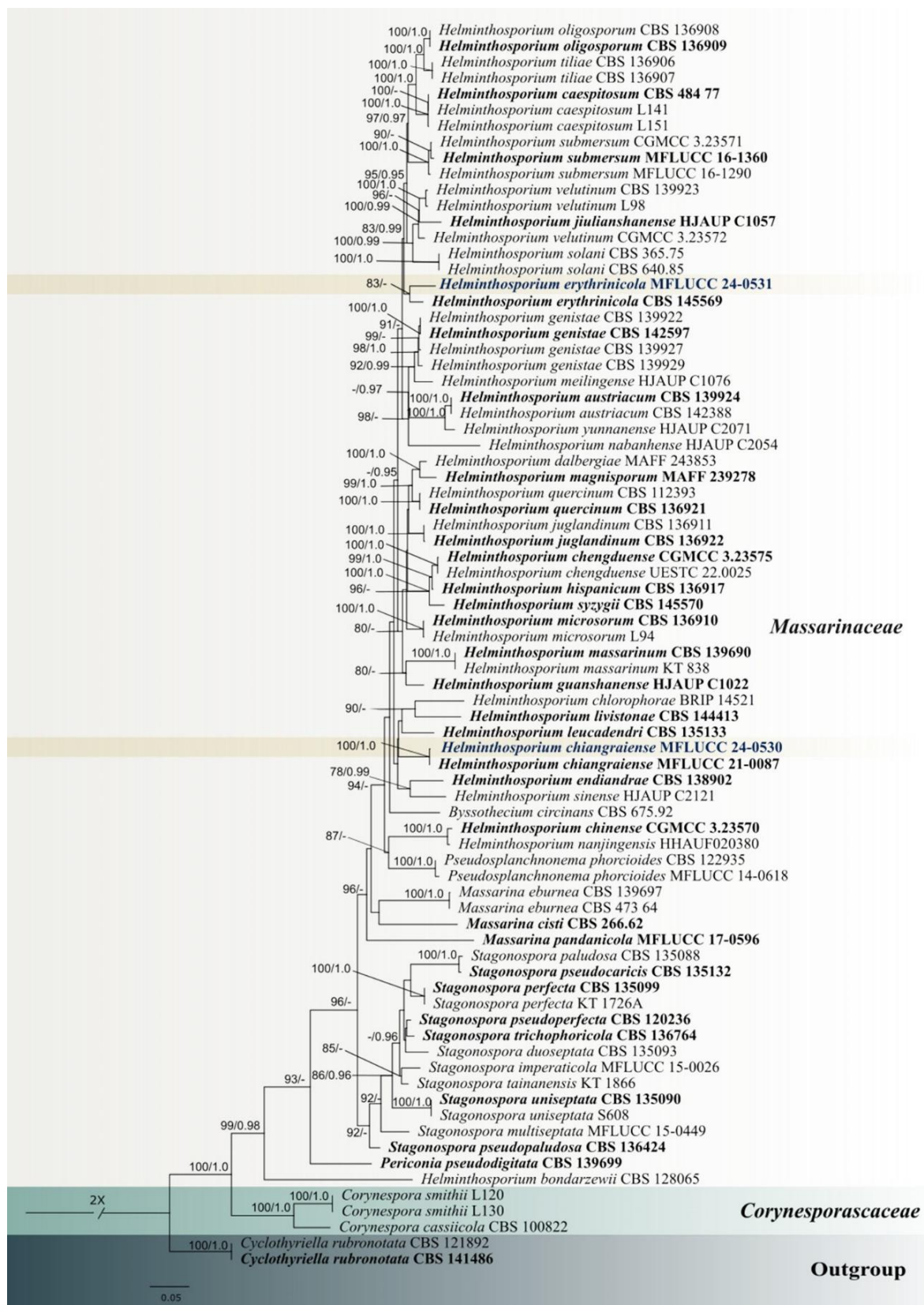


Figure 27 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, SSU, *tef1- α* , and *rpb2* sequence data of *Corynesporaceae*, *Massarinaceae* and *Periconiaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Seventy-eight strains are included in the combined analyses which comprised 4,987 characters (ITS = 581, LSU = 867, SSU = 1,068, *tef1- α* = 1,358, and *rpb2* = 1,113). The best score for log-likelihood of consensus tree is -33915.831. The matrix had 2,011 distinct alignment

patterns, 1,433 parsimony-informative, 253 singleton sites, 3,300 constant sites. Selecting individual models TIM2e+I+G4, TIM2e+I+G4, K2P+I, TN+F+I+G4, and TN+F+I+G4 were applied to ITS, LSU, SSU, *tefl-α*, and *rpb2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.014442. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Cyclothyriella rubronotata* (CBS 121892 and CBS 141486). Ex-type strains are in bold. The isolates generated in this study are indicated in bold and blue.

Helminthosporium chiangraiense Boonmee, Huanraluek & K.D. Hyde, in Boonmee et al. Fungal Diversity 111, 79 (2021). Fig. 28

Index Fungorum number: IF558539; Facesoffungi number: FoF09192

Saprobic on *Azelia xylocarpa* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colony* on the natural substrate effuse, punctiform, hairy, dark brown. *Mycelium* mostly immersed, forming stroma-like aggregations of dark brown pseudoparenchymatous cells. *Conidiophores* 187–403 × 6–12 μm ($\bar{x}$ = 315 × 8.5 μm, n = 25), macronematous, mononematous, brown to dark brown, with dark scars, caespitose, cylindrical to subcylindrical, thick-walled, unbranched, erect, straight to slightly flexuous, smooth, multiple-septate, with apical pore. *Conidiogenous cells* monotretic, integrated, terminal, sometimes becoming intercalary, cylindrical, pale brown, with dark scars, with distinct pores at the apex. *Conidia* (64–)70–188 × 11–22(–24) μm ($\bar{x}$ = 123 × 16 μm, n = 30; L/W ratio = 7.7), solitary, cylindrical to obclavate, straight to moderately flexuous, wider in the middle, truncate and with dark scar at base, upper cell tapering towards apex when mature, pale brown, (1–)7–13(–15)-distoseptate, smooth, *Conidial secession* schizolytic.

Culture characteristics – Conidium germinated on PDA within 24 h. Colonies on PDA reaching 30 mm diam. after one week at room temperature (25–28 °C), effuse, fluffy, dense, radiating towards the margin, non-pigmented, at the upper surface brown, from the reverse radiating from black to pale olive outwardly. Mycelium superficial and relatively immersed.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Azelia xylocarpa* (Fabaceae), 26 March 2022, N. Afshari, 5C1T1R1 (MFLU 24-0401); living culture MFLUCC 24-0530.

GenBank numbers – ITS = PQ800233, LSU = PV072591, *rpb2* = PV138150, SSU = PV072688, *tefl-α* = PX739622.

Known hosts – dead twigs of unidentified plant (Boonmee et al. 2021), *Azelia xylocarpa* (this study).

Known distribution – Thailand (Boonmee et al. 2021, this study).

Notes – In the phylogenetic analysis of combined ITS, LSU, SSU, *tefl-α*, and *rpb2*, our strain (MFLUCC 24-0530) clustered with *H. chiangraiense* (MFLUCC 21-0087), with 100% ML and 1.0 PP bootstrap support (Fig. 27). *Helminthosporium chiangraiense*, which was isolated from dead twigs of an unidentified plant, also in Chiang Rai Province, shares similar characteristics with our collection in size of conidiophores (187–403 × 6–12 μm vs. 168–304.5 × 5.5–12 μm) and conidia ((64–)70–188 × 11–22(–24) μm vs. 141–207 × 14–22 μm) (Boonmee et al. 2021). Based on morphological characters and multigene phylogeny, we conclude that our isolate is *H. chiangraiense*. This study presents a new host record of *H. chiangraiense* on *Azelia xylocarpa*.

Helminthosporium erythrinicola Crous & M.J. Wingf., Persoonia 42, 357 (2019). Fig. 29

Index Fungorum number: IF830852; Facesoffungi number: FoF16089

Saprobic on *Dalbergia cana* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colony* on natural substrate effuse, hairy, punctiform, dark brown to black. *Mycelium* frequently immersed, forming brown stroma-like aggregations on the surface, giving rise conidiophores. *Conidiophores* 290–700 × 6.5–13 μm ($\bar{x}$ = 482 × 10 μm, n = 20), macronematous, mononematous, straight or slightly curved, multiseptate, roughened, cylindrical to subcylindrical, often wider at the base, unbranched, dark brown, at apex pale brown, solitary or grouped in pairs.

Conidiogenous cells 26–41(–51) × 9–12 µm ($\bar{x}$ = 32 × 10 µm, n = 10), terminal, rarely intercalary, with pores, cylindrical, thick-walled, pale brown. *Conidia* 93–172 × 8–18 µm ($\bar{x}$ = 130 × 14 µm, n = 15), L/W ratio = 9.3, obclavate, upper cell tapering towards apex, truncate with dark scar at base, straight to flexuous, sub-obtuse apex, smooth-walled, light brown, 6–14(–19)-distoseptate, with angular lumina, wall 2–4 µm thick. *Conidial secession* schizolytic.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerges from one end cell. Colonies reaching 60 mm diam. after one week on PDA at room temperature (25–28 °C), circular, flat, with moderate aerial mycelium, velvety, medium dense, non-pigmented, at upper surface white, from reverse yellowish white, and black at the center.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cana* (Fabaceae), 26 March 2022, N. Afshari, 4C1T2R2 (MFLU 24-0402); living culture MFLUCC 24-0531.

GenBank numbers – ITS = PQ800234, LSU = PV072592, SSU = PV072618, *tefl-α* = PX739623.

Known hosts – *Erythrina humeana* (Crous et al. 2019b), *Dalbergia cana* (this study).

Known distribution – South Africa (Crous et al. 2019b), Thailand (this study).

Notes – Phylogenetic analyses of ITS, LSU, SSU, *tefl-α*, and *rpb2* support the close affinity of our isolate (MFLUCC 24-0531) to the ex-type of *H. erythrinicola* (CBS 145569) and the two grouped with 83% ML bootstrap support (Fig. 27). Our isolate shares similar characteristics, such as length of conidiogenous cells, shape, and colour of conidia with *H. erythrinicola* (CBS 145569) isolated from leaves of *Erythrina humeana* (Fabaceae) in South Africa (Crous et al. 2019b). However, our collection has shorter conidiophores (290–700 × 6.5–13 µm vs. 500–1200 × 6–10 µm) and larger conidia (93–172 × 8–18 µm vs. (70–)80–90(–110) × (9–)10–11(–12) µm) than those of the holotype (Crous et al. 2019b). Based on morphological and molecular evidence, our new collection represents the first report of *H. erythrinicola* on *Dalbergia cana* from Thailand, identifying it as a new host and geographical record.

Neomassariaceae H.A. Ariyaw., Jaklitsch & Voglmayr

Ariyawansa et al. (2018), introduced *Neomassariaceae* to accommodate *Neomassaria* as the type genus. This classification was supported by phylogenetic studies of single and combined LSU, *rpb2*, SSU, and *tefl-α* gene regions, along with morphological characteristics (Ariyawansa et al. 2018). The taxa of *Neomassariaceae* are distinguishable from *Massariaceae* taxa in having small globose to subglobose ascomata, small asci without a refractive ring and also small, hyaline, 1-septate ascospores (Ariyawansa et al. 2018, Hongsanan et al. 2020a). This family includes three genera (*Neomassaria*, *Pigmentatineomassaria*, and *Pseudoneohendersonia*) (Hyde et al. 2024a). The members in this family are saprobic, growing on dead stems.

Neomassaria Mapook, Camporesi & K.D. Hyde

Index Fungorum number: IF552273; Facesoffungi number: FoF02437

Neomassaria was introduced and placed in *Massariaceae*, as it was morphologically distinct and formed phylogenetically basal to other *Massaria* taxa (Hyde et al. 2016b). Subsequently, the second *Neomassaria* species was introduced by Ariyawansa et al. (2018), who established *Neomassariaceae* to accommodate these two species. In the sexual morph, they have immersed to erumpent, solitary or scattered, globose to subglobose, ostiolate ascomata. The ostiole is crest-like with a slit-like opening or papillate; asci are 8-spored, bitunicate, fissitunicate, cylindrical or cylindric-clavate, and short pedicellate. The ascospores are hyaline, ellipsoid or fusiform, 1-septate, and sometimes surrounded by a gelatinous sheath. In the asexual morph, they are hyphomycetous, with macronematous, mononematous, solitary, erect, unbranched, brown, septate conidiophores, monoblastic, holoblastic, terminal conidiogenous cells, and acrogenous, solitary, obclavate, 5–8-septate, pale brown to brown conidia (Hyde et al. 2016b, Pem et al. 2024, Zhang et al. 2024). In this study we document *Neomassaria thailandica* as a new record on dead wood of *Microcos paniculata* from Doi Tung National Park, Thailand.

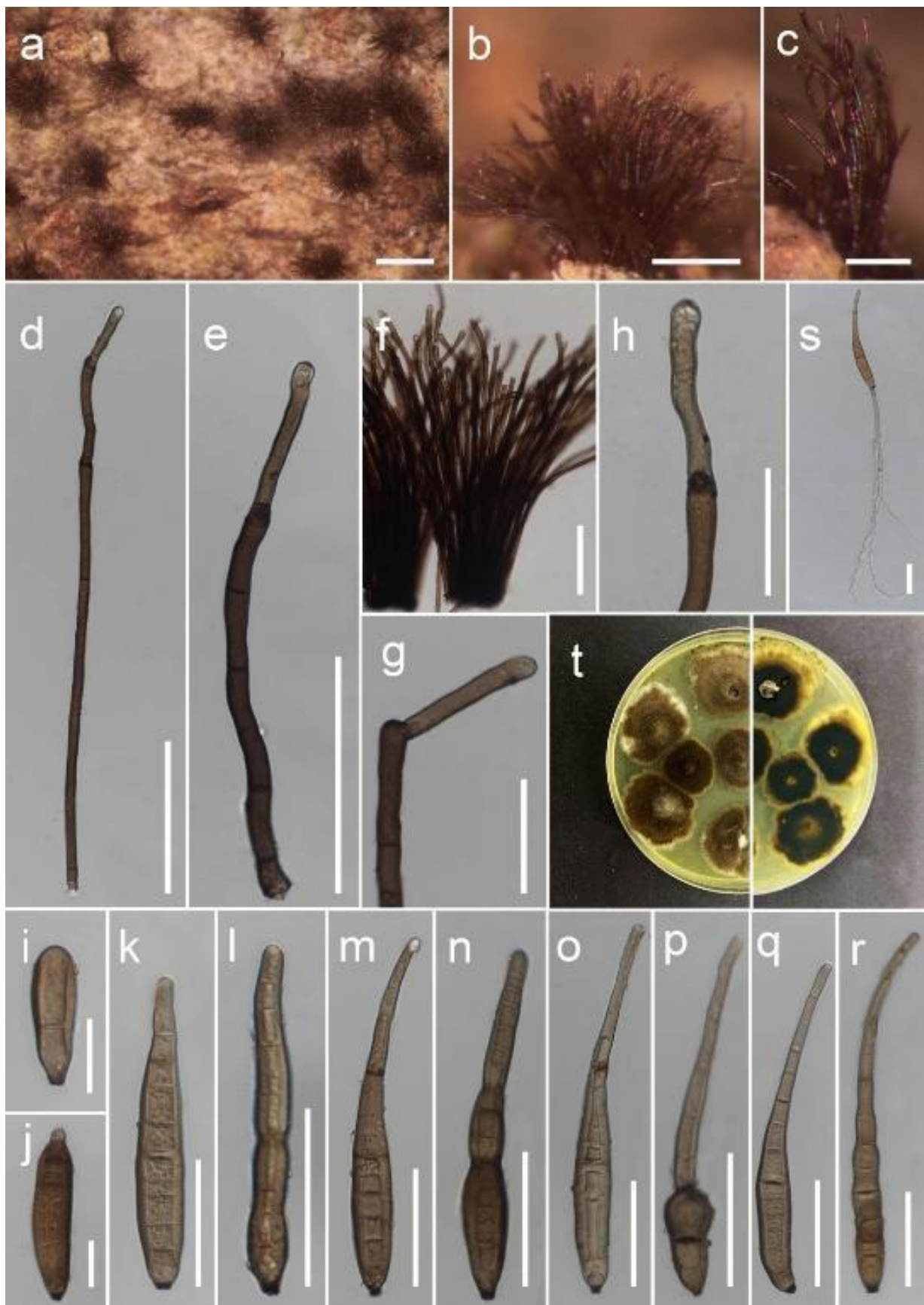


Figure 28 – *Helminthosporium chiangraiense* (MFLU 24-0401, a new host record). a–c Colonies on *Afzelia xylocarpa* woody litter. d–f Conidiophores with conidiogenous cells. g, h Apical

conidiophores and conidiogenesis. i–r Conidia. s A germinated conidium. t Colonies on PDA (front and reverse). Scale bars: a = 500 μ m, b = 200 μ m, c–f = 100 μ m, g, h, k–s = 50 μ m, i, j = 20 μ m.



Figure 29 – *Helminthosporium erythrinicola* (MFLU 24-0402, a new host and geographical record). a, b Colonies on *Dalbergia cana* woody litter. c, d Conidiophores with conidiogenous cells. e Apical conidiophores and conidiogenesis. f–k Conidia. l A germinated conidium. m Colony on (front and reverse). Scale bars: a = 500 μ m, b = 200 μ m, c, d, f–k = 50 μ m, e, l = 20 μ m.

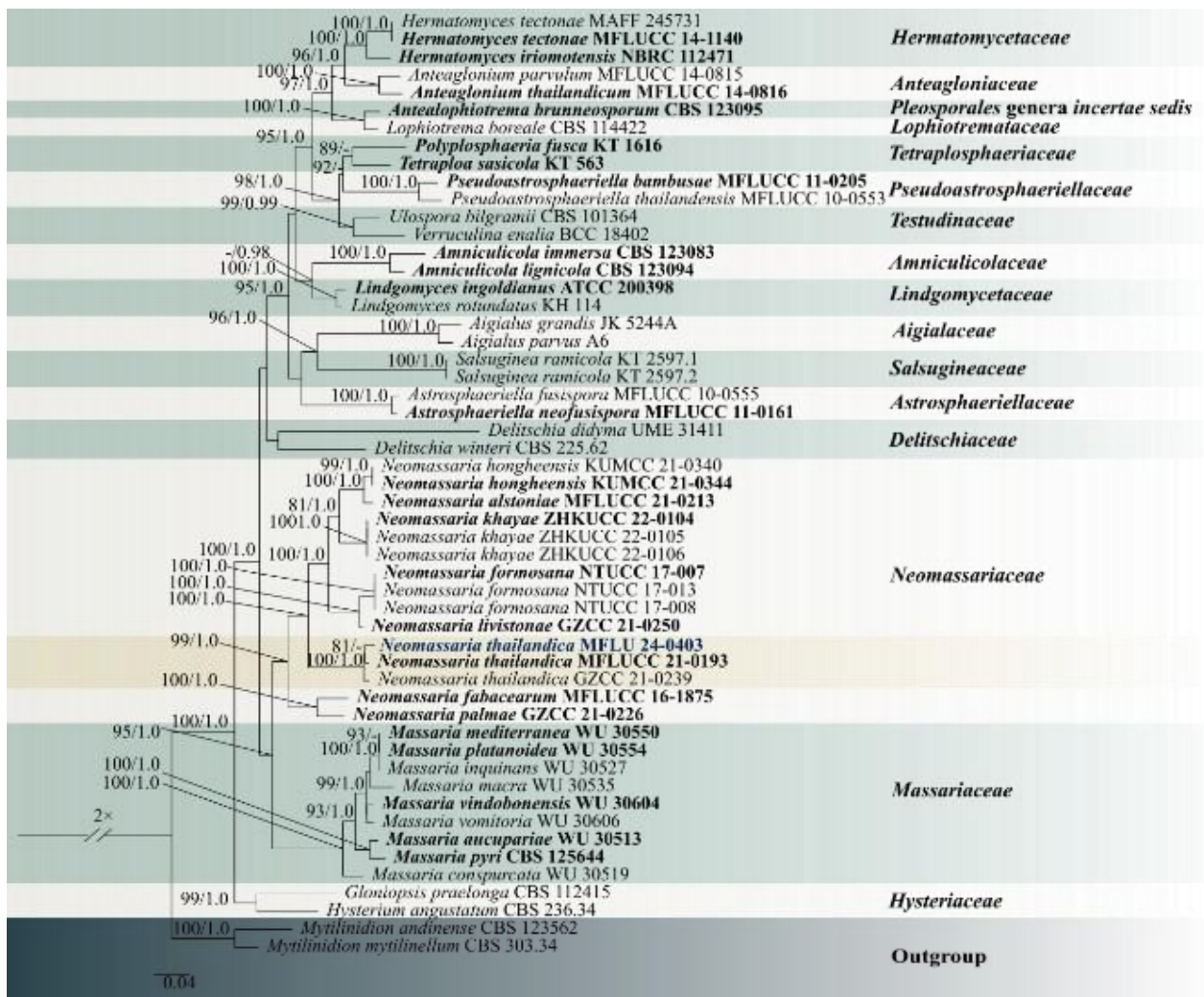


Figure 30 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined LSU, SSU, *rpb2*, and *tefl-α* sequence data of *Neomassariaceae* and some closely related families. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Fifty-three strains are included in the combined analyses which comprised 3,821 characters (LSU = 869, SSU = 1,028, *rpb2* = 1,028, and *tefl-α* = 896). The best score for log-likelihood of consensus tree is -28891.322. The matrix had 1,553 distinct patterns 1,125 parsimony-informative, 220 singleton sites, 2,476 constant sites. Selecting individual models TNe+I+G4, K2P+I+G4, TIM3e+I+G4 and TIM+F+I+G4 were applied to LSU, SSU, *rpb2*, and *tefl-α* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 5,000,000 MCMC generations was calculated as 0.003233. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.98 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Mytilinidion andinense* (CBS 123562) and *M. mytilinellum* (CBS 303.34). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Neomassaria thailandica N.I. de Silva, Lumyong & K.D. Hyde, de Silva, et al. Mycosphere 13, 991 (2022). Fig. 31

Index Fungorum number: IF559520; Facesoffungi number: FoF10718

Saprobic on *Microcos paniculata* woody litter. Sexual morph: *Ascomata* 181–350(–400) µm diam., 150–324 µm high, ($\bar{x}$ = 235 × 270 µm, n = 5), solitary, scattered, semi-immersed, dark brown, globose to subglobose, unilocular, with a carbonaceous central ostiole. *Peridium* 30–45 µm wide, comprising hyaline to brown or dark brown compact cells of *textura angularis*, indistinguishable

from the host tissues. *Hamathecium* comprising 1.2–2.5 µm wide, cylindrical, hyaline, septate, dense, cellular or anastomosing pseudoparaphyses. *Asci* (52–)60–85(–98) × 14–15.5 µm ($\bar{x}$ = 71 × 11.7 µm, n = 20), bitunicate, 8-spored, oblong to cylindrical, with short pedicel and ocular chamber. *Ascospores* (12–)15–26(–27.5) × 4–7.7(–8.5) µm ($\bar{x}$ = 20 × 6 µm, n = 33), overlapping 1–2-seriate, ellipsoid to fusiform, hyaline, when mature 1-septate, constricted at the septum, without a mucilaginous sheath. Asexual morph: Undetermined.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 26 March 2022, N. Afshari, 3C1T2R3a (MFLU 24-0403).

GenBank numbers – (ITS = PQ800235), LSU = PV072593, SSU = PV072689, *rpb2* = PV138135, *tefl-α* = PX739624.

Known hosts – *Anomianthus dulcis* (de Sliva et al. 2022), rachides of *Rhapis Excelsa* (Zhang et al. 2024), *Microcos paniculata* (this study).

Known distribution – Thailand (de Sliva et al. 2022, this study), China (Zhang et al. 2024).

Notes – de Silva et al. (2022) introduced *Neomassaria thailandica* (MFLUCC 21-0193) isolated from *Anomianthus dulcis* (Annonaceae) in Chiang Rai Province, Thailand. Subsequently, the asexual morph (sporidesmium-like hyphomycete) was reported from decaying rachides of *Rhapis excelsa* in China (Zhang et al. 2024). In multigene phylogeny analysis of combined LSU, SSU, *rpb2*, and *tefl-α* sequence data, our isolate (MFLU 24-0403) clustered with the other two strains of *N. thailandica* with 81% ML and 1.0 PP support (Fig. 30). The size of some characters differs slightly, for an example, our isolate has slightly larger ascomata (181–350(–400) µm diam. × 150–324 µm high ($\bar{x}$ = 235 × 270 µm) vs. 200–280 µm diam. × 170–200 µm high ($\bar{x}$ = 190 × 250 µm) than *N. thailandica* (MFLUCC 21-0193). However, there are no significant base pair differences between the LSU, SSU, and *tefl-α* sequences of our isolate and *N. thailandica* (MFLUCC 21-0193), with differences of 0.8%, 0.7%, and 1.8%, respectively. Based on morphology coupled with molecular phylogeny, our collection is identified as a new host record of *N. thailandica*.

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde

Liu et al. (2014) introduced *Roussoellaceae* with *Roussoella* as the type genus. Subsequently, Jaklitsch & Voglmayr (2016) considered *Roussoellaceae* to be a synonym of *Thyridariaceae*. Later, Tibpromma et al. (2017) accepted *Roussoellaceae* as a well-resolved family and this argument was supported by subsequent authors (Tibpromma et al. 2018, Phookamsak et al. 2019, Pasouvang et al. 2022). In its sexual morph, this family exhibits immersed-erumpent to superficial, dome-shaped to elongated linear ascostromata, cylindrical to clavate, bitunicate asci, and yellowish to dark brown, 2-celled ornamented ascospores. The asexual morph produces pycnidial conidiomata (Liu et al. 2014, Ren et al. 2024). Currently, 12 genera are accepted in the family (Hyde et al. 2024a).

Pararoussoella Wanas., E.B.G. Jones & K.D. Hyde

Index Fungorum number: IF554218; Facesoffungi number: FoF04056

The genus was introduced by Wanasinghe et al. (2018) to accommodate *Pararoussoella rosarum*. *Pararoussoella rosarum* was identified from a specimen that was collected from the UK based on combined LSU, SSU, ITS, and *tefl-α* sequence data (Wanasinghe et al. 2018). *Pararoussoella rosarum* morphologically resembles taxa in *Roussoella* by having ascospores with irregular longitudinal striations. However, these two genera are not closely related in phylogenetic analyses. Phookamsak et al. (2019) transferred *Pararoussoella* and *Pseudoneoconiothyrium* from *Thyridariaceae* to *Roussoellaceae* based on multigene phylogenetic analyses and morphological features. This genus has immersed and globose ascomata with small black dots of ostioles, cellular pseudoparaphyses, black, central, papillate ostioles, cylindrical to oblong asci, and uniseriate, brown to dark brown ascospores, with irregular longitudinal striations (Wanasinghe et al. 2018). Phukhamsakda et al. (2020), transferred *Roussoella mangrovei* to *Pararoussoella*, therefore, currently, seven species are accepted in this genus. Herein, we document *Pararoussoella lincangensis* as a new geographical and host record on dead wood of *Dalbergia cana* from Thailand.

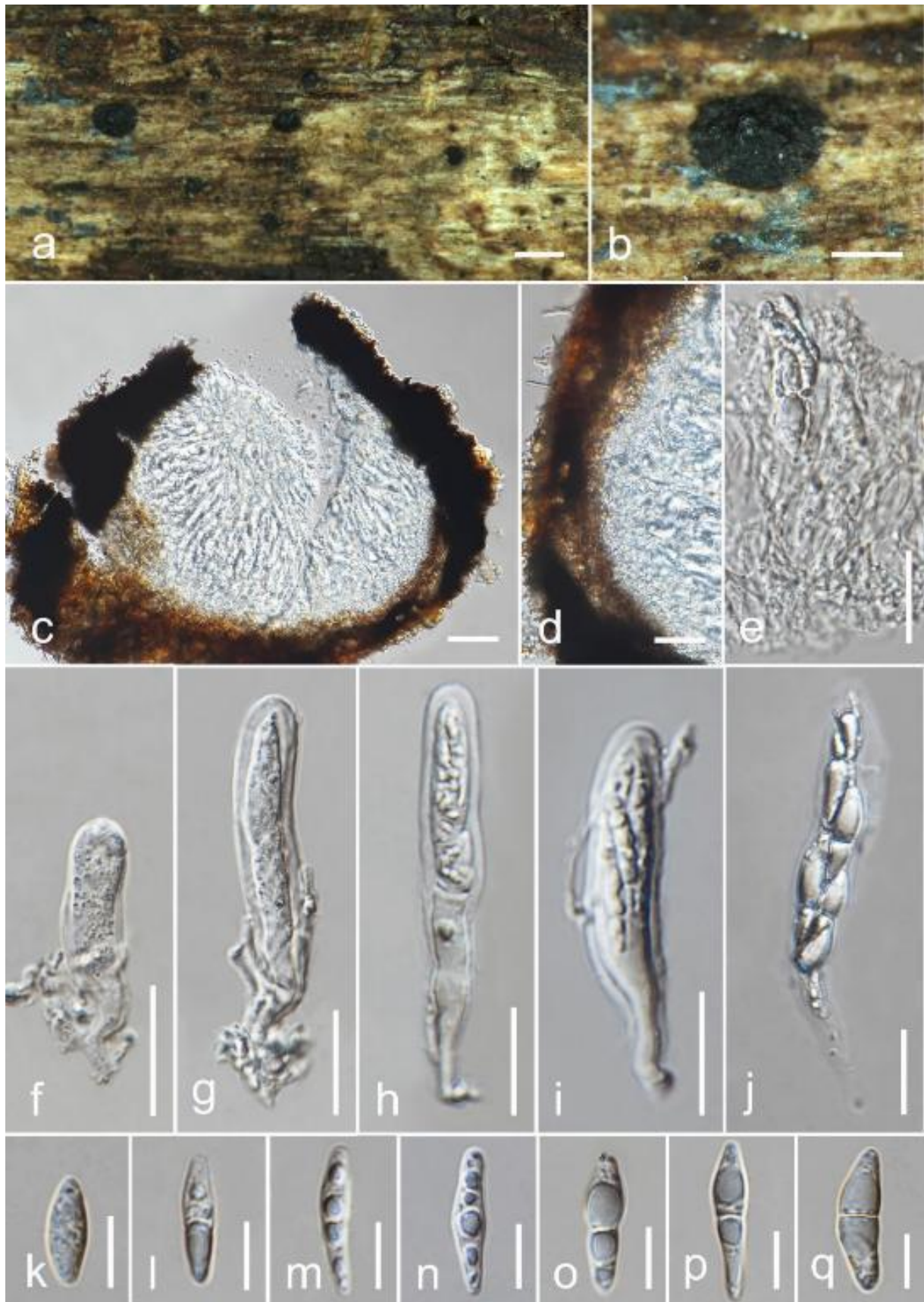


Figure 31 – *Neomassaria thailandica* (MFLU 24-0403, a new host record). a, b Appearance of ascomata on *Microcos paniculata* woody litter. c Vertical section of ascoma. d Section of peridium. e Pseudoparaphyses. f–j Asci. k–q Ascospores. Scale bars: a = 1 mm, b = 500 μm, c = 50 μm, d–j = 20 μm, k–q = 10 μm.

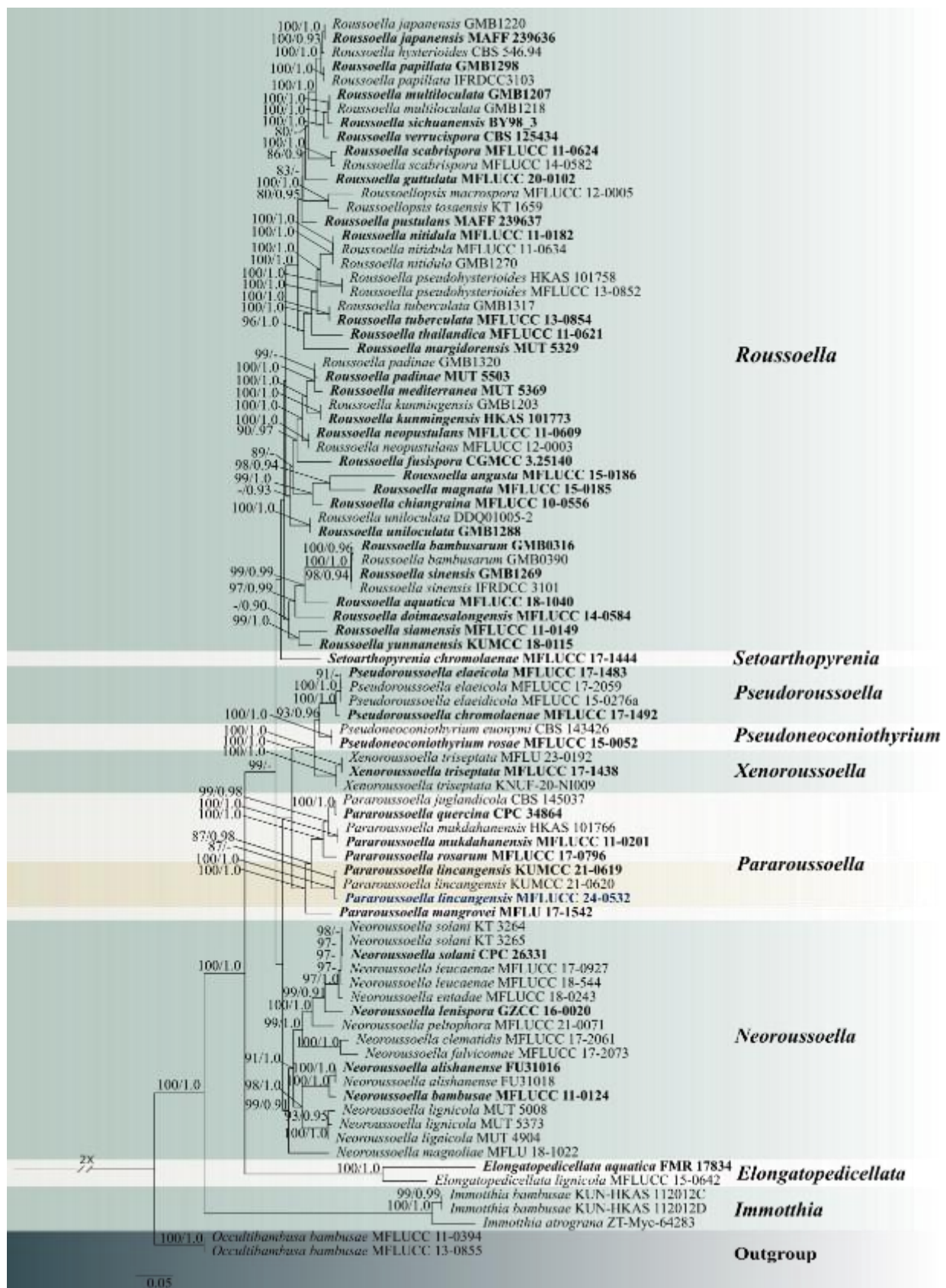


Figure 32 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined LSU, SSU, ITS, *tefl-α* and *rpb2* sequence data of *Roussoellaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Eighty-eight strains are included in the combined analyses which comprised 4,172 characters (LSU = 834, SSU = 958, ITS = 468, *tefl-α* = 893, and *rpb2* = 1,019). The best score for log-likelihood of consensus tree is -

31343.566. The matrix had 1,609 distinct patterns 1,083 parsimony-informative, 254 singleton sites, 2,835 constant sites. Selecting individual models TIM2e+I+G4, TNe+G4, TIM2e+I+G4, TN+F+I+G4 and TIM2e+I+G4 were applied LSU, SSU, ITS, *tefl-α* and *rpb2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.007642. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.9 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Occultibambusa bambusae* (MFLUCC 11-0394 and MFLUCC 13-0855). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Pararoussoella lincangensis G.C. Ren & K.D. Hyde, in Ren et al. Mycosphere (2024). Fig. 33

Index Fungorum number: IF901359; Facesoffungi number: FoF13893

Saprobic on *Dalbergia cana* woody litter. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 135–253 µm diam., 84(–110)–252 µm high ($\bar{x}$ = 190 × 183 µm, n = 10), pycnidial, scattered, mostly solitary, erumpent, globose to mainly sub-globose, dark brown to black, coriaceous, covered by black parenchymatous cells, ostiolate. *Ostiole* centrally located neck, single, papillate. *Conidiomatal wall* 11–17.5 µm wide ($\bar{x}$ = 14 µm, n = 25), composed of several layers, outer layers thick-walled, dark brown cells of *textura angularis*; inner layers thin-walled, hyaline to sub-hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.2–5 × 5–8 µm ($\bar{x}$ = 3.3 × 6.4 µm, n = 30), enteroblastic, phialidic, discrete, ampulliform to doliiform, usually wider at the base, hyaline, smooth-walled, thickening towards apex, arising from the stratum. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 40), L/W ratio = 1.6, ovoid to oblong, aseptate, initially hyaline becoming olivaceous at maturity, with 1–2 guttules, smooth-walled, thick-walled, straight, both ends bluntly rounded.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerged from one end cell. Colonies on PDA reaching 3–4 mm diam. after 7 days at room temperature (25–28 °C), circular, flattened, dense, fluffy, with a lobate margin, after one month; upper surface creamy white, from reverse olivaceous brown.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cana* (Fabaceae), 7 July 2022, N. Afshari, 4C2T1R3 (MFLU 24-0404); living culture MFLUCC 24-0532.

GenBank numbers – LSU = PV072594, SSU = PV072690, ITS = PQ800236, *tefl-α* = PX739625, *rpb2* = PV138136.

Known hosts – *Heliciopsis terminalis* (Ren et al. 2024), *Dalbergia cana* (this study).

Known distribution – China (Ren et al. 2024), Thailand (this study).

Notes – Based on the multigene phylogenetic analyses, our strain (MFLUCC 24-0532) clustered together with two strains of *Pararoussoella lincangensis* (KUMCC 21-0619 and KUMCC 21-0620) with 100% ML bootstrap support and 1.0 PP value (Fig. 32). In a BLASTn search of GenBank, the ITS sequence of our collections had 100% similarity to *P. lincangensis* (KUMCC 21-0619). Ren et al. (2024) described *P. lincangensis* from China, on dead woody twigs of *Heliciopsis terminalis* (Proteaceae), whereas we collected it from Thailand on dead wood of *Dalbergia cana* (Fabaceae). Both of these strains were found as asexual morphs in nature. Herein, we introduce a new host and geographical record for *P. lincangensis*, based on its similar morphology and analysis of the combined LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence dataset.

Teichosporaceae M.E. Barr

This family was established by Barr (2002) to accommodate nine genera (Tennakoon et al. 2021b). *Teichosporaceae* is recognized as a family with a high number of species in *Pleosporales*. *Teichosporaceae* is typified by the genus *Teichospora*, with *Teichospora trabicola* as the type species, that was isolated as a saprobe on oak posts in Germany (Jaklitsch et al. 2016). This family displays a wide range of morphological, ecological, and phylogenetic diversity (Tennakoon et al. 2021c). There are 17 genera are accepted in this family based on phylogeny (a combined ITS, LSU,

SSU, *tefl-α*, and *rpb2* dataset) and morphology (Boonmee et al. 2019, Wijayawardene et al. 2022, Hyde et al. 2024a).

