PEAT SWAMP PALM ASCOMYCETES

OMID KARIMI

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ABSTRACT

Peat swamp forests are unique ecosystems due to their high species diversity and significant role in maintaining a stable global climate. They function as carbon sinks, storing twice as much carbon as all global forest biomass. Beyond carbon storage, peatlands offer valuable benefits. They play vital roles in the water cycle, storing and filtering water and mitigating floods by slowing peak flows. Home to diverse plants and animals, these wetlands support millions of people. These habitats support many flora, including an extensive number of bryophytes, ferns, and palms (Arecaceae). In peat swamp forests, many palm species, including *Eleiodoxa conferta*, can be found, exerting various biological functions. However, this unique habitat is increasingly threatened by deforestation and land-use changes. There are few records of fungal studies in these environments, most of which have been reported from Thailand. The peat swamp forests in Narathiwat, southern Thailand, represent the last remaining primary peat swamp ecosystem in the country. However, studies on microfungi in these habitats remain limited and mostly lack molecular data. Therefore, in the current study, we aimed to investigate fungal species from peat swamp forests in Thailand, focusing on different palm materials, with an emphasis on *Eleiodoxa conferta*, based on morphology and phylogeny. Additionally, we examined one of the dominant palm fungal taxa, *Xylariales*, from non-palm hosts. For this study, fungal samples were collected from ten different hosts, including *Caryota mitis*, *Cyrtostachys renda*, *Eleiodoxa conferta* (the predominant palm species), *Eugeissona tristis*, *Licuala paludosa*, *Quercus kingiana*, and *Swietenia macrophylla*. Morphology and multi-gene phylogenetic analyses (ITS, LSU, SSU, mtSSU, *act*, *rpb*2, *tub*2, *tef1-α*) were used for taxa identification. Taxonomic classification, illustrations, and detailed descriptions for

each taxon are provided. From this research, we introduced one new family, one new genus, 34 new species and 25 new host, habitat and geographical records. Fungi from 19 orders within *Sordariomycetes*, *Dothideomycetes*, and *Leotiomycetes* were recorded. The orders include *Amphisphaeriales*, *Annulatascales*, *Botryosphaeriales*, *Cancellidiales*, *Chaetosphaeriales*, *Conioscyphales*, *Distoseptisporales*, *Helotiales*, *Hypocreales*, *Natipusillales*, *Pleosporales*, *Pleurotheciales*, *Pseudodactylariales*, *Rhytismatales*, *Savoryellales*, *Sporidesmiales*, *Tubeufiales*, Venturiales, and Xylariales. The fungal taxa investigated belong to 26 families, viz., *Amphisphaeriaceae*, *Annulatascaceae*, *Apiosporaceae*, *Astrosphaeriellaceae*, *Botryosphaeriaceae*, *Cancellidiaceae*, *Chaetosphaeriaceae*, *Conioscyphaceae*, *Diatrypaceae*, *Distoseptisporaceae*, *Hypocreaceae*, *Hypoxylaceae*, *Lophiostomataceae*, *Megacapitulaceae*, *Natipusillaceae*, *Oxydothidaceae*, *Pleurotheciaceae*, *Rhytismataceae*, *Savoryellaceae*, *Sporidesmiaceae*, *Striatiguttulaceae*, *Sympoventuriaceae*, *Tetraplosphaeriaceae*, *Tubeufiaceae*, *Vamsapriyaceae*, and *Xylariaceae*. The results of this study contribute to the understanding of microfungi in Thailand by providing additional morphological and phylogenetic evidence for their taxonomic placement. In addition to morphological data, we have generated sequence data for each taxon to address the lack of molecular data from previous studies. This has led to a more accurate taxonomic placement, enhancing our understanding of fungal diversity in peat swamp forests, which remain largely understudied worldwide. This study highlights the rich biodiversity of peat swamp forests, particularly in association with *Eleiodoxa conferta*, emphasizing the importance of conserving these unique ecosystems. The fungal specimens obtained in this study have been deposited in herbarium and culture collections, serving as valuable resources for future research in fungal taxonomy and the exploration of their biomaterial properties.

Keywords: Ascomycota, Dothideomycetes, Sordariomycetes, Peat Swamp Forest, Taxonomy, Phylogeny

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ABBREVIATIONS AND SYMBOLS

cm	centimeter
diam.	diameter
e.g.	for example
et al.	and others
gen.	genus (singular) and genera (plural)
i.e.	that is
mm	millimeter
nov.	novum (Latin for new thing)
sp.	species
spp.	species (plural)
x	average
$°C$	degree centigrade
μm	micrometer
μl	microliter
$\%$	percent

CHAPTER 1

INTRODUCTION

1.1 Peat Swamp Forests

Peatlands are recognized by diverse names globally, such as bogs, fens, mires, and peat swamp forests (Rydin et al. 2013). Peatlands are areas where peat accumulates naturally near the surface. Peat forms through accumulating incomplete microbial decomposition of dead organic materials, a process hindered by oxygen-free (anoxic) conditions, which is provided with elevated water (UNEP 2022). Approximately 50–60% of this peat comprises carbon (Yu et al. 2010; Melton et al. 2022). These wetlands store carbon, which originates from photosynthesis in plant material. Despite their limited distribution, covering about 3–4% of the earth's surface, these regions hold as much as a third of the world's soil carbon (UNEP 2022).

Peatlands cover roughly 436.2 million hectares worldwide, however, only 8.2% of this area is located in the tropics and subtropical regions. Southeast Asia hosts about 60% of these tropical peatlands, predominantly in Indonesia, Malaysia, Brunei, and Thailand, with smaller portions in the Philippines and Vietnam (Rieley et al. 1996; Joosten 2004). In Thailand, peatlands cover 64,555 hectares, mainly concentrated in the southern region, particularly Narathiwat province (Nuyim 2005).

Quantity (water level) and quality of water are vital for peat swamp forests. Excessive water levels disrupt plants' respiration and air exchange processes, while insufficient levels lead to soil drying and the risk of wildfire. In Narathiwat, Thailand, water in peat swamp forests shares global characteristics, with pH levels generally between 5.1 to 6.4, but can vary due to regional factors such as climate and vegetation. Despite acidity and colour resulting from dissolved organic carbon, this water can still be utilized for purposes like fishery, irrigation and animal consumption (Nuyim 2005). In addition to water, soil quality is a pivotal factor in this ecosystem, influencing plant growth, as it provides essential nutrients and water to sustain plant life. In the tropical lands of Southeast Asia, peat soil formation occurs primarily from woody plant debris

in environments, characterized by high rainfall and temperature. This process differs from that in temperate and boreal regions, where peat primarily originates from mosses and herbs (Andriesse 1988; Chimner and Ewel 2005). Peat soil in Thailand has a low density, high carbon content (24–80%) and high water-holding capacity. It is classified as fibric soil with high acidic pH levels (4.2–4.4) (Takai et al. 1987; Kyuma 1995; Grundling and Mazus 1996; Takai 1996). The soil in Narathiwat has a low amount of beneficial nitrogen, less than 2%, and limited nutrient availability (Vijarnsorn and Panichapong 1987).

Despite these demanding conditions, tropical peat swamp forests are habitat to at least 1,524 plant species (UNEP 2023) and have the highest plant diversity of all peatland types globally (Purwaningsih and Yusuf 2000; Corlett 2009). Peat swamp forests in Thailand have a high diversity of plants, comprising over 470 species within 109 families (Niyomdham 1988). Towering trees with up to 30 meters in height include *Baccaurea bracteate, Calophyllym sclerophyllum, Campnosperma coriaceum, Endiandra macrophylla, Eugenia kunstleri* (*Eu.*), *Eu. oblata, Eu. muelleri, Ganua motleyana* (*G.*), *Macaranga pruinosa, Neesia malayana, Sterculia gilva,* and *Stemonurus secundiflorus* (Hara et al. 1995). Undergrowth of the forest floor primarily consists of palm species, dominated by *Aglaonema marantifolium*. *Eleiodoxa conferta* (*El.*), and *Licuala paludosa* (*Lic.*). Additionally, parasitic plants like *Asplinium nidus, Platycerium coronarium,* and *Orchidaceae* species flourish on tree bark. Many of these plant species provide fruits like *El. Conferta,* serve for medicinal treatments like *Croton caudatus* as an analgesic and *Dalbergia parviflora* for heart treatments (Nuyim 2005).

Plants in this extreme environment have adapted their properties, especially their root systems to thrive in deposited peat soil and high-water content conditions. They have developed specialized roots, like large buttresses and stilt roots to help plants navigate peat swamp forests. They have produced pneumatophores emerging from the water, with different root shapes and sizes. For example, pin-shaped roots in *El. conferta;* loop-shaped roots in *Xylopia fusca,* knee-shaped roots in *G. motleyana* and inverted Y-shaped roots in *Elaeocarpus macroerus* (Posa et al. 2011).

This rich plant biodiversity (Crump 2017) makes peat swamp forests an important ecosystem for providing food and shelter for animals and birds (Minayeva and Sirin 2012; Bonn et al. 2016). People, especially local communities, are involved

with and dependent on peat swamps for their living, including beekeeping, fishery, providing timber, using medicinal plants, making crafts using peats and plants and promoting ecotourism (Gearey and Fyfe 2016; Crump 2017). Unfortunately, a significant number of these peat swamp forests are endangering due to human impacts like draining and deforestation for agricultural purposes (Joosten et al. 2012; Cook et al. 2020; Cole et al. 2022), and increasing peatland fires resulting the climate change which might be resulted in a reduction of carbon storage capacity in the region (Cole et al. 2022). For example, between 1990 and 2010, Southeast Asia's peat swamp forests lost more than half of their biomass (UNEP 2023). In Thailand, there were peatlands other than Narathiwat that were degraded or not fertile; Narathiwat province is home to Thailand's last primary peat swamp forest (Nuyim 2005).

The peat swamp forest represents an endangered ecosystem, yet its microbial diversity and ecology remain largely understudied. Thus far, only a limited number of articles have documented the microbial composition of tropical peat swamp forests, encompassing studies on bacteria (Dedysh et al. 2006; Thormann et al. 2007; Sitepu et al. 2007; Kachalkin et al. 2008; Jackson et al. 2009; Kanokratana et al. 2011; Songsumanus et al. 2011; Kachalkin and Yurkov 2012; Roslan et al. 2015; Phongsopitanun et al. 2015; Grum-Grzhimaylo et al. 2016; Sripreechasak et al. 2017; Ong et al. 2020; Klaysubun et al. 2020; Chantavorakit et al. 2021; Weeraphan et al. 2023) and limited studies on fungi associated with palms (Pinruan et al. 2002, 2004a, 2004b, 2004c, 2004d, 2007, 2008, 2010a, 2010b, 2014; Pinnoi et al. 2003a, 2003b, 2004, 2006, 2009, 2010).

1.2 Palm (Arecaceae)

The palm family (Arecaceae) is the world’s third most beneficial plant family, after grasses and legumes. This family belongs to Arecales, comprising around 2600 species across 181 genera (Baker and Dransfield 2016; Faurby et al. 2016) and distributed throughout the tropics and subtropics, mostly in tropical Asia and America (Kahn and de Granville 1992; Pitman et al. 2001; Dransfield et al. 2008). This flowering family exhibits a range of characteristics, including solitary or clustering growth habits, spiny or smooth bark, and forms that can manifest as trees, shrubs or climbers (Rivera

et al. 2008). These plants vary significantly in size, with some specimens measuring as small as 12–25 cm, while others can reach over 50–60 m. Palms represent one of the ancient monocotyledonous flowering plant groups (Janssen and Bremer 2004), with a well-documented fossil history (Harley 2006) spanning approximately 80 million years (Wing et al. 1993; Morley 2000).

Palm trees play an important role in agriculture (Johnson 2011) and are of significant importance to local human communities (Dransfield et al. 2008), especially in rural areas (Sosnowska and Balslev 2009; Johnson 2011). They provide various benefits, including food, oil, medicine, and materials such as wood, fabrics and fuel (Balslev and Barfod 1987; Balick 1988; Balick and Beck 1990; Zambrana et al. 2007; de la Torre et al. 2009; Sosnowska and Balslev 2009). In addition to their economic value, they are also used as ornaments (MacLeod and Hussein 2017). Palms also serve as windbreakers that protect their habitat from erosion and destruction, particularly in coastal mangroves, thus aiding in the protection of coastal areas against tornadoes and cyclones (Marois and Mitsch 2014). They are essential as a keystone resource for pollinator and frugivore communities, playing a vital role in ecosystem dynamics (Terborgh 1986; Zona and Henderson 1989, 2002). Furthermore, their presence may have influenced the evolution of birds and animal groups that depend on them (Dominy et al. 2003). Considering their global dispersion and diversity, palms serve as a model for investigating the factors influencing the abundant tropical biodiversity and its geographical fluctuations (Bjorholm et al. 2005, 2006; Svenning et al. 2008a).

Palms grow in a wide range of habitats, often found in association with water bodies, including freshwater swamps (Baker and Dransfield 2016). In peat swamp forests, many palm species can be found, such as *Areca macrocalyx*, *Calamus caesius* (*Cal.*)**,** *Cal. concinnus*, *Cal. melanochaetes***,** *Caryota mitis* (*Car.*), *Cyrtostachys renda* (*Cyr.*), *El. conferta*, *Eugeissona tristis* (*Eug.*), *Korthalsia laciniosa*, *Lic. longicalycata*, *Lic. paludosa*, *Lic. spinosa*, *Livistona saribus***,** *Metroxylon sagu*, *Nenga pumila*, *Oncosperma tigillarium***,** *Pinanga glaucescens* (*Pi.*), and *Pi. riparia* (Calabon et al. 2022; POWO 2024). The following palm species are native to Thailand and can be found in the peat swamp forests of Narathiwat: *Cal. caesius, Cal. concinnus, Cal. melanochaetes, Car. Mitis, Cyr. renda, El. conferta, Eu. Tristis, Korthalsia laciniosa*,

*Lic. paludosa, Livistona saribus, Nenga pumila, Oncosperma tigillarium***,** *Pi. glaucescens* and *Pi. riparia* (POWO 2024).

1.3 Palm Fungi in Peat Swamp Forests

Fungi associated with palms are known as palm fungi or palmicolous fungi. The exploration of palm fungi has evolved through three distinct phases (Pereira and Phillips 2023). The initial period (1880 to 1920) included historical studies resulting in describing many species, including the earliest documented records of palm fungi, such as *Zygosporium oscheoides* in the order *Xylariales*. The second span (1920 to 1990) includes the first noticeable studies in 1988 and 1989, during which two unique palm genera, *Linocarpon* and *Oxydothis,* were described on mangrove palms (*Nypa fruticans*) (Hyde 1988; Hyde and Nakagiri 1989). The third era, starting in the 1990s and continuing to the present day, includes research conducted by Hyde and his collaborators, who have extensively studied palm fungi (Pereira and Phillips 2023). Their studies provided comprehensive resources on palm fungi including three books and a series of papers (Karimi et al. 2024a, 2024b; Pereira and Phillips 2023; Palmfungi.org 2024). Hyde et al. (2000) published "Genera of ascomycetes from palms" with 100 notes and illustrations on palm fungal genera. Fröhlich and Hyde (2000) published "Palm microfungi", providing a comprehensive review and a collection of palms associated with ascomycetes from Australia, Brunei, Ecuador, and China. Their study showed the high diversity of *Amphisphaeriaceae*, *Oxydothidaceae*, *Hypocreaceae*, *Meliolaceae*, *Mycosphaerellaceae*, *Phyllachoraceae*, and *Xylariaceae* species. Taylor and Hyde (2003) provided a collection of "Microfungi of tropical and temperate palms" from Australia and China. Pereira and Phillips (2023) extensively reviewed global research on palm fungi, indicating palms as an important host for diverse fungal species.

Recently, studies on palm fungi in Thailand have increased, particularly due to the utilization of molecular data, which has led to the discovery of high fungal diversity on *Eleiodoxa conferta*, *Licuala longicalycata*, and *Nypa fruticans* (Karimi et al. 2024a, 2024b; Konta et al. 2022). Pinruan et al. (2004a) described a new genus on palm in Thailand using both morphological and molecular data. Pinnoi et al. (2006) studied

saprobic fungi on *Eleiodoxa conferta* in a peat swamp in Narathiwat Province, Thailand. Their studies were the only research on peat swamp fungi based on the checklist of Thormann and Rice (2007). Pinnoi et al. (2006) recorded 462 taxa but only 251 taxa were identified at the species level and the rest remained poorly identified; the most common taxa mostly isolated from the petioles were, *Astrosphaeriella* sp., *Cancellidium applanatum, Jahnula appendiculate, Lophiostoma frondisubmersa, Microthyrium* sp., *Morenoina palmicola, Nemania eleiodoxae, Phaeoisaria clematidis, Stilbohypoxylon moelleri, and Xylomyces aquaticus.* The other significant research on palm-associated fungi was conducted by Pinruan et al. (2007) who discovered fungi on *Licuala longicalycata* in peat swamp habitats in Thailand. They collected over 350 taxa but were able to identify 177 of them at the species level. The most common taxa included *Annulatascus velatisporus, Microthyrium* sp., *Phaeoisaria clematidis, Massarina bipolaris, Phruensis brunneispora, Thailiomyces setulis,* and *Solheimia costaspora.* Based on previous studies, most fungi inhabiting palms in Thailand's peat swamp forests are saprophytic ascomycetes with a high diversity in submerged palms. Dominant orders are *Pleosporales*, *Xylariales*, and *Chaetosphaeriales*, comprising prominent genera like *Astrosphaeriella*, *Oxydothis*, and *Linocarpon*, respectively. Additionally, numerous species have been classified under undetermined orders, *incertae sedis* (Pinnoi et al. 2006; Pinruan et al. 2007).

1.4 *Xylariales* Taxa Associate with Palms

Xylariales (*Ascomycota*) was circumscribed by Nannfeldt (1932), and since then, members of this order have been traditionally described based on morphological characters (Munk 1953; Hawksworth et al. 1995). A significant study for establishing boundaries for taxa in this order was conducted by Smith et al. (2003), who accepted seven families based on morpho and molecular data. Subsequently, it was subjected to several revisions based on a morpho-molecular approach (Kang et al. 1998; Kang et al. 2002; Kirk et al. 2008; Lumbsch and Huhndorf 2010; Senanayake et al. 2015; Samarakoon et al. 2016; Voglmayr et al. 2018; Wendt et al. 2018; Hyde et al. 2020; Samarakoon et al. 2022; Hernández-Restrepo et al. 2022; Sugita et al. 2022, 2024). Due to the complex nature of these taxa, most of the current taxonomic studies involving

Xylariales employ morphological, multigene phylogenetic, chemotaxonomic, and genomic and comparative genomic approaches (Chethana et al. 2021; Wibberg et al. 2021; Samarakoon et al. 2022). *Xylariales* species produce a wide range of secondary metabolites belonging to various biosynthetic families, including dihydroisocoumarins, punctaporonins, cytochalasins, butyrolactones, and succinic acid derivatives. Hence, chemotaxonomy is frequently used in taxonomic studies to identify *Xylariales* species (Whalley and Edwards 1995; Becker and Stadler 2021). Currently, 22 families are accepted under *Xylariales* (Hernández-Restrepo et al. 2022; Sugita et al. 2022; Hyde et al. 2024), with species found worldwide as saprobes, pathogens and endophytes; however, the tropics and subtropics have the most remarkable diversity, particularly on palm hosts (Arecaceae) (Dayarathne et al. 2017; Li et al. 2017; Ma et al. 2018; Cedeño-Sanchez et al. 2020; Perera et al. 2020; Ma 2022). Voglmayr and Yule (2006) introduced *Polyancora* (*Po.*), as a new genus to accommodate *Po. globosa* within *Xylariales* from tropical peat swamp forests located in Peninsular Malaysia. Konta et al. (2016) introduced *Allodiatrype*, along with five new species (*Allocryptovalsa elaeidis*, *Allodiatrype arengae* (*A.*), *A. elaeidicola*, *A. elaeidis*, and *Diatrypella elaeidis*), within *Xylariales*, from specimens collected from palm materials, including the petioles of *Elaeis guineensis* and *Arenga pinnata* (Arecaceae) in Thailand. Konta et al. (2020) introduced *Neoxylaria* (*Xylariaceae*, *Xylariales*) on dead petiole of *Arenga pinnata* (Arecaceae), based on morphology and combined phylogenetic analyses of *rpb2*, *tub2*, and ITS. Afshari et al. (2023) introduced *Allodiatrype eleiodoxae* (*Diatrypaceae*, Xylariales) on the dead rachis of *Eleiodoxa* sp. (Arecaceae) from peat swamp forest in Narathiwat, Thailand.

1.5 Research Objectives

1.5.1 To investigate ascomycetes in peat swamp forests in Thailand.

1.5.2 To systematically collect, document, and generate molecular data, living cultures, and herbarium specimens for previously studied palm ascomycetes in peat swamp forests with emphasis on *Eleiodoxa conferta*.

1.5.3 To enhance the taxonomic and phylogenetic understanding of *Xylariales* taxa, prominently associated with palm and improving their classification within existing taxonomic frameworks.

1.6 Research Contents

This thesis is divided into 4 chapters.

Chapter 1 provides a general introduction, covering the research background on peat swamp forests, the Arecaceae family, and palm fungi in peat swamp forests in Thailand. It also highlights the importance of the order *Xylariales*.

Chapter 2 provides the materials and methods employed in the study, detailing the sampling techniques, laboratory procedures, and analytical methods used to investigate the fungal communities.

Chapter 3 presents peat swamp *Ascomycota* associated with palms, particularly on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand, supplemented with completed descriptions, photo plates, and a phylogenetic tree, along with a complete account on the order *Xylariales*.

Chapter 4 provides the overall conclusions, summarizing the key findings of the study and their implications for understanding the fungal diversity associated with palms in peat swamp forests and the future directions.

CHAPTER 2

MATERIALS AND METHODS

2.1 Sample Collection, Morphological Study, and Isolation

In this study, samples were collected during 2021–2024 from Chiang Rai (Mae Fah Luang University), Chiang Mai (Doi Inthanon National Park), and Narathiwat provinces (Princess Sirindhorn Wildlife Sanctuary, peat swamp forest) in Thailand. The sampling encompassed both land and freshwater environments and included various hosts, such as palm species, including *Caryota mitis*, *Cyrtostachys renda*, *Eugeissona tristis*, *Licuala paludosa*, and predominantly *Eleiodoxa conferta* and non-palm species (*Afzelia xylocarpa*, *Dalbergia cana*, *Quercus kingiana*, *Swietenia macrophylla*). Detailed information was documented, covering aspects such as host name, collection site, and collection date. Wet (submerged) and dry specimens were placed in plastic bags and brought to the laboratory. The submerged materials were kept moist and examined periodically for fungal fruiting structures, and the dry materials were examined immediately or incubated in moist chambers. Small pieces of the collected specimens were examined using a Motic SMZ 168 Series microscope (Motic Asia, Kowloon, Hong Kong) and isolated into axenic cultures using the single spore technique (Senanayake et al. 2020) on PDA supplemented with 0.5 g/L Streptomycin. Micro-morphological characteristics were examined and photographed using a digital camera (Canon 750D, Japan) attached to a compound microscope (Nikon ECLIPSE 80i, USA), and measurements were taken using the Tarosoft (R) Image Framework program version 0.9.7 (Tarosoft, Thailand). The ex-type living cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC), and the herbarium specimens were deposited in the Mae Fah Luang University Herbarium (MFLU). Facesoffungi (FoF) and Index Fungorum numbers were assigned as described by Jayasiri et al. (2015) and the Index Fungorum (http://www.indexfungorum.org), respectively.

2.2 DNA Extraction, PCR Amplification, and Sequencing

Genomic DNA was extracted from fresh fungal mycelia or fruiting bodies (for spores that could not germinate) using the Mega Genomic DNA Extraction Kit (Omega Bio-tek Inc, The United States), following the manufacturer's standard protocol. Polymerase chain reactions (PCR) were performed using the primers and conditions listed in Table 2.1. The PCR products were visualized on 1% agarose gels stained with 4S Green Stain and sequenced at SolGent Co., Ltd. (South Korea).

2.3 Sequence Alignment and Phylogenetic Analyses

The sequences (ITS, LSU, SSU, mtSSU, *rpb2*, *tef1-α*, *tub2*) were assembled using SeqMan software version 7.1.0 (DNASTAR Inc., WI) and subjected to BLASTn search against the GenBank nucleotide database at National Center for Biotechnology Information (NCBI) to identify closely-related sequences. Data from related taxa were obtained from previous publications and downloaded from the GenBank database. The sequences were aligned using MAFFT v.7 online web server (http://mafft.cbrc.jp/alignment/server/index.html, Katoh et al. 2019) under default settings and manually edited via BioEdit version 7.0.9 (Hall 1999), and alignments were trimmed using trimAl v1.2 (http://trimal.cgenomics.org). The Maximum Likelihood (ML) phylogenetic analysis was run in the CIPRES Science Gateway platform (Miller et al. 2010), using RAxMLHPC2 on the XSEDE (v. 8.2.10) tool (Stamatakis 2014) under the GTRCAT substitution model and 1,000 non-parametric bootstrap replicates. For Bayesian Inference (BI) analysis, the optimal substitution model of each region was determined using jModelTest2 on the CIPRES Science Gateway under the Akaike Information Criterion (AIC) (Darriba et al. 2012). Bayesian analysis was performed using MrBayes v. 3.2.6 on XSEDE at the CIPRES Science Gateway. The resulting trees were visualized in FigTree v. 1.4.2 (Rambaut 2012) and edited in Inkspace v.1.2.2. The pairwise homoplasy index (PHI) test was conducted using the combined sequence dataset of closely related species using Split Tree version 4.18.2 (Huson and Bryant 2006) to evaluate the recombination level.

Table 2.1 Gene regions, primers, and PCR conditions used in this study

Gene Regions	PCR condition						Reference
	Primer	Initial Denaturation	Denaturation	Annealing	Extension	Final extension	
ITS	ITS5/ ITS4	94 °C, 3 min, 1 cycle	94 °C, 45 secs, 35 cycle	53 °C, 55 sec	72 °C, 2 min	72 °C, 10 min, 1 cycle	(White et al. 1990)
LSU	LR0R/LR5	94 °C, 5 min, 1 cycle	94 °C, 30 secs, 35 cycle	55 °C, 50 sec			(Vilgalys and Hester 1990; Rehner and Samuels 1994)
SSU	NS1/NS4	94 °C, 3 min, 1 cycle					(White et al. 1990)
mtSSU	mrSSU1/mrSSU3R	94 °C, 30 secs, 35 cycle		52 °C, 50 sec			(Zoller et al. 1999)
tef1-α	728F/986R	94 °C, 3 min, 1 cycle	94°C, 30 secs, 35 cycles	58°C, 50 sec			(Carbone and Kohn 1999)
	983F/2218R						(Rehner 2001)
	728F/LLErev						(Liu et al. 1999; Carbone and Kohn 1999)

Table 2.1 (continued)

Gene Regions	PCR condition						Reference
	Primer	**Initial Denaturation**	**Denaturation**	**Annealing**	**Extension**	**Final extension**	
rpb2	fRPB2-5f/fRPB2-7cR	95 °C, 5 min, 1 cycle	95 °C, 1 min secs, 35 cycles	52 °C, 1 min			(Liu et al. 1999)
tub2	Bt2a/ Bt2b T1/T22	94 °C, 3 min, 1 cycle	94 °C, 30 sec 35 /40 cycles	58 °C, 50 sec 58 °C, 55 sec	72 °C, 1 min		(Glass and Donaldson 1995) (O'Donnell and Cigelnik 1997)

CHAPTER 3

TAXONOMY AND PHYLOGENY OF PEAT SWAMP ASCOMYCOTA FROM THAILAND

3.1 Introduction

Fungi, a diverse group of organisms, occur in a wide range of habitats, including terrestrial (Phukhamsakda et al. 2020), freshwater (Hyde et al. 2021), and marine (Jones et al. 2019) environments. They play a crucial role in ecosystems, functioning as decomposers, mutualists, and pathogens (Schmit and Mueller 2007; Bhunjun et al. 2022). Beyond their ecological significance, fungi also contribute positively to our daily lives, particularly by decomposing plant materials and aiding in nutrient cycling (Mortimer et al. 2012; Lange et al. 2012).

Ascomycota, the largest phylum within the fungal kingdom, thrives in diverse habitats and on various substrates, including human and animal bodies, plant material, algae, lichens, insects, dung, water, soil, air, and other fungi (Eriksson 2009). *Ascomycota* has been extensively studied on various plants across diverse habitats. Among these, palms (Arecaceae) have gained significant attention from mycologists due to their ecological importance and crucial role in global trade (Hyde 1992a, 1992b; Hyde 1993a, 1993b, 1993c, 1993d, 1993e, 1993f, 1993g, 1993h; Hyde 1994a, 1994b, 1994c, 1994d; Hyde 1995a, 1995b, 1995c, 1995d, 1995e, 1995f, 1995g; Hyde and Fröhlich 1995; Hyde 1996a, 1996b, 1996c, 1996d, 1996e, 1996f; Hyde et al. 1996; Hyde and Aptroot 1997; Hyde 1988; Hyde et al. 1998; Hyde et al. 2000; Fröhlich and Hyde 2000; Pinruan et al. 2002, 2004a, 2004b, 2004c, 2004d, 2007, 2008, 2010a, 2010b; Pinnoi et al. 2003a, 2003b, 2004, 2006, 2009, 2010; Liu et al. 2010; Konta et al. 2016a, 2016b, 2016c; Konta et al. 2017, 2020a, 2020b, 2021a, 2021b, 2023; Zhang et al. 2024).

Arecaceae, commonly known as palm trees, includes approximately 2,600 species within 181 genera distributed globally, mostly in tropical and subtropical regions (Baker and Dransfield 2016). The relationship between palm trees and fungi

involves multiple roles, including those of decomposers, disease-causing agents, and symbionts, with an estimate of over 76,000 fungal species from different habitats (Pereira and Phillips 2023). Peat swamp forests have remarkable palm diversity (Pinnoi et al. 2006), mostly in tropical rainforests where peat remains submerged for most of the year. These forests are characterized by low nutrient content and high acidity due to partially decomposed plant material (Page et al. 1999, 2011; Jackson et al. 2009; Lampela et al. 2016; Ratnayake 2020).

Peat swamp forests are important ecosystems for providing food and shelter for animals and birds (Minayeva and Sirin 2012; Bonn et al. 2016). Local communities are involved with and dependent on peat swamps for their living, including beekeeping, fishery, providing timber, using medicinal plants, making crafts using peats and plants and promoting ecotourism (Gearey and Fyfe 2016; Crump 2017). Thailand's peat swamp forests have a high plant diversity, with over 470 species across 109 families (Chawalit and Wiwat 1991). Narathiwat province is home to Thailand's last primary peat swamp forest (Nuyim 2005), with native palm species such as *Calamus. caesius, Ca. concinnus, Ca. melanochaetes, Caryota mitis, Cyrtostachys renda, Eleiodoxa conferta, Eugeissona tristis, Korthalsia laciniosa, Licuala paludosa, Livistona saribus, Nenga pumila, Oncosperma tigillarium, Pinanga glaucescens,* and *P. riparia* (POWO 2024). The peat swamp forest represents an endangered ecosystem, yet its microbial diversity and ecology remain largely understudied. There are limited studies on fungi in peat swamp forest in Thailand indicating *Ascomycota* as the dominant phylum (Pinnoi et al. 2006; Pinruan et al. 2007). However, many fungi from earlier studies are poorly identified due to a lack of molecular data. To address these research gaps, we investigated the fungal community associated with palms in Narathiwat's peat swamp forest ecosystem, with a particular focus on *El. conferta* and other native species.

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3.2 Results

Phylum *Ascomycota* Caval.-Sm., Biol. Rev. Cambridge Philos. Soc. 73: 247 (1998)

Subphylum *Pezizomycotina* O.E. Erikss. & Winka, Myconet 1: 9 (1997)

Class *Dothideomycetes* O.E. Erikss. & Winka, Myconet 1: 5 (1997)

Subclass *Pleosporomycetidae* C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1048 (2007)

Pleosporales Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

Astrosphaeriellaceae Phookamsak & K.D. Hyde, Fungal Diversity 74: 161 (2015)

Astrosphaeriellaceae was introduced by Phookamsak et al. (2015) within *Pleosporales* to include *Astrosphaeriella* and *Pteridiospora*, based on both morphological features and combined phylogenetic analyses of LSU, SSU, and *tef-1α*. Since then, several additional genera have been incorporated into the family (Liu et al. 2018b; Wanasinghe et al. 2018a; Wijayawardene et al. 2018; Jayasiri et al. 2019; Dong et al. 2020; Konta et al. 2023). Currently, 14 genera are recognized within *Astrosphaeriellaceae* (Hyde et al. 2024; Zhang et al. 2024). Members of *Astrosphaeriellaceae* have been reported as saprobic or parasitic on palms, bamboo, *Quercus* species, or robust grasses (Zhang et al. 2024). The sexual morph is characterised by uni-loculate, solitary to gregarious, erumpent to superficial, glabrous, brittle, and carbonaceous ascomata. These structures are dark opaque, conical or mammiform, thick-walled with uneven thickness, and poorly developed at the base. They may be surrounded by ruptured, reflexed, stellate host tissue remnants at the base. The ascomata are composed of thick, opaque, and melanized cells, with palisade-like cells present at the rim of the peridium. In the hamathecium, dense, anastomosing, trabeculate pseudoparaphyses (Liew et al. 2000) are observed. The asci are 8-spored,

bitunicate, fissitunicate, cylindrical to cylindric-clavate, pedicellate, and rounded apically with an ocular chamber or a J-, subapical ring. The ascospores are subfusoid to fusiform, obclavate to ellipsoidal, or limoniform, hyaline or pale brown to reddish brown, septate, constricted at the septum, and smooth-walled. Appendages and a mucilaginous sheath may be present on the ascospores. The asexual morph is reported as coelomycetous or hyphomycetous (Hongsanan et al. 2020a). An updated tree for the family is shown in Figure 3.1.

Astrosphaeriella Syd. & P. Syd., Annales Mycologici 11: 260 (1913)

Astrosphaeriella is a saprobic genus belonging to *Astrosphaeriellaceae*, *Pleosporales* (*Dothideomycetes*, *Ascomycota*) (Hongsanan et al. 2020). The genus was established by Sydow & Sydow (1913a), with *Astrosphaeriella fusispora* as the type species. This genus is distinguishable from other genera by its distinctive morphological characteristics in both the sexual and asexual stages. Sexual morph: Ascomata are scattered, occasionally forming joined of 2-3 at the base. They can be either superficial or immersed and subepidermal. Upon reaching maturity, they may be covered by the epidermis, except in the ostiolar region. In cross-section, they are unilocular, taking on a range from hemispherical to conical shapes, with a flattened base and an ostiole. The color spectrum spans from dark-purplish brown to nearly black. Peridium are relatively thick and carbonaceous, consisting of thick-walled dark angular pseudoparenchymatous cells. Asci 8-spored, cylindrical, bitunicate. Ascospores are arranged in 2-3 seriate, elongate-fusiform, exhibit a coloration of hyaline or reddish-brown, often accompanied by a mucilaginous sheath (Hyde and Fröhlich 1997). Asexual morph: Coelomycetous, pycnidia, conidiophores arising from the basal cavity, reduced to conidiogenous cells. Conidiogenous cells are holoblastic, phialidic, cylindrical to ampulliform, aseptate, smooth-walled. Conidia hyaline, globose to subglobose, aseptate (Phookamsak et al. 2015). According to Species Fungorum (2025) there are 52 accepted species in this genus, though molecular data is available for only nine of them in GenBank. *Astrosphaeriella* species have been reported on palms, bamboos and grasses. Mostly reported on palms (Arecaceae) including: *Astrosphaeriella angustispora* on dead frond of *Licuala* sp. from Brunei, *A. aosimensis* on leaves of *Livistona subglobosa* from Japan, *A. aquatica* on submerged rachides of *Livistona* sp. from Papua New Guinea, *A. australiensis* on dead stem of *Calamu* sp.

from *Australia*, *A. bakeriana* on dead leaves of *Livistona sinensis* from Singapore, *A. daemonoropis* on dead petiole of *Daemonorops margaritae* from Hong Kong, *A. erumpens* on petioles of palm from Cuba, *A. exorrhiza* on roots of *Iriartea* sp. from Venezuela, *A. fissuristoma* on dead rattan and base of petiole of *Calamus conirostris* from Brunei, *A. floridana* on petioles of *Sabal palmetto* from Florida, *A. fronsicola* on leaf of *Oraniopsis appendiculate* from Australia, *A. immersa* on *Archontophoenix alexandrae* from Hong Kong, *A. lageniformis* on *Cocos nucifera* from China, *A. malayensis* on dead stem of *Daemonorops* sp. from Malaysia, *A. maquilingiana* on dead *Calamus* sp. from Philippines. *A. mauritiae* on dead petiole of *Mauritia flexuosa* from Ecuador, *A. nypae* on decaying intertidal fronds of *Nypa fruticans* from Brunei (Barr 1990; Hawksworth and Boise 1985; Hyde 1994a; Hyde and Fröhlich 1997; Phookamsak et al. 2015).

Javarisimilis S.N. Zhang, K.D. Hyde & Jian K. Liu, Fungal Diversity (2024)

Zhang et al. (2024) introduced *Javarisimilis* (*J.*), to accommodate its type species, *J. palmarum*, which was found on decaying rachides of *Nypa fruticans* submerged in mangrove mud in Thailand. Currently, only one species is listed in Index Fungorum (2024). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *J. narathiwatensis* as the second species in this genus, found on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Javarisimilis narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.2

Index Fungorum number: IF903514; Facesoffungi number: FoF 17517

Etymology – Epithet refers to Narathiwat Province, where the holotype was collected

Holotype – MFLU 24-0484

Saprobic on submerged, decaying rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 350–600 μm diam., ($\bar{x}$ = 503 μm, n = 15), scattered or in small groups, superficial, hemispherical, carbonaceous, grey to brown, showing concentric rings on the surface of ascomata, with a central small black papillate and ruptured host tissue

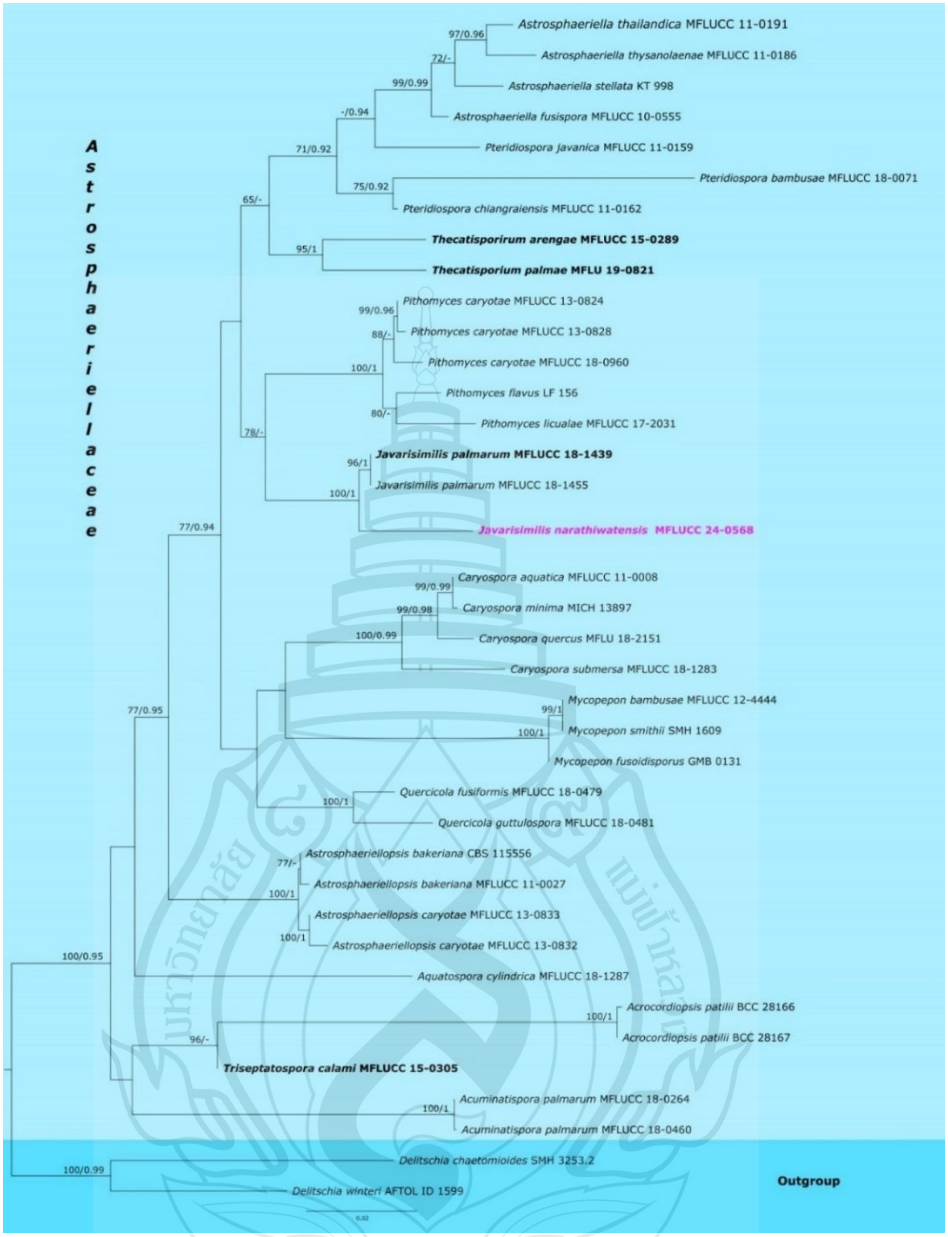
surrounding the surface of the ascomata. *Peridium* 15–20 μm wide, carbonaceous and brittle. *Pseudoparaphyses* 0.9–2.1 μm wide ($\overline{x}$ = 1.3 μm, n = 30), numerous, straight or flexuous, aseptate, branched, filiform, hyaline, sometimes anastomosing and embedded in a gelatinous matrix. *Asci* 98–150 × 11–20 ($\overline{x}$ = 119 × 14 μm, n = 20), 8-spored, bitunicate, cylindrical to clavate, short pedicellate. *Ascospores* 29–38.5 × 3.8–7.6 ($\overline{x}$ = 33.6 × 4.9 μm, n = 40), overlapping uniseriate to biseriate, fusiform, hyaline, tapering toward the ends, 1-septate, constricted at the nearly median septum, slightly curved, guttulate, surrounded by a gelatinous sheath that extends at both ends, forming distinct cap-like appendages. Asexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony circular to irregular, umbonate, dull, velvety, medium dense, surface brown, reverse dark brown with rhizoid reddish-brown margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on decayed, submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 16W (MFLU 24-0484, holotype); ex-type living culture MFLUCC 24-0568.

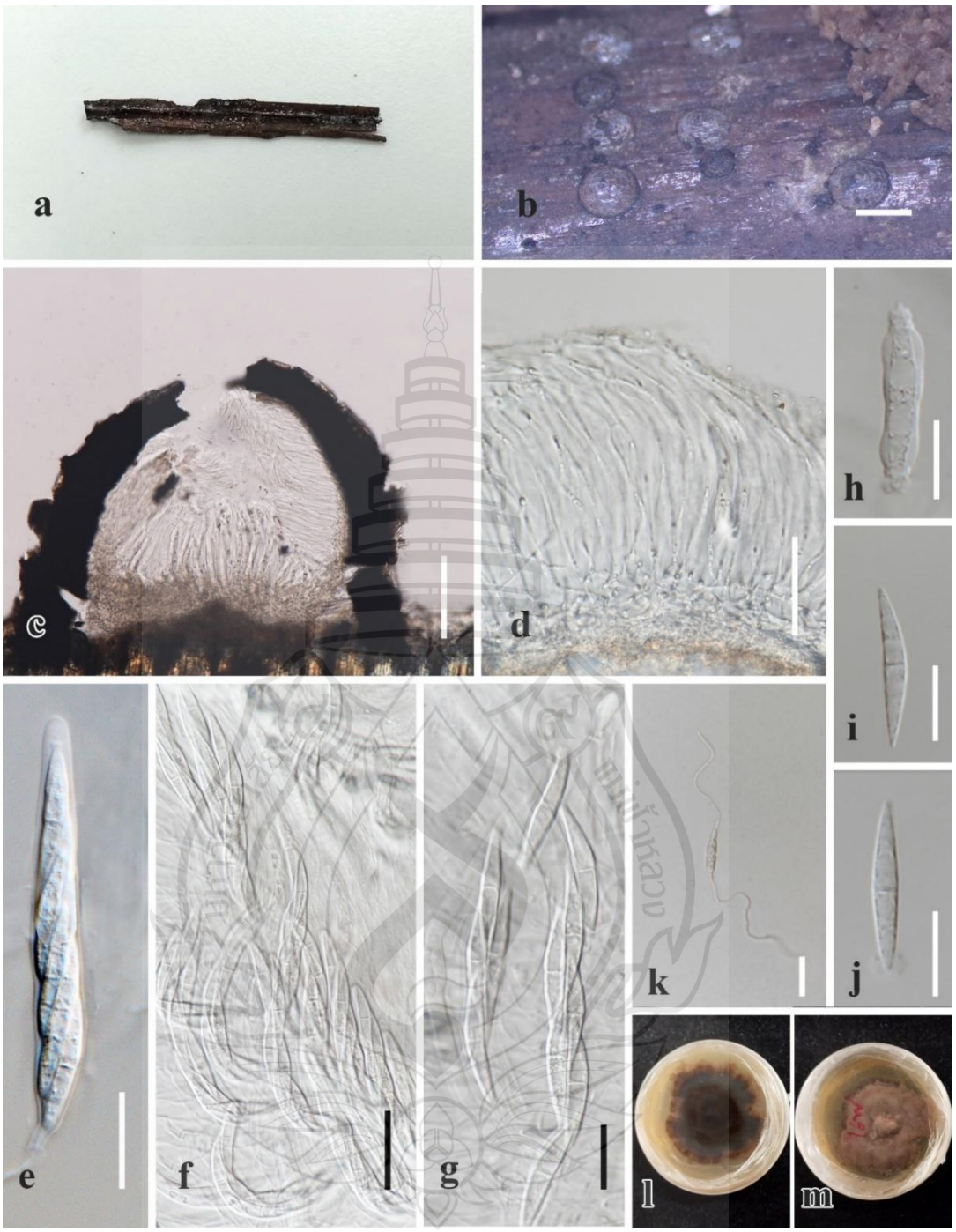
GenBank numbers – MFLUCC 24-0568: ITS = PV271863, LSU = PV271905, *tef-1α* = PV340482.

Notes – Phylogenetically, our strain (MFLUCC 24-0568) clustered with *Javarisimilis palmarum* isolates MFLUCC 18-1439 (ex-type) and MFLUCC 18-1455 with 100% ML, 1.00 PP statistical support in the combined phylogenetic analyses (Figure 3.1). Morphologically, our strain (MFLU 24-0484), differs from *J. palmarum* MFLU 19-0805 (holotype) in having smaller ascomata (350–600 μm vs. 300–1110 μm diam), narrow peridium (15–20 μm vs. 40–57 μm wide), shorter asci (98–150 μm vs. 140–180 μm), shorter ascospores (29–38.5 vs. 37–48 μm), and aseptate pseudoparaphyses in contrast to the septate ones of *J. palmarum* (MFLU 19-0805) (Zhang et al. 2024). Based on pairwise nucleotide comparisons, our strain (MFLUCC 24-0568) differs from *J. palmarum* (MFLUCC 18-1439) by having 4.06% differences (35/860 bp, without including gaps) in the ITS and 5.01% differences (46/917 bp, without including gaps) in *tef-1α* and 0.6% differences (5/860 bp, without including gaps) in the LSU. Therefore, we introduce our strain as *J. narathiwatensis* based on morphological and phylogenetic evidence.



Note D*elitschia chaetomioides* (SMH 3253.2), and *D. winteri* (AFTOL-ID 1599) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.1 Phylogram generated from the ML analysis based on the combined LSU, SSU and *tef-1α* sequence data of *Astrosphaeriellaceae*



Note a Host. b Appearance of ascomata on the substrate. c Vertical section of the ascoma. d Pseudoparaphyses. e–g Asci. h–j Ascospores. k A germinated ascospore. l, m Colonies on the PDA. Scale bars: b = 500 µm, c = 100 µm, d = 40 µm, e, f, k = 30 µm, g–j = 15 µm.

Figure 3.2 *Javarisimilis narathiwatensis* (MFLU 24-0484, holotype)

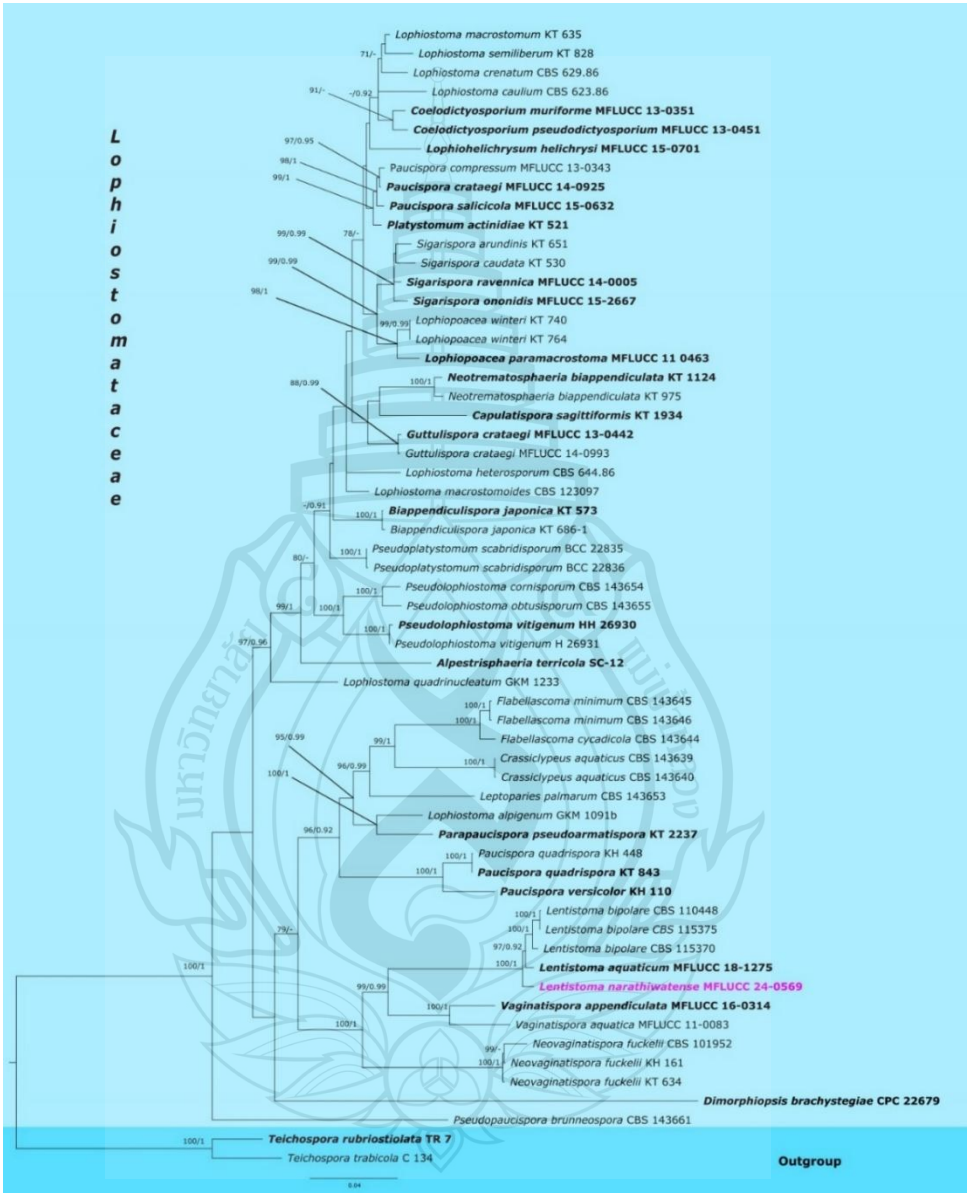
Lophiostomataceae Sacc., Syll. Fung. 2: 672 (1883)

Nitschke (1869) introduced the family *Lophiostomataceae* with *Lophiostoma*, as the type genus. Since then, several genera have been introduced into this family (Trevisan 1877; Kohlmeyer and Kohlmeyer 1991; Crous et al. 2013; Thambugala et al. 2015; Hashimoto et al. 2018; Mapook et al. 2020; Maharachchikumbura et al. 2021; Wanasinghe et al. 2021). Currently, there are 32 accepted genera in *Lophiostomataceae* (Hyde et al. 2024). Members of *Lophiostomataceae* reported as saprobes on twigs, stems or bark of various woody plants and herbaceous plants in terrestrial and aquatic habitats (Mapook et al. 2020). The sexual morph characterized by having superficial or semi-immersed to densely erumpent, globose to subglobose, dark-brown to black and carbonaceous ascomata, with a peridium of lightly pigmented, thin-walled cells of *textura prismatica*, and septate, long, hyaline, anastomosing and branched, cellular pseudoparaphyses. Their asci are 8-spored, bitunicate, fissitunicate, cylindrical to clavate, comprising 1-seriate or partially 2-seriate, hyaline to pale brown, narrowly fusiform, 3–5-septate or muriform ascospores that are slightly constricted at each septum and with acute ends. The ascospores are smooth-walled, with a distinct oil drop in each cell, and with terminal appendages (Hongsanan et al. 2020). The asexual morph is reported as coelomycetous, characterized by semi-immersed, uni-loculate or rarely bi-loculate, subglobose, reddish brown pycnidia, with conidiophores reduced to conidiogenous cells. These conidiogenous cells are cylindrical, phialidic, and hyaline, formed at the end and on the sides, producing subglobose to cylindrical, hyaline, aseptate conidia (Hongsanan et al. 2020). An updated tree for the family is shown in Figure 3.3.

Lentistoma A. Hashim., K. Hiray. & Kaz. Tanaka, Studies in Mycology 90: 169 (2018)

Hashimoto et al. (2018) established *Lentistoma* (*Le*.), as a new genus, accommodating *Massarina bipolaris* K.D. Hyde, which was renamed *Le. bipolaris* and designated as the type species. *Lentistoma aquaticum* was introduced by Dong et al. (2020) as the second species in this genus. Members of *Lentistoma* were found as saprobes on woody plants or submerged wood (Pinnoi et al. 2006; Pinruan et al. 2007; Dong et al. 2020; Hashimoto et al. 2018; Hyde et al. 2024; Pem et al. 2024). To date,

one species of this genus (*Le. bipolaris*) has been reported from peat swamp forests (Pinnoi et al. 2006; Pinruan et al. 2007). In this study, we introduce *Le. narathiwatense* as a novel species found on the submerged rachis of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.



Note *Teichospora rubriostiolata* (TR 7) and *T. trabicola* (C 134) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.3 Phylogram generated from the ML analysis based on the combined LSU, SSU, ITS, *tef-1α* and *rpb2* sequence data of *Lophiostomataceae*

Lentistoma narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.4

Index Fungorum number: IF903515; Facesoffungi number: FoF 17518

Etymology – Epithet refers to Narathiwat Province where the holotype was collected

Holotype – MFLU 24-0485

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 250–280 μm long, 280–332 μm wide, scattered, superficial, conical, carbonaceous, brown to dark brown, ostiolate, and papillate. *Peridium* 12.5–23 μm wide ($\overline{x}$ = 17 μm, n = 20), comprising of carbonaceous, *textura prismatica* to *textura angularis* cells. *Pseudoparaphyses* 1.6–3 μm wide ($\overline{x}$ = 2.3 μm, n = 40), numerous, distantly septate, branched, hypha-like, hyaline. *Asci* 85–108 × 10−16.6 ($\overline{x}$ = 96.2 × 14.4 μm, n = 15), 8-spored, bitunicate, cylindrical to clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 22.4–26.5 × 4–6 ($\overline{x}$ = 24 × 5 μm, n = 40), biseriate, fusiform, hyaline to pale brown, 1-septate, constricted at the nearly median septum, the upper cells slightly swollen towards the septum, thin-walled, smooth, surrounded by a hyaline, narrow sheath, elongated at both ends, with an internal narrow appendage-like chamber at both ends of ascospores up to 3 μm. Asexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 1.8 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, umbonate, felted, medium dense, dull, entire edge, no sporulation, surface grey with white centre and margin, reverse greyish orange with yellowish centre and whitish margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 11B (MFLU 24-0485, holotype); ex-type living culture MFLUCC 24-0569.

GenBank numbers – MFLUCC 24-0569: ITS = PV271865, LSU = PV271907, SSU = PV263309, *rpb2* = PV340515, *tef-1α* = PV340486.