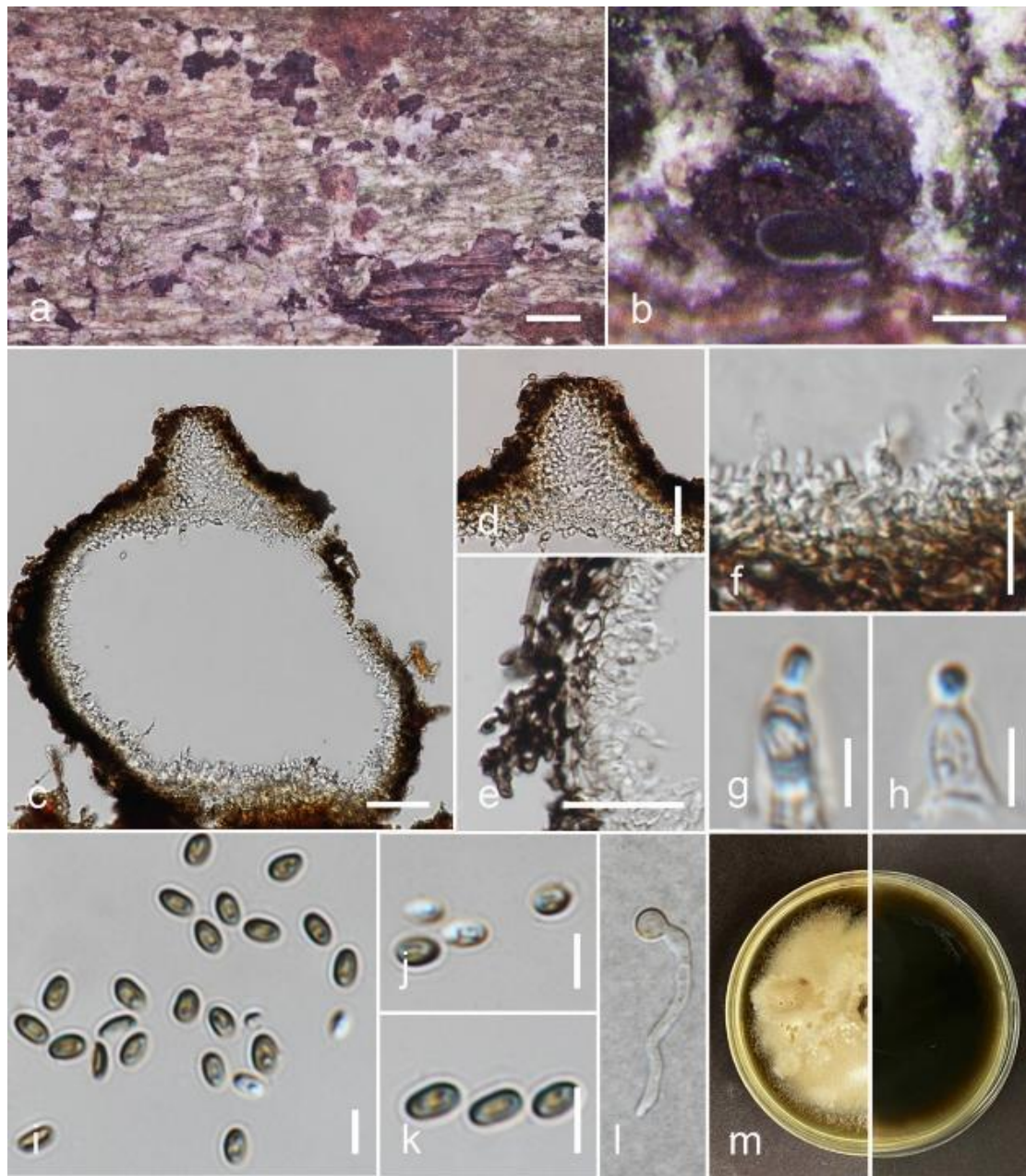


Figure 33 – *Pararoussoella lincangensis* (MFLU 24-0404, a new host and geographical record). a Conidiomata on *Dalbergia cana* woody litter. b Longitudinal section of a conidioma. c Vertical section through conidioma. d Section through ostiole. e Section of conidiomatal wall. f–h Conidiogenous cells and conidia. i–k Conidia. l A germinated conidium. m Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 100 μ m, c = 50 μ m, d–f = 20 μ m, l = 10 μ m, g–k = 5 μ m.

***Misturatosphaeria* Mugambi & Huhndorf**

Index Fungorum number: IF515583; Facesoffungi number: FoF00831

Mugambi & Huhndorf (2009) established *Misturatosphaeria* to accommodate *M. aurantiacinotata* as the type species. In *Misturatosphaeria*, ascomata are solitary or aggregated, semi-immersed or immersed to erumpent, pyriform or globose to subglobose, ostiolar region orange or lighter. The ostiole is central, rounded, and papillate. The asci are eight-spored, bitunicate, fissitunicate, cylindrical-clavate. Ascospores are uniseriate, partially overlapping, brown to dark brown, fusiform, one to three-septate, with one of the central cells often wider than the others, with

or without a mucilaginous sheath. The asexual morph has not been observed (Boonmee et al. 2019, Tennakoon et al. 2021c). Phylogenetically, *Misturatosphaeria* formed a distinct clade in the phylogenetic tree based on a combined LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data. This genus includes three species (*M. aurantiacinotata*, *M. viridibrunnea* and *Misturatosphaeria* sp.) (Tennakoon et al. 2021c). In this study, we document *Misturatosphaeria viridibrunnea* (MFLUCC 24-0534), as a new host record on *Dipterocarpus alatus*, and the first report of asexual morph. Also, *M. viridibrunnea* (MFLUCC 24-0533) is recorded as a new geographical and host record on *Microcos paniculata* from Doi Tung National Park, Thailand.

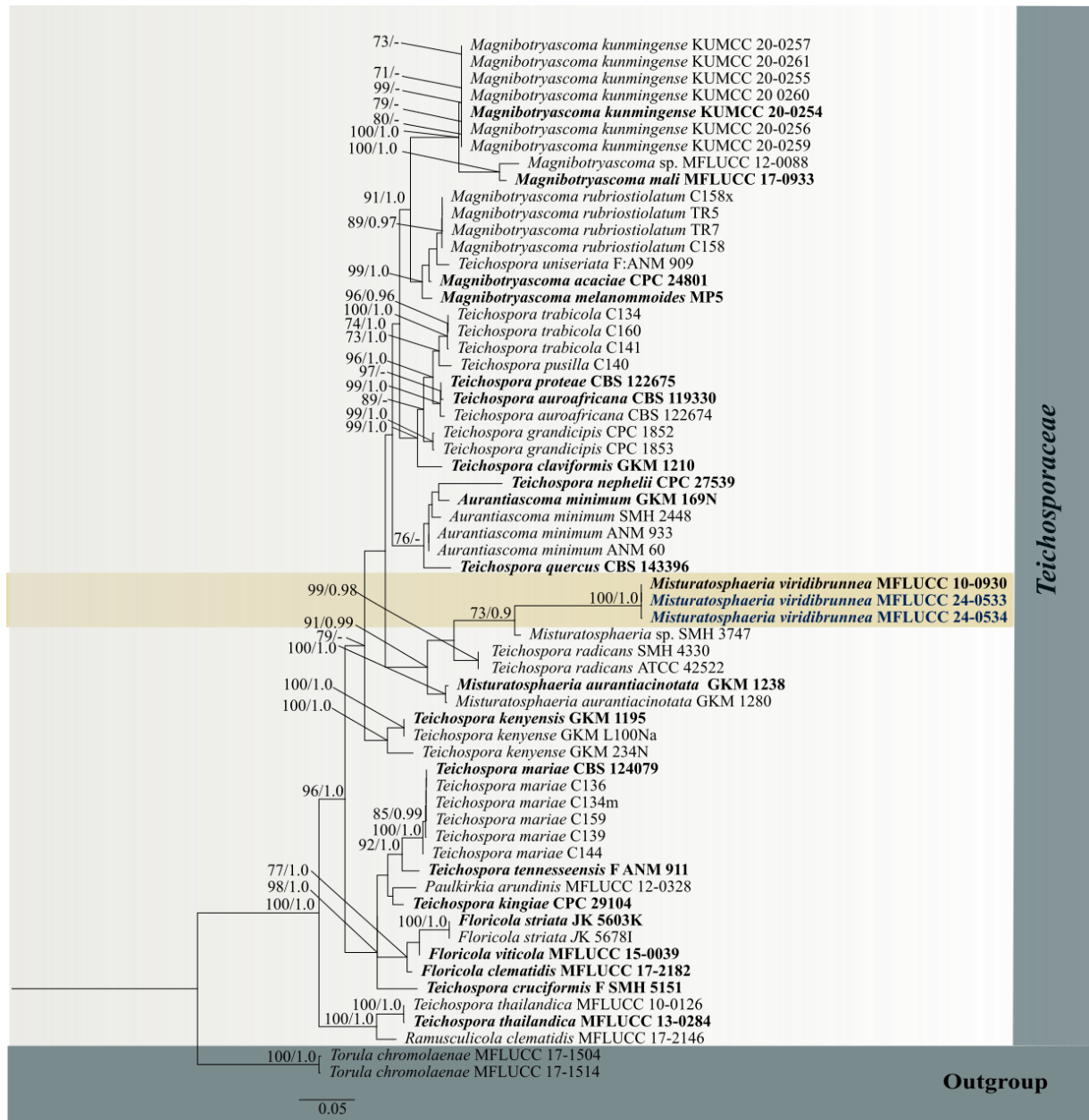


Figure 34 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *rpb2*, SSU, and *tefl-α* sequence data of *Teichosporaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Sixty-two strains are included in the combined analyses which comprised 4,886 characters (ITS = 573, LSU = 874, *rpb2* = 1,059, SSU = 1,014, and *tefl-α* = 1,366). The best RAXML tree with a final optimization likelihood value of -21148.511820 is presented. The matrix had 1,446 distinct alignment patterns, with 49.18% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241324, C = 0.257938, G = 0.277630, T = 0.223108; substitution rates AC = 1.305041, AG = 3.257596, AT = 1.491964, CG =

1.259127, CT = 8.684840, GT = 1.000000; gamma distribution shape parameter α = 0.226052. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.006952. The evolutionary models TrN+I+G, TIM2+I+G, GTR+I+G, TPM1+I, and TIM1+I+G were applied for ITS, LSU, *rpb2*, SSU, and *tef1- α* sequence data, respectively. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.9 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Torula chromolaenae* (MFLUCC 17-1504 and 17-1514). Ex-type strains are in bold. The isolates generated in this study are indicated in bold and blue.

Misturatosphaeria viridibrunnea Boonmee, Wijayaw. & K.D. Hyde, in Boonmee et al. Phytotaxa 388, 127 (2019). Figs 35, 36

Index Fungorum number: IF555392; Facesoffungi number: FoF04909

Saprobic on *Microcos paniculata* and *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 173–235 μ m high, 178–244 μ m diam. ($\bar{x}$ = 198.3 $\times$ 201 μ m, n = 5), superficial, erumpent, mostly solitary, scattered or in small groups, subglobose, dark brown to black, uniloculate, ostiolate. *Ostiole* centrally located, single, rounded, papillate, with pore like opening, rather sulcate or puckered. *Peridium* 20.7–28 μ m wide ($\bar{x}$ = 24.3 μ m, n = 25), outer layers dark brown, inner layers light brown to hyaline, both layers composed of cells of *textura angularis*. *Hamathecium* comprises 1–2.3 μ m wide ($\bar{x}$ = 1.7 μ m, n = 30), dense, hyaline, branched, septate, cylindrical, anastomosing pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 65–83(–87) $\times$ 6.3–9 μ m ($\bar{x}$ = 74 $\times$ 8 μ m, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicel, apically rounded, with a shallow ocular chamber. *Ascospores* 12–15(–16) $\times$ 3.5–5.5 μ m ($\bar{x}$ = 13.4 $\times$ 4.5 μ m, n = 30), uni- or mostly bi-seriate, overlapping, ellipsoidal-fusiform, 1-septate, usually upper cell wider than the lower cell, moderately curved and tapering toward the apex, constricted at septum, brown, guttulate, thick-walled, smooth-walled. Asexual morph: Coelomycetous. *Conidiomata* (including neck) 75–200(–305) μ m diam, 123–285 μ m high ($\bar{x}$ = 156 $\times$ 216 μ m, n = 5), pycnidial, coriaceous, immersed, subepidermal, dark brown to black, mostly solitary or in small groups, globose to subglobose or conical, unilocular, ostiolate. *Conidiomatal wall* 18–25 μ m wide ($\bar{x}$ = 21.7 μ m, n = 20), composed of 2-layers, outer layer brown, thick-walled of *textura angularis* cells, linked with hyaline and compact *textura angularis* cells bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–9 $\times$ 1.7–3 μ m ($\bar{x}$ = 6.5 $\times$ 2.4 μ m, n = 25), phialidic, enteroblastic, hyaline, cylindrical and moderately tapering towards apex, smooth-walled. *Conidia* 2.7–4.4 $\times$ 1.7–2.8 μ m ($\bar{x}$ = 3.6 $\times$ 2.2 μ m, n = 40), L/W ratio = 1.6, globose to oval, with guttule in each cell, hyaline, aseptate, smooth-walled.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes emerged from both end cells. Colonies on PDA reaching 2.5 cm diam. after 10 days at room temperature (25–28 °C), after one month irregular, flattened, medium dense, umbonate elevation, undulate at margin, upper surface cream at center and greenish brown at margin, from reverse reddish brown at center, yellowish at margin. Conidia germinated on PDA within 24 h and germ tube emerged from one end. Colonies reaching 2–2.5 cm diam. after 7 days at room temperature (25–28 °C), irregular, floccose, dense, upper surface cream at the center and grey at margin, from reverse dark grey at the center light brown radiating outwardly with cracks in the middle.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus*, 27 September 2022, N. Afshari, 2C3T2R1 (MFLU 24-0406); living culture MFLUCC 24-0534. Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata*, 26 March 2022, N. Afshari, 3C1T3R3 (MFLU 24-0405); living culture MFLUCC 24-0533.

GenBank numbers – MFLU 24-0406: ITS = PQ800238, LSU = PV072596, *rpb2* = PV138137, SSU = PV072692, *tef1- α* = PX739626; MFLU 24-0405: ITS = PQ800237, LSU = PV072595, SSU = PV072691.

Known hosts – dead branches of an unidentified terrestrial dicotyledonous plant (Boonmee et al. 2019), *Dipterocarpus alatus* and *Microcos paniculata* (this study).

Known distribution – Thailand (Boonmee et al. 2019, this study).

Notes – Our two strains of *Misturatosphaeria viridibrunnea* (MFLUCC 24-0533, MFLUCC 24-0534) clustered together with *M. viridibrunnea* (MFLUCC 10-0930) strain, with 100 ML/ 1.00 PP statistical support (Fig. 34). *Misturatosphaeria viridibrunnea* was introduced by Boonmee et al. (2019), and in their phylogenetic analyses, the species also formed a distinctly long branch, similar to the result observed in the present study. Our collection of *Misturatosphaeria viridibrunnea* (MFLUCC 24-0533) resembles *M. viridibrunnea* (MFLUCC 10-0930) in that both are sexual morphs, and reported on dead wood in Chiang Rai Province, Thailand (Boonmee et al. 2019). This sexual morph collection of *M. viridibrunnea* (MFLUCC 24-0533) represents a new host and geographical record based on morphological and phylogenetic evidence for a fungal collection on *Microcos paniculata*. When it comes to the asexual strain, *M. viridibrunnea* (MFLUCC 24-0534), there is compatible morphology of our strain with other asexual morphs of *Teichosporaceae* taxa (Tennakoon et al. 2021c). This new strain is introduced as a new host record on *Dipterocarpus alatus*, and asexual morph of *M. viridibrunnea* based on multigene phylogenetic analyses of combined ITS, LSU, *rpb2*, SSU, and *tefl-α* sequence data.

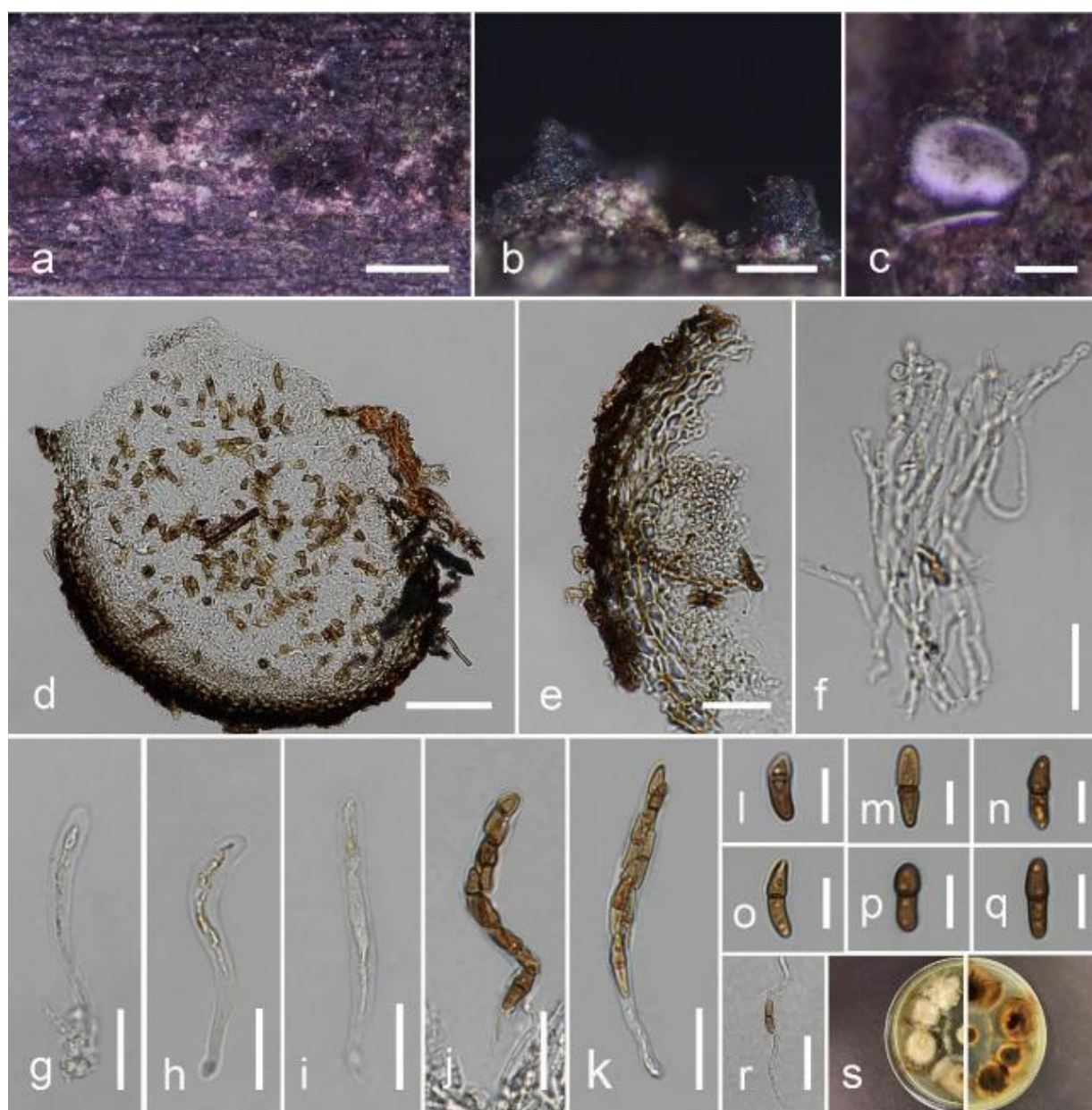


Figure 35 – *Misturatosphaeria viridibrunnea* (MFLU 24-0405, a new host and geographical record). a, b Appearance of ascomata on *Microcos paniculata* woody litter. c Longitudinal section of ascoma.

d Section of ascoma. e Section of peridium. f Pseudoparaphyses. g–k Asci. l–q Ascospores. r A germinated ascospore. s Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d = 50 μ m, e–k, r = 20 μ m, l–q = 10 μ m.

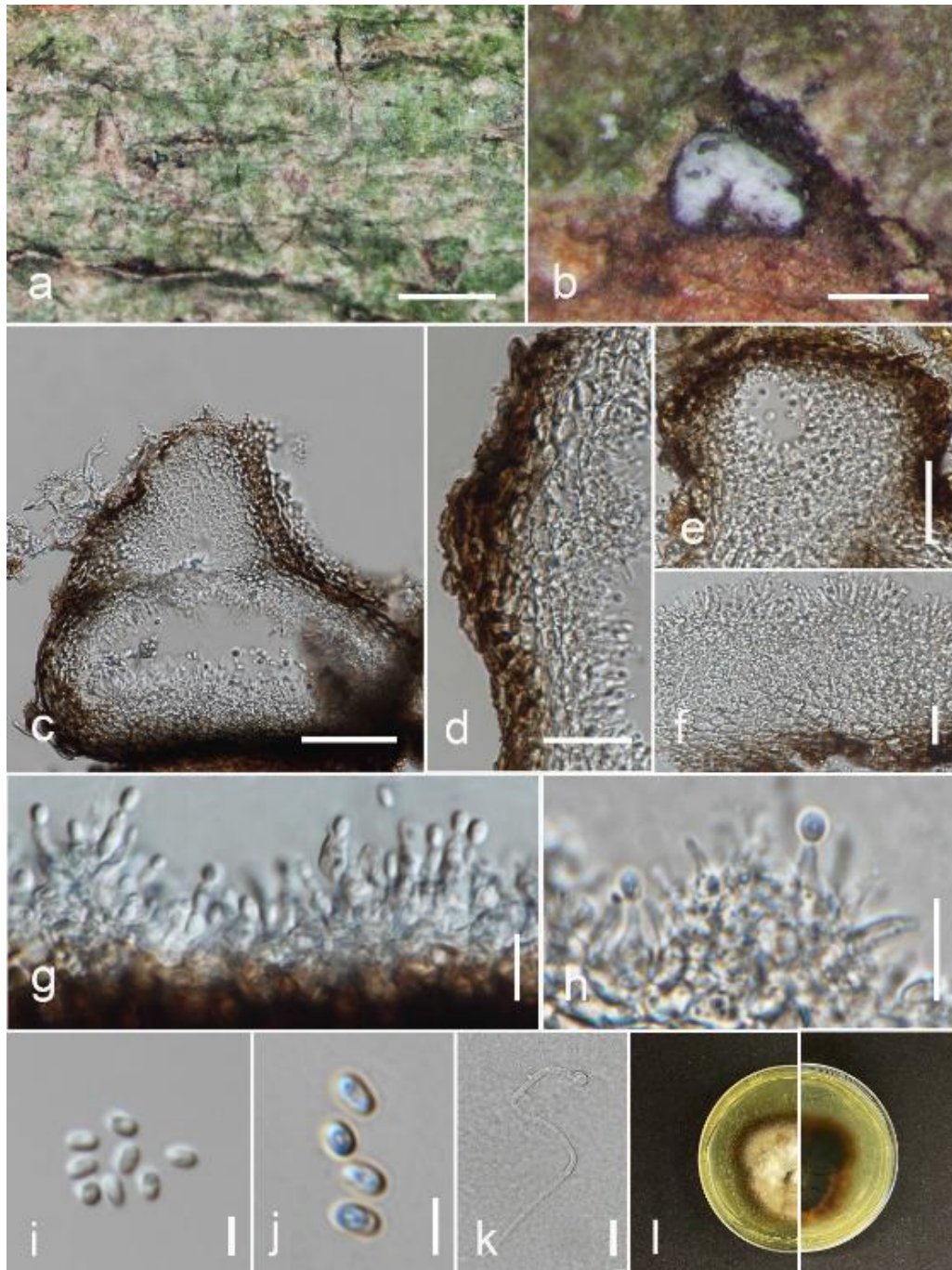


Figure 36 – *Misturatosphaeria viridibrunnea* (MFLU 24-0406, a new host record and first report of the asexual morph). a Appearance of conidiomata on *Dipterocarpus alatus* woody litter. b Longitudinal section of conidioma. c Vertical section through conidioma. d Section of conidiomatal wall. e Section through ostiole. f–h Conidia attached to conidiogenous cells. i, j Conidia. k A germinated conidium. l Colony on PDA (front and reverse). Scale bars: a = 500 μ m, b = 200 μ m, c = 50 μ m, d–f, k = 20 μ m, g, h = 10 μ m, i, j = 5 μ m.

Eurotiomycetes O.E. Erikss. & Winka
Sclerococomycetidae Réblová, Unter. & W. Gams
Sclerococcales Réblová, Unter. & W. Gams

Dactylosporaceae Bellem. & Hafellner (= *Sclerococcaceae* Réblová, Unter. & W. Gams)

Réblová et al. (2017) established *Sclerococcaceae* to accommodate *Dactylospora*, *Rhopalophora*, *Sclerococcum*, and *Fusichalara minuta*. Phylogenetic analyses based on LSU, SSU, *rpb2*, *rpb1*, and mtSSU were applied to introduce this family. *Cylindroconidiis*, *Fusichalara*, *Gamsomyces*, *Rhopalophora*, and *Sclerococcum* genera are listed in this family (Hyde et al. 2024a).

Cylindroconidiis H. Zhang & X.D. Yu

Index Fungorum number: IF555307; Facesoffungi number: FoF04855

Yu et al. (2018) established *Cylindroconidiis* to accommodate *Cylindroconidiis aquaticus*, as the type species, based on morphological characteristics and phylogenetic analysis of combined LSU, SSU, and ITS datasets. This species was isolated from submerged decaying wood in a freshwater habitat. In the phylogenetic tree, it was positioned between *Rhopalophora* species and *Fusichalara minuta*. The sexual morph of this genus is undetermined. The asexual morph is characterized by superficial, effuse, gregarious, hairy colonies, which are partly immersed, and composed of septate, smooth hyphae. The conidiophores are macronematous, mononematous, cylindrical, erect, smooth, unbranched, septate, and thin-walled. Conidiogenous cells are holoblastic, polyblastic, integrated, determinate, terminal or intercalary and conidia are acrogenous and pleurogenic, cylindrical to oblong, euseptate, pigmented, solitary (Yu et al. 2018). In this study, we introduce *Cylindroconidiis doitungensis* as a novel species found on dead wood of *Microcos paniculata* from Doi Tung National Park, Thailand.

Cylindroconidiis doitungensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 38

Index Fungorum number: IF904745; Facesoffungi number: FoF17225

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which the fungus was collected.

Holotype – MFLU 24-0464

Saprobic on *Microcos paniculata* woody litter. Sexual morph: Undetermined. Asexual morph: *Mycelium* semi-immersed, consisting of pale brown, smooth, and septate hyphae. *Conidiophores* 50–113 × 1.5–3.5 µm ($\bar{x}$ = 72 × 2.3 µm, n = 25), macronematous, mononematous, erect, cylindrical, mostly straight or slightly flexuous, smooth, thin-walled, pale brown to brown, paler at apex, simple and rarely branched, septate, constricted at the septa. *Conidiogenous cells* polyblastic, holoblastic, with occasional sympodial proliferation, determinate, integrated, terminal and intercalary nodose. *Conidia* 5.1–2.2 × 1.5–2.6 µm ($\bar{x}$ = 3.5 × 2 µm, n = 50; L/W ratio = 1.8), acrogenous and pleurogenic, globose, ellipsoidal to amygdaliform, straight, at base truncate, slightly tapering toward base, aseptate to rarely 1-septate, not constricted at septum, subhyaline and guttulate when immature, pale brown to brown and without guttules at maturity, smooth, thin-walled.

Culture characteristics – Conidium germinated on PDA within 24 h. Colonies on PDA reached 1 mm diam. after 10 days at room temperature (25–28 °C), irregularly rugose, raised, felty, flesh, umbonate, margin undulate, at upper surface grey, reverse olivaceous brown, white at periphery.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 26 March 2022, N. Afshari, 3C1T2R4b (MFLU 24-0464, holotype); ex-type living culture MFLUCC 24-0554.

GenBank numbers – LSU = PV072609, ITS = PQ800255.

Notes – Multigene phylogenetic analyses indicate that *Cylindroconidiis doitungensis* (MFLUCC 24-0554) clusters sister to the type strain of *Cylindroconidiis aquaticus* (MFLUCC 11-0294), with 77% ML bootstrap support and 0.99 PP value (Fig. 37). In a BLASTn search of NCBI, the ITS sequence of our strain (MFLUCC 24-0554) has 95.59% similarity in 100% query cover to *C. aquaticus* (MFLUCC 11-0294). The SSU gene region was not amplified in our study; therefore, comparisons were made based on the LSU and ITS gene regions. Sequence comparison between *C. doitungensis* and *C. aquaticus* revealed 3.3% and 8% base pair differences in ITS and LSU, respectively (excluding gaps). Both *Cylindroconidiis aquaticus* (MFLU 11-1070), which was

collected from submerged decaying wood in freshwater habitat, and our isolate have macronematous, mononematous conidiophores, polyblastic, holoblastic conidiogenous cells, and acrogenous and pleurogenic conidia. However, our collection occasionally proliferates sympodially and has smaller conidiophores compared to those of *C. aquaticus* $50\text{--}113 \times 1.5\text{--}3.5 \mu\text{m}$ ($\bar{x} = 72 \times 2.3 \mu\text{m}$), vs. $240\text{--}380 \times 6\text{--}10 \mu\text{m}$ ($\bar{x} = 312 \times 7.3 \mu\text{m}$). The conidia of *C. doitungensis* are predominantly aseptate and smaller than those of *C. aquaticus* (MFLU 11-1070) ($\bar{x} = 3.5 \times 2 \mu\text{m}$, vs. $\bar{x} = 20.6 \times 8.3 \mu\text{m}$) (Yu et al. 2018). Therefore, *Cylindroconidiis doitungensis* is introduced as a new species based on different morphological characterization and the phylogenetic distinctiveness.

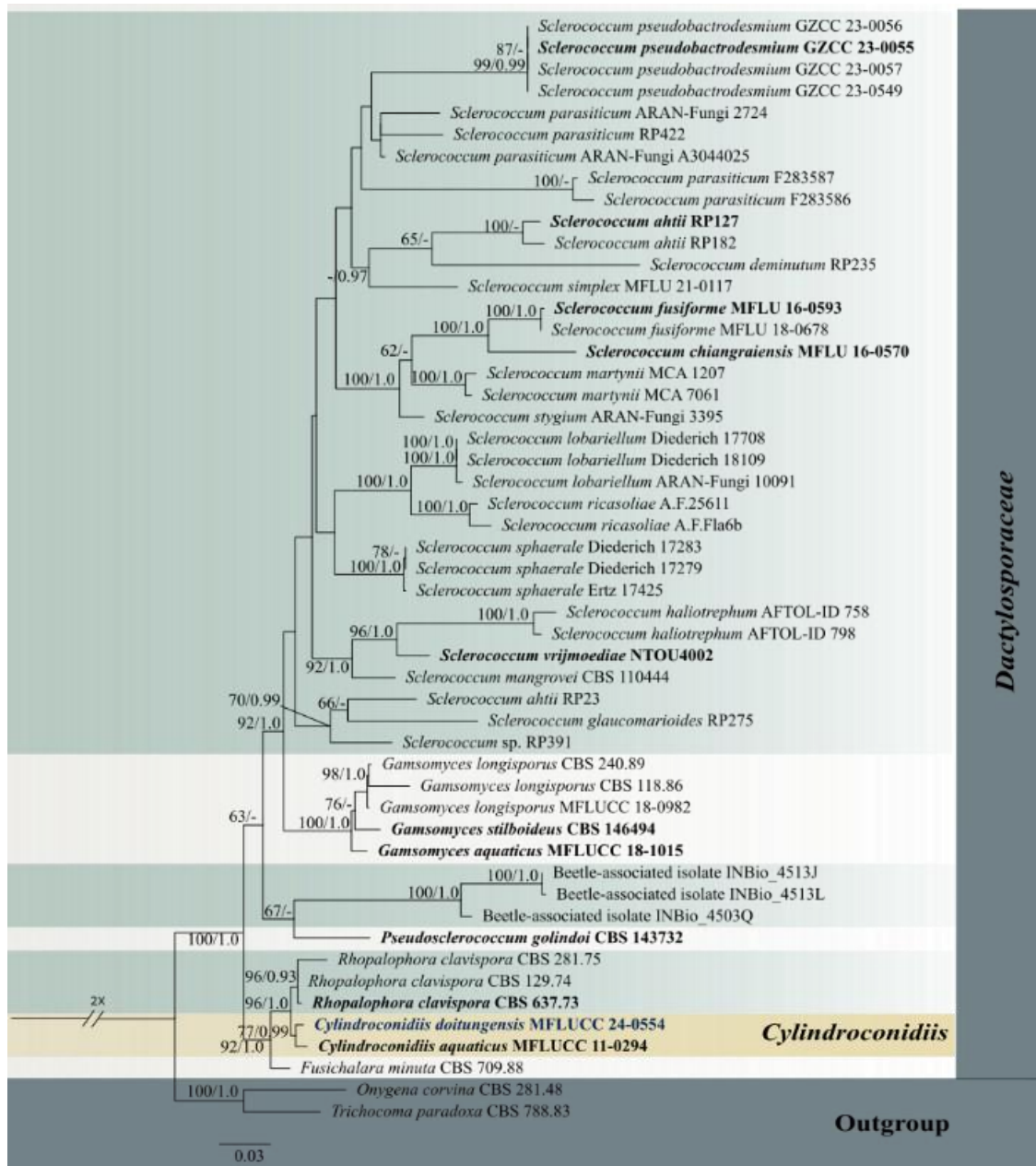


Figure 37 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, SSU, and ITS sequence data of *Dactylosporaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Fifty-one strains are included in the combined analyses which comprised 2,909 characters (LSU = 920, SSU = 1,512, and ITS = 477). The best RAxML tree with a final optimization likelihood value of -15390.605671 is presented. The matrix had 952 distinct alignment patterns, with 51.61% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.261540, C = 0.212678, G = 0.272721, T = 0.253060; substitution rates AC = 1.201286, AG = 2.320882, AT = 1.229950, CG = 1.005588, CT = 5.385489, GT = 1.000000; gamma

distribution shape parameter $\alpha = 0.257248$. In the Bayesian analysis, average standard deviation of split frequencies at the end of 5,000,000 MCMC generations was calculated as 0.006714. The evolutionary models TrN+I+G, TrN+G, and TIM2ef+I+G were applied to combined LSU, SSU, and ITS sequence data respectively. Bootstrap support values for ML greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Onygena corvina* (CBS 281.48) and *Trichocoma paradoxa* (CBS 788.83). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.



Figure 38 – *Cyllindroconidiis doitungensis* (MFLU 24-0464, holotype). a Colonies on *Microcos paniculata* woody litter. b, c Colony on MEA (front and reverse). d–i Conidiophores, conidiogenous cells, and conidia. j–o Conidia. Scale bars: a = 200 μm , d–i = 10 μm , j–o = 5 μm .

Sordariomycetes O.E. Erikss. & Winka
Amphisphaeriales D. Hawksw. & O.E. Erikss.
Oxydothidaceae S. Konta & K.D. Hyde

Oxydothidaceae was introduced by Konta et al. (2016) in *Xylariales* (*Sordariomycetes*) based on morphology and phylogeny. Later, Samarakoon et al. (2022) and Hyde et al. (2024a) accepted this family within the order *Amphisphaeriales*. Only one genus was reported in this family (Hyde et al. 2024a). Species of *Oxydothidaceae* are mostly saprobic or endophytic, occurring on the leaves, rachides, or petioles of palms (Konta et al. 2016).

Oxydothis Penz. & Sacc.

Index Fungorum number: IF3661; Facesoffungi number: FoF05091

As the type genus of *Oxydothidaceae*, *Oxydothis* was established by Penzig & Saccardo (1897), with *O. grisea* as the type species, along with two additional species (*O. nigricans* and *O. maculosa*), assigned to family *Amphisphaeriaceae* (Eriksson & Hawksworth 1991). Hyde (1993) transferred *Oxydothis* from *Amphisphaeriaceae* to *Hyponectriaceae* based on ascus, ascospore, and peridium characteristics. Subsequently, it was transferred to *Clypeosphaeriaceae* (Kang et al. 1999). Later, based on DNA sequence data, Jeewon et al. (2003) proposed that this genus is related to *Leiosphaerella* (*Xylariales*, genera *incertae sedis*). Later, Konta et al. (2016) transferred *Oxydothis* to *Oxydothidaceae* (*Xylariales*). Currently, *Oxydothis* comprises 80 species (Hyde et al. 2024a). In this study, we introduce *Oxydothis dalbergiae* as a novel species found on dead wood of *Dalbergia cana* from Doi Tung National Park, Thailand.

Oxydothis dalbergiae N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 40

Index Fungorum number: IF904748; Facesoffungi number: FoF17226

Etymology – Referring to the host genus “*Dalbergia*”, from which the holotype was isolated.

Holotype – MFLU 24-0472

Saprobic on *Dalbergia cana* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetes. Colonies on the substrate, effuse, hairy, scattered or gregarious, glistening, black. Mycelium superficial and immersed in the substratum, composed of septate, branched, pale brown to hyaline, smooth-walled hyphae. Conidiophores 46–81(–88) × 4–5.5 µm ($\bar{x}$ = 60 × 4.6 µm, n = 20), macronematous, mononematous, solitary or rarely grouped in 2, branched, mostly straight or slightly flexuous, cylindrical, thick-walled, brown, wider at the base, truncate and slightly wider at apex, 2–6-septate. Conidiogenous cells 8.5–16.5 × 3.3–5 µm ($\bar{x}$ = 12.5 × 4 µm, n = 15), terminal, integrated, monotretic, monoblastic, cylindrical, thick-walled, brown. Conidia 52(–38)–85(–91) × 5.8–9.3 µm ($\bar{x}$ = 68 × 7.5 µm, n = 20; L/W ratio = 9), solitary, acrogenous, obclavate to cylindrical, upper and basal cells tapered, truncate at base, hila darkened, straight or curved, thick-walled, pale brown, 4–10-distoseptate.

Culture characteristics – Colonies on PDA reaching 1–1.5 cm diam. after 10 days at room temperature (25–28 °C); after one month irregular, dense, wavy at edge, mycelia radiating outwards; upper surface grey in the center and dark grey towards outer zone, and radially folded; reverse dark grey to black.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cana* (Fabaceae), 26 March 2022, N. Afshari, 4C1T1R3c (MFLU 24-0472, holotype); ex-type living culture MFLUCC 24-0552.

GenBank numbers – ITS = PQ800263, LSU = PV072614, *rpb2* = PV138143, *tub2* = PX739612.

Notes – Phylogenetic analyses of combined SSU, ITS, LSU, *rpb2*, and *tefl-α* sequence data indicate that *Oxydothis dalbergiae* (MFLUCC 24-0552) forms a distinct branch among *Oxydothis* taxa with 98% ML, 1.0 PP support values (Fig. 39). The asexual morph of *Oxydothis*, which is hyphomycetous (*Selenosporella* sp.), has only been reported from culture by Samuels & Rossman (1987). The asexual morph was not obtained in media by Hyde (1994) and Konta et al. (2016). Since morphological comparisons are not possible, *O. dalbergiae* (MFLUCC 24-0552) is introduced based

solely on phylogenetic and sequence data. This study represents the first collection of the new asexual morph species of *Oxydothis* from a natural substrate.