Notes – Phylogenetically, our strain (MFLUCC 24-0569) formed a robust subclade with *Lentistoma aquaticum* (MFLUCC 18-1275) and *Le. bipolare* (CBS 115370, CBS 115375, CBS 110448), with 100% ML and 1.00 PP statistical support in

the combined phylogenetic analyses of LSU, SSU, ITS, *tef-1α* and *rpb2* (Figure 3.3). Morphologically, *Le. narathiwatense* (MFLU 24-0485) is similar to *Le. bipolare,* but differs in having superficial, longer and narrower ascomata (250–280 × 280–332 μm vs. 160–200 × 470–540 μm), narrower carbonaceous peridium (12.5–23 μm vs. 25–45 μm), shorter asci (85–108 μm vs. 105–140 μm), slightly shorter ascospores (22.4–26.5 μm vs. 20–33 μm), longer sheaths at both ends of the ascospores (15–19 μm vs. 5–10 μm) and an appendage-like chamber at both ends of the ascospores despite a short chamber in the latter (Hashimoto et al. 2018). *Lentistoma narathiwatense* (MFLU 24-0485) is easily distinguishable from *Le. aquaticum* in having smaller and narrower ascospores (22.4–26.5 × 4–6 μm vs. 38–43 × 6.5–8.5 μm) and the presence of a sheath surrounding the ascospore, which is absent in *Le. aquaticum* (Dong et al. 2020). Therefore, we introduce *Le. narathiwatense* as a novel species based on morphological and phylogenetic evidence.

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016)

Dictyosporium Corda, Beiträge zur gesammten Natur- und Heilwissenschaften: 87 (1836)

Dictyosporium was established by Corda (Witenweber 1836) to accommodate *Dictyosporium elegans*. Based on Species Fungorum (2024) there are 72 accepted morphological species in this genus. Sexual morph: the genus is characterized by having subglobose superficial ascomata, cylindrical, bitunicate asci, uniseptate, fusiform, hyaline ascospores, with or without a sheath. Asexual morph: sporodochial colonies, micronematous to macronematous conidiophores and cheiroid, digitate complanate conidia with several parallel rows of cells (Boonmee et al. 2016; Yang et al. 2018). *Dictyosporium aquaticum* was described by Abdel-Aziz as a new species on date palm from Egypt (Liu et al. 2015). Batista (1951) described *Dictyosporium coccophilum* as a new species on *Cocos nucifera* in Brazil. Manoharachary et al. (2007) introduced *Dictyosporium dkagarwalii* as a new species on the epicarp of dead coconut from India. McKenzie (2010) described *Dictyosporium hughesii*, *Dictyosporium rhopalostylidis* on dead leaves of *Rhopalostylis sapida* (Aceraceae) in New Zealand. *Dictyosporium palmae* was described by Abdel-Aziz (2016) on submerged decaying fronds of *Phoenix dactylifera* (Aceraceae) in Egypt.

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

Didymosphaeria Fuckel, Jahrb. Nassauischen Vereins Naturk. 23-24: 140 (1870)

Didymosphaeria is a saprobic or parasitic on plants and other fungi. There are 25 accepted morphological species, of which only 4 species have molecular (Hyde et al. 2024; Pem et al. 2024). Further research utilizing molecular markers is necessary to fully elucidate the taxonomy of *Didymosphaeria*. The genus characterized by having solitary, scattered, immersed ascomata, papillate ostiole with a pore-like opening, bitunicate, fissitunicate, cylindrical asci with 2–4-spored, or 8-spored (Fuckel 1870). The asexual morph is coelomycetes. Conidiomata separate or aggregated, conidiogenous cells phialidic, conidia aseptate, fusiform, ellipsoidal to obovoid (Zhang et al. 2012; Ariyawansa et al. 2014). Hyde et al. (1999) described *Didymosphaeria calamicola* on dead rachis of *Calamus* sp. (Arecaceae) from Australia.

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

Leptospora Rabenh., Hedwigia 1: 116 (1857)

Leptospora Rabenh (1857) is a saprobic genus belonging to the family *Phaeosphaeriaceae* (*Pleosporales, Dothideomycetes*) (Hongsanan et al. 2020) and comprises 25 species up to date (Species Fungorum 2025). *Leptospora* is characterized by large, flask-shaped ascomata and long, cylindrical asci with filiform, multi-septate and thin ascospores. Species in this genus have been reported to have red colored apical part in the ostiolar canal and stains the host tissue with reddish-purple pigments (Shoemaker 1976; Crous et al. 2006; Hyde et al. 2016). *Leptospora* was introduced by Rabenh (1857) to accommodate *L. rubella*, the type species of *Leptospora*, which was previously known as *Sphaeria rubella* Pers.

Leptospora and *Ophiobolus* Riess share a similar ascospore morphology (Shoemaker 1976; Crous et al. 2006); therefore, Hyde et al. (2016) updated the phylogenetic analyses for *Phaeosphaeriaceae* and described three new species, *L. aquatica, L. galii, L. thailandica* and provided reference specimen from UK for *L. rubella*. Zhang et al. (2019) introduced *L. hydei*, and Mapook et al. (2020) introduced two new species based on phylogenetic analyses of combined LSU, ITS, SSU, TEF1 and RPB2 sequence data.

The genus was reported worldwide from America, Asia and Europe on various hosts, such as Arecaceae, Asteraceae, Betulaceae, Celastraceae, Euphorbiaceae, Fagaceae, Musaceae, Orobanchaceae, Poaceae, Ranunculaceae, Rubiaceae and Verbenaceae. *Leptospora jubaeae*, introduced from dead leaves of *Jubaea spectabilis* in Chile (Spegazzini 1921).

Table 3.1 World distribution of *Leptospora* species

Taxa	Host/Substrate	Location	References
Leptospora jubaeae	dead leaves of *Jubaea spectabilis* (Arecaceae)	Chile, Atacama	(Spegazzini 1921)
Leptospora chromolaenae	dead stems of *Chromolaena odorata*	Thailand	(Mapook et al. 2020)
Leptospora clematidis	dead stems of *Clematis patens*	Belgium	(Phukhamsakda et al 2020)
Leptospora elaeodendri	stem of *Elaeodendron roxburghii*	India	(Patil and Ramesh 1986)
Leptospora euphrasiae	dead stems of *Euphrasia*	NA	(Murashkinsky 1924)
Leptospora hydei	decaying branch	China	(Zhang et al. 2019)
Leptospora implexa	dead roots of *Sorghum halepense* and on lower part of sheathing leaves of *Andropogon*	USA	(Walker 1980)
Leptospora indica	dead herbaceous stems	India	(Pande 1979)

Table 3.1 (continued)

Taxa	Host/Substrate	Location	References
Leptospora inquinans	-	Japan	(Hino and Katum 1955)
Leptospora macarangae	dead leaf petioles of *Macaranga tanarius*	China	(Tennakoon et al. 2021)
Leptospora musae	*Musa sapinetum*	USA	(Landb. Suriname 1912)
Leptospora nuda	dead branches of *Fagus taurica*:	Crimea	(Gucevič 1955)
Leptospora ovina	rotten trunk	Germany	(Persoon 1801)
Leptospora phraeana	dead stems of *Chromolaena odorata*	Thailand	(Mapook et al. 2020)
Leptospora rubella	Paper is not available	-	(Rabenhorst 1857)
Leptospora thailandica	dead branches of *Duranta*	Italy	(Hyde et al. 2016)

Pseudoastrosphaeriellaceae Phookamsak & K.D. Hyde, Fungal Diversity 74: 181 (2015)

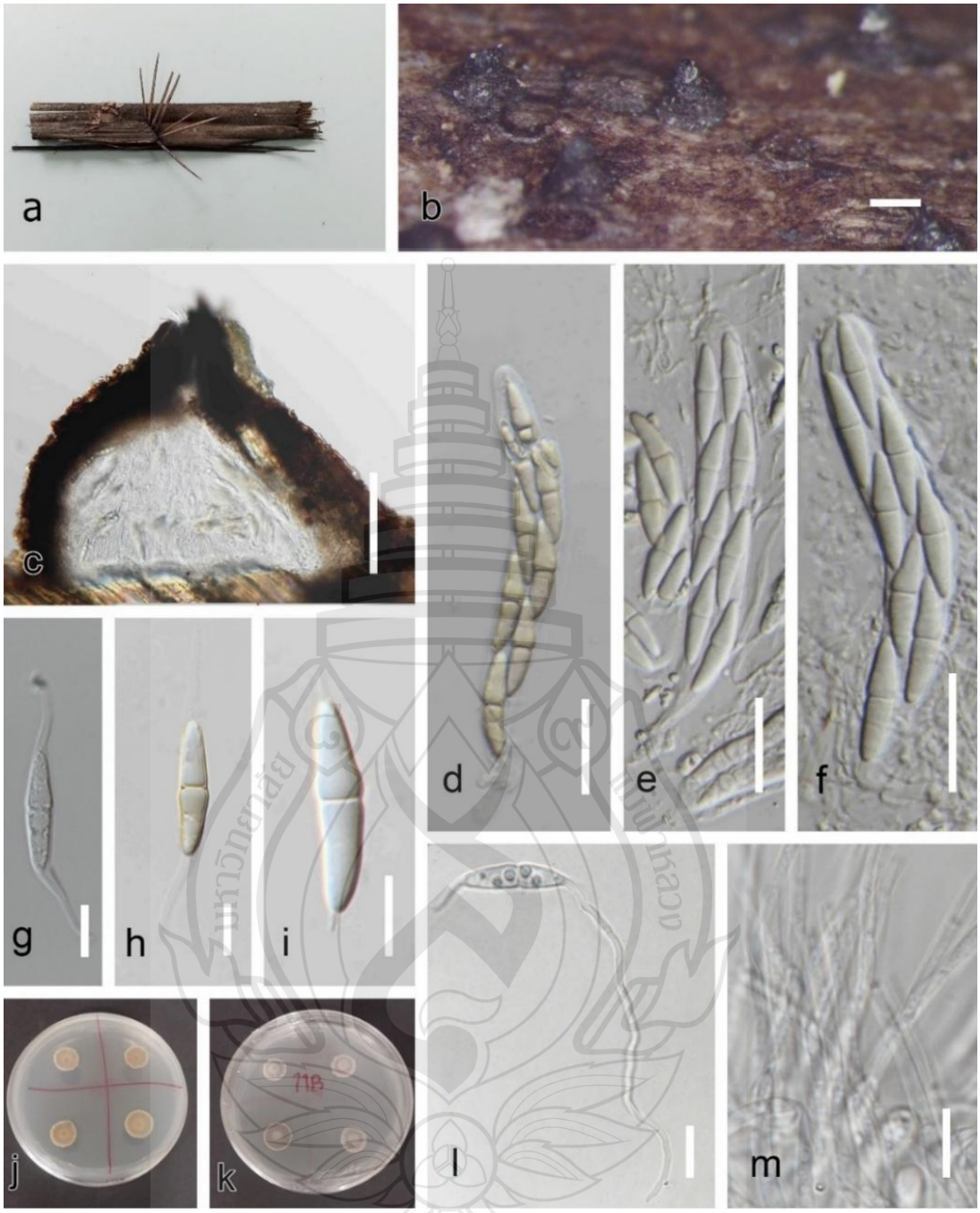
Carinispora K.D. Hyde, Botanical Journal of the Linnean Society 110: 97 (1992)

Carinispora was introduced as a new genus by Hyde (1992a) on *Nypa fruticuns* from Brunei. Based on Species Fungorum (2025) there are 2 accepted morphological species while molecular data is limited, only the small subunit ribosomal RNA (SSU) and translation elongation factor-1 alpha (EF1a) are available for *Carinispora nypae* BCC 36316.

Morphologically, the *Carinispora* genus is characterized by its sexual morph, where the ascomata emerged, presenting a brown, crust-like appearance with a circular shape and a small central ostiole. They are lenticular and submerged beneath a clypeus, exhibiting variable stromatic development. The peridium presents a light brown hue, featuring slender, thin-walled elongate cells along the sides and robust, thick-walled cells with a textura epidermoidea structure at the base. Asci are 8-spored, taking on a clavate-cylindrical form, featuring a pedunculate structure and a fissitunicate arrangement, along with the presence of an ocular chamber. Ascospores are arranged in two rows (biseriate), exhibiting 7-8 septa, with the two central cells being the largest. They present a yellow to light brown color and are enveloped by a gelatinous sheath (Hyde 1992a). Hyde (1992a), introduced *Carinispora nypae* in the intertidal region on decaying fronds of *Nypa fruticans* from Brunei. Hyde (1994) introduced *Carinispora velatispora* in intertidal region on rachis of *Oncosperma tigillarium* from Brunei.

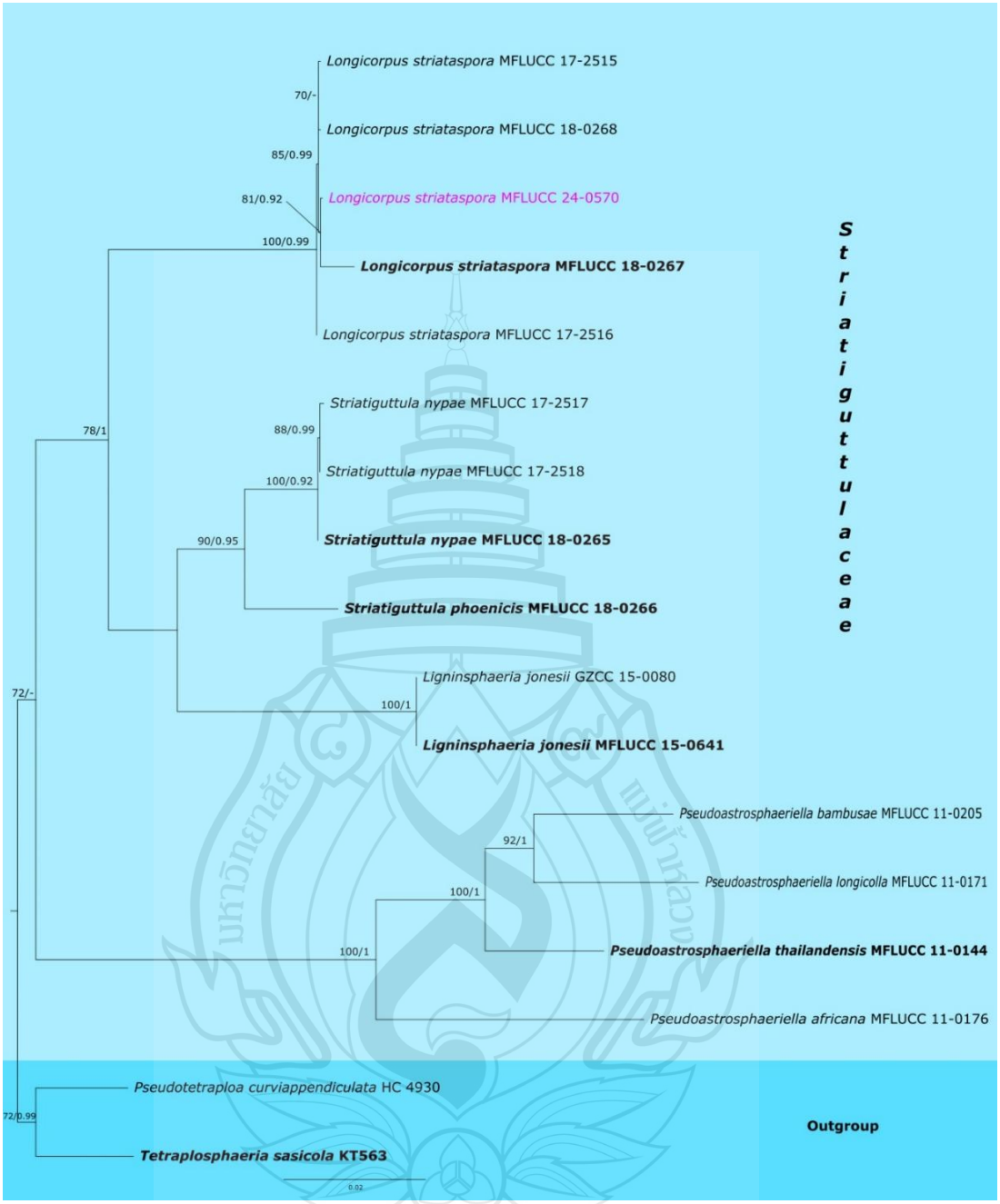
Striatiguttulaceae S.N. Zhang, K.D. Hyde & J.K. Liu, MycoKeys 49: 110 (2019)

Zhang et al. (2019) introduced *Striatiguttulaceae* based on the polyphasic approaches of morphology, phylogeny and divergence time estimates. Their phylogenetic analysis, based on the combined LSU, SSU, *tef-1α* and *rpb2* data, revealed a distinct clade of *Striatiguttulaceae* within *Pleosporales*, which comprises two separate subclades, prompting the introduction of two novel genera in this family: *Longicorpus* and *Striatiguttula*. Phylogenetically, the family is closely related to *Ligninsphaeriaceae* and *Pseudoastrosphaeriellaceae*, but it differs in the morphology of its ascomata and ascospores (Zhang et al. 2016, 2019). Species in *Striatiguttulaceae* are saprobic on palm hosts in mangrove habitats. The sexual morph is characterised by immersed, erumpent or superficial, papillate, ostiolate stromata, a several-layered, brown to hyaline peridium, trabeculate pseudoparaphyses, cylindric-clavate, pedicellate asci, and eight fusiform or ellipsoidal, 1–3-septate, striate, hyaline to brown ascospores with paler end cells and a mucilaginous sheath (Zhang et al. 2019). An updated tree for the family is shown in Figure 3.5.



Note a Host. b Appearance of ascomata on the host substrate. c A vertical section of an ascoma. d–f Asci. g–i Ascospores. j, k Colonies on the CMA. l Germinated ascospore. m Pseudoparaphyses. Scale bars: b = 200 μm, c = 100 μm, d–f = 25 μm, g–i, m = 10 μm.

Figure 3.4 *Lentistoma narathiwatense* (MFLU 24-0485, holotype)



Note *Pseudotetraploa curviappendiculata* (HC 4930) and *Tetraplosphaeria sasicola* (KT563) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.5 Phylogram generated from the ML analysis based on the combined LSU, SSU, *tef-1α* and *rpb2* sequence data of *Striatiguttulaceae*

Longicorpus S.N. Zhang, K.D. Hyde & J.K. Liu, MycoKeys 49: 117 (2019)

Longicorpus (*L.*), was introduced by Zhang et al. (2019), with *L. striataspora* as the type species, which was found as a saprobe on mangrove palm (*Nypa fruticans*). Currently, there is only one accepted species listed in Index Fungorum (2024). To date, no report of this genus has been documented from peat swamp forests. In this study, we found *L. striataspora* as a saprobe on submerged rachides of *Eleiodoxa conferta* in the peat swamp forest in Narathiwat, Thailand, and report this as a new host and habitat record.

Longicorpus striataspora (K.D. Hyde) S.N. Zhang, K.D. Hyde & J.K. Liu (2019) Figure 3.6

Index Fungorum number: IF 838919; Facesoffungi number: FoF 05037

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 250–450 × 200–500 µm ($\overline{x}$ = 435 × 350 µm, n = 15), scattered to gregarious, immersed, and erumpent, sometimes visible as a slightly raised, dome-shaped area, ostiolate, papillate, long neck up to 990 µm, black. *Peridium* 11–15 µm wide, composed of brown to pale brown angular cells. *Hamathecium* comprising up to 1.7 µm wide, septate, branched, filamentous, trabeculate, anastomosing pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 90–140 × 10−15 µm ($\overline{x}$ = 112 × 12 µm, n = 15), 8-spored, bitunicate, cylindric to clavate, pedicellate, rounded apex, with an ocular chamber. *Ascospores* 25–38 × 5.4–7.3 µm ($\overline{x}$ = 31 × 6.2 µm, n = 30), overlapping uniseriate to biseriate, pale brown to brown, fusiform, upper end rounded, basal end slightly acute, 1–3-septate, constricted at the central septum, the upper middle cell slightly swollen towards the central septum, middle cells larger and longer, apical cells paler and smaller, straight or slightly curved, striate, guttulate, surrounded by a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, fluffy, smooth, surface white with brownish orange centre, reverse greyish yellow with whitish margin and brown centre.

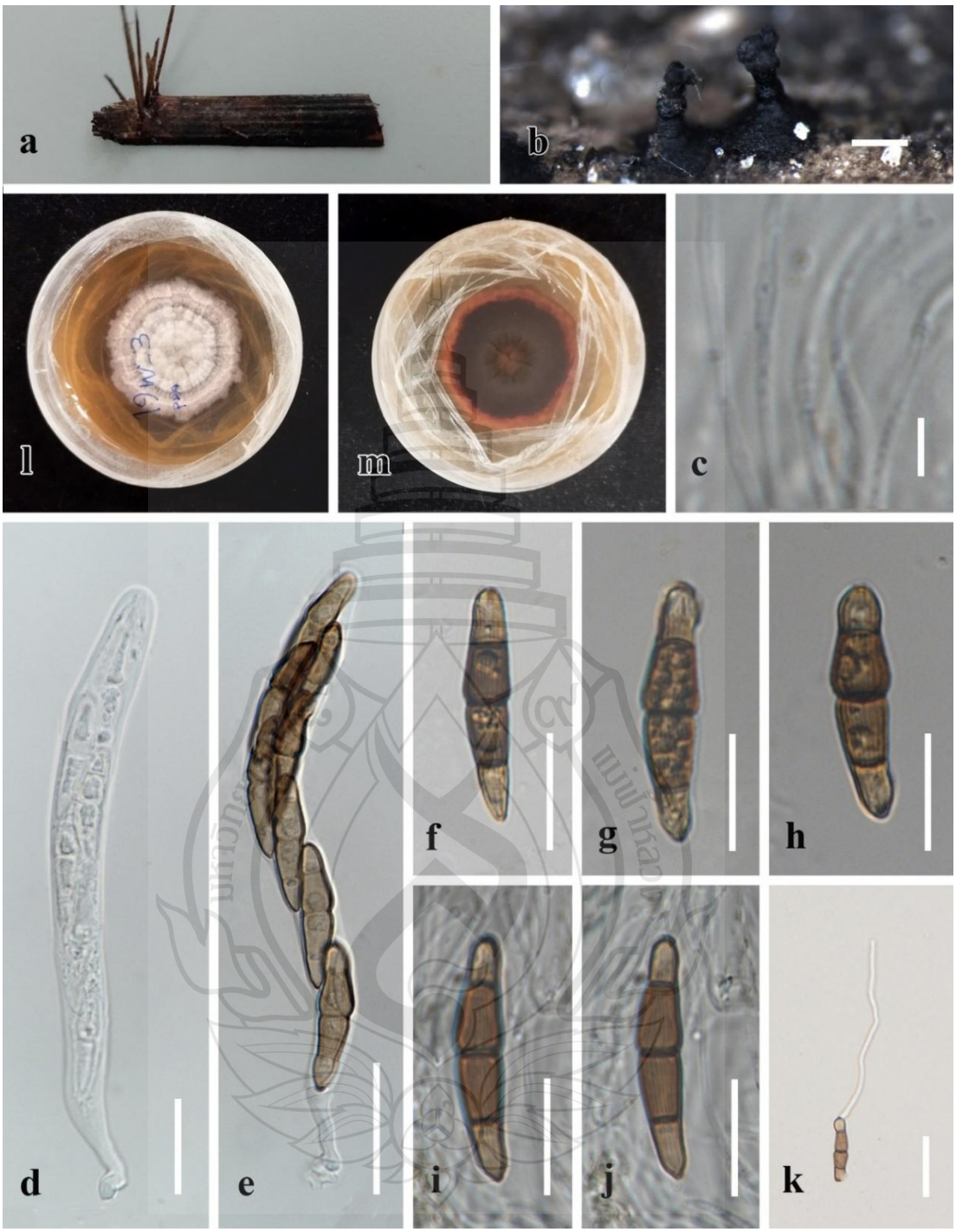
Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta,* 4 August 2023, O. Karimi, 19W-3 (MFLU 24-0486); living culture MFLUCC 24-0570.

Known hosts – *Eleiodoxa conferta* (This study), *Nypa fruticans* (Hyde 1988, Zhang et al. 2019), *Phoenix paludosa* (Zhang et al. 2019).

Known distribution – Brunei (Hyde 1988), Thailand (Zhang et al. 2019, this study).

GenBank numbers – MFLUCC 24-0570: ITS = PV271866, LSU = PV271908, SSU = PV263310, *rpb2* = PV340516, *tef-1α* = PV340487.

Notes – Our strain (MFLUCC 24-0570) clustered with *Longicorpus striataspora* (MFLUCC 18-0267) in the combined phylogenetic analysis of LSU, SSU, *tef1-α,* and *rpb2* data, with statistical support of 81% ML and 0.92 PP (Figure 3.5). Comparing the nucleotide sequences between our strain (MFLUCC 24-0570) and the type species, there is one nucleotide difference in LSU, three nucleotide differences in *rpb2*, and six nucleotide differences in *tef-1α.* Morphologically, our strain (MFLU 24-0486) resembles *L. striataspora* (MFLU 18-1580) in having immersed, carbonaceous ascomata with a long neck, and the striate, guttulate, fusiform, 1–3-septate ascospores, with larger middle cells and relatively smaller and paler apical cells, surrounded by a mucilaginous sheath, with slight differences in the size of asci (90–140 × 10−15 μm vs. 85–160 × 10−17 μm), and ascospores (25–38 × 5.4–7.3 μm vs. 24–45 × 7–8.8 μm) (Zhang et al. 2019). Therefore, we report our strain (MFLU 24-0486) as a new host record of *L. striataspora* on *Eleiodoxa conferta* from Thailand based on morphology and phylogenetic data. Additionally, we document *L. striataspora* as a new habitat record from the peat swamp forest.



Note a Host. b Appearance of ascomata on natural substrate. c Pseudoparaphyses. d, e Asci. f–j Ascospores. k Germinated ascospore. l, m Colonies on the PDA. Scale bars: b = 250 µm, c = 5 µm, d = 20 µm, e, k = 30 µm, f–j= 15 µm.

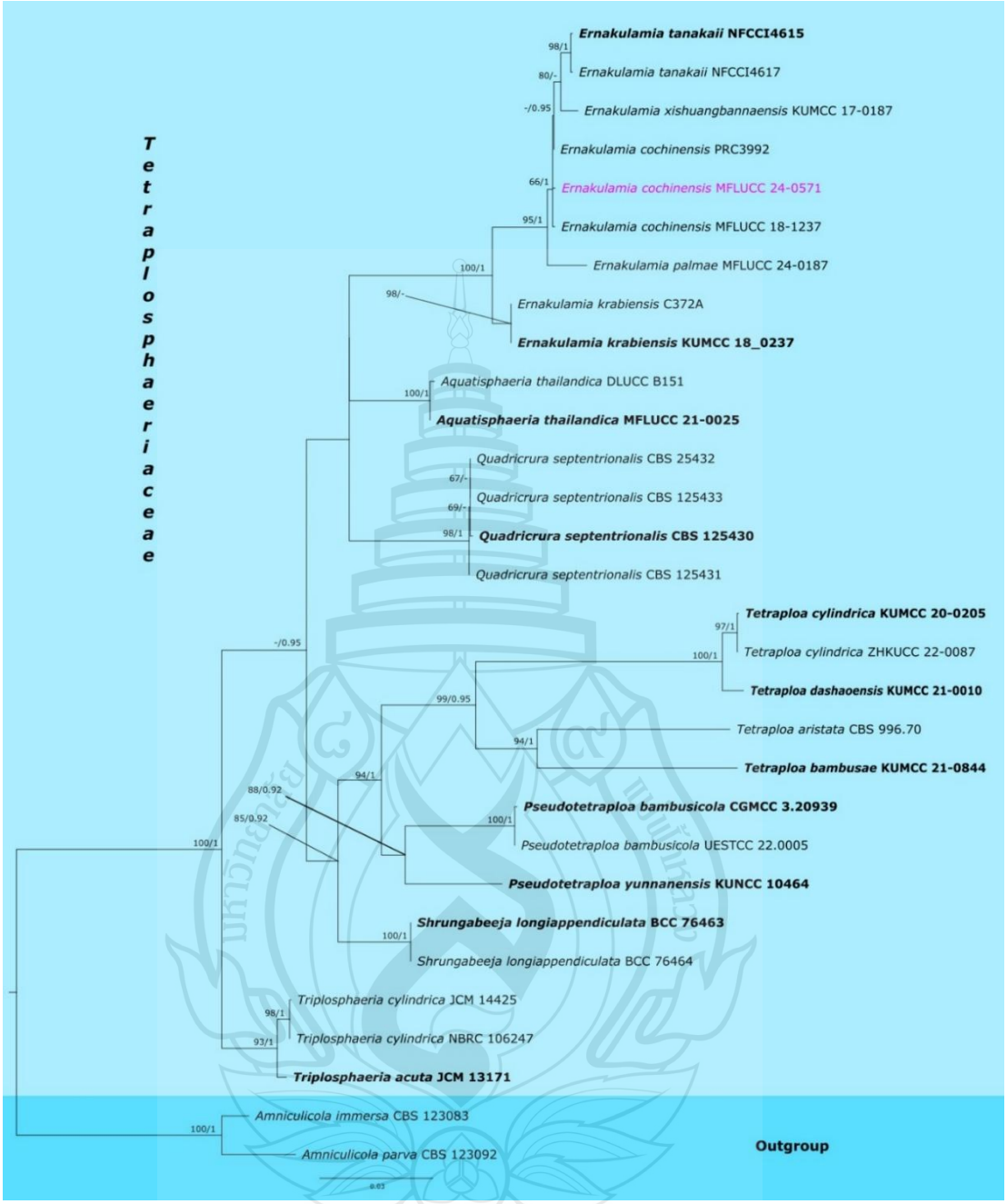
Figure 3.6 *Longicorpus striataspora* (MFLU 24-0486, new host and habitat record)

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., Studies in Mycology 64: 177 (2009)

Tanaka et al. (2009) introduced *Tetraplosphaeriaceae* with *Tetraplosphaeria* as the type genus, along with the genera *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria*, and *Triplosphaeria*, based on morphological characteristics and the combined phylogenetic analyses of SSU and LSU data. Hyde et al. (2013) considered *Tetraplosphaeria* a synonym of *Tetraploa* and prioritized the latter name due to the nomenclatural precedence. Recently, Zhang et al. (2023) introduced *Pseudopolyplosphaeria* in this family. Currently, ten genera are accepted in *Tetraplosphaeriaceae*: *Aquatisphaeria*, *Byssolophis*, *Ernakulamia* (*E.*), *Polyplosphaeria*, *Pseudopolyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa*, and *Triplosphaeria* (Tanaka et al. 2009; Hyde et al. 2013, 2024; Pem et al. 2024; Zhang et al. 2024). The family is characterised by Massarina-like sexual morphs, defined by hyaline, 1–3-septate ascospores surrounded by a sheath. Its asexual morphs are distinguished by conidia with setose appendages (Tanaka et al. 2009; Hyde et al. 2013; Tibpromma et al. 2018). An updated tree for the family is shown in Figure 3.7.

Ernakulamia Subram., Kavaka 22/23: 67 (1996)

Ernakulamia cochinensis was originally described as *Petrakia cochinensis* by Subramanian (1957). Ellis (1976) transferred *Petrakia cochinensis* to *Piricauda*, which was subsequently transferred to *Ernakulamia* (Subramanian 1994) based on morphological and ecological evidence. Delgado et al. (2017) provided molecular sequence data for *E. cochinensis* and placed *Ernakulamia* within the family *Tetraplosphaeriaceae*. Currently, there are five accepted species of *Ernakulamia* listed in the Species Fungorum (2024). To date, no species of this genus have been reported from peat swamp forests. In this study, we found *E. cochinensis* on *Cyrtostachys renda* from the peat swamp forest in Narathiwat, Thailand.



Note *Amniculicola parva* (CBS 123092) and *A. immersa* (CBS 123083) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in red, while the type strains are in bold.

Figure 3.7 Phylogram generated from ML analysis based on the combined LSU, ITS, SSU, *tub2* and *tef-1α* sequence data of *Tetraplosphaeriaceae*

Ernakulamia cochinensis (Subram.) Subram., Kavaka 22/23: 67 (1996) [1994] Figure 3.8

Index Fungorum number: IF374840; Facesoffungi number: FoF 09277

Saprobic on the submerged petiole of *Cyrtostachys renda*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host scattered or in small groups, black, glistening. *Conidiophores* and *conidiogenous cells* not seen. *Conidia* 38–45 × 21–31 μm, variable in shape, subglobose, obconical, broadly pyriform, dark brown to black, with 3–7 appendages. *Appendages* 17–117 × 2–5 μm ($\overline{x}$ = 53 × 3.9 μm, n = 20), cylindrical, straight or flexuous, septate, brown, smooth.

Culture characteristics – Colonies on the PDA reaching 3 cm diam. after 14 days at room temperature (25–28 °C). Colony lobate to irregular, dense, umbonate, mycelia superficial to immersed, dull, surface greyish-brown with light grey to whitish margin, reverse dark brown with dark orange margin.

Material examined – Thailand, Narathiwat, peat swamp forest, on submerged petiole of *Cyrtostachys renda*, 4 August 2023, O. Karimi, 45R (MFLU 24-0487); living culture MFLUCC 24-0571.

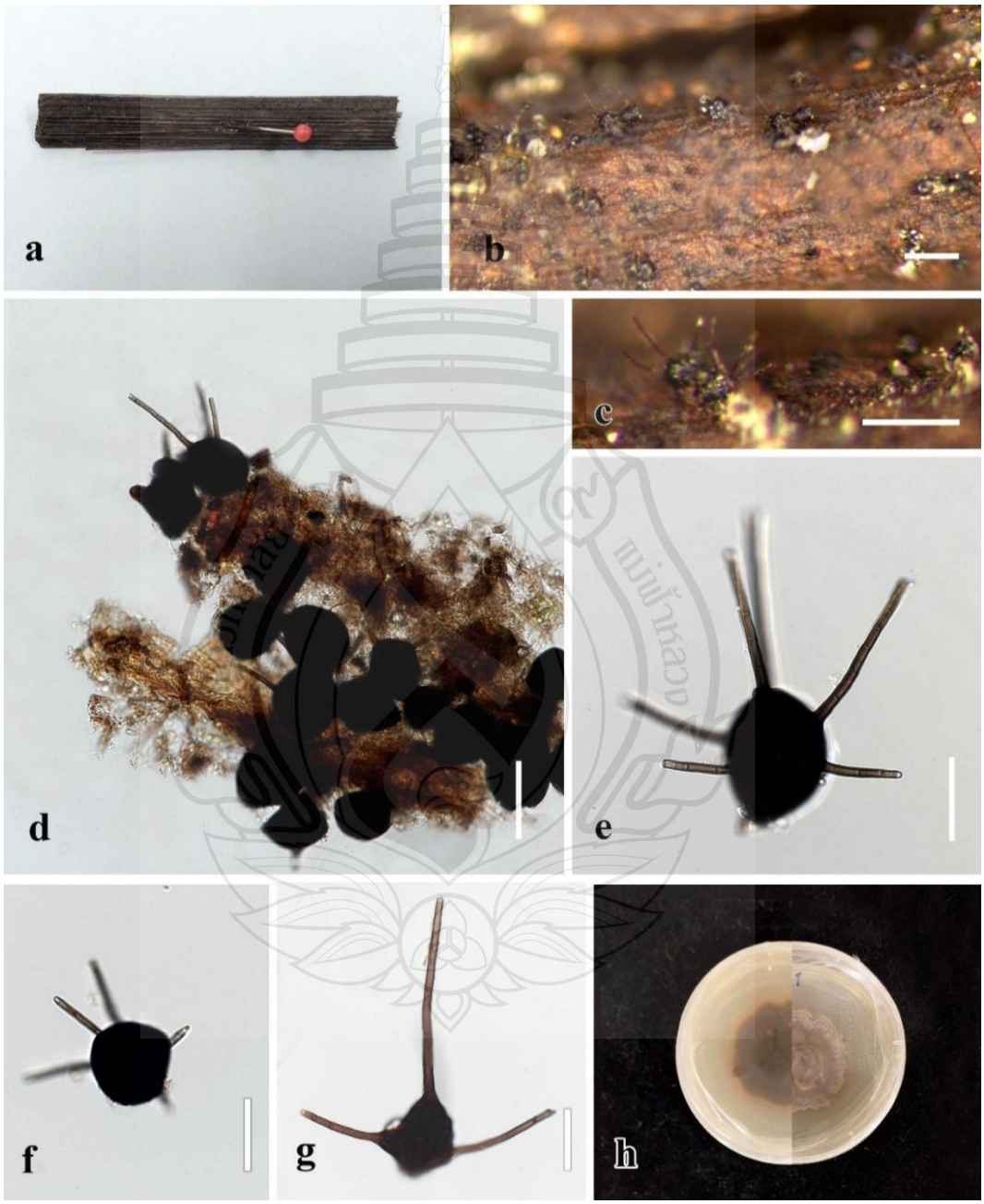
Known hosts – *Astrocaryum standleyanum* (Delgado et al. 2017), *Cocos nucifera* (Subramanian 1957), *Cyrtostachys renda* (This study).

Known distribution – India (Subramanian 1957), Panama (Delgado et al. 2017), Thailand (This study).

GenBank numbers – MFLUCC 24-0571: ITS = PV271867, LSU = PV271909, SSU = PV263311, *tef-1α* = PV340483.

Notes – Phylogenetically, our strain (MFLUCC 24-0571) clustered with *Ernakulamia cochinensis* strains (PRC3992, MFLUCC 18-1237) with 66% ML and 1.00 PP statistical support (Figure 3.7). The nucleotide comparisons showed that our strain has similar ITS, LSU, and *tub2* sequence data with *E. cochinensis* (PRC 3992). However, SSU and *tef1-α* sequences cannot be compared, as they are unavailable for *E. cochinensis* (PRC 3992). Morphologically, our strain (MFLU 24-0487) resembles *E. cochinensis* (PRC 3992) due to having variable-shaped (subglobose, obconical, broadly pyriform) conidia that are dark brown to black with cylindrical, straight or flexuous, septate, brown, smooth appendages. However, our isolate differs from PRC 3992 in their smaller conidial size (38–45 × 21–31 μm vs. 24–60 × 18–53 μm) and smaller

appendages (17–117 × 2–5 μm vs. up to 132 × 3–5 μm). Thus, we identified our strain (MFLU 24-0487) as *E. cochinensis* based on phylogenetic analyses and morphological characters. We report our strain (MFLU 24-0487) as a new host record of *E. cochinensis* on *Cyrtostachys renda* from Thailand. Additionally, we document *E. cochinensis* as a new habitat record from the peat swamp forest.



Note a Host. b, c Colonies on the host. d–g Conidia. h Colonies on the PDA. Scale bars: b, c = 250 μm, d, e = 20 μm, g = 40 μm.

Figure 3.8 *Ernakulamia cochinensis* (MFLU 24-0487, a new host and habitat record)

Megacapitulaceae O. Karimi, R. Asghari & K.D. Hyde fam. nov.

Index Fungorum number: IF903516; Facesoffungi number: FoF 17519

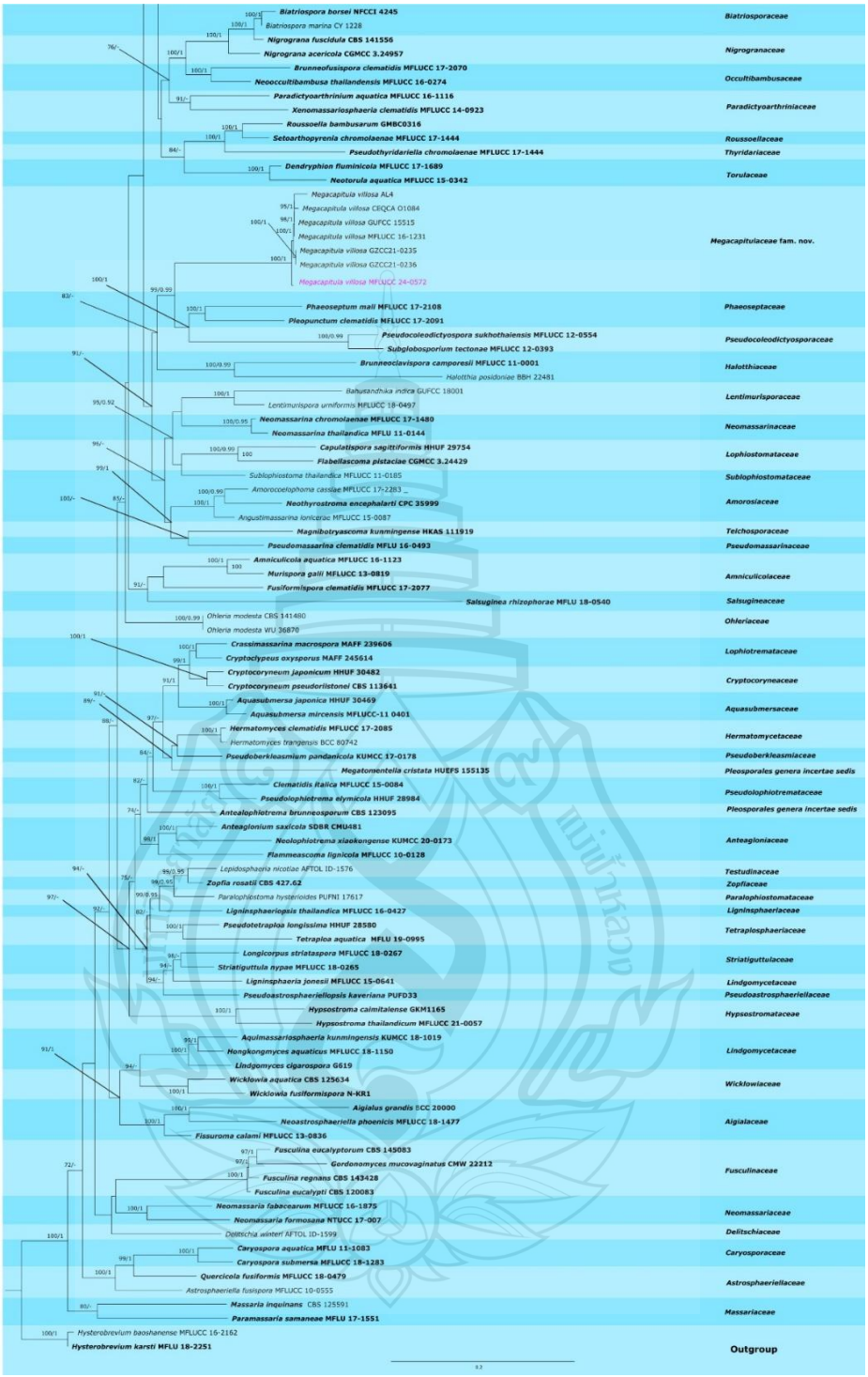
Etymology – The name reflects the type genus.

Type genus – *Megacapitula* Chen & Tzean

Saprobic on decaying leaves. Asexual morph: Hyphomycetous. *Mycelium* composed of branched, septate, smooth, roughened, verrucose, hyaline or pigmented hyphae. *Conidiophores* micronematous. semimacronematous, mononematous, simple or branched, pale brown to brown, smooth, roughened or verrucose. *Conidiogenous cells* integrated, terminal, lateral or rarely intercalary, determinate. *Conidia* holoblastic, solitary, ovoid, obclavate, ellipsoidal or obpyriform, muriform, pigmented with densely packed, branched or unbranched, hairlike appendages at the apex. Sexual morph: Not observed.

Notes – Based on the morphology and multi-gene phylogeny, a new family, *Megacapitulaceae*, is introduced within *Pleosporales* to accommodate *Megacapitula* (*M*.). *Megacapitula* has been placed in *Pleosporales* genera *incertae sedis* (Wijayawardene et al. 2022; Hyde et al. 2024). In our phylogenetic analysis, all the *Megacapitula* isolates clustered in a single cluster separated from the families *Phaeoseptaceae* and *Pseudocoleodictyosporaceae*, with 99% ML and 0.99 PP statistical support (Figure 3.9). Morphologically, *Megacapitulaceae* differs from *Pseudocoleodictyosporaceae* in lacking sporodochial colonies on the substrate and dictyosporous conidia and having hair-like appendages at the apex of the conidia (Doilom et al. 2017). *Megacapitulaceae* differs from *Phaeoseptaceae* in lacking sporodochial colonies on the substrate, acrogenous conidia, and a hyaline, elliptical to globose basal cell in the conidia. Additionally, *Megacapitulaceae* possesses hair-like appendages at the apex of the conidia, which are absent in *Phaeoseptaceae* (Liu et al. 2019).

Figure 3.9 Phylogram generated from the ML analysis based on the combined LSU, ITS, SSU and *tef-1α* sequence data of *Pleosporales*



Note *Hysterobrevium baoshanense* (MFLUCC 16-2162) and *H. karsti* (MFLU 18-2251) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in red, while the type strains are in bold.

Figure 3.9 (continued)

Megacapitula J.L. Chen & Tzean, Mycological Research 97: 347 (1993)

Chen and Tzean (1993) introduced *Megacapitula*, with *M. villosa* as the type species. Prabhugaonkar and Bhat (2011) provided the ITS sequence data for the type species *M. villosa* based on a collection from India. To date, no species of this genus have been reported from peat swamp forests. In this study, we report *M. villosa* on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Megacapitula villosa J.L. Chen & Tzean, Mycological Research 97: 347 (1993). Figure 3.10

Index Fungorum number: IF359484; Facesoffungi number: FoF11816

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on the host solitary, scattered, black. *Mycelium* mostly immersed, composed branched, septate, brown to dark brown hyphae. *Conidiophores* not seen. *Conidiogenous cells* not seen. *Conidia* 150–180 × 50–60 μm ($\overline{x}$ = 165 × 54 μm, n = 10), holoblastic, solitary, scattered, oblong to ovoid, ellipsoidal, brown, dark brown or black, smooth, with up to 90 μm long and 1.5 μm wide, hairy, aseptate, unbranched, hyaline apical appendages. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 3 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, dense, dull, umbonate, felted, entire edge, surface brown with grey margin and reverse dark brown to black.

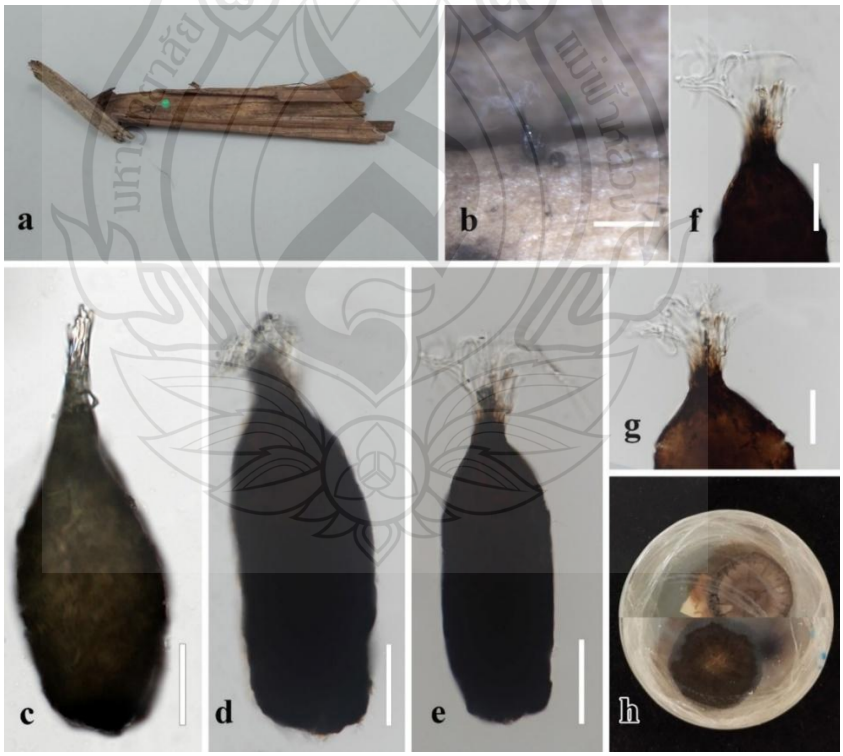
Material examined – Thailand, Narathiwat, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, S5PP8N3 (MFLU 24-0488), living culture MFLUCC 24-0572.

Known hosts – broad-leaved trees (Chen and Tzean 1993), decaying fronds of *Caryota urens* (Prabhugaonkar and Bhat 2011), *Eleiodoxa conferta* (This study), dead rachides of *Roystonea regia* (Zhang et al. 2024).

Known distribution – China (Chen and Tzean 1993; Zhang et al. 2024), India (Prabhugaonkar and Bhat 2011), Thailand (Boonmee et al. 2021; this study).

GenBank numbers – MFLUCC 24-0572: ITS = PV271868, LSU = PV271910, *rpb2* = PV340518, *tef-1α* = PV340484.

Notes – We recognised our strain (MFLU 24-0488) as *Megacapitula villosa* based on morphology and phylogenetic analyses. Our strain (MFLUCC 24-0572) has identical ITS sequence data with *M. villosa* (GUFCC 15515) (Prabhugaonkar and Bhat 2011), with only 2 nucleotide differences across the 500 bp of the ITS gene region, without including gaps. However, other gene regions of our strain (MFLUCC 24-0572) are not comparable as they are unavailable for *M. villosa* (GUFCC 15515). In the combined phylogenetic analysis of LSU, ITS, SSU and *tef-1α* sequences (Figure 3.9), *M. villosa* (MFLUCC 24-0572) clustered with other *M. villosa* strains, with 100% ML and 1.00 PP statistical support. Morphologically, our collection (MFLU 24-0488) fits well with *Megacapitula*, although it has shorter and narrower conidia (150–180 × 50−60 µm vs. 79.4–230 × 47.6−119 µm) and shorter appendages (up to 400 vs. up to 556 µm long) than the type strain (PPH17) (Chen and Tzean 1993). We report our strain (MFLU 24-0488), as a new host record of *M. villosa* on *Eleiodoxa conferta* from Thailand. Additionally, we document *M. villosa* as a new habitat record from the peat swamp forest.



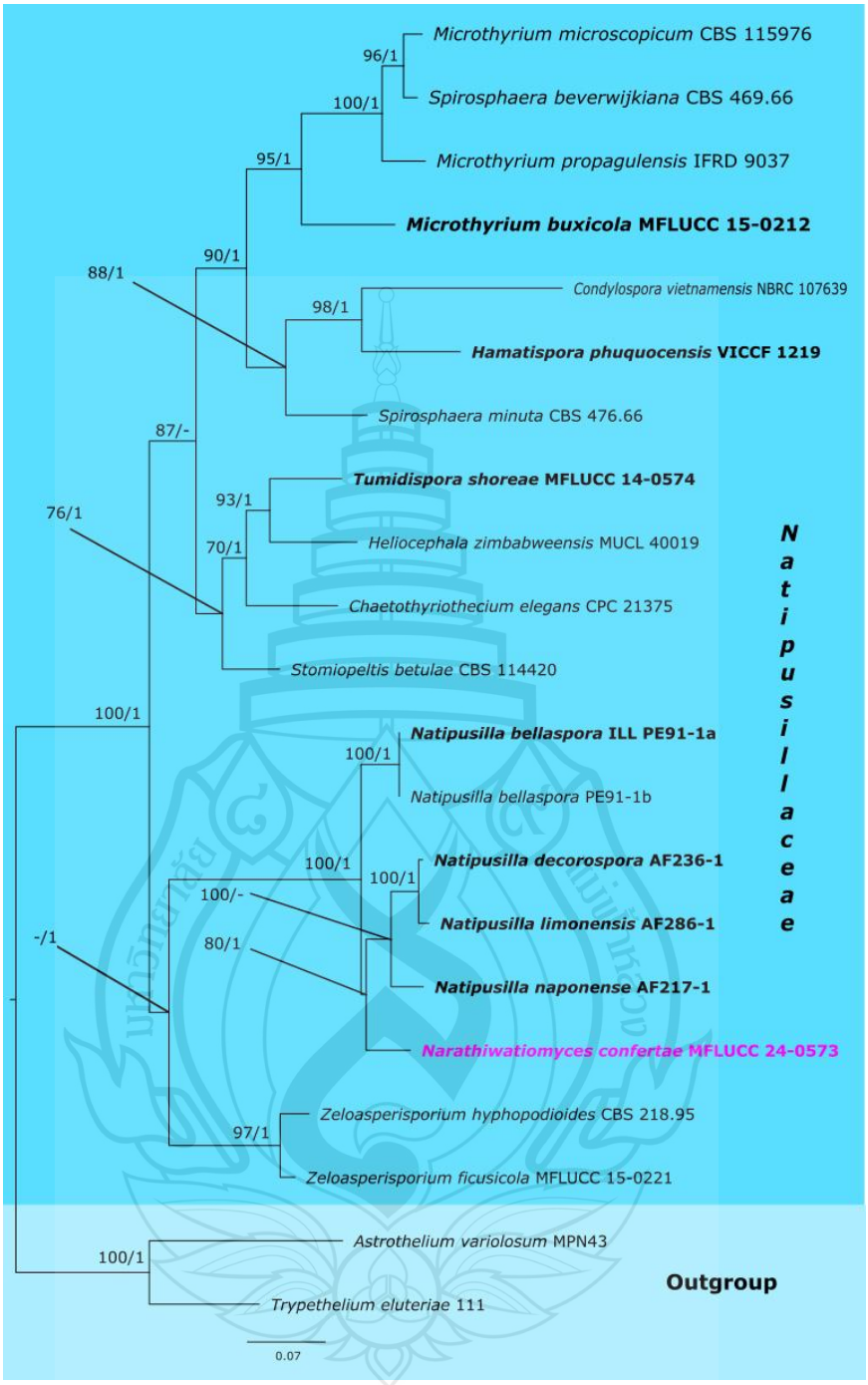
Note a Host. b Colonies on the host. c–g Conidia with appendages. h Colonies on the PDA. Scale bars: b = 250 µm, c = 35 µm, d, e = 40 µm, f, g = 35 µm.

Figure 3.10 *Megacapitula villosa* (MFLU 24-0488, new host and habitat record)

Natipusillales Raja, Shearer, A.N. Mill. & K.D. Hyde, Fungal Diversity 63 (1): 9 (2013)

Natipusillaceae Raja, Shearer & A.N. Mill., Mycologia 104 (2): 570 (2012)

Raja et al. (2012) established the family *Natipusillaceae* to accommodate the genus *Natipusilla* (*Nat.*), comprising four species (*Nat. bellaspora*, *Nat. decorospora, Nat. limonensis*, and *Nat. naponensis*) within *Dothideomycetes*. Subsequently, Hyde et al. (2013) introduced *Natipusillales* to accommodate *Natipusillaceae* based on the combined phylogenetic analyses of LSU and SSU sequence data. Members of *Natipusillaceae* have been reported as saprobes, occurring on submerged, decorticated, or corticated woody debris in freshwater streams and swamps (Ferrer et al. 2011; Raja et al. 2012; Hyde et al. 2013; Yang et al. 2023; Pem et al. 2024). The family is characterised by small ascomata that are globose to subglobose, hemispherical, umbonate, erumpent to superficial, and hyaline to light brown or black, occurring on submerged wood. The peridium wall is membranous, composed of pseudoparenchymatous cells arranged in a *textura angularis* pattern in surface view. Pseudoparaphyses are sparse and septate. Asci are globose, subglobose, obclavate, or clavate, eight-spored, with or without a short pedicel. Ascospores are fusiform to cylindrical, one to several septate, multi-guttulate or eguttulate, hyaline, brown to olivaceous brown, and may possess a gelatinous sheath and/or appendages. In this study, we describe a new genus, *Narathiwatiomyces* (*Nar.*), to accommodate *Nar. confertae*, based on morpho-phylogenetic analyses. An updated tree for the family is shown in Figure 3.11.



Note *Astrothellium variolosum* (MPN43), and *Trypethelium eluteriae* (111) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.11 Phylogram generated from the ML analysis based on the combined LSU and SSU sequence data of *Natipusillaceae*

Narathiwatiomyces O. Karimi, R. Asghari & K.D. Hyde, gen. nov. Figure 3.12

Index Fungorum number: IF903517; Facesoffungi number: FoF 17520

Etymology – The genus name refers to Narathiwat, the region where the fungus was collected.

Holotype – MFLU 24-0489

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* superficial, hemispherical, effused-pulvinate, umbonate, black, papillate. *Peridium* brown, slightly translucent, arranged in cells of *textura angularis*. *Pseudoparaphyses* hyaline, subcylindrical to irregular, septate. *Asci* 8-spored, clavate, rounded at the apex, with or without an apical chamber, with a short pedicellate or absent. *Ascospores* irregularly overlappingly arranged, fusiform, 1-septate, sometimes becoming 3-septate at maturity, brown to olivaceous brown, guttulate, straight or curved. Asexual morph: Not observed.

Notes – *Narathiwatiomyces* has a single species, *Nar. confertae* (MFLUCC 24-0573), formed a robust subclade to *Natipusilla* species (*Nat. decorospora, Nat. limonensis, Nat. naponensis*) with 80% ML and 1.00 PP statistical support in the combined phylogenetic analyses of the LSU and SSU sequence data (Figure 3.11). In the phylogenetic tree, *Nat. bellaspora* isolates clustered separately from other *Natipusilla* species. This may be due to the insufficient sequence data, as only LSU and SSU are available for *Natipusilla* species. However, morphologically, our isolate differs significantly from the *Natipusilla* species. The newly introduced genus, *Narathiwatiomyces* differs from *Natipusilla* species by having hemispherical, effused-pulvinate, umbonate, black, papillate ascomata, septate, hyaline pseudoparaphyses and clavate, short pedicellate asci, whereas the latter has globose to subglobose, hyaline to light brown ascomata, few or absent pseudoparaphyses and globose to obclavate asci (Ferrer et al. 2011). Based on BLAST search results of LSU and SSU sequences, *Nar. confertae* (MFLUCC 24-0573) demonstrates 97.70% and 91.83% similarities to *Nat. bellaspora* (ILL PE91 1a), respectively, with 100% query cover. Based on the pairwise comparison of LSU and SSU nucleotides, *Nar. confertae* (MFLUCC 24-0573) differs from *Nat. bellaspora* (ILL PE91 1a) by 8.3% (74/889 bp) for LSU and 2.8% (30/1040 bp) for SSU without including gaps. However, comparisons for the ITS and *rpb2* sequences cannot be performed due to the lack of sequences for *Natipusilla* species.