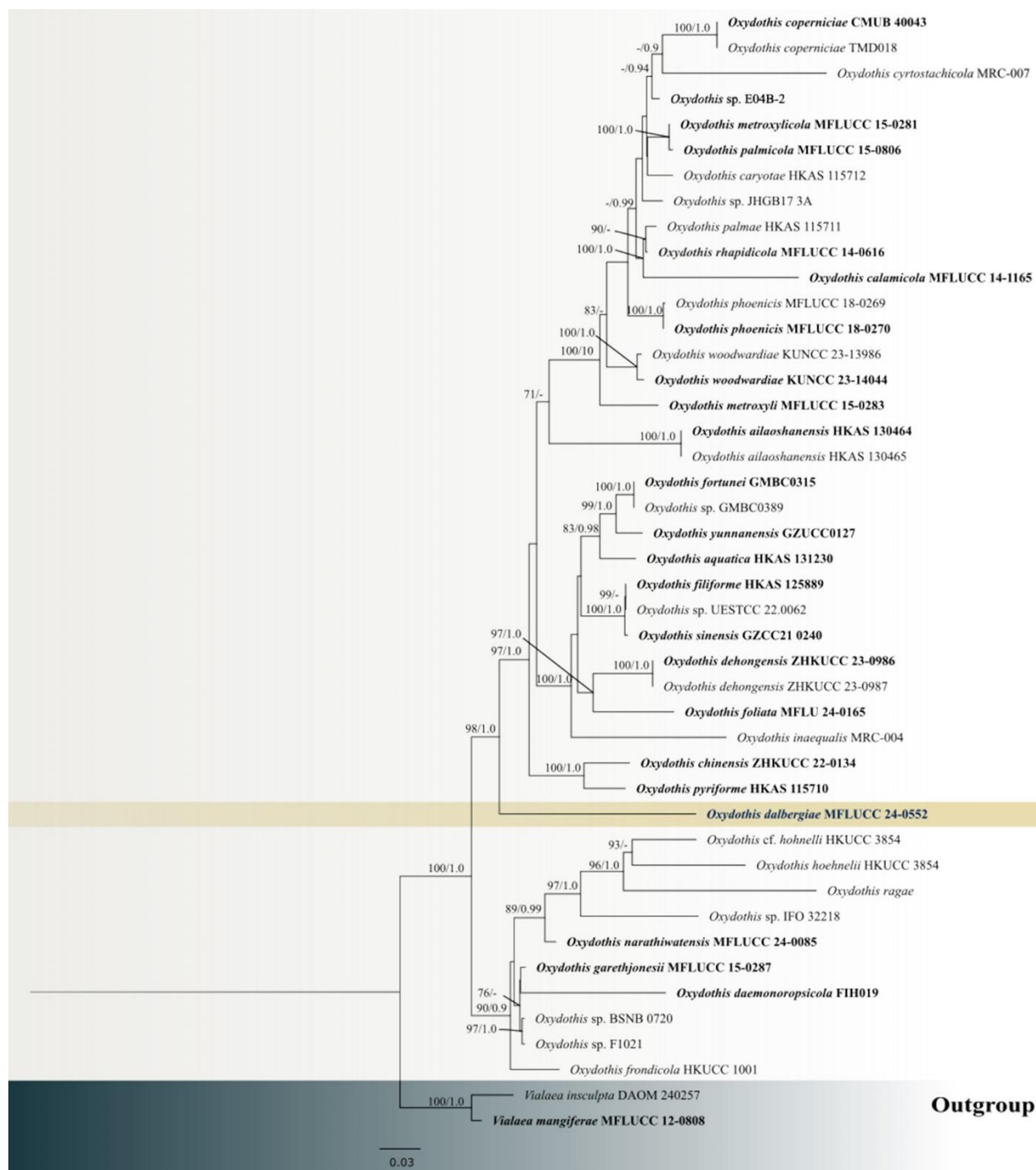


Figure 39 – Phylogram generated maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined SSU, ITS, LSU, *rpb2*, and *tefl-α* sequence data of *Oxydothis*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Forty-four strains are included in the combined analyses which comprised 4,527 characters (SSU = 1,028, ITS = 583, LSU = 922, *rpb2* = 1,068, and *tefl-α* = 926). The best RAXML tree with a final optimization likelihood value of -21824.945 is presented. The matrix had 1,344 distinct patterns 866 parsimony-informative, 609 singleton sites, 3,052 constant sites. Selecting individual models K2P+G4, TIM2e+G4, TNe+I+G4, TIM3e+G4 and TN+F+G4 were applied for SSU, ITS, LSU, *rpb2*, and *tefl-α* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 2,000,000 MCMC generations was calculated as 0.015276. Bootstrap support values for ML greater

than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Vialaea insculpta* (DAOM 240257) and *V. mangiferae* (MFLUCC 12-0808). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.



Figure 40 – *Oxydothis dalbergiae* (MFLU 24-0472, holotype). a, b Colonies on *Dalbergia cana* woody litter. c–h Conidiophores and conidiogenous cells. i–o Conidia. p Colony on PDA (front and reverse). Scale bars: a = 200 μ m, b = 100 μ m, c–o = 20 μ m.

Barbatosphaeriales K.D. Hyde & Hongsanan

Barbatosphaeriaceae Huang Zhang, K.D. Hyde & Maharachch.

Zhang et al. (2017) established *Barbatosphaeriaceae* with *Barbatosphaeria* as the type genus. They were not able to phylogenetically assign to any order, and therefore, it was placed in

Diaporthomycetidae family *incertae sedis*. This family includes four genera, *Appendopyricularia*, *Barbatosphaeria*, *Ceratostomella*, and *Xylomelasma* (Hyde et al. 2024a).

***Barbatosphaeria* Réblová**

Index Fungorum number: IF505954; Facesoffungi number: FoF05073

Barbatosphaeria was established by Réblová (2007) for *Calosphaeria barbirostris* ($\equiv$ *Barbatosphaeria barbirostris*), isolated from decayed wood of deciduous trees based on cultivation experiments, revision of herbarium material, and molecular phylogenetics of LSU sequences. This genus is characterized by nonstromatic perithecia, dark ascomata with long decumbent necks, and ellipsoid to oblong, hyaline, 1-septate ascospores in unitunicate, clavate asci with a nonamyloid apical ring (Réblová 2007, Zhang et al. 2017). Réblová et al. (2015b) revised the taxonomy of the genus. Zhang et al. (2017) accommodated *Barbatosphaeria* in to a new family, *Barbatosphaeriaceae*, along with *Ceratostomella* and *Xylomelasma*. The known anamorphs produced *in vitro* are ramichloridium- and sporothrix-like taxa with holoblastic denticulate conidiogenesis, conidiophores of two types are formed in succession during development of the colony (Réblová 2007, Réblová et al. 2015b, Zhang et al. 2017). To date, nine species have been introduced (Réblová 2007, Réblová et al. 2015b, Zhang et al. 2017, Hyde et al. 2018, Luo et al. 2019, Index Fungorum 2025). In this study, we document *Barbatosphaeria lignicola* as a new record of habitat, geographical distribution and host on dead wood of *Dipterocarpus alatus* from Doi Tung National Park, Thailand.

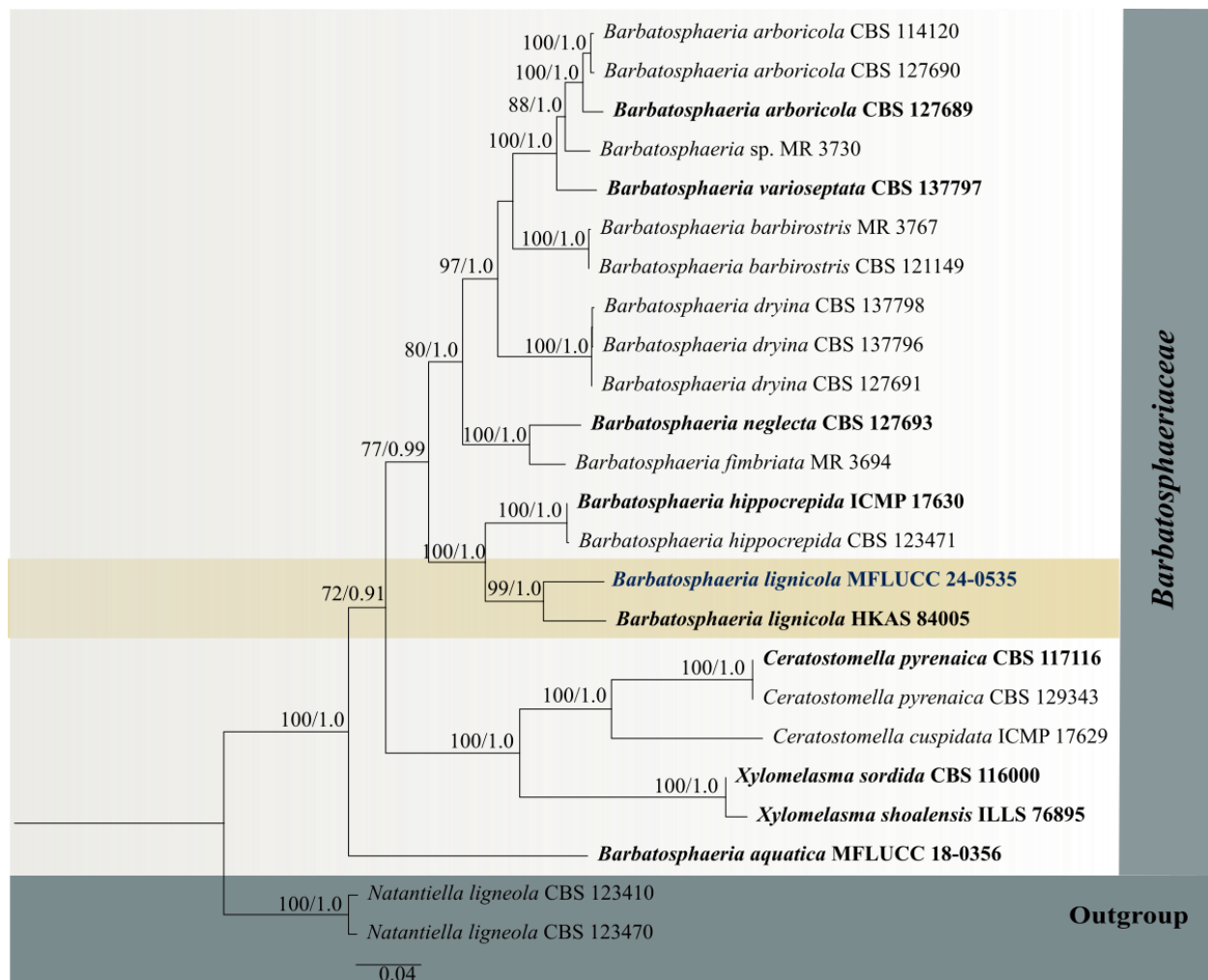


Figure 41 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *rpb2*, and *tub2* sequence data of *Barbatosphaeriaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Twenty-four strains are included in the combined analyses which comprised 3,220 characters (ITS = 495, LSU = 1,112, *rpb2* = 1,119, and

tub2 = 494). The best RAxML tree with a final optimization likelihood value of -15267.035159 is presented. The matrix had 1,053 distinct alignment patterns, with 22.07% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233558, C = 0.265521, G = 0.283437, T = 0.217485; substitution rates AC = 1.126369, AG = 2.664778, AT = 1.793777, CG = 1.596146, CT = 7.489623, GT = 1.000000; gamma distribution shape parameter α = 0.202386. In the Bayesian analysis, average standard deviation of split frequencies at the end of 2,000,000 MCMC generations was calculated as 0.001214. The evolutionary models SYM+I+G, GTR+I+G, TIM2+I+G, and TIM3+I+G were applied for ITS, LSU, *rpb2* and *tub2* sequence data. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Natantiella lignicola* (CBS 123410 and CBS 123470). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Barbatosphaeria lignicola Z.L. Luo, H.Y. Su & K.D. Hyde, in Luo et al. Fungal Diversity [72] (2019). Fig. 42

Index Fungorum number: IF555658; Facesoffungi number: FoF05430

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 263–330 μ m high, 332–380 μ m diam. excluding neck ($\bar{x}$ = 302 $\times$ 357 μ m, n = 5), immersed in the substratum, aggregated in round groups, dark brown to black, coriaceous, globose to mostly subglobose, with ostiole. *Ostioles* central, cylindrical, black, converging radially, mostly straight to slightly curved, periphyses filling the ostiole canal. *Peridium* 24–44 μ m wide, slightly fragile, composed of 2-layers, outer layer brown, thick-walled cells of *textura prismatica* to *textura angularis*, inner layer consisting of layers of thin-walled subhyaline to hyaline compact and flattened cells. *Hamathecium* comprises 2.5–4.5(–5.2) μ m ($\bar{x}$ = 3.4 n = 30), abundant, septate, slightly constricted at the septa, tapering toward the apex, wider in the base, paraphyses longer than asci. *Asci* 19.6–30.4 $\times$ 4.1–6.3 μ m ($\bar{x}$ = 24.5 $\times$ 5.3 μ m, n = 25), unitunicate, 8-spored, clavate, tapering toward the base, apically broadly rounded to obtuse. *Ascospores* 5–9.5 $\times$ 0.9–1.8 μ m ($\bar{x}$ = 7.3 $\times$ 1.2 μ m, n = 30), arranged obliquely, 1–2-seriate, occasionally overlapping, allantoid, U-shaped to horseshoe shaped, narrow at both ends, hyaline, aseptate. Asexual morph: Undetermined.

Culture characteristics – Colonies reached 10 mm diam. after 10 days on PDA at room temperature (25–28 °C), irregular, pigment diffusing in the agar, narrow towards the margin, brownish grey at upper and reverse.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T1R5a (MFLU 24-0407); living culture MFLUCC 24-0535.

GenBank numbers – ITS = PQ800239, LSU = PV065627, *rpb2* = PV138138, *tub2* = PX739617.

Known hosts – decaying wood submerged in freshwater (Luo et al. 2019), *Dipterocarpus alatus* (this study).

Known distribution – China (Luo et al. 2019), Thailand (this study).

Notes – In the multilocus phylogenetic analyses, our strain (MFLUCC 24-0535) grouped with *Barbatosphaeria lignicola* (HKAS 84005) with 99% ML and 1.0 PP bootstrap support (Fig. 41). They share similar characteristics, including globose to subglobose, dark brown to black ascomata; black, cylindrical ostiole; septate paraphyses, tapering toward the tip, and wider near the base; size and unitunicate, 8-spored, asci; and allantoid, horseshoe to U-shaped, hyaline, aseptate, similar sized ascospores (Luo et al. 2019). We conclude that our collection is *B. lignicola* based on morphological and molecular evidence. *Barbatosphaeria lignicola* was introduced by Luo et al. (2019) on submerged decaying wood in freshwater habitats in Yunnan Province, China. Our new collection is the first report of *B. lignicola* on *Dipterocarpus alatus* in a terrestrial habitat, Chiang Rai Province, Thailand, and identifies as a new host, habitat, and geographical record.

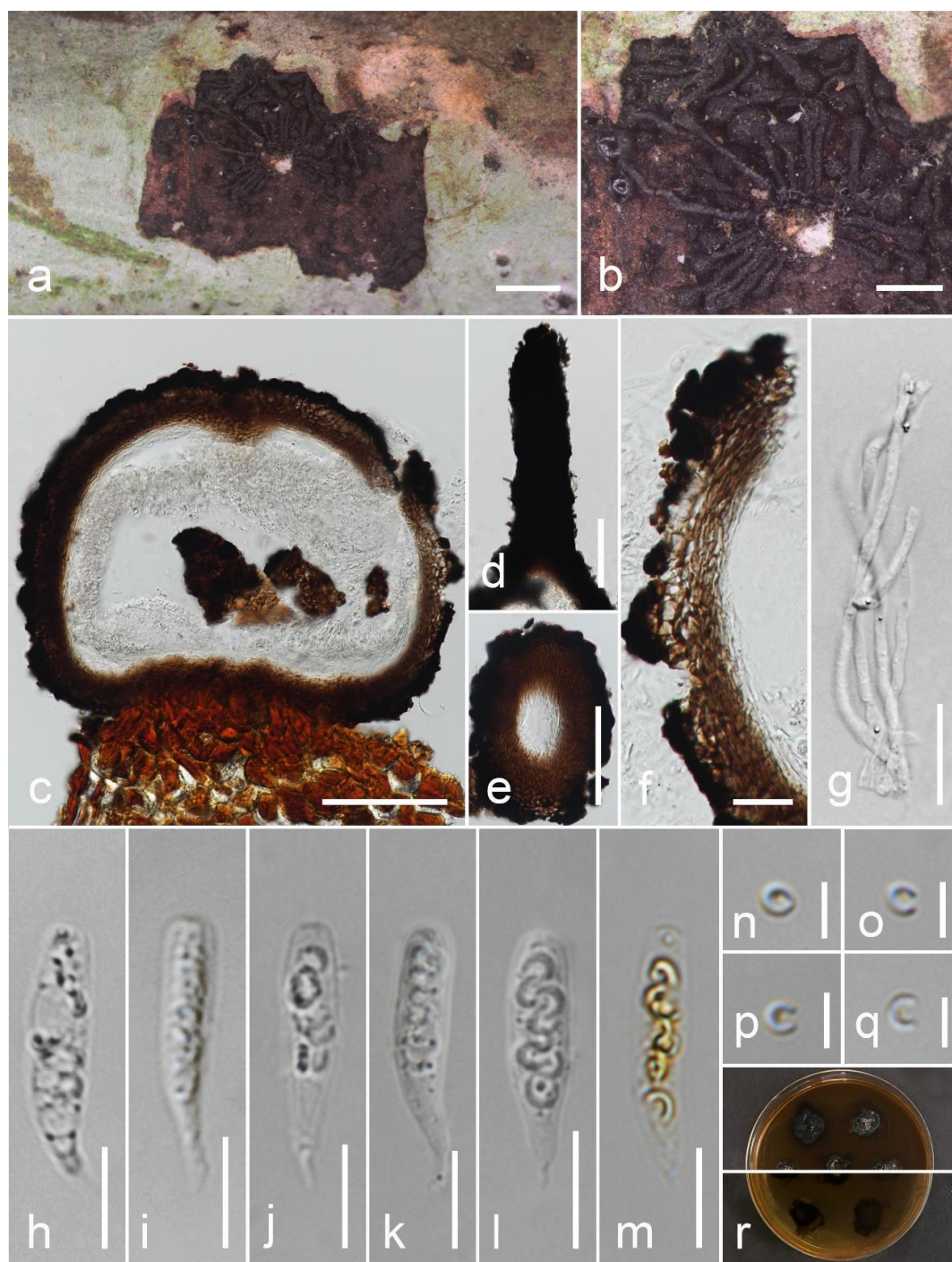


Figure 42 – *Barbatosphaeria lignicola* (MFLU 24-0407, a new host, habitat, and geographical record). a, b Appearance of ascomata on *Dipterocarpus alatus* woody litter. c Horizontal section of ascoma. d Sections through ostiole. e Ostiole with periphyses. f Section of peridium. g Paraphyses. h–l Asci. m Ascus in Melzer's reagent. n–q Ascospores. r Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 500 μ m, c, d = 100 μ m, e = 50 μ m, f, g = 20 μ m, h–m = 10 μ m, n–q = 5 μ m.

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

Based on LSU sequence data, *Chaetosphaeriales*, positioned within the *Sordariomycetes*, was delineated by Huhndorf et al. (2004). This order encompasses six families: *Chaetosphaeriaceae*, *Helminthosphaeriaceae*, *Leptosporrellaceae*, *Linocarpaceae*, *Neoleptosporrellaceae*, and *Pseudocapsulosporaceae* as supported by subsequent studies (Hongsanant et al. 2017, Konta et al. 2017, Wijayawardene et al. 2022, Hyde et al. 2024a).

Linocarpaceae S. Konta & K.D. Hyde

Linocarpaceae was established by Konta et al. (2017) based on phylogenetic analysis of a combined ITS and LSU dataset. *Linocarpon* and *Neolinocarpon* cluster together in a clade and formed a distinct clade sister to *Chaetosphaeriaceae*. The species belongs in this family are saprobes on monocotyledons and dicotyledons plants (Konta et al. 2017). Currently, *Claviformispora*, *Linocarpon*, and *Neolinocarpon* (Hyde et al. 2024a).

Claviformispora X.L. Xu & C.L. Yang

Index Fungorum number: IF557395; Facesoffungi number: FoF14621

Claviformispora was erected by Xu et al. (2020) as a monotypic genus to accommodate *Claviformispora phyllostachydis* as the type species. This species was isolated from dead branches of *Phyllostachys heteroclada* in China. Morphological distinctions and analyses of a combined ITS, LSU, SSU, and *tef1-α* sequence dataset confirmed validity of the new genus and its classification within *Linocarpaceae*, *Chaetosphaeriales*, *Sordariomycetes*, *Ascomycota* (Xu et al. 2020). The sexual morph has stromata that are either solitary or gregarious, black, and erumpent. Ascomata are solitary or aggregated, immersed, subglobose, and form slightly raised blistered areas with a central ostiole containing periphyses. The outer cells of the peridium integrate with the host tissues, comprising pale to dark brown cells of *textura angularis*. The hamathecium comprises hyaline, septate paraphyses, that are longer than asci, broader at the base, and taper toward the apex. Asci are 8-spored, cylindrical to cylindric-clavate, unitunicate, short-pedicellate, and apically rounded with a doughnut-shaped, refractive, J- apical ring. Ascospores are overlapping, uniseriate or 2-seriate, clavate with a thin pedicel, 1-celled, hyaline, smooth-walled, and lack appendages and refringent bands. The asexual morph has not been observed in this genus (Xu et al. 2020). In this study, we document *Claviformispora phyllostachydis* as a new geographical and host record on dead wood of *Nayariophyton zizyphifolium* from Doi Tung National Park, Thailand.

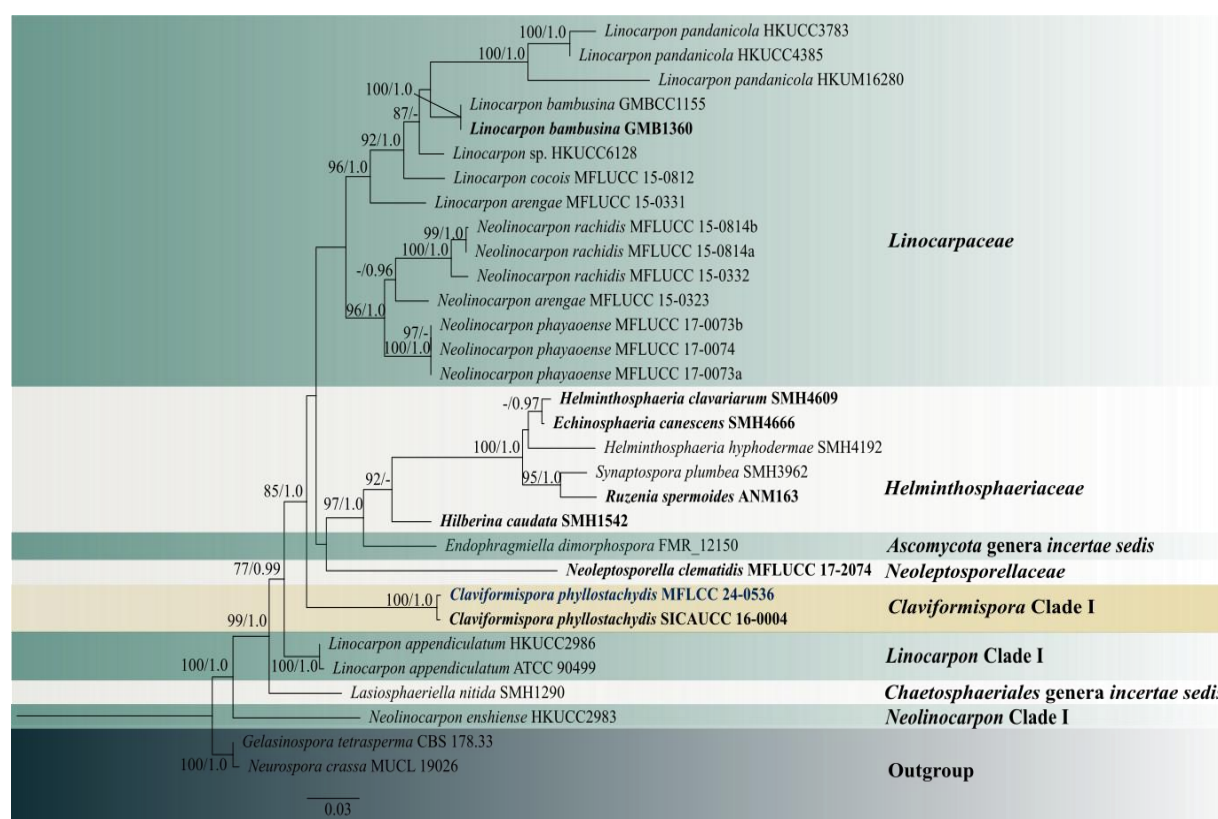


Figure 43 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, SSU, and *tef1-α* sequence data of *Linocarpaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Thirty-one strains are included in the combined analyses

which comprised 2,672 characters (LSU = 800, SSU = 971, and *tef1- α* = 901). The best RAxML tree with a final optimization likelihood value of -10733.547378 is presented. The matrix had 646 distinct alignment patterns, with 45.41% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232837, C = 0.264789, G = 0.309802, T = 0.192572; substitution rates AC = 0.745108, AG = 2.109548, AT = 0.620391, CG = 1.222153, CT = 5.710740, GT = 1.000000; gamma distribution shape parameter α = 0.274996. In the Bayesian analysis, average standard deviation of split frequencies at the end of 3,000,000 MCMC generations was calculated as 0.005390. The evolutionary models TIM2+I+G, TrN+G, and TIM2+G were applied for LSU, SSU, and *tef1- α* sequence data. Bootstrap support values for ML greater than or equal to 75% and Bayesian posterior probabilities greater than or equal to 0.95 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Gelasinospora tetrasperma* (CBS 178.33) and *Neurospora crassa* (MUCL 19026). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Claviformispora phyllostachydis X.L. Xu & C.L. Yang, in Xu et al. MycoKeys 70, 8 (2020). Fig. 44
Index Fungorum number: IF557396; Facesoffungi number: FoF14622

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: *Stromata* solitary, scattered or gregarious, well-developed, consisting of black, elliptical or circular spots, moderately raised through epidermis with slit-like openings on the host surface. *Ascomata* 311–524 μ m high, 430–607 μ m diam. ($\bar{x}$ = 455 $\times$ 527 μ m, n = 10), perithecial, immersed, erumpent, globose to mostly subglobose, ostiolate. *Peridium* 23–45 μ m wide ($\bar{x}$ = 36 μ m, n = 20), outer layer composed of dark brown *textura angularis* cells merging with the host tissues, inner layer composed of hyaline to sub-hyaline cells of *textura angularis*. *Hamathecium* comprises 1.8–3.6 μ m diam. ($\bar{x}$ = 2.6 μ m, n = 30), with abundant, compact, hyaline paraphyses, occasionally branched, septate, tapering towards the apex. *Asci* 109–192 $\times$ 14–23 μ m ($\bar{x}$ = 155 $\times$ 17.7 μ m, n = 20), unitunicate, 8-spored, cylindrical to cylindric-clavate, with short pedicel, rounded at the apex, with a doughnut-shaped, refractive, J-, apical ring. *Ascospores* 42–55 $\times$ 6.3–9.6 μ m ($\bar{x}$ = 49.2 $\times$ 8.2 μ m, n = 30), overlapping, uniseriate or mostly biseriate, aseptate, claviform with a narrow pedicel, hyaline, guttulate, straight or slightly curved. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes emerged from one side. Colonies on PDA reaching 1–2 cm diam. after 14 days at room temperature (25–28 °C), circular, with entire margin, dense, pigment diffusing in the agar with age, upper surface orange in center and yellowish-white at outer zone, from reverse dark brown and black.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 6 June 2022, N. Afshari, 1C2T1R1 (MFLU 24-0408); living culture MFLUCC 24-0536.

GenBank numbers – ITS = PQ800240, SSU = PV072619, *tef1- α* = PX739628.

Known hosts – *Phyllostachys heteroclada* (Xu et al. 2020), *Nayariophyton zizyphifolium* (this study).

Known distribution – China (Xu et al. 2020), Thailand (this study).

Notes – In the phylogenetic analyses, our strain (MFLUCC 24-0536) grouped with the holotype of *Claviformispora phyllostachydis* (SICAU 16-0007) with 100% ML and 1.00 PP statistical support (Fig. 43). Xu et al. (2020) introduced *Claviformispora* as a new genus to accommodate *C. phyllostachydis*, which was reported from dead branches of *Phyllostachys heteroclada* in China. Our new isolate is similar to *C. phyllostachydis* (SICAU 16-0007), except for the larger ascomata ($\bar{x}$ = 455 $\times$ 527 μ m vs. $\bar{x}$ = 189 $\times$ 345 μ m), asci ($\bar{x}$ = 155 $\times$ 17.7 μ m vs. $\bar{x}$ = 118 $\times$ 13 μ m), and ascospores ($\bar{x}$ = 49.2 $\times$ 8.2 μ m vs. $\bar{x}$ = 45.7 $\times$ 7.0 μ m) (Xu et al. 2020). Nevertheless, based on nucleotide comparisons, *C. phyllostachydis* (MFLUCC 24-0536) is identical to *C. phyllostachydis* (SICAU 16-0007) in SSU (0%), and no significantly difference in *tef1- α* (0.8%). Thus, the current study presents a new host record of *C. phyllostachydis* on *Nayariophyton zizyphifolium*, and a new geographical record from Thailand.



Figure 44 – *Claviformispora phyllostachydis* (MFLU 24-0408, a new host and geographical record). a Appearance of stomata on *Nayariophyton zizyphifolium* woody litter. b Longitudinal section through the ascomata. c, d Vertical sections of ascomata. e Section of peridium. f Paraphyses. g–j Asci. k Ascus in Melzer's reagent. l–o Ascospores. p A germinated ascospore. q, r Colonies on PDA (front and reverse). Scale bars: a = 2.5 mm, b = 750 μ m, c, d = 200 μ m, g–k = 50 μ m, e, f, l–p = 20 μ m.

***Conioscyphales* Réblová & Seifert**

***Conioscyphaceae* Réblová & Seifert**

Réblová et al. (2016) established *Conioscyphaceae* with *Conioscypha* as the type genus. Sexual morph of this family features perithecial ascomata, unitunicate, cylindrical-clavate, stipitate asci, and fusiform to fusiform-navicular, transversely multi-septate ascospores. In the asexual morph, conidiophores are micronematous, mononematous; conidiogenous cells blastic, cyathiform to doliiform, and conidia brown, aseptate.

***Conioscypha* Höhn.**

Index Fungorum number: IF7754; Facesoffungi number: FoF05191

Conioscypha, a dematiaceous hyphomycete genus, was first described by Höhnelt (1904), with *Conioscypha lignicola* as the type species, collected from submerged *Carpinus* wood in Austria. Shearer (1973) described the genus as having compact, erumpent colonies consisted of hyaline to subhyaline, branched, septate hyphae. One-celled, dark-brown, smooth-walled conidia with a noticeable scar at the point of detachment are produced by enteroblastic, short-stalked conidiogenous cells. Shearer (1973) described a second species, *Conioscypha varia*. This species was found on balsa wood and is different from *Conioscypha lignicola* in having smaller, more elongated, thinner-walled, and more variably shaped conidia. Subsequently, *C. varia* was given a sexual morph under the new genus *Conioscyphascus* by Réblová & Seifert (2004). *Conioscypha* and *Conioscyphascus* are congeneric according to molecular phylogeny based on LSU sequence data, which strongly supported a single clade containing both. *Conioscyphascus* was synonymized under *Conioscypha* in accordance with the "one fungus, one name" principle (Zelski et al. 2015, Réblová et al. 2016). Using a multigene phylogenetic analysis (LSU–SSU–*rpb2*), Réblová et al. (2016) erected the monotypic order *Conioscyphales* (*Conioscyphaceae*) within the subclass *Hypocreomycetidae*. This classification was later revised by Hongsanan et al. (2017), who transferred *Conioscyphales* to the subclass *Savoryellomycetidae*, retaining *Conioscypha* as its sole genus placed in sole family, *Conioscyphaceae* (Hyde et al. 2024a). According to Species Fungorum (2025), there are currently 35 accepted species in this genus. In this study we reported *C. chiangmaiensis* as a new host record on *Microcos paniculata* in Thailand confirmed through both morphological and phylogenetic analyses.

***Conioscypha chiangmaiensis* (X.G. Tian & Karun.) Y.R. Sun, Yong Wang bis & K.D. Hyde, in Sun et al. Fungal Diversity 131, 223 (2025).** Fig. 46

Index Fungorum number: IF903093; Facesoffungi number: FoF10569

Saprobic on *Microcos paniculata* woody litter. Sexual morph: Undetermined. Asexual morph: Colonies on the natural substrate, sporodochia, black, scattered. Mycelium immersed, consisting of branched, hyaline, septate hyphae. Conidiophores hypha-like, micronematous, septate, cylindrical, simple or occasionally branched, smooth-walled, hyaline. Conidiogenous cells 4.8–6.7(–7.3) μm wide ($\bar{x}$ = 5.7 μm , n = 10), terminal, monoblastic, holoblastic, integrated, granulate, cylindrical. Separating cells 13–30 $\times$ 6–11 μm ($\bar{x}$ = 19.5 $\times$ 8 μm , n = 15), clavate to vermiform, hyaline. Conidia 23.6–28.4 $\times$ 14.7–21 μm ($\bar{x}$ = 25.7 $\times$ 17.9 μm , n = 20; L/W ratio = 1.4), solitary, acrogenous, ellipsoidal, aseptate, pale brown to dark brown with age, 1 or 2-guttulate in mature conidia, darker brown in the guttulate spots, smooth or verruculose, with a thin sheath, mostly separating cell attached to the conidium.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerges from one end cell. Colonies on PDA reached 10 mm diam. after 2 weeks at room temperature (25–28 °C), irregular, radially folded, dense, mycelia radiating outwards, after one month at upper and reverse yellow.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 27 September 2022, N. Afshari, 3C3T1R5 (MFLU 24-0409).

GenBank numbers – ITS = PQ800241, LSU = PV072597, SSU = PV072693.

Known hosts – decaying wood of an unidentified host (Phukhamsakda et al. 2022), *Microcos paniculata* (this study).

Known distribution – Thailand (Phukhamsakda et al. 2022, this study).

Notes – Phylogenetically, our new isolate (MFLU 24-0409) clustered with the ex-type strain of *Conioscypha chiangmaiensis* (MFLUCC 21-0158) based on combined ITS, LSU, and SSU sequence data, with 100% ML and 1.0 PP bootstrap support (Fig. 45). The morphological characteristics of our strain resemble the features given by Phukhamsakda et al. (2022). However, our isolate has some differences from *C. chiangmaiensis* (MFLUCC 21-0158) in the size of separating cells ($\bar{x} = 19.5 \times 8 \mu\text{m}$, vs. $\bar{x} = 30 \times 10 \mu\text{m}$), and the numbers of guttules (1 or 2 guttulate vs. one guttulate). Based on morphology and phylogeny we conclude our collection is *C. chiangmaiensis*. The collection of *C. chiangmaiensis* (MFLUCC 21-0158) was found on decaying wood in Thailand. Here, we present a new host record of *C. chiangmaiensis* on *Microcos paniculata* in Thailand.

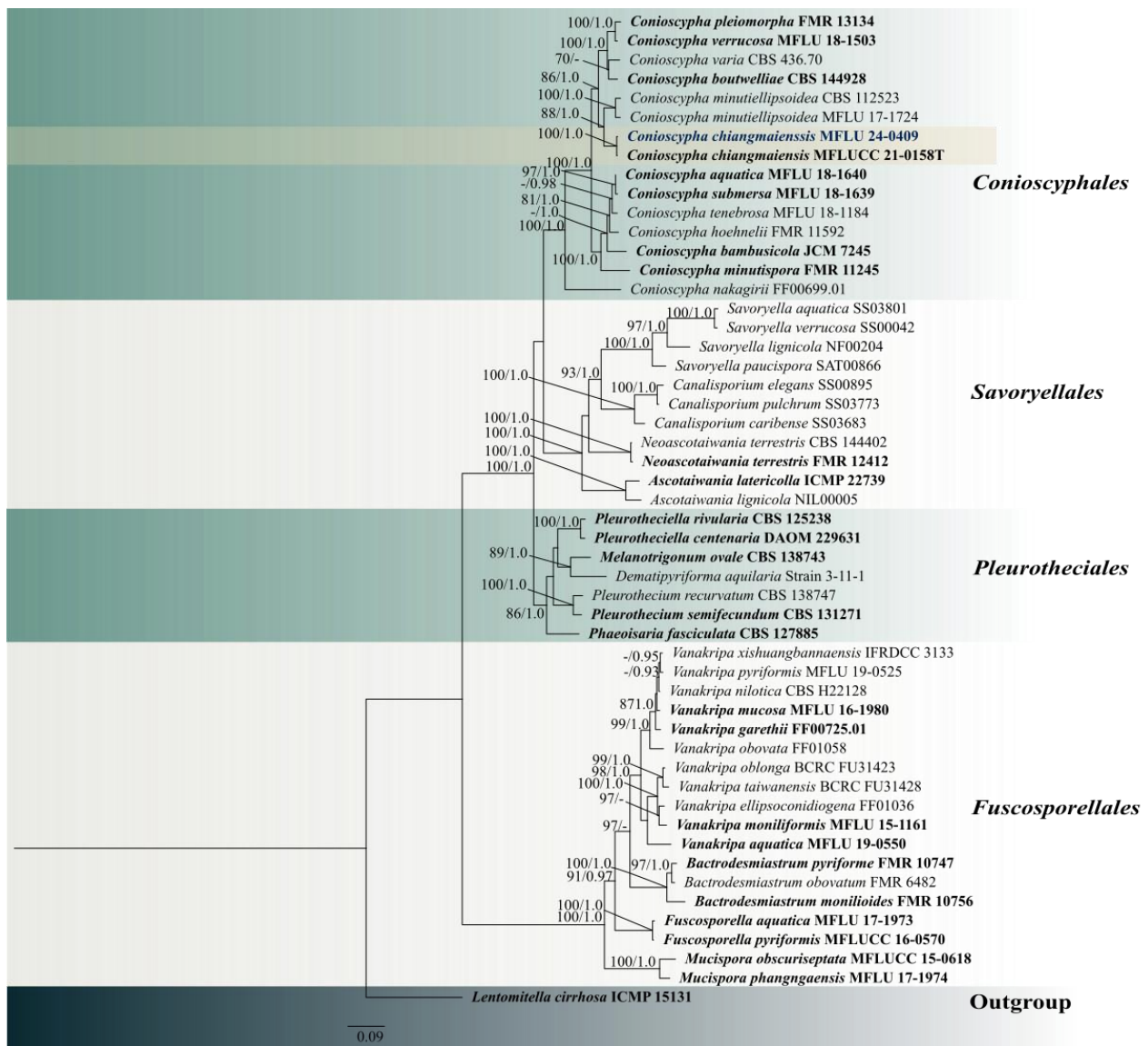


Figure 45 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, and SSU sequence data for *Conioscyphales* with other taxa in some other close orders. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Fifty-two strains are included in the combined analyses which comprised 2,453 characters (ITS = 559, LSU = 869, and SSU = 1,025). The best RAXML tree with a final optimization likelihood value of -22534.880049 is presented. The matrix had 1,157 distinct alignment patterns, with 22.27% of

undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234705, C = 0.258165, G = 0.294689, T = 0.212441; substitution rates AC = 1.464347, AG = 2.436346, AT = 1.701655, CG = 0.979405, CT = 5.788590, GT = 1.000000; gamma distribution shape parameter α = 0.256428. In the Bayesian analysis, average standard deviation of split frequencies at the end of 7,000,000 MCMC generations was calculated as 0.001723. The evolutionary models GTR+I+G, TIM3+I+G, and TIM2ef+I+G were applied to combined ITS, LSU, and SSU, sequence data respectively. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Lentomitella cirrhosa* (ICMP 15131). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

***Diaporthales* Nannf.**

Diaporthales includes terrestrial or aquatic fungi found on plants, animals, or in soil, as saprobes, endophytes, and pathogens (Senanayake et al. 2017, 2018). The sexual morphs of the order form perithecia and unitunicate asci, and typically exhibits a coelomycetous characteristics (Senanayake et al. 2018).

***Cryphonectriaceae* Gryzenh. & M.J. Wingf.**

Cryphonectriaceae was established to accommodate the type genus *Cryphonectria*, and four allied genera, *Amphilogia*, *Chrysosporthe*, *Endothia*, and *Rostraureum* by Gryzenhout et al. (2006). Members of this family differ from the other diaporthalean taxa by having orange stromatic tissues at some stage, that became yellow in lactic acid and purple in KOH. Jiang et al. (2020) redefined *Cryphonectriaceae* and established two new families within *Diaporthales*. Hyde et al. (2024a) listed 29 genera in this family.

***Doitungomyces* N. Afshari, Lumyong & K.D. Hyde, gen. nov.**

Fig. 48

Index Fungorum number: IF904750; Facesoffungi number: FoF17228

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which the specimen was collected.

Holotype – MFLU 24-0465

Type species – *Doitungomyces dipterocarpi* N. Afshari, Lumyong & K.D. Hyde

Saprobic on dead branches of *Dipterocarpus alatus*. Sexual morph: *Stromata* solitary, scattered, well-developed, comprising elliptical and black spots, slightly raised through epidermis on host surface. *Ascomata* perithecial, immersed, erumpent, pyramid shape to subglobose, coriaceous to carbonaceous. *Peridium* outer layer composed of brown, compact, thick-walled *textura angularis* cells, inner layer composed of hyaline, loosely arranged cells of *textura angularis*. *Hamathecium* comprises hyaline, unbranched, septate, constricted at septum, tapering towards the apex, paraphyses longer than asci. *Asci* 8-spored, unitunicate, clavate to cylindric-clavate, with small pedicel, apex oblong, J- apical ring. *Ascospores* uniseriate, ellipsoid to fusiform, slightly narrow toward ends, straight to mostly curved hyaline, medianly 1-septate, constricted at septa, with 2–4 guttules. Asexual morph: Undetermined.

Notes – *Doitungomyces* is introduced for a fungus occurring on dead branches of *Dipterocarpus alatus*. *Doitungomyces*, is typified by *Doitungomyces dipterocarpi* and formed a separate lineage and is distinct from other genera in *Cryphonectriaceae* based on the combined ITS, LSU, *tefl- α* and *rpb2* sequence data with 69% ML support value (Fig. 47). In a BLASTn search of GenBank, the closest match of the ITS sequence of or isolate is *Endothia cerciana* (CSF 15423) with 89.04% similarity. *Aurantiosacculus castaneae* is the only taxon in the family that does not produce orange stromatic tissues based on published data. The morphological comparison showed that our species has unique characteristics among related taxa in lacking elongated perithecia beaks, but is similar in having asci with a refractive apical annulus (Voglmayr et al. 2012, Senanayake et al. 2018, Jaklitsch & Voglmayr 2019, Fan et al. 2020, Huang et al. 2022, Wang & Chen 2023). Here, we introduce *Doitungomyces* as a new genus within the *Cryphonectriaceae* based on

morphology and phylogenetic evidence. Additional collections, together with detailed molecular characterization are required to further validate the phylogenetic placement of the genus.

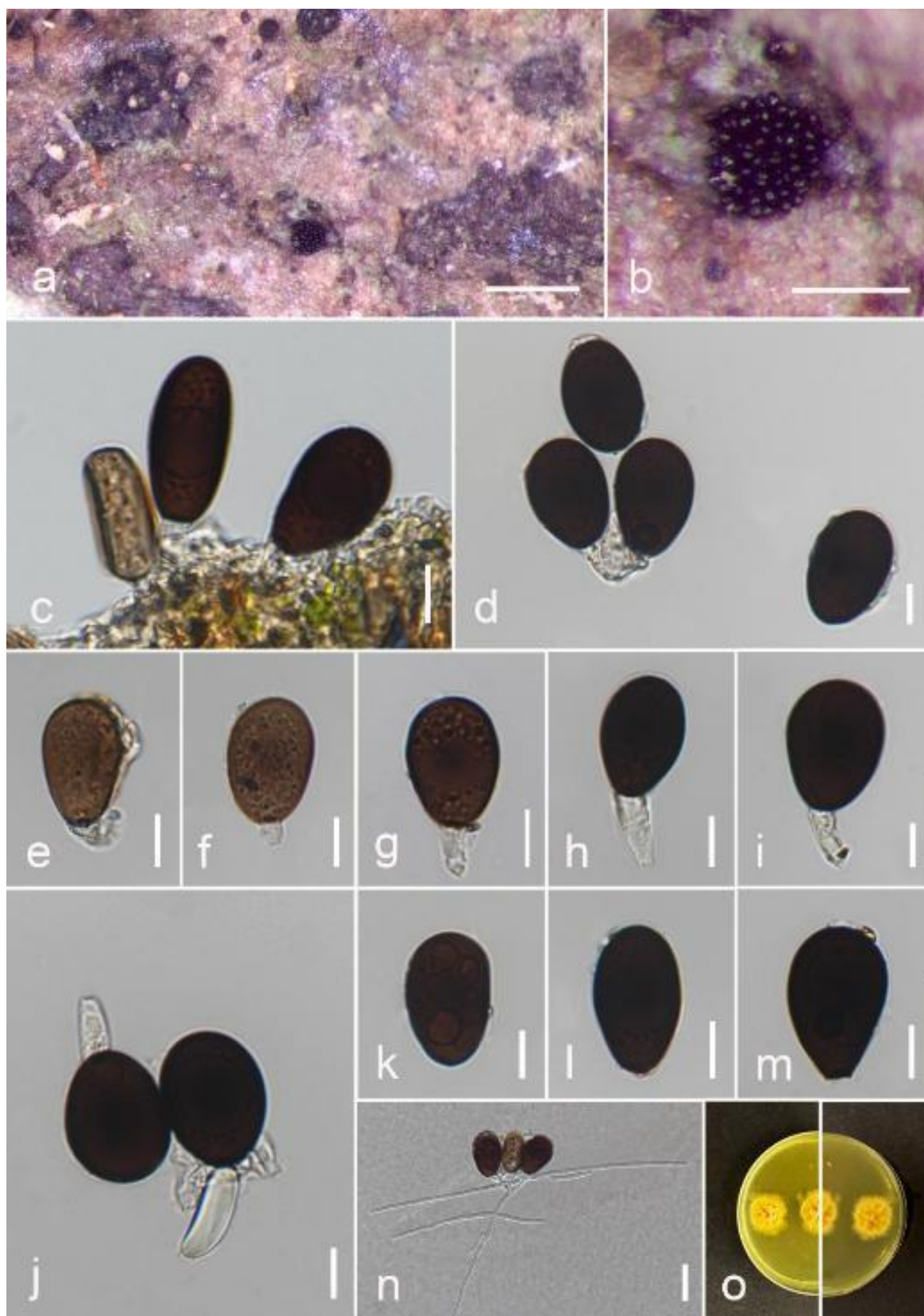


Figure 46 – *Conioscypha chiangmaiensis* (MFLU 24-0409, a new host record). a, b Sporodochia on *Microcos paniculata* woody litter. c–j Conidiophores with conidia. k–m Conidia. n Germinated

conidia. o Colonies on (front and reverse). Scale bars: Scale bars: a = 200 μ m, b = 100 μ m, n = 20 μ m, c–m = 10 μ m.

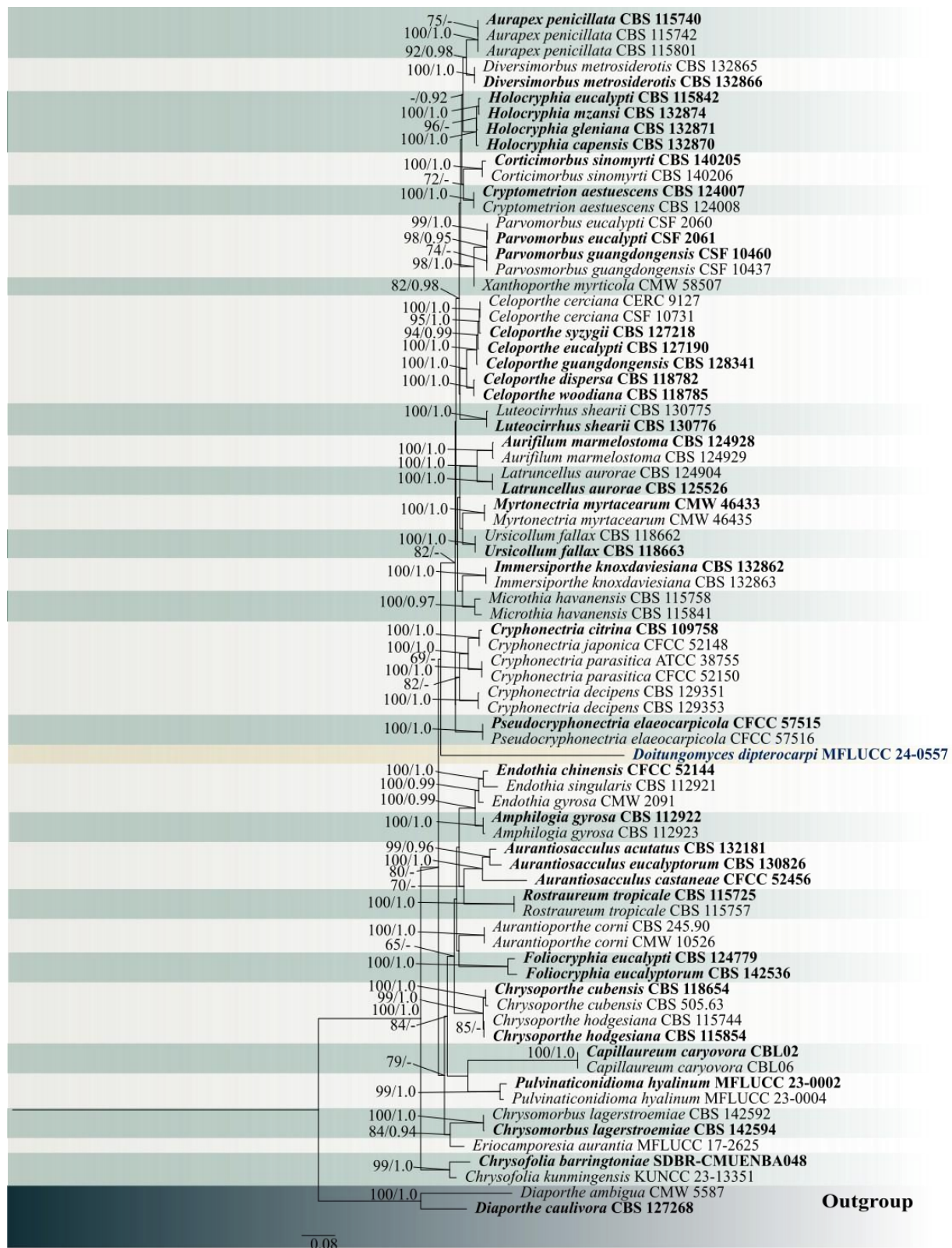


Figure 47 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, *tef1- α* and *rpb2* sequence data of *Cryphonectriaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Seventy-seven strains are included in the combined analyses which comprised 2,703 characters (ITS = 513, LSU = 846, *tef1- α* = 563, and *rpb2* = 780). The best score for log-likelihood of consensus tree is -20406.917.

The matrix had 1,239 distinct patterns 846 parsimony-informative, 247 singleton sites, 1,610 constant sites. Selecting individual models TIM2e+I+G4, TIM2e+I+G4, HKY+F+G4 and TN+F+I+G4 were applied to ITS, LSU, *tefl-α* and *rpb2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 8,000,000 MCMC generations was calculated as 0.015648. Bootstrap support values for ML greater than or equal to 65% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Diaporthe ambigua* (CMW5587) and *D. caulivora* (CBS 127268). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Doitungomyces dipterocarpi N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 48

Index Fungorum number: IF904749; Facesoffungi number: FoF17229

Etymology – Referring to the host genus “*Dipterocarpus*”, from which the holotype was isolated.

Holotype – MFLU 24-0465

Saprobic on dead branches of *Dipterocarpus alatus*. Sexual morph: *Stromata* solitary, scattered, well-developed, comprising elliptical and black spots, slightly raised through epidermis on host surface. *Ascomata* 245–300 μm high, 315–500 μm diam. ($\bar{x}$ = 268 × 382 μm, n = 5), perithecial, immersed, erumpent, pyramid shape to subglobose, coriaceous to carbonaceous. *Peridium* 29.5–49.5 μm wide ($\bar{x}$ = 38.5 μm, n = 35), outer layer composed of brown, compact, thick-walled *textura angularis* cells, inner layer composed of hyaline, loosely arranged cells of *textura angularis*. *Hamathecium* comprises 2.2–5.5(–6) μm diam. ($\bar{x}$ = 4 μm, n = 35), hyaline, unbranched, septate, constricted at septum, tapering towards apex, paraphyses longer than asci. *Asci* 46.5–36 × 8.8–5.3 μm ($\bar{x}$ = 41 × 6.9 μm, n = 20), 8-spored, unitunicate, clavate to cylindric-clavate, with small pedicel, apex oblong, J- apical ring. *Ascospores* 6.5–10.2 × 2–3.9 μm ($\bar{x}$ = 8.6 × 2.8 μm, n = 50), uniseriate, overlapping, ellipsoid to fusiform, slightly narrow toward ends, straight to mostly curved hyaline, 1-septate at middle, constricted at septa, with 2–4 guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 48 h and a germ tube emerges from one end cell. Colonies on PDA reaching 60 mm diam. after one week at room temperature (25–28 °C), flat, thinly felty, center creamy white, brown to grey at periphery, edge dendritic, reverse pale brown at center, dark brown at periphery, pigment diffusing in the agar after two months.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 27 September 2022, N. Afshari, 2C3T1R4b (MFLU 24-0465, holotype); ex-type living culture MFLUCC 24-0557.

GenBank numbers – ITS = PQ800256, LSU = PV072610, *tefl-α* = PX739631, *rpb2* = PV138151.

Notes – *Doitungomyces dipterocarpi* (MFLUCC 24-0557) formed an independent lineage in *Cryphonectriaceae* with 69% ML support value (Fig. 47). *Striatiseptata paniculatae* is characterized by lacking elongated perithecia beaks (Fig. 48). Our isolate is similar to other members of *Cryphonectriaceae* in having refractive apical annulus asci (Voglmayr et al. 2012, Senanayake et al. 2018, Jaklitsch & Voglmayr 2019, Fan et al. 2020, Huang et al. 2022, Wang & Chen 2023). The species was collected as a saprobe from *Dipterocarpus alatus* dead branches in its sexual morph. Based on the morphological differences along with the multigene phylogeny analyses, we introduce *Doitungomyces dipterocarpi* as a novel wood-dwelling micofungi from Doi Tung National Park, Thailand.

Cytosporaceae Fr. (= *Valsaceae* Tul. & C. Tul.)

Fries (1823) introduced *Cytosporaceae* with *Cytospora chrysosperma* as the type species. This family includes phytopathogenic and saprobic species (Wehmeyer 1975, Castlebury et al. 2002, Lin et al. 2023). Hyde et al. (2024a) accepted six genera in *Cytosporaceae* in the outline of Fungi and fungus-like taxa (*Cryptascoma*, *Cytospora*, *Pachytrype*, *Paravalsa*, *Waydora*, and *Xenotypha*).

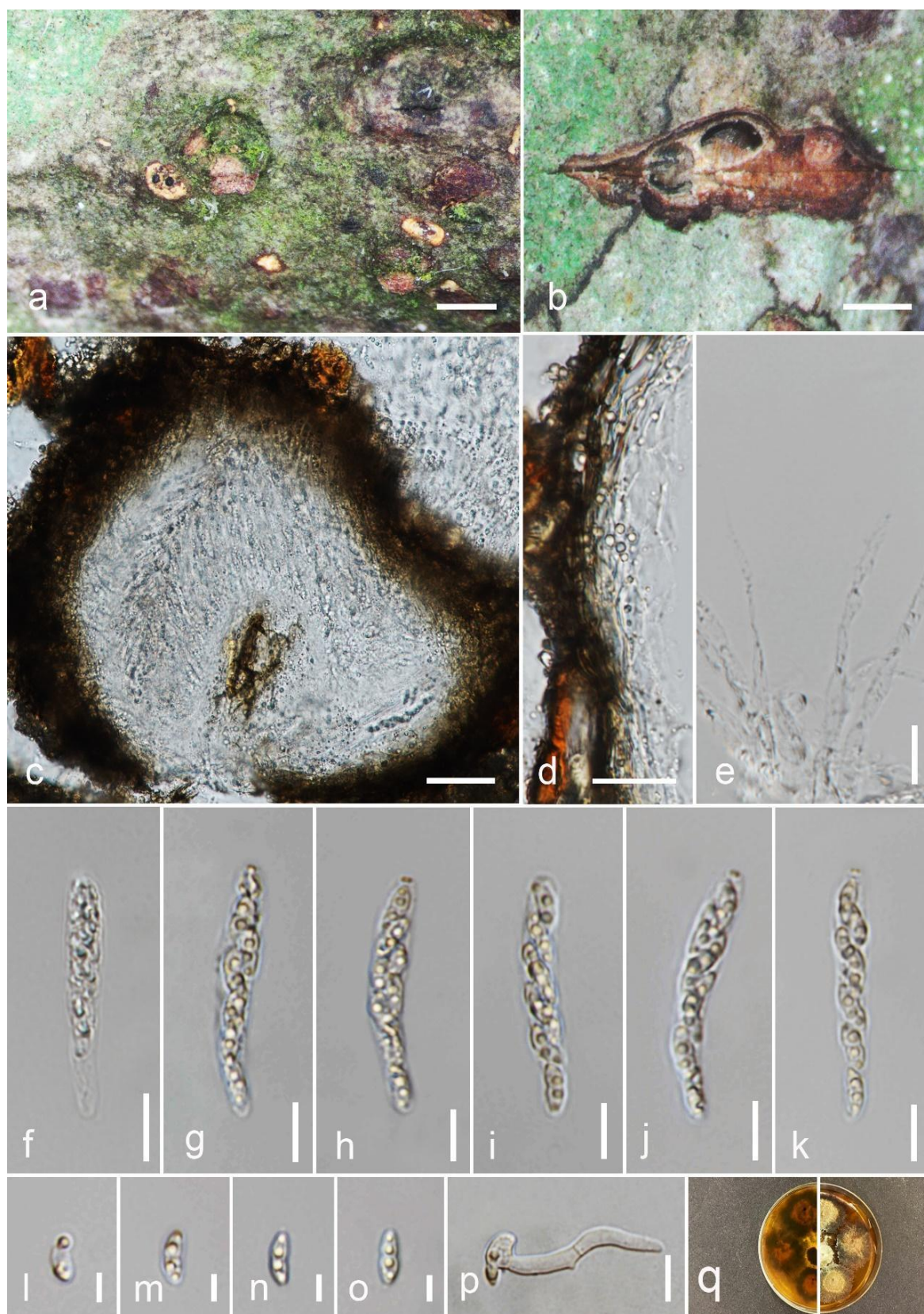


Figure 48 – *Doitungomyces dipterocarpi* (MFLU 24-0465, holotype). a Appearance of ascomata on *Dipterocarpus alatus* woody litter. b Longitudinal section of ascomata. c Vertical section of ascoma. d Section of peridium. e Paraphyses. f–k Asci. l–o Ascospores. p A germinated ascospore. q Colonies on PDA (front and reverse). Scale bars: a, b = 500 µm, c = 50 µm, d, e = 20 µm, f–k, p = 10 µm, l–o = 5 µm.

***Cytospora* Ehrenb.**

Index Fungorum number: IF7904; Facesoffungi number: FoF01378

The genus, *Cytospora* was erected by Ehrenberg (1818) and belongs to *Cytosporaceae* within *Diaporthales* (Wijayawardene et al. 2017). *Cytospora*, established as an asexual name, predates all the sexual synonyms such as *Valsa*, *Leucocytospora*, *Leucostoma*, *Valsella*, and *Valseutypella*, making it the primary name in nomenclature (Adams et al. 2004, Fan et al. 2015 a, b, Zhang et al. 2019). *Cytospora* species are plant pathogens, endophytes or saprobes. They are found globally and are responsible for canker and dieback diseases on various plant species (Norphanphoun et al. 2018, Monkai et al. 2021b). In the past, identifying species within *Cytospora* was challenging because of similar morphological characters and diverse host ranges. A comprehensive method, incorporating host association, geographic distribution, morphological features, and multigene phylogeny, is now commonly used to distinguish *Cytospora* species (Monkai et al. 2021b). *Cytospora* is distinguished by its coelomycetous asexual morphology. The sexual form of *Cytospora* features solitary ascostromata that are immersed to erumpent, consisting of prosenchymatous or pseudoparenchymatous cells with valsoid or diatrypelloid configurations, enclosed in an ectostromatic disc; ellipsoid to clavate, J- apical ring asci; and hyaline, ellipsoid to allantoid, aseptate ascospores (Monkai et al. 2021b). *Cytospora* can be distinguished from other diaporthalean genera by its elongated, hyaline conidia and ascospores (Wang et al. 2024b). The classification of *Cytospora* now relies more on a combination of DNA sequence data, morphology, and ecological characteristics rather than solely on species morphology and host associations (Wang et al. 2024b). In this study, we document *Cytospora heveae* as the first report of its sexual morph and as a new host record on dead wood of *Microcos paniculata* from Doi Tung National Park, Thailand. An updated phylogeny for the genus is shown in Fig. 49.

Cytospora heveae Senwanna, Cheew. & K.D. Hyde, in Senwanna et al. Mycosphere 12(1), 1402 (2021). Fig. 50

Index Fungorum number: IF559362; Facesoffungi number: FoF16091

Saprobic on *Microcos paniculata* woody litter. Sexual morph: *Stromata* solitary, immersed, uni- or multi-loculate. *Ascomata* 105–253 µm high, 150–280 µm wide ($\bar{x}$ = 179 × 214 µm, n = 5), perithecial, immersed or semi-immersed in a stroma, erumpent, scattered, mostly subglobose, glabrous, brown to dark brown, with ostiolar neck. *Peridium* 14–26(–30) µm wide, composed of two layers, brown outer layer and sub-hyaline inner region, outer layer comprising compact thick-walled cells of *textura angularis*, inner layer comprising thin-walled cells of *textura angularis* to *textura prismatica*. *Paraphyses* 3.2–6(–6.9) µm wide ($\bar{x}$ = 4.5 µm, n = 20), cylindrical, hyaline, septate, moderately constricted at septa. *Asci* (17.4–)19–29 × 3.4–6.3(–6.8) µm ($\bar{x}$ = 24.6 × 4.7 µm, n = 25), 8-spored, unitunicate, sessile, clavate to elongate obovoid, apically truncate, with a J- apical ring. *Ascospores* (5.5–)6–8(–8.5) × 1.7–2.6 µm ($\bar{x}$ = 7.2 × 2.2 µm, n = 35), biseriate, overlapping, elongate-allantoid, straight to slightly curved, aseptate, hyaline to light yellow, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h and germ tubes emerge from one or both sides. Colonies on PDA reached 8 cm diam. after 7 days at room temperature (25–28 °C), circular, medium dense, umbonate elevation, upper surface white becoming whitish cream with age, reverse buff becoming brown with age.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Microcos paniculata* (Malvaceae), 09 September 2022, N. Afshari, 3C3T1R8 (MFLU 24-0410); living culture MFLUCC 24-0537.

GenBank numbers – *act* = PX753037, ITS = PQ800242, LSU = PV072598, *rpb2* = PV138149, *tefl-α* = PV138147.

Known hosts – *Hevea brasiliensis* (Senwanna et al. 2021), *Microcos paniculata* (this study).

Known distribution – Thailand (Senwanna et al. 2021, this study).



Figure 49 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, *act*, *tef1-α*, and *rpb2* sequence data of *Cytospora*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. One hundred and sixty-nine

strains are included in the combined analyses which comprised 2,621 characters (ITS = 549, LSU = 544, *act* = 245, *tefl-α* = 556, and *rpb2* = 727). The best score for log-likelihood of consensus tree is -39955.155. The matrix had 1 1,287 distinct patterns, 893 parsimony-informative, 183 singleton sites, 1,545 constant sites. Selecting individual models TIM2e+I+G4, K2P+I+G4, TIM2+F+I+G4, TIM2+F+I+G4 and TN+F+I+G4 were applied for ITS, LSU, *act*, *tefl-α*, and *rpb2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 40,000,000 MCMC generations was calculated as 0.011304. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Diaporthe vaccinii* (CBS 160.32). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

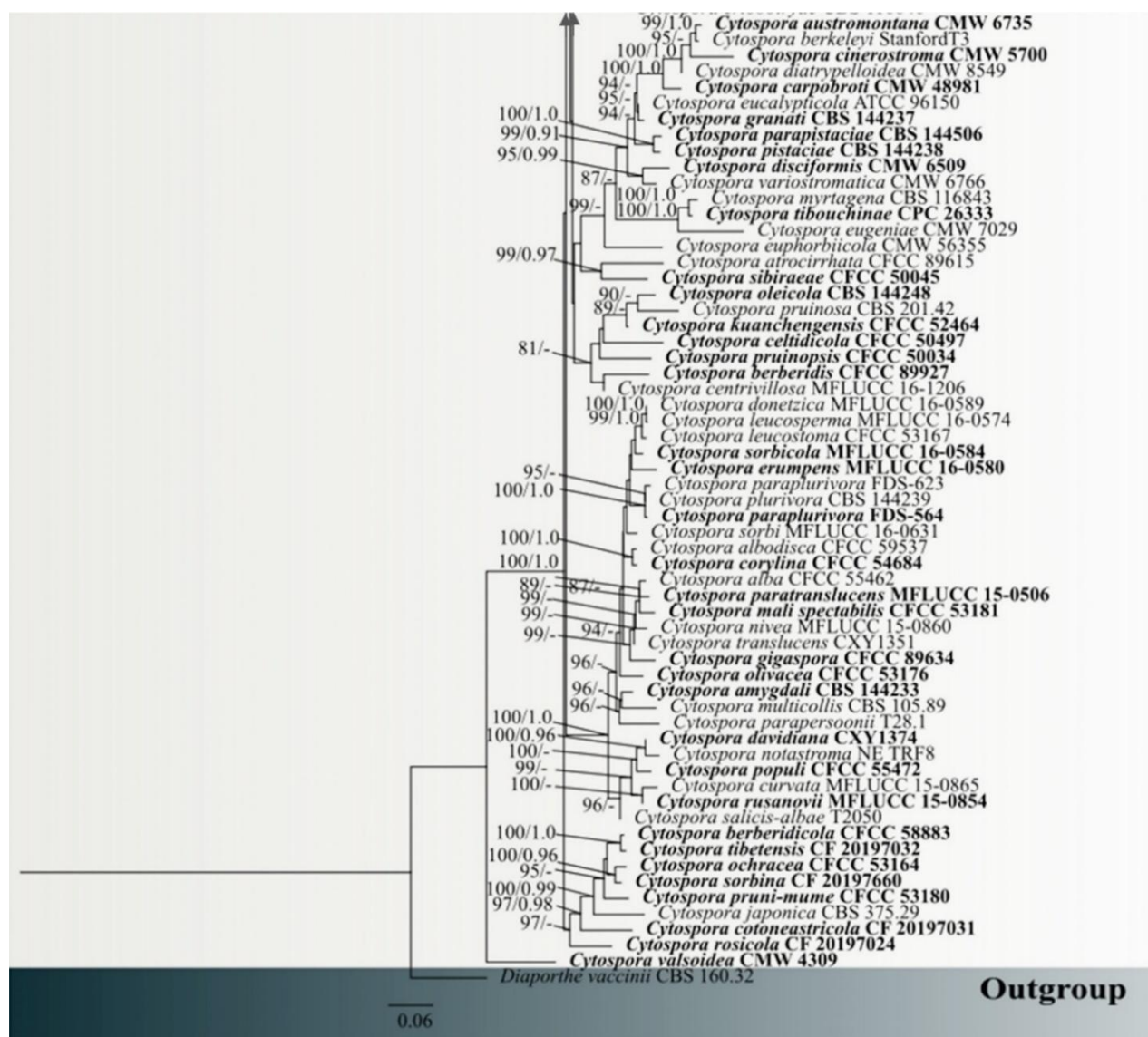


Figure 49 – Continued.

Notes – The asexual morph of *C. heveae* (MFLU 21-0203) identified as a coelomycete, was isolated from canker on a seedling stem of *Hevea brasiliensis* (Euphorbiaceae), in Thailand by Senwanna et al. (2021). The morphology could not be compared since we reported its sexual morph. However, morphological characters of our collection are congruent to the sexual morphs of other *Cytospora* species in having immersed to erumpent, solitary ascostromata, ellipsoid to clavate, J-apical ring asci, and aseptate, hyaline, and ellipsoid to allantoid ascospores (Shang et al. 2020, Monkai et al. 2021b, Senwanna et al. 2021, Wang et al. 2024b). In the phylogeny (Fig. 49) our isolate

(MFLUCC 24-0537) clustered together with *C. heveae* (MFLUCC 17-0358) with high support (100% ML, 0.99 PP). There is not significant sequence difference among these isolates. Therefore, based on the guidelines of Jeewon & Hyde (2016), we consider the new collection (MFLU 24-0410) to be a new host record and new record of the sexual morph of *C. heveae*.

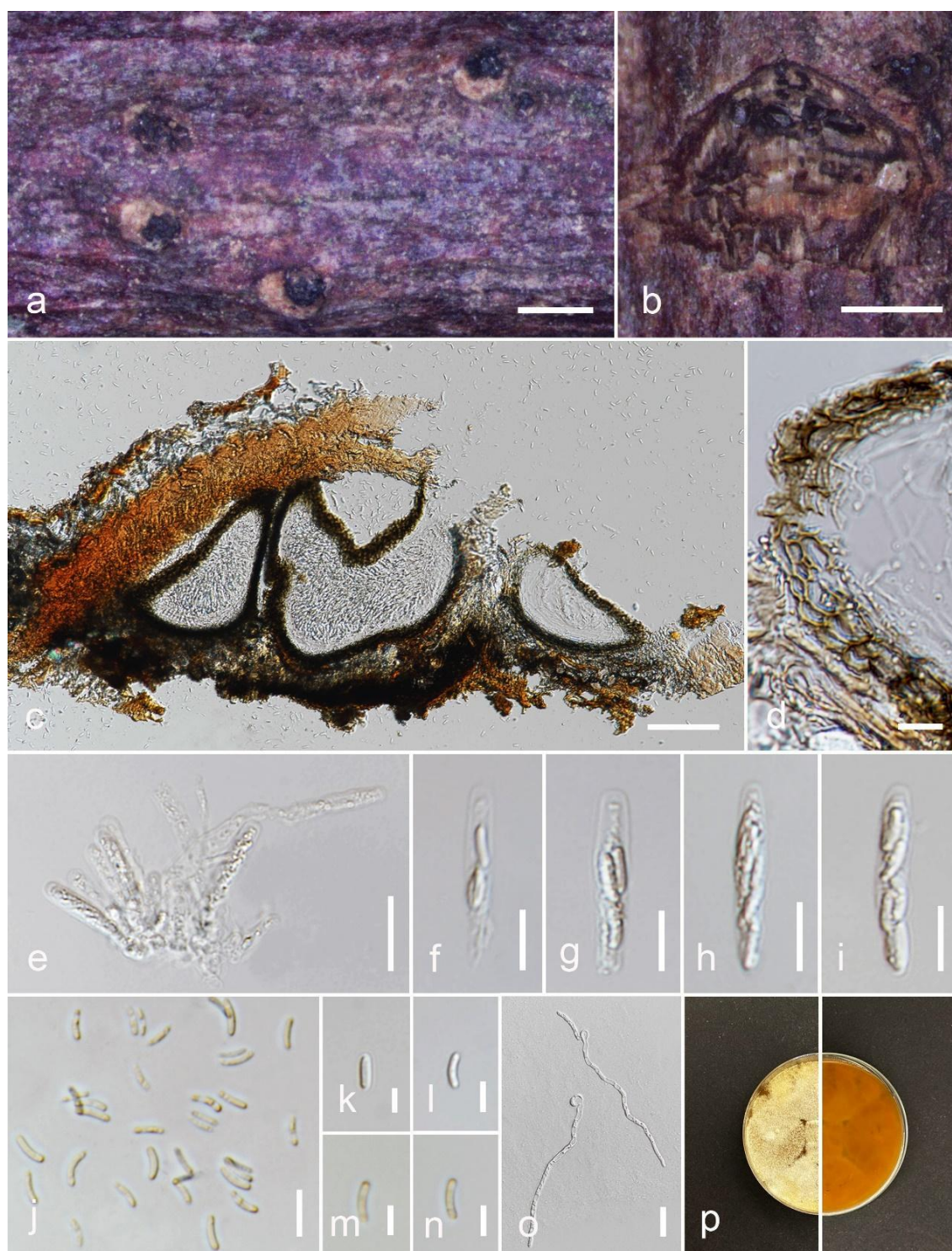


Figure 50 – *Cytospora heveae* (MFLU 24-0410, a new host record and first report of the sexual morph). a Close-up of ascomata on *Microcos paniculata* woody litter. b Longitudinal section of the ascomata. c Vertical section through ascomata. d Section of peridium. e Asci and paraphyses. f–i Asci. j–n Ascospores. o Germinated ascospores. p Colonies on PDA (front and reverse). Scale bars: a, b = 500 μ m, c = 100 μ m, e = 20 μ m, d, f–j, o = 10 μ m, k–n = 5 μ m.

Diaporthomycetidae families *Incertae sedis*

Woswasiaceae Huang Zhang, K.D. Hyde & Maharachch.

Zhang et al. (2017) established *Woswasiaceae* to accommodate *Cyanoannulus*, *Woswasia* and *Xylochrysis* in *Diaporthomycetidae* families *incertae sedis* typified by *Woswasia*. Afterwards, based on multigene phylogenetic analyses combined with divergent time estimation, *Pararamichloridiales* was introduced for *Pararamichloridiaceae* and *Woswasiaceae* (Hyde et al. 2021). Hyde et al. (2021) accommodated this family in *Diaporthomycetidae* families *incertae sedis*.

Xylochrysis Réblová

Index Fungorum number: IF805253; Facesoffungi number: FoF10306

Réblová et al. (2014) erected the monotypic and lignicolous genus *Xylochrysis* for *X. lucida* based on LSU, SSU, and *rpb2* datasets. This genus was placed within *Sordariomycetidae* but without close ordinal or familial affiliation. Morphological and molecular DNA data supported recognition of the genus and suggested that it is closely related to *Ceratolenta*, *Cyanoannulus*, and *Woswasia* (Réblová et al. 2014). Song et al. (2023) introduced another species in *Xylochrysis* based on combined ITS, LSU, SSU, *rpb2*, and *tefl-α* sequence data. It has perithecial, superficial or erumpent, golden yellow, globose to conical ascomata; black, glabrous, papillate or beaked necks; 3-layered ascomatal wall; abundant, septate, persistent paraphyses; long-stipitate, cylindrical, unitunicate asci with a non-amyloid apical annulus; unicellular, ellipsoidal, and hyaline ascospores. It produces hyaline conidiophores with terminally arranged branches bearing metulae, conidiogenous cells, and holoblastic conidia in culture. Currently, *Xylochrysis* comprises four species listed in Species Fungorum (2025). In this study, we introduce *Xylochrysis Chiangraiensis* as a novel species on dead wood of *Dipterocarpus alatus* from Doi Tung National Park, Thailand.

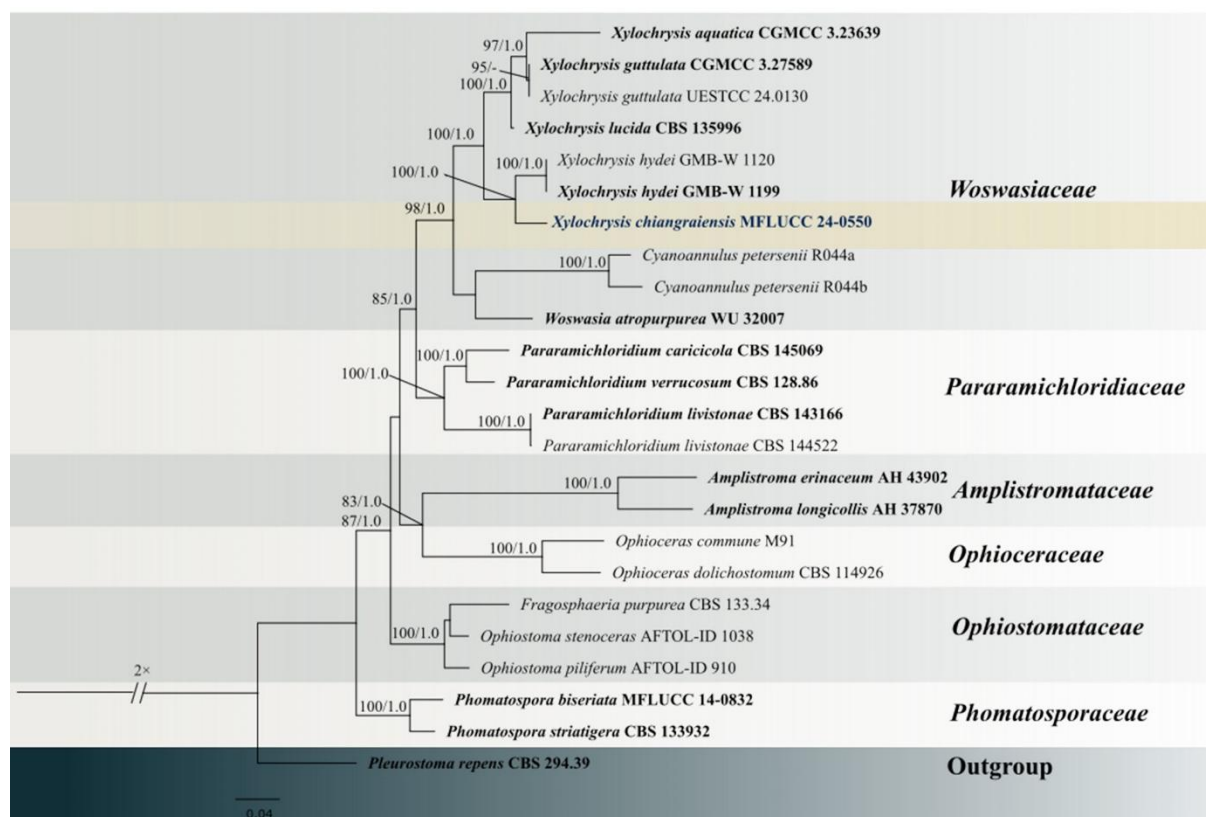


Figure 51 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, *rpb2*, SSU, and *tefl-α* dataset of *Woswasiaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Twenty-four strains are included in the combined analyses which comprised 4,604 characters (ITS = 580, LSU = 850, *rpb2* = 1,185,

SSU = 970, and *tef1*- α = 1,019). Estimated base frequencies were as follows: A = 0.243, C = 0.256, G = 0.279, T = 0.222; substitution rates AC = 1.23125, AG = 2.03636, AT = 1.00000, CG = 1.23125, CT = 4.93365, GT = 1.00000; gamma distribution shape parameter α = 0.567. In the Bayesian analysis, average standard deviation of split frequencies at the end of 3,000,000 MCMC generations was calculated as 0.003395. The evolutionary models GTR+G, TIM3+I+G, TIM1+I, TrNef+G, and TIM2+G were applied to combined ITS, LSU, *rpb2*, SSU, and *tef1*- α , sequence data respectively. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 1.0 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Pleurostoma repens* (CBS 294.39). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Xylochrysis chiangraiensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 52

Index Fungorum number: IF904751; Facesoffungi number: FoF17230

Etymology – The specific epithet is derived from Chiang Rai, location where the holotype was collected.