Hence, based on these morphological and phylogenetic differences, we establish a new genus to accommodate *Nar. confertae*.

Narathiwatiomyces confertae O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.12

Index Fungorum number: IF903518; Facesoffungi number: FoF 17521

Etymology – The epithet "confertae" refers to the host plant "*Eleiodoxa conferta*"

Holotype – MFLU 24-0489

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 200–280 μm ($\overline{x}$ = 250 μm, n = 10), hemispherical, superficial, scattered, effused-pulvinate, umbonate, raised and mostly wrinkled at the centre, flat at the margin, black, papillate. *Peridium* brown, slightly translucent, comprising of *textura angularis* cells. *Pseudoparaphyses* 2.5–4 μm, septate, hyaline, subcylindrical to irregular, sometimes with swollen cells. *Asci* 55–77.4 × 11–17.7 ($\overline{x}$ = 64.6 × 14 μm, n = 30), 8-spored, bitunicate, clavate, rounded at the apex, with or without an apical chamber and with or without a short pedicel. *Ascospores* 31.6–36.2 × 3.6–5 μm ($\overline{x}$ = 33.8 × 4.3 μm, n = 40), triseriate or irregularly overlapping, narrowly fusiform, 1-septate nearly median, constricted at the septa, sometimes becoming 3-septate at maturity, olivaceous brown, guttulate, slightly curved, without a sheath. Asexual morph: Not observed.

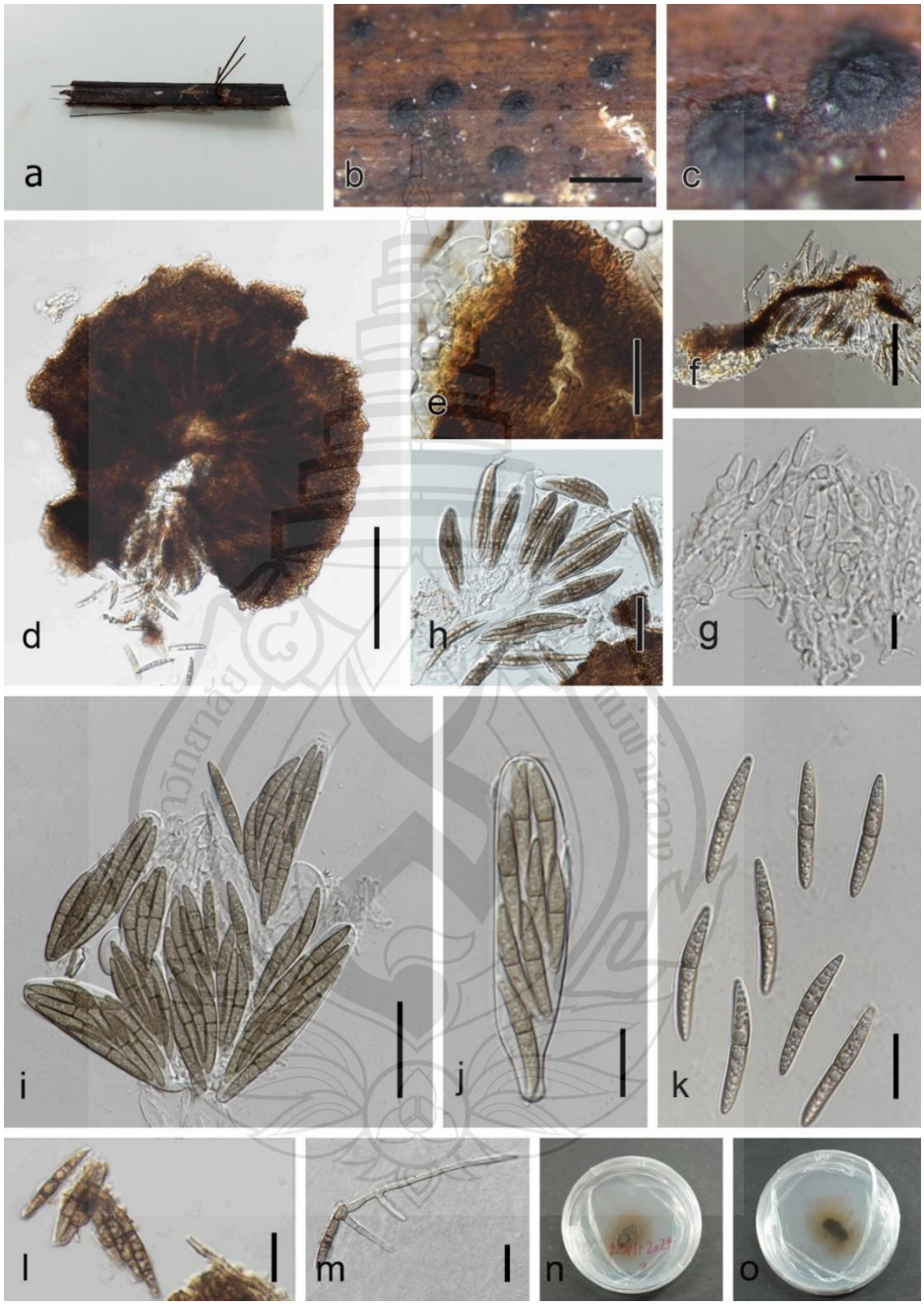
Culture characteristics – Colonies on the PDA reaching 2.5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, flat, fimbriate, medium sparse, dull, no sporulation, surface greyish brown, reverse brown.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 9W (MFLU 24-0489, holotype); ex-type living culture MFLUCC 24-0573.

GenBank numbers – MFLUCC 24-0573: ITS = PV271869, LSU = PV271911, SSU = PV263312, *rpb2* = PV340535.

Note – *Narathiwatiomyces confertae* (MFLUCC 24-0573) formed a subclade with *Nat. decorospora*, *Nat. limonensis*, and *Nat. naponensis*, supported by 80% ML and 1.00 PP statistical support in the combined phylogenetic analyses of LSU and SSU

sequence data (Figure 3.11). *Nar. confertae* is introduced as a novel species and the sole species of *Narathiwatiomyces* based on morphological and phylogenetic evidence. Detailed information is provided in the generic note of *Narathiwatiomyces*.



Note a Host. b, c Appearance of ascomata on the host substrate. e, f A section of the ascoma. g Pseudoparaphyses. h–j Asci. k, l Ascospores. m A germinated ascospore. n, o Colonies on the CMA. Scale bars: b = 500 μm, c–e = 100 μm, f = 50 μm, g = 6 μm, h, i = 30 μm, j–m = 15 μm.

Figure 3.12 *Narathiwatiomyces confertae* (MFLU 24-0489, holotype)

Tubeufiales Boonmee & K.D. Hyde, Fungal Diversity 68 (1): 245 (2014)

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

Tubeufiaceae was introduced by Barr (1979) based on the type genus *Tubeufia* (*Tu*.), along with five other genera: *Letendraeopsis*, *Melioliphila*, *Podonectria*, *Rebentischia*, and *Thaxteriella*. To date, the family comprises 54 genera (Hyde et al. 2024). Most species in *Tubeufiaceae* were reported as saprobes on decaying woody substrates in terrestrial and freshwater habitats (Lu et al. 2018; Lu and Kang 2020; Li et al. 2022; Ma et al. 2023, 2024). The sexual morph of *Tubeufiaceae* is characterised by superficial, white to yellow, pale brown, or black ascomata, with or without setae, seated on a subiculum, with a pseudoparaphysate hamathecium, bitunicate asci, and hyaline to pale brown, cylindrical ascospores (Boonmee et al. 2014). The asexual morph is hyphomycetous, typically dictyosporous, helicosporous, or phragmosporous-like (Zhao et al. 2000; Boonmee et al. 2014; Lu et al. 2018). In this study, we introduce nine new species and report one new record from the palm in the peat swamp forest of Narathiwat, Thailand. An updated tree for the order is shown in Figure 3.13.

Berkleasmium Zobel, Icones fungorum hucusque cognitorum 6: 4 (1854)

Berkleasmium is a saprobic genus on decaying wood in freshwater or terrestrial habitats. This genus was established by Zobel (Corda 1854) and typified by *Berkleasmium concinnum*. Moore (1958) re-established *Berkleasmium* to accommodate sporodochial species previously placed in *Sporidesmium*. The genus is characterized by distinct features of sexual and asexual morph; Ascomata are superficial, appearing solitary or scattered, and are sub globose to globose, with a color range from dark brown to black. Pseudoparaphyses are filiform, septate, and branched. Asci are 8-spored, bitunicate, and cylindrical. Ascospores are biseriate, fusiform, tapering towards the rounded ends, slightly curved, guttulate, multi-septate, not constricted at septa, and have a hyaline, smooth-walled appearance. Asexual morph: two types of asexual morph have been reported for this genus: (1) Hyphomycetous and produces dictyoconidia, sporodochia are black, well-defined. Conidia are broad-cylindrical, multicellular, featuring large and fairly regular cells, and have a fuscous color. They are borne on short conidiophores, which become less distinct as they mature (Moore 1958), (2) Hyphomycetous, helicosporous. Mycelium is composed of both partly immersed and

partly superficial brown, septate, and branched hyphae, accompanied by masses of closely packed, glistening conidia. Conidiophores are macronematous, mononematous, erect. They are short, cylindrical, 0–3-septate, brown, and have a smooth wall. Conidiogenous cells are holoblastic, mono- to polyblastic, integrated, sympodial, terminal, cylindrical, and truncate at the apex. Conidia are solitary, acrogenous, helicoid, tapering to the apex and base, coiled 1–3 times, becoming loosely coiled or uncoiled in water (Lu et al. 2018). Based on Species Fungorum (2025) there are 45 accepted species in this genus, though molecular data is available for seven of them in GenBank. Pinnoi et al. (2007) described *Berkleasmium crunisia* on decaying rachis of *Calamus* sp. from the peat swamp forest in Narathiwat, Thailand. *Berkleasmium micronesicum* has been reported on dead petiole of *Cocos nucifera* from Guam (Matsushima 1981), and *B. sinense* on dead petiole of *Trachycarpus fortunei* from China (Taylor and Hyde 2003).

Helicoma Corda, Icones fungorum hucusque cognitorum 1: 15 (1837)

Corda (1937) established the genus *Helicoma* (*H.*), based on the type species *H. muelleri*. Currently, there are 65 accepted *Helicoma* species listed in Species Fungorum (2024). *Helicoma* has a worldwide distribution and is reported from both freshwater and terrestrial habitats (Boonmee et al. 2014; Lu et al. 2018; Lu and Kang 2020; Li et al. 2022; Ma et al. 2023). To date, one species of this genus (*H. gigasporum*) and one unidentified *Helicoma* taxon (*Helicoma* sp.) have been reported from peat swamp forests (Pinnoi et al. 2006; Pinruan et al. 2007). In this study, we describe *H. narathiwatense* and *H. eleiodoxae* as novel species found on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogenetic tree for the genus, including all species, has been constructed.

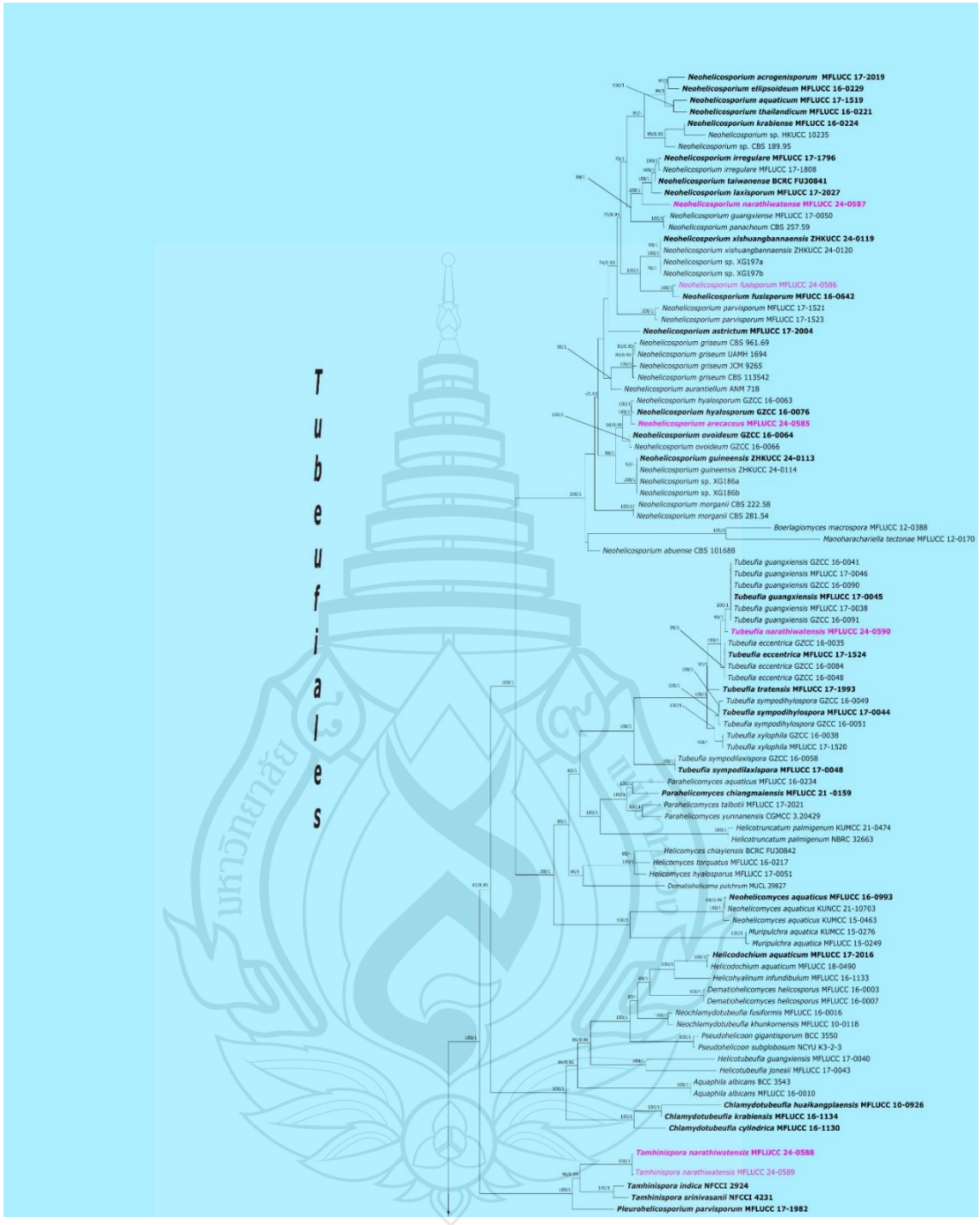
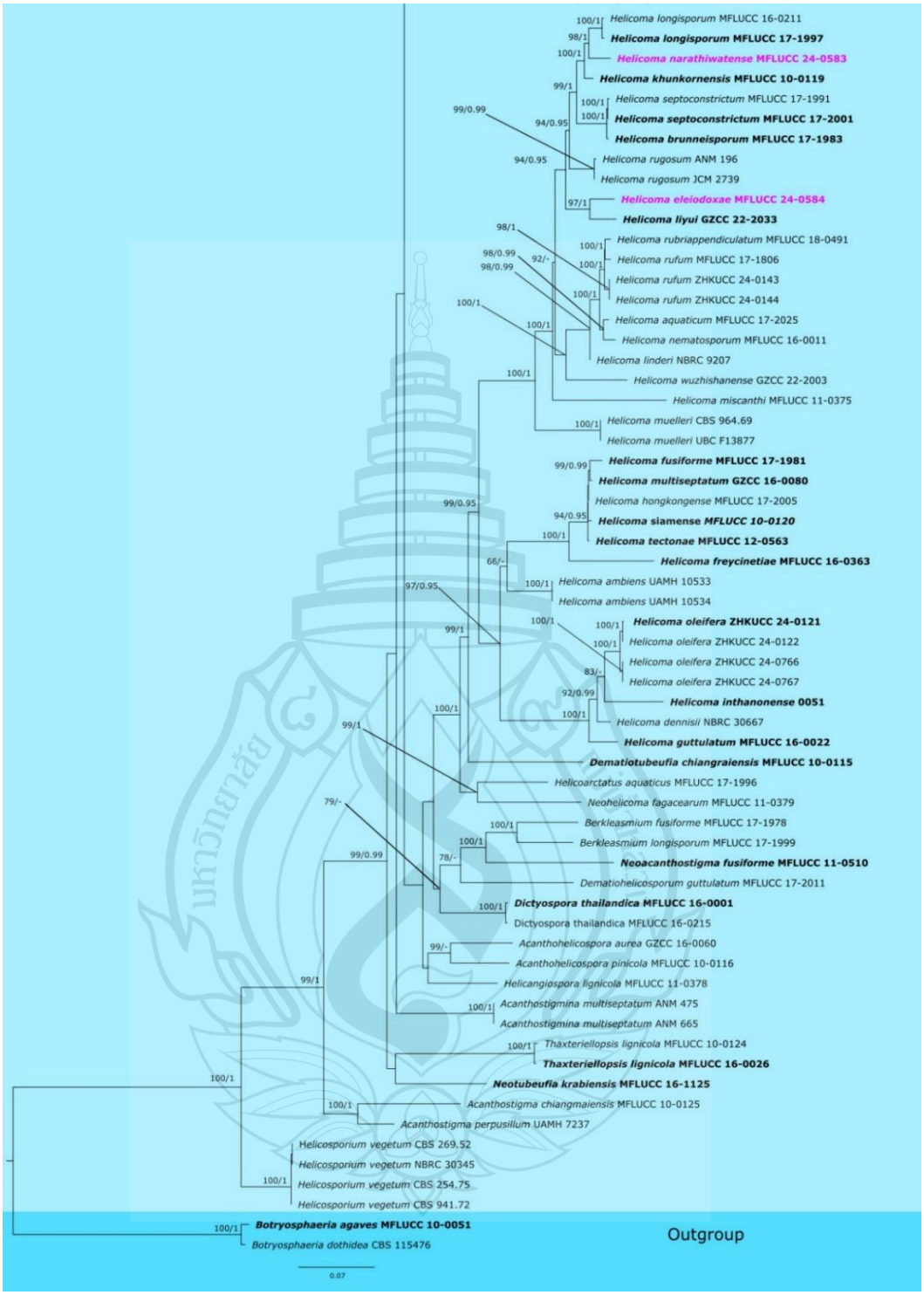


Figure 3.13 Phylogram generated from ML analysis based on ITS, LSU, *rpb2* and *tef1-α* sequence data of *Tubeufiales*



Note *Botryosphaeria agaves* (MFLUCC 10-0051) and *B. dothidea* (CBS 115476) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. Strain of the newly described species is in purple, while type strains are in bold.

Figure 3.13 (continued)

Helicoma narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.14

Index Fungorum number: IF903519; Facesoffungi number: FoF 17522

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region where the fungus was collected

Holotype – MFLU 24-0498

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on natural substrate superficial, effuse, gregarious, brown, glistering. *Mycelium* superficial to immersed, brown, septate, branched. *Conidiophores* 235–276 × 5–10 µm ($\bar{x}$ = 253 × 8 µm, n = 15), macronematous, mononematous, erect, cylindrical, tapering toward the apex, straight, unbranched, septate, brown, pale brown to hyaline toward the apex, smooth-walled. *Conidiogenous cells* 10–18 × 7–9 µm ($\bar{x}$ = 15 × 8 µm, n = 15), holoblastic, monoblastic, intercalary with denticles. *Conidia* 190–199 µm diam. ($\bar{x}$ = 195 µm, n = 15), conidial filament 7–9 µm wide ($\bar{x}$ = 8.5 µm, n = 15), 802–871 µm long ($\bar{x}$ = 835 µm, n = 15), helicoid, tightly coiled 1–1½ times, becoming loose in water, rounded at the apical end, up to 55-septate, pale brown to brown, smooth, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 2.8 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, medium sparse, flat, dull, slightly radiating, without pigment diffusion and sporulation, the surface and reverse brown.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 7W (MFLU 24-0498, holotype); ex-type living culture MFLUCC 24-0583.

GenBank numbers – MFLUCC 24-0583: ITS = PV271870, LSU = PV271912, *rpb2* = PV340519, *tef-1α* = PV340485.

Notes – Phylogenetically, our strain (MFLUCC 24-0583) clustered separated from *Helicoma longisporum* (MFLUCC 16-0211, MFLUCC 17-199711), with 98% ML and 1.00 PP statistical support in the combined phylogenetic analyses of ITS, LSU, *rpb2* and *tef-1α* (Figure 3.16), and also separated from *H. khunkornensis* (MFLUCC10–

0119) with 100% ML and 1.00 PP support. Morphologically, our strain (MFLU 24-0498) is similar to *H. longisporum* (MFLU 17-1137) in having macronematous, mononematous, erect, cylindrical conidiophores, conidiogenous cells with denticles and helicoid conidia, but it differs in having longer conidiophores (235–276 µm vs. 135–210 µm), longer conidial filaments (802–871 µm vs. 620–770 µm), and larger conidia (190–199 vs. 70–150 µm diam.) with less coiled times when tight (1–1½ vs. 1–2½) (Lu et al. 2018). Our strain (MFLU 24-0498) is significantly different from the asexual morph of *H. khunkornensis* (MFLUCC10–0119), which has club-shaped, brown, muriform conidia-like structures formed on hyphae (Boonmee et al. 2011), in contrast to the helicoid conidia with distinct conidiophores and conidiogenous cells of our species. Therefore, based on morphology and phylogenetic analyses, we introduce *H. narathiwatense* as a novel species on *Eleiodoxa conferta* from the peat swamp forest in Thailand.

Helicoma eleiodoxae O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.15

Index Fungorum number: IF903520; Facesoffungi number: FoF 17523

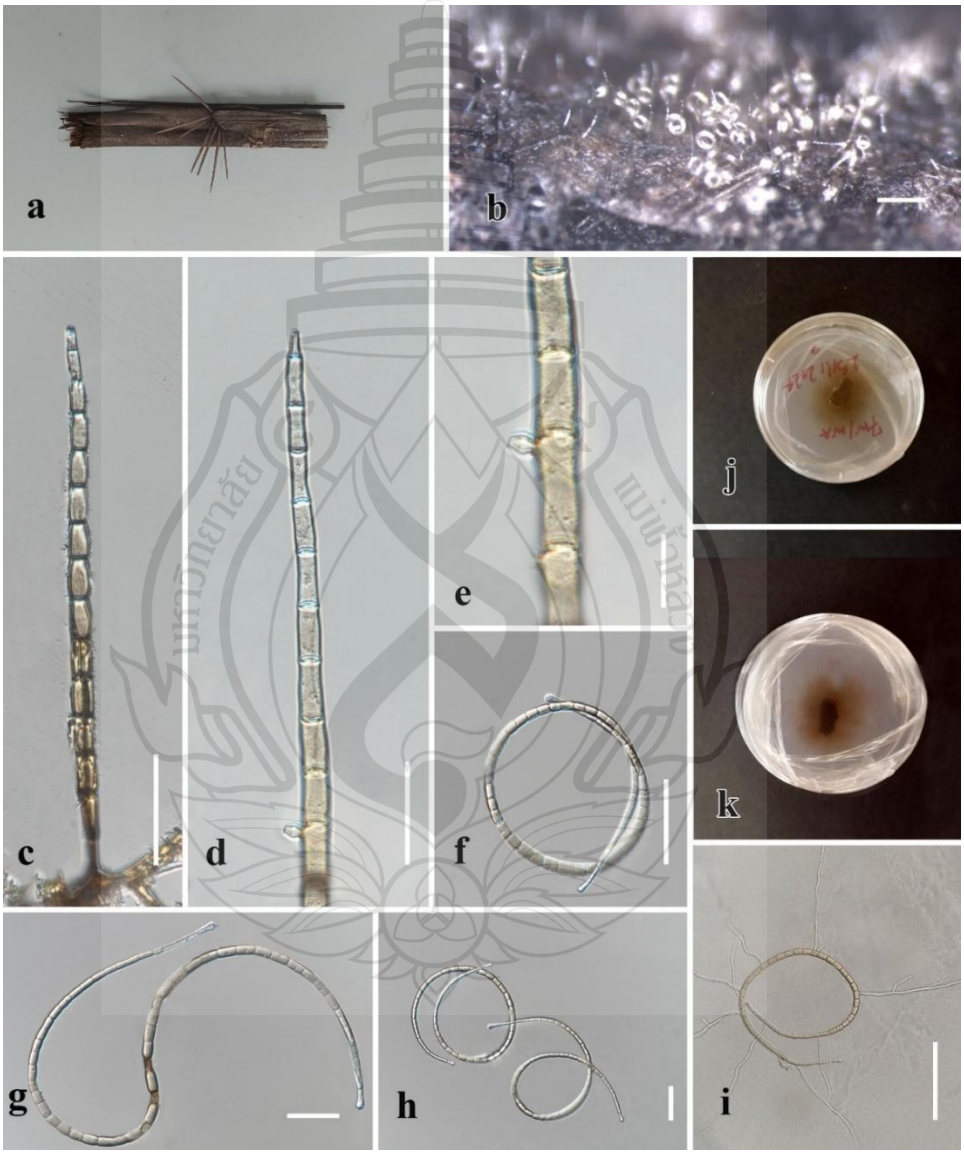
Etymology – The epithet "eleiodoxae" refers to the host plant "*Eleiodoxa conferta*"

Holotype – MFLU 24-0499

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on natural substrate superficial, solitary, brown, glistering. *Mycelium* superficial to immersed, brown, septate, branched. *Conidiophores* 150–163 × 5–7.5 µm ($\bar{x}$ = 160 × 6 µm, n = 15), macronematous, mononematous, erect, cylindrical, tapering toward the apex, straight, unbranched, septate, brown, paler brown to hyaline toward the apex, smooth-walled. *Conidiogenous cells* 15–17 × 6–7 µm ($\bar{x}$ = 16.8 × 6 µm, n = 15), holoblastic, polyblastic, intercalary, cylindrical with barrel-shaped denticles 6–6.5 × 2–3 µm. *Conidia* 178–112 µm diam., ($\bar{x}$ = 91.5 µm, n = 15), conidial filaments 3–8.5 µm wide ($\bar{x}$ = 6.5 µm, n = 20), 546–670 µm long ($\bar{x}$ = 600 µm, n = 20), helicoid, tightly coiled 2–3 times, becoming loose in water, rounded at apical end, multi-septate, guttulate, hyaline to pale brown, smooth, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 3 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, sparse, flat, dull, rhizoid, without pigment diffusion, surface and reverse light orange.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 8B (MFLU 24-0499, holotype); ex-type living culture MFLUCC 24-0584.



Note a Host. b Colonies on the natural substrate. c–e Conidiophores and conidiogenous cells. f–h Conidia. i Germinated conidium. Scale bars: b = 200 µm, c = 50 µm, d = 30 µm, e = 15 µm, f = 100 µm, g = 50 µm, h, i = 65 µm.

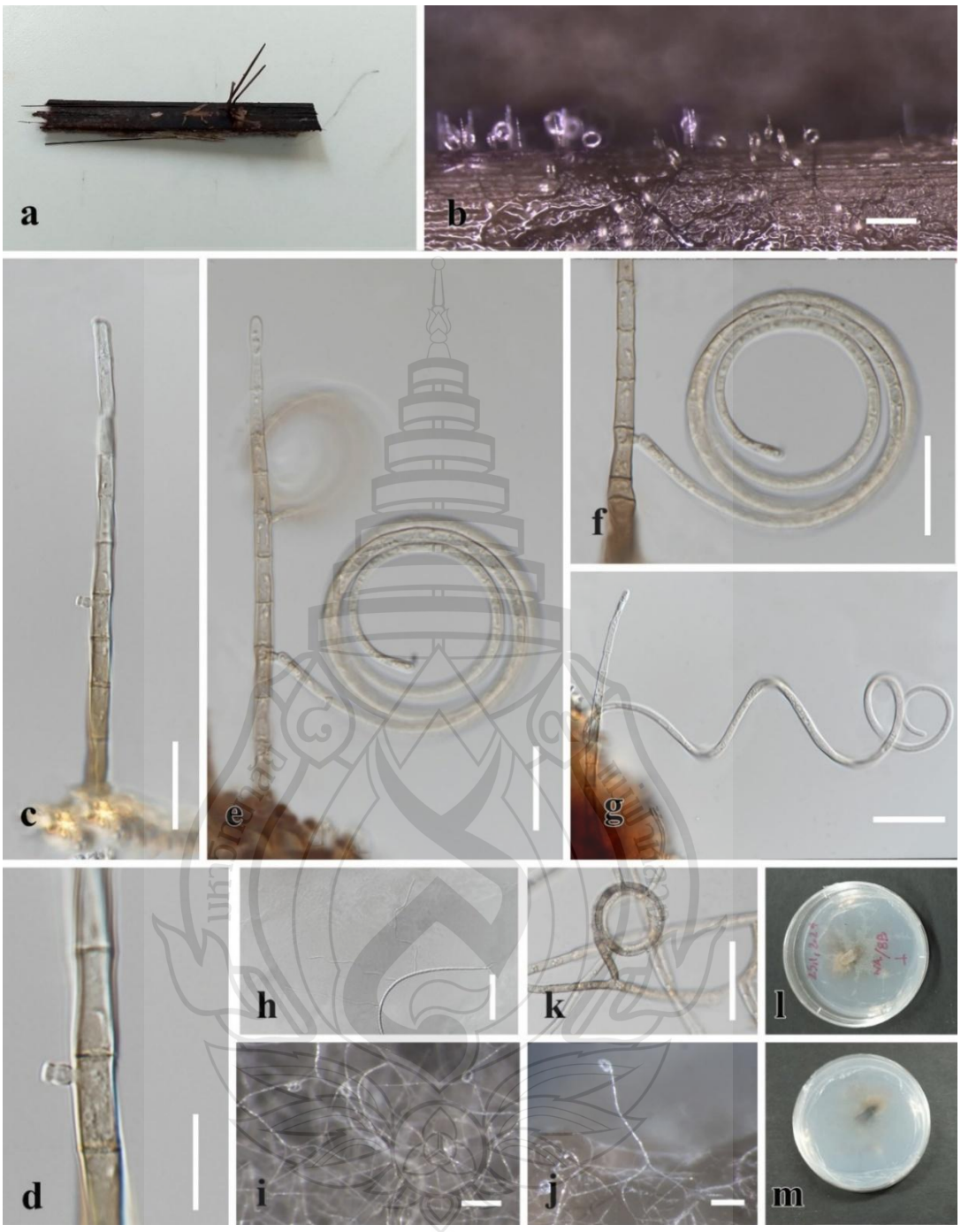
Figure 3.14 *Helicoma narathiwatense* (MFLU 24-0498, holotype)

GenBank numbers – MFLUCC 24-0584: ITS = PV271871, LSU = PV271913, *rpb2* = PV340508, *tef-1α* = PV340488.

Notes – Phylogenetically, our strain (MFLUCC 24-0584) clustered with *Helicoma liyui* (GZCC 22-2033), with 97% ML, 1.00 PP statistical support in the combined phylogenetic analyses of ITS, LSU, *rpb2* and *tef-1α* (Figure 3.13). Morphologically, it is similar to *H. liyui* (GZAAS 22–2033) in having macronematous, mononematous, erect, cylindrical, straight, septate, smooth-walled conidiophores, holoblastic, polyblastic, intercalary, cylindrical conidiogenous cells and helicoid conidia. However, *H. eleiodoxae* (MFLU 24-0499) differs from *H. liyui* in having shorter and narrower conidiophores (150−163 × 5−7.5 vs. 103–200 × 7–11 μm), narrower conidiogenous cells (6−7 vs. 7−11 μm), longer conidial filaments (546–670 vs. 276–395 μm) (Lu et al. 2023). Based on a pairwise comparison of ITS, LSU and *tef-1α* nucleotides, *H. eleiodoxae* (MFLUCC 24-0584) differs from *H. liyui* (GZCC 22-2033) in 6.4% (37/577 bp, excluding gaps) in the ITS, 0.63% (5/800 bp, excluding gaps) in the LSU and 4.5% (43/950 bp, excluding gaps) in *tef-1α* (without including gaps). However, *rpb2* is not comparable as it is unavailable for *H. liyui* (GZCC 22-2033). Thus, we introduce *H. eleiodoxae* as a novel species based on morphological and molecular data.

Neohelicosporium Y.Z. Lu, J.C. Kang & K.D. Hyde, Mycol. Progr. 17 (5): 637 (2017)

Lu et al. (2018a) introduced *Neohelicosporium* (*Ne.*), with *Ne. parvisporum* as the type species. Currently, there are 23 accepted species of *Neohelicosporium* listed in Species Fungorum (2024). Members of *Neohelicosporium* are reported as saprobes on decaying wood in freshwater habitats in China, India, Thailand, and the United States (Lu et al. 2018; Pem et al. 2024). To date, no species of this genus have been reported from peat swamp forests. In this study, we describe *Ne. arecaceus* and *Ne. narathiwatense* as novel species found on palm materials (Arecaceae) and report *Ne. fusisporum* as a new host record on *Eleiodoxa conferta* from the peat swamp forest in Thailand.



Note a Host. b Colonies on the natural substrate. c, d Conidiophores and conidiogenous cells. e–g Conidiophores, conidiogenous cells and conidia. h Germinated conidium. i–k Colonie in culture (water agar). m, l Upper surface and reverse overview of culture (PDA). Scale bars: b = 200 μm, c, e, f = 30 μm, d = 15 μm, g = 50 μm, h = 100 μm, i, j = 250 μm, k = 40 μm.

Figure 3.15 *Helicoma eleiodoxae* (MFLU 24-0499, holotype)

Neohelicosporium arecacearum O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.16

Index Fungorum number: IF903521; Facesoffungi number: FoF 17524

Etymology – The epithet "arecaceus" refers to the host family, Arecaceae

Holotype – MFLU 24-0500

Saprobic on dead rachis of *Caryota mitis*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on the natural substrate superficial, effuse, gregarious, white. *Mycelium* composed of immersed or superficial, hyaline to pale brown, septate, branched hyphae, with masses of crowded, glistening conidia. *Conidiophores* up to 300 μm long, 2–5 μm wide ($\bar{x}$ = 4 μm, n = 30 μm), micronematous, mononematous, flexuous, long, cylindrical, branched, septate, smooth-walled, pale brown to brown. *Conidiogenous cells* 9.5–19.5 μm long ($\bar{x}$ = 15 μm, n = 20), 3–4.5 μm wide ($\bar{x}$ = 4 μm, n = 20), holoblastic, monoblastic to polyblastic, integrated, intercalary, pale brown, smooth-walled, cylindrical, with denticles. *Conidia* 14.5–19 μm diam. ($\bar{x}$ = 17, n = 50) and conidial filament 1–2 μm wide ($\bar{x}$ = 1.5 μm, n = 25), 104–127 μm long ($\bar{x}$ = 113 μm, n = 30), tightly coiled 2.5–3.5 times, and no changes to coiling in water, multi-septate, guttulate, smooth-walled or roughened, hyaline. Sexual morph: Not observed.

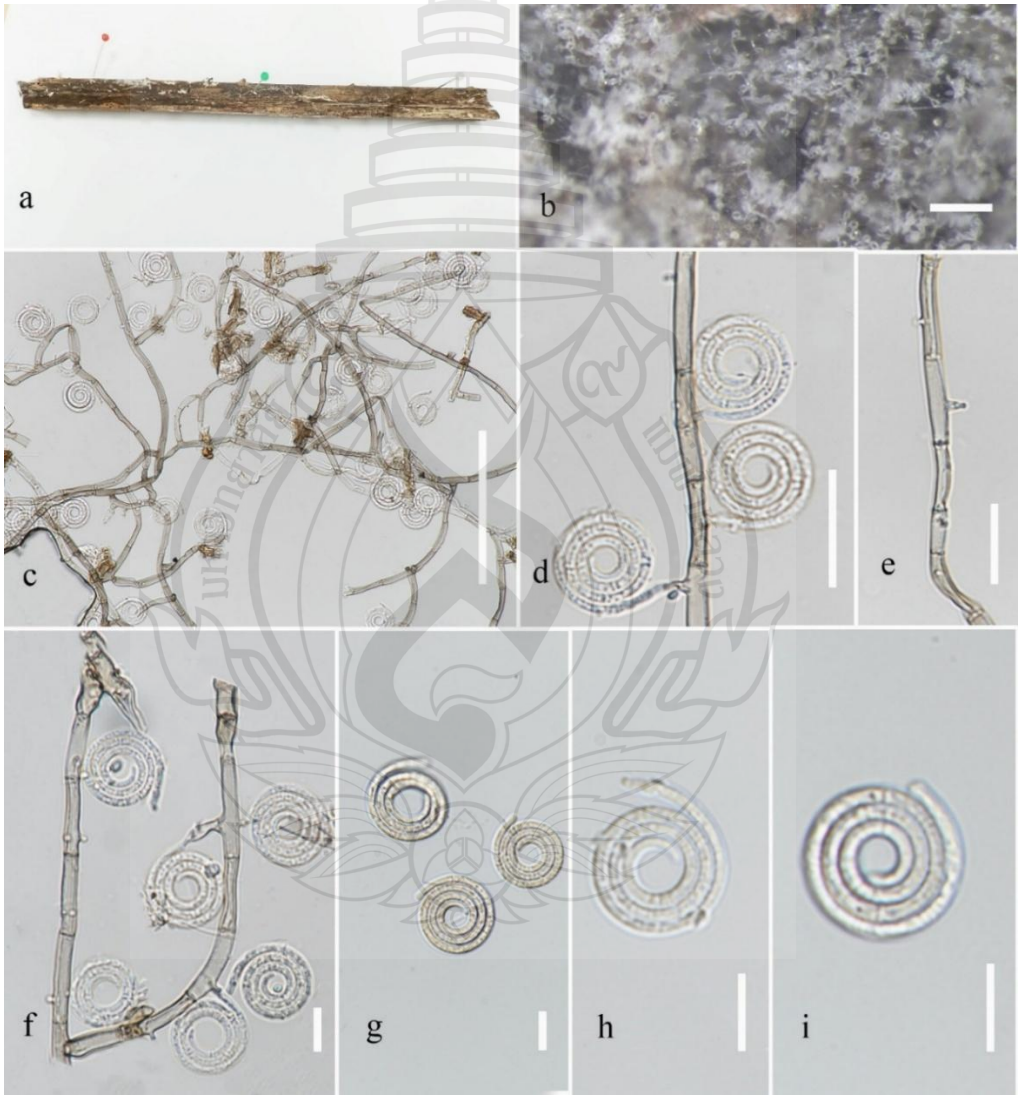
Culture characteristics – Colonies on the PDA reaching 5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, medium dense, flat, dull, without pigment diffusion, from the surface and reverse light orange.

Material examined – Thailand, Narathiwat, peat swamp forest, on the dead rachis of *Caryota mitis*, 24 April 2022, O. Karimi, S5PP3SSEFD (MFLU 24-0500, holotype); ex-type living culture MFLUCC 24-0585.

GenBank numbers – MFLUCC 24-0585: ITS = PV271872, LSU = PV271914, *rpb2* = PV340520, *tef-1α* = PV340489.

Notes – Phylogenetically, our strain (MFLUCC 24-0585) clustered separately from *Neohelicosporium hyalosporum* (GZCC 16-0076, GZCC 16-0063), with 100% ML and 1.00 PP support. Morphologically, *Ne. arecacearum* is similar to *Ne. hyalosporum* (GZAAS 16-0088), but easily distinguished from *Ne. hyalosporum* (GZAAS 16-0088) in having shorter and thinner conidiophores (up to 300 μm long, 2–5 μm wide vs. up to 540 μm long, 4–5.5 μm wide), smaller conidia (14.5–19 μm diam. vs. 25–33 μm diam.), with narrower conidial filaments (1–2 μm wide, vs. 3–4 μm wide)

that do not become loose in water, while the conidial filaments in *Ne. hyalosporum* (GZAAS 16-0088) become loose in water (Lu et al. 2018). Based on a pairwise comparison of ITS, *tef-1α*, *rpb2* and LSU nucleotides, *Ne. arecacearum* (MFLUCC 24-0585) differs from *Ne. hyalosporum* (GZCC 16-0076) in 2.1% (12/550 bp, without including gaps) in the ITS, 1.8% (15/820 bp, without including gaps) in *tef-1α*, and 0.9% (9/1045 bp, without including gaps) in *rpb2*. However, no differences were observed between the LSU sequences. Thus, we introduce *Ne. arecacearum* as a novel species based on morphological characters and high phylogenetic support.



Note a Host. b Colonies on the natural substrate. c–f Conidiophores, conidiogenous cells and conidia. g–i Conidia. Scale bars: b = 150 μm, c = 70 μm, d = 50 μm, e = 30 μm, f, i = 60 μm, g = 55 μm, h = 45 μm.

Figure 3.16 *Neohelicosporium arecaceus* (MFLU 24-0500, holotype)

Neohelicosporium fusisporum Jayasiri & K.D. Hyde, Index Fungorum 352: 1 (2018) Figure 3.17

Index Fungorum number: IF 553637; Facesoffungi number: FoF 03785

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on natural substrate effuse, gregarious, white with aerial hyphae. *Mycelium* mostly superficial and partly immersed, brown, septate, branched. *Conidiophores* 112–295 × 3.5–9 µm ($\bar{x}$ = 180 × 5.5 µm, n = 30), micronematous, mononematous, straight or flexuous, cylindrical, branched, rarely anastomosing, septate, brown to pale brown, smooth, thin-walled. *Conidiogenous cells* 11–22 × 3.5–6 µm ($\bar{x}$ = 17 × 5 µm, n = 30), holoblastic, polyblastic, integrated, intercalary, cylindrical with denticles, pale brown to brown, smooth-walled. *Conidia* 14–24.5 µm diam., ($\bar{x}$ = 19 µm, n = 35), conidial filaments 1.5–2.5 µm wide, 118–129 µm long, helicoid, tightly coiled 2½–3 times, rounded at the apical end, septate, hyaline, smooth, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 2.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium sparse, umbonate, dull, entire edge, felted, without pigment diffusion and sporulation, from surface brown with white margin, from reverse greyish orange with white margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 14B (MFLU 24-0501); living culture MFLUCC 24-0586.

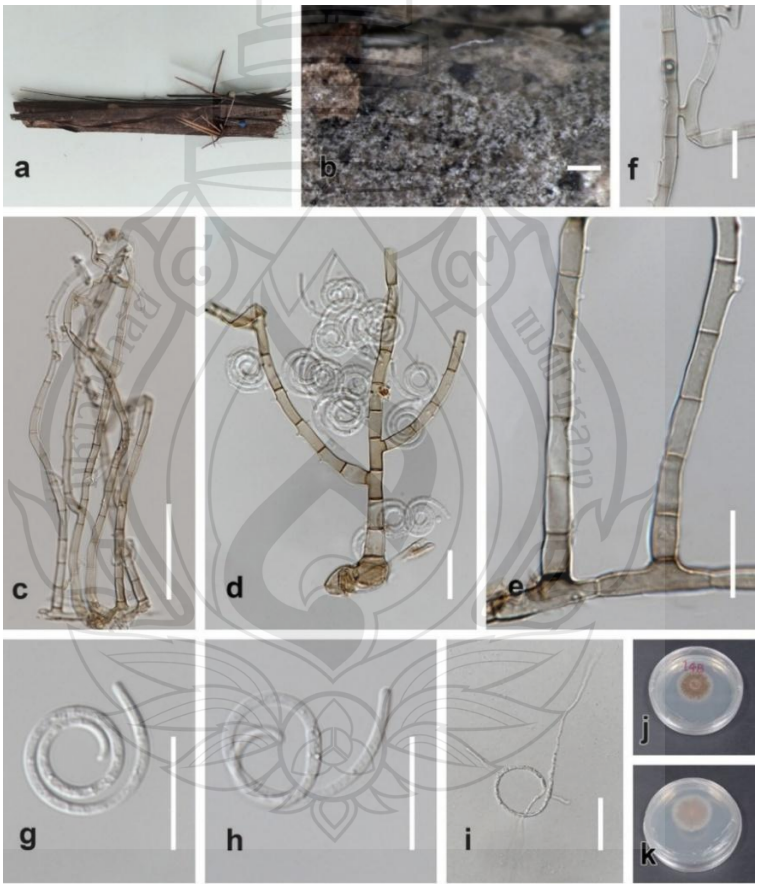
Known host – decaying fruit of *Malvaceae* (Jayasiri et al. 2017), *Eleiodoxa conferta* (This study).

Known distribution – Thailand (Jayasiri et al. 2017; this study).

GenBank numbers – MFLUCC 24-0586: ITS = PV271873, LSU = PV271915, *rpb2* = PV340521, *tef-1α* = PV340490.

Notes – Phylogenetically, our strain (MFLUCC 24-0586) clustered with *Neohelicosporium fusisporum* (MFUCC 16-0642) with 100% ML and 1.00 PP statistical support (Figure 3.13). Based on a pairwise comparison of ITS, *tef-1α*, and LSU nucleotides, our strain (MFLUCC 24-0586) differs from *Ne. fusisporum* (MFUCC 16-0642) by 0.5% (3/570 bp, excluding gaps) in the ITS, 0.2% (2/910 bp, excluding gaps) in the *tef-1α*, and shows no differences in the LSU sequences. However, *rpb2* is

not comparable as it is unavailable for *Ne. fusisporum* (MFUCC 16-0642). Morphologically, our strain resembles *Ne. fusisporum* (MFLU 16-0950) in having micronematous, mononematous, straight or flexuous, cylindrical, branched, septate conidiophores, holoblastic, polyblastic, integrated, intercalary, cylindrical conidiogenous cells and helicoid conidia with almost comparable dimensions (Jayasiri et al. 2017). Thus, we identified our strain (MFLU 24-0501) as *Ne. fusisporum* based on morphological characters and phylogenetic analyses. We report our strain (MFLU 24-0501) as a new host record of *Ne. fusisporum* on *Eleiodoxa conferta* from Thailand. Additionally, we document *Ne. fusisporum* as a new habitat record from the peat swamp forest.



Note a Host. b Colonies on natural substrate. c, e, f Conidiophores and conidiogenous cells. d Conidiophores and conidia. g, h Conidia. i Germinated conidium. j, k Colonie on PDA. Scale bars: b = 200 μm, c = 50 μm, e, d, g, h = 20 μm, f = 15 μm, i, g = 40 μm.

Figure 3.17 *Neohelicosporium fusisporum* (MFLU 24-0501, a new host and habitat record)

Neohelicosporium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.18

Index Fungorum number: IF903522; Facesoffungi number: FoF 17525

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region from where the fungus was collected

Holotype – MFLU 24-0502

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on natural substrate superficial, effuse, brightly coloured or brown. *Mycelium* mostly superficial and partly immersed, pale brown to brown, septate, branched. *Conidiophores* 159–340 × 3–6 µm ($\bar{x}$ = 200 × 5 µm, n = 15), macronematous, mononematous, straight or flexuous, cylindrical, sometimes the upper part is sterile, branched, septate, brown to pale brown toward the apex, smooth-walled. *Conidiogenous cells* 11–30 × 4.5–9 µm ($\bar{x}$ = 16.5 × 6 µm, n = 15), holoblastic, polyblastic, integrated, intercalary, cylindrical with denticles. *Conidia* 57.5–87 µm diam., ($\bar{x}$ = 71.5 µm, n = 15), conidial filaments 3–5 µm wide, with 223–364 µm long, helicoid, tightly coiled 1½–3 times, rounded at the apical end, multi-septate, hyaline, smooth or rough, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 3.3 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, umbonate, dull, felted, without pigment diffusion and sporulation, from surface Persian orange with white margin, from reverse pale orange with white margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 11W (MFLU 24-0502, holotype); ex-type living culture MFLUCC 24-0587.

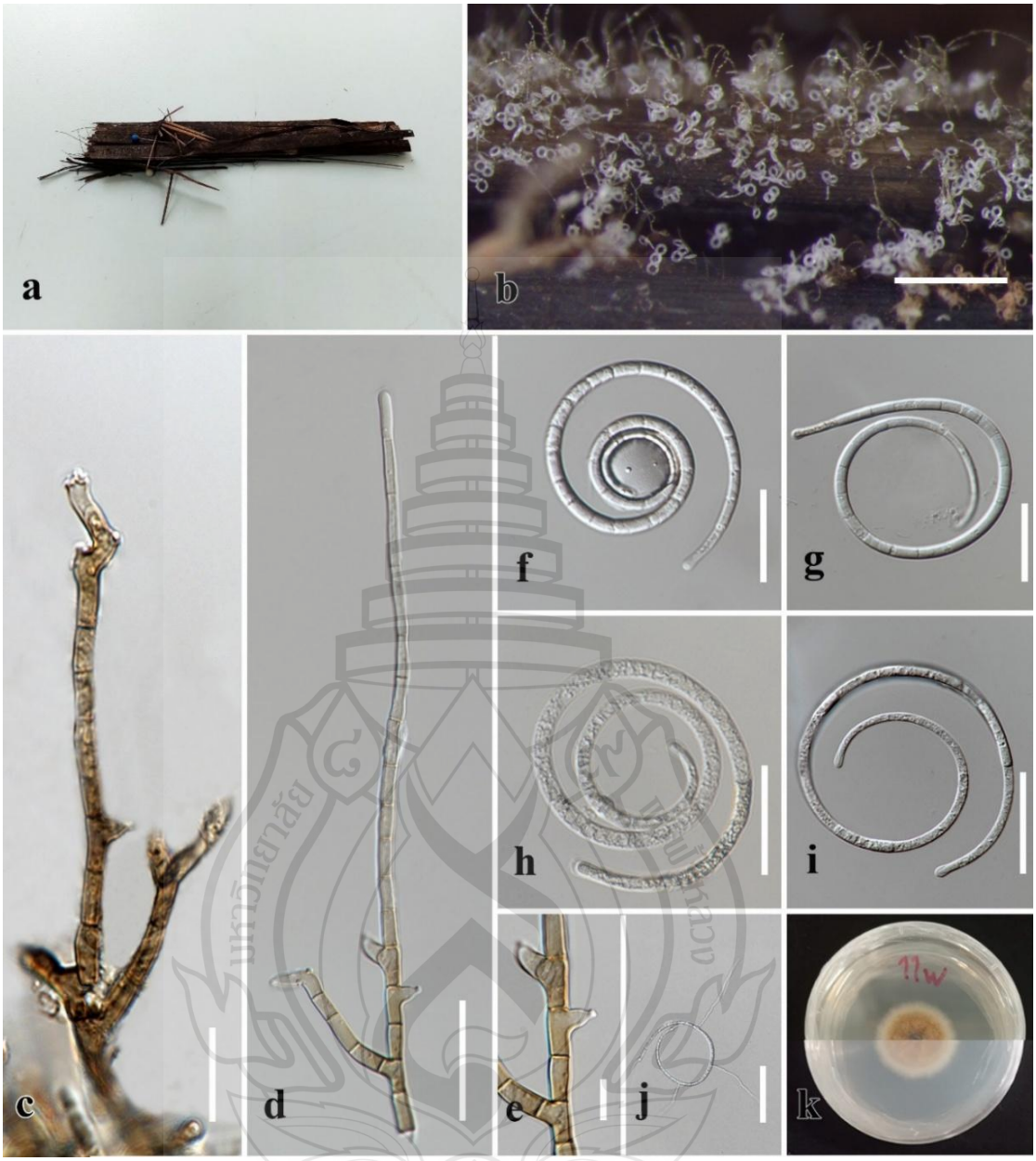
GenBank numbers – MFLUCC 24-0587: ITS = PV271874, LSU = PV271916, *rpb2* = PV340522, *tef-1α* = PV340491.

Notes – Phylogenetically, our strain (MFLUCC 24-0587) clustered basal to the subclade comprising *Neohelicosporium irregulare* (MFLUCC 17-1808, MFLUCC 17-1796), *Ne. taiwanense* (BCRC FU30841) and *Ne. laxisporum* (MFLUCC 17-2027), with 100% ML, 1.00 PP statistical support in the combined phylogenetic analyses of ITS, LSU, *rpb2* and *tef-1α* (Figure 3.13). Morphologically, our collection (MFLU 24-

0502) is similar to *Ne. taiwanense* (TNM F31001) in having macronematous, mononematous, straight or flexuous, cylindrical, branched, septate, smooth-walled conidiophores, polyblastic, integrated, cylindrical conidiogenous cells and helicoid conidia. However, *Ne. narathiwatense* can be distinguished from *Ne. taiwanense* by having longer and wider conidiogenous cells (11−30 × 4.5−9 vs. 2.2−3.7 × 1−1.5 μm) and larger conidia (57.5–87 vs. 37−48 μm diam.) (Kuo and Goh 2018). Our collection (MFLU 24-0502) is easily distinguishable from *Ne. laxisporum* (MFLU 17–1107) in having branched longer conidiophore (159–340 μm vs. 20–160 μm), which lacks a bulb at the apex, and larger (57.5–87 μm diam. vs. 27–33 μm diam.) and longer (223–364 μm vs. 150–240 μm) conidia (Lu et al. 2018). Our collection (MFLU 24-0502) differs from *Ne. irregulare* (MFLU 17–1095), as the latter has two kinds of shorter and longer conidiophores, both of which are shorter than our strain (MFLU 24-0502), (the shorter one: 35–55 μm vs. 159–340 μm and the longer one: 90–265 vs. 159–340 μm), with mostly unbranched conidiophores in the latter despite the branched ones in our strain. Additionally, conidia of *Ne. irregulare* (MFLU 17–1095) are smaller (25–40 μm diam. vs. 57.5–87 μm diam.) and shorter (150–270 μm vs. 223–364 μm) compared to our species (Lu et al. 2018). Therefore, we introduce *Ne. narathiwatense* (MFLU 24-0502) as a novel species based on morphological and phylogenetic evidence.

Tamhinispora Rajeshk. & Rah. Sharma, Mycosphere 4 (2): 166 (2013)

Rajeshkumar and Sharma (2013) introduced *Tamhinispora* (*Ta.*), to accommodate *Ta. indica*, the type species, which was found on decaying culms of *Bambusa bambos* in India. Currently, three accepted species of *Tamhinispora* are listed in Species Fungorum (2024). To date, no species of this genus have been reported from peat swamp forests. In this study, we describe *Ta. narathiwatensis* as a novel species, saprobic on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.



Note a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f–i Conidia. j Germinated conidium. k Colonie on the PDA. Scale bars: b = 400 µm, c= 20 µm, d = 40 µm, e = 10 µm, f, g = 30 µm, h, i = 25 µm, j = 100 µm.

Figure 3.18 *Neohelicosporium narathiwatense* (MFLU 24-0502, holotype)

Tamhinispora narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.19

Index Fungorum number: IF903523; Facesoffungi number: FoF 17526

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0503

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, dictyosporous. *Colonies* on natural substrate scattered or in small groups, glistening, black. *Mycelium* mostly immersed and partly superficial, brown, septate, branched. *Conidiophores* not seen. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindric, terminal or lateral, brown. *Dictyospores* 60–80 × 54–75 µm ($\bar{x}$ = 68 × 63 µm, n = 20), solitary, indistinctly dictyoseptate, black, globose to subglobose. Sexual morph: Not observed.

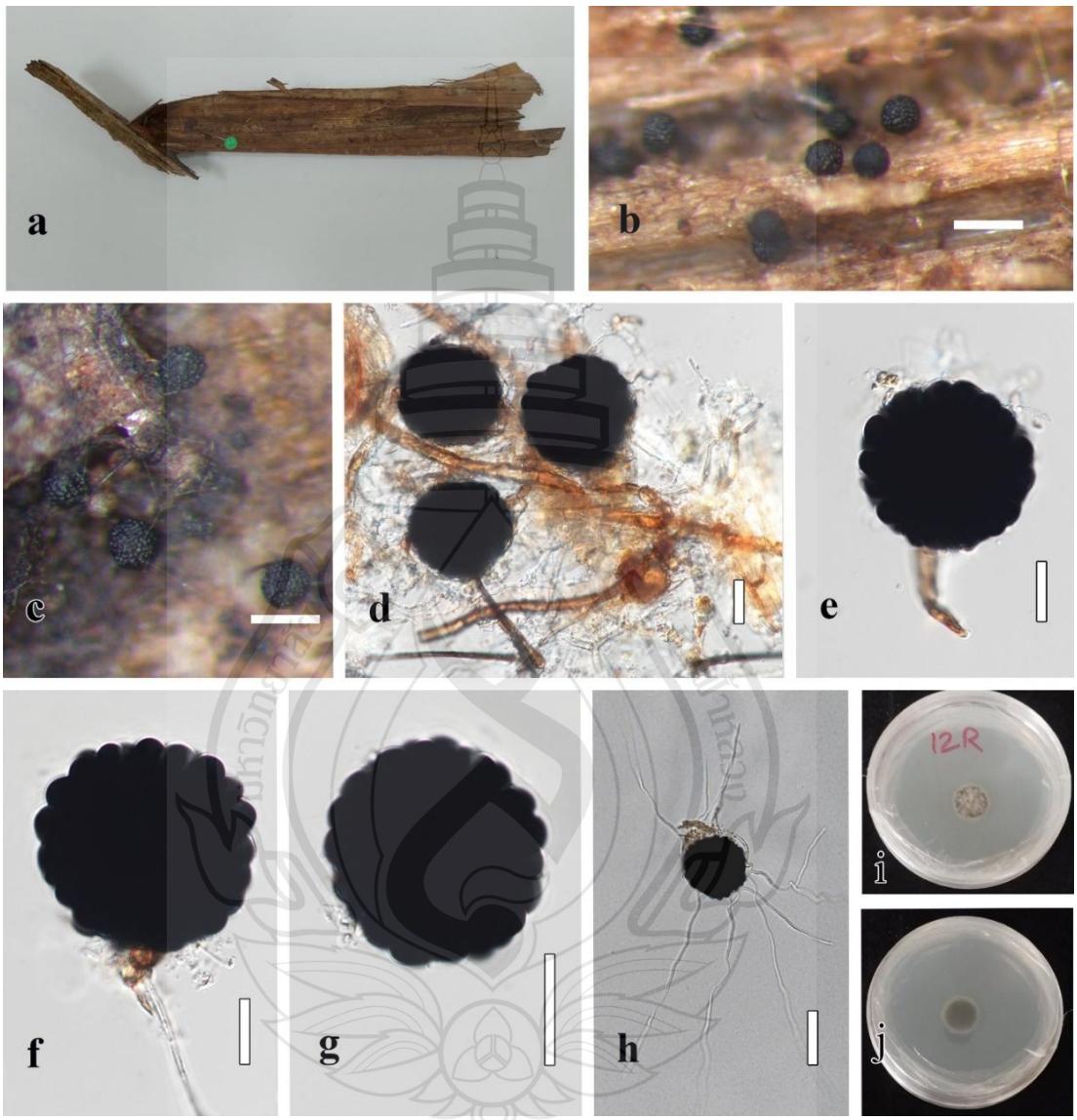
Culture characteristics – Colonies on the PDA reaching 1.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, raised, dull, entire edge, without pigment diffusion and sporulation, from surface whitish grey with white margin, from reverse grey with white margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 12R (MFLU 24-0503, holotype); ex-type living culture MFLUCC 24-0588; 26Y (MFLU 24-0504, isotype); ex-isotype living culture MFLUCC 24-0589.