Holotype – MFLU 24-0470

Saprobic on *Dipterocarpus alatus* woody litter. Sexual morph: *Ascomata* 138–282 μ m diam., 130–216 μ m high ($\bar{x}$ = 188 μ m $\times$ 164 μ m, n = 6), scattered to mostly gregarious, globose to subglobose and mostly flat at base, glabrous, uniloculate, immersed, erumpent through the bark, visible as black spots on the host surface, coriaceous to carbonaceous, short ostiole. *Peridium* two-layered, outer layer 19–40.5 μ m thick ($\bar{x}$ = 29.3 μ m, n = 30), composed of brown to dark brown thick-walled *textura angularis* cells, inner layer 7–18.3 μ m thick ($\bar{x}$ = 11.5 μ m, n = 30), composed of compact, hyaline *textura angularis* cells. *Hamathecium* comprises 2.2–5.1 μ m wide ($\bar{x}$ = 3.7 μ m, n = 35) abundant paraphyses, branched, septate, slightly constricted at the septa, cylindrical, not embedded in a gelatinous matrix. *Asci* (58.5–)65–135(–138) μ m $\times$ 3.8–6.3 μ m ($\bar{x}$ = 93 $\times$ 5 μ m, n = 20), 8-spored, unitunicate, cylindrical, tapering to base, long pedicellate, inamyloid wedge-shaped apical ring. *Ascospores* 4.2–6.2 μ m $\times$ 2.8–4.1 μ m ($\bar{x}$ = 5.4 $\times$ 3.3 μ m, n = 35), L/W 1.5–1.5 ($\bar{x}$ = 1.6, n = 35), 1-seriate, aseptate, ellipsoidal, hyaline, smooth- and thin-walled, straight, two guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h and a germ tube emerged from both ends of the ascospore. Colonies on PDA reached 4–5.4 cm diam. after 10 days at room temperature (25–28 °C), circular, flattened, entire edge, at upper surface white, reverse brown to white outwards.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dipterocarpus alatus* (Dipterocarpaceae), 26 March 2022, N. Afshari, 2C1T3R2a (MFLU 24-0470, holotype); ex-type living culture MFLUCC 24-0550.

GenBank numbers – ITS = PQ800261, LSU = PV072612, *rpb2* = PV138141, SSU = PV072702.

Notes – In our phylogenetic analysis, the new collection (MFLUCC 24-0550) formed a basal clade to the *X. hydei* (GMB-W 1199, GMB-W 1120) with 100% ML bootstrap support and 1.00 PP value (Fig. 51). *Xylochrysis chiangraiensis* (MFLUCC 24-0550), and ex-type of *X. hydei* (GMB-W 1199) have 5.4%, 1.6%, and 9% base pair differences in ITS, LSU, and *rpb2*, respectively. *Xylochrysis hydei* was reported from dead branches in terrestrial habitats in China (Hongsan et al. 2025), while *X. chiangraiensis* was isolated from dead wood of *Dipterocarpus alatus* in Thailand. *Xylochrysis chiangraiensis* is introduced as a new species based on distinct morphology and phylogeny of the combined ITS, LSU, *rpb2*, SSU, and *tef1*- α datasets.

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Glomerellales nested within *Hypocreomycetidae*, represents a fascinating array of fungi, ranging from endophytes and saprobes to plant and animal pathogens. These versatile fungi thrive in diverse ecosystems across the world (Hyde et al. 2020b). What sets them apart are their distinctive apostromatal and endostromatal ascomata, alongside their hyaline and aseptate ascospores. *Glomerellales* boasts a rich

diversity further delineated into five families, *Australiascaceae*, *Glomerellaceae*, *Malaysiascaceae*, *Reticulascaceae*, *Trichosphaeriaceae* (Hyde et al. 2024a).

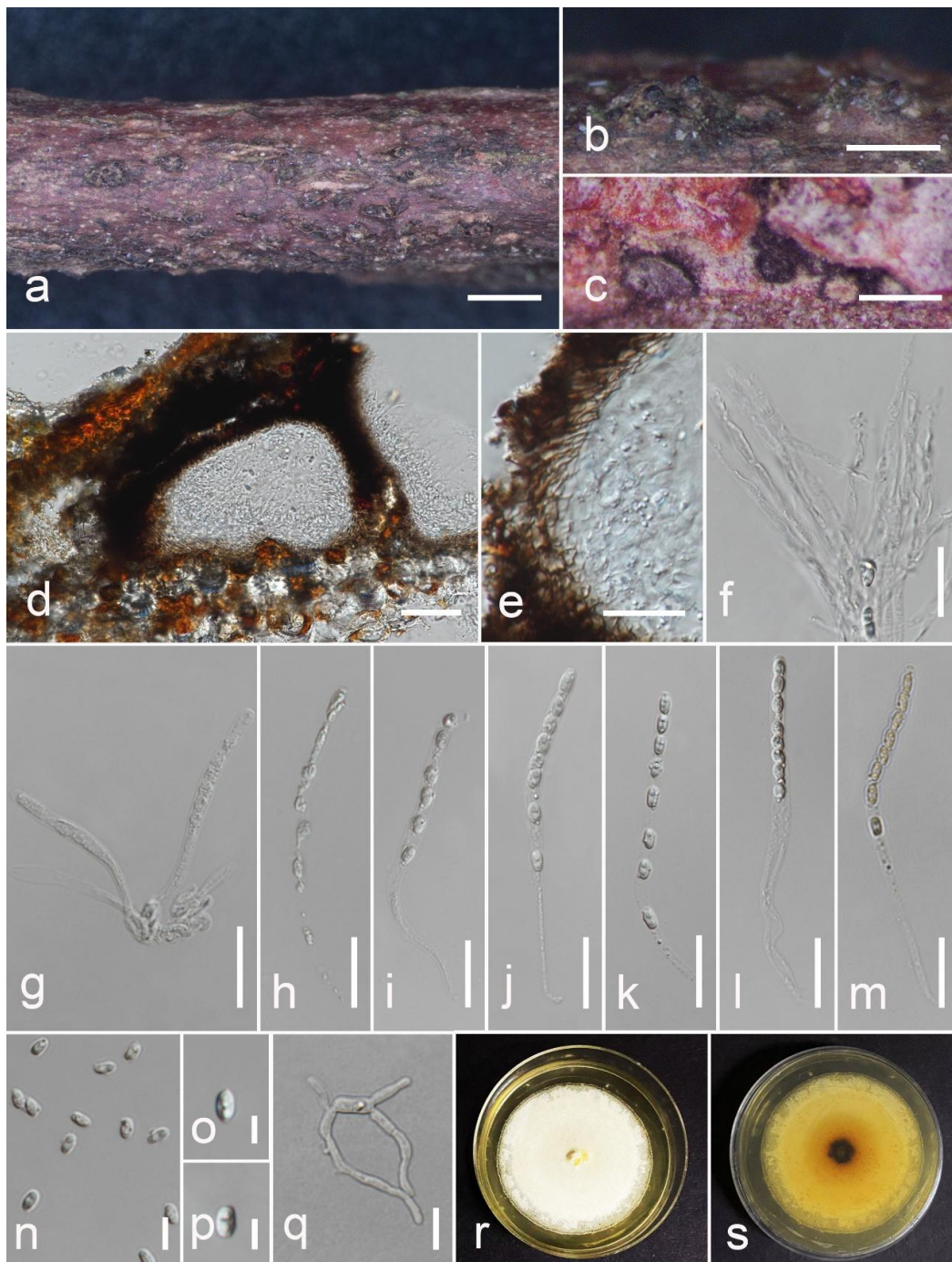


Figure 52 – (MFLU 24-0470, holotype). a, b Appearance of ascomata on *Dipterocarpus alatus* woody litter. c Longitudinal section through ascomata. d Vertical section through ascoma. e Section of peridium. f Paraphyses. g–l Asci. m Ascus in Melzer's reagent. n–p Ascospores. q A germinated ascospore. r, s Colony on PDA (front and reverse). Scale bars: a = 1mm, b = 500 μ m, c = 200 μ m, d = 50 μ m, e–m = 20 μ m, n, q = 10 μ m, o, p = 5 μ m.

Glomerellaceae Locq. ex Seifert & W. Gams

Locquin (1984) introduced *Glomerellaceae* with *Glomerella* as the type genus. Later, this family validated by Zhang et al. (2006) & Réblová et al. (2011). *Colletotrichum*, the asexual morph of *Glomerella*, is included to accommodates both sexual and asexual morphs (Damm et al. 2009,

Maharachchikumbura et al. 2016). Maharachchikumbura et al. (2015), synonymized *Glomerella* with *Colletotrichum*. Members of the family exhibit pathogenic, endophytic, and saprobic lifestyles, and recent phylogenetic studies place *Glomerellaceae* as a monophyletic lineage within *Glomerellales* (Maharachchikumbura et al. 2016).

***Colletotrichum* Corda**

Index Fungorum number: IF7737; Facesoffungi number: FoF00144

Colletotrichum is a coelomycetous genus that incorporates the sexual morph *Glomerella*. This genus exhibits a broad ecological spectrum, functioning as endophytes, saprophytes, or pathogens to plants, insects, and humans (Zhang et al. 2015, Bhunjun et al. 2019, Hyde et al. 2020b, c, Liu et al. 2022b). *Colletotrichum* is taxonomically structured into 16 species complexes and 15 singleton species (Jayawardena et al. 2021, Bhunjun et al. 2021a). It is typified by *C. lineola*, which was isolated from the stem of Apiaceae in the Czech Republic. The asexual morph has dark brown to black conidiomata, occurring solitarily, in clusters, or confluent, and either semi-immersed or erumpent. The conidiomata are subglobose, glabrous, unilocular, and have thick-walled, smooth cells forming the conidiomatal wall. The wall composition ranges from *textura globulosa* to *textura epidermoidea*, *textura porrecta*, and sometimes *textura angularis*. Conidiophores are reduced to conidiogenous cells, originating from the basal stroma. They are hyaline, enteroblastic, phialidic, cylindrical to subcylindrical, determinate, and possess smooth walls. Conidia are hyaline, ellipsoid or falcate, and thick- and smooth-walled. Appressoria are brown and may have entire, crenate, or irregular margins (Sutton 1981, Liu et al. 2022b, Armand et al. 2023, Gomdola et al. 2025). In this study, we introduce *Colletotrichum nayariophyti* as a novel species on *Nayariophyton zizyphifolium* woody litter. As well as, we report the first sexual morph of *C. gigasporum*, and also *C. gigasporum* and *C. durionigenum* as new host records on *Dalbergia cultrata* woody litter from Doi Tung National Park, Thailand.

Colletotrichum durionigenum A. Armand, Jayawar. & K.D. Hyde, in Armand, Huanraluek, Jayawardena & Hyde, Mycosphere 14(2), 117 (2023). Fig. 55

Index Fungorum number: IF559996; Facesoffungi number: FoF13362

Saprobic on *Dalbergia cultrata* woody litter. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 105–250 µm ($\bar{x}$ = 168.5 µm, n = 10) diam., acervulus, globose to oval, black, solitary, comprises dark brown to black cylindrical to sub-cylindrical cells from which originate setae and conidial mass. *Setae* dark grey to black, straight or bent, smooth-walled, paler in the base and apex, opaque, 2–4-septate, 57–79 µm long ($\bar{x}$ = 69 µm, n = 10), base cylindrical and inflated, 6–8.3 µm diam. ($\bar{x}$ = 7 µm, n = 10), apex acute or obtuse. *Conidiophores* rarely observed, septate, single or branched. *Conidiogenous cells* 10–22 × 5–8 µm ($\bar{x}$ = 15 × 6.5 µm, n = 20), cylindrical to pyriform, hyaline to pale brown, smooth-walled. *Conidia* (16.6–)19–25.5(–27) × 5.8–8 µm ($\bar{x}$ = 23 × 7 µm, n = 25; L/W ratio = 3.3), subhyaline to light brown, smooth or verruculose, aseptate, rarely tapering towards the apex, mostly both ends rounded, guttulate.

Culture characteristics – Conidia germinated on PDA within 24 h and germ tubes emerged from one side of the conidia. Colonies on PDA reaching 2 cm diam. after 10 days at room temperature (25–28 °C), irregular, medium dense, undulate at margin, upper surface dirty-white, acervuli appeared mainly on the edge of the colony, from reverse black in the center and pale brown at margin.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cultrata* (Fabaceae), 26 March 2022, N. Afshari, 6C1T1R2 (MFLU 24-0466); living culture MFLUCC 24-0558.

GenBank numbers – ITS = PQ800257, *chs-1* = PX753042, *act* = PX753038.

Known hosts – durian rotting fruit (Armand et al. 2023), *Dalbergia cultrata* (this study).

Known distribution – Thailand (Armand et al. 2023, this study).

Notes – Based on the phylogenetic tree, *C. durionigenum* (MFLUCC 24-0558) clustered together with *C. durionigenum* (MFLUCC 22-0111, ex-holotype) with 60 ML/ 0.92 PP support values (Fig. 53). The base pair differences between *C. durionigenum* (MFLUCC 24-0558) and *C. durionigenum* (MFLUCC 22-0111) revealed 5/237 bp in *chs-1*, and 15/221 bp in *act*.

Morphologically, *C. durionigenum* (MFLUCC 24-0558) is similar to *C. durionigenum* (MFLUCC 22-0111) in having conidiomata with dark pigmentation, septate and branched conidiophores, and conidiogenous cells that are cylindrical to clavate/pyriform, hyaline to pale brown. The setae in both strains are septate, with inflated bases. Two strains produce conidia with a same shape. However, it produces smaller conidiogenous cells than *C. durionigenum* (MFLUCC 22-0111) ((10–22 × 5–8 µm ($\bar{x}$ = 15 × 6.5 µm) vs. 18.5–39 × 6.5–10 µm ($\bar{x}$ = 28.5 × 8 µm)), and smaller conidia ((16.6–)19–25.5(–27) × 5.8–8 µm ($\bar{x}$ = 23 × 7 µm) vs. 29–40 × 8.5–11.5 µm ($\bar{x}$ = 35 × 10 µm)) (Fig. 55) (Armand et al. 2023). *Colletotrichum durionigenum* was introduced by Armand et al. (2023) on rotting durian fruit in Thailand. Due to the lack of *gapdh* and *tub2* sequence data for our isolate and its morphological and DNA similarity, our strain is introduced as a new isolate of *C. durionigenum* from dead wood of *Dalbergia cultrat*.

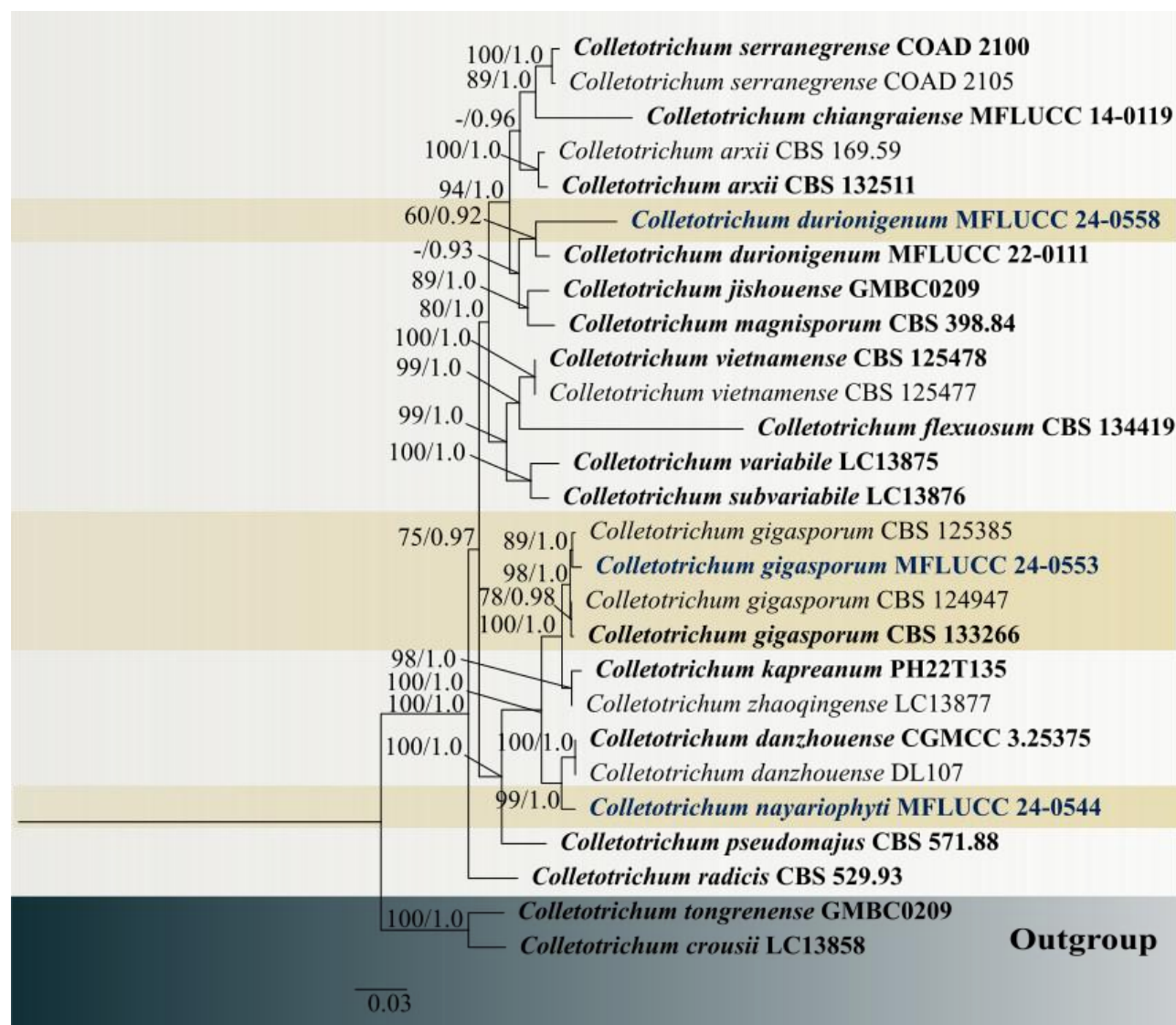


Figure 53 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequence data of *Colletotrichum*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Twenty-seven strains are included in the combined analyses which comprised 1,739 characters (ITS = 519, *gapdh* = 154, *chs-1* = 299, *act* = 234, and *tub2* = 533). The best RAxML tree with a final optimization likelihood value of -7135.156011 is presented. The matrix had 594 distinct alignment patterns, with 12.26% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.227315, C = 0.300657, G = 0.251024, T = 0.221003; substitution rates AC = 1.316529, AG = 5.848166, AT = 1.343640, CG = 1.194254, CT = 8.931147, GT = 1.000000; gamma distribution shape parameter α

= 0.314661. In the Bayesian analysis, average standard deviation of split frequencies at the end of 2,000,000 MCMC generations was calculated as 0.000874. The evolutionary models TrN+I+G, TPM2uf+I, TrN+I+G, HKY+I, and TIM3+I+G were applied for ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequence data. Bootstrap support values for ML greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Colletotrichum tongrenense* (GMBC0209) and *C. crousii* (LC13858). Ex-type strains are in bold. The isolates generated in this study are indicated in bold and blue.

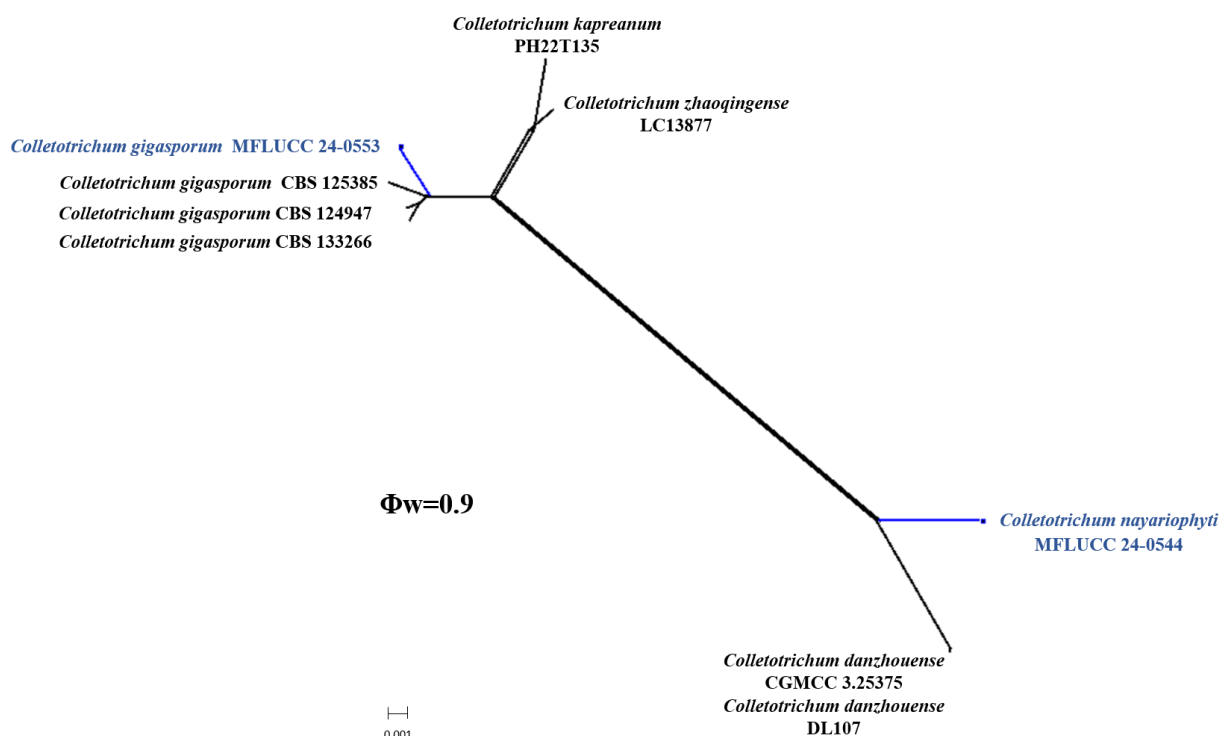


Figure 54 – The splits diagram from the pairwise homoplasy index (PHI) test created from the concatenated data set of ITS, *gapdh*, *chs-1*, *act*, and *tub2* using splits decomposition and LogDet transformation. The PHI test (Φ_w) < 0.05 indicates significant recombination within the dataset. The novel taxa are in blue and squared edges. *Colletotrichum nayariophyti* and *Colletotrichum gigasporum* and closely related taxa.

Colletotrichum nayariophyti N. Afshari, Lumyong & K.D. Hyde, sp. nov. Fig. 56
Index Fungorum number: IF904752; Facesoffungi number: FoF17232
Etymology – Referring to the host genus “*Nayariophyton*”, from which the holotype was isolated.

Holotype – MFLU 24-0467

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 180–335 μm ($\bar{x}$ = 244 μm , n = 5) diam., acervulus, oval, black, solitary, scattered, comprising dark brown to brown, cylindrical to sub-cylindrical cells. *Setae* dark brown, straight or bent, smooth-walled, paler at the apex, 2–5 septate, 59–80 μm long ($\bar{x}$ = 70 μm , n = 10), base cylindrical, 4–6 μm diam. ($\bar{x}$ = 5 μm , n = 10), with acute to rounded tip. *Conidiophores* rarely observed, aseptate, single or branched. *Conidiogenous cells* 7.8–20 $\times$ 5.2–7.8 μm ($\bar{x}$ = 15 $\times$ 6.6 μm , n = 25), cylindrical or clavate, hyaline to subhyaline. *Conidia* 18–26 $\times$ 5.5–8.3 μm ($\bar{x}$ = 22 $\times$ 7 μm , n = 30; L/W ratio = 3), cylindrical to subcylindrical, straight to slightly curved, moderately truncate and tapering at the base, rounded at apex, hyaline, smooth-walled, aseptate, guttulate.

Culture characteristics – Conidium germinated on PDA within 24 h and germ tubes emerged from one or both ends of the conidium. Colonies on PDA reached 4–4.5 cm diam. after 7 days at

room temperature (25–28 °C), after one month irregular, undulate at edge, zonate, mycelia radiating outwards, upper surface greenish brown with white raised ring, acervuli appeared mainly at margin, from reverse dark brown to black.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T1R1 (MFLU 24-0467, holotype); ex-type living culture MFLUCC 24-0544.

GenBank numbers – ITS = PQ800258, *gapdh* = PX753043, *act* = PX753039, *tub2* = PX739618.

Notes – Based on the phylogenetic tree, *Colletotrichum nayariophyti* (MFLUCC 24-0544) clustered with two strains of *C. danzhouense* (CGMCC 3.25375 (=DL52), DL107) with 99% ML/1.0 PP support values (Fig. 53). The GCPSR concept was used to the concatenated gene set of *C. nayariophyti* and the closely related taxa (*C. danzhouense* (CGMCC 3.25375, DL107), *C. gigasporum* (CBS 125385, CBS 124947, CBS 133266, MFLUCC 24-0553), *C. kapreanum* PH22T135, *C. zhaoqingense* LC13877). A PHI test of the multilocus dataset detected nonsignificant recombination among these isolates ($\Phi_w = 0.9$, Fig. 54). *Colletotrichum nayariophyti* differs from *C. danzhouense* (CGMCC 3.25375) by a 0.8% bp difference in ITS, 4% bp difference in *act*, 3% bp difference in *gapdh*, and 1% bp difference in *tub2*. Morphologically, *C. nayariophyti* (MFLU 24-0467) differs from *C. danzhouense* (CGMCC 3.25375) in having smaller setae (59–80 μm vs. 70.8–113.4 μm), and larger conidia (18–26 $\times$ 5.5–8.3 μm vs. 14.4–21.6 $\times$ 5.6–7.2 μm) (the size of conidiogenous cells for *C. danzhouense* (CGMCC 3.25375) is not available) (Fig. 56) (Cao et al. 2023). *Colletotrichum danzhouense* was isolated from diseased leaves of *Litchi chinensis* by Cao et al. (2023) in China. We describe *C. nayariophyti* as a new species in the *C. gigasporum* species complex using morphological, phylogenetic, and PHI test approaches.

Colletotrichum gigasporum Rakotonir. & Munaut, in Rakotoniriana et al. Mycol. Progr. 12(2), 407 (2013). Fig. 57

Index Fungorum number: IF800175; Facesoffungi number: FoF10777

Saprobic on *Dalbergia cultrata* woody litter. Sexual morph: *Ascomata* 160–254 μm high, 129–229 μm wide ($\bar{x} = 205 \times 167 \mu\text{m}$, $n = 5$), perithecium, lignicolous, immersed or semi-immersed, erumpent, coriaceous, rarely solitary to mostly gregarious, globose to ovoid, dark brown to black, lacking setae. *Peridium* 30–45 μm wide ($\bar{x} = 37.5 \mu\text{m}$, $n = 35$), comprising 2–3 layers of dark brown to hyaline cells, arranged in a *textura angularis*. *Paraphyses* 5–9 μm wide ($\bar{x} = 7 \mu\text{m}$, $n = 30$), cylindrical, guttulate, septate, constricted at the septa, slightly exceeding asci, hyaline, smooth-walled. *Asci* (74–)85–130(–143) $\times$ 14–22 μm ($\bar{x} = 107 \times 18 \mu\text{m}$, $n = 15$), unitunicate, 6–8-spored, smooth-walled, broadly cylindrical to clavate, mostly curved, tapering towards base and apex, truncate at apex, short pedicellate. *Ascospores* (40–)53–85(–90) $\times$ 5–8.5 μm ($\bar{x} = 77 \times 6 \mu\text{m}$, $n = 25$), fusoid to cylindrical, mostly curved, rounded at both ends, hyaline, aseptate, smooth-walled, contents granular. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h and germ tubes emerge from one side. Colonies on PDA reached 8.5 cm diam. after 10 days at room temperature (25–28 °C), circular, flattened, with entire margin, dense at the center, rough at surface, upper surface grey in center and pale grey at outer zone, from reverse olivaceous-green to dark grey outwardly.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cultrata* (Fabaceae), 26 March 2022, N. Afshari, 6C1T3R1b (MFLU 24-0468); living culture MFLUCC 24-0553.

GenBank numbers – ITS = PQ800259, *gapdh* = PX753044, *chs-1* = PX753041, *act* = PX753040, *tub2* = PX739619.

Known hosts and distribution – *Colletotrichum gigasporum* has a cosmopolitan distribution and is associated with different hosts (Farr & Rossman 2025). This study presents the first report of *C. gigasporum* on *Dalbergia cultrate* from Thailand.

Notes – Rakotoniriana et al. (2013) introduced *Colletotrichum gigasporum* as an asexual fungus based on morphology and phylogeny. It was isolated from healthy leaves of *Centella asiatica*

in Madagascar, *Stylosanthes guianensis* in Mexico, and *Coffea arabica* in Colombia. A phylogenetic tree derived from an alignment of combined ITS, *gapdh*, *chs-1*, *act*, and *tub2* sequence data of *C. gigasporum* (MFLUCC 24-0553) has 89% ML and 1.0 PP support, and it clusters together with three other *C. gigasporum* strains (CBS133266, CBS 125385, CBS 124947) (Figs. 53, 54). Based on multilocus sequence analyses combined with morphology and the analysis of genealogical concordance phylogenetic species recognition analysis (GCPSR) result applied to the concatenated gene set of the closely related taxa, a first sexual morph of *C. gigasporum* (MFLU 24-0468) is introduced. This morph was found on dead wood of *Dalbergia cultrata* from Thailand.

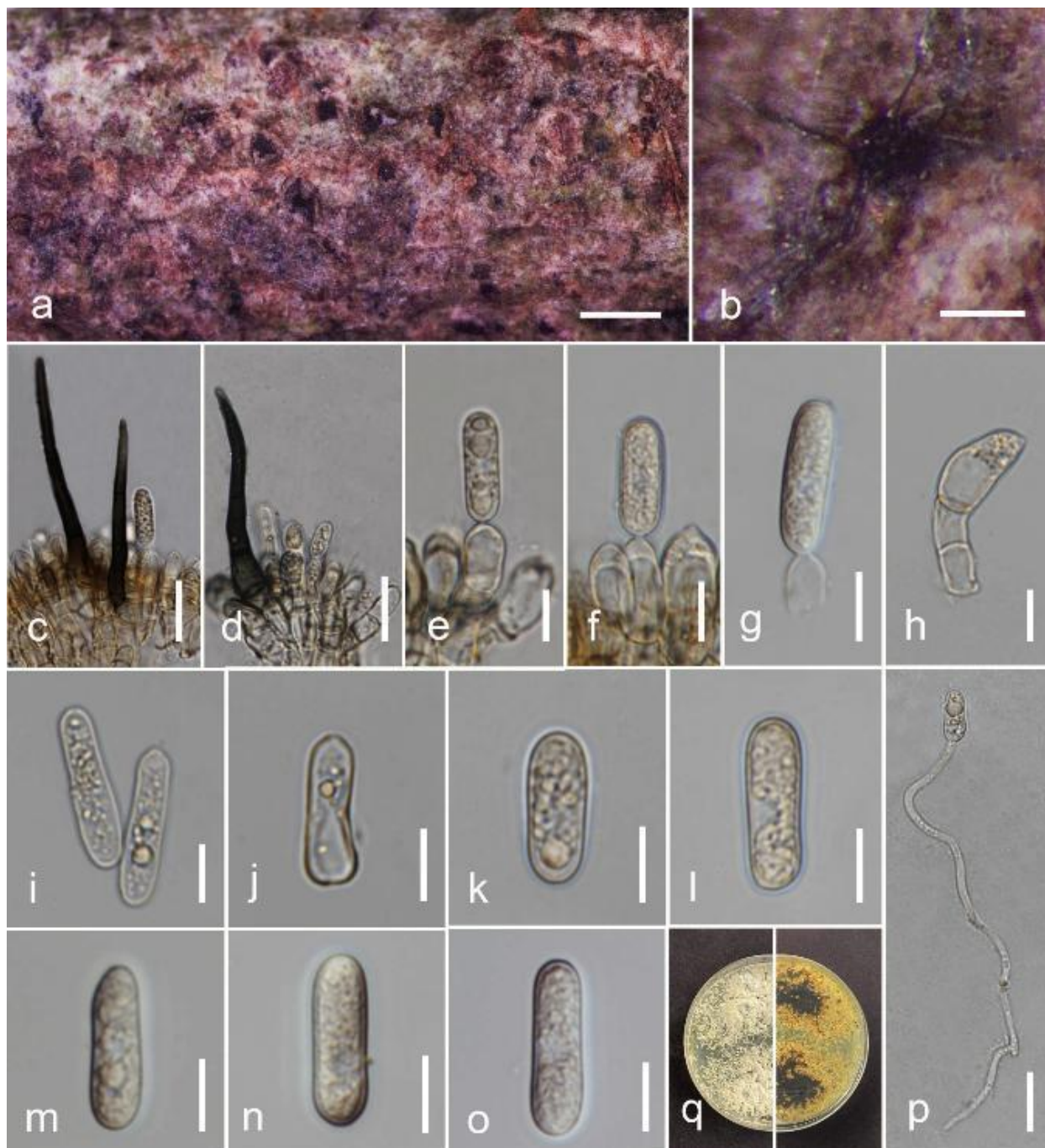


Figure 55 – *Colletotrichum durionigenum* (MFLU 24-0466, a new host record). a, b Acervuli on *Dalbergia cultrata* woody litter. c, d Conidiophores, conidia, and setae. e–h Conidia arising from conidiogenous cells. i–o Conidia. p A germinated conidium. q Colonies on PDA (front and reverse). Scale bars: a = 500 μ m, b = 100 μ m, c, d, p = 20 μ m, e–o = 10 μ m.

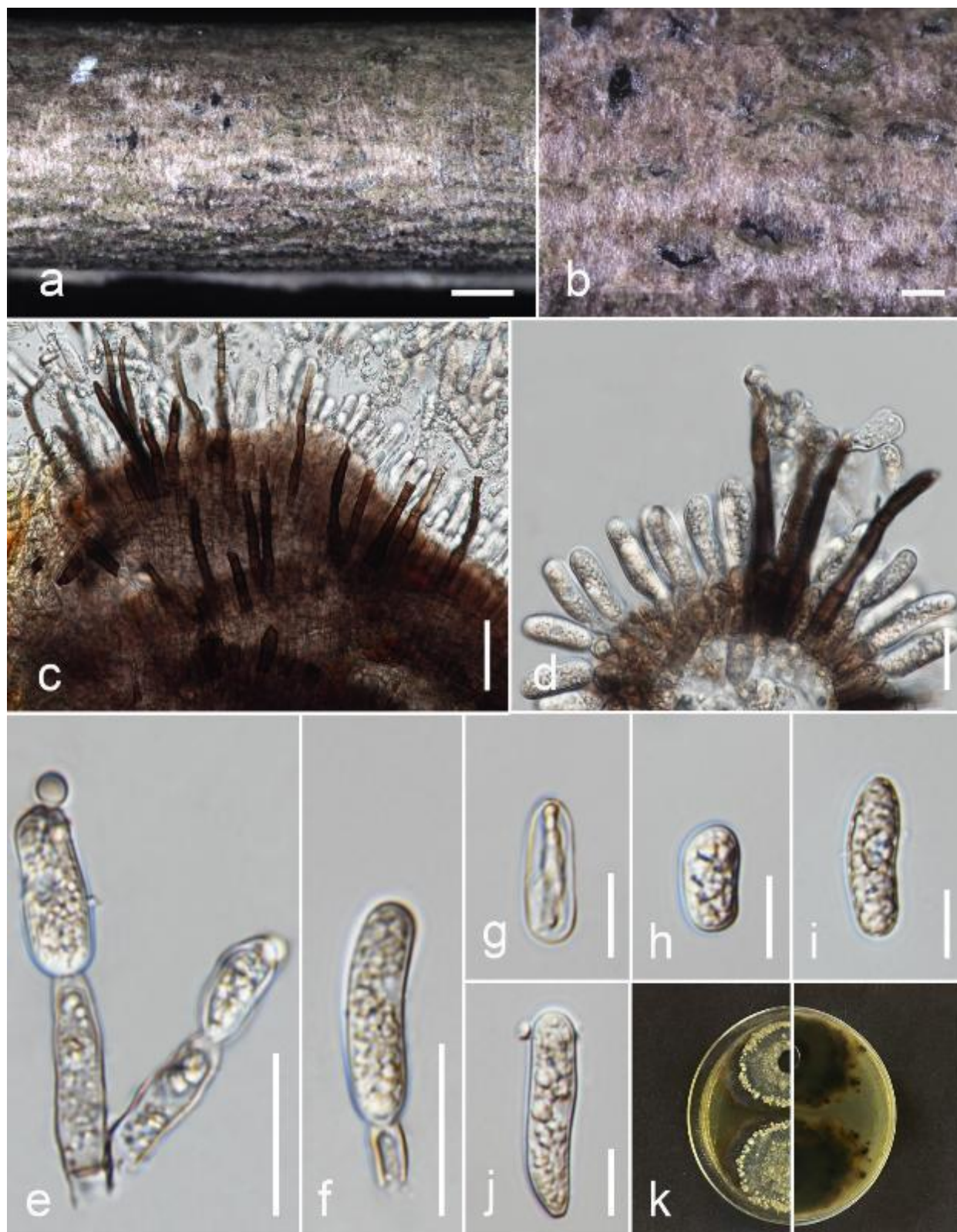


Figure 56 – *Colletotrichum nayariophyti* (MFLU 24-0467, holotype). a, b Acervuli on *Nayariophyton zizyphifolium* woody litter. c, d Conidiophores, conidia, and setae. e, f Conidia arising from conidiogenous cells. g–j Conidia. k Colonies on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 μ m, c = 50 μ m, d–f = 20 μ m, g–j = 10 μ m.



Figure 57 – *Colletotrichum gigasporum* (MFLU 24-0468, a new host record and first report of the sexual morph). a Appearance of ascomata on *Dalbergia cultrata* woody litter. b Vertical section of ascomata. c Section of peridium. d Paraphyses. e–g Asci. h–j Ascospores. k A germinated ascospore. l, m Colonies on PDA (front and reverse). Scale bars: a = 200 μm , b = 100 μm , c–g, k = 50 μm , h–j = 20 μm .

***Trichosphaeriaceae* G. Winter**

Trichosphaeriaceae was introduced by Winter (1887) with *Trichosphaeria* as the type genus and seven other genera. Later these seven genera were excluded from this family by molecular evidence. In multigene phylogenetic analyses of LSU, SSU, *tefl-α* and *rpb2* sequence data *Trichosphaeriaceae* had affinities with *Papulosaceae* and *Thyridiaceae*, but they maintained *Trichosphaeriaceae* as a separate family until more sequence data (Maharachchikumbura et al. 2015). Certain species in this family are coprophilic, and other members are saprobic or pathogenic on plants (Hudson 1963, Calatayud & Aguirre-Hudson 2001). Hyde et al. (2024a), listed 31 genera in *Trichosphaeriaceae*.

***Chordomyces* Bilanenko, Georgieva & Grum-Grzhim.**

Index Fungorum number: IF811265; Facesoffungi number: FoF13530

Grum-Grzhimaylo et al. (2016) established the monotypic genus *Chordomyces* with *C. antarcticus* as the type species. This species was discovered in soda soil on the periphery of a lake in Altay, China. Through comprehensive analysis of LSU and ITS sequence data, alongside detailed morphological examination, this genus was placed within *Plectosphaerellaceae*, *Glomerellales* (Grum-Grzhimaylo et al. 2016). The sexual morph has not been observed in this genus. The asexual morph has white tufts, composed of intricate bundles of hyaline hyphae that gradually taper into synnemata. These occasionally branching tufts create a bristling effect due to numerous radiating phialides. Conidiation is abundant, predominantly synnematogenous, with some plectonemagenous development. Stroma, setae, and hyphopodia are notably absent. Conidiophores exhibit diverse branching patterns and conidiogenous cells are mainly phialidic. Conidia are elliptical to cylindrical, hyaline, and smooth-walled (Grum-Grzhimaylo et al. 2016). In this study, we report an additional collection of *Chordomyces zizyphifolii* on dead branches of *Nayariophyton zizyphifolium* from Doi Tung National Park, Thailand.

***Chordomyces zizyphifolii* Samarad., Lumyong & K.D. Hyde, in Samaradiwakara et al. Fungal Diversity, [85] (2025).** Fig. 59

Index Fungorum number: IF855738; Facesoffungi number: FoF16512

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Synnemata* 305–610 µm high, 115–190(–300) µm diam. ($\bar{x}$ = 415 × 145 µm, n = 10) at apical parts, scattered, gregarious or rarely caespitose, clavate or cylindrical, dark brown at apical part, straight or slightly bent, unbranched, sporulating along their entire length, with lentil- to obovoid-shaped head, with a compact capitulum. *Stipe* 120–370 µm high, (33–)55–110(–160) µm wide ($\bar{x}$ = 254 × 70 µm, n = 10), pale orange brown, unbranched, consisting of parallel adpressed conidiophores. *Conidiophores* (24–)35–58(–66) µm × 2–3.3 µm ($\bar{x}$ = 46.6 × 2.7 µm, n = 20), moderately flared on capitulum, abundant, septate, flexuous, pale brown to brown at maturity. *Conidiogenous cells* 1.2–3 µm wide, 2.3–4.3 µm long ($\bar{x}$ = 1.8 × 3.3 µm, n = 30), phialides mostly solitary or rarely in small groups, terminal, hyaline, cylindrical or subulate, wide at the base, straight or sinuous, smooth- and thick-walled, predominantly proliferating percurrently. *Conidia* 4–6.8 × 2–3.2 µm ($\bar{x}$ = 5.8 × 2.6 µm, n = 30), L/W ratio = 2.2, ellipsoidal to cylindrical, aseptate, rounded at apex, hyaline to sub-hyaline, thick-walled, verruculose, without a mucilaginous sheath.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerged from one or both sides of conidium. Colonies on PDA reached 1–1.5 cm diam. after 10 days at room temperature (25–28 °C), mucoid, irregular, dense, crenated margin, no pigment diffusing into agar, at upper surface white, reverse pale yellow.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 6 June 2022, N. Afshari, 1C2T2R6 (MFLU 24-0412); living culture MFLUCC 24-0539.

GenBank numbers – ITS = PQ800244, LSU = PV072599.

Known hosts – *Nayariophyton zizyphifolium* (Samaradiwakara et al. 2025), *N. zizyphifolium* (this study).

Known distribution – Thailand (Samaradiwakara et al. 2025, this study).

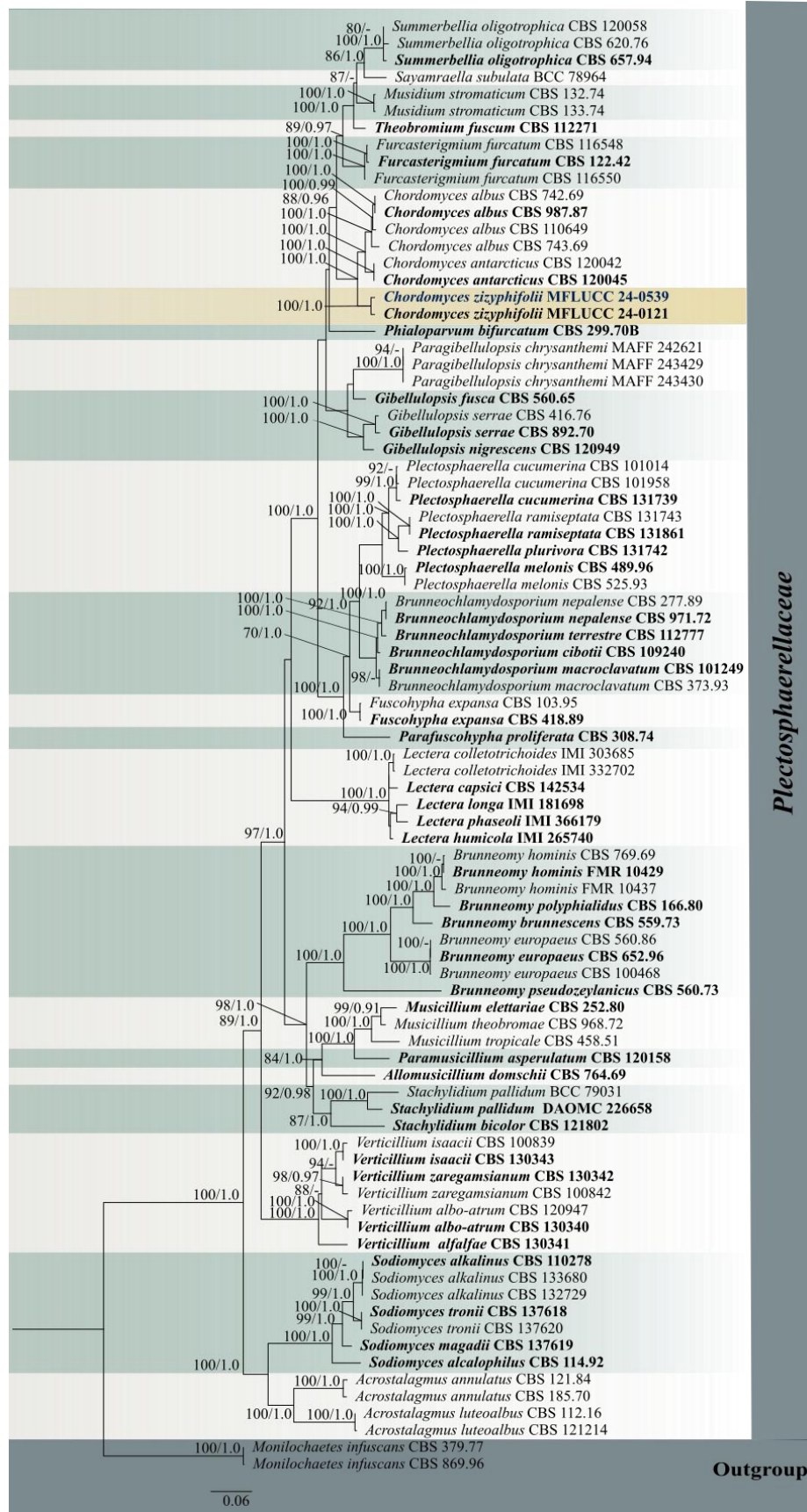


Figure 58 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined LSU, ITS, *rpb2*, and *tef1-α* sequence data of *Plectosphaerellaceae*. Tree

topology of the maximum likelihood analysis is similar to the Bayesian analysis. Eighty-six strains are included in the combined analyses which comprised 3,026 characters (LSU = 784, ITS = 409, *rpb2* = 1,061, *tefl-α* = 772). The best score for log-likelihood of consensus tree is -26634.910. The matrix had 1,150 distinct patterns, 1,003 parsimony-informative, 108 singleton sites, 1,915 constant sites. Selecting individual models TIM3e+I+G4, SYM+I+G4, TN+F+I+G4, and GTR+F+I+G4 were applied LSU, ITS, *rpb2* and *tefl-α* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 6,000,000 MCMC generations was calculated as 0.007992. Bootstrap support values for ML greater than or equal to 80% and Bayesian posterior probabilities greater than or equal to 0.9 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Monilochaetes infuscans* (CBS 379.77 and CBS 869.96). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Notes – In the phylogenetic analysis, our isolate (MFLUCC 24-0539) clustered together with the strains of *Chordomyces zizyphifolii* (MFLUCC 24-0050) with 100% ML bootstrap support and 1.00 PP value (Fig. 58). Our isolate is synnematus, therefore it is difficult to compare morphology with *C. zizyphifolii* (MFLUCC 24-0121) which was introduced based on culture morphology by Samaradiwakara et al. (2025). The ex-type strain of *C. zizyphifolii* (MFLUCC 24-0121) was isolated from dead leaves of *Nayariophyton zizyphifolium*, while our isolate was obtained from dead branches of the same host and locality. Also, *C. zizyphifolii* (MFLUCC 24-0539) morphologically differs from *C. albus* in having synnemata (Giraldo et al. 2017). *Chordomyces antarcticus* (CBS 120045) produces synnemata on culture. Conidiogenous cells of *C. antarcticus* proliferate sympodially, with schizophialides, however our collection has mostly solitary phialides or rarely in small groups, and often proliferate percurrently. Also, conidia of *C. antarcticus* are held in slimy spherical heads and are rarely 2-celled, while *C. nayariophyti* has single and aseptate conidia (Grum-Grzhimaylo et al. 2016). Therefore, based on phylogenetic evidence we propose *C. zizyphifolii* as a new collection of from dead branches of *Nayariophyton zizyphifolium*.

***Hypocreales* Lindau**

***Myrotheciomycetaceae* Crous**

Crous et al. (2018b) established *Myrotheciomycetaceae* with *Myrotheciomyces*. as the type genus. It includes *Leucosphaerina*, *Myrotheciomyces* and *Trichothecium* (Hyde et al. 2024a). Conidiomata solitary to sporodochia, with crystalline to white or orange conidial mass; conidiophores hyaline, subcylindrical, with terminal and lateral conidiogenous cells that are phialidic or retrogressive; and conidia aggregated in slimy mass, aseptate or 1-septate, hyaline, fusoid-ellipsoid (Crous et al. 2018b).

***Trichothecium* Link**

Index Fungorum number: IF10303; Facesoffungi number: FoF13427

Trichothecium was erected by Link (1809) to accommodate *T. roseum* as the type species and was reported on dried pods of *Delonix regia*. Summerbell et al. (2011) revised this genus using D1/D2 sequences for sequence-based identification. Hou et al. (2023), introduced *T. hongkongense* based on combined LSU, ITS, and *rpb2* sequence data. Both sexual and asexual morphs have been observed in this genus. *Trichothecium* species are usually considered as a contaminant. They cause pink rot on diverse fruits and vegetables (Summerbell et al. 2011). They are mycoparasitic in cultivated mushrooms, resulting in economic losses to different degrees (Zare et al. 2005, Sun et al. 2019, Liu et al. 2021). The sexual morph is characterized by clavate to spherical asci containing eight ellipsoidal or reniform ascospores with refractile walls and a gelatinous sheath. In the asexual morph, conidiogenous apparatus varies by species. Conidiophores long, often septate and unbranched, with terminal phialides producing unicellular, hyaline, smooth-walled conidia. Chlamydospores may be present. There are 37 species of *Trichothecium* recorded in Species Fungorum (2025). In this study, we report *Trichothecium roseum* as a new host record on dead branches of *Dalbergia cultrata* from Thailand.

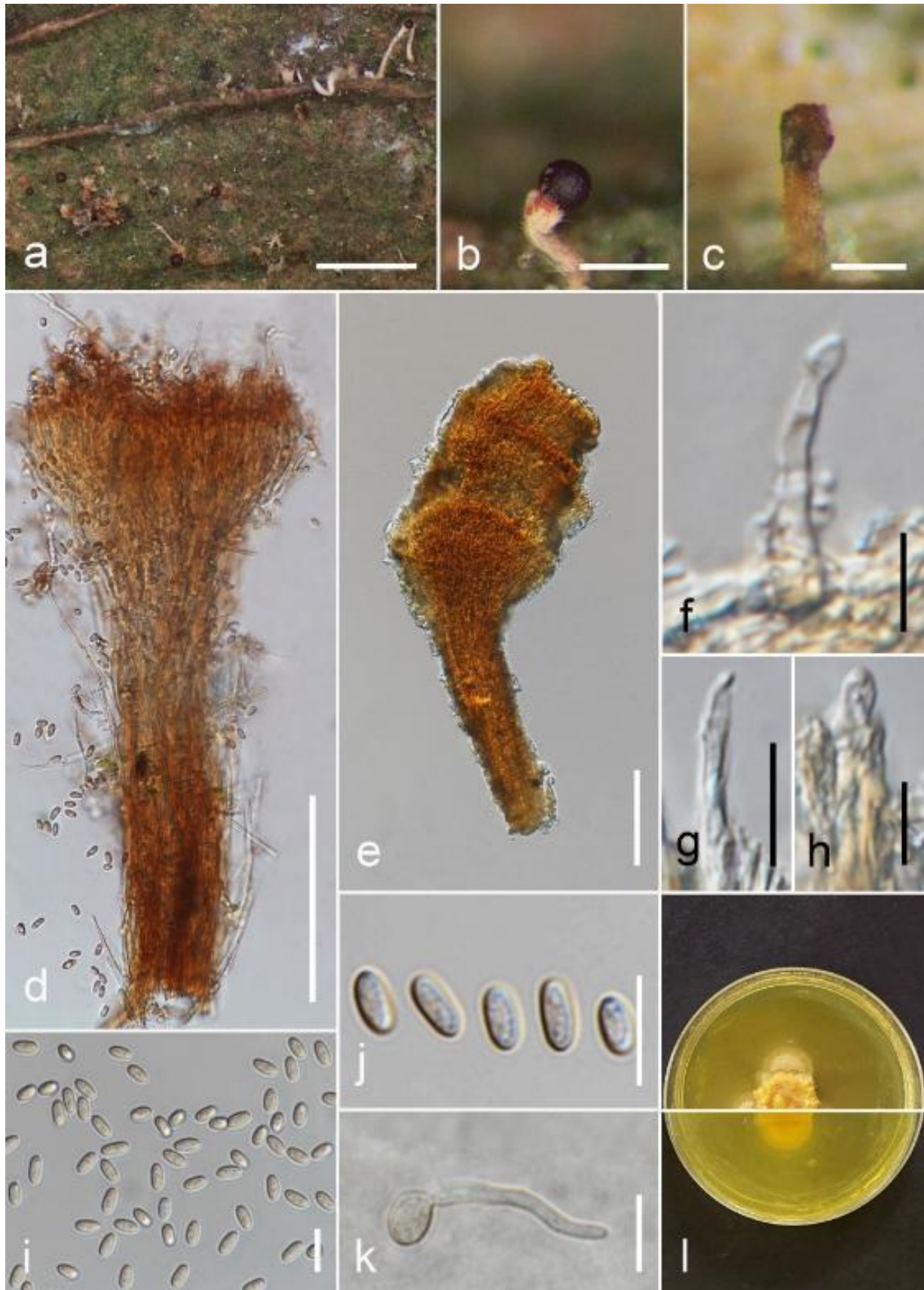


Figure 59 – *Chordomyces zizyphifolii* (MFLU 24-0412, additional collection from dead wood). a–c Synnemata on *Nayariophyton zizyphifolium* woody litter. d, e Vertical section synnemata. f–h Conidiogenous cells. i, j Conidia. k A germinated conidium. l Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 200 μ m, c–e = 100 μ m, f–k = 10 μ m.

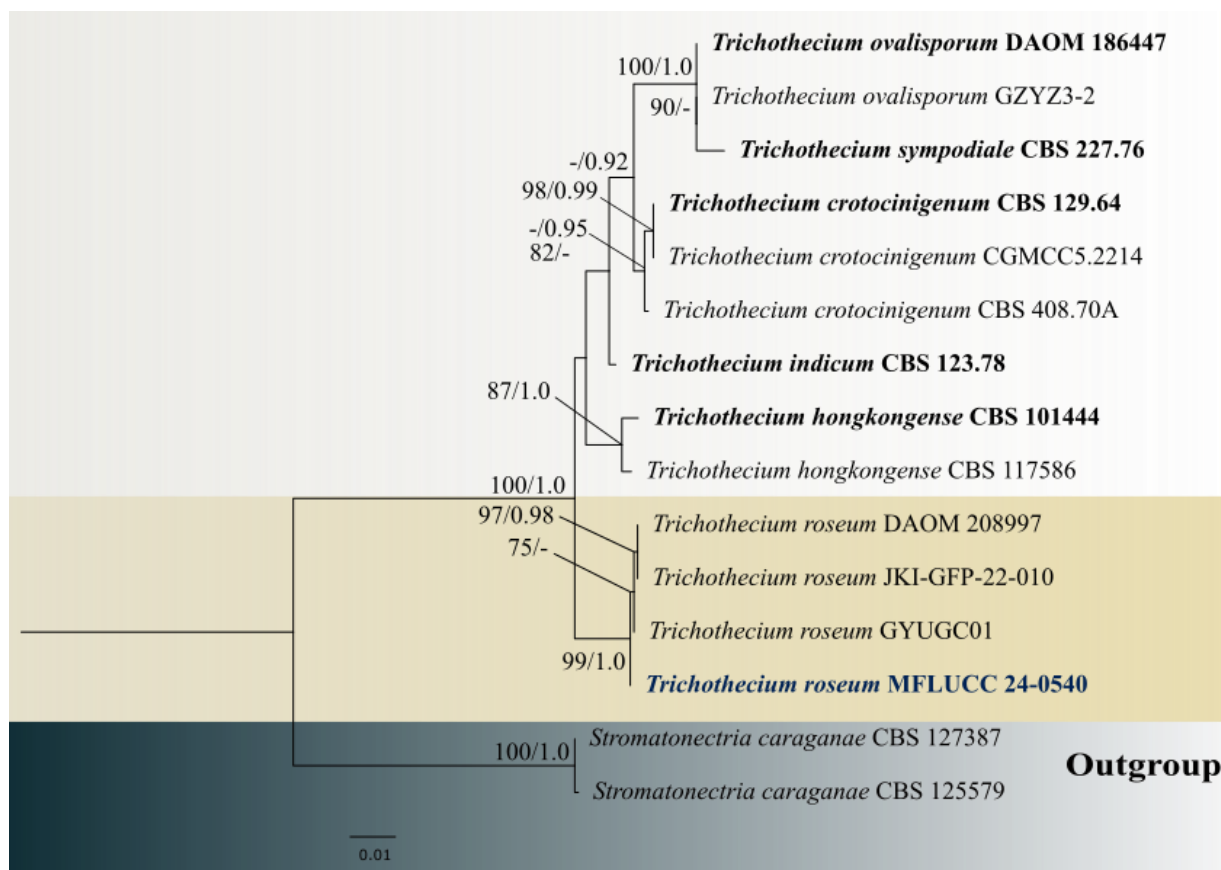


Figure 60 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, and LSU sequence data of *Trichothecium*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Fifteen strains are included in the combined analyses which comprised 1,252 characters (ITS = 475, and LSU = 777). The best RAxML tree with a final optimization likelihood value of -2706.902309 is presented. The matrix had 139 distinct alignment patterns, with 14.39% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.228017, C = 0.270026, G = 0.298204, T = 0.203753; substitution rates AC = 2.102218, AG = 2.106836, AT = 2.085904, CG = 1.759619, CT = 8.853385, GT = 1.000000; gamma distribution shape parameter α = 0.191047. In the Bayesian analysis, average standard deviation of split frequencies at the end of 1,000,000 MCMC generations was calculated as 0.004002. The evolutionary models TIM2+G, and TrN+G were applied to combined ITS, and LSU sequence data respectively. Bootstrap support values for ML greater than or equal to 75% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Stromatonectria caraganae* (CBS 127387 and CBS 125579). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Trichothecium roseum (Pers.) Link, Mag. Gesell. naturf. Freunde, Berlin 3, 18 (1809). Fig. 61

Index Fungorum number: IF152448; Facesoffungi number: FoF07768

Saprobic on *Dalbergia cultrata* woody litter. Sexual morph: Undetermined. Asexual morph: Colonies on the natural substrate, whitish-salmon becoming rosy, scattered. *Conidiophores* 96–198 × 2.7–4.1 μm ($\bar{x}$ = 144 × 3.4 μm , n = 20), simple or branched, hyaline, septate. *Conidiogenous cells* not observed. *Conidia* 10.2–19 × 5–10.8 μm ($\bar{x}$ = 14.4 × 7.6 μm , n = 30; L/W ratio = 1.9), retrogressive modes of conidial development, produced in basipetal chains, hyaline to sub-hyaline, aseptate at immaturity, 1-septate at maturity, slightly constricted at the septum, ellipsoidal to pyriform, mostly obliquely prominent truncated basal scar, abruptly narrowed toward base, rounded at apex, smooth to verrucous, thick-walled. *Chlamydospores* when present hyaline, frequently in intercalary position, smooth-walled.

Culture characteristics – Conidium germinated on PDA within 24 h and a germ tube emerged from one end cell. Colonies on PDA reached 4–5 cm diam. after 9 days at room temperature (25–28 °C), suede-like to powdery, umbonate, with white ring at periphery, upper surface white, reverse yellow at center, buff at periphery.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Dalbergia cultrata* (Fabaceae), 26 March 2022, N. Afshari, 6C1T3R1a (MFLU 24-0413); living culture MFLUCC 24-0540.

GenBank numbers – ITS = PQ800245, LSU = PV072600.

Known hosts and distribution – *Trichothecium roseum* has a cosmopolitan distribution and is associated with different hosts (Farr & Rossman 2025). This study presents the first report of *T. roseum* on *Dalbergia cultrata* from Thailand.

Notes – *Trichothecium roseum* (MFLUCC 24-0540) clustered in a clade containing three strains of *T. roseum* (DAOM 208997, JKI-GFP-22-010, GYUGC01) with combined ITS, and LSU sequence data (Fig. 60). The characteristics of our strain are consistent with the characters of *T. roseum* as previously documented (Kwon et al. 2010, Oh et al. 2014, Lin et al. 2016, Harishchandra et al. 2023). *Trichothecium roseum* is an important post-harvest fungus that causes pink rot and white stain disease in many fruits and vegetables globally; it is also important due to its ability to produce mycotoxins (Harishchandra et al. 2023). This fungus is also associated with decaying plant material, and can also be found from soil (Domsch et al. 1993). *Trichothecium roseum* was reported from many different plant hosts worldwide (Farr & Rossman 2025). Therefore, we propose *T. roseum* (MFLU 24-0413) as a new host record on dead *Dalbergia cultrata* wood.

***Stachybotryaceae* L. Lombard & Crous**

Stachybotryaceae was established by Crous et al. (2014a). Subsequently, Lombard et al. (2016) revised this family based on morphological characteristics and molecular analyses of combined LSU, ITS, *rpb2*, *cmdA*, *tef1-α*, and *tub2* sequence data. Hyde et al. (2024a) reported 41 genera within this family.

***Striaticonidium* L. Lombard & Crous**

Index Fungorum number: IF816042; Facesoffungi number: FoF05582

All *Myrothecium* species with striate conidia were synonymised under *M. cinctum* based on the similarity in marginal ornamentation and conidial dimensions (Tulloch 1972). Subsequently, Nag Raj (1993) synonymised *M. cinctum* under *Hymenopsis ellipsospora*. Lombard et al. (2016) preserved the epithet “*cinctum*” for the type species of *Striaticonidium* and designated an epitype. Therefore, *Striaticonidium* was introduced as an asexual genus to accommodate myrothecium-like species (Lombard et al. 2016). Nine species are known in this genus (Lombard et al. 2016, Crous et al. 2017, Dong et al. 2025). *Striaticonidium* is characterized by synnematosus or sporodochial conidiomata or simple conidiophores. Synnemata are cylindrical to pyriform, comprising bundles of parallel, longitudinal, compacted hyphae; sporodochia stromatic, superficial, scattered or gregarious, oval or irregular in outline, with a white to grey setose fringe; stroma hyaline of *textura globulosa* or *textura angularis* cells; conidiophores macronematous, hyaline, solitary or rarely in groups; setae short, septate, sinuous, subhyaline to olivaceous green, and verrucose; conidiogenous cells phialidic, hyaline, smooth, cylindrical to subcylindrical; and conidia aseptate, olivaceous green to brown, fusiform to ellipsoidal, longitudinally striate. In this study, we introduce *Striaticonidium chiangraiense* as a novel species on *Nayariophyton zizyphifolium* woody litter from Thailand.

***Striaticonidium chiangraiense* N. Afshari, Lumyong & K.D. Hyde, sp. nov.**

Fig. 63

Index Fungorum number: IF904753; Facesoffungi number: FoF17233

Etymology – The specific epithet is derived from Chiang Rai, location where the holotype was collected.

Holotype – MFLU 24-0469



Figure 61 – *Trichothecium roseum* (MFLU 24-0413, a new host record). Whitish-salmon conidial mass on *Dalbergia cultrata* woody litter. b, c Colonies on PDA (front and reverse). d–h Conidiophores, conidiogenous cells, and conidia. i–n Conidia. o A germinated conidium. Scale bars: a = 1 mm, d–h, o = 20 µm, i–n = 10 µm.

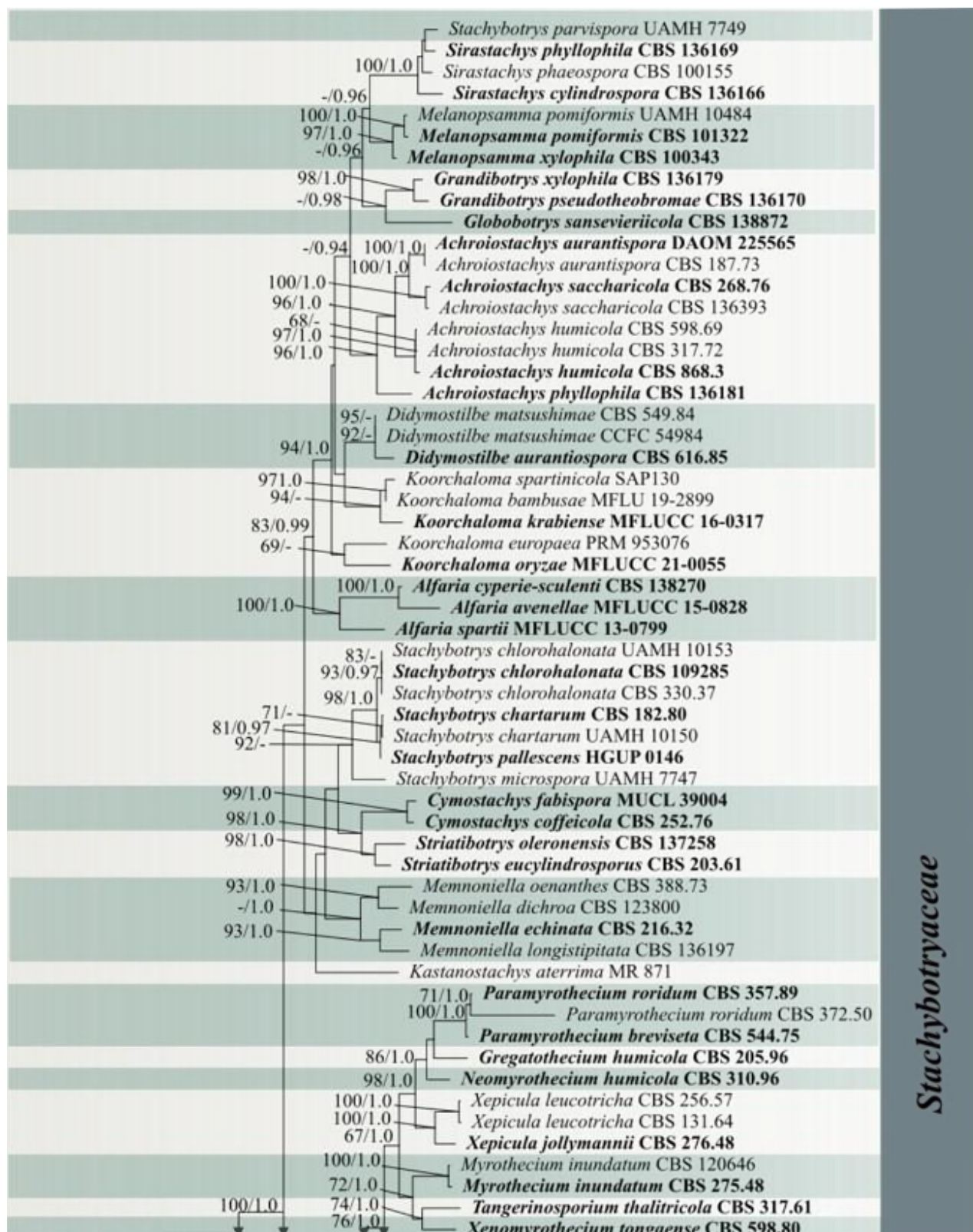


Figure 62 – Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *rpb2*, and *tub2* sequence data of *Striaticonidium* and other genera in *Stachybotryaceae*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Eighty-eight strains are included in the combined analyses which comprised 2,501 characters (ITS = 588, LSU = 827, *rpb2* = 721, and *tub2* = 365). The best RAXML tree with a final optimization likelihood value of -30492.592453 is presented. The matrix had 1,132 distinct alignment patterns, with 19.27% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242211, C =

0.262148, G = 0.280472, T = 0.215169; substitution rates AC = 1.577535, AG = 4.119297, AT = 1.403329, CG = 1.002381, CT = 7.199957, GT = 1.000000; gamma distribution shape parameter α = 0.205299. In the Bayesian analysis, average standard deviation of split frequencies at the end of 15,000,000 MCMC generations was calculated as 0.004291. The evolutionary models TIM2+I+G, TIM2+I+G, GTR+I+G, and TPM2uf+G were applied to combined ITS, LSU, *rpb2*, and *tub2* sequence data respectively. Bootstrap support values for ML greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Fusarium sambucinum* (CBS 146.95) and *Calonectria ilicicola* (CBS 190.50). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

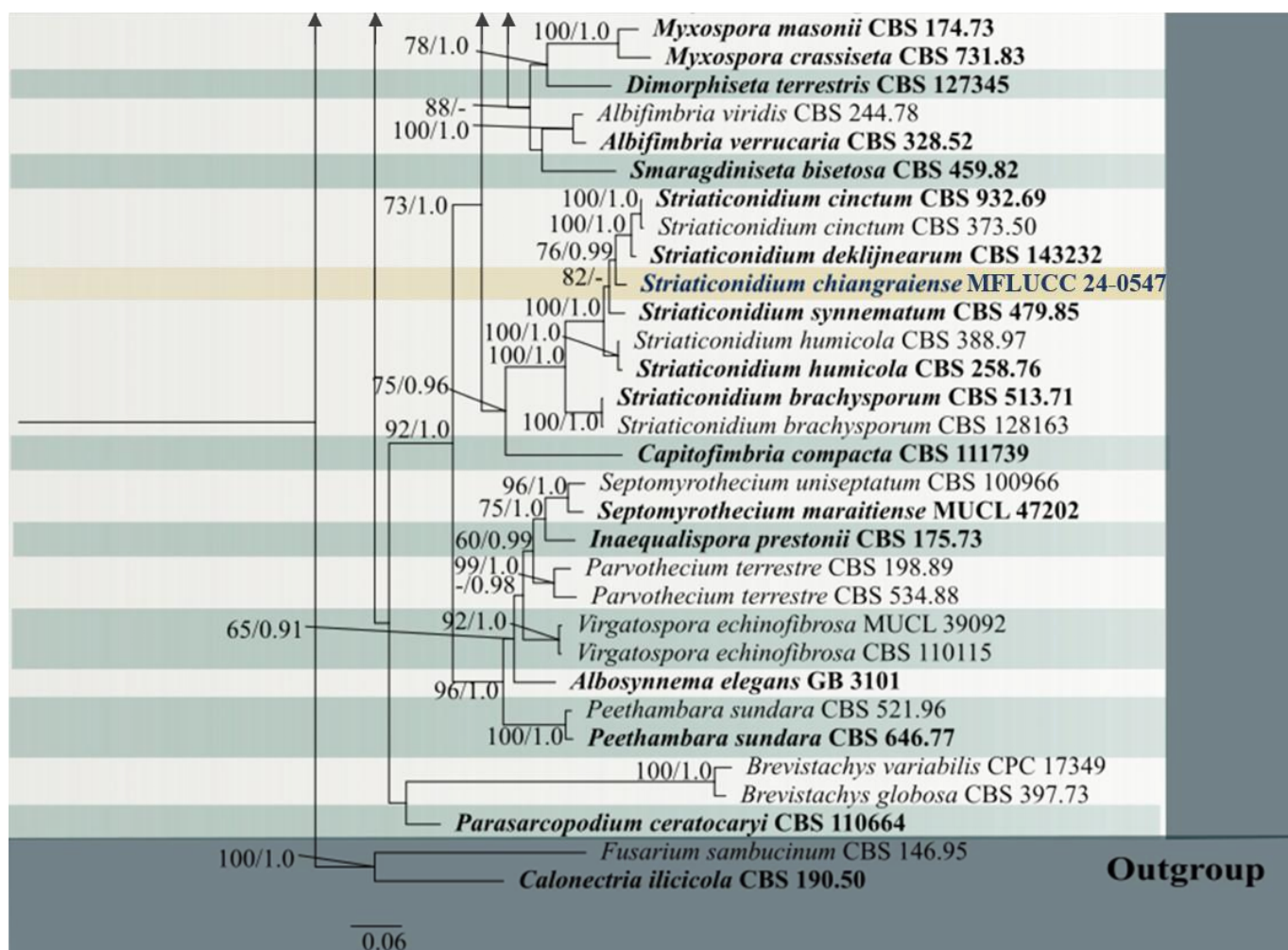


Figure 62 – Continued.

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 238–400 μm diam., sporodochia, shallow-cupulate, oval to circular, occasionally irregular, mostly scattered, solitary, formed of loosely arranged hyphae arising from a compact or pseudoparenchymatous base, terminating in a dense disk-like layer, an olivaceous green to black surrounded by a white to grey edge of hyphae. *Setae* 12.5–20.5 μm $\times$ 2.6–3.7 μm , sinuous, verrucose, unbranched, subhyaline to olivaceous green, apically blunt. *Conidiophores* 6–17.5 $\times$ 1.8–3 μm ($\bar{x}$ = 2.5 $\times$ 11.5 μm , n = 20), unbranched, arising from the basal stroma, hyaline, septate, smooth-walled, primary and secondary branches not observed. *Conidiogenous cells* 4.5–11.5 $\times$ 1.6–3 μm ($\bar{x}$ = 7 $\times$ 2.1 μm , n = 20), phialidic, clavate to cylindrical to doliiform, hyaline, smooth to slightly verrucose, straight to slightly curved or bent at the upper third, with periclinal thickenings. *Conidia* 3.8–7.8 $\times$ 2.7–4.1 μm ($\bar{x}$ = 6 $\times$ 3.4 μm , n = 30; L/W ratio = 1.8), fusiform to ellipsoidal, occasionally

spherical at immaturity, aseptate, hyaline olivaceous green at maturity, with a guttule at each end, longitudinally finely striate, thick-walled.

Culture characteristics – Conidium germinated on PDA within 24 h and germ tube emerged from one or both ends of conidium. Colonies on PDA reaching 3.5–4 cm diam. after one week at room temperature (25–28 °C), irregular, wrinkled, curled, medium sparse, undulate at margin, flat, at upper surface: white, reverse yellow

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 26 March 2022, N. Afshari, 1C1T3R3b (MFLU 24-0469, holotype); ex-type living culture MFLUCC 24-0547.

GenBank numbers – ITS = PQ800260, LSU = PV072611, *tub2* = PX739620.

Notes – In our phylogenetic study *S. chiangraiense* (MFLUCC 24-0547) constitutes a single lineage between ex-types of *S. dekljnearum* (CBS 143232) and *S. synnematum* (CBS 479.85) with 76% ML bootstrap support and 0.99 PP value (Fig. 62). Based on a BLASTn search of *tub2* data of *S. chiangraiense* (MFLUCC 24-0547) in GenBank, it is most similar to a strain of *S. synnematum* (CBS 479.85) and *S. dekljnearum* (CBS 143232) with 95.25% and 94.26% identity, respectively. Morphologically, *S. chiangraiense* (MFLU 24-0469) fits well within the genus; however, *S. chiangraiense* (MFLU 24-0469) differs from *S. synnematum* in conidiomata type (sporodochia vs. synnemata). *Striaticonidium chiangraiense* (MFLU 24-0469) can be distinguished from *S. dekljnearum* (culture morphology) by having darkly pigmented setae, shorter conidiophores and conidiogenous cells (6–17.5 µm vs. 10–24 µm; and 4.5–11.5 µm vs. 8–15 µm). Also, conidia have guttules and they are darker, shorter and wider than those of *S. dekljnearum* ($\bar{x} = 3.4 \times 6 \mu\text{m}$, vs. $\bar{x} = 7 \times 2 \mu\text{m}$) (Lombard et al. 2016, Crous et al. 2017). *Striaticonidium dekljnearum* was reported from soil in The Netherlands (Crous et al. 2017), while we report *S. chiangraiense* (MFLUCC 24-0547) from dead wood of *Nayariophyton zizyphifolium* in Thailand. Therefore, based on morphology and phylogeny we introduce *S. chiangraiense* as a new species.

Pisorisporiales Réblová & J. Fourn.

Pisorisporiaceae Réblová & J. Fourn.

Pisorisporiaceae was established by Réblová et al. (2015a) with *Pisorisporium* as the type genus and is known only from its sexual morph. The members of this family are characterized by non-stromatic, immersed to superficial, papillate or with a long central neck ascomata. Unitunicate, 8-spored, cylindrical-clavate asci, and fusiform to cylindrical, hyaline, transversely multiseptated ascospores. Currently, this family accommodates *Achroceratosphaeria* and *Pisorisporium* (Hyde et al. 2024a).

Pisorisporium Réblová & J. Fourn.

Index Fungorum number: IF810340; Facesoffungi number: FoF01287

Réblová et al. (2015a) described *Pisorisporium* to house *P. cymbiforme* (as the type species) and *P. glaucum* which was collected on decaying wood submersed in fresh water, based on combined sequence data from LSU, SSU, and *rpb2* genes. The asexual morph of this genus is unidentified, and conidia were not produced *in vitro* or on a natural substrate. *Pisorisporium* has astromatic, minute, black, immersed to superficial perithecial ascomata, the outer ascomatal wall is carbonaceous, grading outwards into 2–3 layers of subhyaline to pale brown, polyhedral to angular cells, fragile, cylindrical, persistent paraphyses, unitunicate, persistent asci with an amyloid apical annulus and hyaline, fusiform, cymbiform to cylindrical, and multiseptate, hyaline ascospores with conspicuous guttules (Réblová et al. 2015a). In this study, we introduce *Pisorisporium nayariophyti* as a novel species on *Nayariophyton zizyphifolium* woody litter from Doi Tung National Park, Thailand.

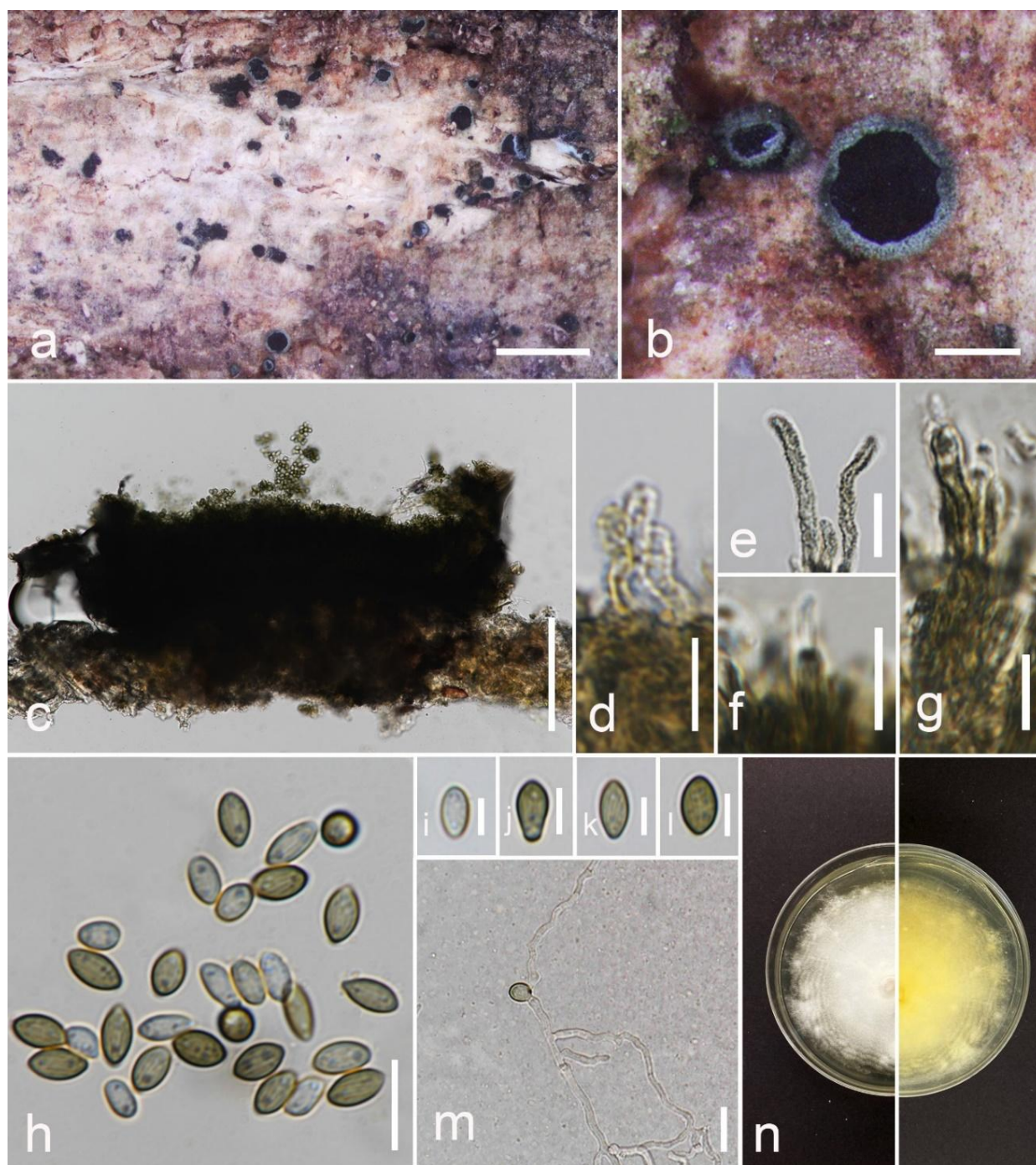


Figure 63 – *Striaticonidium chiangraiense* (MFLU 24-0469, holotype). a, b Sporodochia on *Nayariophyton zizyphifolium* woody litter. c Section through the sporodochia. d, e Setae. f, g Conidiophore and conidiogenous cells. h–l Immature and mature conidia. m A germinated conidium. n Colony on PDA (front and reverse). Scale bars: a = 1 mm, b = 200, μm , c = 100, μm , m = 20 μm , d–h = 10 μm , i–l = 5 μm .