GenBank numbers – MFLUCC 24-0588: ITS = PV271875, LSU = PV271917, *rpb2* = PV340523, *tef-1α* = PV340492; MFLUCC 24-0589: ITS = PV271876, LSU = PV271918.

Notes – Phylogenetically, our strains (MFLUCC 24-0588, MFLUCC 24-0589) formed a distinct clade separately from *Tamhinispora indica* (NFCCI 2924), and *Ta. srinivasanii* (NFCCI 4231) with 96% ML, 0.99 PP support in the combined phylogenetic analyses of ITS, LSU, *rpb2* and *tef-1α* (Figure 3.13). Morphologically, our species is similar to *Ta. srinivasanii*, but it differs from *Ta. srinivasanii* (AMH 9942) in having globose to subglobose dictyospores, lacking appendages, in contrast to the ovoid or branched or Y-shaped dictyospores of *Ta. srinivasanii* with rudimentary or well-developed arm-like appendages (Rajeshkumar et al. 2018). Similarly, it differs

from *Ta. indica* (AMH 9555) with the latter having ovoid or irregular dictyospores with apical appendages (Rajeshkumar and Sharma 2013). Therefore, based on morphological and phylogenetical evidence, we introduce *Ta. narathiwatensis* (MFLU 24-0503) as a novel species from peat swamp forests.



Note a Host. b, c Colonies on the host substrate. d–g Conidia. h Germinated conidium. i, j Colonie on the PDA. Scale bars: b, c = 100 μm, c = 50 μm, d, f = 20 μm, e, g = 25 μm, h = 30 μm.

Figure 3.19 *Tamhinispora narathiwatensis* (MFLU 24-0503, holotype)

Tubeufia Penz. & Sacc., Malpighia 11: 517 (1898)

Penzig and Saccardo (1897) established *Tubeufia* within *Tubeufiaceae*, with *Tu. javanica* as the type species. Boonmee et al. (2014) designated the epitype for *Tu. javanica* based on phylogenetic analyses. Currently, there are 60 accepted species of *Tubeufia* listed in Species Fungorum (2024). *Tubeufia* species are reported as saprobes on decaying wood in freshwater or terrestrial habitats (Boonmee et al. 2014; Chaiwan et al. 2017; Lu et al. 2018a; Dong et al. 2020). To date, one species of this genus (*Tu. claspisphaeria*) has been reported from peat swamp forests (Pinnoi et al. 2006; Pinruan et al. 2007). In this study, we introduce *Tu. narathiwatensis* as a novel species found on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogenetic tree for the genus, including all species, has been constructed (Supplementary S3).

Tubeufia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.20

Index Fungorum number: IF903524; Facesoffungi number: FoF 17527

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0505

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous, helicosporous. *Colonies* on natural substrate superficial, effuse, gregarious, brown. *Mycelium* superficial to immersed, brown, septate, branched. *Conidiophores* 37–53 × 4–6.8 µm ($\bar{x}$ = 47 × 5.5 µm, n = 15), macronematous, mononematous, erect, cylindrical, tapering toward the apex, straight or curved, unbranched, septate, brown, paler brown to hyaline toward the apex, smooth-walled. *Conidiogenous cells* 13–28.5 × 4–5.5 µm ($\bar{x}$ = 20 × 4.5 µm, n = 15), holoblastic, monoblastic, terminal, straight or curved, pale brown to hyaline, sub cylindrical tapering toward the apex. *Conidia* 86–132 µm diam. ($\bar{x}$ = 111.5 µm, n = 15), conidial filaments 3.5–6.5 µm wide ($\bar{x}$ = 5.2 µm, n = 20), with 417–529 µm long ($\bar{x}$ = 474 µm, n = 20), tightly coiled 1½–2½ (−3) times, becoming loose in water, rounded at the apical end, up to 70-septate, not constricted at septa, hyaline, guttulate, smooth-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 4.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, slightly raised, dull, velvety, with 3–4 concentric rings, entire edge, without pigment diffusion and sporulation, surface olive brown with dark brown to black margin, reverse whiteish grey with brown to dark brown margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 3W (MFLU 24-0505, holotype); ex-type living culture MFLUCC 24-0590.

GenBank numbers – MFLUCC 24-0590: ITS = PV271877, LSU = PV271919, *rpb2* = PV340524, *tef-1α* = PV340493.

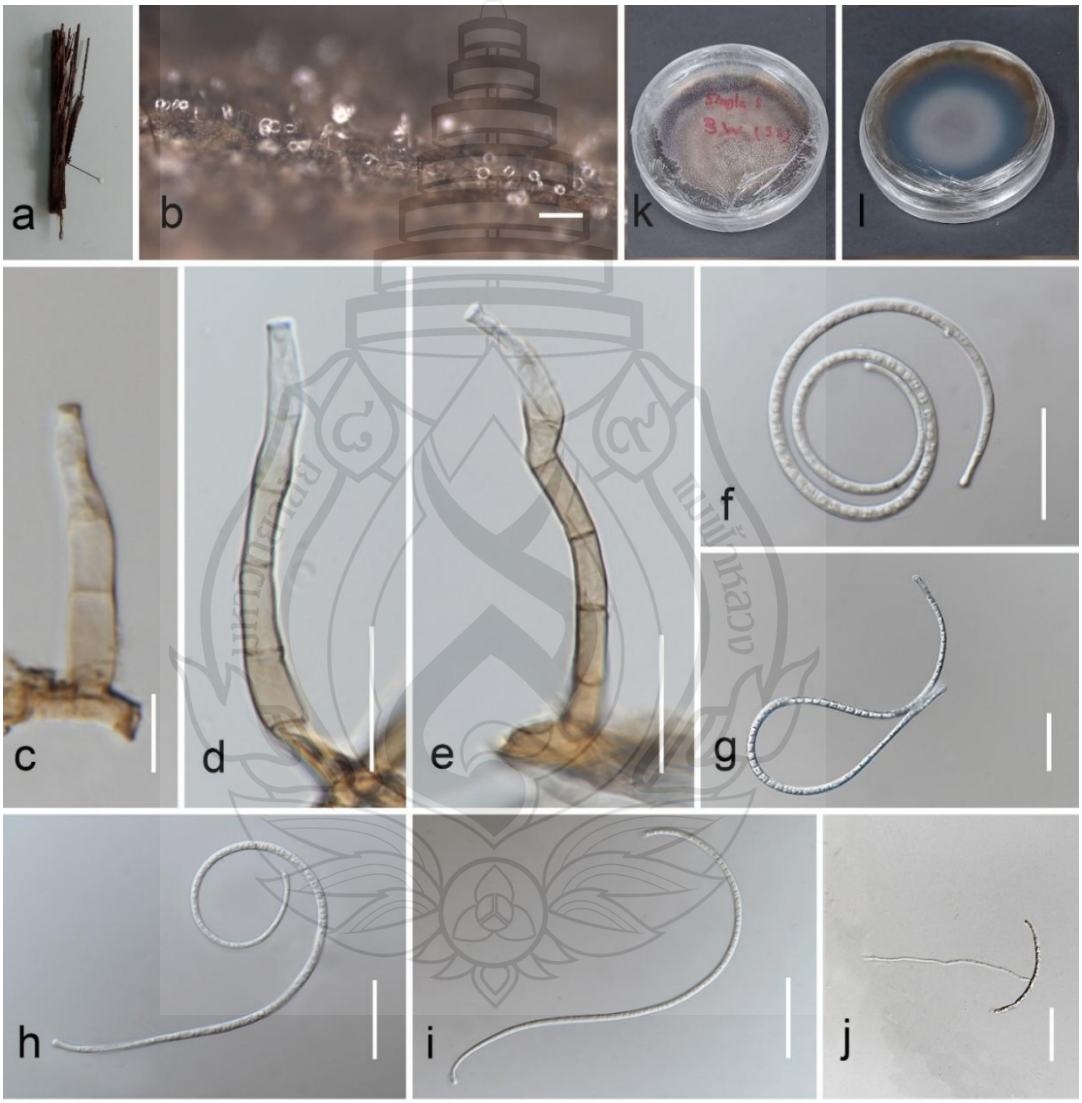
Notes – Phylogenetically, our strain (MFLUCC 24-0590) clustered separately from the sub clade comprising *Tubeufia guangxiensis* strains with 100% ML and 1.00 PP statistical supports in the combined phylogenetic analysis of ITS, LSU, *rpb2* and *tef-1α* (Figure 3.13). Morphologically, *Tu. narathiwatensis* is similar to *Tu. guangxiensis* (GZAAS 16–0042), but it differs in having longer and wider conidiophores (37–53 × 4–6.8 µm vs. 24–39 × 3.5–5 µm), and longer conidiogenous cells (13–28.5 vs. 10–17 µm), and longer conidia (417–529 µm vs. 360–460 µm) with more septa (up to 70-septate vs. up to 50-septate) (Chaiwan et al. 2017). Therefore, we introduce *Tu. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde, Fungal Diversity 51: 251 (2011)

Sympoventuriaceae Y. Zhang ter, C.L. Schoch & K.D. Hyde, Fungal Diversity 51: 255 (2011)

Sympoventuriaceae comprises 22 accepted genera that are saprobic, endophytic, or plant pathogenic (Hyde et al. 2024). It was first described by Zhang et al. (2011) based on phylogenetic analyses using the combined SSU, LSU, *tef-1α*, and *rpb*1 and *rpb*2 sequence data, forming a distinct clade close to *Venturiaceae* in *Venturiales* and included genera like *Sympoventuria*, *Veronaeopsis simplex*, and Fusicladium-like species. Wei et al. (2022) re-evaluated the family, accepting 22 genera based on

morphology and molecular data. Both sexual and asexual morphs occur, with many hyphomycetous genera producing conidia through rhexolytic secession (Wei et al. 2022; Zhang et al. 2024). Sexual morphs have subglobose to globose ascomata with brown setae or hyphal-like appendages, bitunicate asci, and hyaline or brown, fusoid-ellipsoidal, clavate, or muriform ascospores, with or without a mucilaginous sheath (Wei et al. 2022; Zhang et al. 2024). An updated tree for the family is shown in Figure 3.21.



Note a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f–i Conidia. j A germinated conidium. k, l Colonies on the PDA. Scale bars: b = 200 µm, c = 10 µm, d, e = 20 µm, f, g, h, j = 50 µm, i= 70 µm.

Figure 3.20 *Tubeufia narathiwatensis* (MFLU 24-0505, holotype)

Yunnanomyces Tibpromma & K.D. Hyde, Fungal Diversity 93: 75 (2018)

Yunnanomyces (*Y.*), was introduced by Tibpromma et al. (2018) with *Y. pandanicola* as the type species, which was found as a saprobe on decaying leaves or wood in terrestrial habitats in China. Zhang et al. (2019) described *Y. phoenicis* on fallen rachides and leaves of *Phoenix paludosa*. Currently, four species of *Yunnanomyces* are listed in Species Fungorum (2024). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *Y. narathiwatensis* as a novel species found on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Yunnanomyces narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.22

Index Fungorum number: IF903525; Facesoffungi number: FoF 17528

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0490

Saprobic on the submerged leaflet of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* scattered, granular, black, glistening, gregarious, rarely solitary. *Mycelium* mostly superficial, composed of branched, septate, pale brown to dark brown, smooth hyphae. *Conidiophores* semi-macronematous, mostly reduced to conidiogenous cells, pale brown to dark brown, smooth, thick-walled. *Conidiogenous cells* 3–8 μm ($\overline{x}$ = 6.5 μm, n = 10), integrated, determinate, holoblastic, monoblastic, terminal, cylindrical, brown to dark brown. *Conidia* 22–29 × 14–19.8 μm ($\overline{x}$ = 26 × 17 μm, n = 20), acrogenous, solitary or arranged in a small chain, subglobose to ellipsoidal or obovoid, muriform, brown to black, thick-walled, comprises 14–40 cells per conidium, apical row containing 1–3 cells.

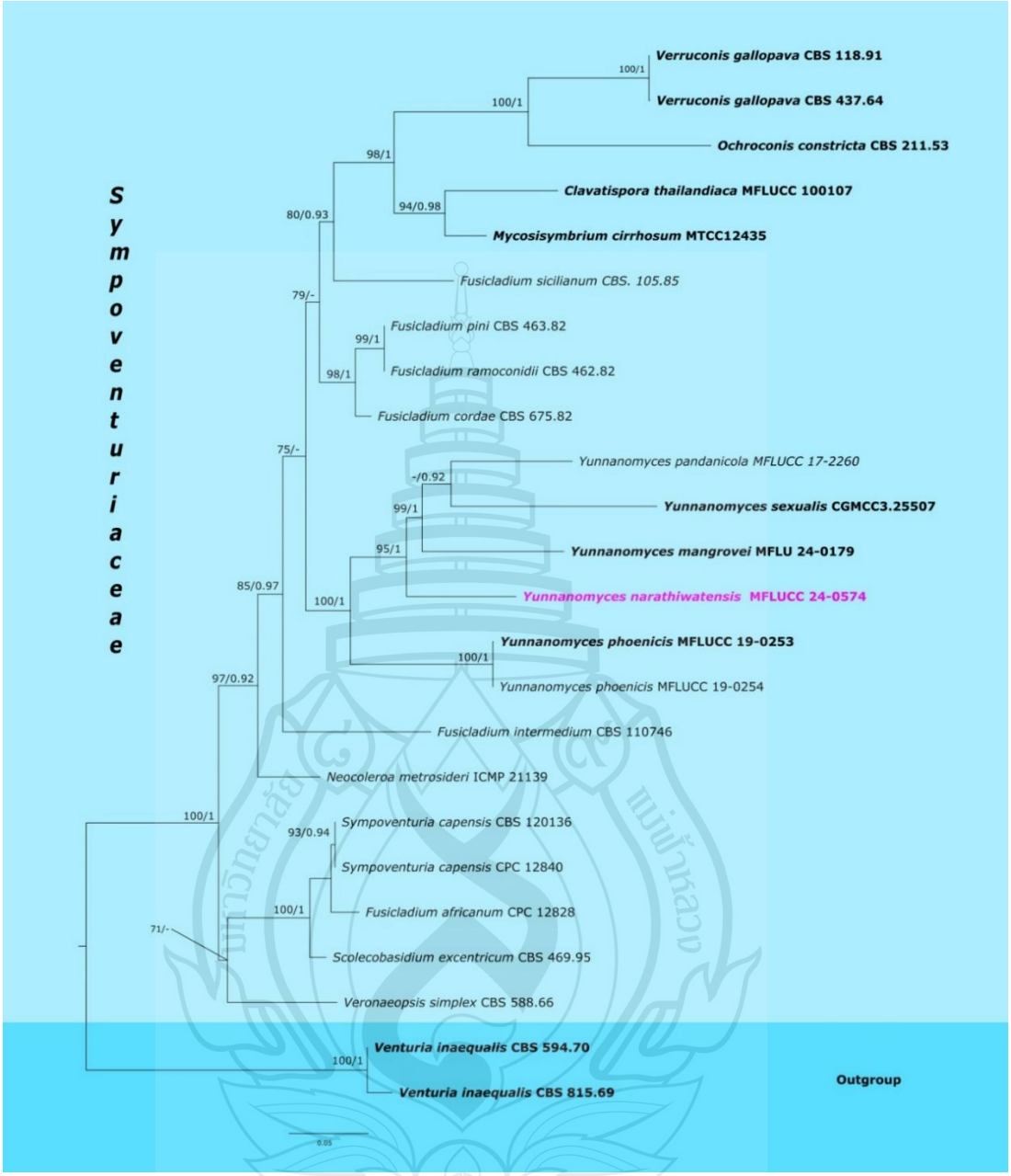
Culture characteristics – Colonies on the PDA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, lobate, medium dense, slightly raised, mycelia submerged in media at the margin, dull, felted, surface greyish brown, reverse dark brown to black.

Material examined – Thailand, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, Narathiwat, on the submerged leaflet of *Eleiodoxa conferta*, 4 August

2023, O. Karimi, S4PP38N1(MFLU 24-0490, holotype); ex-type living culture MFLUCC 24-0574.

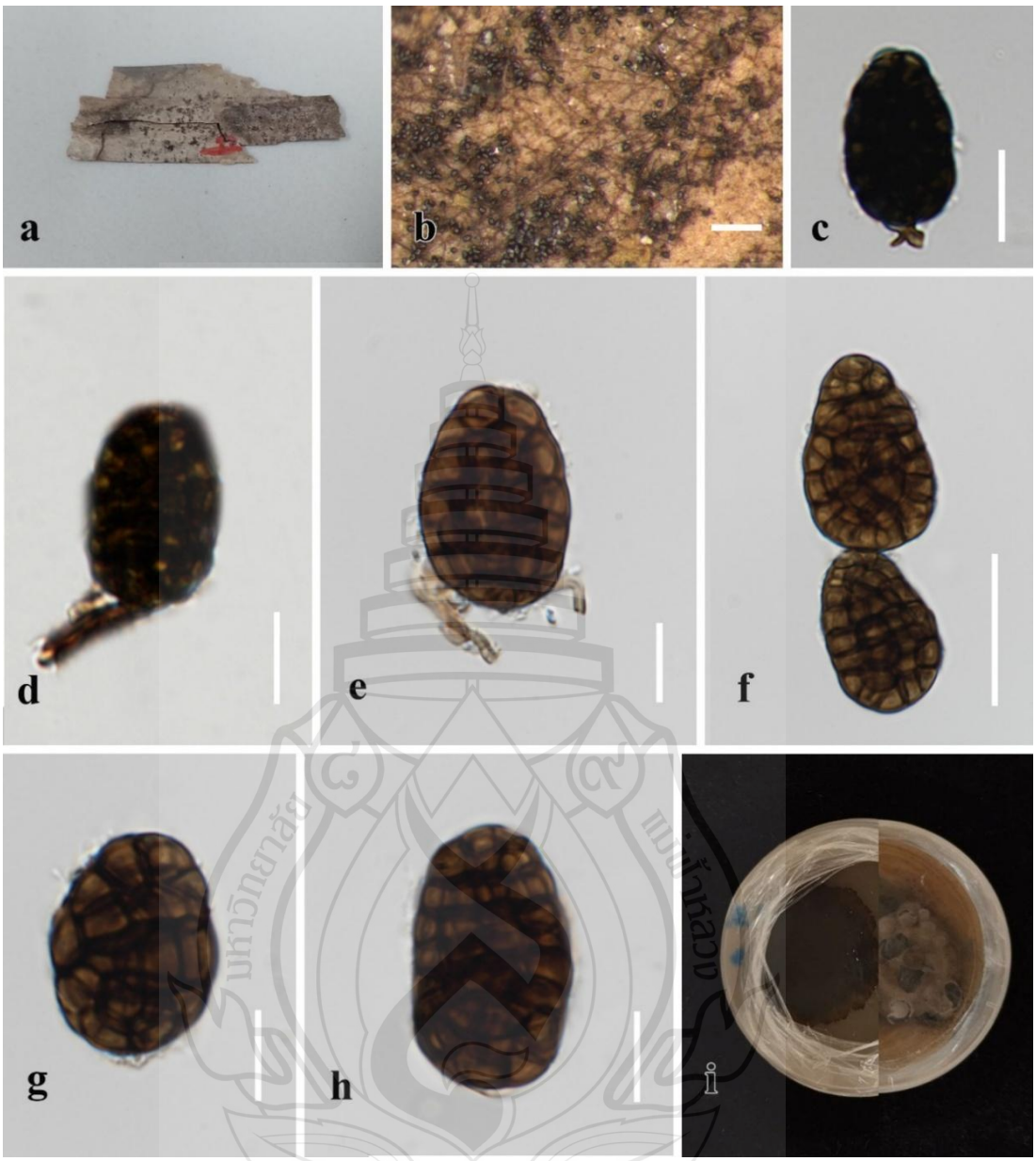
GenBank numbers – MFLUCC 24-0574: ITS = PV271878, LSU = PV271920, *rpb2* = PV340525.

Notes – Phylogenetically, *Yunnanomyces narathiwatensis* (MFLUCC 24-0574) clustered separately from the clade comprising *Y. mangrovei* (MFLU 24-0179), *Y. sexualis* (CGMCC3.25507), *Y. pandanicola* (MFLUCC 17-2260) with 95% ML and 1.00 PP statistical support in the combined phylogenetic analysis of LSU, SSU and *rpb*2. Furthermore, *Y. narathiwatensis* separated from *Y. phoenicis* (MFLUCC 19-0253, MFLUCC 19-0254) in the combined phylogenetic tree with 100% ML and 1.00 PP statistical support (Figure3.21). Morphologically, *Y. narathiwatensis* (MFLU 24-0490) is similar to *Y. phoenicis* (MFLU 19-0811) in having semi-macronematous conidiophores, integrated, determinate, holoblastic, monoblastic, terminal, cylindrical conidiogenous cells, acrogenous, muriform conidia. However, it differs in having gregarious colonies on the substrate, longer (3–8 µm vs. 0.7–1.2 µm), brown conidiogenous cells and shorter (22–29 × 14–19 µm vs. 18–34 × 12−22 µm), brown to black conidia with more cells per conidium (14–40 vs 10–30), in contrast to the punctiform colonies, subhyaline to pale brown conidiogenous cells and brown and hyaline conidia in *Y. phoenicis* (MFLU 19-0811) (Zhang et al. 2019). *Yunnanomyces narathiwatensis* (MFLUCC 24-0574) differs from *Y. pandanicola* (HKAS 96206) in having mostly superficial, pale brown to dark brown mycelium, mostly reduced conidiophores, brown to dark brown conidiogenous cells, and subglobose to ellipsoidal or obovoid, brown to black conidia, despite the immersed hyaline mycelium, fasciculate conidiophores, hyaline conidiogenous cells, and globose to broadly oval, flattened, yellow–brown conidia of the *Y. pandanicola* (HKAS 96206) (Tibpromma et al. 2018). Morphologically, *Y. narathiwatensis* is not comparable with *Y. mangrovei* (MFLU 24-0179) and *Y. sexualis* (ZY H-22.033) as they were described only in their sexual morphs (Zhang et al. 2024). Thus, we introduce *Y. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.



Note *Venturia inaequalis* (CBS 594.70, CBS 815.69) were used as the outgroup taxon. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strain of the current study is in purple, while type strains are in bold.

Figure 3.21 Phylogram generated from the ML analysis based on the combined LSU, SSU and *rpb2* sequence data of *Sympoventuriaceae*



Note a Host. b Colonies on the host. c, d Conidiogenous cells and developing conidia. e–h Conidia. i Culture characters on the PDA. Scale bars: b = 250 μm, c, d = 15 μm, e, g, h = 10 μm, f = 25 μm.

Figure 3.22 Yunnanomyces *narathiwatensis* (MFLU 24-0490, holotype)

Dothideomycetes orders *incertae sedis*

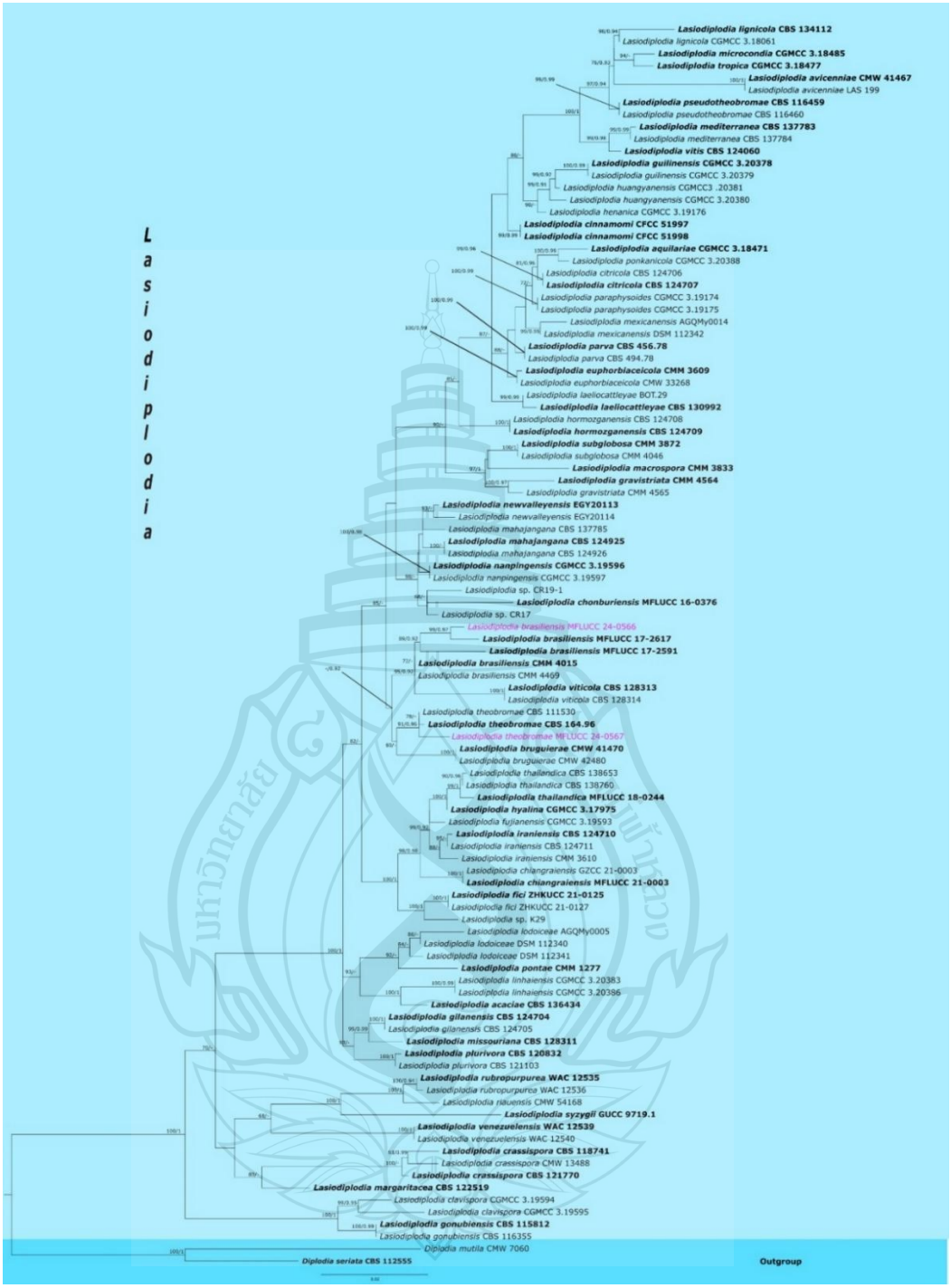
Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2007)

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

Theissen and Sydow (1918) established *Botryosphaeriaceae* with *Botryosphaeria* as the type genus, along with *Botryosphaeria*, *Dibotryona*, and *Phaeobotryon*. Currently, there are 22 accepted genera in *Botryosphaeriaceae* (Hyde et al. 2024). Members of this family are reported as plant pathogens, endophytes, and saprobes on various hosts (Phillips et al. 2013; Manawasinghe et al. 2021, 2022; Wu et al. 2023b; Samarakoon et al. 2024; Yu et al. 2024b; Tian et al. 2024). The family *Botryosphaeriaceae* is characterized by its sexual morph, which features uni- to multi-loculate ascostromata with 8-spored, bitunicate asci and ascospores that are hyaline to brown, aseptate, or septate (Phillips et al. 2013). The asexual morph includes coelomycetes that produce uni- to multi-loculate pycnidia, hyaline phialidic conidiogenous cells, and large conidia that may be hyaline or dematiaceous (Phillips et al. 2013).

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

Clendenin (1896) established *Lasiodiplodia* (*La*.), with *La. theobromae* as the type species. Species in this genus are known to infect various woody plants, causing diseases such as cankers, dieback, fruit and root rot, and branch blights (Alves et al. 2008; Tibpromma et al. 2018; Zhang et al. 2021; Tian et al. 2024; Samarakoon et al. 2024). Currently, 88 records of *Lasiodiplodia* species are listed in Species Fungorum (2024). To date, one species of this genus (*La. theobromae*) has been reported from peat swamp forests (Pinuruan et al. 2007). In this study, we document *La. brasiliensis* and *La. theobromae* as new records on *Cyrtostachys renda* from the peat swamp forests in Narathiwat, Thailand. An updated tree for the genus *Lasiodiplodia* is shown in Figure 3.23.



Note *Diplodia seriata* (CBS 112555) and *D. mutila* (CMW 7060) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolates of the current study are in purple, while the type strains are in bold.

Figure 3.23 Phylogram generated from ML analysis based on ITS, *tef1-α* and *tub*2 sequence data of *Lasiodiplodia*

Lasiodiplodia brasiliensis M.S.B. Netto et al., Fungal Diversity 67: 134 (2014) Figure 3.24

Index Fungorum number: IF812566; Facesoffungi number: FoF 14085

Saprobic on a dead leaflet of *Cyrtostachys renda*. Asexual morph: *Pycnidia* 610–720 × 200–340 µm ($\overline{x}$ = 700 × 315.5 µm, n = 7), scattered to gregarious, immersed, dark brown. *Pycnidial wall* 50–76 µm wide, composed of several layers of thick-walled, brown to dark brown cells of *textura angularis. Paraphyses* 25–80 µm long, aseptate, hyaline, straight, smooth, thin-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 13–17 × 3–4 µm ($\overline{x}$ = 15 × 3.5 µm, n = 20), annellidic, cylindrical, thick-walled, smooth. *Conidia* 22–29 × 11.2–14.5 µm ($\overline{x}$ = 27 × 13 µm, n = 20), subglobose to oval, aseptate, hyaline, guttulate. Sexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 5 cm diam. after seven days at room temperature (25–28 °C). Colony circular, medium dense with aerial mycelia, slightly raised, dull, entire edge, without pigment diffusion, initially white and gradually turning black with age.

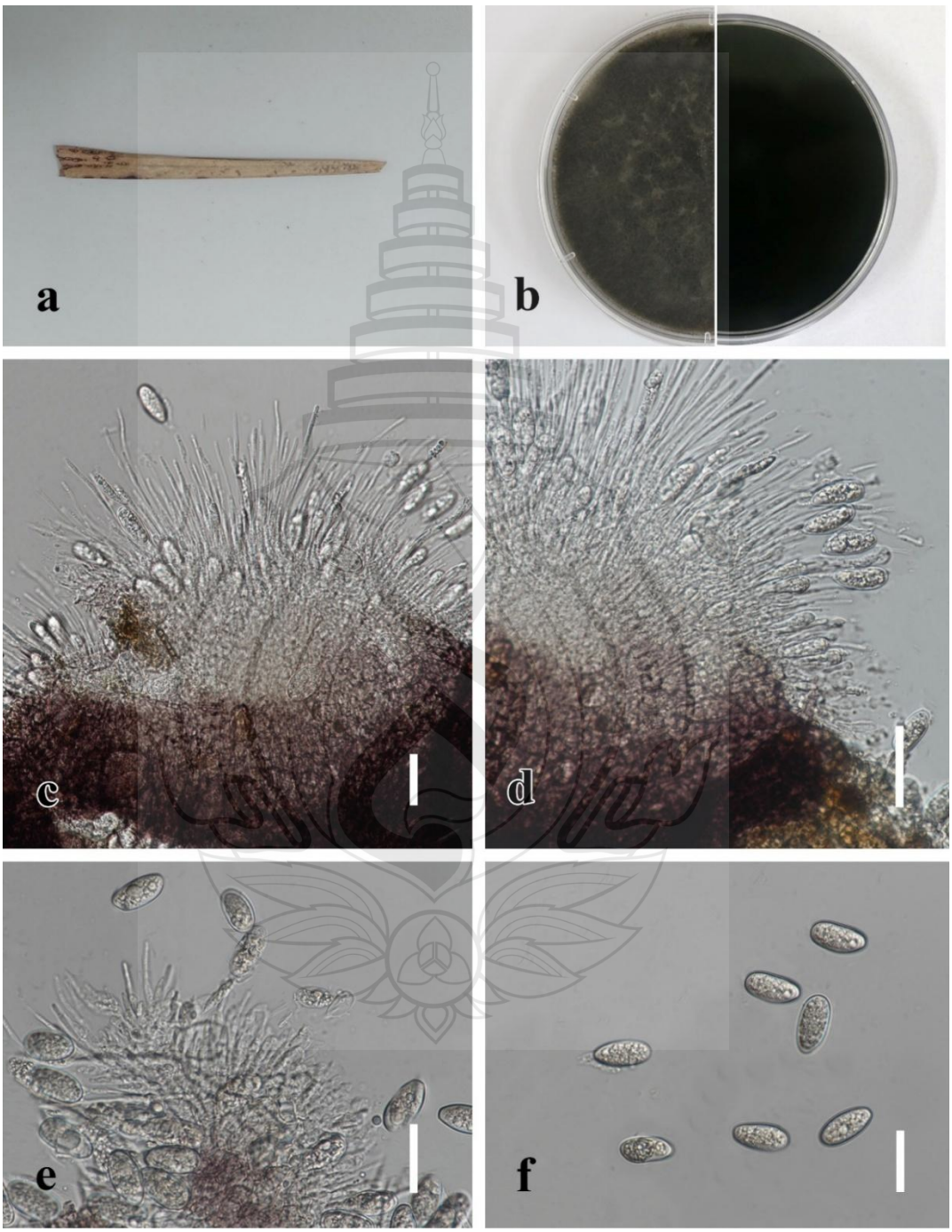
Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on *Cyrtostachys renda*, 4 August 2023, O. Karimi, F10 (MFLU 24-0482), living culture MFLUCC 24-0566.

Known hosts and distribution – *Lasiodiplodia brasiliensis* has a cosmopolitan distribution and is associated with different host species (Farr and Rossman 2025). This study presents the first report of *La. brasiliensis* on *Cyrtostachys renda* from the peat swamp forest in Narathiwat, Thailand.

GenBank numbers – MFLUCC 24-0566: ITS = PV271879, LSU = PV271921, *tef-1α* = PV340494.

Notes – Phylogenetically, our strain (MFLUCC 24-0566) clustered as a sister taxon of *Lasiodiplodia brasiliensis* (MFLUCC 17-2617) with 99% ML Bootstrap and 0.97 posterior probability support (Figure 3.13). Nucleotide comparisons showed that our strain (MFLUCC 24-0566) has similar ITS and *tef-1α* sequences with *La. brasiliensis*, however, *tub*2 data cannot be compared as it is unavailable for the holotype. Morphologically, our strain has similar morphology to the *La. brasiliensis* (URM 85580) (Netto et al. 2014), with slightly longer conidiogenous cells (13–17 µm

vs. 7–14) and larger conidia (22–29 × 11.2–14.5 µm vs. 20–25 × 10–14). Therefore, we identified our strain (MFLU 24-0482) as *La. brasiliensis* based on phylogenetic analyses and morphological characters. We report our strain (MFLU 24-0482) as a new host record of *La. brasiliensis* on *Cyrtostachys renda* from Thailand.



Note a Host. b Colonies on the PDA. c–e Conidiogenous cells, paraphyses and conidia. f Conidia. Scale bars: c, e = 30 µm, d = 40 µm, f = 25 µm.

Figure 3.24 *Lasiodiplodia brasiliensis* (MFLU 24-0482, new host record)

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909) Figure 3.25

Index Fungorum number: IF188476; Facesoffungi number: FoF 00167

Saprobic on *Cyrtostachys renda*. Asexual morph: Coelomycetous. *Pycnidia* 150–350 µm high × 120–279 µm diam. ($\bar{x}$ = 220 × 190 µm, n = 20), solitary, superficial, subglobose, uniloculate, black. *Pycnidial wall* 20–60 µm wide, comprising cells of *texture angularis*, multi layers of thick-walled, brown to dark brown cells. *Mycelium* hyaline to brown, branched, smooth, thin-walled, septate. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 7–19 × 3–9 µm ($\bar{x}$ = 12 × 6 µm, n = 20), hyaline, smooth, cylindrical, holoblastic. *Conidia* 25–32 × 10–17 µm. ($\bar{x}$ = 26 × 14 µm, n = 20), oblong to ovoid, thick-walled, aseptate, hyaline and become brown, striate and 1-septate with age. Sexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after seven days at room temperature (25–28 °C). Colony circular, medium dense, flat with aerial mycelia, dull, entire edge, without pigment diffusion, surface brownish grey and reverse black.

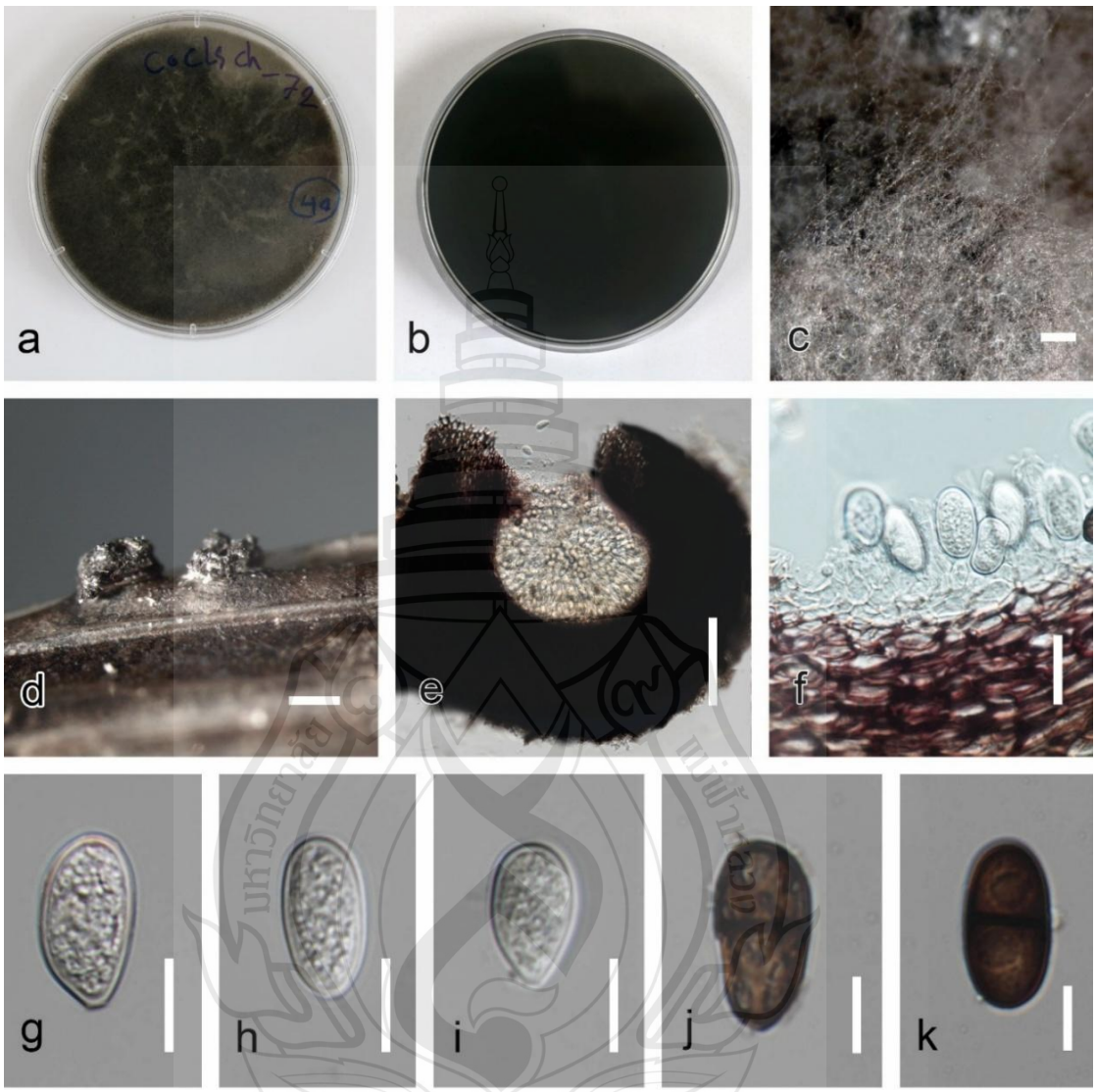
Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on *Cyrtostachys renda*, 4 August 2023, O. Karimi, 316 (MFLU 24-0483), living culture MFLUCC 24-0567.

Known hosts and distribution – *Lasiodiplodia theobromae* is distributed worldwide and infects a wide variety of host species (Farr and Rossman 2025). This study presents the first report of *La. theobromae* on *Cyrtostachys renda* from the peat swamp forest in Narathiwat, Thailand.

GenBank numbers – MFLUCC 24-0567: ITS = PV271880, *tef-1α* = PV340495.

Notes – Phylogenetically, our strain (MFLUCC 24-0567) clustered with the ex-neotype strain (CBS 164.96) and another strain (CBS 111530) of *Lasiodiplodia theobromae* with 91% ML bootstrap and 0.96 posterior probability support (Figure 3.23). Nucleotide comparisons showed that our strain (MFLUCC 24-0567) has similar ITS and *tub*2 sequences to *La. theobromae* (CBS 164.96), and the *tef-1α* sequence shows two bp differences. Morphologically, our strain (MFLU 24-0483) is similar to the neotype (MBT176098) (Alves et al. 2008). Therefore, we identified our strain (MFLU 24-0483) as *La. theobromae* based on phylogenetic analyses and

morphological characters. We report our strain (MFLU 24-0483) as a new host record of *La. theobromae* on *Cyrtostachys renda* from Thailand.



Note a, b Colonies on the PDA, above (a), and below (b). c, d Colonies and conidiomata on the host. e Vertical section through a conidioma. f Conidiomatal wall. g–i Immature conidia. j, k Mature conidia. Scale bars: c = 1 mm, d = 750 µm, e = 25 µm, f = 15 µm, g–k = 10 µm.

Figure 3.25 *Lasiodiplodia theobromae* (MFLU 24-0483, a new host record)

Class *Leotiomycetes* O.E. Erikss. & Winka, Myconet 1: 7 (1997)

Helotiales genera incertae sedis

Strossmayeria Schulzer, Oesterr. Bot. Z. 31 (10): 313 (1881)

Strossmayeria (*St.*), was introduced by Schulzer (1881) with *St. rackii* as the type species. Currently, there are 20 accepted *Strossmayeria* species listed in Species Fungorum (2024). Members of this genus have been reported on various plant hosts, including bamboo from Panama, *Calamus moti* from Australia, *Corylus* sp. from France, *Fagus* sp. from Germany and the USA, *Quercus* sp. from Italy, and *Rhipogonum scandens* from New Zealand (Schulzer 1881; Iturriaga and Korf 1990; Fröhlich and Hyde 2000). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *St. narathiwatensis* as a novel species, saprobic on the submerged rachis of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogeny for *Strossmayeria* is shown in Figure 3.26.

Strossmayeria narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.27

Index Fungorum number: IF903526; Facesoffungi number: FoF 17529

Etymology – The epithet “narathiwatensis” refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0491

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host effuse, hairy, dark brown to black. *Mycelium* mostly immersed, composed of smooth, thick-walled, brown hyphae. *Conidiophores* up to 577 µm long and 4–13 µm wide ($\overline{x}$ = 7 µm, n = 30), macronematous, mononematous, fasciculate, branched, septate, erect, straight or flexuous, verrucose, cylindrical, sinuate or geniculate, brown, dark brown to black, paler towards the apex. *Conidiogenous cells* 10–34 × 3.4–8.4 µm ($\overline{x}$ = 19.5 × 5.9 µm, n = 20), holoblastic, polyblastic, indeterminate, terminal or intercalary, pale brown to brown, integrated, with percurrent proliferations. *Conidiogenous loci* inconspicuous or slightly prominent, narrow. *Conidia* 15–30 × 8–12 µm ($\overline{x}$ = 22 × 9.8 µm, n = 20),

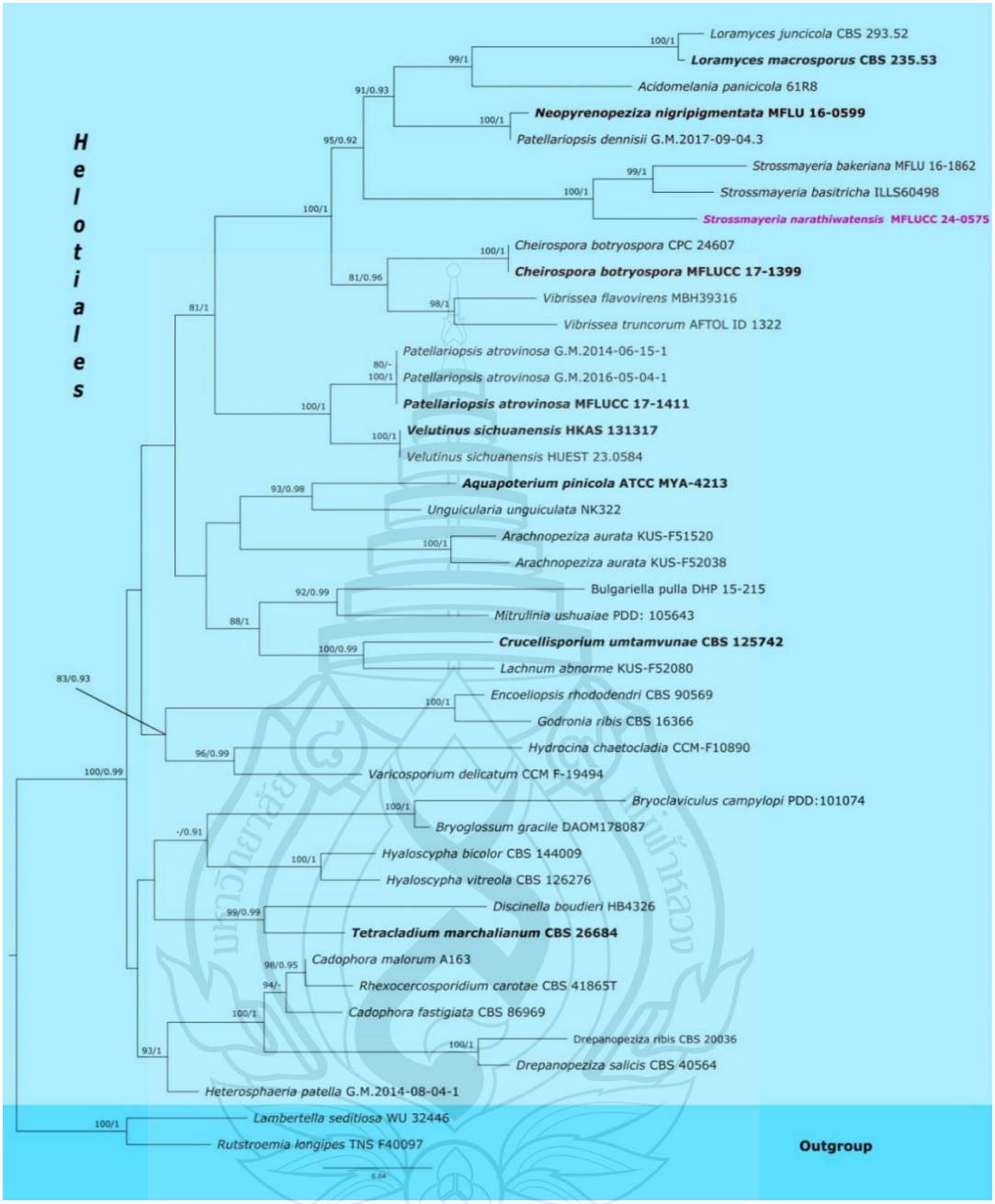
secession schizolytic, broad fusiform, solitary, dry, smooth, acropleurogenous, pale olivaceous, to pale brown, 3–7-pseudoseptate.

Culture characteristics – Colonies on the CMA reaching 2.5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, flat, dull, smooth, mycelium mostly submerged to media, from surface pale yellow, from reverse yellowish orange.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 4Y (MFLU 24-0491, holotype); ex-type living culture MFLUCC 24-0575.

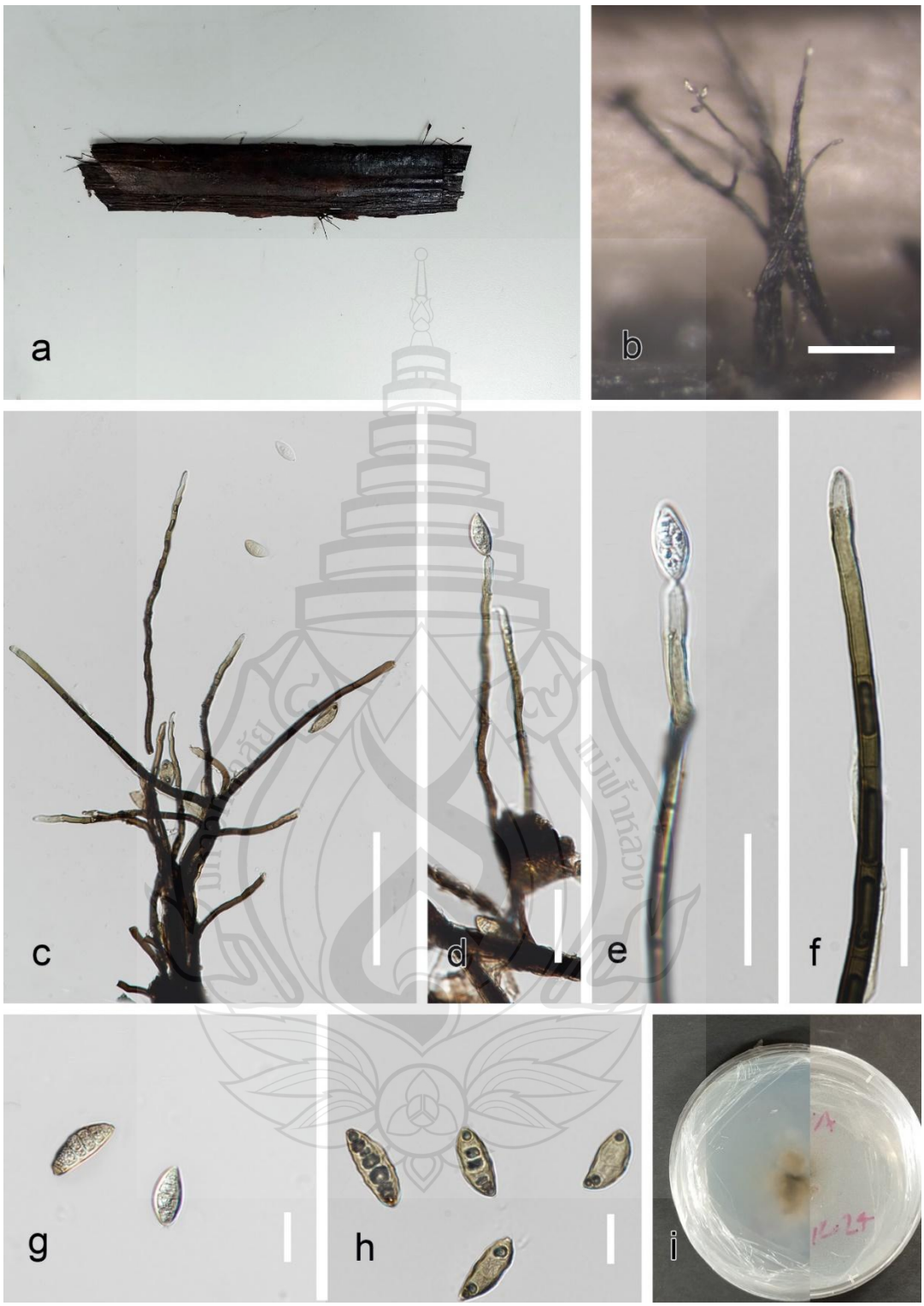
GenBank numbers – MFLUCC 24-0575: ITS = PV271881, LSU = PV271922, SSU = PV263313, *rpb2* = PV340526.

Notes – Phylogenetically, our strain (MFLUCC 24-0575) clustered separately from *Strossmayeria basitricha* (ILLS60498) and *St. bakeriana* (MFLU 16-1862), in the combined phylogenetic analysis of LSU and ITS (Figure 3.26), with 100% ML and 1.00 PP statistical support. Morphologically, it is similar to the asexual morph of *St. bakeriana* (Ellis 1971; Ruiz et al. 2001), but it differs in having longer and wider conidiophores (up to 577 × 4−13 μm vs. up to 400 × 4.5−6.5 μm), shorter conidia (15–30 μm vs. 26–44 μm) with less pseudosepta (3−7 vs. 6−11). Our strain is different with *St. basitricha* in having shorter and wider conidia (22 × 9.8 μm vs. 35 × 8 μm) and forming laterally or terminally on distinguished conidiophores and conidiogenous cells despite the latter species producing conidia terminally on filamentous hyphae (Saccardo 1875). Morphologically our strain (MFLUCC 24-0575) is similar to *St. josserandii* in having brown conidiophores lighter toward the apex, polyblastic, terminal or intercalary conidiogenous cells and solitary, dry, acropleurogenous, fusiform conidia, but it differs in lacking bulbous base in conidiophores, protruding pale scars in conidiogenous cells and dark brown basal cell in conidia despite the conidiophores with swollen bases, conidiogenous cells bearing slightly protruding pale scars and basal cells usually dark brown in the latter (Bertault 1970). Therefore, we introduce *St. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.



Note *Lamertella seditiosa* (WU-32446) and *Rutsroemia longipes* (TNS F40097) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strain of the current study is in purple, while the type strains are in bold.

Figure 3.26 Phylogram generated from the ML analysis based on the combined LSU and ITS sequence data of *Helotiales*



Note a Host. b Colonies on the host substrate. c–f Conidiophores, conidiogenous cells and conidia. g, h Conidia. i Colonies on the CMA. Scale bars: b, c = 100 μm, d = 40 μm, e, f = 30 μm, g, h = 15 μm.