Pisorisporium nayariophyti N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 65

Index Fungorum number: IF904754; Facesoffungi number: FoF17234

Etymology – Referring to the host genus “*Nayariophyton*”, from which the holotype was isolated.

Holotype – MFLU 24-0471

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph *Ascomata* 193.5–208 μm high, 120–156 μm wide ($\bar{x}$ = 202 $\times$ 136 μm , n = 5), nonstromatic, semi-immersed to superficial, mostly solitary or in small groups, subglobose, membranaceous, subhyaline to dark brown, standing

or obliquely to horizontally, papillate, ostiole central. *Peridium* 22.5–39 µm wide, slightly thicker in the neck, thick-walled, composed of pale brown cells of *textura angularis*. *Paraphyses* 1.3–2.7 µm wide ($\bar{x}$ = 1.7 µm, n = 30) with abundant, hyaline, septate, unbranched the same length as asci. *Asci* (102–)112–172(–182) × 8–11.5 µm ($\bar{x}$ = 140.3 × 9.7 µm, n = 20), unitunicate, 8-spored, cylindrical-clavate, straight to mostly curved, with a J-, apical ring. *Ascospores* 22.3–30 × 3.4–5.6 µm ($\bar{x}$ = 25 × 4.3 µm, n = 25), overlapping, arranged 2-seriately in the ascus fusiform, tapering towards the ends, smooth-walled, hyaline, 3–8-septate, not constricted at the septa, with guttules in each cell. Asexual morph: Undetermined.

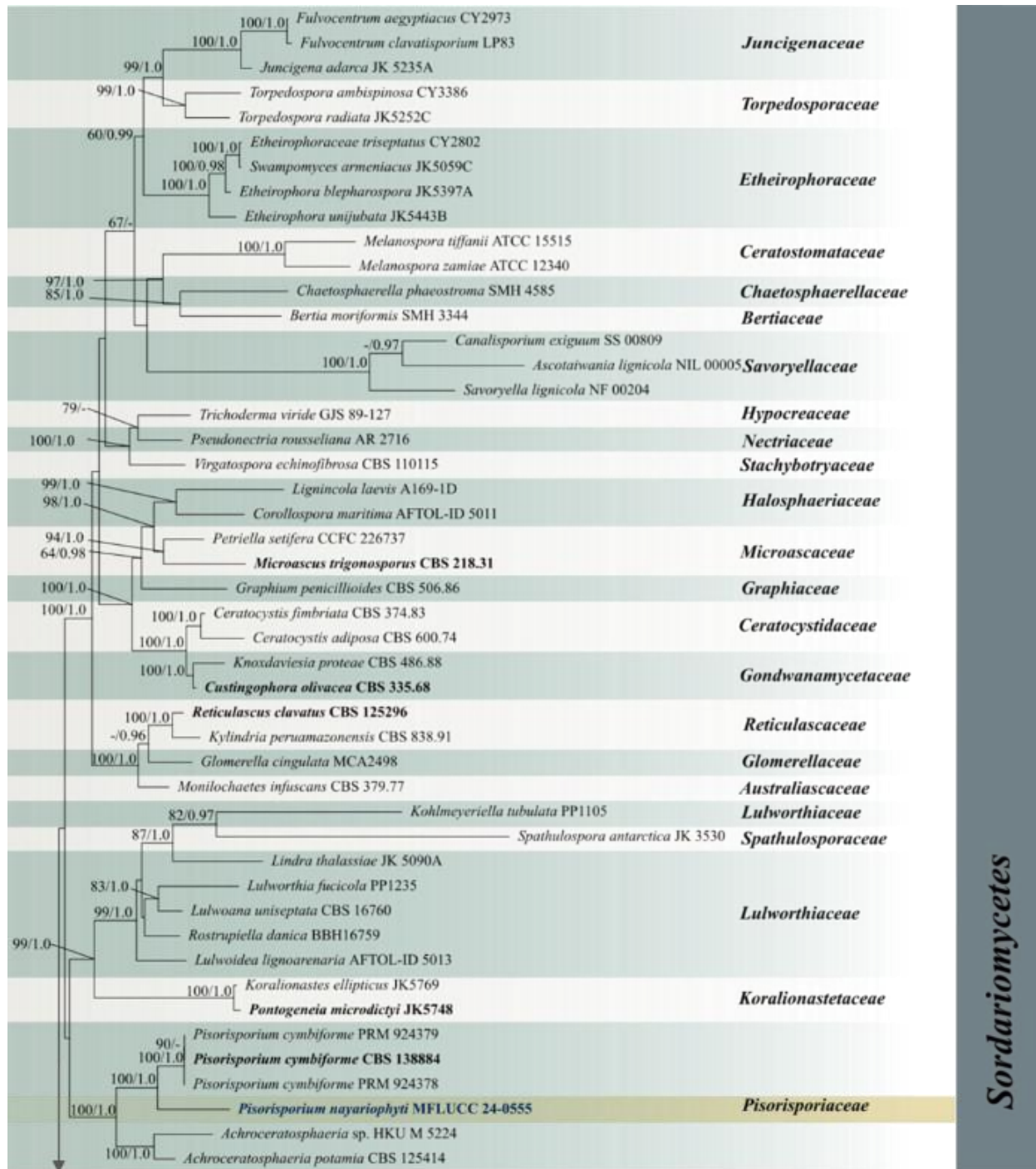


Figure 64 – Phylogram generated from the maximum likelihood analysis based on the combined LSU, *rpb2*, and SSU, sequence data of *Sordariomycetes*. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Eighty strains are included in the combined analyses which comprised 3,801 characters (LSU = 1,111, *rpb2* = 1,064, and SSU = 1,626). The best RAxML

tree with a final optimization likelihood value of -61988.481859 is presented. The matrix had 2,503 distinct alignment patterns, with 27.77% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250339, C = 0.233692, G = 0.283417, T = 0.232552; substitution rates AC = 1.366874, AG = 2.861911, AT = 1.129540, CG = 1.363142, CT = 5.621380, GT = 1.000000; gamma distribution shape parameter α = 0.317442. In the Bayesian analysis, average standard deviation of split frequencies at the end of 10,000,000 MCMC generations was calculated as 0.006457. The evolutionary models GTR+I+G, were applied to combined LSU, and *rpb2*, and TIM2+I+G were applied to SSU sequence data. Bootstrap support values for ML greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Leotia lubrica* (AFTOL-ID 1) and *Microglossum rufum* (AFTOL-ID 1292). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

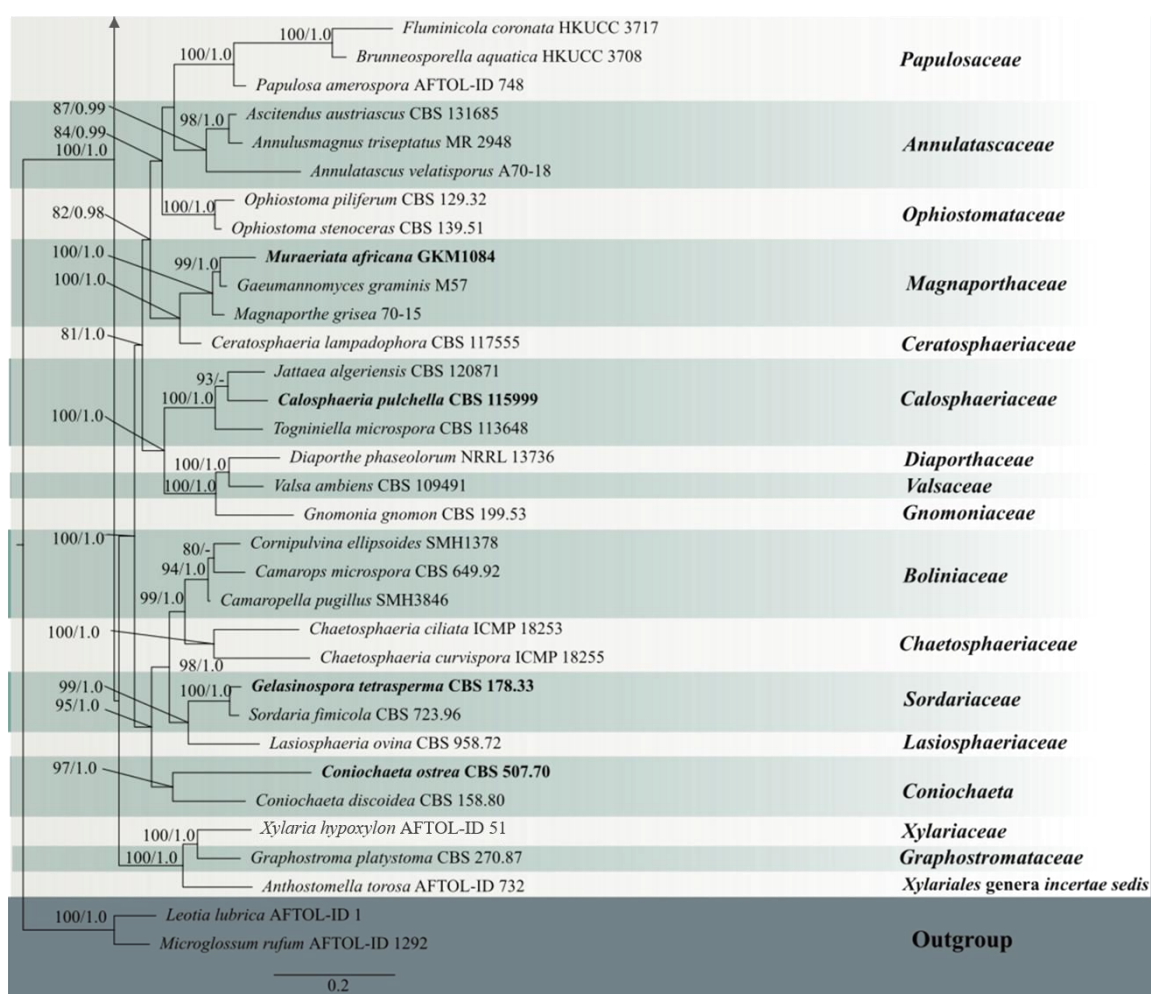


Figure 64 – Continued.

Culture characteristics – Ascospore germinated on PDA within 24 h and a germ tube emerged from both end cells of the ascospore. Colonies on PDA reached 1.5–2 cm diam. after two weeks at room temperature (25–28 °C), irregular, flattened, felty, medium dense mycelium, at upper surface cream with yellow at the edge; reverse pale brown, outwardly with yellow radiations.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 6 June 2022, N. Afshari, 1C2T2R5b (MFLU 24-0471, holotype); ex-type living culture MFLUCC 24-0555.

GenBank numbers – (ITS = PQ800262), LSU = PV072613, *rpb2* = PV138142.

Notes – Our new collection, separately groups with three strains of *Pisorisporium cymbiforme* (CBS 138884, PRM 924379, PRM 924378), with 100% ML bootstrap support and 1.00 PP value (Fig. 64). The holotype (CBS 138884) was isolated from submerged decorticated wood of *Alnus glutinosa*, while two other strains were obtained from the same branch of submerged decorticated wood of *Fraxinus excelsior* in France (Réblová et al. 2015a). Among the two species in this genus, molecular data are lacking for *P. glaucum* (isolated from driftwood of *Acer pseudoplatanus* in Belgium). The LSU and *rpb2* sequences of *Pisorisporium nayariophyti* (MFLUCC 24-0555) differ by 9.9% and 15% (excluding gaps) respectively, from those of *P. cymbiforme* (CBS 138884). *Pisorisporium nayariophyti* differs from the type material of *P. cymbiforme* (CBS 138884), in having membranaceous, subhyaline to dark brown ascomata, wider ascomatal wall (22.5–39 µm vs. (12–)14–26), smaller and narrower asci and ascospores ($\bar{x} = 140.3 \times 9.7 \mu\text{m}$ vs. $\bar{x} = 199.7 \pm 5.4 \times 12.5 \pm 1.2 \mu\text{m}$; and $\bar{x} = 25 \times 4.3 \mu\text{m}$ vs. $\bar{x} = 43.7 \pm 1.9 \times 4.5 \pm 0.3 \mu\text{m}$) respectively, and fewer guttules in the ascospores (Réblová et al. 2015a). Our collection also differs from *P. cymbiforme* in size of asci and ascospores ($\bar{x} = 140.3 \times 9.7 \mu\text{m}$ vs. $\bar{x} = 209.7 \pm 12.8 \times 12.8 \pm 1.2 \mu\text{m}$; and $\bar{x} = 25 \times 4.3 \mu\text{m}$ vs. $\bar{x} = 59.5 \pm 4.5 \times 4.9 \pm 0.3 \mu\text{m}$). Hence, the new isolate is described as a new species.

Xylariales Nannf.

Maharachchikumbura et al. (2016) accepted *Xylariales* as the only order under the subclass *Xylariomycetidae*, which included 22 families.

Xylariaceae Tul. & C. Tul.

Xylariaceae is one of the largest and most diverse family in *Xylariales*. Daranagama et al. (2018) recognized 37 genera, subsequently Hyde et al. (2020b) accepted 32 genera in the family. Recently, new genera such as *Dematophora*, *Albicollum*, *Nigropunctata*, *Oligostoma*, and *Spiririma* have been added to this family and comprises 42 genera and almost 852 species (Hyde et al. 2024a, Li et al. 2024). Most xylariaceous species are saprobes or endophytes, with a few classified as plant pathogens (Rogers 2000, Stadler et al. 2013, Konta et al. 2020, Pourmoghaddam et al. 2022). *Xylariaceae* is characterized by embedded, well-developed ascomata with dark stromata that may be reduced or absent. Unitunicate, cylindrical, and 8-spored, often with amyloid apical ring asci, and pigmented and typically possess germ slits or pores ascospores (Rogers 2000).

Nemania Gray

Index Fungorum number: IF3437; Facesoffungi number: FoF03055

Nemania is known for its rich diversity, with *N. serpens* as the type species (Daranagama et al. 2018, Wendt et al. 2018, Dissanayake et al. 2024). Due to the initial unclear taxonomic description of this genus, taxonomists have frequently considered certain *Nemania* species as synonymous with those of *Hypoxylon*. To illustrate, *Nemania angusta* was previously identified as a synonym of *Hypoxylon angustum* (Miller 1961, Whalley et al. 1983, Ju & Rogers 2002). Subsequent modifications to the generic concept were made by Petrini & Rogers (1986). An inclusive overview of *Nemania* confirmed the existence of 37 species (Granmo et al. 1999, Ju & Rogers 2002). Sánchez-Ballesteros et al. (2000) conducted a phylogenetic analysis using ITS sequences. Hsieh et al. (2005) utilized *tub2* and *act* to assess the phylogenetic relationships among various xylariaceous genera. Tang et al. (2007) subsequently redefined the phylogenetic connections of this genus with related genera using a combined dataset of ITS, and *rpb2*. As a result of these studies, the boundaries of *Nemania* have become clearer, with *Nemania* established as a distinct genus within *Xylariaceae* (Ju & Rogers 2002, Pi et al. 2021). *Nemania* species are recognized by their carbonaceous, multi-peritheciate stromata that are effused-pulvinate in form, with papillate ostioles and displaying a range of internal tissues that can be soft, whiteish, brownish grey, or yellow, and which do not release pigments in 10% KOH. They also have unitunicate cylindrical asci and ascospores with a germ slit (Daranagama et al. 2018). Currently, 78 species have been documented worldwide within this genus (Li et al. 2024). In this study, we introduce *Nemania doitungensis* as a novel species on *Nayariophyton zizyphifolium* woody litter from Doi Tung National Park, Thailand.

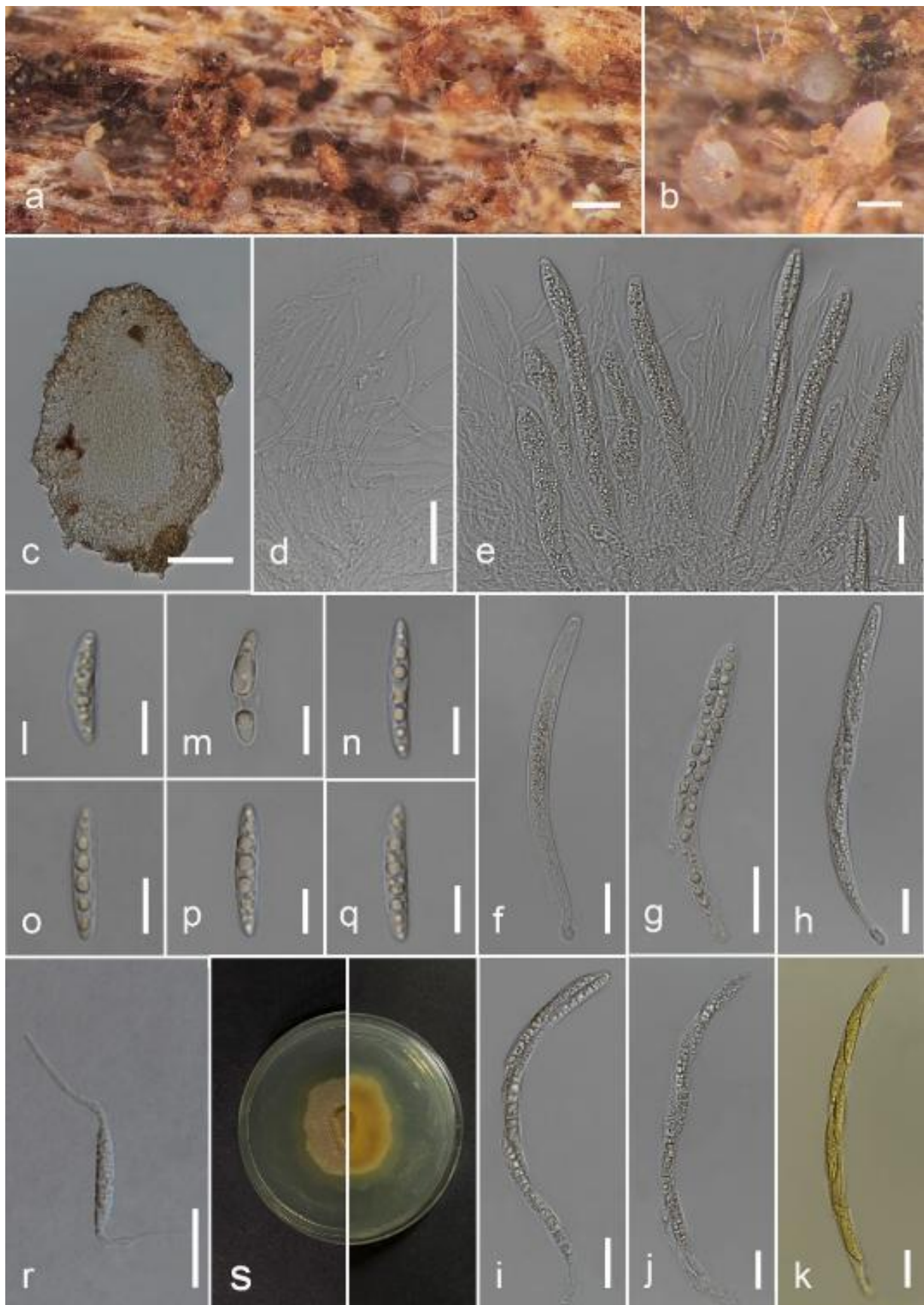


Figure 65 – *Pisorisporium nayariophyti* (MFLU 24-0471, holotype). a, b Appearance of ascomata on *Nayariophyton zizyphifolium* woody litter. c Vertical section of ascoma. d Paraphyses. e–j Asci. k Ascus in Melzer's reagent. l–q Ascospores. r A germinated ascospore. s Colony on PDA (front and reverse). Scale bars: a = 200 μ m, b = 100 μ m, c = 50 μ m, d–k, r = 20 μ m, l–q = 10 μ m.

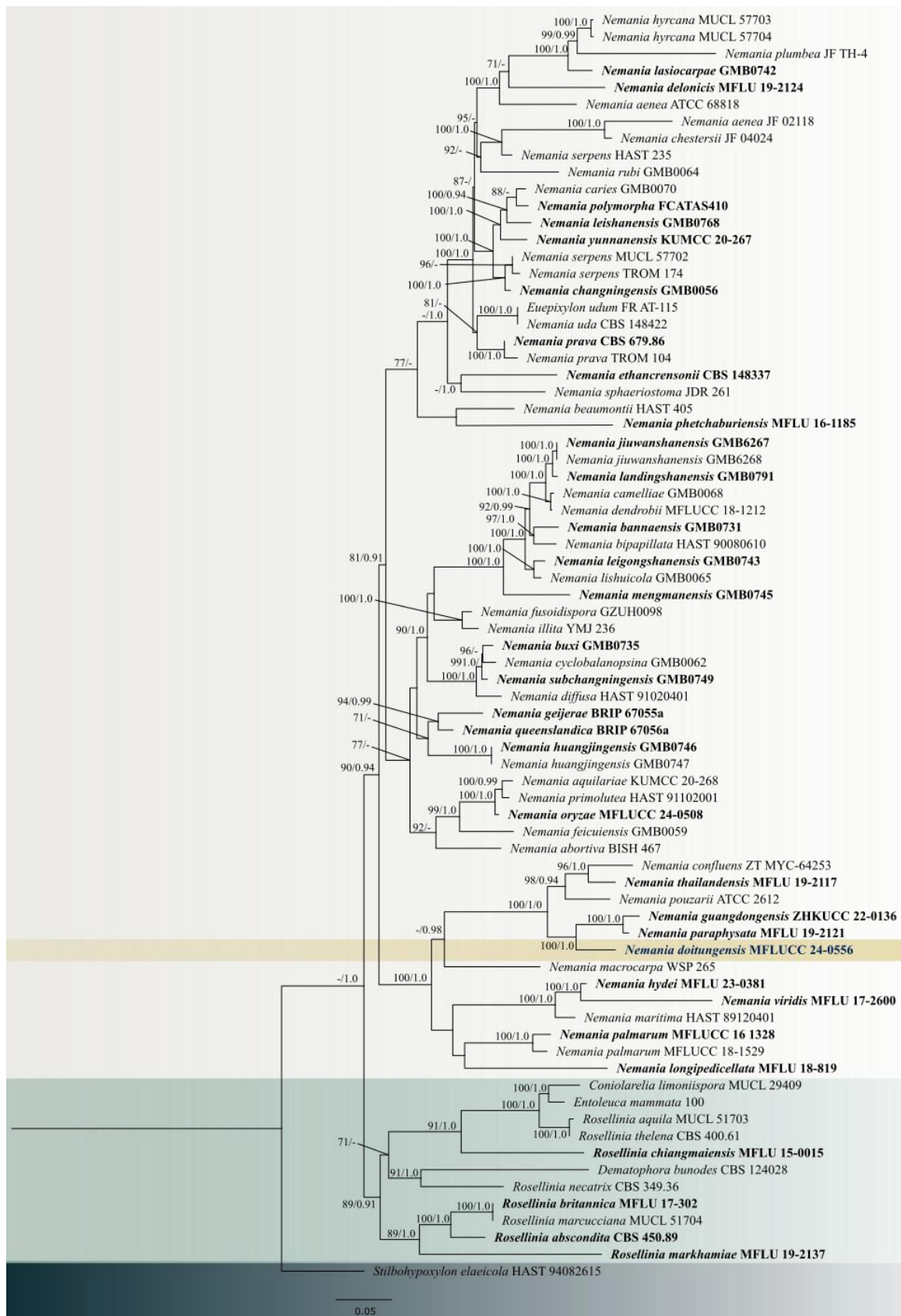


Figure 66 – Phylogram by maximum-likelihood (ML) method generated using IQ-TREE analysis based on the combined ITS, LSU, *rpb2*, and *tub2* sequence data of *Nemania* and closely related genera. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Seventy-five strains are included in the combined analyses which comprised 3,894 characters (ITS = 576, LSU = 841, *rpb2* = 1,082, and *tub2* = 1,395). The best score for log-likelihood of consensus tree

is -43601.140. Selecting individual models TIM2+F+I+G4, K2P+I+G4, TIM3e+I+G4, and TN+F+I+G4 were applied for ITS, LSU, *rpb2*, and *tub2* using BIC. In the Bayesian analysis, average standard deviation of split frequencies at the end of 4,000,000 MCMC generations was calculated as 0.018748. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.90 are given above the nodes. The strain codes are noted after the species names. The tree is rooted with *Stilbohypoxyton elaeicola* (HAST 94082615). Ex-type strains are in bold. The isolate generated in this study is indicated in bold and blue.

Nemanja doitungensis N. Afshari, Lumyong & K.D. Hyde, sp. nov.

Fig. 67

Index Fungorum number: IF904755; Facesoffungi number: FoF17235

Etymology – The epithet refers to “Doi Tung National Park”, the forest from which the fungus was collected.

Holotype – MFLU 24-0473

Saprobic on *Nayariophyton zizyphifolium* woody litter. Sexual morph: *Ascomata* 622–810 µm diam. ($\bar{x}$ = 705 µm, n = 10), visible as sharp black spots on the host surface, spherical, solitary or aggregated, uniperitheciate, superficial, black, carbonaceous, ostiole black, papillate. *Paraphyses* 125.5–181.5 × 2.2–5.2 µm ($\bar{x}$ = 150.8 × 4 µm, n = 25), abundant, branched, septate, longer than asci. *Asci* 81–132 × 7.7–12.4 µm ($\bar{x}$ = 109 × 10.2 µm, n = 20) total length, the spore-bearing parts 68.6–86.6 µm long ($\bar{x}$ = 77.3 µm, n = 10), non-spore bearing apical apparatus 6.1–12.2 µm long ($\bar{x}$ = 9.4 µm, n = 10), unitunicate, cylindrical, 8-spored, mostly uniseriate, with inverted hat-shaped apical ring, bluing in Melzer’s reagent (J^+). *Ascospores* 9–13.5(–15) µm × 6–8.5 µm ($\bar{x}$ = 12 × 7 µm, n = 30), globose to subglobose when immature becoming ellipsoidal and inequilateral with age, narrowly to broadly rounded ends, hyaline becoming olivaceous brown to dark brown at maturity, uni-seriate or rarely bi-seriate, guttulate (mostly 1–3 or rarely more), with straight spore-length germ slit, aseptate, episore smooth, perispore dehiscent in 10% KOH. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 24 h and a germ tube emerged from both ends of the ascospore. Colonies on PDA reached 60 mm diam. after 2 weeks at room temperature (25–28 °C), irregular, dense, flattened, at upper surface white, reverse light yellow.

Material examined – Thailand, Chiang Rai Province, Doi Tung National Park, on dead wood of *Nayariophyton zizyphifolium* (Malvaceae), 6 June 2022, N. Afshari, 1C2T2R3 (MFLU 24-0473, holotype); ex-type living culture MFLUCC 24-0556.

GenBank numbers – ITS = PQ800264, LSU = PV072615, *rpb2* = PV138144, *tub2* = PX739613.

Notes – Phylogenetic analyses based on a multilocus analysis of ITS, LSU, *rpb2*, and *tub2* sequences indicate that *Nemanja doitungensis* (MFLUCC 24-0556) clusters in a well-supported basal lineage to *N. paraphysata* (MFLU 10-2121) and *N. guangdongensis* (ZHKUCC 22-0136), with MP/Bi support values of 100%/1.00 (Fig. 66). The base pair differences between the sequences of ITS, LSU, and *rpb2* of our isolate and *N. paraphysata* (MFLU 10-2121) are 7.5%, 1.1%, 8.3%, respectively; no *tub2* sequence is available for *N. paraphysata*. Morphologically, *N. doitungensis* is similar to *N. paraphysata* and *N. guangdongensis* in size of ascospores and presence of amyloid J^+ apical rings, but it is distinct based on characteristics of the stromata as *N. doitungensis* has spherical ascomata while those of *N. paraphysata* and *N. guangdongensis* are mostly with a broader base. Our isolate also has longer and wider asci compared to *N. paraphysata* and *N. guangdongensis* ($\bar{x}$ = 109 × 10.2 µm vs. $\bar{x}$ = 88.5 × 8.6 µm, and $\bar{x}$ = 88.5 × 8.6 µm, respectively), and wider paraphyses ($\bar{x}$ = 4 µm vs. $\bar{x}$ = 3.5 µm, $\bar{x}$ = 1.6 µm, respectively) (Samarakoon et al. 2022, Senanayake et al. 2023). These findings support the introduction of *N. doitungensis* as a novel species.

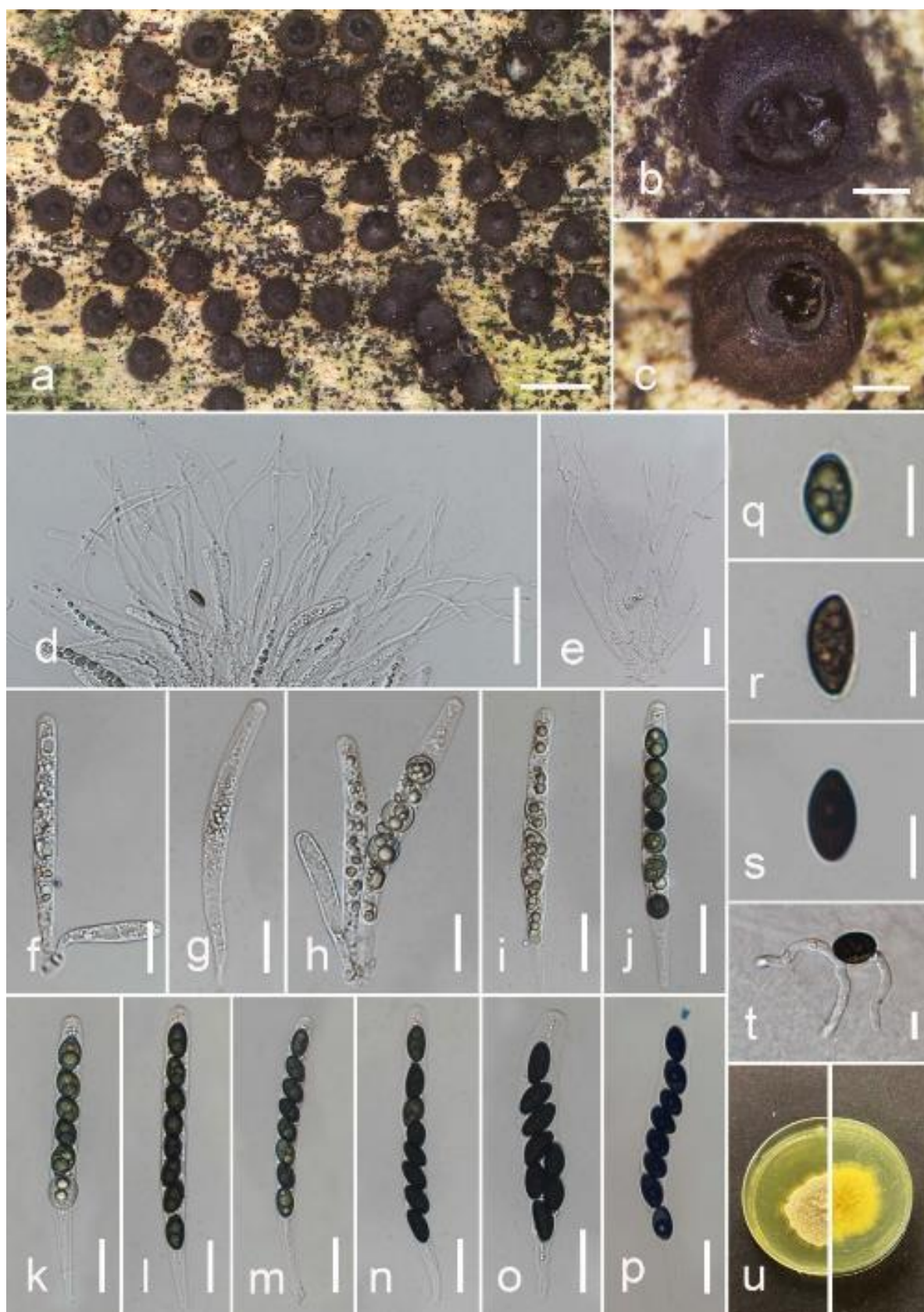


Figure 67 – *Nemanja doitungensis* (MFLU 24-0473, holotype). a Appearance of ascomata on *Nayariophyton zizyphifolium* woody litter. b Longitudinal section of ascoma. c Transverse section of the ascoma. d Asci and paraphyses. e Paraphyses. f–o Asci. p Ascus demonstrating J⁺ reaction in Melzer's reagent. q–s Ascospores. t A germinated ascospore. u Colony on PDA (front and reverse). Scale bars: a = 1 mm, b, c = 200 µm, d = 50 µm, e–p = 20 µm, q–t = 10 µm.

Fungal community composition across different hosts

The analysis of saprobic fungal communities is based on only those strains that could be isolated and sequenced to establish their identities, which limits the results to saprobic species (Table S1). The degree of separation derived from hierarchical clustering based on the Bray-Curtis similarity of fungal species diversity associated with phylogenetically related host levels (order, family, genus, and species) indicates minor compositional differences in fungal community structures ranging between 0.046–0.195 (Fig. 68). The results indicate that similarity among fungal communities does not consistently decline with increasing phylogenetic distance between host plants (Table S2). However, at certain taxonomic levels, higher similarity was observed among closely related taxa, for example, at family level, fungal community similarity between Dipterocarpaceae and Malvaceae belonging to the same order (Bray-Curtis similarity = 0.143) is relatively high compared to Malvaceae and Fabaceae from which are from different orders (Bray-Curtis similarity = 0.091). At genus level, the fungal community similarity between *Dipterocarpus* and *Microcos* from two distinct families is 0.092, that is lower than between *Afzelia* and *Dalbergia* belonging to same family (Bray-Curtis similarity = 0.195). At species level, the fungal community similarity between *Afzelia xylocarpa* and *Dalbergia cana* (both within the Fabaceae family) is relatively higher (Bray-Curtis similarity = 0.146) compared to that between *Afzelia xylocarpa* and *Microcos paniculata* (belonging to different families and orders), which shows a lower similarity value of 0.098. The highest specificity is noted at the genus level, where fungal communities are unique and closely associated with specific host species.

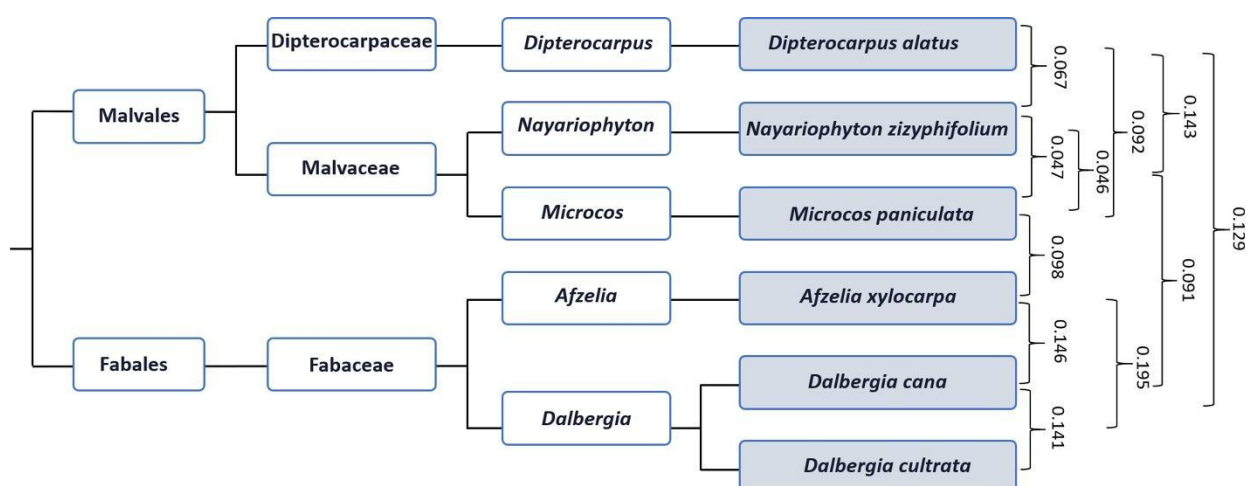


Figure 68 – Degree of separation of fungal community composition within the host phylogenetic hierarchy (order, family, genus, and species) based on Bray-Curtis similarity values. Bray-Curtis similarity value ranges from 0 to 1, where 0 represents complete dissimilarity and 1 complete similarity.

To evaluate fungal diversity across different host taxa, we calculated the Shannon Diversity Index (H'), which considers both species richness and evenness. A Shannon diversity index (H') heatmap was constructed at the fungal species level for the fungi identified using both molecular and morphological methods. The Shannon diversity index was visualized for diversity measurement, with intensity of colour white (no diversity) to dark blue (maximum diversity) (Figs 69–72). The analysis shows that species diversity is distributed across both host orders, although significant number of species show index between 0 to 2 H' values (Fig. 69). A few fungal species evenly distributed across hosts (the higher diversity values of 3 to 4). Fig. 70 compares the Shannon Diversity Index of fungal species across three different tree families. In Fabaceae, fungal species show a broad range of diversity values. Several species display high diversity (values between 2–3). In Malvaceae, fungal species diversity is more uniform with few higher diversities. The majority of species ranging 0.5–

1.5. There are no species reaching the maximum diversity value 3. In Dipterocarpaceae, fungal species demonstrate lower diversity values overall. Most species show values 0–1, with very few reaching moderate diversity. In general, Fabaceae supports higher fungal diversity, with several species achieving Shannon Index values between 2–3. The heat map compares the Shannon Diversity Index of fungal species diversity across five tree genera (Fig. 71). *Dalbergia* and *Afzelia* show higher fungal diversity compared to other tree genera. *Microcos*, *Nayariophyton*, and *Dipterocarpus* exhibit lower fungal diversity, with values between 0–1.5. The Shannon Diversity Index of fungal species diversity across six tree species is shown in Fig. 72. These results indicate the importance of host identity in shaping fungal community structure and suggest that some tree species and genera may act as biodiversity hotspots for fungal taxa.