Figure 3.27 *Strossmayeria narathiwatensis* (MFLU 24-0491, holotype)

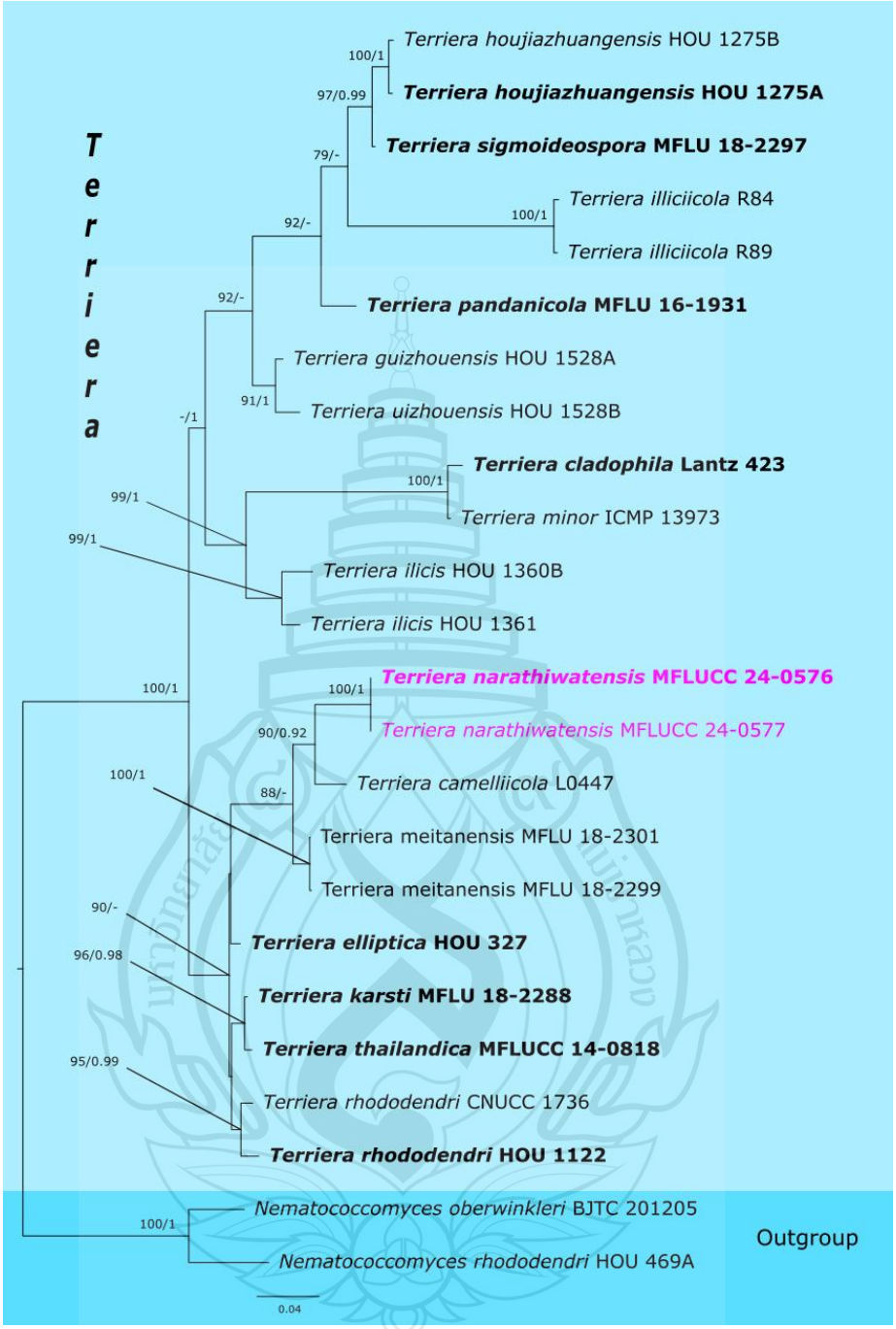
Rhytismatales M.E. Barr ex Minter, Syst. Ascomycetum 5: 182 (1986)

Rhytismataceae Chevall., Flore Générale des Environs de Paris 1: 439 (1826)

Rhytismataceae species are saprobic or parasitic on plant material, with *Rhytisma* as the type genus (Wang et al. 2006, 2023). The family was established by Chevallier (1826) and placed in *Rhytismatales* by Hawksworth and Eriksson (1986). Sexual morph is characterised by apothecial long-stipitate, clypeate ascomata, opened via longitudinal split or radial fissures. Paraphyses are mostly present, filiform, curved, hyaline and sometimes with swollen apex. Asci are cylindric-clavate, mostly non-amyloid with 4–8 ascospores. Ascospores are hyaline, mostly unicellular, tapered base and variable in shape, including ovoid, ellipsoid, clavate, sub-cylindrical, fusoid or filiform, sometimes with gel cap at the apex (Wang et al. 2006; Ge et al. 2014; Tanney and Seifert 2017; Ekanayaka et al. 2019). Asexual morph is coelomycetous with sympodial proliferating holoblastic conidiogenous cells, bearing hyaline, unicellular, ellipsoid to fusoid, rod-shape conidia (Wang et al. 2006; Ge et al. 2014; Ekanayaka et al. 2019). The *rpb2*, *tef-1α* and *act* gene regions are effective barcodes for the phylogeny of *Rhytismataceae.* However, many taxa in this family lack sequences for these genes (Ekanayaka et al. 2019; Wang et al. 2023). Currently, there are 65 accepted genera in this family (Hyde et al. 2024).

Terriera B. Erikss., Symbolae Botanicae Upsalienses 19 (4): 58 (1970)

Terriera (*Te.*), was introduced by Eriksson (1970), with *Te. cladophila* as the type species. Currently, there are 40 accepted *Terriera* species listed in Species Fungorum (2024). Members of *Terriera* have been reported on woody plant materials from various regions, including Argentina, Brazil, China, India, Indonesia, New Zealand, Norway, Puerto Rico, Sri Lanka, Thailand, and the USA (Johnston 2001; Hyde et al. 2016; Tibpromma et al. 2018; Zhang et al. 2020). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *Te. narathiwatensis* as a novel species found on submerged leaf sheaths of *Cyrtostachys renda* from the peat swamp forest in Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.28.



Note *Nematococcomyces oberwinkleri* (BJTC 201205) and *N. rhododendri* (HOU 469A) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strain produced by the current study is in purple, while the type strains are in bold.

Figure 3.28 Phylogram generated from the ML analysis based on the combined LSU, ITS and mtSSU sequence data of *Terriera*

Terriera narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.29

Index Fungorum number: IF903527; Facesoffungi number: FoF 17530

Etymology – The epithet “narathiwatensis” refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0492

Saprobic on the submerged leaf sheath of *Cyrtostachys renda*. Sexual morph: *Ascomata* 430–1100 × 70–250 ($\overline{x}$ = 650 × 185 μm, n = 25), black, scattered or in small groups, semi-immersed to superficial, elliptical or oblong-elliptical, straight or curved, with a black area on the host surface, raising the host surface, opened via a single longitudinal split almost entire the length. *Apothecium* covered by host tissue at the sides, slit area is uncovered and open. *Covering stroma* 20–57 μm wide ($\overline{x}$ = 40 μm, n = 15), carbonaceous, brittle, dark brown to black, cellular structure not obvious, with brown *textura angularis* thick-walled cells toward the inner layers. *Basal stroma* 10–38 (−63) μm wide ($\overline{x}$ = 29 μm, n = 10), dark-brown to reddish brown, irregularly combined with the host tissue. Sometimes a triangular-shaped space present at the joining area of the covering stroma with the basal stroma, at both or one side, 11–50 μm wide ($\overline{x}$ = 29 μm, n = 10), composed of thick-walled, brown, *textura prismatica* to *textura angularis* or *textura globosa* cells. *Subhymenium* 5.5−11 μm wide ($\overline{x}$ = 8 μm, n = 15), hyaline, *textura angularis* to *textura intricata*, thin-walled cells. *Paraphyses* 68–88 × 0.9−2.2 μm ($\overline{x}$ = 78 × 1.5 μm, n = 25), filiform, hyaline, branched, rarely septate, slightly swollen and irregular in at the apices. *Asci* 70–96 × 4−8 μm ($\overline{x}$ = 80 × 5.7 μm, n = 25), cylindrical, short-stalked, flattened apex, thin-walled. *Ascospores* 48–53 × 2.3−2.7 μm ($\overline{x}$ = 50 × 2.5 μm, n = 30), fascicle, filiform, slightly tapering towards the ends, hyaline, guttulate, aseptate, straight or slightly curved, lacking a gelatinous sheath. Asexual morph: Not observed.

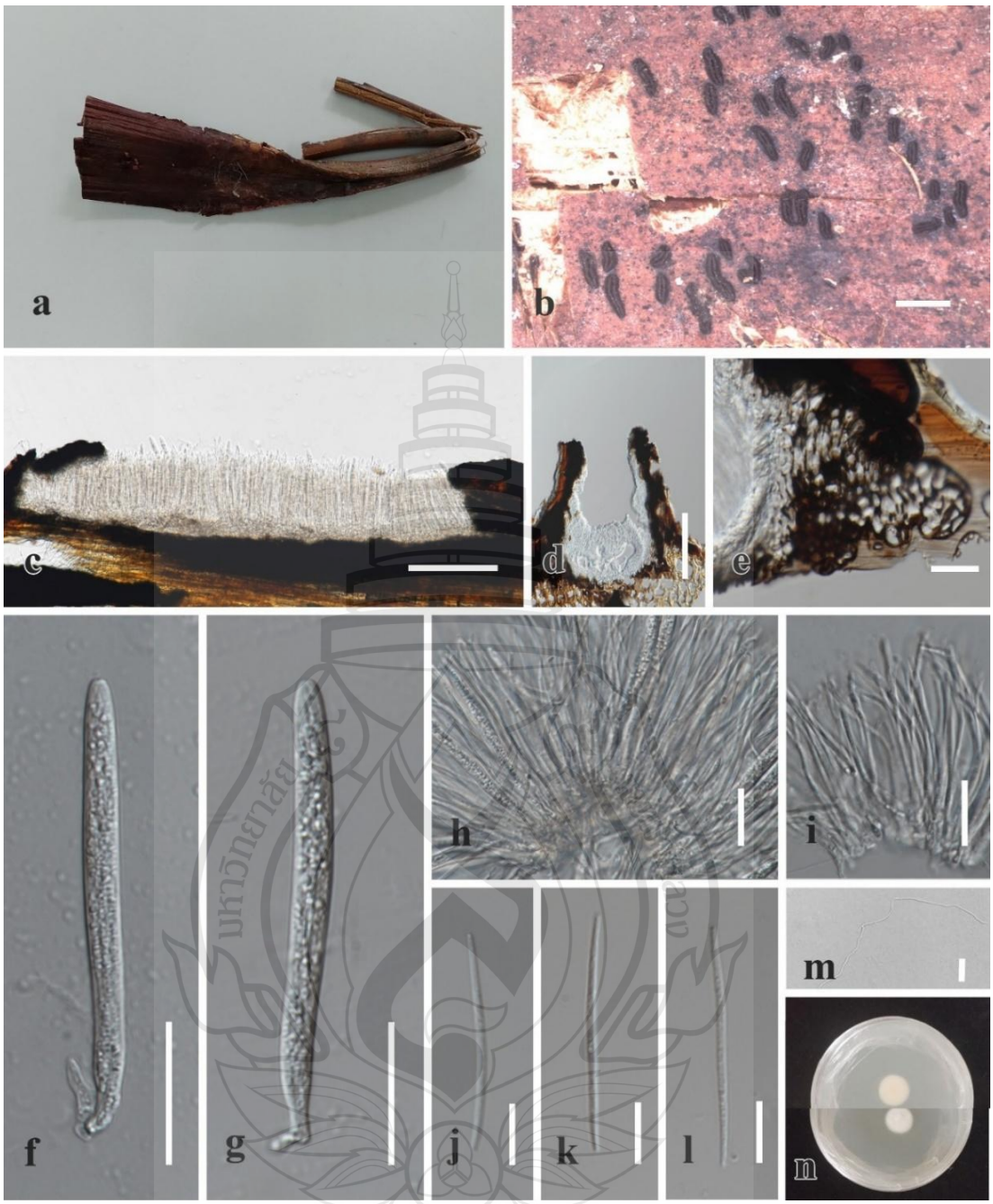
Culture characteristics – Colonies on the PDA reaching 1.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, umbonate, dull, entire edge, no sporulation, surface and reverse white.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged leaf sheath of *Cyrtostachys renda*, 4 August 2023, O. Karimi, 21R-a (MFLU 24-0492, holotype); ex-type living culture

MFLUCC 24-0576; 21R-b (MFLU 24-0493, isotype); ex-isotype living culture MFLUCC 24-0577.

GenBank numbers – MFLUCC 24-0576: ITS = PV271882, LSU = PV271923, mtSSU = PV271943, MFLUCC 24-0577: ITS = PV271883, mtSSU = PV271944.

Notes – Phylogenetically, our strain (MFLUCC 24-0576) formed a sister clade to *Terriera camelliicola* (L0447) with 90% ML and 0.92 PP statistical support in the combined phylogenetic analyses of LSU, ITS and mtSSU (Figure 3.28). Morphologically, it differs from *Te. camelliicola* in having larger ascomata (430–1100 μm vs. 500–900 μm), lacks protrusion at right angles from the substrate-covered part of the clypeus around the split, have thick basal stroma, shorter asci (70–96 vs. 80–110 μm), with a short stalk and flattened apex, and shorter and wider ascospores (48–53 × 2.3–2.7 μm vs. 50–70 × 1 μm), without a sheath in contrast to the long-stalked ascospores with a rounded apex and a surrounding sheath in *Te. camelliicola* (Minter and Sharma 1982). Based on a pairwise comparison of LSU and mtSSU nucleotides, *Te. narathiwatensis* (MFLUCC 24-0576) differs from *Te. camelliicola* (L0447) by 5.37% (63/1173 bp) in the LSU and 3.23% (31/959 bp) in mtSSU, without including gaps. The ITS region was not comparable as it is not available for *Te. camelliicola*. Therefore, we introduce *Te. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.



Note a Host. b Appearance of apothecia on the host substrate. c Horizontal section through an apothecium. d Vertical section through an apothecium. e Triangular space in the section between the covering stroma and basal stroma. f, g Asci. h, i Paraphyses. j–l Ascospores. m A germinated ascospore. n Colonies on the PDA. Scale bars: b = 1000 μm, c, i = 25 μm, d = 100 μm, e, j–l = 15 μm, f, g = 30 μm, h, m = 20 μm.

Figure 3.29 *Terriera narathiwatensis* (MFLU 24-0492, holotype)

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

Subclass *Diaporthomycetidae* Senan., Maharachch. & K.D. Hyde, Fungal Diversity 72: 208 (2015)

Annulatascales D'souza, Maharachch. & K.D. Hyde, Fungal Diversity 72: 212 (2015)

Annulatascaceae S.W. Wong, K.D. Hyde & E.B.G. Jones, Systema Ascomycetum 16: 18 (1998)

Wong et al. (1998d) introduced the family *Annulatascaceae* with *Annulatascus* as the type genus. Subsequently, *Annulatascales* was established by Maharachchikumbura et al. (2015) through combined phylogenetic analyses using LSU, SSU, *tef1-α*, and *rpb*2 sequence data to accommodate species within *Annulatascaceae*. Currently, the family comprises 12 genera, including *Annulatascus, Annulusmagnus, Aqualignicola, Ascitendus, Ayria, Cataractispora, Chaetorostrum, Fusoidigranularius, Longicollum, Longivarius, Submersisphaeria,* and *Vertexicola* (Hyde 1996; Wong et al. 1998d; Hyde et al. 1999; Ranghoo et al. 2001; Campbell and Shearer 2004; Fryar and Hyde 2004; Zelski et al. 2011; Maharachchikumbura et al. 2015; Dong et al. 2021). Members of *Annulatascaceae* were reported as saprobes on woody substrates in freshwater and terrestrial habitats (Maharachchikumbura et al. 2015). The sexual morph of *Annulatascaceae* is characterised by unilocular, rarely clypeate ascomata, with black or hyaline necks, coriaceous or membranous peridium, and tapering paraphyses. Asci are 8-spored, unitunicate, pedicellate, and usually feature a massive, J-, refractive apical ring. Ascospores are uniseriate, hyaline or sometimes brown, with or without septa. The asexual morph of *Chaetorostrum* is reported as Taeniolella-like (Maharachchikumbura et al. 2015). An updated phylogeny for the family is shown in Figure 3.30.

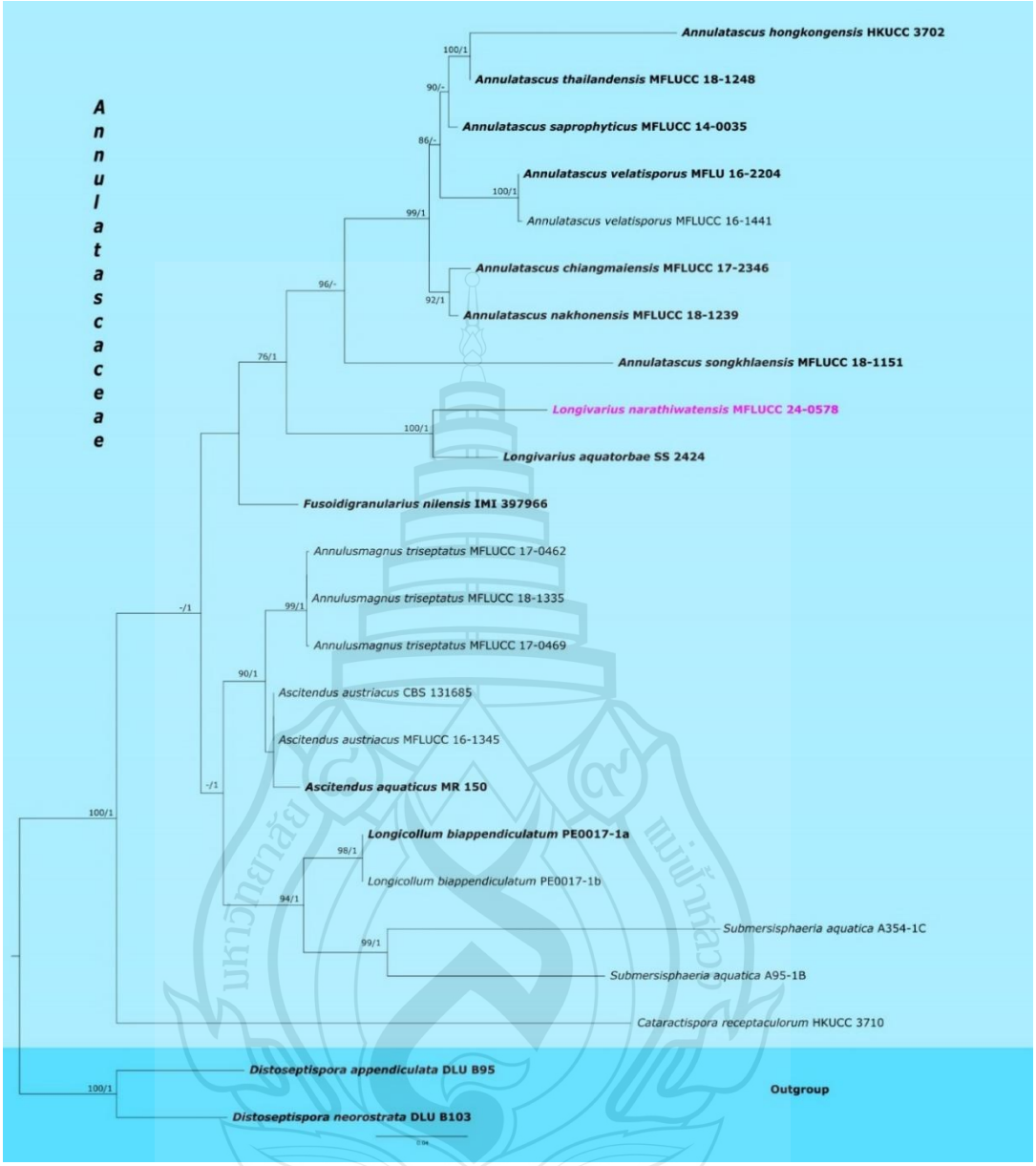
Annulatascus K.D. Hyde, Austral. Syst. Bot. 5: 118 (1992)

Hyde (1992a) introduced *Annulatascus* as a novel genus in order *Annulatascales* based on *A. velatisporus* as the type species and *A. bipolaris*, which were collected from Millaa Millaa Falls and the Clohesy River in north Queensland on submerged wood in freshwater habitat. Based on Species Fungorum (2025) there are 20 accepted species in this genus and molecular data is available for seven species, most

of which are isolated from freshwater habitats in tropical areas. Dayarathne et al. (2016) designated an epitype specimen for *A. velatisporus* due to the inadequate condition of the type species, which had a limited number of ascomata. The genus is defined by its distinctive features, including solitary, partially submerged to superficial, carbonaceous, papillate, and black ascomata. The ascomata have a central black ostiole with a neck, and the peridium is brown to black, composed of two layers. Paraphyses are septate and unbranched. Asci are cylindrical, unitunicate, and 8-spored. Ascospores are uniseriate, fusiform, hyaline, guttulate, and surrounded by a mucilaginous sheath. Fröhlich and Hyde (2000) introduced *A. citriosporus* on dead petiole of *Licuala* sp. from Brunei and *A. licualae* on dead petiole of *Licuala ramsayi* from Australia, Queensland.

Longivarius W. Dong, H. Zhang & K.D. Hyde, Mycosphere 12 (1): 20 (2021)

Annulatascus aquatorbae was originally introduced by Boonyuen et al. (2012) based on a collection from submerged wood test blocks of *Erythrophleum teysmannii* in Thailand. Later, Dong et al. (2021a) studied Annulatascaceae-like taxa and revealed that *Annulatascus aquatorbae* formed a distinct clade, separate from other *Annulatascus* species, based on the combined phylogenetic analyses of LSU, ITS, *tef-1α*, and *rpb*2. Consequently, they established a new genus, *Longivarius* (*Lo.*), to accommodate *Lo. aquatorbae*. Currently, there is only one species in this genus listed in Species Fungorum (2024). The type species *Lo. aquatorbae* has been reported from peat swamp forests in Narathiwat, Thailand (Boonyuen et al. 2012). In this study, we introduce *Lo. narathiwatensis* as a novel species, found on submerged rachides of *Eleiodoxa conferta* in the peat swamp forest of Narathiwat, Thailand.



Note *Distoseptispora appendiculata* (B95), and *D. neorostrata* (B103) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.30 Phylogram generated from the ML analysis based on the combined LSU and ITS sequence data of *Annulatascaceae*

Longivarius narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.31

Index Fungorum number: IF903530; Facesoffungi number: FoF 17531

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0494

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host effuse, scattered or in small groups, granular, glistening, black. *Mycelium* superficial to semi-immersed, composed of smooth, thick-walled, brown hyphae. *Conidiophores* 10.5–28 × 1.2–3.2 μm ($\overline{x}$ = 16.5 × 2.2 μm, n = 15), micronematous, mononematous, cylindrical, flexuous, smooth, hyaline to pale brown. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindrical or ampulliform, up to 5 μm long and 5 μm wide at the apex, terminal, pale brown to brown. *Conidia* 21.5–46 × 19–35 μm ($\overline{x}$ = 34 × 26.7 μm, n = 35), solitary, terminal or lateral, globose to subglobose or irregular, thick-walled, septate, constricted at septa, muriform, guttulate, pale brown to dark brown.

Culture characteristics – Colonies on the PDA reaching 3.5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, medium sparse, flat, dull, submerged, slightly irregular, no sporulation, surface greyish orange, reverse light orange.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 13G (MFLU 24-0494, holotype); ex-type living culture MFLUCC 24-0578.

GenBank numbers – MFLUCC 24-0578: ITS = PV271884, LSU = PV271924, SSU = PV263314, *rpb2* = PV340507.

Notes – Our strain (MFLUCC 24-0578) clustered with *Longivarius aquatorbae* (SS 2424) in the combined phylogenetic analysis of LSU and ITS (Figure 3.30), with 100% ML and 1.00 PP statistical support. The morphology of our strain is not comparable to *Lo. aquatorbae* (SS 2424), as the latter was described with a sexual morph. Based on a pairwise comparison of LSU nucleotides, *Lo. narathiwatensis* (MFLU 24-0494) differs from *Lo. aquatorbae* (SS 2424) by 3.3% (33/995 bp,

excluding gaps), and ITS, SSU, *rpb*2, and *tef-1α* sequences of *Lo. narathiwatensis* cannot be compared, as they are unavailable for *Lo. aquatorbae* (SS 2424). Therefore, based on the phylogeny and sequence comparison, we introduce *Lo. narathiwatensis* (MFLU 24-0494) as a novel species. However, further sampling of these fungal specimens is required to confirm the status of this novel species in future.

Cancellidiales K.D. Hyde & Hongsanan, Fungal Diversity 107: 86 (2021)

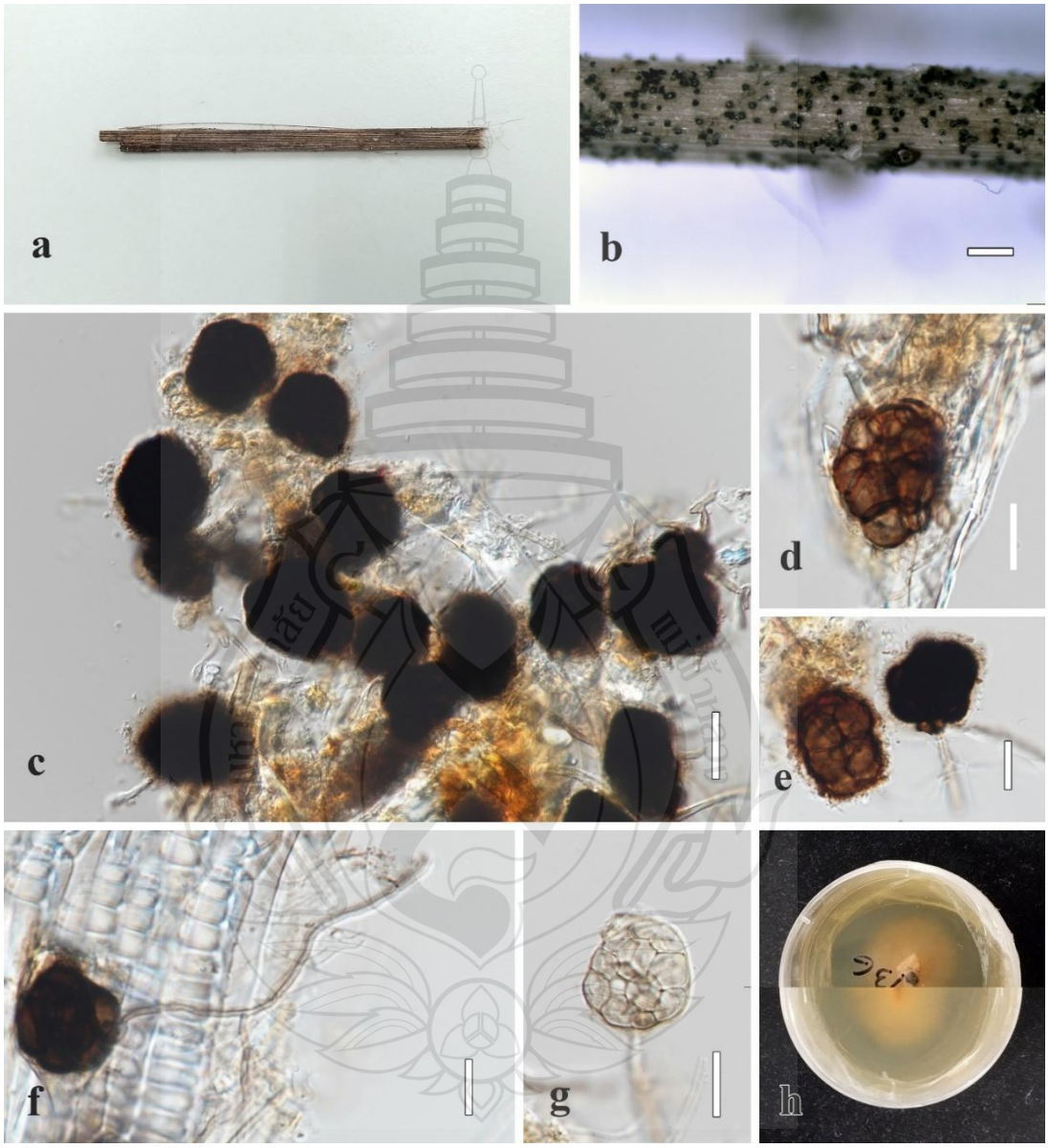
Cancellidiaceae K.D. Hyde & Hongsanan, Fungal Diversity 107: 86 (2021)

Hyde et al. (2021) established the family *Cancellidiaceae* to accommodate the asexual genus *Cancellidium* (*Ca.*) within *Cancellidiales*, based on a divergence time analysis, which indicated a stem age of 137 MYA. Subsequently, Dong et al. (2021) introduced *Obliquiminima* as the first sexual morph genus in this family. Currently, *Cancellidiaceae* comprises two genera: *Cancellidium*, with eight species and *Obliquiminima*, with a single species (Dong et al. 2021; da Silva and Gusmão 2024). Species of *Cancellidiaceae* are reported as saprobes on wood and twigs in freshwater habitats (Dong et al. 2021; Hyde et al. 2021). The sexual morph is characterised by small, scattered, superficial, ellipsoidal to subglobose, black, coriaceous, ostiolate ascomata with a lateral neck. Paraphyses are dense, hypha-like, septate, unbranched, and hyaline. Asci are unitunicate, 8-spored, narrowly obclavate, slightly truncate at the apex, sessile, and feature a small, refractive apical ring. Ascospores are uni- to biseriate, oval to narrowly ellipsoidal, straight, aseptate, guttulate, hyaline, thin-walled, smooth, and surrounded by a thin gelatinous sheath. The asexual morph is distinguished by unique, large, flattened, fan-shaped conidia (Dong et al. 2021).

Cancellidium Tubaki, Trans. Mycol. Soc. Japan 16: 357 (1975)

Tubaki (1975) established *Cancellidium* as a new genus, with *Ca. applanatum* as the type species. Currently, seven accepted species of *Cancellidium* are listed in Species Fungorum (2024). Members of *Cancellidium* are reported as saprobes on *Eleiodoxa conferta* from Thailand (Pinnoi et al. 2006), *Licuala longicalycata* from Thailand (Pinruan et al. 2007), decayed needles of *Pinus massoniana* from China (Yeung et al. 2006), and also primarily in freshwater habitats. To date, one species of this genus (*Ca. applanatum*) and two unidentified Cancellidium-like species have been

reported from peat swamp forests (Pinnoi et al. 2006; Pinruan et al. 2007). In this study, we introduce *Ca. narathiwatense* as a novel species, found on submerged rachides of *Eleiodoxa conferta* in the peat swamp forest of Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.32.



Note a Host. b Colonies on the host substrate. c–g Conidia, conidiophores and conidiogenous cells. h Colonies on the PDA. Scale bars: b = 200 μm, c = 25 μm, e, f = 15 μm, g = 10 μm.

Figure 3.31 *Longivarius narathiwatensis* (MFLU 24-0494, holotype)

Cancellidium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.33

Index Fungorum number: IF903541; Facesoffungi number: FoF 17532

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0521

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host scattered, sometimes gregarious, brown, shiny. *Mycelium* mostly immersed, composed of branched, septate, brown hyphae. *Conidiophores* not seen. *Conidiogenous cells* 7–13 × 2.5–5 μm, holoblastic, monoblastic, brown. *Conidia* 127.5–212.7 × 100–197 μm ($\overline{x}$ = 172 × 161 μm, n = 20), solitary, dry, thick-walled, smooth-walled, subglobose, ovoid, ellipsoidal, fan-shaped, dictyoseptate, olivaceous brown to dark brown, composed of several parallel, adherent rows radiating from the base, rows 1.7–7 μm wide ($\overline{x}$ = 4.9, n = 30), septate, containing rectangular and moniliform cells, radiating from point of attachment with conidiogenous cells.

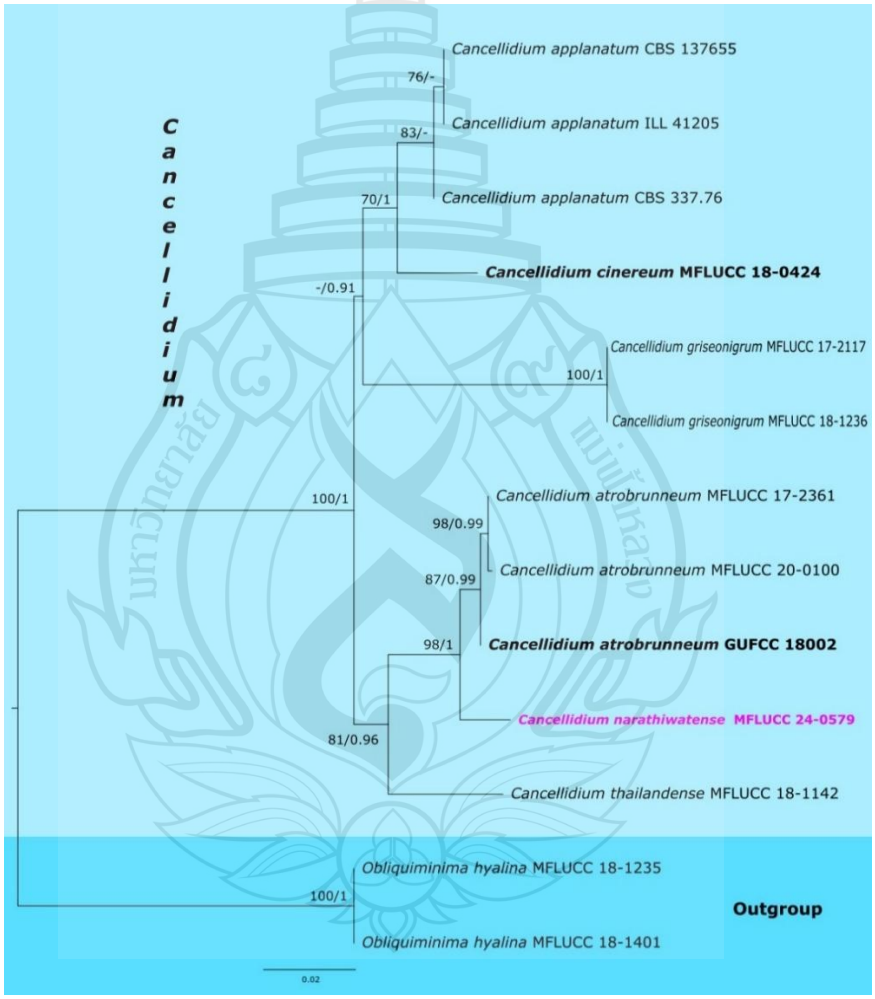
Culture characteristics – Colonies on the PDA reaching 2 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, dense, umbonate, dull, surface grey, reverse black with olive grey margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 15Y (MFLU 24-0521, holotype); ex-type living culture MFLUCC 24-0579.

GenBank numbers – MFLUCC 24-0579: ITS = PV271885, LSU = PV271925, SSU = PV263315, *rpb2* = PV340527, *tef-1α* = PV340496.

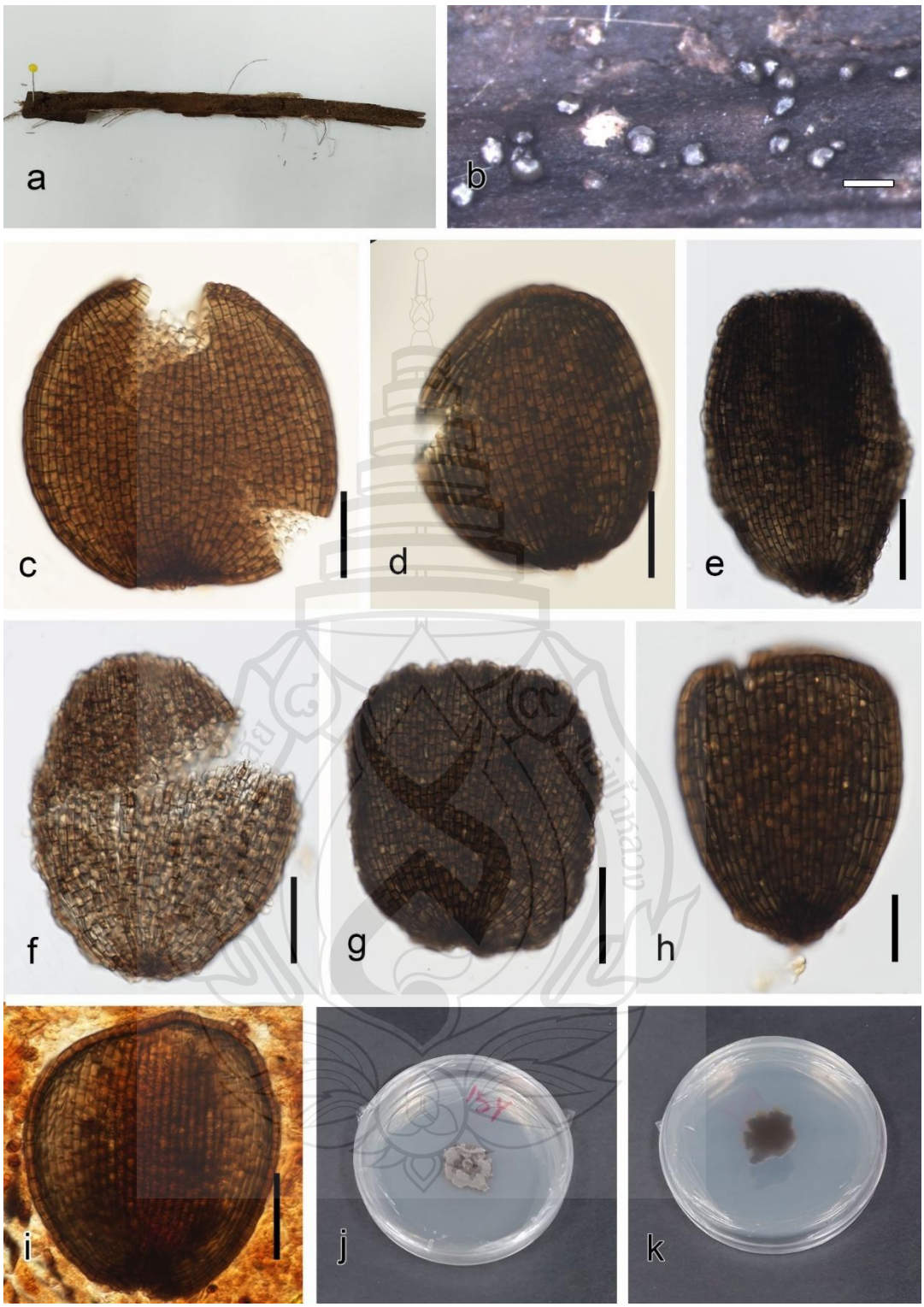
Notes – Phylogenetically, our strain (MFLUCC 24-0579) formed a robust subclade to *Cancellidium atrobrunneum* (MFLUCC 20-0100), with 98% ML and 1.00 PP statistical support (Figure 3.32). It separated from *Ca. thailandense* (MFLUCC 18-1142) by 81% ML and 0.96 PP statistical support (Figure 3.32). Morphologically, our species differs from *Ca. atrobrunneum* (MFLU 20-0429) in having conidiophores reduced to conidiogenous cells, and subglobose, ovoid, ellipsoidal-shaped, and longer and wider conidia (127.5–212.7 × 100−197 μm vs. 111–147 × 83.8–56.6 μm), in

contrast to the mononematous, micronematous to semi-macronematous conidiophores and obovate to obcordate conidia in *Ca. atrobrunneum* (MFLU 20-0429). Our species (MFLU 24-0521) also differs from *Ca. thailandense* (MFLU 18-1510), in having reduced conidiophores and larger conidia (127.5–212.7 × 100–197 µm vs. 78– 105 × 60–100 µm), despite having micronematous, mononematous, subcylindrical, flexuous conidiophores in the latter (25–55 × 3.5–4 µm). Therefore, we introduce *Ca. narathiwatense* (MFLU 24-0521) as a novel species based on morphological and phylogenetical evidence.



Note *Pseudotetraploa curviappendiculata* (HC 4930) and *Tetraplosphaeria sasicola* (KT563) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.32 Phylogram generated from the ML analysis based on the combined LSU, SSU, *tef-1α* and *rpb2* sequence data of *Cancellidium*



Note a Host. b Colonies on the host substrate. c–g, i Conidia. h Conidiogenous cell and conidium. j, k Colonies on PDA. Scale bars: b = 200 μm, c–f, i = 50 μm, g = 60 μm, h = 40 μm.

Figure 3.33 *Cancellidium narathiwatense* (MFLU 24-0521, holotype)

Diaporthales genera *incertae sedis*

Phruensis Pinruan, Mycologia 96(5): 1165 (2004)

Phruensis Pinruan, a saprobic genus in *Sordariomycetes* and comprises one species with sequence data (Pinruan et al. 2004; Hyde et al. 2024). *Phruensis* was introduced by Pinruan et al. (2004) and typified with *Phruensis brunneispora* Pinruan. Wijayawardene et al. (2022) and Hyde et al. (2020) accepted this genus. This genus was characterized by immersed, subglobose, black, coriaceous, ostiolate ascomata with a long neck, and septate, broad, hyaline paraphyses attached at the base of the centrum. The peridium consists of two layers; the inner layer comprises elongated, hyaline cells, and the outer layer comprises parenchymatous, intensely brown cells that merge with the host cells. *Asci* are unitunicate, cylindrical to fusiform with a J-, subapical ring, bearing cylindrical, straight or curved, brown, trans-septate ascospores. The asexual morphs resemble *Phialophora*. *Phruensis brunneispora* is collected on decaying trunks of palm host (*Licuala longecalycata*) from Sirindhorn peat swamp forest, Thailand.

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 99: 482 (2019)

Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80: 402 (2016)

Su et al. (2016b) established *Distoseptisporaceae* to accommodate a single genus *Distoseptispora*. *Distoseptispora* is a saprobic genus in freshwater and terrestrial habitats. Based on Species Fungorum (2024). There are 68 accepted species in this genus with molecular data for all the species in the GenBank. The genus was established by Su et al. (2016) with *D. fluminicola* as type species. Except for two species (*D. hyaline*, *D. licualae*) most *Distoseptispora* species have been recorded as having an asexual morph (Su et al. 2016; Hyde et al. 2024; Karimi et al. 2024a). Asexual morph hyphomycetous and characterized by having macronematous, mononematous, septate, unbranched, straight or flexuous, smooth, olive-green, cylindrical conidiophores, monoblastic, integrated, determinate, terminal conidiogenous cells, acrogenous, solitary, dry, dark, distoseptate, cylindrical conidia (Su et al. 2016). Konta et al. (2023) described *D. licualae* from dead leaves of *Licuala glabra* in terrestrial habitats. Hyde et al. (2019) described *D. palmarum* as a new species from *Cocos nucifera*. Karimi et al. (2024) described three novel species of *Distoseptispora* from peat swamp forest in

Narathiwat, Thailand, including: *D. arecacearum* on submerged rachis of *Licuala paludosa*, *D. eleiodoxae* on submerged rachis of *Eleiodoxa conferta* and *D. narathiwatensis* on dead petiole of *Eugeissona tristis*.

Distoseptispora K.D. Hyde, McKenzie & Maharachch., Fungal Diversity 80: 402 (2016)

Distoseptispora (*Dis*.), is a saprobic genus in freshwater and terrestrial habitats. Based on Species Fungorum (2024) there are 68 accepted species in this genus with molecular data for all the species in the GenBank. The genus was stablished by Su et al. (2016) with *Dis. fluminicola* as type species. Except for two species (*Dis. hyaline*, *Dis. licualae*) most *Distoseptispora* species have been recorded as having an asexual morph (Karimi et al. 2024a). Asexual morph hyphomycetous and characterized by having macronematous, mononematous, septate, unbranched, straight or flexuous, smooth, olive-green, cylindrical conidiophores, monoblastic, integrated, determinate, terminal conidiogenous cells, acrogenous, solitary, dry, dark, distoseptate, cylindrical conidia (Su et al. 2016). Konta et al. (2023) described *Dis. licualae* from dead leaves of *Licuala glabra* in terrestrial habitats. Hyde et al. (2019) described *Dis. palmarum* as a new species from *Cocos nucifera*. Karimi et al. (2024a) described three novel species of *Distoseptispora* from peat swamp forest in Narathiwat Thailand inculing: *Dis. arecacearum* on submerged leaf of *Licuala paludosa*, *Dis. eleiodoxae* on submerged rachis of *Eleiodoxa conferta* and *Dis. narathiwatensis* on dead petiole of *Eugeissona tristis*.

Distoseptispora arecacearum O. Karimi, Q.R. Li & K.D. Hyde, sp. nov. Figure 3.34

Index Fungorum number: IF900843; Facesoffungi number: FoF14756

Etymology – The epithet ‘‘*arecacearum*’’ refers to host family, Aceraceae.

Holotype – MFLU 23-0276.

Saprobic on submerged leaf of *Licuala paludosa*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* gregarious or scattered, effuse, hairy, dark brown to black. *Mycelium* mostly immersed, composed of branched, septate, smooth hyphae. *Conidiophores* 70–140 × 5.1–6.3 µm ($\bar{x}$ = 110 × 5.5 µm, n = 20),

macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, smooth, thick-walled, brown, 4–7 septa, sometimes consists a swollen cell in the middle or towards the apex. *Conidiogenous cells* 13–25 × 4.5–6 µm ($\bar{x}$ = 17 × 5 µm, n = 20), monoblastic or polyblastic, terminal or subterminal, determinate, cylindrical, brown. *Conidia* 25–60 × 7–17 µm ($\bar{x}$ = 44 × 10 µm, n = 30), acrogenous, solitary, cylindrical, obclavate to obpyriform or irregular, straight or curved, 4–10-distoseptate, brown, thick-walled, smooth, round apex, truncated base, sometimes with percurrent regeneration forming a secondary conidium from the conidial apex.

Culture characteristics – Colonies grown on PDA, reaching 50 mm in diameter after 15 days at 25 °C, under dark conditions, circular, fimbriate edge, flat, dull surface, radiating outwards, felted, medium dense, without pigment diffusion and sporulation, brown on the top, reverse dark brown to black.

Material examined – Thailand, Narathiwat Province, Yi-ngo District, peat swamp forest, on submerged leaf of *Licuala paludosa*, 06 April 2022, Omid Karimi, S5PP3SG (MFLU 23-0276, holotype); ex-type culture MFLUCC 23-0211, additional living culture MFLUCC 23-0212.

Notes – Morphologically, our proposed new species is similar to *Distoseptispora dehongensis* W. Dong, H. Zhang & K.D. Hyde and *Dis. obpyriformis* Z.L. Luo & H.Y. Su in having macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, septate conidiophores, terminal, determinate, cylindrical, brown conidiogenous cells and acrogenous, distoseptate, straight or curved conidia (Luo et al. 2018; Hyde et al. 2019). However, our isolate differs from *Dis. dehongensis* (HKAS 101738) in having longer and wider conidiophores (70–140 × 5.1–6.3 µm vs. 45–80 × 4–5 µm), with swollen cells, longer and wider conidia (25–60 × 7–17 µm vs. 17–30 × 7.5–10 µm) and more distosepta (4–10-distoseptate vs. 3–5-distoseptate). *Distoseptispora arecacearum* (MFLU 23-0276) differs from *Dis. obpyriformis* (MFLU 18–0476) in having conidiophores with swollen cells and shorter conidia (25–60 µm vs. 53–71 µm) (Luo et al. 2018). The BLASTn searches of the ITS sequence of *Dis. arecacearum* (MFLUCC 23-0211) resulted in *Dis. aquatica* Z.L. Luo, H.Y. Su & K.D. Hyde (MFLUCC 18- 0646) with 92.21% similarity across 100% of the query sequence coverage, while the LSU sequence of *Dis. arecacearum* has 99.09% similarity across 100% of the sequence coverage with *Dis. phangngaensis* J. Yang,

Maharachch. & K.D. Hyde (MFLUCC 16-0857). *Distoseptispora arecacearum* (MFLU 23-0276) is easily distinguishable from *Dis. aquatica* (HKAS 83991) in having longer conidiophores (70–140 µm vs. 29–41 µm) and shorter conidia (25–60 µm vs. 110–157 µm) with less distosepta (4–10-distoseptate vs. 15–28-distoseptate) (Su et al. 2016). *Distoseptispora arecacearum* (MFLU 23-0276) differs from *Dis. phangngaensis* (MFLU 17-0855) in having longer conidiophores (70–140 µm vs. 18–30(–40) µm) and shorter conidia (25–60 µm vs. 165–350 µm) (Yang et al. 2018). Therefore, we introduced *Dis. arecacearum* (MFLU 23-0276) as a novel species, based on morphological and phylogenetic analyses.

Distoseptispora eleiodoxae O. Karimi, Q.R. Li & K.D. Hyde, sp. nov. Figure 3.35

Index Fungorum number: IF900844; Facesoffungi number: FoF14757

Etymology – The epithet "*eleiodoxae*" refers to the name of the host genus, *Eleiodoxa conferta*.

Holotype – MFLU 23-0277.

Saprobic on submerged rachis of *Eleiodoxa conferta*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* immersed to superficial, septate, smooth, brown to dark brown. *Colonies* on submerged rachis, solitary, scattered, dark brown to black. *Conidiophores* 71–161 × 5–6.5 µm ($\bar{x}$ = 110 × 5.7 µm, n = 20), macronematous, mononematous, cylindrical, erect, straight to flexuous, unbranched, smooth or finely verrucose, thick-walled, dark brown, 5–10-septate with lobed basal cells, percurrent proliferations at the apex. *Conidiogenous cells* 13.5–18.8 × 5–6.8 µm ($\bar{x}$ = 15.96 × 5.6 µm, n = 20), holoblastic, monoblastic, terminal, integrated, cylindrical to ampulliform, percurrent, brown to dark brown, smooth. *Conidia* 31.5– 48 × 13.5–15.8 µm ($\bar{x}$ = 40.8 × 14.8 µm, n = 30), secession schizolytic, solitary, obpyriform, rostrate, truncated base, 6–7-septate, verrucose, thick-walled, brown with dark brown to black cells in the middle, paler towards the apex.

Culture characteristics – Colonies grown on PDA, reaching 30 mm in diameter after 15 days at 25 °C, under dark conditions, circular, entire to radially with lobate edge, well-defined margin, low convex, dull surface, felted, dense, mycelium

superficial to immersed, without pigment diffusion and sporulation, greyish-brown on the top with dark brown margin, reverse brown with dark brown center and margin.

Note a Host material b Colonies on the substrate c–e Conidiophores and conidia f–i Conidia j, k Culture on PDA. Scale bars: 200 µm (b); 50 µm (c–e); 10 µm (f–i).

Figure 3.34 *Distoseptispora arecacearum* (MFLU 23-0276, holotype)

Material examined – Thailand, Narathiwat Province, Yi-ngo District, peat swamp forest, on submerged rachis of *Eleiodoxa conferta*, 06 April 2022, Omid Karimi, S5PP8N1SG (MFLU 23-0277, holotype); ex-type culture MFLUCC 23-0213, additional living culture MFLUCC 23-0214.

Notes – *Distoseptispora eleiodoxae* (MFLU 23-0277) shares similar characteristics with *Dis. tropica* J. Ma & Y.Z. Lu (HKAS 123761), in having macronematous, mononematous, cylindrical, erect, straight, unbranched conidiophores with holoblastic, monoblastic, terminal, cylindrical, thick-walled conidiogenous cells and verrucose, rostrate conidia (Ma et al. 2022). However, *Dis. eleiodoxae* (MFLU 23-0277) differs from *Dis. tropica* (HKAS 123761) in having shorter and wider obpyriform conidia (31.5–48 × 13.5–15.8 µm vs. 39–75 × 7.5–10.5 µm), with broad and darker middle cells, no guttules and lacking conspicuous hyphae attachment to conidia. The BLAST search against GenBank showed that the ITS and LSU sequences of the new isolate, *Dis. eleiodoxae* (MFLUCC 23-0213), share 84.25% similarity across 100% sequence coverage with *Dis. tropica* (GZCC 22-0076) and 96.09% similarity across 100% sequence coverage with *Dis. effusa* L.L. Liu & Z.Y. Liu, respectively. *Distoseptispora eleiodoxae* (MFLU 23-0277) differs from *Dis. effusa* (GZAAS 20-0427) in having shorter conidia (31.5–48 vs. 35.5–113 µm) (Yang et al. 2021). Based on a pairwise comparison of ITS, LSU, *rpb2* and *tef1-α* nucleotides, *Dis. eleiodoxae* (MFLUCC 23-0213) differs from *Dis. tropica* (GZCC 22-0076) in 70/536 bp (13.05%) for ITS, 50/834 bp (5.99%) for LSU, 141/1052 bp (13.40%) for *rpb2* and 96/888 bp (10.8%) for *tef1-α* (without including gaps). Therefore, we introduced *Dis. eleiodoxae* (MFLU 23-0277) as a novel species, based on the morphological evidence and according to the species delimitation guidelines proposed by Chethana et al. (2021) and Maharachchikumbura et al. (2021).

Distoseptispora narathiwatensis O. Karimi, Q.R. Li & K.D. Hyde, sp. nov. Figure 3.36

Index Fungorum number: IF900845; Facesoffungi number: FoF14758

Etymology – The epithet "*narathiwatensis*" refers to Narathiwat Province, where the holotype was collected.

Holotype – MFLU 23-0278.

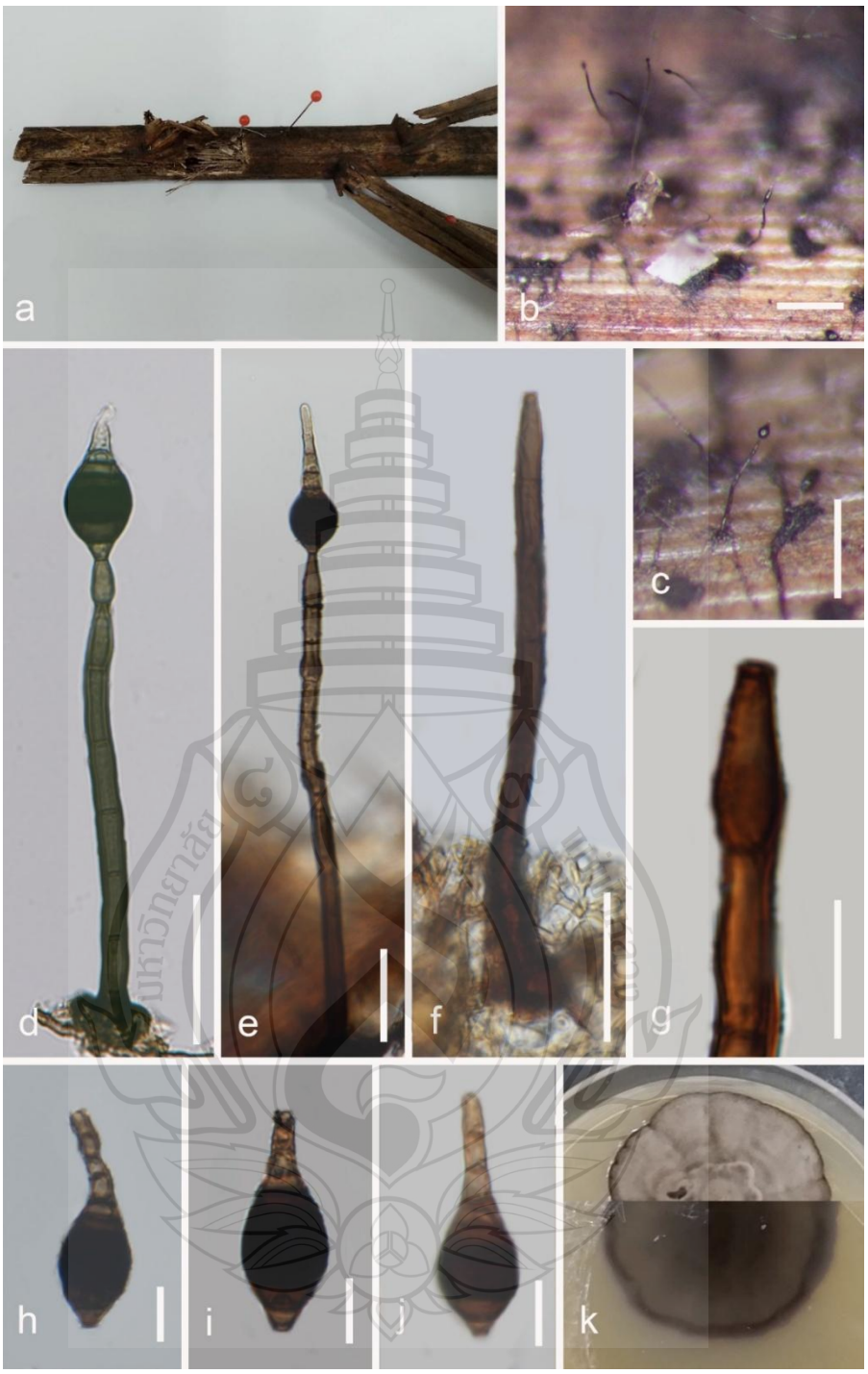
Saprobic on dead petiole of *Eugeissona tristis.* Asexual morph*:* Hyphomycetous. *Colonies* superficial, effuse, hairy, gregarious, brown. *Mycelium* immersed to superficial, composed of septate, branched, pale brown hyphae. *Conidiophores* 27–155 × 3–6.5(–7) μm ($\bar{x}$ = 104 × 5 μm, n = 50), macronematous, mononematous, cylindrical, straight or flexuous, occasionally slightly curved in the middle and near the base and the apex, up to 10 septa, slightly constricted at septa, unbranched, brown, thin-walled, smooth, often containing inflated or constricted cells at the apex or middle, sometimes percurrent with annellations. *Conidiogenous cells* 7–17 × 4–5.5 μm ($\bar{x}$ = 12.5 × 5 μm, n = 30), holoblastic, mono- to polyblastic, integrated, determinate, terminal and intercalary, subcylindrical, brown, smooth. *Conidia* 12–38 × 4.5–8 μm ($\bar{x}$ = 27 × 6.5 μm, n = 30), secession schizolytic, solitary or occasionally catenate, dry, thin-walled, smooth, subcylindrical to obclavate to conical, straight or curved, 1–7-distoseptate, slightly constricted at septa, olivaceous to brown, apex rounded, truncated base with slightly pigmented scar, often the primary cells of conidia are narrower than the second ones which are often inflated. Sexual morph: Undetermined.

Culture characteristics – Colonies grown on PDA, reaching 50 mm in diameter after 15 days at 25 °C, under dark conditions, circular, entire margin, well-defined margin, low convex, dull surface, felted, dense, mycelium mostly superficial, without pigment diffusion and sporulation, medium brown to reddish-brown with dark brown edge on the top, reverse-side dark brown to black.

Material examined – Thailand, Narathiwat Province, Yi-ngo District, peat swamp forest, on dead petiole of *Eugeissona tristis*, 06 April 22, Omid Karimi, 35Y (MFLU 23-0278, holotype); ex-type culture MFLUCC 23-0215, additional living culture MFLUCC 23-0216.

Notes – *Distoseptispora narathiwatensis* (MFLU 23-0278) is similar to *Dis. saprophytica* (MFLU 18-1568), but it can be distinguished in having longer and wider conidiophores (27–155 × 3–6.5 (–7) μm vs. 50–140 × 3.2–4.2 μm) and conidiogenous cells (7–17 × 4–5.5 μm vs. 5–11.5 × 3–4.5 μm). In *Dis. narathiwatensis* (MFLU 23-0278), the conidiophore is slightly curved at the base, middle and near the top in contrast to *Dis. saprophytica* (MFLU 23-0278), which is characterised by sharp curving near the base; also in *Dis. narathiwatensis*, the conidiophore cells are often inflated or

constricted at the apex or middle which is not observed in *Dis. saprophytica* (Dong et al. 2021). Conidiogenous cells of *Dis. narathiwatensis* are terminal and intercalary and their conidia are not acrogenous as in *Dis. saprophytica*. The primary cell in the conidium is often narrower than the second one, and the second cell is often inflated, which is not observed in *Dis. saprophytica*. The BLAST search against the GenBank showed that the ITS and *rpb2* sequences of the new isolate, *Dis. narathiwatensis* (MFLUCC 23-0215), share 98.33% similarity across 100% sequence coverage and 98.63% similarity across 78% sequence coverage with *Dis. saprophytica* (MFLUCC 18-1238), respectively. In a BLAST search against GenBank, the LSU and *tef1-α* sequences of *D. narathiwatensis* (MFLUCC 23-0215) share 99.3% similarity across 85% sequence coverage and 94.12% similarity across 94% sequence coverage with *Dis. palmarum* (MFLU 18-0588), respectively. However, *Dis. palmarum* is distinguished in having longer (12–38 μm vs. 35–180 μm), elongated, greenish-black to brown conidia (Hyde et al. 2019). Based on a pairwise comparison of ITS and LSU nucleotides, *Dis. narathiwatensis* (MFLUCC 23-0215) differs from *Dis. saprophytica* (MFLUCC 18-1238) by 22/580 bp (3.8%), 16/870 bp (1.8%) differences, respectively (without including gaps). Therefore, we introduced *Dis. narathiwatensis* (MFLU 23-0278) as a novel species, based on the morphological evidence and according to the species delimitation guidelines proposed by Chethana et al. (2021) and Maharachchikumbura et al. (2021).

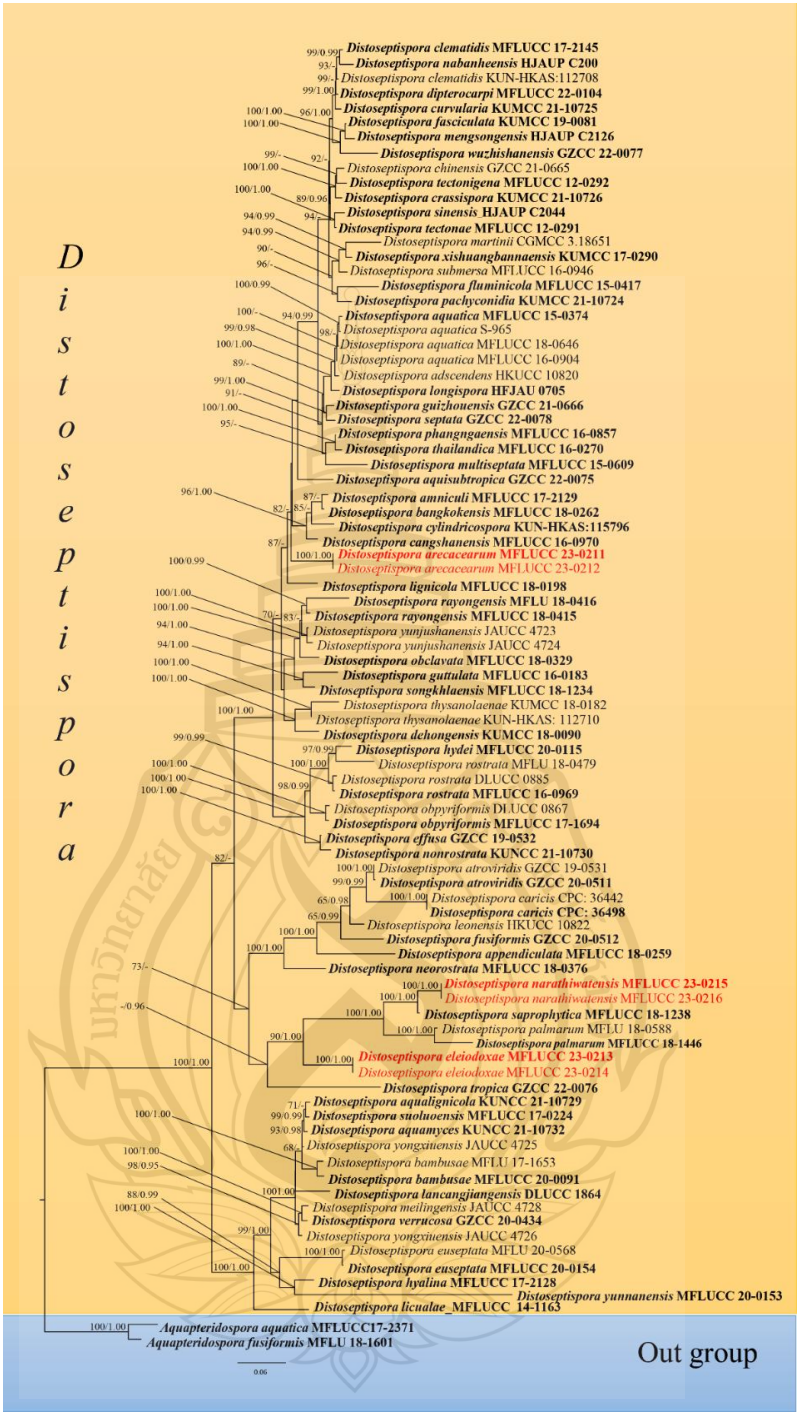


Note a Host material b, c Colonies on the substrate d–f Conidiophores and conidia g Conidiogenous cell h–j Conidia k Culture on PDA (top and reverse). Scale bars: 100 µm (b, c); 30 µm (d–f); 10 µm (g–j).

Figure 3.35 *Distoseptispora eleiodoxae* (MFLU 23-0277, holotype)

Note a Host material b Colonies on the substrate c–e Conidiophores and conidia f Conidiogenous cell g–j Conidia k, l Culture on PDA. Scale bars: 100 μm (b); 50 μm (c–e); 10 μm (f–j).

Figure 3.36 *Distoseptispora narathiwatensis* (MFLU 23-0278, holotype)



Note Bootstrap support values ≥ 65% and Bayesian posterior probabilities ≥ 0.95 are demonstrated at the nodes. The new taxa are indicated in red bold. Ex-type strains are in black bold.

Figure 3.37 Maximum likelihood tree generated from combined ITS, LSU, *rpb2*, and *tef1-α* sequence data of *Distoseptispora*

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

Ophioceraceae Klaubauf, M.-H. Lebrun & Crous, Studies in Mycology 79: 103 (2014)

Ophioceras Sacc., Syll. fung. (Abellini) 2: 358 (1883)

Ophioceras is a saprobic genus belonging to the family *Ophioceraceae* (*Magnaporthales*, *Sordariomycetes*) and comprises 30 species (Hyde et al. 2024). The genus is characterized by black, immersed to superficial ascomata with long periphysate necks, cylindrical asci with a J-, apical ring and filiform, hyaline, pale brown or olivaceous ascospores without sheaths (Teng 1934; Conway and Barr 1977; Tsui et al. 2001; Thongkantha et al. 2009; Klaubauf et al. 2014). *Ophioceras freycinetiae* is the only asexual morph reported with hyaline, smooth, septate hyphae, *conidiophores* reduced to hyaline, elongated ampulliform conidiogenous cells, and aseptate, hyaline conidia of subcylindrical, falcate shape (Crous et al. 2021).

Ophioceras was introduced by Saccardo (1883) and typified by *O. dolichostomum*. Chen et al. (1999) and Inderbitzin and Berbee (2001) placed the genus in the family *Magnaporthaceae* based on phylogenetic analyses based on SSU rDNA. Based on the combined analyses of LSU and *rpb*1, Thongkantha et al. (2009) showed that *Ophioceras* clusters separately from *Magnaporthaceae* in *Magnaporthales*. Based on the combined LSU and *rpb*1 phylogenetic analyses, Klaubauf et al. (2014) introduced the monotypic family *Ophioceraceae* (*Magnaporthales*) to accommodate *Ophioceras*. Based on the updated phylogenetic analyses of *Magnaporthales*, Jiang et al. (2021) synonymized *Ceratosphaerella* under *Ophioceras* and introduced *Ophioceras castillensis*, but Wijayawardene et al. (2022) discussed that the phylogenetic analyses based on few strains are not enough to produce a good resolution and morphological characters should be considered carefully, and reinstated *Ceratosphaerella* back as a separate genus in *Ophioceraceae*. *Ophioceras* species have been generally found on decaying wood in aquatic habitats worldwide (Shearer et al. 1999; Tsui et al. 2001; Thongkantha et al. 2009; Hu et al. 2012). *Ophioceras palmae* and *Ophioceras tambopataense* were reported on palm hosts from the Philippines and Peru, respectively (Tsui et al. 2001; Matsushima 2003).

Table 3.2 World distribution of *Ophioceras* species

Species	Host/Substrate	Country	Reference
Ophioceras palmae	*Calamus ornatus*	Philippines	(Tsui et al. 2001)
Ophioceras tambopataense	decaying leaf of palm	Peru	(Matsushima 2003)
Ophioceras aquaticum	wood submerged	China	(Hu et al. 2012)
Ophioceras arcuatisporum	wood submerged in lake	USA	(Shearer et al. 1999)
Ophioceras bacillatum	decorticated rotten branch	Great Britain	(Saccardo 1883)
Ophioceras bambusae	bamboo	Indonesia	(Höhnel 1909)
Ophioceras castillensis	bark	Nicaragua	(Jiang et al. 2021)
Ophioceras cecropiae	leaves of Cecropia	Venezuela	(Müller 1965)
Ophioceras chiangdaoense	dead leaves of *Dracaena loureiroi*	Thailand	(Thongkantha et al. 2009)
Ophioceras commune	stem of *Medicago sativa* submerged in creek	Panama	(Shearer et al. 1999)
Ophioceras dolichostomum	dead wood	Cuba	(Saccardo 1883)
Ophioceras ficinum	dead leaves of *Ficus septica*	Taiwan	(Tennakoon et al. 2021)
Ophioceras filiforme	rotten leaf sheaths of Amomum	Indonesia	(Höhnel 1911)
Ophioceras freycinetiae	leaves of *Freycinetia banksii*	New Zealand	(Crous et al. 2021)
Ophioceras fusiforme	decorticated woody debris submerged in small stream	India	(Shearer et al. 1999)
Ophioceras junci	dead culms of *Juncus effusus*	Netherlands	(Crous et al. 2021)
Ophioceras guttulatum	wood submerged in river	Hong Kong	(Tsui et al. 2001)

Table 3.2 (continued)

Species	Host/Substrate	Country	Reference
Ophioceras hongkongense	wood submerged in river	Hong Kong	(Tsui et al. 2001)
Ophioceras indicus	dried twigs of Ficus infectoria	India	(Lal 1987)
Ophioceras leptosporum	rotten stems of *Umbelliferae*	Great Britain	(Walker 1980)
Ophioceras miyazakiense	decaying litter in broad-leaved forest	Japan	(Matsushima 2003)
Ophioceras parasiticum		China	(Teng 1934)
Ophioceras petrakii	dead stems of Vitex negundo	India	(Tilak and Kale 1969)
Ophioceras rhizomorpha	decaying wood, on ground	Kenya	(Jiang et al. 2021)
Ophioceras sichuanense	submerged decaying branches of *Bambusoideae*	China	(Jiang et al. 2021)
Ophioceras sorghi	Sorghum vulgare	Central Africa	(Saccas 1954)
Ophioceras submersum	decaying wood submerged in freshwater stream	Thailand	(Luo et al. 2019)
Ophioceras tenuisporum		Panama	(Shearer et al. 1999)
Ophioceras thailandense	decaying wood submerged in a freshwater stream	Thailand	(Jing Yang et al. 2023)
Ophioceras zeae	dead *Zea mays*	Central Africa	(Saccas 1951)

Trichosphaeriaceae genera *incertae sedis*

Unisetosphaeria Pinnoi, E.B.G. Jones, McKenzie & K.D. Hyde, Mycoscience 44 (5): 377 (2003)

Unisetosphaeria is a saprobic genus which was introduced by Pinnoi et al. (2003) as freshwater ascomycete on submerged petiole of *Eleiodoxa conferta* in a peat swamp forest in Narathiwat, Thailand. *Unisetosphaeria* is a monotypic genus and typified by *Unisetosphaeria penguinoides*. There is one accepted morphological

species in this genus based on Species Fungorum (2024), with no available sequence data in the GenBank. The genus is characterized by having immersed, semi-immersed to superficial, pyriform ascomata, angular peridium which consist of brown ell walls, sparse, obscure paraphyses with ovoid to oblong cells, 8-spored, clavate, unitunicate asci, J-apical ring, ovoid to fusoid, septate, hyaline ascospore (Pinnoi et al. 2003).

Subclass *Hypocreomycetidae* O.E. Erikss. & Winka, Myconet 1: 6 (1997)

Hypocreales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 343 (1897)

Hypocreaceae De Not., Giornale Botanico Italiano 2: 48 (1844)

Lindau (1897) established the family *Hypocreaceae* (*Hypocreales*), based on the genus *Hypocrea*, introduced earlier by Fries (1825). The family has undergone several taxonomic revisions over the years (Seaver 1909a, b; 1910a, b; 1911; Nannfeldt 1932; Petch 1938; Miller 1949; Luttrell 1951; Dingley 1951a; Munk 1957; Gäumann 1964; Kreisel 1969; Rogerson 1970; Barr 1990; Rossman et al. 1999). Currently, the family includes 17 accepted genera: *Arachnocrea*, *Dialhypocrea*, *Escovopsioides*, *Escovopsis*, *Hypocreopsis*, *Hypomyces*, *Kiflimonium*, *Lichenobarya*, *Mycogone*, *Protocrea*, *Rogersonia*, *Sepedonium*, *Sphaerostilbella*, *Sporophagomyces*, *Stephanoma*, *Trichoderma*, and *Verticimonosporium* (Hyde et al. 2024). Members of *Hypocreaceae* are characterised by perithecia that are typically immersed in a stroma or seated on a subiculum and often disarticulating ascospores (Perera et al. 2023).

Trichoderma Pers., Neues Mag. Bot. 1: 92 (1794)

Trichoderma (*T.*), was established by Persoon in 1794, with *T. viride* designated as the type species. Currently, approximately 500 *Trichoderma* species are recorded in Species Fungorum (2024). Members of *Trichoderma* are distributed worldwide and are found on various hosts and substrates, such as *Abies alba*, *Dactylis glomerata*, *Lycopersicon esculentum*, *Medicago sativa*, and *Phaseolus vulgaris* from Poland (Mulenko et al. 2008), *Eucalyptus* sp. from South Africa (Bissett et al. 2015), *Fomes pinicola* from the USA (Bissett et al. 2015), *Ipomoea batatas* from China (Yang et al. 2021), *Lycopersicon esculentum* from Brazil (Mendes et al. 1998), *Prunus padus* from Austria (Urbez-Torres et al. 2020), *Solanum lycopersicum* from Canada (Johnston-

Monje et al. 2017), and *Vitis vinifera* from Italy (Lorenzini et al. 2016). In this study, we report *T. virens* as a new record on dead leaves of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.38.

Trichoderma virens (J. Miller, Giddens & Foster) von Arx, Beih. Nova Hedwigia 87: 288. 1987 Figure 3.39

Index Fungorum number: IF128198; Facesoffungi number: FoF 17532

Saprobic on the dead leaf of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on the host substrate compact and green. *Mycelium* superficial, branched, septate, subhyaline to pale green. *Conidiophores* 80−105 × 2−4 µm ($\bar{x}$ = 99 × 3 µm, n = 10), macronematous, straight or flexuous, septate, branched, smooth, thick-walled, subhyaline. *Phialides* 4−12 × 3−5 µm ($\bar{x}$ = 10 × 3.8 µm, n = 20), lageniform to ampulliform, smooth, thick-walled, mostly arising in closely appressed verticils of 2–5 on terminal branches, occasionally solitary or in pairs laterally on the conidiophore and branches. *Conidia* 4−6 × 2.8−4.3 µm ($\bar{x}$ = 4.8 × 3.5 µm, n = 20), broad, ellipsoidal to obovoid, smooth, thin-walled, pale to dark green.

Culture characteristics – Colonies on the PDA reaching 6 cm diam. after 10 days at room temperature (25–28 °C). Colony circular, medium dense, slightly raised, dull, entire edge, without pigment diffusion and sporulated after 20 days, surface pale yellow with dark olive-brown in the centre, reverse dull yellow with a dull green centre.

Material examined – Thailand, Narathiwat, peat swamp forest, dead leaf of *Eleiodoxa conferta*, 24 April 2022, O. Karimi, 22B (MFLU 24-0495), living culture MFLUCC 24-0580.

Known hosts – *Betula pendula* (Mulenko et al. 2008), *Cucumis sativus* (Kindermann et al. 1998), *Eleiodoxa conferta* (This study), *Fraxinus excelsior* (Przybyl 2002), *Guizotia abyssinica* (Nagaraja and Krishnappa 2009), *Pinus nigra* (Mulenko et al. 2008), *Pinus sylvestris* (Tokumasu et al. 1994), *Pseudotsuga menziesii* (Nelson et al. 1987), *Ricinus communis* (Liu 1977), *Triticum aestivum* (Mulenko et al. 2008), *Theobroma cacao* (Hanada et al. 2010).

Known distribution – Poland (Przybyl 2002; Mulenko et al. 2008), India (Nagaraja and Krishnappa 2009), USA (Zabel et al. 1985; Nelson et al. 1987), Malaysia

(Liu 1977), Canada (Kindermann et al. 1998), Germany (Tokumasu et al. 1994), Brazil (Hanada et al. 2010), New Zealand (Kindermann et al. 1998), Thailand (This study).

GenBank numbers – MFLUCC 24-0580: ITS = PV271886, *rpb2* = PV340528.

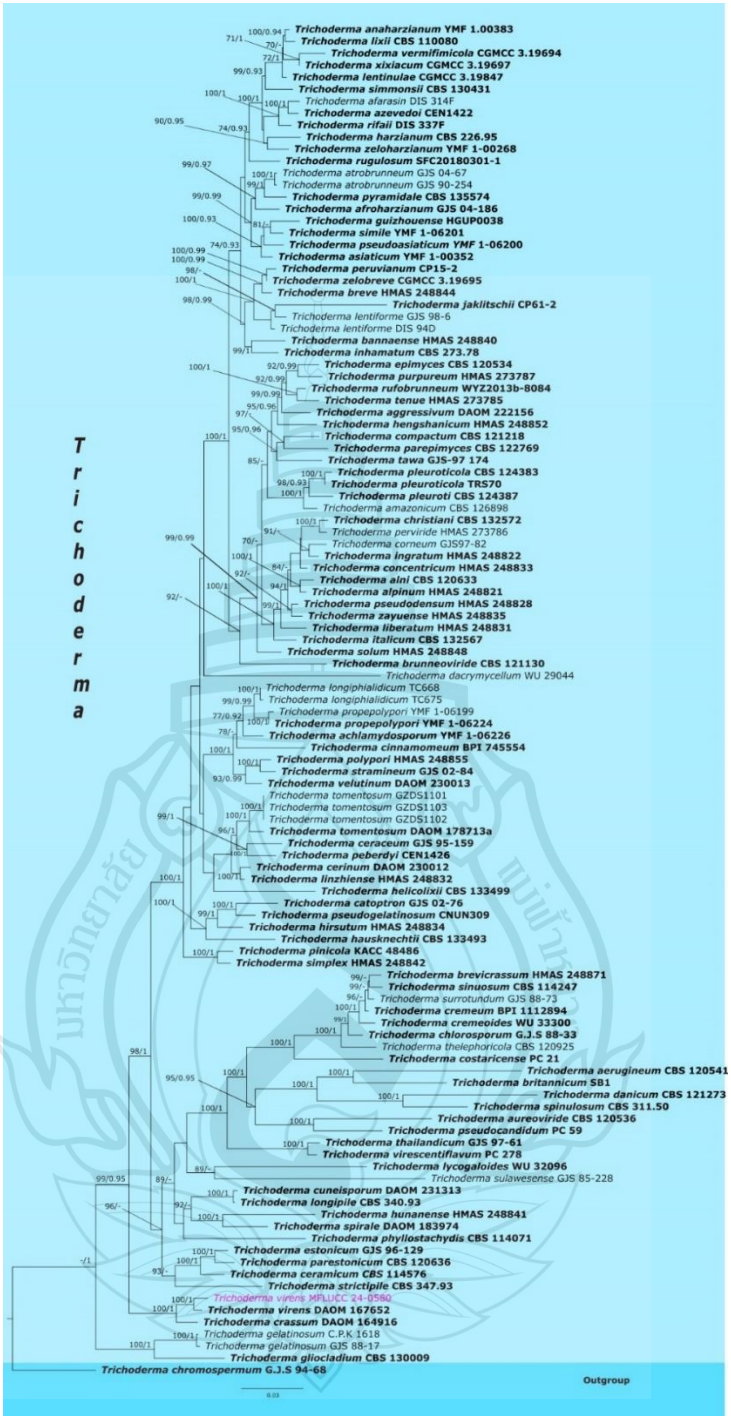
Notes – In the multi-gene phylogeny of the combined ITS, *rpb2* and *tef-1α* sequence data, our strain (MFLUCC 24-0580) clustered with *T. virens* (DAOM 167652) with 100% ML and 1.00 PP statistical support (Figure 3.39). Morphologically, our strain resembles *T. virens* in having similar conidiophores, phialides, and conidia with almost identical sizes (Kubicek and Harman 1998). Thus, we identified our strain (MFLU 24-0495) as *T.* virens based on phylogenetic analyses and morphological characters. We report our strain (MFLU24-0495) as a new host record of *T. virens* on *Eleiodoxa conferta* from Thailand. Additionally, we document *T. virens* as a new habitat record from the peat swamp forest.

Subclass *Savoryellomycetidae* Hongsanan, K.D. Hyde & Maharachch., Fungal Diversity 84: 35 (2017)

Conioscyphales Réblová & Seifert, Persoonia 37: 63 (2015)

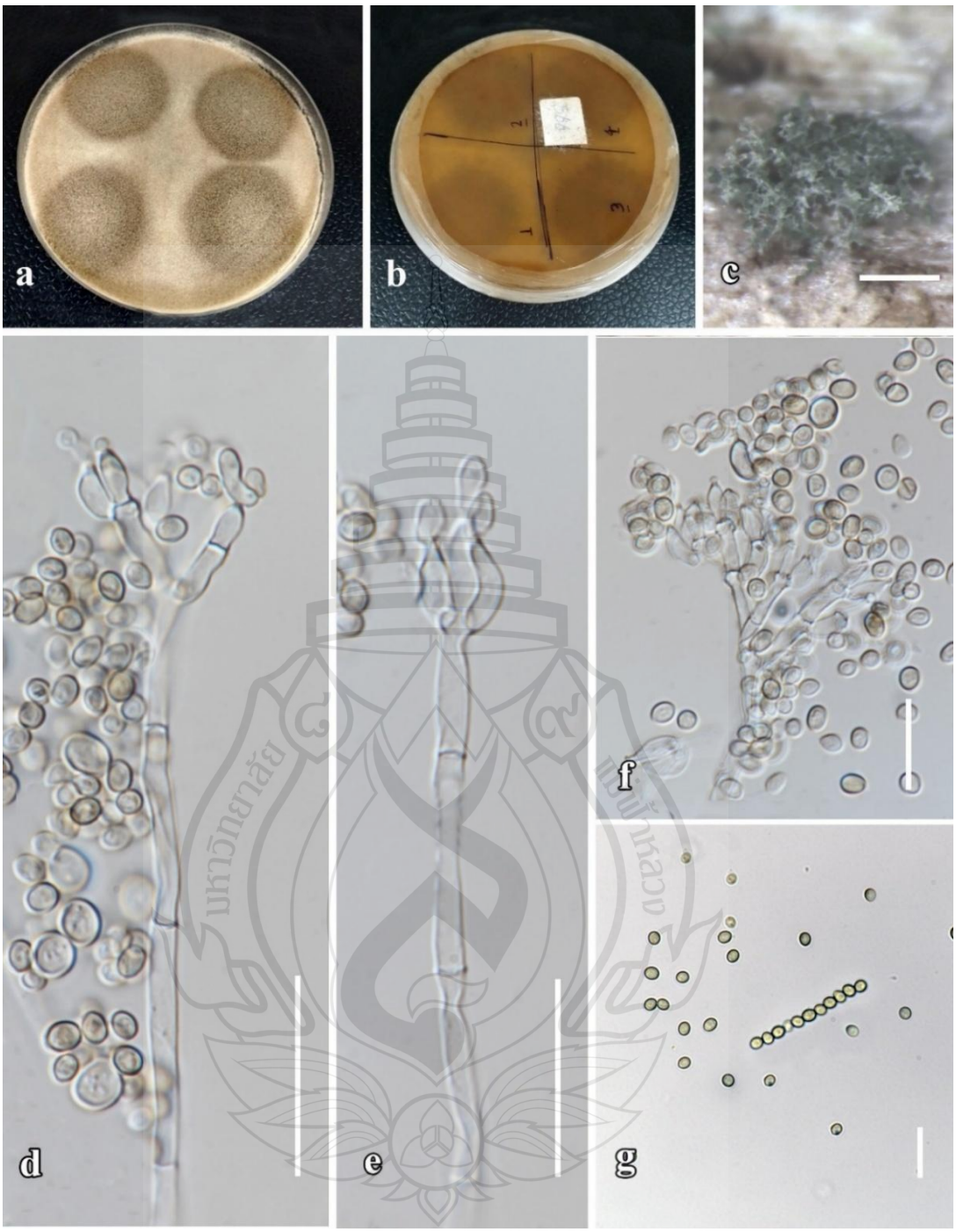
Conioscyphaceae Réblová & Seifert, Persoonia 37: 63 (2015)

Réblová et al. (2016) established *Conioscyphaceae* with a single genus, *Conioscypha* (*C.*), within *Conioscyphales*, based on morphology and combined phylogenetic analyses of SSU, LSU, and *rpb2* sequences. Their phylogenetic tree showed *Savoryellaceae* (from *Savoryellales*) as the closest clade to *Conioscyphaceae*. Recently, Yu et al. (2024a) performed a combined phylogenetic analysis (SSU, ITS, LSU, *rpb2*, and *tef1α*) and accepted *Vanakripa* as the second genus in *Conioscyphaceae*. The family now includes *Conioscypha* and *Vanakripa* (Yu et al. 2024a, b; Hyde et al. 2024). The sexual morphs of *Conioscyphaceae* feature perithecial, immersed to superficial ascomata with a papillate or elongated neck, filiform unbranched paraphyses, and unitunicate, persistent, 8-spored, cylindrical-clavate, stipitate asci with a pronounced, non-amyloid apical annulus. Ascospores are fusiform to fusiform-navicular, hyaline, transversely multi-septate, and lack mucilaginous sheaths or appendages. The asexual morphs are characterised by micronematous, mononematous, hyaline conidiophores, blastic, cyathiform to doliiform conidiogenous cells, and brown or black, aseptate conidia (Réblová et al. 2016).



Note *Trichoderma chromospermum* (G.J.S. 94-68) was used as the outgroup taxon. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is generated sequence is in purple, while the type strains are in bold.

Figure 3.38 Phylogram generated from the ML analysis based on the combined *tef-1α*, *rpb2* and ITS sequence data of *Trichoderma*

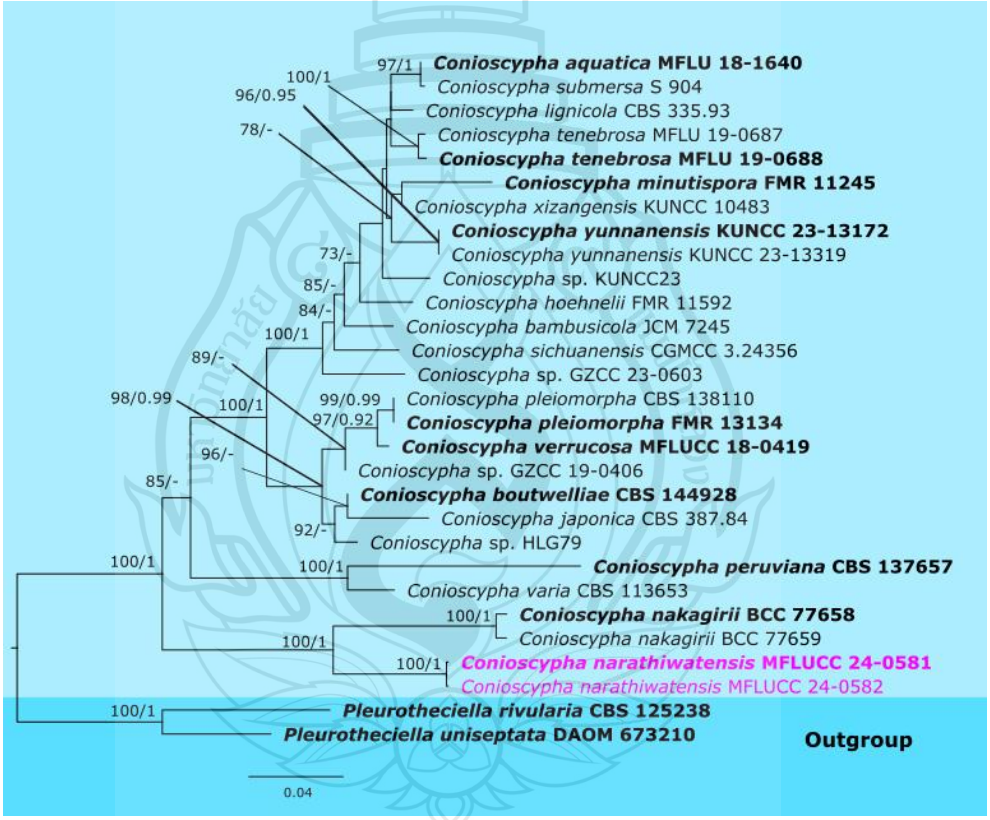


Note a, b Upper surface and reverse overview of the culture on the PDA. c Colonies on the host substrate. d–f Conidiophores and conidiogenous cells. g Conidia. Scale bars: c = 200 μm, d = 25 μm, e = 20 μm, f = 15 μm, g = 15 μm.

Figure 3.39 *Trichoderma virens* (MFLU 24-0495, a new host and habitat record)

Conioscypha Höhn., Ann. Mycol. 2 (1): 58 (1904)

Höhnel (1908) established *Conioscypha* with *C. lignicola* as the type species, which was found on submerged *Carpinus* wood. Currently, there are 20 accepted species of *Conioscypha* listed in Species Fungorum (2024). Members of *Conioscypha* have been reported as saprobes from submerged wood and twigs in freshwater habitats and soil (Chuaseeharonnachai et al. 2017; Liu et al. 2019b; Hyde et al. 2020). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *C. narathiwatensis* as a novel species found on the submerged rachis of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.40.



Note *Pleurotheciella rivularia* (CBS 125238) and *Pleurotheciella uniseptata* (DAOM 673210) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strains of the current study are in purple, while the type strains are in bold.

Figure 3.40 Phylogram generated from the ML analysis based on the combined ITS, LSU, SSU and *rpb2* sequence data of *Conioscypha*

Conioscypha narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.41

Index Fungorum number: IF903542; Facesoffungi number: FoF 17533

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the fungus was collected

Holotype – MFLU 24-0496

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* scattered or in small groups, granular, black, glistening. *Mycelium* 1.7–3.2 μm diam., mostly immersed and partly superficial, composed of branched, pale brown to hyaline, smooth hyphae. *Conidiophores* 15–20 × 2–3.5 μm ($\overline{x}$ = 17 × 2.5 μm, n = 15), micronematous, mononematous, laterally from the hyphae, hyaline. *Conidiogenous cells* 5–8 × 2–5 μm ($\overline{x}$ = 6.5 × 3.5 μm, n = 15), monoblastic, integrated or discrete, sessile or on short conidiophores, arising laterally from the hyphae, cylindrical, smooth-walled, hyaline, rarely with a cup-shaped, single layer collarette, up to 28 μm at the apex. *Conidia* 29–41 × 30–42 μm ($\overline{x}$ = 36 × 36.5 μm, n = 20), solitary, turbinate to pyriform, black, smooth-walled, aseptate, rounded at the apex, rounded to truncate at the base.

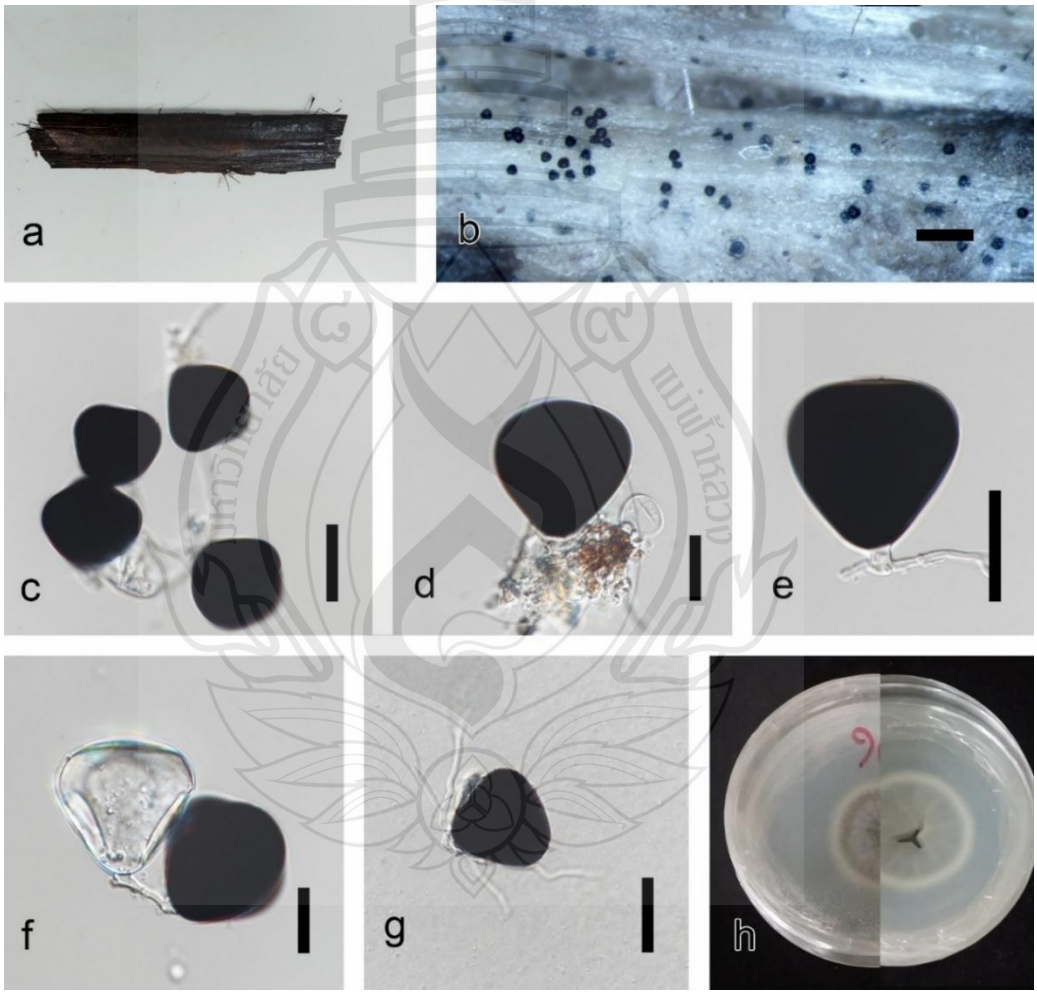
Culture characteristics – Colonies on the PDA reaching 3 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, flat, mycelia superficial to immersed, dull, entire edge, radially furrowed, felted, surface medium grey with a whitish margin, reverse light grey with a whitish margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 9G (MFLU 24-0496, holotype); ex-type living culture MFLUCC 24-0581; 10R (MFLU 24-0497, isotype); ex-isotype living culture MFLUCC 24-0582.

GenBank numbers – MFLUCC 24-0581: ITS = PV271887, LSU = PV271926, SSU = PV263316, *rpb2* = PV340529. MFLUCC 24-0582: ITS = PV271888, LSU = PV271927, SSU = PV263317.

Notes – Phylogenetically, our strain (MFLUCC 24-0581) clustered separately from *Conioscypha nakagirii* (BBH40587) with 100% ML and 1.00 PP support in the combined phylogenetic tree of ITS, LSU, SSU and *rpb2* (Figure 3.40). Morphologically, *C. narathiwatensis* (MFLU 24-0496) is similar to *C. nakagirii*

(BBH40587), but it differs in having hyaline, narrower conidiophores (15–20 × 2–3.5 µm vs. 45 × 2–13.5 µm), with a single layer collarette, and lacks a pore at the attachment site of the conidia to the conidiogenous cells, in contrast to the multi-collarette cup-shaped *C. nakagirii* (BBH40587). Based on the pairwise comparison of ITS, SSU and *rpb2* nucleotides, *C. narathiwatensis* (MFLUCC 24-0581) differs from *C. nakagirii* (BBH40587) by 9.32%, (55/590 bp, without including gaps) in the ITS, 0.9% (10/1076 bp, without including gaps) in SSU and 7.2% (70/967 bp, without including gaps) in *rpb2*. Therefore, we introduce *C. narathiwatensis* (MFLU 24-0496) as a novel species based on morphological and phylogenetic evidence.



Note a Host. b Colonies on the host. c Conidiophores and conidia. d–f Conidiogenous cells and developing conidia. g A germinated conidium. h Culture characters on the PDA. Scale bars: b = 200 µm, c = 35 µm, d, f = 20 µm, e = 25 µm, g = 30 µm.

Figure 3.41 *Conioscypha narathiwatensis* (MFLU 24-0496, holotype).

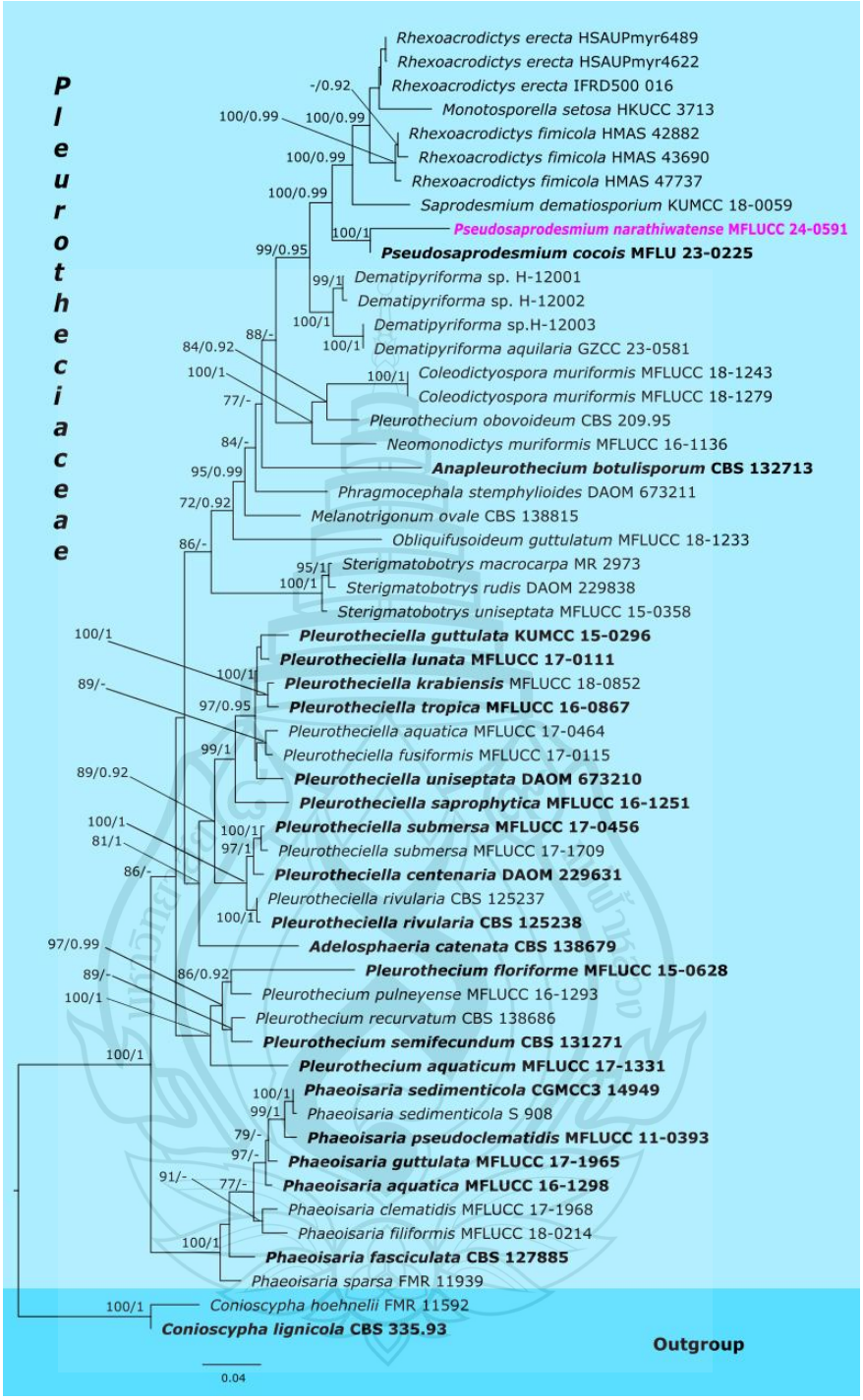
Pleurotheciales Réblová & Seifert, Persoonia 37: 63 (2015)

Pleurotheciaceae Réblová & Seifert, Persoonia 37: 63 (2015)

Réblová et al. (2016) introduced *Pleurotheciaceae* within *Pleurotheciales*, based on morphology and the combined phylogenetic analyses of ITS, SSU, LSU, *tub2*, and *mcm*7 sequence data, with *Pleurothecium* as the type genus, which was earlier established by Höhnel (1923). Currently, the family comprises 14 accepted genera (Samarakoon et al. 2024). Members of *Pleurotheciaceae* are mostly reported as saprobes in aquatic habitats, with some genera, such as *Dematipyriforma*, occasionally reported as endophytes (Cheng et al. 2014; Réblová et al. 2016; Sun et al. 2017; Dong et al. 2021). The sexual morph is characterised by dark, papillate, perithecial ascomata without stromata, unitunicate asci, abundant paraphyses, and transversely multi-septate ascospores, which are hyaline or versicolorous with hyaline polar cells and brown middle cells. The asexual morph was reported as variable hyphomycetous forms, including Acrodictys-like, Helicon-like, Monodictys-like, and Dactylaria-like structures. It is characterised by macronematous or semi-macronematous conidiophores, which are often loosely fasciculate or aggregated in indeterminate synnemata, holoblastic conidiogenous cells, and hyaline, brown, or versicolorous conidia that are septate or non-septate (Cheng et al. 2014; Réblová et al. 2016; Sun et al. 2017; Dong et al. 2021; Tian et al. 2024; Samarakoon et al. 2024). An updated phylogeny for the family is shown in Figure 3.42.

Pseudosaprodesmium X.G. Tian, K.D. Hyde & Tibpromma, Mycosphere 15 (1): 152 (2024)

Tian et al. (2024) introduced *Pseudosaprodesmium* (*P.*), with *P. cocois* as the type species, found on dead leaves of *Cocos nucifera* in Thailand. Currently, there is only one species of *Pseudosaprodesmium* listed in the Index Fungorum (2024). To date, *P. cocois* has not been reported from peat swamp forests. In this study, we describe *P. narathiwatense* as a novel species on the submerged rachis of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.



Note *Conioscypha hoehnelii* (FMR 11592), and *C. lignicola* (CBS 335.93) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.42 Phylogram generated from the ML analysis based on the combined ITS, LSU, and SSU sequence data of *Pleurotheciaceae*

Pseudosaprodesmium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.43

Index Fungorum number: IF903544; Facesoffungi number: FoF 17533

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0506

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host scattered or in small groups. *Mycelium* immersed, composed of smooth, hyaline, thin-walled hyphae. *Conidiophores* 8–15 × 2.1–3.6 μm ($\overline{x}$ = 11.5 × 2.8 μm, n = 20), micronematous, mononematous, cylindrical, smooth, hyaline. *Conidiogenous cells* holoblastic, monoblastic, integrated, ampulliform, slightly curved, terminal, determinate, hyaline to pale brown, smooth, thick-walled. *Conidia* 15–48 × 11–33 μm ($\overline{x}$ = 30 × 21 μm, n = 35), solitary, globose to subglobose, cylindrical, obovoid, or irregular, thick-walled, muriform, composed of irregularly ornamented cells, septate, constricted at septa, brown to dark brown.

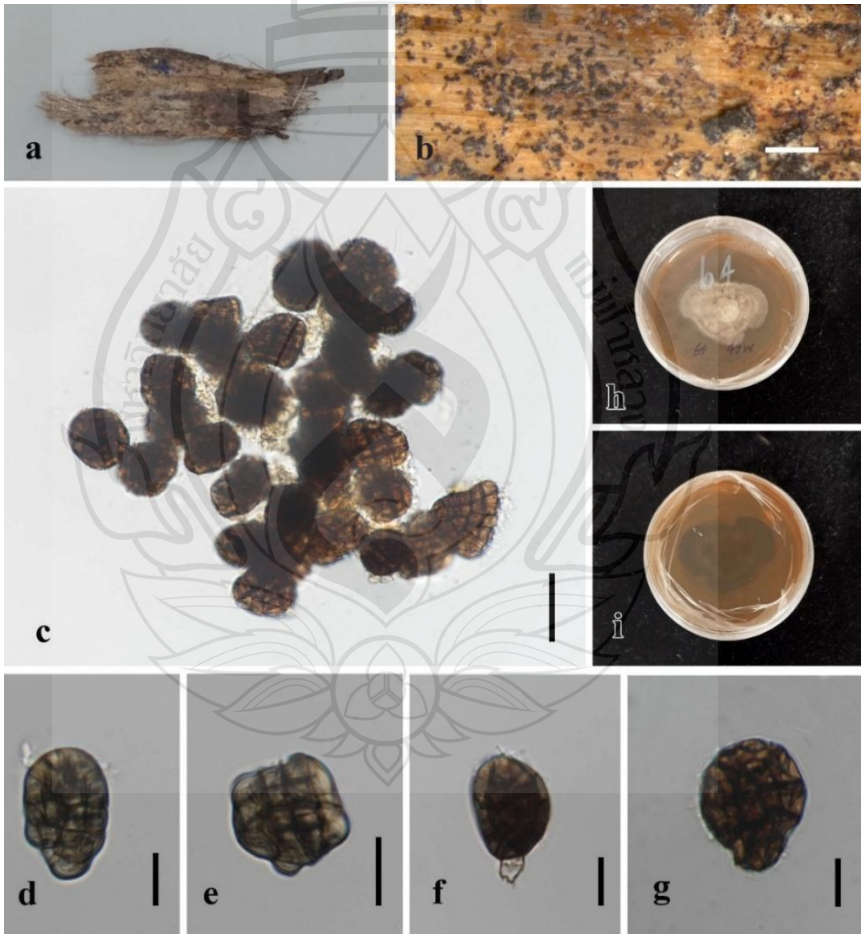
Culture characteristics – Colonies on the PDA reaching 3.5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, umbonate, dull, velvety, uneven, no sporulation, mycelium superficial to immersed, from surface brownish grey, from reverse dark brown to black.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 49W (MFLU 24-0506, holotype); ex-type living culture MFLUCC 24-0591.

GenBank numbers – MFLUCC 24-0591: ITS = PV271889, LSU = PV271928, SSU = PV263318, *rpb2* = PV340530, *tef-1α* = PV340497.

Notes – Phylogenetically, our strain (MFLUCC 24-0591) clustered with *Pseudosaprodesmium cocois* (MFLU 23-0225) in the combined phylogenetic tree of ITS, LSU, and SSU sequence data with 100% ML and 1.00 PP statistical support (Figure 3.42), but morphologically differs in having shorter and narrower conidiophores (8–15 × 2.1−3.6 μm vs. 15–30 × 3–7 μm), ampulliform, thick-walled conidiogenous cells, and longer, wider conidia (15–48 × 11−33 μm vs. 25–35 × 20–25

μm), composed of cells with ornamented surfaces, in contrast to cylindrical, thin-walled conidiogenous cells and conidia, lacking conidia with ornamented surface (Tian et al. 2024). The culture characters of our strain (MFLU 24-0506) are not comparable with *P. cocois* (MFLU 23-0225) as these details are missing in the *P. cocois* description (Tian et al. 2024). Based on nucleotide comparison, our strain (MFLUCC 24-0591) differs from *P. cocois* (MFLU 23-0225) by 8.7% (91/1023 bp, without including gaps) in SSU, 0.25% (2/863 bp, without including gaps) in LSU and a similar percentage in the ITS, without including gaps. The *rpb2* and *tef-1α* regions of our strain cannot be compared with *P. cocois*, as they are unavailable for *P. cocois* (MFLU 23-0225). Therefore, we introduce *P. narathiwatense* as a novel species based on morphological and molecular evidence.



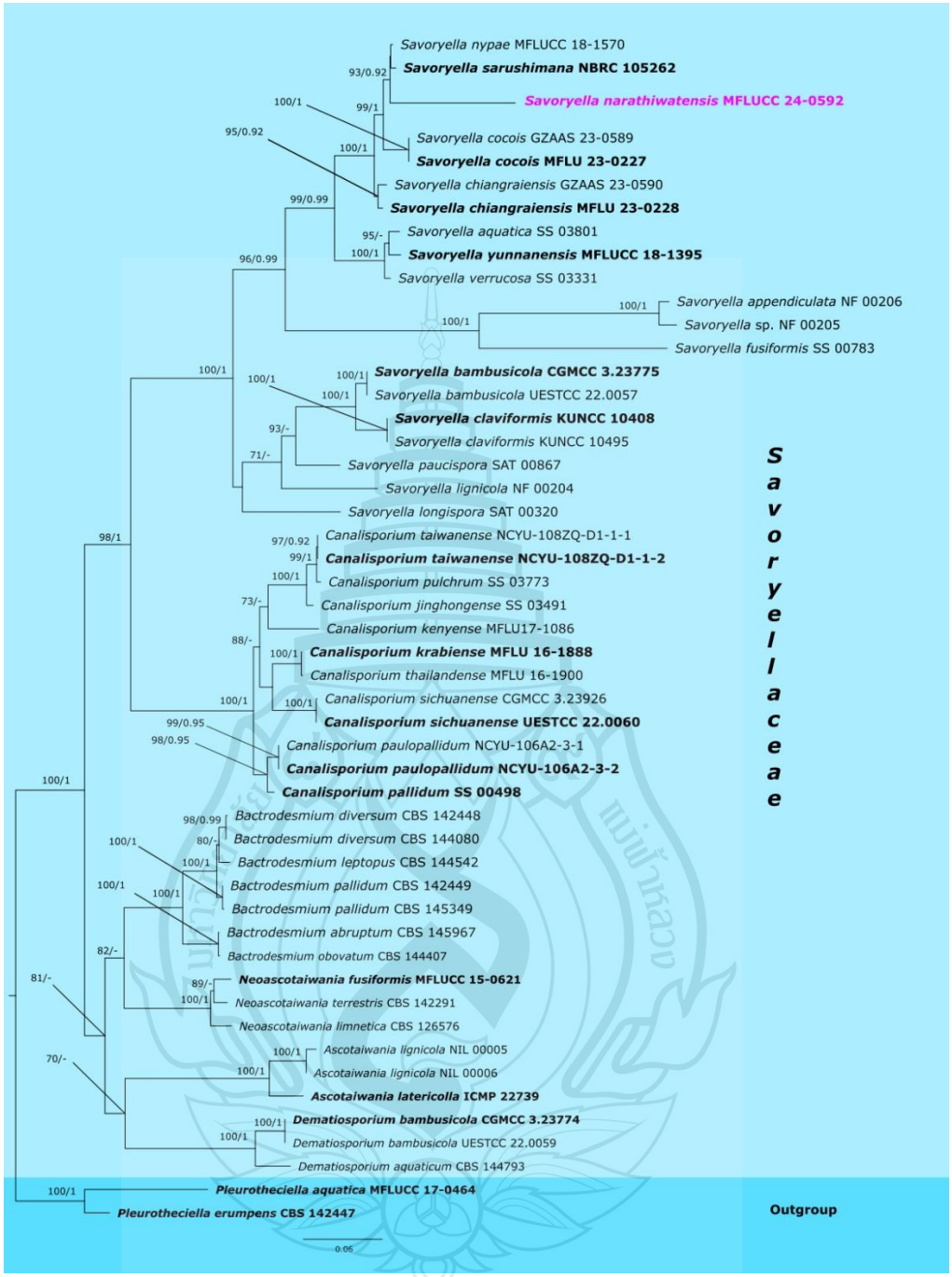
Note a Host. b Colonies on the host substrate. c–g Conidia and conidiogenous cells. h, i Colonies on the PDA. Scale bars: b = 1000 μm, c = 25 μm, d = 15 μm, e, f = 20 μm, g = 10 μm.

Figure 3.43 *Pseudosaprodesmium narathiwatense* (MFLU 24-0506, holotype)

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones, Mycologia 103 (6): 1368 (2011)

Savoryellaceae Jaklitsch & Réblová, Index Fungorum 209: 1 (2015)

The family *Savoryellaceae* was first established by Jaklitsch and Réblová (2015) to include the genus *Savoryella* (*Sa.*). Previously, *Savoryellaceae* was placed in *Sordariales* as genera *incertae sedis* (Jones et al. 2009), and later in *Savoryellales* by Boonyuen et al. (2011). The order *Savoryellales* was later proposed to accommodate genera such as *Ascotaiwania*, *Ascothailandia*, and *Canalisporium*, which were shown to cluster within *Sordariomycetes* (Jaklitsch 2015; Dayarathne et al. 2019). Dayarathne et al. (2019) revised *Savoryellaceae*, accepting three genera: *Ascotaiwania*, *Ascothailandia*, and *Canalisporium*, while synonymizing *Neoascotaiwania* under *Ascotaiwania*. Additionally, *Dematiosporium* was introduced as a new genus in the family by Luo et al. (2019), and *Bactrodesmium* was also assigned to the family based on phylogenetic evidence. Later, Réblová et al. (2020) recognised *Neoascotaiwania* as a distinct genus and placed it in *Savoryellaceae*. The family now includes six genera: *Ascotaiwania*, *Ascothailandia*, *Bactrodesmium*, *Canalisporium*, *Dematiosporium*, and *Neoascotaiwania* (Luo et al. 2019; Réblová et al. 2020). The sexual morph of *Savoryellaceae* is characterised by non-stromatic, heavily pigmented, coriaceous ascomata that can be immersed, semi-immersed, or superficial. These ascomata contain unitunicate asci with a non-amyloid apical annulus and fusiform to ellipsoidal, transversely septate ascospores with hyaline end cells and brown median cells. The asexual morphs in the family show significant diversity, including forms such as Monotosporella-like, Monodictys-like, Trichocladium-like, and Bactrodesmium-like morphs (Ranghoo and Hyde 1998; Sivichai et al. 1998; Hernández-Restrepo et al. 2017). An updated phylogeny for the family is shown in Figure 3.44.



Note *Pleurotheciella aquatica* (MFLUCC 17-0464) and *Pleurotheciella erumpens* (CBS 142447) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strains of the current study are in purple, while the type strains are in bold.