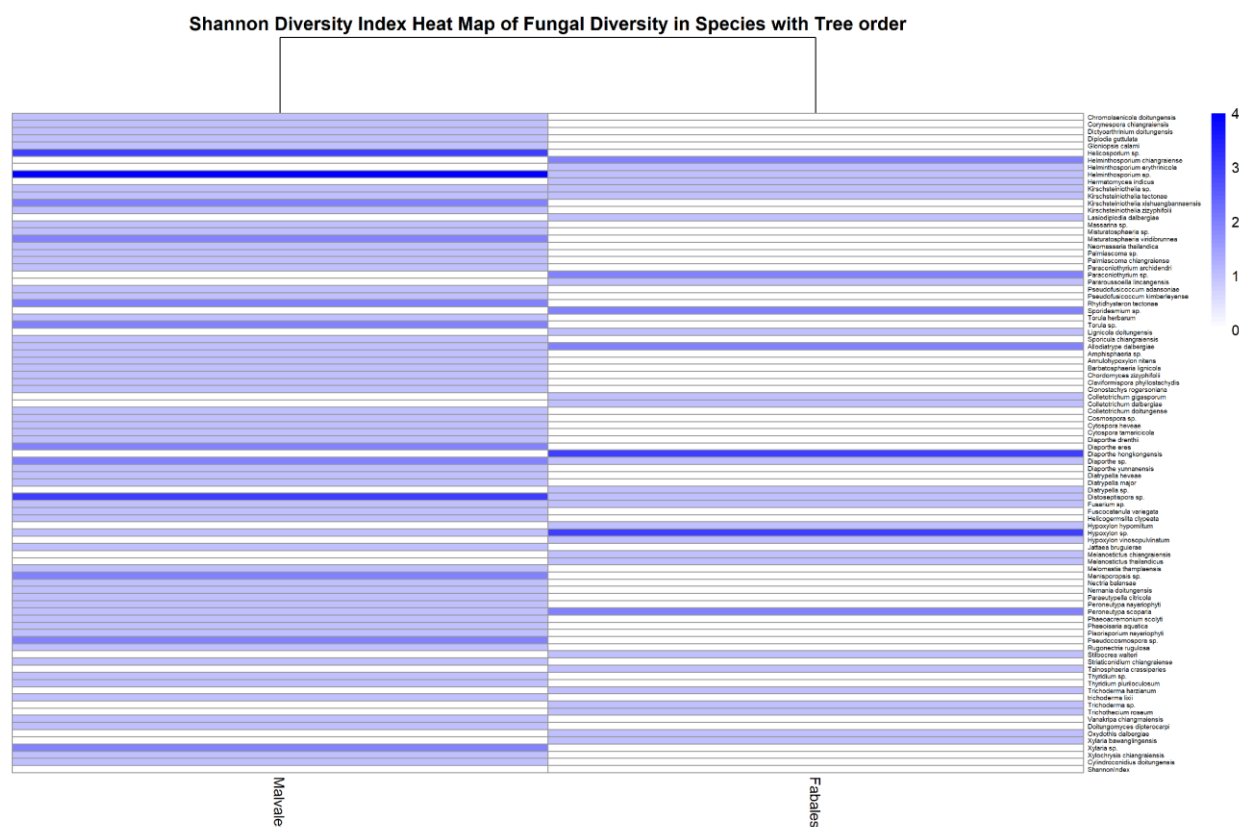


Figure 69 – Shannon diversity index heatmap of fungal species across host tree orders. Shannon diversity index ranges from 0 to 4, where 0 represents no diversity and 4 represents maximum diversity (high-resolution image available in the Supplementary Material).

Fungal community composition based on Jaccard similarity

The Jaccard similarity heatmap is a visual tool that in this research clearly show how fungal species diversity overlaps across different host plants with highlighting the proportion of shared species with colour gradient. The Jaccard similarity coefficient ranges from 0 (yellow) lower similarity and fewer shared taxa, to 1 (Green) shows more shared and overlapped species. This visualization allows us to quickly identify relationships in fungal community composition. The heatmap includes hierarchical clustering, which groups hosts with similar fungal communities together (Figs 73–76). Heatmaps based on the Jaccard similarity index are presented, at the order (Fig. 73), family (Fig. 74), genus (Fig. 75), and host species (Fig. 76) levels. High Jaccard similarity is consistently observed within certain groups at all levels, suggesting that closely related tree orders, families, or genera share fungal communities. Based on this result, a higher proportion of shared fungal species is observed at higher taxonomic levels (order and family). However, this pattern of species overlap is seen across all levels examined.

When comparing the overlap of fungal communities among different host taxonomic levels (Fig. 77), it was revealed that 40 and 11 fungal genera were isolated from Malvales and Fabales, respectively, with 13 genera common to both. At the family level, the composition included 27 (Malvaceae), 10 (Fabaceae), and 9 (Dipterocarpaceae) fungal genera. Six genera are shared among the three plant families, and 4 are shared between Malvaceae and Dipterocarpaceae, Dipterocarpaceae and Fabaceae, as well as between Malvaceae and Fabaceae. Regarding the host genera, 16, 11, 7, 9, and 2 genera were isolated from *Nayariophyton*, *Microcos*, *Dalbergia*, *Dipterocarpus*, and *Afzelia*, respectively, with no intersection among the host genera and only a few members shared between each host genera. Overall, most unique fungal genera were isolated from Malvaceae, while *Nayariophyton* and *Microcos* have the highest number of specific fungal genera, and *Afzelia* possesses the lowest fungal diversity. This relatively limited overlap observed at all taxonomic levels reflects significant differences in the composition of the fungal community and diversity of isolated fungi. In general, the overlap decreases at lower taxonomic levels, with a large proportion of the fungal community being unique to specific host groups.

Variations of woody litter microfungi between wet and dry Seasons

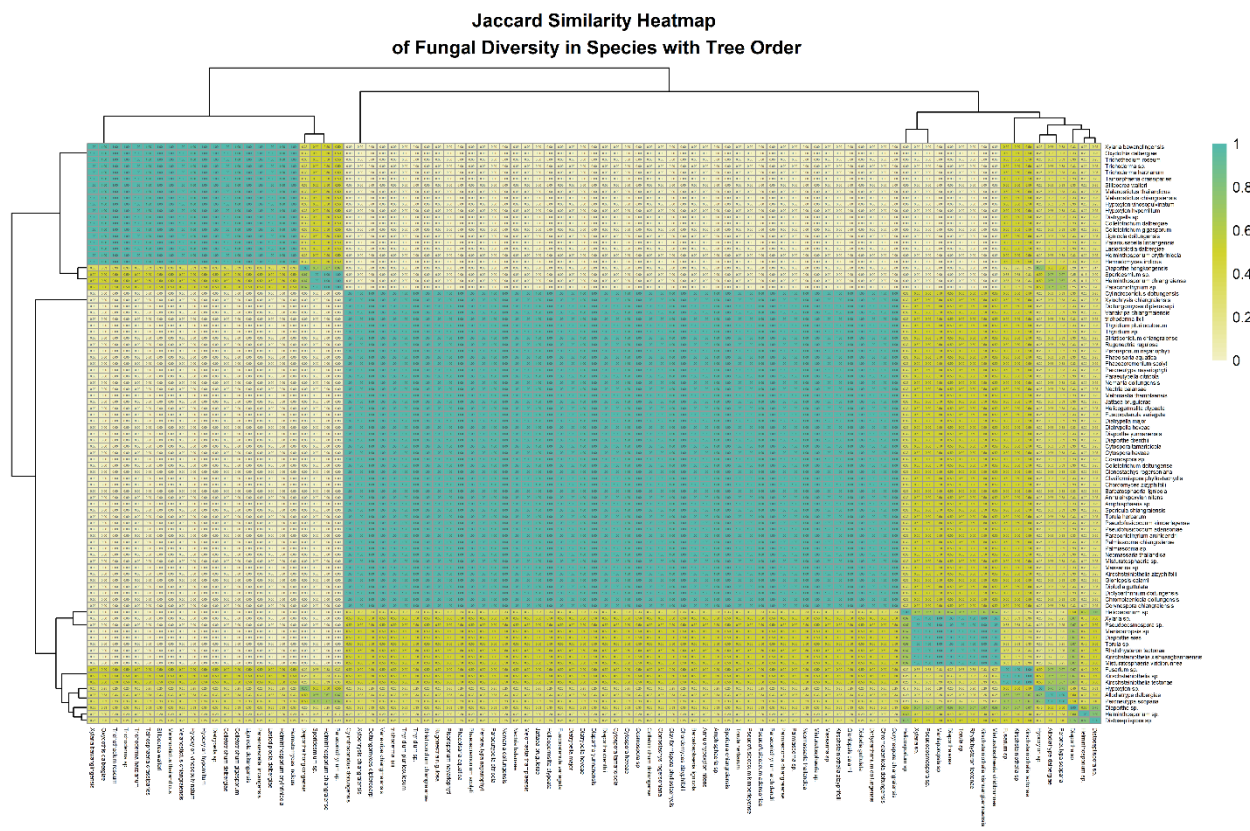


Figure 73 – Jaccard similarity heatmap of fungal species diversity across tree orders (high-resolution image available in the Supplementary Material).

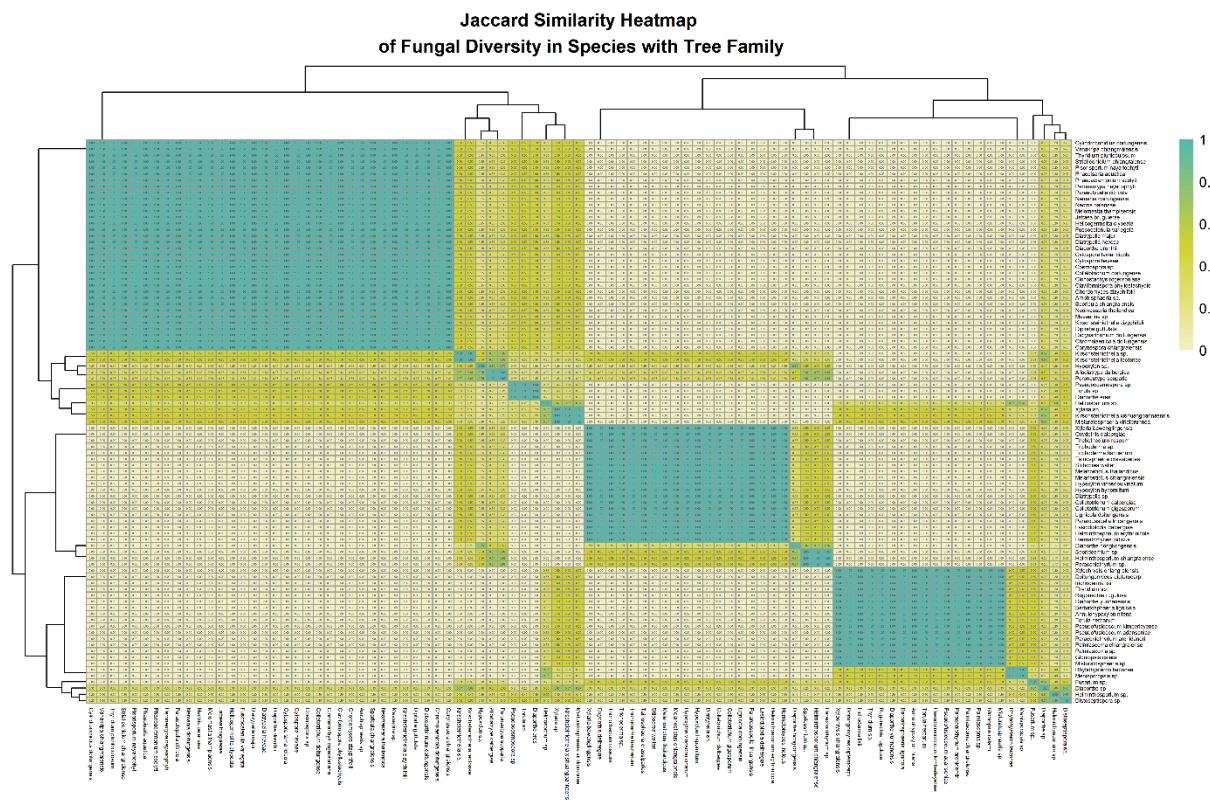


Figure 74 – Jaccard similarity heatmap of fungal species diversity across tree families (high-resolution image available in the Supplementary Material).

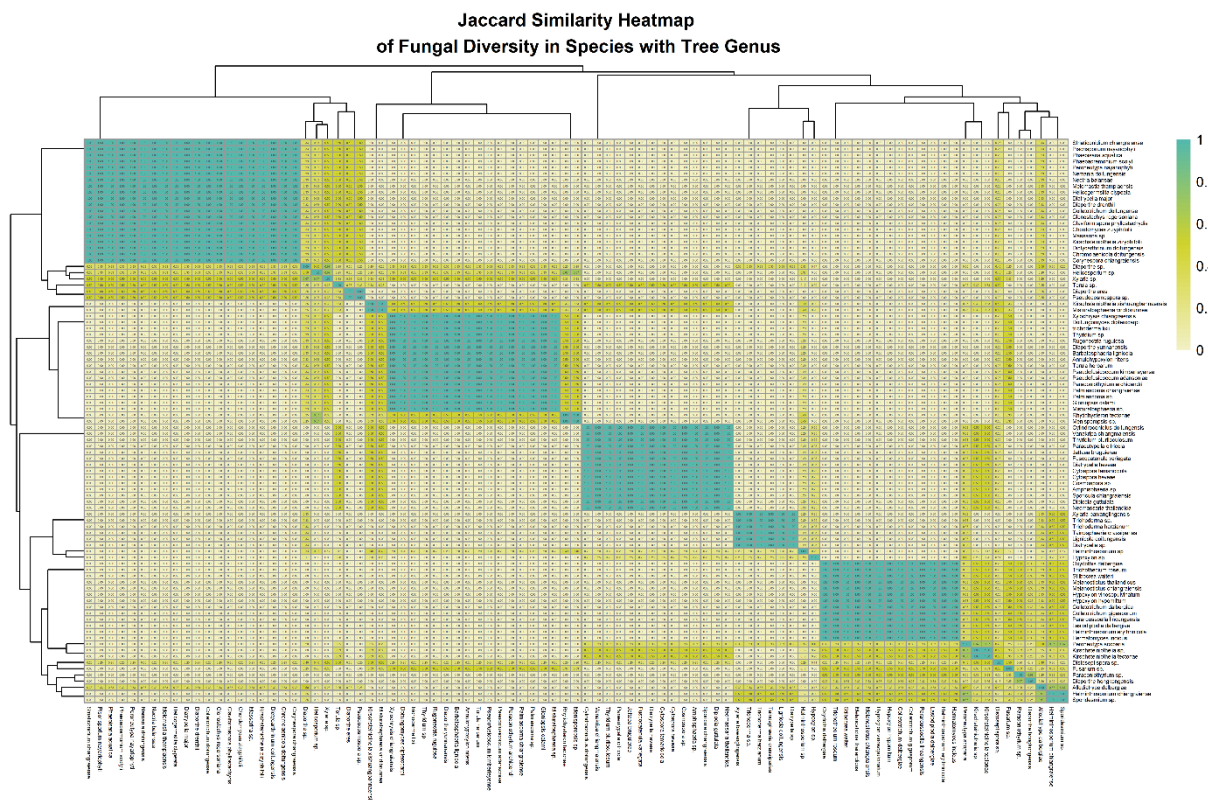


Figure 75 – Jaccard similarity heatmap of fungal species diversity across tree genera (high-resolution image available in the Supplementary Material).

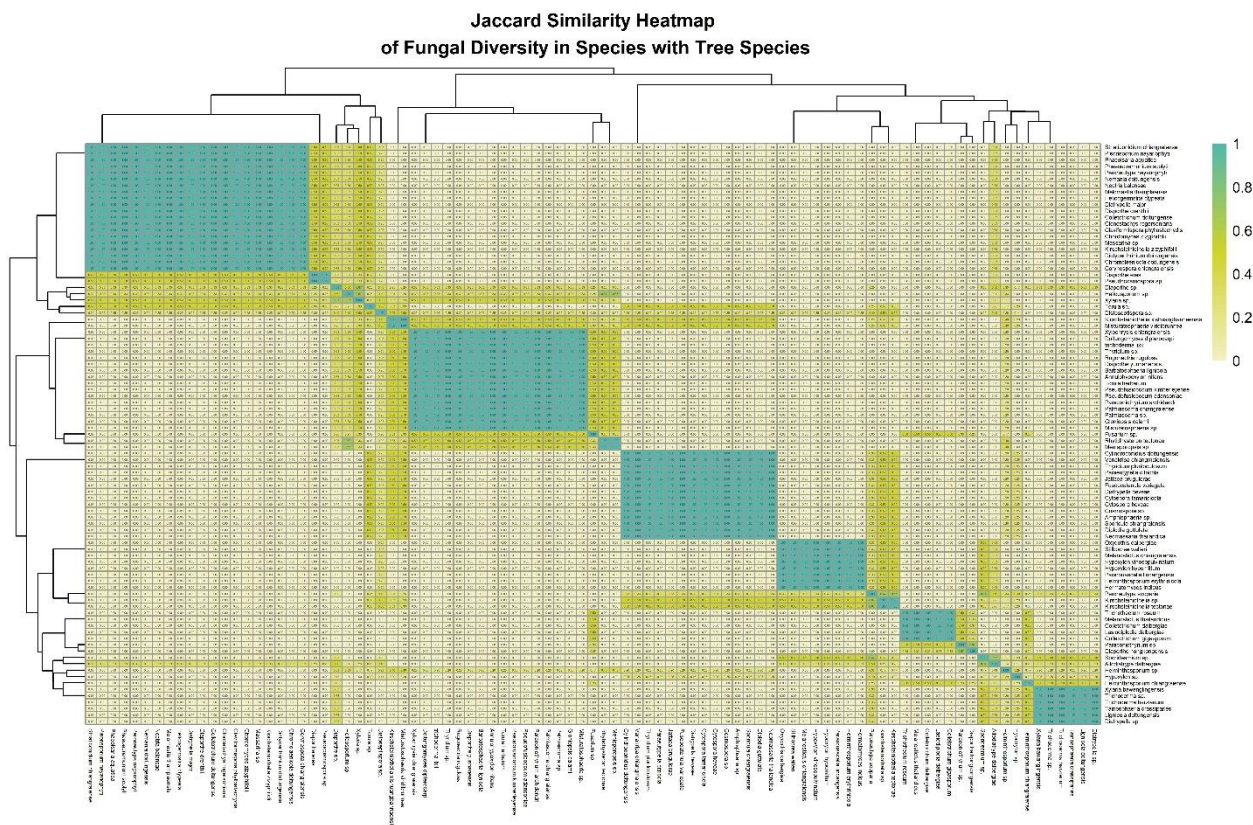


Figure 76 – Jaccard similarity heatmap of fungal species diversity across tree species (high-resolution image available in the Supplementary Material).

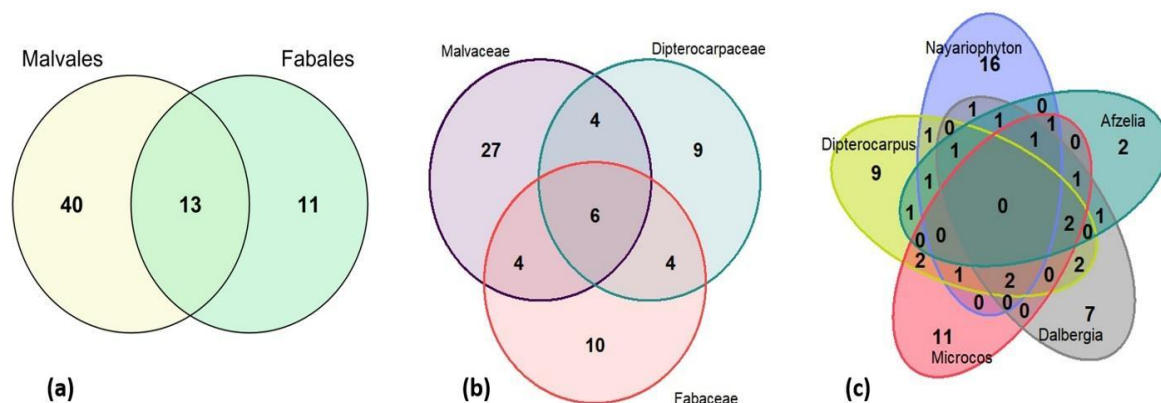


Figure 77 – Venn diagram shows the fungal genera shared between host (a) orders, (b) families, and (c) genera.

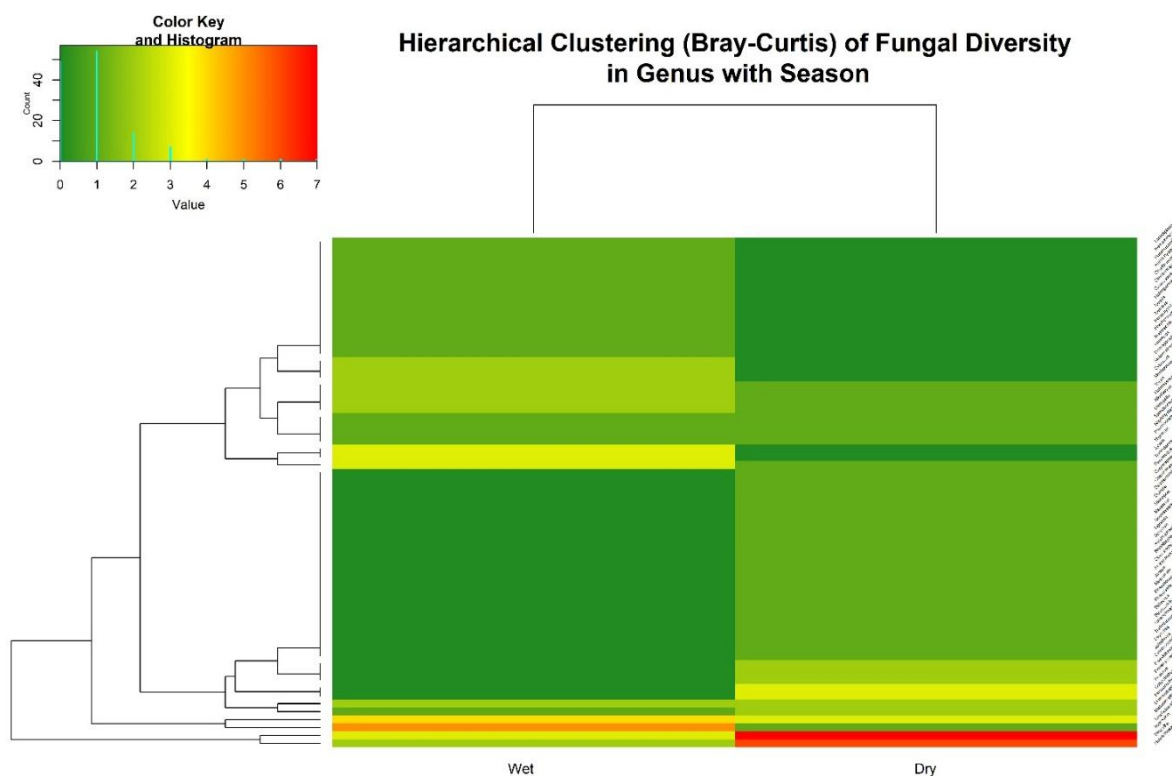


Figure 78 – The heatmap and hierarchical clustering (Bray-Curtis) of fungal genera diversity during dry and wet seasons (high-resolution image available in the Supplementary Material).

Variations of woody litter microfungi across different stages of wood litter decomposition

Comparative analysis of fungal generic diversity across decomposition stages is shown in Fig. 79, and the quantitative details are provided in Table S4. This heatmap presents hierarchical clustering (Bray-Curtis similarity). The histogram in the heatmap illustrates values ranging from 0–5, corresponding to the colour gradient in this dataset. The composition and clustering patterns reveal significant temporal shifts in fungal community structure. In the early-stage, highest fungal diversity was observed with distinct clusters of dominant genera. Several genera, including *Helminthosporium*, *Diaporthe*, *Hypoxyton*, *Peroneutypa*, *Paraconiothyrium*, and *Colletotrichum* exhibit yellow to red intensities, indicating high abundances. The clustering is more complex, with many genera forming distinct groups. In the middle stage, diversity declines with only *Kirschsteiniotelia* and *Diaporthe*

remain prominent, represented by yellow zones. Most genera display green intensities, indicating low relative abundance and less fungal activity. In the late stage, clustering becomes simplified, with most genera displaying low relative abundance.

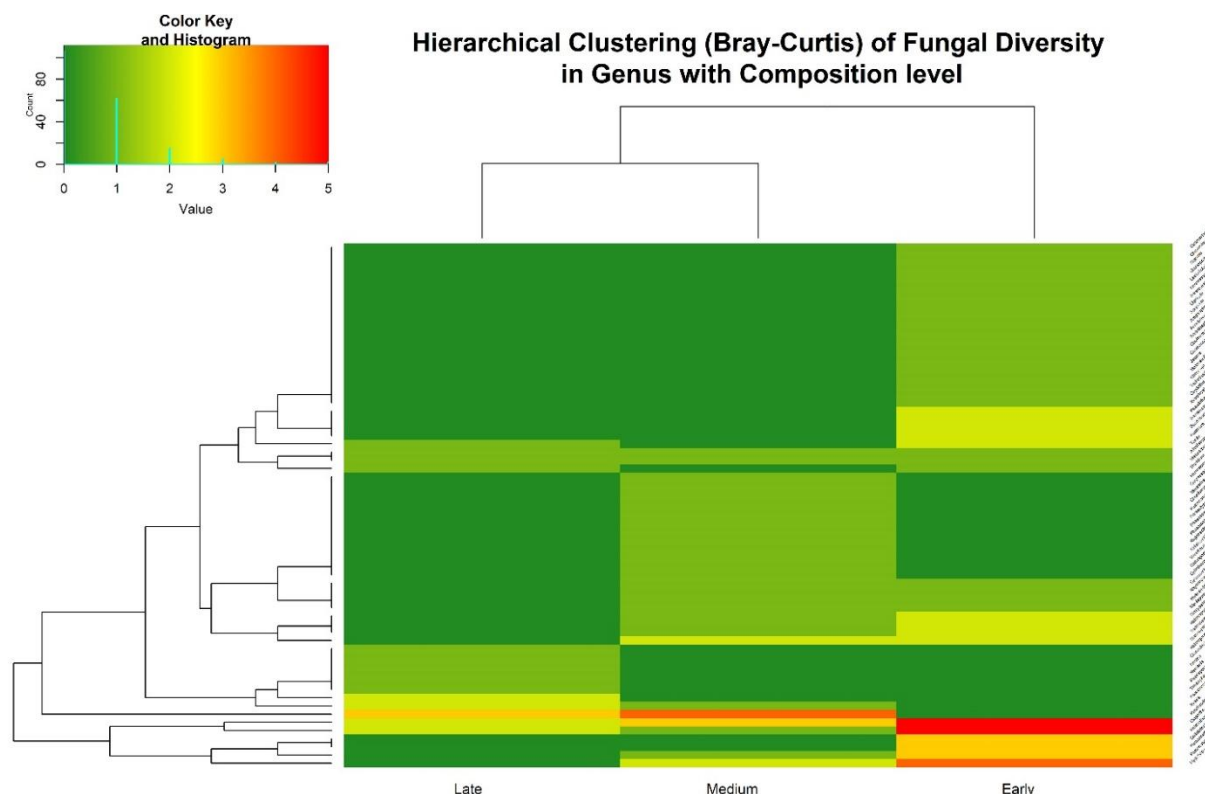


Figure 79 – The heatmap and hierarchical clustering (Bray-Curtis) of fungal genera diversity during different decomposition levels (high-resolution image available in the Supplementary Material).

DISCUSSION

Fungi are the most dominant microorganisms and are important degraders of dead wood (Bailey et al. 2002). Furthermore, the diversity and composition of microfungi isolated from dead wood underscore the ecological significance of these fungi in wood decomposition (Stokland et al. 2012, Purahong et al. 2019). This research contributes to understanding woody litter microfungal diversity in a tropical conserved ecosystem (Doi Tung National Park).

During the study, one hundred and twenty-five fungal isolates were identified using morphological characteristics with DNA-based identification, representing three classes, 24 orders, 45 families, 63 genera, and 91 species. Among these in this study, 14 novel taxa (11 new species, two new genera, and one new family) were described. The exploration of wood-associated fungi in Thailand's terrestrial ecosystems led to the discovery of new saprobic species from Dothideomycetes: *Corynespora chiangraiensis* (Corynesporascaceae), *Chromolaenicola doitungensis* and *Dictyoarthrinium doitungensis* (Didymosphaeriaceae), *Novolignicola doitungensis* (Novolignicolaceae), *Palmiascoma chiangraiense* (Bambusicolaceae), *Sporicula chiangraiensis* (Fusculinaceae); from Eurotiomycetes: *Cylindroconidiis doitungensis* (Dactylosporaceae); and from Sordariomycetes: *Colletotrichum nayariophyti* (Glomerellaceae), *Doitungomyces dipterocarpi* (Cryphonectriaceae), *Nemania doitungensis* (Xylariaceae), *Oxydothis dalbergiae* (Oxydothidaceae), *Pisorisporium nayariophyti* (Pisorisporiaceae), *Striaticonidium chiangraiense* (Stachybotryaceae), and *Xylochrysis chiangraiensis* (Woswasiaceae). The results indicate that members of Sordariomycetes (62%, 77 isolates) are the dominant groups of isolated fungi. Sordariomycetes comprising a diverse range of taxa and members of this class were reported from a wide range of substrates, including woody materials

and plant-associated habitats. Most of them are found in terrestrial habitats, although a number of taxa have also been reported from aquatic environments (Maharachchikumbura et al. 2015, 2016). Karimi et al. (2025), reported 57% *Sordariomycetes*, 38% *Dothidiomycetes*, and 5% *Leotiomycetes* from peat swamp forests. This research also resulted in the isolation of known saprobic species (from *Dothideomycetes* and *Sordariomycetes*) among them five new sexual or asexual morphs: *Pseudofusicoccum kimberleyense* (*Phyllostictaceae*), *Paraconiothyrium archidendri* (*Didymosphaeriaceae*), *Misturatosphaeria viridibrunnea* (*Teichosporaceae*), *Cytospora heveae* (*Cytosporaceae*), *Colletotrichum gigasporum* (*Glomerellaceae*), were identified. In this study, *Sordariomycetes* constituted a significant proportion of the isolated fungi; within this class, *Xylariales*, *Hypocreales*, and *Diaporthales* were prominent orders. *Dothideomycetes*, the second most abundant class, included highly prevalent orders such as *Pleosporales*, *Kirschsteinietheliales*, and *Botryosphaeriales*. The dominance of *Dothideomycetes* and *Sordariomycetes* supports previous studies that highlight their prevalence in wood-associated habitats (Zhang et al. 2006, de Silva et al. 2022, Ren et al. 2024). Several studies have emphasized the ability of *Dothideomycetes* to thrive in various environments, including severe droughts, high temperatures, and elevated solar radiation levels (Pem et al. 2021). *Pleosporales*, which are particularly abundant, represent the largest group within the *Dothideomycetes*, with the majority being saprobic on decaying plant matter (Ren et al. 2022, Yang et al. 2022b). Conversely, the limited representation of *Eurotiomycetes* contrasts with some reports that emphasize their roles in arid and extreme environments, suggesting that their ecological roles may be limited by environmental factors at the sampling locations of this study (Coleine et al. 2024). Generally, woody litter fungi demonstrate broad host ranges, particularly in tropical and subtropical regions (Lindblad 2000, de Silva et al. 2022). This aligns with our findings, as new host records of woody-associated fungi have been documented during the diversity study.

In this study, the composition and diversity of fungal communities was also assessed. The results are based on those fungi that could be isolated and subjected to phylogenetic study and may therefore not be fully represented. The Bray-Curtis similarity analysis shows distinct patterns of fungal community structuring across host phylogenetic levels (orders, families, genera, and species) (Fig. 68). Host-recurrence of fungi, or repeated association of particular fungal species with specific host, can be inferred at different taxonomic levels of the host plants. Based on the results of this study, host-recurrence was observed between closely related taxa like species within the same genus (*Dalbergia cana* and *D. cultrata*) or genera within the same family (*Azelia* and *Dalbergia*). This finding aligns with previous studies that showed host phylogeny plays a key role in shaping fungal diversity and composition (Tennakoon et al. 2022b, Samaradiwakara et al. 2025). Tennakoon et al. (2022b) showed that tree species influence fungal diversity and community composition. These findings collectively reinforce the hypothesis that phylogenetically related host plants tend to have similar fungal taxa, leading to host-recurrent patterns in fungal assemblages. These results underscore the concept of host-recurrence among fungal taxa, evident in fungi that are mainly associated with a primary host but also occur on other hosts within the same habitat (Mukwevho et al. 2020). *Distoseptospora* and *Diaporthe* displayed patterns indicating their ability to colonize multiple hosts within shared environments, demonstrating they are not confined to specific hosts. It was suggested that the reduced host range observed in recently described fungal species often reflects limited sampling rather than their true host-recurrence (Abdollahzadeh et al. 2010). In our study, we identified novel fungi such as *Nemania doitungensis*, *Striaticonidium chiangraiense*, and *Pisorisporium nayariophyti*, exclusively associated with the dead wood of *Nayariophyton zizyphifolium*. Most likely, the host range may increase with additional sampling from different substrates and habitats. For example, *Pararoussoella lincangensis* from the Greater Mekong Subregion in China is found on dead woody twigs of *Heliciopsis terminalis* (*Proteaceae*) (Ren et al. 2024), whereas we collected it in Thailand on dead wood of *Dalbergia cana* (*Fabaceae*). Consequently, accurately describing host-recurrence trends in saprobes is challenging, as it often depends on various factors (Kubicek et al. 2014). Moreover, resource availability and competitive dynamics during fungal succession

contribute to the high diversity observed in these communities (Mukwevho et al. 2020). Another interesting result of this research is the isolation of *Diplodia guttulata*, which was recently identified by Samaradiwakara et al. (2025), from the leaf litter of *Microcos paniculata* from Doi Tung National Park, Chiang Rai Province, Thailand, as we also isolated it from the dead wood of the same host and locality. Additionally, *Chordomyces zizyphifolii* was isolated from the woody litter of *Nayariophyton zizyphifolium*, while Samaradiwakara et al. (2025) identified it from the dead leaves of the same host in their recent study. Some species demonstrated flexibility, transitioning between saprobic and pathogenic roles. Endophytic fungi such as *Diaporthe chiangmaiensis* exhibited dual lifestyles, existing endophytically in healthy leaves and transitioning to saprobic roles in dead twigs (Promputtha et al. 2010). In this research, we also found *Colletotrichum gigasporum*, previously recorded as a pathogen, was recorded as the first sexual morph saprobe on *Dalbergia cultrata*.

During decomposition, fungal communities undergo succession influenced by both abiotic and biotic factors (Pioli et al. 2018). Besides biotic factors, abiotic environmental elements, such as temperature, soil moisture, and pH significantly influence the composition of saprobic fungal communities. Seasonal variations influence litter decomposition rates. Fungi generally demonstrate more efficient decomposition in relatively dry conditions (Rousk et al. 2010, van der Wal et al. 2013). This heatmap clustering analysis groups fungal genera with seasonal abundance trends, providing insights into their ecological niches. Fungal diversity and abundance vary with seasonal changes, highlighting the ecological influence of moisture availability. Based on the results of this study, specific genera are likely adapted to wet conditions such as *Hypoxylon* and *Kirschsteiniothelia*, while others like *Helminthosporium* and *Diaporthe* are resilient during dry periods.

In our studied area, we did not observe completely distinct seasonal patterns and wide temperature differences, however, fungal diversity still varied between the two seasons. Tennakoon et al. (2022b) demonstrated that leaf litter chemistry significantly influences fungal diversity and community composition. Also, it was demonstrated that fungal diversity initially increased during the early stages of leaf decay for each tree species, reached its highest levels at mid-decay, and then declined in the later stages. Similarly, in our results, decomposition stages affected fungal community structure, with early decomposition stages supporting higher diversity and declined at later stages which is dominated by specialized genera. The rate of decomposition can vary among different tree species (Weedon et al. 2009). Logging, which increases sunlight exposure by opening the forest canopy, has been shown to adversely impact the diversity of wood-decaying fungi in forest ecosystems (Bässler et al. 2010). Krah et al. (2018) demonstrated the independent effects of host tree species and environmental factors on the diversity of wood-inhabiting fungi. Based on their results, host tree species is more influential than other factors like canopy openness or host size in determining fungal richness and community composition, while local amount and heterogeneity of dead wood had not affected on the fungal diversity measures. Persistent genera form a few broad clusters, representing stable, low-activity of communities adapted to nutrient-depleted environments. The reduction in distinct clusters suggests a shift toward niche specialization, where a subset of fungi dominate under the changing substrate conditions. Members of *Xylariales* are well-documented wood degraders, capable of decomposing lignocellulose. Their ability to cause a type of soft rot in wood decay has been demonstrated across various ecosystems, including the Amazon rainforest, where they were frequently found (Rajtar et al. 2023). *Xylaria* species can cause significant biomass loss in a short incubation period when decomposing lignin-rich material, underscoring their essential role in nutrient cycling (Osono et al. 2011, van der Wal et al. 2013).

One of the earliest estimates of global fungal diversity that was based on a plant-to-fungus ratio of 1:6, suggested the existence of almost 1.5 million fungal species (Hawksworth 1991). Based on plant-to-fungus ratios, unexplored habitats, high-throughput sequencing (HTS) data, and the continued discovery of new taxa, Hawksworth & Lücking (2017) estimated global fungal diversity to be 2.2–3.8 million species. Subsequently, Wu et al. (2019) expanded these estimates to

11.7–13.2 million species, later studies suggested approximately 6.3 million species (Baldrian et al. 2022, 2023). Several studies have employed HTS, a culture-independent method, to identify fungi inhabiting woody litter (Kubartová et al. 2012, Runnel et al. 2015, Yamashita et al. 2015, Hoppe et al. 2016, Vaz et al. 2017). The integration of culture-based approaches with culture-independent methods has been used to assess fungal diversity in highly diverse environments and to detect taxa that are non-culturable or slow-growing (Dissanayake et al. 2018, Hyde et al. 2024b). This study applied culture-based methods combined with phylogenetic analyses to assess the fungal diversity of wood-dwelling microfungi. These findings emphasize their ecological significance, particularly in forest ecosystems, where they play a vital part in the decomposition process and the recycling of organic matter (Afshari et al. 2023, Rajtar et al. 2023). These comprehensive findings significantly expand the current understanding of fungal taxonomy, their host associations, habitat diversity, as well as the ecological preferences of different fungal taxa providing valuable information for further plant-associate fungal studies. Based on these findings, future research should implement both culture-dependent and culture-independent methods to obtain more accurate assessments of fungal diversity and expand host-recurrence studies by examining additional time intervals. Long-term studies are also needed to evaluate the effects of seasonal variability, temperature, and rainfall on fungal communities. Finally, targeted investigations of decomposition stages through long-term successional studies on selected wood samples would enhance our understanding of fungal succession dynamics.

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DECLARATION ON CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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SUPPLEMENTAL TABLES

All supplementary tables are available at DOI: <https://zenodo.org/records/18093265>

Table S1 – Taxonomic classification of isolated fungal species.

Table S2 – Distribution of isolated fungal species across different host species.

Table S3 – Distribution of fungal genera in dry and wet seasons.

Table S4 – Distribution of fungal genera across decomposition stages.

Figure 69 – Shannon diversity index heatmap of fungal species across host tree orders.

Figure 70 – Shannon diversity index heatmap of fungal species across host tree families.

Figure 71 – Shannon diversity index heatmap of fungal species across host tree genera.

Figure 72 – Shannon diversity index heatmap of fungal species across host tree species.

Figure 73 – Jaccard similarity heatmap of fungal species diversity across tree orders.

Figure 74 – Jaccard similarity heatmap of fungal species diversity across tree families.

Figure 75 – Jaccard similarity heatmap of fungal species diversity across tree genera.

Figure 76 – Jaccard similarity heatmap of fungal species diversity across tree species.

Figure 78 – The heatmap and hierarchical clustering (Bray-Curtis) of fungal genera diversity during dry and wet seasons.

Figure 79 – The heatmap and hierarchical clustering (Bray-Curtis) of fungal genera diversity during different decomposition levels.