Figure 3.44 Phylogram generated from the ML analysis based on the combined LSU, SSU and ITS sequence data of *Savoryellaceae*

Savoryella E.B.G. Jones & R.A. Eaton, Transactions of the British Mycological Society 52 (1): 161 (1969)

Jones et al. (1969) introduced *Savoryella*, with *Sa. lignicola* as the type species, originally found on Scots pine (*Pinus sylvestris*) test blocks in a water-cooling tower in the UK (Eaton and Jones 1971). Currently, 15 accepted *Savoryella* species are listed in Index Fungorum (2024). Members of *Savoryella* have been reported on different hosts and substrates, such as *Avicennia marina* and *Rhizophora mucronata* (Pande 2008) from India, *Platanus* sp. from France (Reblova et al. 2011), *Pinus massoniana* (Zhuang et al. 2001), *Machilus velutina*, *Bambusa* sp. (Lu et al. 2000) from China, *Phragmites australis* (Eriksson 2014) from Sweden, and submerged decaying wood from Australia (Hyde and Goh 1998). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *Sa. narathiwatensis* as a novel species on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Savoryella narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.45

Index Fungorum number: IF903545; Facesoffungi number: FoF 17534

Etymology – The epithet “narathiwatensis” refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0507

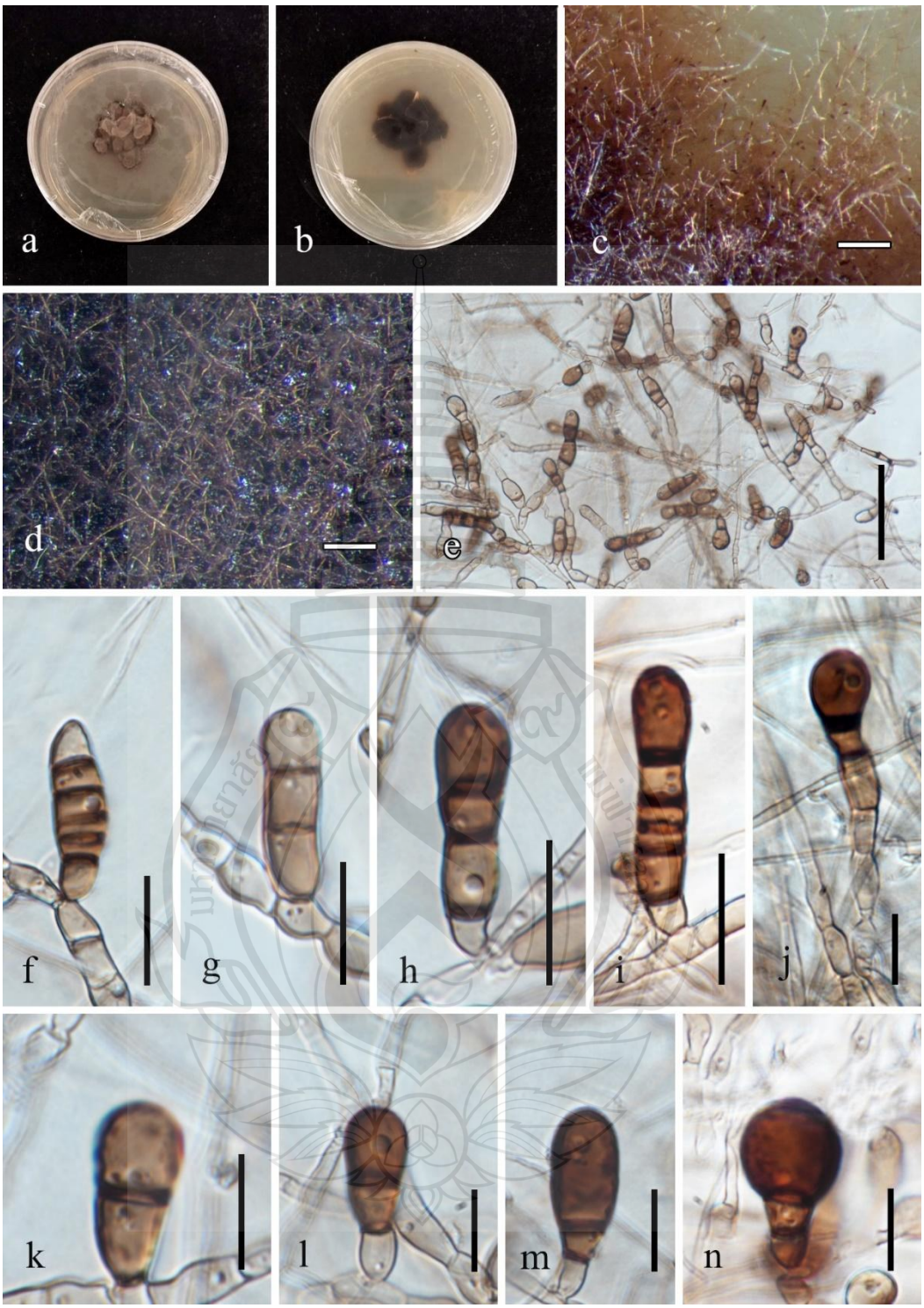
Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on culture effuse, hairy, pale brown to dark brown, glistening. *Mycelium* 1.8–5.8 μm diam., mostly superficial and partly submerged in media, composed of branched, pale brown to dark brown, thin-wall, smooth hyphae. *Conidiophores* 2–7 μm diam., micronematous, mononematous, laterally from the hyphae, septate, pale brown to brown. *Conidiogenous cells* 7–10 × 2.5–5 μm ($\overline{x}$ = 9 × 3.5 μm, n = 15), holoblastic, determinate, integrated or discrete, mostly intercalary, subcylindrical, hyaline to pale brown. *Conidia* 12–35 × 5–13 μm ($\overline{x}$ = 24 × 6 μm, n = 20), solitary, cylindrical, pyriform to obovoid, rounded at the apex, straight or slightly curved, thick-walled, 1–5-septate, thick septa, dividing the conidium into unequal cells, the apical cell brown, mostly being the largest, with pale brown to subhyaline basal cell.

Culture characteristics – Colonies on the PDA reaching 2 cm diam. after 14 days at room temperature (25–28 °C). Colony lobate to irregular, dense, raised, uneven surface, mycelia superficial to immersed, dull, surface brown, reverse dark brown to black.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 47W (MFLU 24-0507, holotype); ex-type living culture MFLUCC 24-0592.

GenBank numbers – MFLUCC 24-0592: ITS = PV271890, LSU = PV271929, SSU = PV263319.

Notes – Phylogenetically, *Savoryella narathiwatensis* (MFLUCC 24-0592) separated from *Sa. nypae* (MFLUCC 18-1570) and *Sa. sarushimana* (NBRC 105262) with 93% ML and 0.92 PP statistical support (Figure 3.44). Morphologically, *Sa. narathiwatensis* (MFLU 24-0507) is similar to *Sa. nypae* (MFLU 19-0011), but it differs in having longer conidia (12–35 μm vs. 15–21 μm) with more septa (1−5 vs. 2), and presence of cylindrical conidia despite the globose to subglobose conidia in *Sa. nypae* (Zhang et al. 2019). *Savoryella narathiwatensis* (MFLUCC 24-0592) is easily distinguishable from *Sa. sarushimana* (CBS H-2385) by its smaller and narrower conidia (12–35 × 5–13 μm vs. 42–63 × 32–50 μm), which are cylindrical, pyriform to obovoid, in contrast to the clavate conidia of the latter. Additionally, mature black conidia are absent in the former (Zhang et al. 2019). Based on the pairwise comparison of ITS, LSU and SSU nucleotides, *Sa. narathiwatensis* (MFLUCC 24-0592) differs from *Sa. nypae* by 1.6% (8/490 bp, without including gaps) in the ITS and 5.2% (55/1040 bp, without including gaps) in SSU, and no changes were observed among the LSU sequences. Therefore, we introduce *Sa. narathiwatensis* (MFLU 24-0507) as a novel species based on morphological and phylogenetic evidence.



Note a, b Culture characters on the PDA (a = from above, b = from down). c–d Mycelia on the PDA. e Conidiophores and conidia in the pure culture. f–n Sporulating conidia in the culture Scale bars: c, d = 250 μm, e = 35 μm, f–i = 15 μm, j–m = 10 μm.

Figure 3.45 *Savoryella narathiwatensis* (MFLU 24-0507, holotype)

Subclass *Sordariomycetidae* O.E. Erikss. & Winka, Myconet 1: 10 (1997)

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycological Research 108 (12): 378 (2004)

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

Locquin (1984) initially introduced *Chaetosphaeriaceae* as a new family with 106 genera (Hyde et al. 2024). Later, the family was validated by Réblová et al. (1999), who accepted six sexual genera, including *Ascocodinaea*, *Melanochaeta*, *Melanopsammella*, *Porosphaerella*, *Porosphaerellopsis*, and *Striatosphaeria*, along with 13 asexual genera within *Chaetosphaeriaceae*. Since then, several studies have expanded the family (Locquin 1984; Réblová 1999; Maharachchikumbura et al. 2016; Lin et al. 2019; Zheng et al. 2020). Wu and Diao (2022) conducted a comprehensive study of anamorphic chaetosphaeriaceous fungi from China, analysing over 300 herbarium specimens and 1100 strains, which expanded the family to 89 accepted genera. More recently, Réblová and Nekvindová (2023) examined species within *Chloridium sensu lato*, introducing six new genera: *Caliciastrum*, *Caligospora*, *Capillisphaeria*, *Geniculoseta*, *Papillospora*, and *Spicatispora*. The sexual morph of this family features dark brown to black, immersed, globose ascomata with unitunicate, clavate to cylindrical asci, containing hyaline to brown, fusiform, or ellipsoid ascospores, often with guttules, sheaths, or appendages. The asexual morphs are coelomycetous or hyphomycetous. Coelomycetous forms have setose, unilocular conidiomata, while hyphomycetous forms exhibit septate conidiophores and distinct funnel-shaped collarettes, producing diverse conidial types, ranging from hyaline to dark brown, often septate, cylindrical, or fusiform (Hyde et al. 2020d). An updated phylogeny for the selected genera in *Chaetosphaeriaceae* and *Linocarpaceae* in *Chaetosphaeriales* is shown in Figure 3.46.

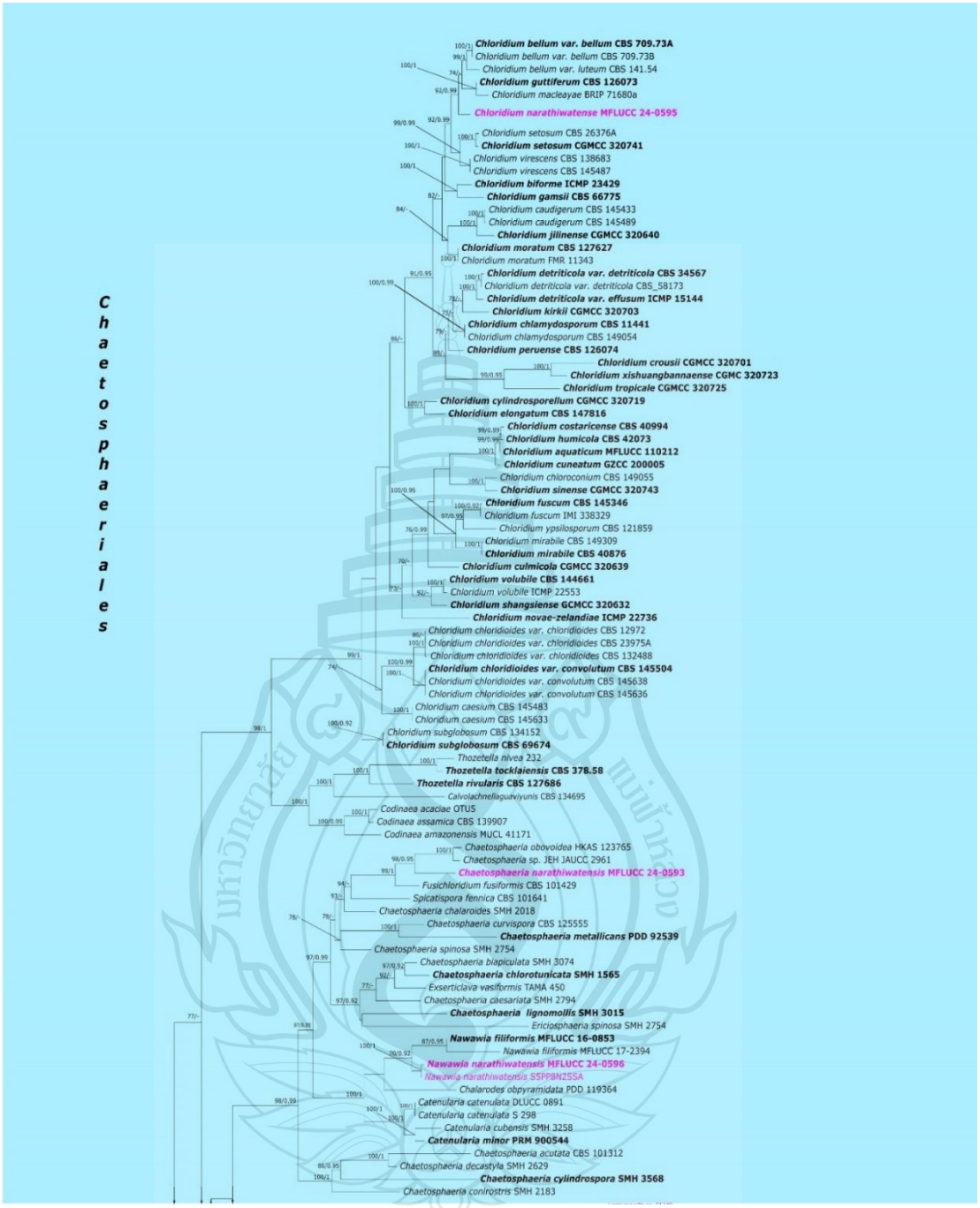
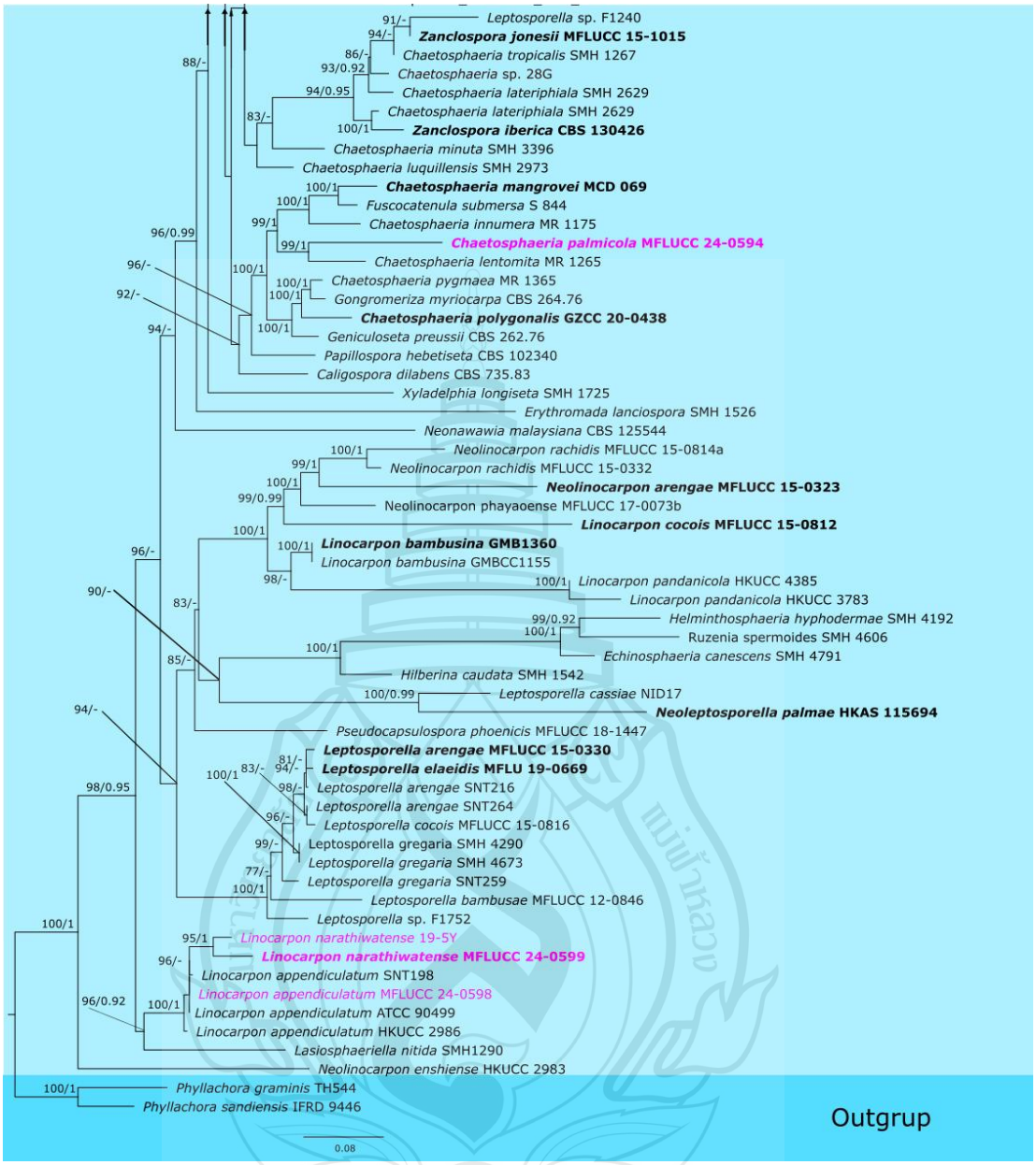


Figure 3.46 Phylogram generated from ML analysis based on the combined ITS, LSU and *tef-1α* sequence data of *Chaetosphaeriales*



Note *Phyllachora graminis* (TH544) and *Ph. sandiensis* (IFRD 9446) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolates of the current study are in purple, while the type strains are in bold.

Figure 3.46 (continued)

Chaetosphaeria Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei – Valsei – Sphaeriei 2: 252 (1863)

Tulasne and Tulasne (1863) introduced *Chaetosphaeria* (*Cha.*), as a new genus, with *Cha. Innumera* as the type species. Currently, approximately 100 *Chaetosphaeria* species are listed in Species Fungorum (2024). *Chaetosphaeria* species have a worldwide distribution and are commonly reported as saprobes on decaying plant material in terrestrial and freshwater habitats (Booth 1957; Sarbhoy and Varshney 1971; Kirk and Spooner 1984; Dennis 1986; McKenzie et al. 1992; Eriksson and Yue 1998; Lu et al. 2000; Irsenaite and Treigiene 2001; Fernández and Huhndorf 2005; Chlebicki and Chmiel 2006; Atkinson et al. 2007; Kobayashi 2007; Nasr et al. 2018; Hyde et al. 2024). Hyde et al. (1999) described *Cha. Arecacensis* on *Licuala* sp. From Brunei, *Cha*. *Hongkongensis* on *archontophoenix alexandrae* from Hong Kong and *Cha. Saltuensis* on dead petiole of *Cocos nucifera* from Seychelles. Holubová-Jechová (1982) described *Cha. Cubensis* on dead trunk of palm from Cuba. To date, only one unidentified *Chaetosphaeria* taxon (*Chaetosphaeria* sp.) has been reported from peat swamp forests (Pinruan et al. 2007). In this study, we describe *Cha. Narathiwatensis* and *Cha. Palmicola* as novel taxa, which are found as saprobes on submerged leaves of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Chaetosphaeria narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.47

Index Fungorum number: IF903546; Facesoffungi number: FoF 17535

Etymology – The epithet “narathiwatensis” refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0508

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph**:** Hyphomycetous. *Colonies* on the host scattered or in small groups, dark brown with glistening conidial masses at the apex. *Mycelium* mostly immersed, composed of smooth, thick-walled, brown, hyphae. *Conidiophores* 61–160 × 4.4–5.2 µm ($\overline{x}$ = 118 × 4.7 µm, n = 15), macronematous, mononematous, unbranched, septate, erect, straight or curved, smooth, thick-walled, cylindrical, brown, paler towards the apex. *Conidiogenous cells* 20–35.5 × 4–5 µm ($\overline{x}$ = 28 × 4.4 µm, n = 15), monophialidic,

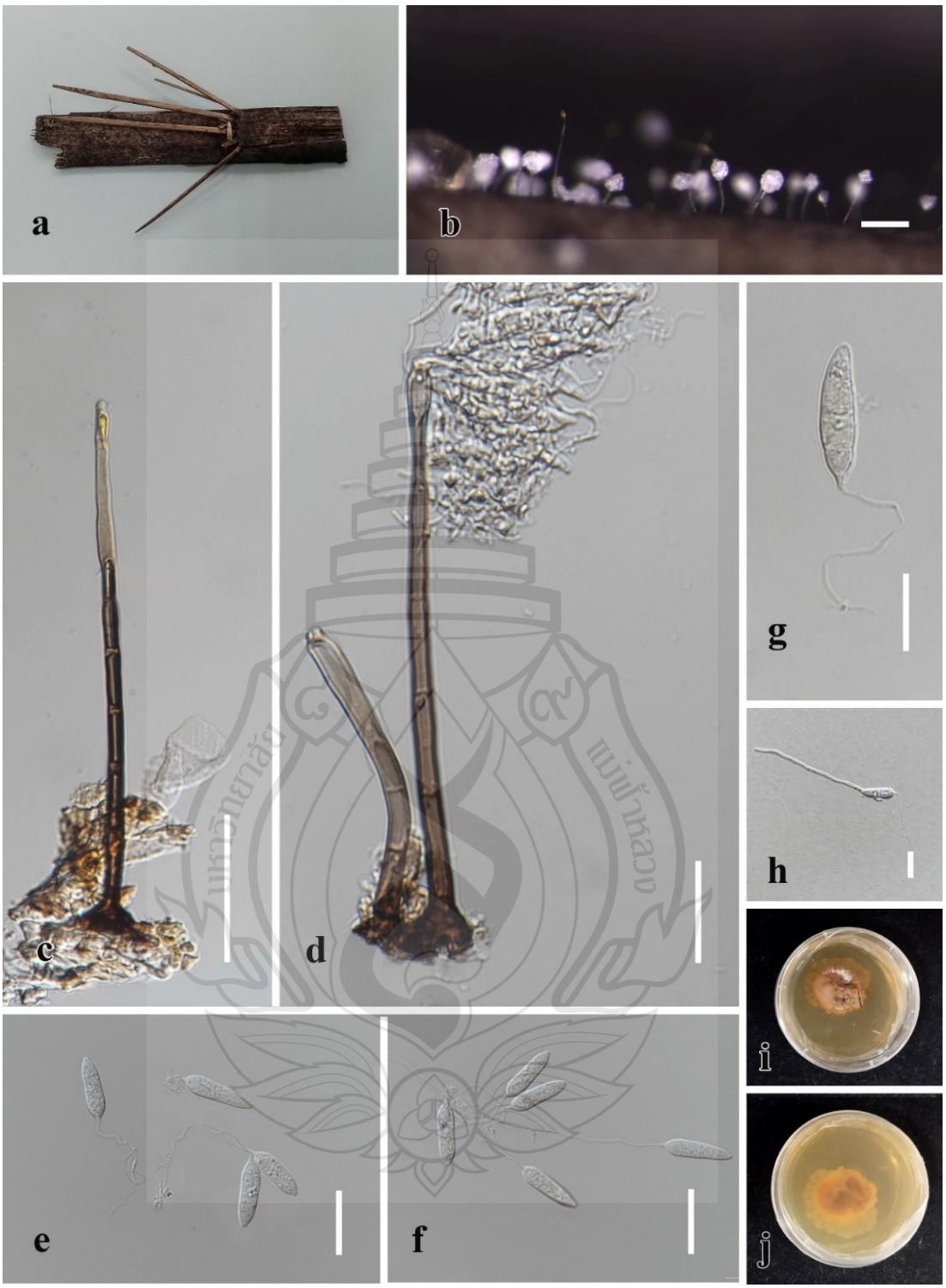
integrated, terminal, smooth, pale brown to subhyaline, apex with collarette of 2–3 μm. *Conidia* 21–27 × 5.2–7.5 μm ($\overline{x}$ = 24 × 6.4 μm, n = 20), fusiform, tapering toward the apex, hyaline, aseptate, smooth, thin-walled with a long hair-like appendage in one side up to 80 μm and 0.8–1.4 μm wide. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, dense, raised, dull, felted, surface light orange and reverse deep orange with a yellow margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 8W (MFLU 24-0508, holotype); ex-type living culture MFLUCC 24-0593.

GenBank numbers – MFLUCC 24-0593: ITS = PV271892, LSU = PV271931, *tef-1α* = PV340498.

Notes –Phylogenetically, *Chaetosphaeria narathiwatensis* (MFLUCC 24-0593) clustered basal to the subclade comprising *Cha. obovoidea* (HKAS 123765) and *Chaetosphaeria* sp. (EH-2019 JAUCC) with 98% ML, 0.95 PP statistical support in the combined phylogenetic tree for LSU, ITS and *tef-1α* (Figure 3.46). Morphologically, *Cha. narathiwatensis* (MFLU 24-0508) differs from *Cha. obovoidea* (HKAS 123765) in having shorter conidiophores (61–160 μm vs. 93–234(–291) μm), monophialidic conidiogenous cells, and fusiform conidia with a long hair-like appendage in one side, while *Cha. obovoidea* (HKAS 123765) have mono to polyphialidic conidiogenous cells and obovoid, pyriform to broadly clavate conidia without appendages (Zhang et al. 2022). Therefore, we introduce *Cha. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.



Note a Host. b Colonies on the host substrate. c, d Conidiophores and conidiogenous cells. e–g Conidia. h A germinated conidium. i, j Colonies on the PDA. Scale bars: b = 100 µm, c = 50 µm, d, h = 20 µm, e, f = 25 µm.

Figure 3.47 *Chaetosphaeria narathiwatensis* (MFLU 24-0508, holotype)

Chaetosphaeria palmicola O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.48

Index Fungorum number: IF903547; Facesoffungi number: FoF 17536

Etymology – The epithet "palmicola" refers to the host plant, palm

Holotype – MFLU 24-0509

Saprobic on the submerged leaflet of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on the host effuse, gregarious, dark brown to black with glistening conidial masses at the apex. *Mycelium* mostly immersed, composed of smooth, thick-walled, brown hyphae. *Conidiophores* 117–200 × 4–8 μm ($\overline{x}$ = 150 × 5.4 μm, n = 20), macronematous, mononematous, unbranched, septate, erect, straight or slightly curved, smooth, thin-walled, cylindrical, brown to dark brown, paler towards the apex, with 1–2 percurrent proliferations. *Conidiogenous cells* 24–32 × 2.3–3.7 μm ($\overline{x}$ = 26.5 × 3 μm, n = 15), monophialidic, integrated, terminal, smooth, thin-walled, brown to pale brown, apex with flared collarettes of 4–6 μm diam. *Conidia* 1.2–4.5 × 1.5–2.9 μm ($\overline{x}$ = 3.8 × 2.1 μm, n = 25), aggregating in mucoid mass, cylindrical to ellipsoidal, aseptate, hyaline, smooth, thin-walled. Sexual morph: Not observed.

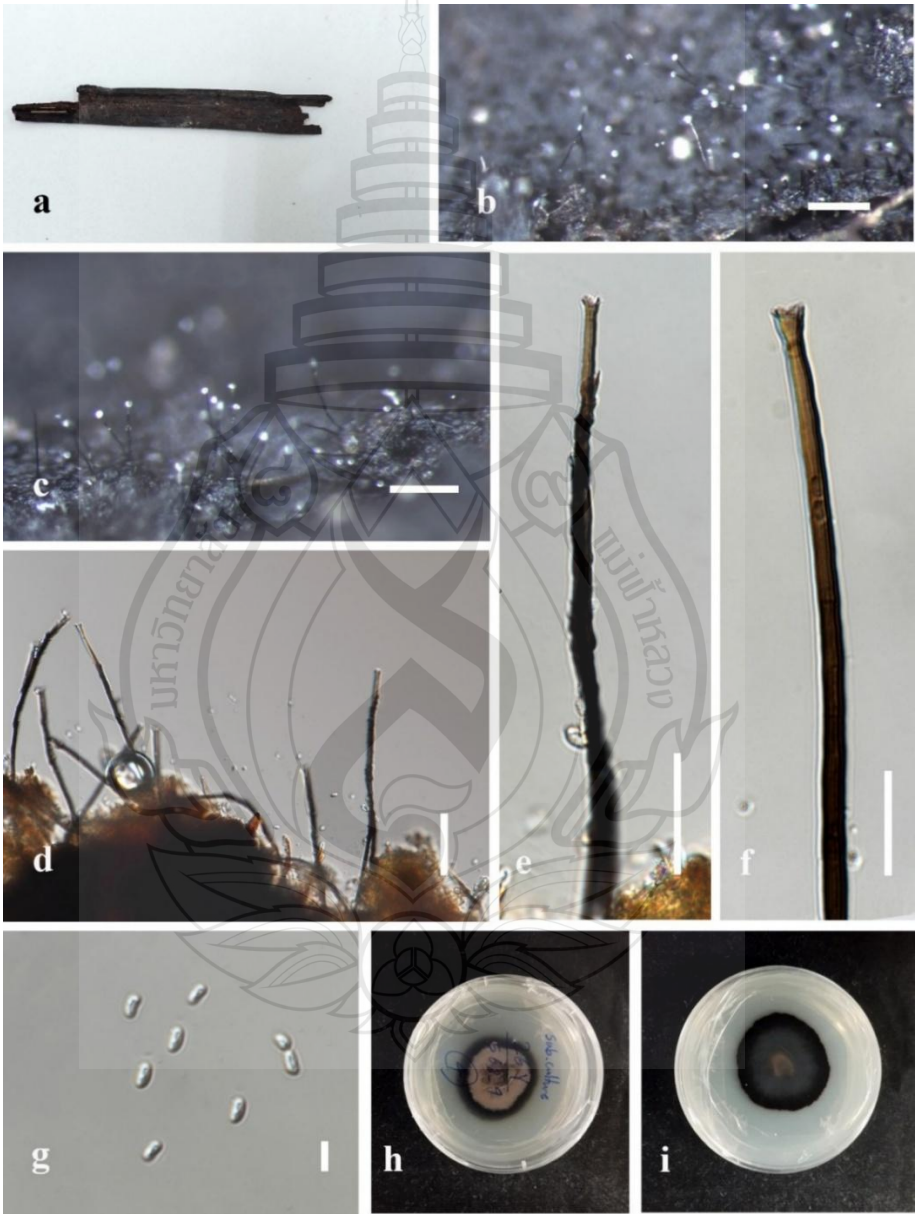
Culture characteristics – Colonies on the PDA reaching 3.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, slightly raised, dull, entire edge, surface brown with a black margin and reverse grey with a black margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged leaflet of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 15-5R (MFLU 24-0509, holotype); ex-type living culture MFLUCC 24-0594.

GenBank numbers – MFLUCC 24-0594: ITS = PV271893, LSU = PV271932, *tef-1α* = PV340499.

Notes – Phylogenetically, *Chaetosphaeria palmicola* (MFLUCC 24-0594) clustered with *Cha. lentomita* (MR 1265), with 99% ML and 1.00 PP statistical support in the phylogenetic tree (Figure 3.46). Morphologically, *Cha. palmicola* differs from *Cha. lentomita* in having unbranched, shorter conidiophores (117–200 μm vs. 60−250 μm), longer conidiogenous cells (24–32 μm vs. 7–20 μm), and shorter, narrower conidia (1.2–4.5 × 1.5–2.9 vs. 4–9 × 2–3.5), compared to the branched conidiophores of *Cha.*

lentomita (Gams and Holubová-Jechová 1976). Based on the pairwise comparison of ITS and LSU sequences, *Cha. palmicola* (MFLUCC 24-0594) differs from *Cha. lentomita* (MR 1265) by 15% (80/524 bp, without including gaps) in the ITS and 5% (59/1159 bp, without including gaps) in LSU. However, *tef1-α* cannot be compared as it is unavailable for *Cha. lentomita* (MR 1265). Therefore, we introduce *Cha. palmicola* as a novel species based on morphological and phylogenetic evidence.



Note a Host. b, c Colonies on the host substrate. d–f Conidiophores and conidiogenous cells. g Conidia. h, i Colonies on the PDA. Scale bars: b, c = 250 μm, d = 40 μm, e = 25 μm, f = 15 μm, g = 5 μm.

Figure 3.48 *Chaetosphaeria palmicola* (MFLU 24-0509, holotype)

Chloridium Link, Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin 3 (1): 13 (1809)

Chloridium (*Chl.*), was introduced by Link (1809) and typified by the hyphomycetous species *Chl. viride* (currently *Chl. virescens*). Réblová et al. (1999) considered *Melanopsammella* as the sexual morph of *Chloridium sensu stricto, Gonytrichum*, and *Chl. preussii*. Later, Réblová et al. (2016) proposed that *Gonytrichum*, *Melanopsammella*, and *Chloridium* are synonyms, which was later confirmed by Hyde et al. (2020). Based on polyphasic approaches, Réblová et al. (2022) defined *Chloridium* as a monophyletic genus distributed across eight sections. *Chloridium* comprises over 30 species, mostly isolated as saprobes from decaying plants or soil in freshwater and terrestrial habitats, predominantly in moist environments (Réblová et al. 2022; Hyde et al. 2024). To date, only one unidentified *Chloridium* taxon (as *Chloridium* sp.) has been reported from peat swamp forests (Pinnoi et al. 2006). In this study, we introduce *Chl. narathiwatense* as a novel species on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Chloridium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.49

Index Fungorum number: IF903548; Facesoffungi number: FoF 17537

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region from where the fungus was collected

Holotype – MFLU 24-0510

Saprobic on the submerged leaflet of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* in culture scattered or in small groups, dark brown to black with glistening conidial masses at the apex, vegetative hyphae 1–5.3 µm diam., numerous, branched, septate, smooth, thin-walled, hyaline to pale brown. *Conidiophores* 37.5–262.5 × 2.5–4 µm ($\overline{x}$ = 122 × 3.2 µm, n = 300), macronematous, mononematous, solitary or in small groups (up to 8), unbranched, septate, erect, straight or curved, cylindrical, brown, paler towards the apex, with 1–2 percurrent proliferations. *Conidiogenous cells* 17.5–43 × 2.5–4 µm ($\overline{x}$ = 2.2 × 3.2 µm, n = 20), monophialidic, cylindrical to subcylindrical, integrated, terminal, smooth, thin-walled, pale brown, subhyaline towards the apex, with collarettes of 2–3 µm wide. *Conidia* 2.3–

4 × 1.5–2.5 µm ($\overline{x}$ = 3 × 1.9 µm, n = 30), aggregating in mucoid mass, obovate, ellipsoid, aseptate, hyaline, smooth, thin-walled. *Chlamydospores* 4–7 × 4–5 µm ($\overline{x}$ = 5 × 4.2 µm, n = 30), intercalary or lateral, sessile or on a short stipe, globose to subglobose or pyriform, smooth, brown. Sexual morph: Not observed.

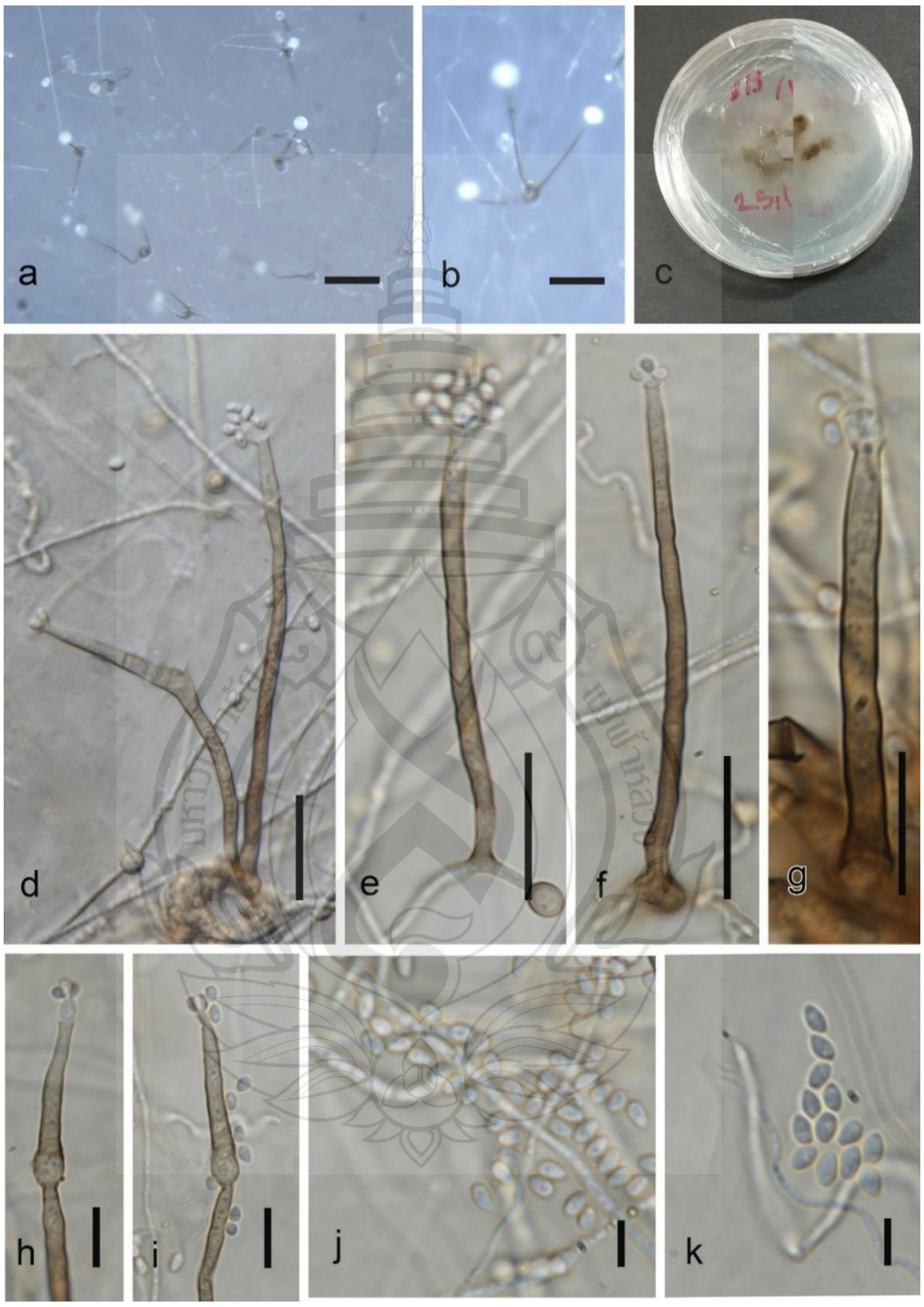
Culture characteristics – Colonies on the CMA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, medium spares, raised, dull, rhizoid, white with brown centre in surface and reverse.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged leaflet of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 1B (MFLU 24-0510, holotype); ex-type living culture MFLUCC 24-0595.

GenBank numbers – MFLUCC 24-0595: ITS = PV271894, LSU = PV271933, *tef-1α* = PV340500.

Notes – Phylogenetically, *Chloridium narathiwatense* (MFLUCC 24-0595) clustered basal to the subclade comprising *Chl. bellum var. bellum* (CBS 709.73A, CBS 709.73B), *Chl. bellum var. luteum* (CBS 14154), *Chl. guttiferum* (CBS 126073), and *Chl. macleayae* (BRIP 71680a) with 92% ML and 0.99 PP statistical support in the combined phylogenetic analysis (Figure 3.46). Morphologically, our species is similar to *Chl. guttiferum* (CBS 126073), but it differs in having shorter conidiophores (37.5–262.5 µm vs. 80–314 µm) and longer conidiogenous cells (17.5–43 µm vs. 15.5–27 µm) (Réblová et al. 2022). Our species differs from *Chl. bellum var. bellum* (CBS 709.73A) in having less percurrent proliferations in conidiophores (1–2 vs. 3–6 and up to 15 in older cultures) and longer conidiogenous cells (17.5–43 µm vs. 12–29) (Réblová et al. 2022). *Chloridium narathiwatense* differs from *Chl. bellum var. luteum* (CBS 141.54) in having longer conidiophores (37.5–262.5 µm vs. 60–182) with less percurrent proliferations (1–2 vs. 1–4) (Réblová et al. 2022). Our strain cannot be compared with *Chl. macleayae* (BRIP 71680a) as its morphology has not been provided (Tan and Shivas 2023). Based on the pairwise comparison nucleotides, *Chl. narathiwatense* (MFLUCC 24-0595) differs from *Chl. guttiferum* (CBS 126073) by 2.2% (28/1259 bp, without including gaps) in *tef-1α* and 6.7% (51/751bp, without including gaps) in *tub2*, 1.2% (6/492 bp, without including gaps) in the ITS and 0.7% (7/1060 bp, without

including gaps) in LSU. Therefore, we introduce *Chl. narathiwatense* as a novel species based on morphological and phylogenetic evidence.



Note a, b Colonies on the CMA. c Surface and reverse overview of the culture. d–i Conidiophores and conidiogenous cells. j, k Conidia. Scale bars: a, b =100 μm, d–g = 20 μm, h, i = 10 μm, j, k = 5 μm.

Figure 3.49 *Chloridium narathiwatense* (MFLU 24-0510, holotype)

Cryptophiale Piroz., Canadian Journal of Botany 46 (9): 1123 (1968)

Cryptophiale was introduced by Pirozynski (1968) with *Cryptophiale kakombensis* as type species. Based on Species Fungorum (2024) there are 21 accepted morphological species with only two species with sequence data. *Cryptophiale* species distinguished by having unbranched or apically dichotomous or verticillate, setiform, monophialidic, obscured conidiogenous cells in two rows and unicellular to multiseptate, conidia hyaline, formed on one side of the conidiophore with slimy masses (Pirozynski 1968; Seifert et al. 2011; Yang et al. 2018a). Farr (1980) described *Cryptophiale minor* as a new species on dead leaves of *Astrocaryum* sp. (Arecaceae) in Brazil, Amazonas.

Nawawia Marvanová, Transactions of the British Mycological Society 75 (2): 227 (1980)

Marvanová (1980) established *Nawawia* (*Naw.*), as a new genus, designating *Naw. filiformis* (originally described as *Clavatospora filiformis*) as the type species. Currently, five accepted species (*Naw. antennata*, *Naw. filiformis*, *Naw. oviformis*, *Naw. quadrisetulata*, and *Naw. sasae-kurilensis*) are listed in Species Fungorum (2024). Members of *Nawawia* have been reported from aquatic habitats, such as submerged wood or leaves, as well as terrestrial habitats (Nawawi 1973; Kuthubutheen et al. 1992; Hyde et al. 1996; Mel'nik and Hyde 2006; Goh et al. 2014; Peng et al. 2016). To date, one species of this genus (*Naw. fusiformis*) has been reported from peat swamp forests (Pinnoi et al. 2006; Pinuruan et al. 2007). In this study, we introduce *Naw. narathiwatensis* as a novel species, discovered on submerged rachises of *Eleiodoxa conferta* in the peat swamp forest of Narathiwat, Thailand.

Nawawia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.50

Index Fungorum number: IF903549; Facesoffungi number: FoF 17538

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0511

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on the host substrate effuse, gregarious, dark brown to black with glistening conidial masses at the apex. *Mycelium* mostly immersed, brown, septate. *Conidiophores* 80–180 × 5–9 µm ($\bar{x}$ = 126 × 6.5 µm, n = 20), macronematous, mononematous, single or in small groups (2–3), erect, straight or slightly curved, smooth, thick-walled, septate, brown or dark brown, paler toward the apex. *Conidiogenous cells* integrated, terminal, monophialidic, pale brown smooth, thick-walled, cylindrical, with collarette and without percurrent proliferation. *Conidia* 14–18 × 11–16 µm ($\bar{x}$ = 16 × 13 µm, n = 30), hyaline, aseptate, smooth, thin-walled, triangular- or quadrangular-shaped with a long hair-like appendage from each corner of 15.5–53 × 1–2 µm, and sometimes conidia have four appendages and when viewed from above are square. Sexual morph: Not observed.

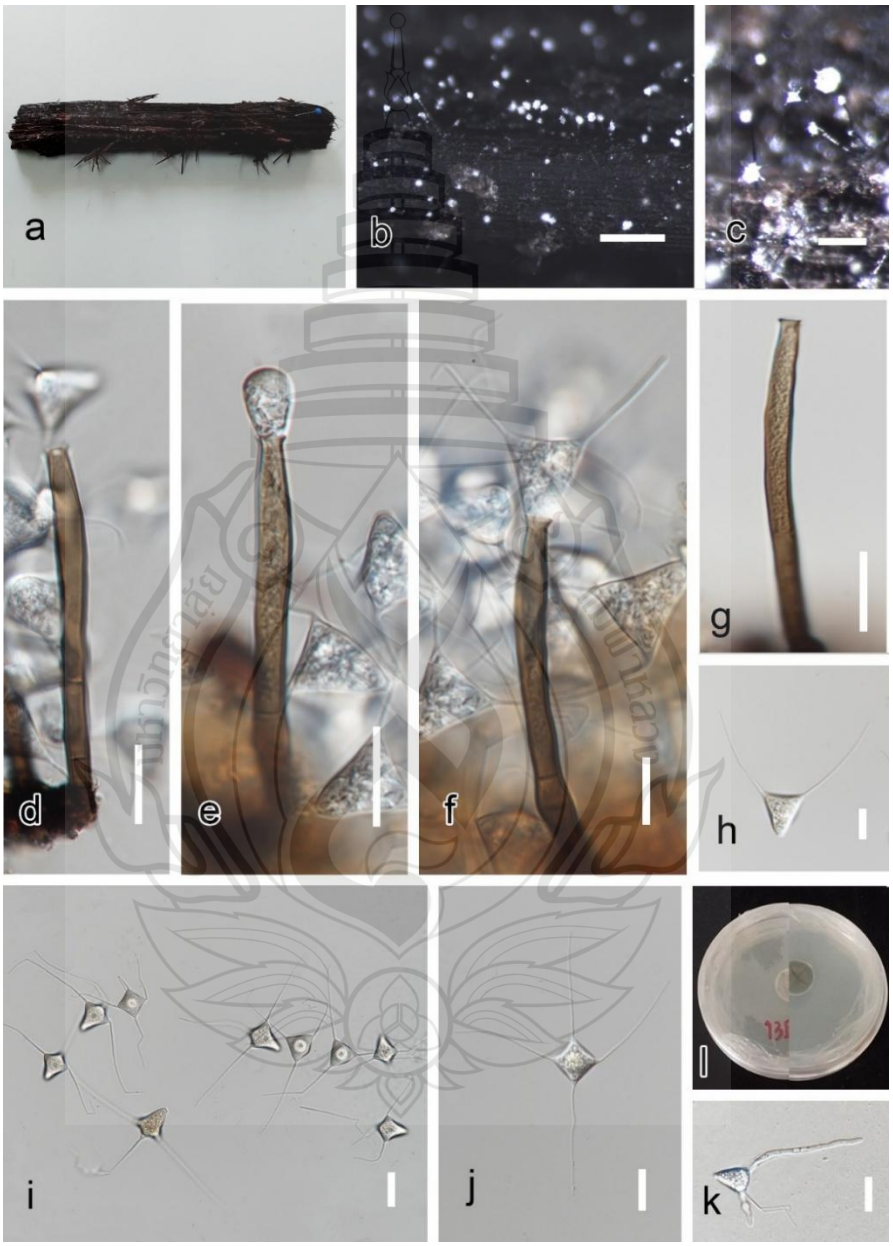
Culture characteristics – Colonies on the PDA reaching 1.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, umbonate, dull, entire edge, without pigment diffusion and sporulation, surface pale brown with a white margin, reverse grey.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 13B (MFLU 24-0511, holotype); ex-type living culture MFLUCC 24-0596.

GenBank numbers – MFLUCC 24-0596: ITS = PV271895, LSU = PV271934, *tef-1α* = PV340501.

Notes – Phylogenetically, *Nawawia narathiwatensis* (MFLUCC 24-0596) formed a separate clade with *Naw. filiformis* (MFLUCC 17-2394, MFLUCC 16-0853) with 70% ML and 0.92 PP statistical support in our phylogenetic analyses (Figure 3.46). Morphologically, *Naw. narathiwatensis* (MFLU 24-0511) is similar to *Naw. filiformis* (MFLU 18-1500) in having macronematous, mononematous conidiophores, monophialidic conidiogenous cells and hyaline appendaged conidia, but it differs in having shorter and wider conidiophores (80–180 × 5–9 µm vs. (49–)77–215(–236) × 4.1–5.9 µm), longer appendages (15.5–53 µm vs. 15–34 µm), and conidiogenous cells without percurrent proliferations, compared to *Naw. filiformis* with up to three percurrent proliferations (Yang et al. 2018; Nawawi 1973). Based on the pairwise

comparison of the ITS, *Naw. narathiwatensis* (MFLUCC 24-0596) differs from *Naw. filiformis* (MFLUCC 17-2394) by 15.09% (80/530 bp, excluding gaps). However, *rpb2* and *tef1-α* sequences of *Naw. narathiwatensis* cannot be compared, as they are unavailable for *Naw. filiformis*. Therefore, we introduce *Naw. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.

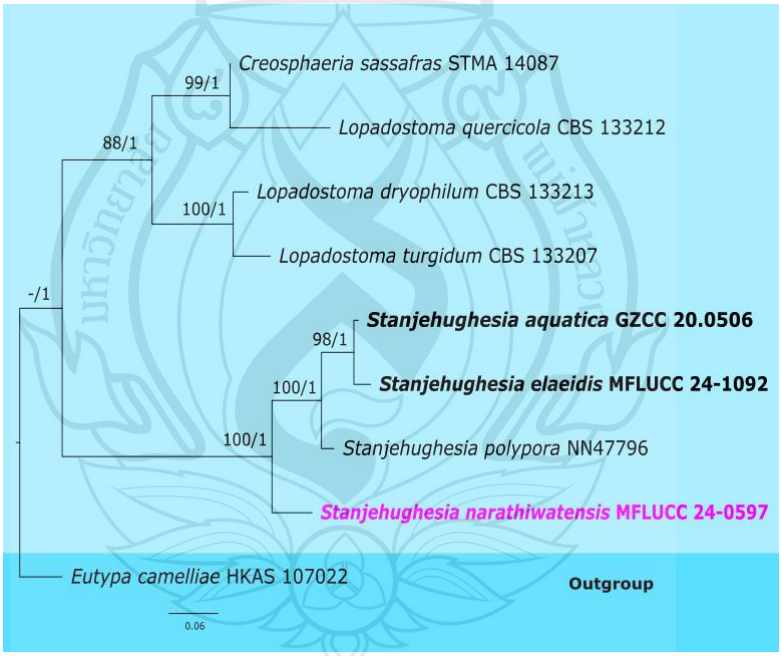


Note a Host. b, c Colonies on the host substrate. d–g Conidiophores and conidiogenous cells. h–j Conidia. k A germinated conidium. l Colony on the PDA. Scale bars: b = 200 μm, c = 100 μm, d, e, g, i–k = 20 μm, f, h = 15 μm.

Figure 3.50 *Nawawia narathiwatensis* (MFLU 24-0511, holotype)

Stanjehughesia Subram., Proc. Indian Acad. Sci., Pl. Sci. 58 (4): 184 (1992)

Subramanian (1992) established *Stanjehughesia* (*S.*), as a new genus, with *S. hormiscioides* as the type species. Currently, there are 20 accepted species of *Stanjehughesia* listed in Species Fungorum (2024). Members of *Stanjehughesia* have a wide distribution and have been reported on various hosts, such as *Elaeis guineensis* from Thailand (Zhang et al. 2024), *Roystonea regia* from Cuba (Mena-Portales et al. 2016), rachides and petioles of *Sabal* from the USA (Delgado 2008), branches of bamboo and *Michelia skinneriana* from China (Ma et al. 2011), *Juniperus virginiana* from the USA (Subramanian 1992), and dead wood from Spain (Mena-Portales et al. 2016). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *S. narathiwatensis* as a novel species found on the submerged petiole of *Eleiodoxa conferta* in the peat swamp forest of Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.51.



Note *Eutypa camelliae* (HKAS 107022) was used as the outgroup taxon. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.51 Phylogram generated from the ML analysis based on the combined LSU, ITS, SSU, *tef-1α, rpb2* and *tub2* sequence data of *Stanjehughesia*

Stanjehughesia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.52

Index Fungorum number: IF903550; Facesoffungi number: FoF 17539

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the holotype was collected.

Holotype – MFLU 24-0512

Saprobic on the submerged petiole of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host substrate gregarious, dark brown to black, glistening, conidia white at the apex. *Mycelium* mostly immersed, composed of branched, septate, brown hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–16 × 3.9–6.2 ($\bar{x}$ = 12.9 × 5 μm, n = 20), monoblastic, terminal, erect, solitary or caespitose, straight or curved, cylindrical or lageniform, aseptate, smooth-walled, thick-walled, dark brown to black, truncate at the apex. *Conidia* 90–120 × 11–16 μm ($\bar{x}$ = 108.3 × 12.4 μm, n = 20), solitary, 13–17-septate, acrogenous, straight or curved, obclavate, fusiform, falcate, rostrate with dark bands at septa, verrucose, with horizontal striation, brown to dark brown, the apical cell hyaline with a sheath and often with broken apical cells.

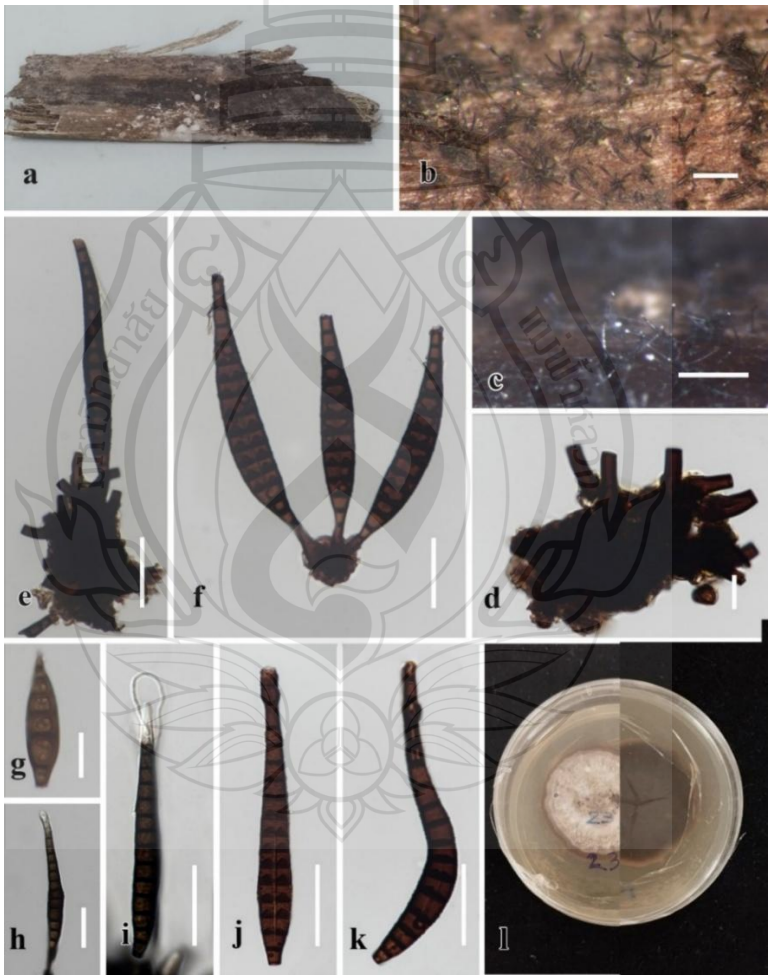
Culture characteristics – Colonies on the PDA reaching 3 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, entire to lobate margin, raised, medium dense, dull, velvety, surface white with a greyish orange at the margin, reverse brown with a whitish margin.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged petiole of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 8F (MFLU 24-0512, holotype); ex-type living culture MFLUCC 24-0597.

GenBank numbers – MFLUCC 24-0597: ITS = PV271897, LSU = PV271936, *tef-1α* = PV340502.

Notes – In the multi-gene phylogenetic analyses (LSU, ITS, SSU, *tef-1α*, *rpb2*), *Stanjehughesia narathiwatensis* (MFLUCC 24-0597) clustered separated from the subclade comprising *S. aquatica* (GZCC 20.0506), *S. elaeidis* (MFLUCC 24-1092), and *S. polypora* (NN47796) with 100% ML, 1.00 PP statistical support (Figure 3.51). Morphologically, *S. narathiwatensis* (MFLU 24-0512) is similar to *S. polypore*, but it

can easily be distinguished by having mucilage sheath at the apex and lacking germination pore in each cell in conidia, in contrast to *S. polypore* with its germination pore in each cell of conidia, lacking a mucilage sheath. *Stanjehughesia narathiwatensis* (MFLUCC 24-0597) differs from *S. aquatica* (HKAS 112612) in having longer and wider conidiogenous cells (8–16 × 3.9–6.2 µm vs. 7–12 × 2–3.5 µm), falcate, striate conidia with dark thick septa and an apical sheath despite lacking these characters in *S. aquatica* (HKAS 112612) (Yang et al. 2023). *Stanjehughesia narathiwatensis* (MFLUCC 24-0597) cannot be compared with *S. elaeidis* (HKAS 115744) as it was introduced based on its sexual morph (Zhang et al. 2024). Therefore, we introduce *S. narathiwatensis* as a novel species, based on morphological and phylogenetic evidence.



Note a Host. b, c Colonies on the host substrate. d Conidiogenous cells. e, f Conidiogenous cells and conidia. g–k Conidia. l Colonies on the PDA. Scale bars: b = 500 µm, c = 250 µm, d = 10 µm, e, i–k = 30 µm, g = 15 µm, h = 20 µm.

Figure 3.52 *Stanjehughesia narathiwatensis* (MFLU 24-0512, holotype)

Leptosporellaceae Konta & K.D. Hyde, Mycosphere 8 (10): 1956 (2017)

Leptosporella Penz. & Sacc., Malpighia 11(9-10): 406 (1897)

Leptosporella belongs to the *Leptosporellaceae* (*Chaetosphaeriales*, *Sordariomycetes*, *Ascomycota*) (Konta et al. 2017) and comprises 10 species reported as endophytes or saprobes (Hyde et al. 2024). *Leptosporella* is characterized by solitary, superficial and ostiolate ascomata, comprising carbonaceous, dome-shaped areas through the host tissues with 8-spored, cylindrical asci with a J-, subapical ring. *Ascospores* are aseptate, long filiform, spiral and hyaline or pale-yellowish in mass, with or without polar mucilaginous appendages. The asexual morph has not been determined yet. *Leptosporella* has ascomata and asci similar to *Linocarpon* and *Neolinocarpon*, but it has narrower ascospores, which gradually taper to the end, and an indistinct mucilaginous appendage, if present (Konta et al. 2017).

Leptosporella was introduced by Penzig and Saccardo (1897) and typified with *L. gregaria* Penz. & Sacc. Lumbsch and Huhndorf (2010) placed the genus in *Sordariomycetidae* genera *incertae sedis*. Huhndorf and Miller (2011) re-examined the holotype and freshly collected specimens, and transferred the genus to *Chaetosphaeriales* based on molecular data. Maharachchikumbura et al. (2015) did not determine a family for *Leptosporella*. The genus was placed in *Chaetosphaeriales incertae sedis* by Dai et al. (2016). Konta et al. (2017) reported *L. arengae* on *Arenga pinnata* and *L. cocois* on *Cocos nucifera* from palm hosts and based on analysis of combined LSU and ITS sequence data, established *Leptosporellaceae* to accommodate *Leptosporella* in the order *Chaetosphaeriales*, which was confirmed by Wijayawardene et al. (2018). Hyde et al. (2020) reported *L. elaeidis* on *Elaeis guineensis* (Arecaceae) based on phylogenetic analyses and also accepted *Leptosporella* in the family *Leptosporellaceae* (*Chaetosphaeriales*).

Leptosporella members were reported on Arecaceae, Dicksoniaceae, Fabaceae, Lamiaceae, Leucodontaceae, Poaceae, Polypodiales and Rosaceae (Penzig and Saccardo 1897; Rehmit 1901; Spegazzini 1912; Chardón and Toro 1934; Sydow 1938; Chardón 1939; Sousa da Camara and da Luz 1939; Sawada 1943; Hansford 1957; Racovitza 1959; Edward et al. 1972; Huhndorf et al. 2004; Huhndorf and Miller 2011; Dai et al. 2016; Del and Arnold 2017). *Leptosporella* species are widespread and reported from Argentina, Australia, Brazil, France, India, Indonesia, Portugal and

Thailand (Penzig and Saccardo 1897; Rehmit 1901; Spegazzini 1912; Sydow 1938; Sousa da Camara and da Luz 1939; Hansford 1957; Racovitza 1959; Edward et al. 1972; Konta et al. 2017).

Table 3.3 World distribution of *Leptosporella* species

Species	Host/Substrate	Country	References
Leptosporella arengae	dead rachis of *Arenga pinnata*	Thailand	(Konta et al. 2017)
Leptosporella elaeidis	On rachis and petioles of *Elaeis guineensis*	Thailand	(Hyde et al. 2020)
Leptosporella cocois	dead rachis of *Cocos nucifera*	Thailand	(Konta et al. 2017)
Leptosporella ambiens	living stems of *Compositae*	Brazil	(Rehm 1901)
Leptosporella andina	stems of *Ephedra andina*	Argentina, Mendoza	(Spegazzini 1912)
Leptosporella bambusae	dead culms of bamboo	Thailand	(Dai et al. 2016)
Leptosporella clelandii	dead branches of *Acacia kempeana*	Central Australia	(Hansford 1957)
Leptosporella dicksoniae	*Dicksonia squarrosa*	Portugal	(Sousa da Câmara and Luz 1939)
Leptosporella gregaria	rotten wood	Indonesia	(Penzig and Saccardo 1897)
Leptosporella leucodontis	dead leaves of *Leucodon sciuroides*	France	(Racovitza 1959)
Leptosporella macrotheca	on wood	Australia, New South Wales	(Sydow 1938)
Leptosporella rosae	dead branches of *Rosa*	India	(Edward et al. 1972)

Linocarpaceae Konta & K.D. Hyde

Konta et al. (2017) introduced *Linocarpaceae* within *Chaetosphaeriales* based on morphology and the combined phylogenetic analyses of ITS and LSU sequences, including two genera (*Linocarpon* and *Neolinocarpon*). Later, Xu et al. (2020) introduced a third genus, *Claviformispora*, into this family based on morphology and the combined LSU, SSU, and *tef1-α* gene phylogeny, emending the family description. Currently, three genera (*Claviformispora*, *Linocarpon*, and *Neolinocarpon*) are accepted in *Linocarpaceae* (Zhang et al. 2023, 2024; Hyde et al. 2024). The sexual morph is characterized by solitary or aggregated ascomata, either superficial or immersed, dome-shaped or subglobose with a central ostiole or immersed papilla. The peridium consists of dark brown to black cells of *textura angularis*, and the hamathecium includes septate paraphyses that are longer than the asci. *Asci* are 8-spored, unitunicate, cylindrical, with a J-apical ring, developing from the base and periphery of the ascomata. *Ascospores* are parallel or spiral, hyaline or pale yellowish in mass, filiform or claviform, straight or curved, unicellular, with or without refringent bands and polar appendages. For the asexual morph, only Phialophora-like species have been reported by Hyde (1992a) from the cultures of *Linocarpon appendiculatum* and *L. elaeidis* (Konta et al. 2017; Zhang et al. 2023). In this study, we introduce *Linocarpon narathiwatense* as a novel species and *Linocarpon appendiculatum* as a new host record.

Linocarpon Syd. & P. Syd., Annls mycol. 15(3/4): 210 (1917)

Linocarpon Syd. & P. Syd., a saprobic genus on monocotyledonous and dicotyledonous plants, is the type genus of the family *Linocarpaceae* (*Sordariomycetes*, *Ascomycota*) (Konta et al. 2017). The asexual morph of this genus includes phialophora-like spp. and has been reported from two species viz., *Linocarpon appendiculatum* and *L. elaeidis*. In the sexual morph, ascomata are solitary, superficial, subglobose and flat-based with black, domed blistering areas and a central ostiole. The outer cells of the peridium merge with the cells of the host epidermis, consisting of dark brown to black cells of *textura angularis*. The hamathecium comprises hyaline and septate paraphyses that are longer than asci, wider at the base and taper towards the apex. Asci are 8-spored, cylindrical, unitunicate and apically rounded, with a small non-

amyloid apical ring, which develops from the base and periphery of the ascomata. Ascospores are filiform, hyaline or pale yellowish, parallel or spiral in asci with round ends. The ascospores are inflated, appendage or acute and contain numerous refringent septum-like bands (Sydow and Sydow 1917; Hyde 1992). *Linocarpon* was introduced by Sydow and Sydow (1917) and typified with *Linocarpon pandani* Syd. and P. Syd. Hyde (1992) provided a monograph with twenty-three accepted species and was later updated and accommodated in *Xylariaceae* (*Xylariales*) (Hyde 1997; Dulymamode et al. 1998; Hyde and Alias 1999; Fröhlich and Hyde 2000; Thongkantha et al. 2003; Cai et al. 2004). Konta et al. (2017) introduced *Linocarpaceae* as a new family to accommodate *Linocarpon*, which was further confirmed by Wijayawardene et al. (2022). Wijayawardene et al. (2022) accepted forty-two species in this genus. It is difficult to differentiate *Linocarpon* and *Neolinocarpon* (*Linocarpaceae*) from *Leptosporella* (*Leptosporellaceae*) due to their similar ascomata and ascus morphologies. *Linocarpaceae* genera (*Linocarpon* and *Neolinocarpon*) are distinguished from *Leptosporella* by their distinct ascospore appendages at the apex (Poonyth et al. 2000; Yanna and Hyde 2003; Cai et al. 2004). Most *Linocarpon* species have been collected from *Pandanaceae* and Arecaceae hosts. *Linocarpon* has also been reported from other hosts, including *Zingiberaceae*, *Poaceae*, *Fabaceae*, *Fagaceae*, *Euphorbiaceae* and *Smilacaceae* (Sydow and Sydow 1917; Petrak 1952; Petrak and Deighton 1952; Hansford 1954; Petrak 1956; Schrantz 1960; Turner 1971; Pirozynski 1972; Liu 1977; Barr 1978; Sivanesan and Hsieh 1989; Hyde 1992; Barr 1993; Hyde 1997, 1988, 1989; Dulymamode et al. 1998; Hsieh et al. 1998; Hyde and Alias 1999; Fröhlich and Hyde 2000; Lu et al. 2000; Zhuang 2001; Taylor and Hyde 2003; Cai et al. 2004; Huhndorf et al. 2004; Miller and Huhndorf 2005; Bahl 2006; Pinruan et al. 2007; Konta et al. 2017). Bahl (2006) found that the species were often isolated from *Pandanus* and rarely occur on bamboo (Thongkantha et al. 2003). *Linocarpon* members have been collected from Australia, Brazil, Brunei, China, Ecuador, India, Malaysia, Mauritius, Papua New Guinea, Thailand, Tanzania, Philippines, Sierra Leone, Indonesia and the United States.

Table 3.4 World distribution of *Linocarpon* species

Species	Host/Substrate	Location	Reference
L. angustatum	on intertidal petiole of *Nypa fruticans*	Malaysia, Peninsular	(Hyde and Alias 1999)
L. apiculatum	on decaying petiole of palm in freshwater swamp	Papua New Guinea, Irian Jaya	(Hyde 1997)
L. appendiculatum	on rotten fronds of *Nypa fruticans*	Brunei	(Hyde 1988)
L. aquaticum	on rachis of palm (Arecaceae)	Australia, Queensland	(Hyde 1997)
L. arengae	on dead rachis of *Arenga pinnata* (Arecaceae)	Thailand	(Konta et al. 2017)
L. australiense	on rachis of *Licuala ramseyi*, *Archontophoenix alexandrae*	Australia, Queensland	(Hyde 1997)
L. bipolare	on intertidal fronds of *Nypa fruticans*	Brunei	(Hyde 1992)
L. bruneiense	on dead petiole of *Calamus pogonacanthus* (Arecaceae)	Brunei	(Fröhlich and Hyde 2000)
L. cajani	on *Elaeis guineensis* (Arecaceae)	Sierra Leone	(Petrak and Deighton 1952)
L. calamicola	on dead rattan of *Calamus australis, C. conirostris, Archontophoenix alexandrae* (Arecaceae)	Australia, Queensland	(Fröhlich and Hyde 2000)
L. carinisporum	on dead rachis of *Licuala ramsayi*, (Arecaceae)	Peninsular Malaysia	(Hyde 1997)

Table 3.4 (continued)

Species	Host/Substrate	Location	Reference
L. clavatum	on rachis of Pinanga (Arecaceae)	Peninsular Malaysia	(Hyde 1997)
L. cocois	on dead rachis of *Cocos nucifera* (Arecaceae)	Thailand	(Konta et al. 2017)
L. eccentricollum	on dead petiole of *Mauritia flexuosa* (Arecaceae)	Ecuador	(Fröhlich and Hyde 2000)
L. elaeidis	on dead rachis of *Elaeis guineensis*	Sierra Leone	(Petrak and Deighton 1952)
L. livistonae	on dead petioles of *Livistona* sp.	Philippines	(Hyde 1988)
L. longisporum	on intertidal fronds of *Nypa fruticans* (Arecaceae)	Brunei	(Hyde 1992)
L. luteocollum	on dead rachis of *Archontophoenix alexandrae* (Arecaceae)	Australia	(Taylor and Hyde 2003)
L. mauritiae	on dead petiole of *Mauritia flexuosa* (Arecaceae)	Ecuador	(Fröhlich and Hyde 2000)
L. nipae	on *Nypa fruticans* (Arecaceae)	from Philippines,	(Hyde 1988)
L. palmetto	on dead places in living leaves of Sabal palmetto (Arecaceae)	from United States	(Barr 1978)

Table 3.4 (continued)

Species	Host/Substrate	Location	Reference
L. pandani	On dead leaves of *Pandanus utilissimus*: (Arecaceae)	Philippines	(Sydow and Sydow 1917)
L. pandanicola	on decaying leaves of *Pandanus* in freshwater swamp	Papua New Guinea (Iryan Jaya)	(Hyde 1997)
L. versisporum	on dead petioles of Sabal serrulata (Arecaceae)	Florida.	(Petrak 1952)
L. williamsii	on dead culms of Poaceae	South Australia	(Hansford 1954)
L. zingiberaceicola	on basal stem of Zingiberaceae	Peninsular Malaysia	(Hyde 1997)

Linocarpon appendiculatum K.D. Hyde, Transactions of the Mycological Society of Japan 29: 339 (1989) Figure 3.53

Index Fungorum number: IF135907; Facesoffungi number: FoF 17540

Saprobic on the submerged rachis of *Cyrtostachys renda*. Sexual morph: *Ascomata* 350–420 μm × 110–130 μm ($\bar{x}$ = 327 × 82 μm, n = 15), solitary or aggregated, superficial, black, dome-shaped, raised, lenticular and with a central ostiole. *Peridium* 10–15 μm wide ($\bar{x}$ = 12.5 μm, n = 20), outer cells merging with the host epidermal cells, composed of dark brown to black cells of *textura angularis*. *Paraphyses* longer than asci, 2–4 μm wide ($\bar{x}$ = 3 μm, n = 30), straight or flexuous, septate, hypha-like, hyaline. *Asci* 100–148 × 7−9 ($\bar{x}$ = 130 × 7.8 μm, n = 20), 8-spored, cylindrical, straight or curved toward the apex, with a J-subapical ring. *Ascospores* 80–120 × 2.4–3 ($\bar{x}$ = 93.5 × 2.8 μm, n = 25), filiform, straight or curved toward the apex, containing numerous refringent septum-like bands, hyaline, with bell-shaped mucilage at the base. Asexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 5.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, slightly raised, dull, felted, medium dense, no sporulation, surface pale orange, reverse pale yellow.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Cyrtostachys renda*, 4 August 2023, O. Karimi, 19W (MFLU 24-0513); living culture MFLUCC 24-0598.

Known hosts – *Nypa fruticans* (Hyde 1988), *Cyrtostachys renda* (This study).

Known distribution – Brunei (Hyde 1988), Papua New Guinea (Hyde 1992), Thailand (Pilantanapak et al. 2005; this study).

GenBank numbers – MFLUCC 24-0598: LSU = PV271937, *tef*= PV340503.

Notes – Phylogenetically, our strain (MFLUCC 24-0598) clustered with *Linocarpon appendiculatum* with 100% ML and 1.00 PP statistical support. Morphologically, it resembles *Li. appendiculatum* (IMI 326619) with almost similar-sized ascomata, paraphyses, asci and ascospores. Thus, we identified our strain (MFLU24-0513) as *Li. appendiculatum* based on phylogenetic analyses and morphological characters. We report our strain (MFLU24-0513) as a new host record of *Li. appendiculatum* on *Cyrtostachys renda* from the peat swamp forest in Thailand.

Linocarpon narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.54

Index Fungorum number: IF903551; Facesoffungi number: FoF 17541

Etymology – The epithet “narathiwatense” refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0514

Saprobic on the submerged petiole of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 250–350 μm × 50–80 μm ($\bar{x}$ = 300 × 73 μm, n = 15), aggregated, semi-immersed, black, dome-shaped, raised, lenticular with a central ostiole. *Peridium* 15–20 μm wide ($\bar{x}$ = 17.5 μm, n = 20), outer cells merging with the host epidermal cells, composed of dark brown cells of *textura angularis*. *Paraphyses* up to 85 μm long, 4.5–6 μm wide ($\bar{x}$ = 5 μm, n = 30), straight or flexuous, septate, hypha-like, branded, hyaline. *Asci* 90–120 × 11–14 μm ($\bar{x}$ = 115 × 12.5 μm, n = 20), 8-spored, long-cylindrical, straight or slightly curved, short-pedicellate, with a J- subapical ring. *Ascospores* 80–

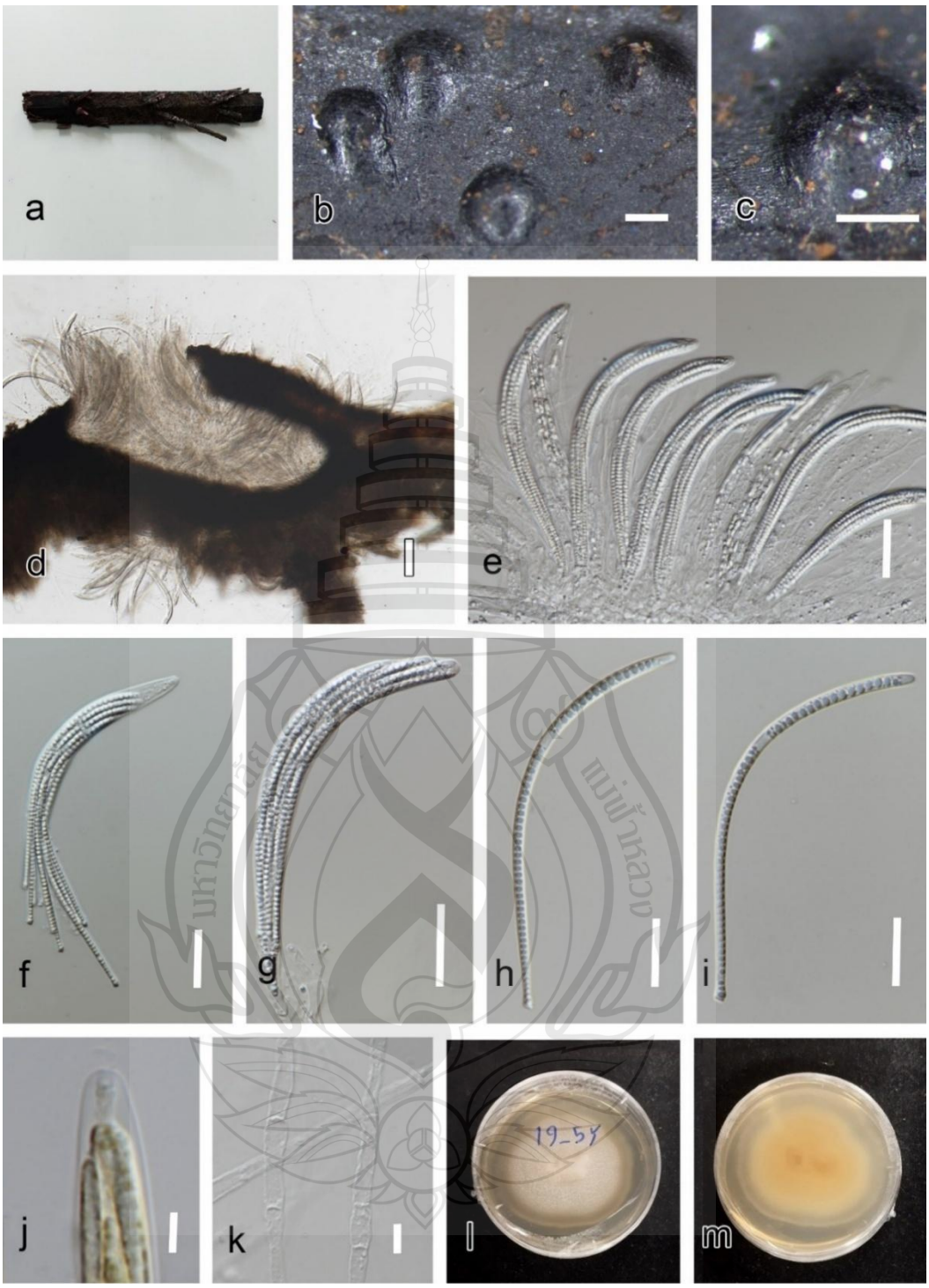
100 × 2–4 μm ($\bar{x}$ = 94.5 × 2.5 μm, n = 25), filiform, straight or slightly curved, without containing refringent septum-like bands, hyaline, apex rounded and base with bell-shape appendage. Asexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 4.5 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, raised, dull, submerged, dense, no sporulation, surface pale orange with a white centre, reverse pale orange.

Material examined – Thailand, Narathiwat, peat swamp forest, the submerged petiole of *Eleiodoxa conferta*, 24 April 2022, O. Karimi, 22W (MFLU 24-0514, holotype); ex-type living culture MFLUCC 24-0599.

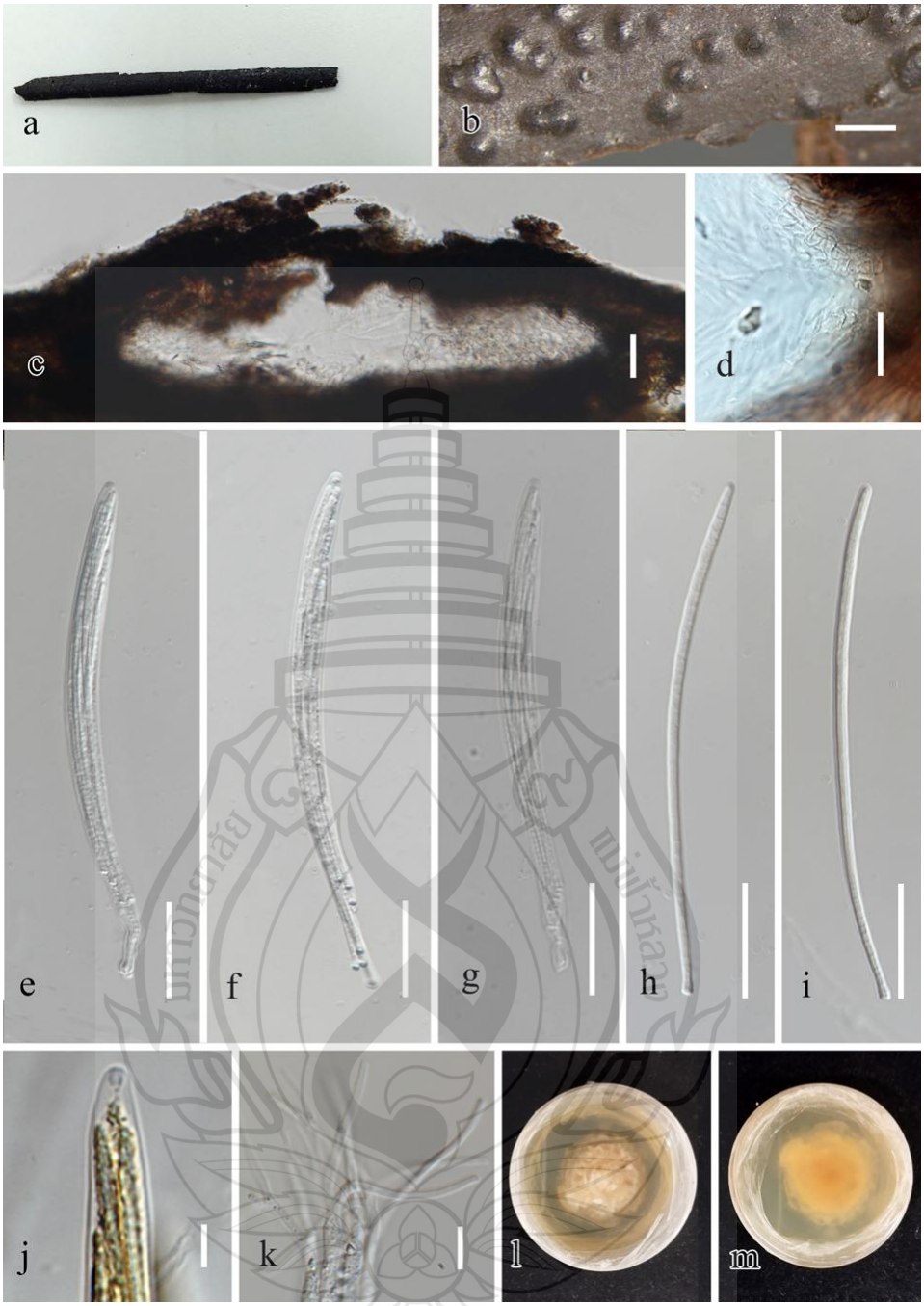
GenBank numbers – MFLUCC 24-0599, ITS = PV271898, LSU = PV271938, *tef-1α* = PV340504.

Notes – Phylogenetically, our strain (MFLUCC 24-0599), grouped with *Linocarpon appendiculatum* strains with 100% ML and 1.00 PP support in the phylogenetic analyses (Figure 3.46), but morphologically it differs from *Li. appendiculatum* (IMI 326619) in having smaller ascomata (250–350 × 50–80 μm vs. 330–510 × 120–180 μm), shorter and branched paraphyses (up to 85 μm vs. longer than asci, 169 μm), shorter and wider asci (90–120 × 11−14 μm vs.110.5–169 × 7.8−9.8 μm), and shorter ascospores (80–100 μm vs. × 72–120 μm). Based on the pairwise comparison of the LSU, *Li. narathiwatense* (MFLUCC 24-0599) differs from *Li. appendiculatum* (ATCC 90499) by 3% (27/900 bp, excluding gaps). However, ITS and *tef-1α* cannot be compared, as they are unavailable for *Li. appendiculatum* (ATCC 90499). Therefore, we introduce *Li. narathiwatense* (MFLU 24-0514) as a novel species based on morphological and phylogenetic evidence.



Note a Host. b, c Colonies on the host substrate. d A vertical section through an ascoma. e–g Asci. h, i Ascospore j The apex of ascus stained in the Melzer's reagent. k Paraphyses. l, m Colony on the PDA. Scale bars: b, c = 250 µm, d = 80 µm, e–g = 35 µm, h, i = 25 µm, j, k = 5 µm.

Figure 3.53 *Linocarpon appendiculatum* (MFLU 24-0513, a new host record)



Note a Host. b Colonies on the host substrate. c A vertical section through an ascoma. d Peridium. e–g Asci. h, i Ascospore j The apex of ascus stained in the Melzer's reagent. k A germinated ascospore. l Paraphyses. m Colony on the PDA. Scale bars: b = 2.5 mm, c = 80 µm, d = 20 µm, e, f, h, i = 20 µm, g = 30 µm, j = 5 µm, k, l = 10 µm.

Figure 3.54 *Linocarpon narathiwatense* (MFLU 24-0514, holotype)

Neolinocarpon K.D. Hyde, Bot. J. Linn. Soc. 110(2): 104 (1992)

Neolinocarpon K.D. Hyde, a saprobic genus in *Sordariomycetes*, belongs to the family *Linocarpaceae* (Konta et al. 2017) and comprises 15 species (Hyde et al. 2024). The asexual morph has not been determined for this genus. In this genus, ascomata are solitary, deeply immersed, and developing beneath a slightly raised or flattened clypeus. They have ostiole with periphyses and a pale yellowish mass. Asci are long, cylindrical, unitunicate and 8-spored with a rounded apex, and some have a refractive apical ring. Ascospores are hyaline and filiform with refringent bands and with or without apical appendages (Hyde 1992; Hyde et al. 1998; Vitoria et al. 2013; Konta et al. 2017). *Neolinocarpon* was introduced by Hyde (1992) to accommodate a linocarpon-like species and is typified by *N. globosicarpum* K.D. Hyde. *Neolinocarpon* and *Linocarpon* are similar, but *Neolinocarpon* differs in having deeply immersed ascomata forming below a slightly raised or flattened clypeus and the presence of a refractive globose body below the ascus apical ring (Hyde 1992). *Neolinocarpon* was introduced in *Xylariaceae* based on morphological characters (Hyde 1992). Hyde (1997) transferred it to *Hyponectriaceae* in a subsequent study but was excluded later by Wang and Hyde (1999) based on the morphology of the apical ring. Kirk et al. (2001) and Eriksson (2006) placed *Neolinocarpon* in *Sordariomycetes* genera *incertae sedis*. Bahl (2006) showed that *Neolinocarpon* was not monophyletic and transferred it to *Xylariales* and *Chaetosphaeriales* according to phylogenetic analysis of LSU and *rpb2* DNA sequence data. According to morphology, *Neolinocarpon* cannot be definitively placed in any family in *Xylariales*, and therefore, it was established as *Xylariales* genera *incertae sedis* by Jones et al. (2009). Maharachchikumbura et al. (2015, 2016) did not accept this placement. Konta et al. (2017) placed *Neolinocarpon* in *Linocarpaceae* (*Chaetosphaeriales*) based on phylogenetic analysis, which was further confirmed by Wijayawardene et al. (2021). *Neolinocarpon arengae* S. Konta & K.D. Hyde (2017), *N. rachidis* S. Konta & K.D. Hyde (2017) and *N. phayaoense* Senwanna & K.D. Hyde (2018) were analyzed with combined LSU and ITS sequence data and morphological data.

Neolinocarpon species differ in dimension of ascomata, asci and ascospores, shape of ascomata and lack mucilaginous appendages on ascospores. *Neolinocarpon* was first reported from decaying fronds of *Nypa fruticans* in Brunei subsequently

collected from Australia, Brazil, China, Indonesia, Malaysia, Singapore and Thailand (Hyde 1992; Hyde et al. 1998; Hyde and Alias 1999; Lu et al. 2000; Bahl et al. 2006; Bhilabutra et al. 2006; Vitoria et al. 2013; Jasrotia et al. 2014; Konta et al. 2017; Senwanna et al. 2018). Most *Neolinocarpon* species have been collected on palms. *N. penniseti* and *N. phayaoense*, which were identified from different host families, *Poaceae* and *Euphorbiaceae*, respectively (Hyde 1992; Hyde et al. 1998; Hyde and Alias 1999; Lu et al. 2000; Bahl et al. 2006; Bhilabutra et al. 2006; Vitoria et al. 2013; Jasrotia et al. 2014; Konta et al. 2017; Senwanna et al. 2018).

Table 3.5 World distribution of *Neolinocarpon* species

Species	Host/Substrate	Location	Reference
N. arengae	dead leaflet of *Arenga pinnata* (Arecaceae)	Thailand	(Konta et al. 2017)
N. attaleae	dead rachis of *Attalea funifera* (Arecaceae)	Brazil	(Vitoria et al. 2013)
N. australiense	dead rattan of *Calamus moti*, (Arecaceae)	Australia	(Hyde et al. 1998)
N. calami	dead petiole of *Calamus conirostris* (Arecaceae)	Brunei	(Hyde et al. 1998)
N. enshiense	dead petiole of *Trachycarpus fortunei* (Arecaceae),	China, southwest Hubei, Enshi	(Hyde et al. 1998)
N. eutypoides	*Acrocomia sclerocarpa, Archontophoenix alexandrae, Calamus conirostris, Cocos nucifera, Plectocomia elongata* (Arecaceae) *Livistona chinensis,*	Australia, Brunei Darussalam, Hong Kong, Indonesia, Malaysia	(Hyde et al. 1998)

Table 3.5 (continued)

Species	Host/Substrate	Location	Reference
N. eutypoides	*Daemonorops margaritae, Licuala* spp., *Livistona chinensis, Plectocomia elongata* (Arecaceae)		
N. globosicarpum	decaying intertidal fronds of *Nypa fruticans* (Arecaceae)	from Brunei	(Hyde 1992)
N. inconspicuum	dead rachis of *Archontophoenix alexandrae* (Arecaceae)	Australia, Queensland	(Hyde et al. 1998)
N. nonappendiculatum	dead petiole of *Archontophoenix alexandrae* (Arecaceae),	Australia, Queensland	(Hyde et al. 1998)
N. nypicola	dead aerial rachids of *Nypa fruticans* (Arecaceae)	Malaysia	(Hyde and Alias 1999)
N. rachidis	dead rachis of *Arenga pinnata* (Arecaceae)	Thailand	(Konta et al. 2017)
N. penniseti	dead stem of *Pennisetum purpureum*	Hong Kong	(Bhilabutra et al. 2006)
N. phayaoense	*Hevea brasiliensis*	Thailand	(Senwanna et al. 2018)

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

Phyllachoraceae Theiss. & P. Syd., Annales Mycologici 13 (3-4): 168 (1915)

Ophiodothella Henn., Hedwigia 43: 258 (1904)

Ophiodothella, belonging to the family *Phyllachoraceae* (*Phyllachorales***,** *Sordariomycetes*), comprises saprobic species that are characterized by perithecial ascomata that form immersed ostiolate perithecia in host tissue, a blackened clypeus surrounding and opposite to the ostiole under the perithecium (Hanlin et al. 1992). The genus has J+, unitunicate asci with hyaline, scolecosporous ascospores (Hanlin et al. 2002). These bi-ostiolate perithecia are unique for *O. casearіae* and *O. vaccinii* (Boyd 1934; Hanlin et al. 2002).

Ophiodothella was described by Höhnel (1910) and typified by *Ophiodothella atromaculans* in *Phyllachoraceae* (Eriksson and Hawksworth 1993) based on the morphological characters. Based on the conidial similarities between *Ophiodothella* and *Xylariales*, a relationship was suggested between these taxa, which was confirmed with molecular analyses (Silva 1996; Glawe and Rogers 1982a, 1982b). There are 30 epithets in the Index Fungorum for this genus (Index Fungorum 2025).

Most species of *Ophiodothella* are leaf parasites, such as *O. angustissima*, causing leaf spot disease on *Vaccinium arboretum* (Hanlin and González 2013). Boyd (1934), who introduced this anamorphic species, described acervulus, hyaline and filiform conidia without assigning it to a particular genus. Hanlin and González (2013) studied *O. angustissima* and synonimized *Septoria angustissima* and *Acerviclypeatus poriformans* under *O. angustissima* based on re-examination of the type specimens and similarity of morphological characters. Three species of *Ophiodothella* were reported from the palm hosts; *O. arengae* found on the rachis of *Arenga engleri* from China (Hsieh et al. 1997), *O. calami* on the leaves of *Calamus pseudotenuis* from India (Hosagoudar 1994) and *O. palmicola* on the leaf rachis of *Palmae* from Ghana (Batista and Peres1960). This genus has also been reported on Anacardiaceae, Annonaceae, Apocynaceae, Asteraceae, Bignoniaceae, Boraginaceae, Ericaceae, Faboideae, Fagaceae, Lythraceae, Moraceae, Myrtaceae, Ochnaceae, Orchidaceae, Platanaceae, Polygonaceae and Salicaceae from Africa, Australia, Brazil, Colombia, Costa Rica, Guatemala, Philippines, United States and Venezuela.

Table 3.6 World distribution of *Ophiodothella* species

Species	Host	Location	Reference
Ophiodothella arengae	rachis of *Arenga engleri*	China	(Hsieh et al. 1997)
O. calami	leaves of *Calamus pseudotenuis*	India	(Hosagoudar 1994)
O. palmicola	leaf rachis of *Palmae*	Ghana	(Batista and Peres 1960)
O. atromaculans	leaves of *Lonchocarpus*	Brazil	(Höhnel 1910)
O. balansae	living leaves of *Bignoniaceae*	Paraguay	(Höhnel 1910)
O. bignoniacearum	*Bignoniaceae*	Brazil	(Chardón et al. 1940)
O. casearíae	leaves of *Casearia tremula*	Venezuela	(Hanlin et al. 2002)
O. cuervoi	living leaves of *Vaccinium caracasanum*	Colombia	(Toro and Chardón 1934)
O. cyclobalanopsidis	leaves of *Cyclobalanopsis*	China	(Hsieh et al. 1998)
O. edax	leaves of *Tephrosia suberosa*	Sri Lanka	(Höhnel 1910)
O. ferruginea	leaves of *Andromeda ferruginea*	USA	(Barr 1978)
O. fici	leaves of *Ficus aurea*	USA	(Bessey 1919)
O. floridana	–	USA	(Chardón 1929)
O. galophila	living leaves of *Ficus jimenezii*	Costa Rica	(Sydow 1925)
O. ingae	leaves of *Inga*	Brazil	(Theissen and Sydow 1915)
O. lagerstroemiae	leaves of *Lagerstroemia microcarpa*	India	(Hosagoudar and Nair 1985)
O. leptospora	living leaves	Brazil	(Spegazzini 1889)

Table 3.6 (continued)

Species	Host	Location	Reference
O. leucospila	leaves of *Platanus occidentalis*	United States	(Miller and Thompson 1940)
O. liebenbergii	leaves of *Ochna pulchra*	South Africa	(Doidge 1942)
O. longispora	leaves of *Eucalyptus goniocalyx*	Australia	(Swart 1982)
O. neurophila	leaves of *Streptocaulon baumii*	Philippines	(Petrak and Sydow 1931)
O. orchidearum	*Laelia superbiens*	Guatemala	(Cash and Watson 1955)
O. panamensis	leaves of *Cordia heterophylla*	Panama	(Stevens 1927)
O. paraguariensis	living leaves of *Annonaceae*	Paraguay	(Spegazzini 1885)
O. ruprechtiae	*Ruprechtia laxiflora*	Argentina	(Catania et al. 2019)
O. sydowii	Cavendishia	Ecuador	(Petrak 1948)
O. syzygii	leaf of *Syzygium suborbiculare*	Australia	(Pearce and Hyde 1993)
O. tithoniae	living leaves of *Tithonia rotundifolia*	Venezuela	(Chardón and Toro 1934)
O. trichocarpa	leaves of *Dracontomelon cumingianum*	Philippines	(Sydow 1925)
O. ulei	leaves of *Leguminosae*	Brazil	(Höhnel 1910)

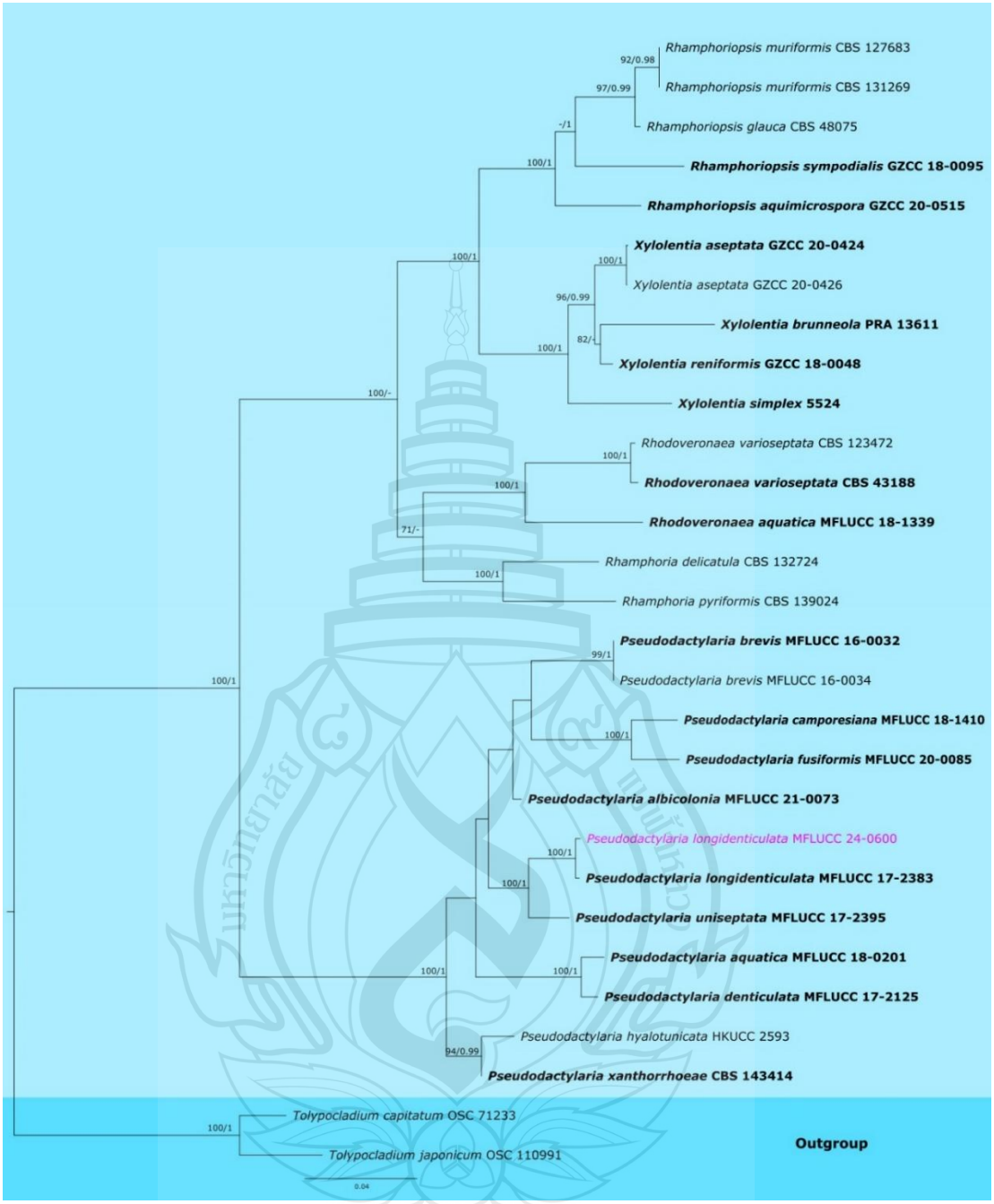
Pseudodactylariales Crous, Persoonia 39: 421 (2017)

Pseudodactylariaceae Crous, Persoonia 39: 421 (2017)

Crous et al. (2017) introduced *Pseudodactylariaceae* to accommodate a single genus, *Pseudodactylaria* (*Ps.*), based on the morphology and an LSU phylogenetic tree within *Pseudodactylariales*. Their phylogenetic analysis showed that *Vermiculariopsiellaceae* from *Vermiculariopsiellales* and *Chaetosphaeriaceae* from *Chaetosphaeriales* were the closest clades to this family. Currently, there is only one genus, *Pseudodactylaria*, with 20 accepted species in *Pseudodactylariaceae* (Crous et al. 2017; Hyde et al. 2024). The family is characterised by hyaline, smooth, branched, septate hyphae, erect, hyaline, smooth, subcylindrical, straight to flexuous, unbranched, thick-walled, septate conidiophores and terminal, integrated, subcylindrical conidiogenous cells with apical taper. The apical part forms a rachis with numerous aggregated cylindrical denticles, and the scars are cicatrized, not thickened or darkened. Conidia are solitary or aggregated in slimy masses, fusoid-ellipsoid, hyaline, smooth, surrounded by a thin mucilaginous sheath, guttulate, and 1-septate at the middle. An updated phylogeny for the family and related genera is shown in Figure 3.56.

Pseudodactylaria Crous, Persoonia 39: 421 (2017)

Crous et al. (2017) established the genus *Pseudodactylaria* to accommodate *Ps. xanthorrhoeae*, the type species, and *Ps. hyalotunicata*. The type species was found on *Xanthorrhoea* sp. (*Asphodelaceae*) in Nullica State Forest, New South Wales, Australia (Crous et al. 2017). Currently, there are 10 accepted species of *Pseudodactylaria* listed in Species Fungorum (2024). *Pseudodactylaria* species have been reported on submerged decaying wood and twigs in freshwater habitats from China and Thailand (Tsui et al. 1997; Crous et al. 2017; Lin et al. 2018; Hyde et al. 2020b; Lu et al. 2020; Bao et al. 2021b; Boonmee et al. 2021), as well as in terrestrial habitats on *Xanthorrhoea* sp. (*Asphodelaceae*) from Australia (Crous et al. 2017). To date, no species of this genus have been reported from peat swamp forests. In this study, we found *Ps. longidenticulata* on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.



Note *Tolypocladium capitatum* (OSC 71233) and *Tolypocladium japonicum* (OSC 110991) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.55 Phylogram generated from the ML analysis based on the combined LSU, ITS, SSU, *tef-1α* and *rpb2* sequence data of *Pseudodactylariaceae*

Pseudodactylaria longidenticulata Jing Yang, E.B.G. Jones & K.D. Hyde, Fungal Diversity 119: 166 (2023) Figure 3.57

Index Fungorum number: IF 559823; Facesoffungi number: FoF 12834

Saprobic on the submerged petiole of *Eleiodoxa conferta*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host effuse, scattered or in small groups, yellowish white with glistening conidial masses at the apex. *Mycelium* immersed to superficial, composed of branched, pale brown, smooth hyphae. *Conidiophores* 150–173 × 3–5 ($\overline{x}$ = 160 × 4 μm, n = 10), macronematous, mononematous, erect, straight or slightly flexuous, cylindrical, smooth-walled, septate, unbranched, dark brown, paler to hyaline towards the apex, thick-walled. *Conidiogenous cells* 53–65 × 4–5 ($\overline{x}$ = 60 × 4.7 μm, n = 15), polyblastic, discrete, terminal, cylindrical, denticulate, hyaline. *Conidia* 25–34 × 3–5.3 μm ($\overline{x}$ = 30 × 4.3 μm, n = 25), fusiform, hyaline, uniseptate, smooth-walled, thin-walled, mostly with a hyaline sheath 2.7–8 μm wide, and polar hairy appendages at one or both ends up to 25 μm long.

Culture characteristics – Colonies on the PDA reaching 2 cm diam. after 14 days at room temperature (25–28 °C). Colony lobate to irregular, dense, raised, uneven surface, mycelia superficial to immersed, dull, surface brown, reverse dark brown to black.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged petiole of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 7Y (MFLU 24-0515); living culture MFLUCC 24-0600.

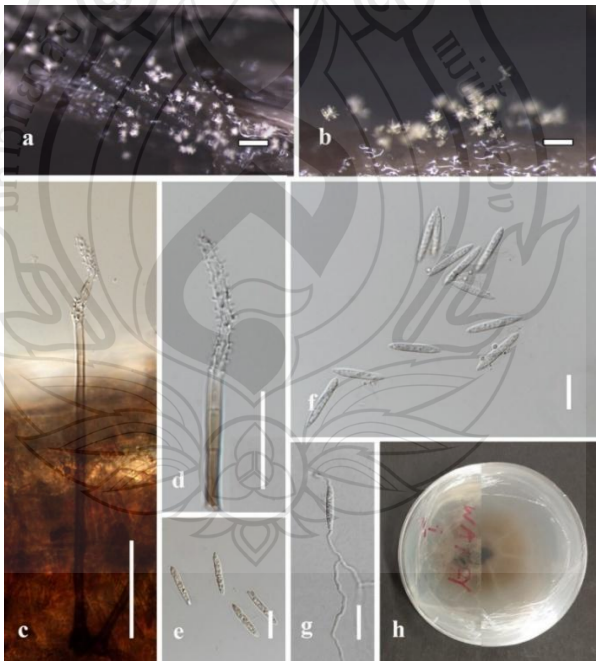
Known host – *Eleiodoxa conferta* (This study).

Known distribution – Thailand (Yang et al. 2023; this study).

GenBank numbers – MFLUCC 24-0600: ITS = PV271899, LSU = PV271940, SSU = PV263321, *tef-1α* = PV340505.

Notes – In the multigene phylogeny of the combined LSU, ITS, SSU, *tef-1α* and *rpb2* sequence data, our strain (MFLUCC 24-0600) clustered with *Pseudodactylaria longidenticulata* (MFLUCC17-2383), with 100% ML and 1.00 PP statistical support (Figure 3.56). Morphologically, our strain (MFLU 24-0515) is similar to *Ps. longidenticulata* and *Ps. uniseptata* (MFLU 22-0072), in having macronematous, mononematous, dark brown, paler to hyaline towards the apex conidiophores, and

polyblastic, terminal, cylindrical, denticulate, hyaline conidiogenous cells, hyaline, uniseptate conidia. However, it differs from *Ps. longidenticulata* (MFLU 22-0075), in having longer conidiophores (150–173 × 3−5 vs. (55–)80–130(–175) × 3–5 µm), shorter conidiogenous cells (53–65 × 4−5 vs. 20–145 × 2.5–5), longer conidia (25–34 × 3−5.3 µm vs. 18–27×3–4.5), and differs from *Ps. uniseptata* (MFLU 22-0072), in having shorter conidiophores (150–163 vs. 90–185 × 3–5 µm), longer conidiogenous cells (53–65 × 4−5 vs. 27–50×2.5–4) and longer conidia (25–34 × 3−5.3 µm vs. 19–25×2.5–4). Based on a pairwise comparison of ITS and LSU nucleotides, our strain differs from *Ps. longidenticulata* (MFLUCC17-2383) by 0.5% (3/520 bp, without including gaps) for ITS, 0.2% (2/900 bp, without including gaps) for LSU. Therefore, we identified our strain (MFLU 24-0515) as *Ps. longidenticulata* based on phylogenetic analyses and morphological characters. We report our strain as a new host record of *Ps. longidenticulata* on *Eleiodoxa conferta* from the peat swamp forest in Thailand. Additionally, we document *Ps. longidenticulata* as a new habitat record from the peat swamp forest.



Note a, b Colonies on the host substrate. c, d Conidiophores and conidiogenous cells. e, f Conidia. g A germinated conidium. h Colonies on the PDA. Scale bars: a, b = 100 µm, c = 50 µm, d = 30 µm, e = 15 µm, f, g = 15 µm.

Figure 3.56 *Pseudodactylaria longidenticulata* (MFLU 24-0515, a new host and habitat record)

Subclass *Xylariomycetidae* O.E. Erikss & Winka

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

Oxydothidaceae Konta & K.D. Hyde

Oxydothis Penz. & Sacc., Malpighia 11(11-12): 505 (1897)

Oxydothis, belonging to the *Oxydothidaceae* (*Sordariomycetes, Ascomycota*), comprises 79 species (Index Fungorum 2024). The taxa include generally tropical saprobes on monocotyledons, and rarely associated with leaf spots such as palms, bamboo and *Pandanus* (Hyde 1993a, 1993b; Wang and Hyde 1999; Wong and Hyde 2001; Fröhlich and Hyde 2000; Taylor and Hyde 2003; Shenoy et al. 2005; Hidayat et al. 2006; Tibpromma et al. 2018) and has also been found as pathogens on palms (Fröhlich and Hyde 1994) and endophytes on palms and *Pandanus* (Hyde 1994b). The characteristic feature of this genus is two types of ascomata; Type 1 with common, cylindrical ascomata, occurring as solitary or in clusters in darkened, ellipsoidal, raised areas on the host surface with distinctive eccentric ostioles that curve upward and pierce the host tissue; and Type 2 with pyriform ascomata that develop under a raised sheet of host epidermis, usually not darkened with eccentric ostioles that pierce the host epidermis through the edge cracks (Fröhlich and Hyde 2000). In addition, species having ascomata with central ostioles are also known, such as *O. asymmetrica* J. Fröhl. & K.D. Hyde (Fröhlich and Hyde 2000). Asci are long cylindrical with a round or truncated apex, usually with a J+, subapical ring. Ascospores are fusiform, 1-septate with a central, non-constricted septum and hyaline but are sometimes yellow in mass (Hyde 1993c; 1994a). The morphology of asci, ascal ring and ascospore apices and sizes are important characters for species identification (Hyde 1994a). *Oxydothis* species have not formed anamorph in pure culture, except *O. selenosporellae* which is the only species that formed a *Selenosporella* anamorph (Samuels and Rossman 1987). *Oxydothis* was introduced by Penzig and Saccardo (1897) with the type species *O. grisea* and two more species, *O. nigricans* and *O. maculosa* and placed in the family *Amphisphaeriaceae* (sensu Eriksson and Hawksworth 1991). Hyde (1993c) reviewed the genus and proposed that *Oxydothis* should be transferred from *Amphisphaeriaceae* to the *Hyponectriaceae* based on ascus, ascospore and peridium morphologies. He also emphasized the consistency of ascus and ascospore morphology that is important for identifying species and compared it with the closely related genera *Ceriospora*,

Frondispora, *Lasiobertia* and *Leiosphaerella* (Hyde 1993c). Kang et al. (1999) transferred the genus to *Clypeosphaeriaceae* but Jeewon et al. (2003) suggested that it was related to *Leiosphaerella* (*Xylariales*, genera *incertae sedis*) based on DNA sequence data. Konta et al. (2016) transferred *Oxydothis* to *Oxydothidaceae* (*Xylariales*) which was accepted by Hyde et al. (2020) and Wijayawardene et al (2022).

Most *Oxydothis* species were found on palms, except *O. pandani*, *O. bambusicola* and *O. miscanthicola*. However, this genus members are mainly saprobes, Hyde (1994b) discussed that they may be endophytes on leaves or petioles of palms or leaves of *Pandanus*. Rodrigues (1994) reported *O. poliothea* as a rare endophyte on *Euterpes oleracea* (Arecaceae) and Taylor and Hyde (2003) introduced *O. ianei* as a common endophyte. *Oxydothis parasitica* has been reported as the only record of a pathogen in *Oxydothis*, which collected on *Licuala ramsayi* (Arecaceae) leaf spots from Australia (Fröhlich and Hyde 1994). *Oxydothis* is generally reported from tropical and subtropical regions, such as Australia, Brazil, Brunei, China, Congo, Ecuador, French Polynesia, Hong Kong, Indonesia, Papua New Guinea, Peninsular Malaysia, Philippines, Sierra Leone, Thailand and Venezuela (Konta et al. 2016).

Table 3.7 World distribution of *Oxydothis* species

Species	Host/Substrate	Location	Reference
Oxydothis acutata	On dead leaves of Orania	Philippines	(Hyde 1994)
O. aequalis	On culms of *Bambusoideae*	Philippines	(Sydow and Sydow 1917)
O. alexandrarum	On rotten rachis of *Archontophoenix alexandrae*	Queensland	(Hyde 1993)
O. angustispora	On dead petiole of Licuala ramsayi	Queensland	(Fröhlich and Hyde 2000)
O. asiatica	On dead rattan of *Calamus flabellatus*	Brunei	(Fröhlich and Hyde 2000)
O. asymmetrica	On dead petiole of *Calamus conirostris*	Brunei	(Fröhlich and Hyde 2000)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. australiensis	In forest litter on rachis of *Archontophoenix*	Queensland	(Hyde 1993)
O. atypica	In peat swamp on dead leaves of Licuala longicalycata	Thailand	(Liu et al. 2015)
O. bambusicola	On senescent culms of *Indocalamus*	Hong Kong	(Shenoy et al. 2005)
O. batuapoiensis	On dead petiole and rachis of *Daemonorops oxycarpa*	Brunei	(Shenoy et al. 2005)
O. belalongensis	On dead petiole of *Licuala* sp.	Brunei	(Fröhlich and Hyde 2000)
O. bruneiensis	On dead petiole of *Licuala* sp.	Brunei	(Fröhlich and Hyde 2000)
O. calami	On trunk of *Calamus* sp.	Philippines	(Sydow and Sydow 1917)
O. calamicola	On rachis of *Calamus*	Thailand	(Konta et al. 2016)
O. cyrtospora	On dead petiole of *Licuala ramsayi*	Queensland	(Fröhlich and Hyde 2000)
O. cyrtostachicola	On petiole of fronds of *Cyrtostachys renda*	Thailand	(Hidayat 2006)
O. daemonoropis	On dead *Daemonorops gaudichaudii*	Philippines	(Sydow and Sydow 1917)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. daemonoropsicola	On dead rachis of *Daemonorops margaritae*	Hong Kong	(Fröhlich and Hyde 2000)
O. dispariapicis	On dead petiole of *Daemonorops oxycarpa*	Brunei	(Fröhlich and Hyde 2000)
O. elaeidicola	On dead *Elaeis guineensis*	Sierra Leone	(Petrak and Deighton 1952)
O. elaeidis	On leaves of Elaeis	Congo	(Sivanesan 1970)
O. elaeidicola	On dead *Elaeis guineensis*	Sierra Leone	(Petrak and Deighton 1952)
O. extensa	On dead petiole of *Licuala ramsayi*	Queensland	(Fröhlich and Hyde 2000)
O. froehlichiae	On leaves of *Calamus radicalis*	Queensland	(Hyde 1994)
O. frondicola	On palm frond	Queensland	(Hyde 1993)
O. garethjonesii	On petiole of Elaeis	Thailand	(Konta et al. 2016)
O. gigantea	n dead petiole of Palmae:	Irian Jay	(Hyde 1994)
O. grisea	On culms	Java	(Penzig and Saccardo 1898)
O. hoehnelii	On dead petioles of Arenga	Philippines	(Hyde 1994)
O. hongkongensis	On dead petiole of *Daemonorops margaritae*	Hong Kong	(Fröhlich and Hyde 2000)
O. ianei	On dead petiole of Trachycarpus fortunei	Hubei	(Taylor and Hyde 2003)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. inaequalis	On decaying rachis of fronds of *Wallichia siamensis*	Thailand	(Hidayat et al. 2006)
O. insignis	On leaves of Eugenia	São Paulo	(Spegazzini 1908)
O. licualae	On dead petioles of *Licuala spinosa*	Philippines	(Hyde 1993)
O. licualicola	On dead petiole of Licuala	Brunei	(Fröhlich and Hyde 2000)
O. linospadicis	On *Linospadix microcarya*	Queensland	(Fröhlich and Hyde 1994)
O. livistonae	On petioles of Livistona	Philippines	(Sydow and Sydow 1917)
O. livistonica	Livistona subglobosa	Japan	(Hyde 1994)
O. livistonicola	On Livistona	Philippines	(Hyde 1994)
O. luteaspora	On rachis of Calamus	Queensland	(Hyde 1993)
O. magnicolla	On dead petiole of Calamus conirostris	Brunei	(Fröhlich and Hyde 2000)
O. manokwariensis	In freshwater swamp on Palmae	Irian Jaya	(Hyde 1994)
O. maquilingiana	On dead petiole of Daemonorops sp.	Philippines	(Hyde 1994)
O. mauritiae	On dead petiole of Mauritia flexuosa	Ecuador	(Fröhlich and Hyde 2000)
O. megalospora	On dead petiole of *Calamus*	Brunei	(Fröhlich and Hyde 2000)
O. metroxyli	On petiole of Metroxylon sagu	Thailand	(Konta et al. 2016)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. metroxylicola	On petiole of Metroxylon sagu	Thailand	(Konta et al. 2016)
O. miscanthicola	On standing senescent leaf sheath of *Miscanthus floridulus*	Hong Kong	(Wong and Hyde 2001)
O. nigra	On petioles of Licuala	Peninsular Malaysia	(Hyde 1994)
O. nonamyloidea	On petiole of Livistona	Sulawesi	(Hyde 1994)
O. nonspecifica	On dead petiole of *Calamus pogonacanthus*	Brunei	(Fröhlich and Hyde 2000)
O. nontincta	On dead petiole of Licuala: Brunei	Brunei	(Fröhlich and Hyde 2000)
O. nypae	On rotten fronds of Nypa fruticans	Brunei	(Hyde and Nakagiri 1989)
O. nypicola	On rotten petiole of Nypa fruticans	Brunei	(Hyde 1994)
O. obducens	On leaves of *Linospadix microcarya*	Queensland	(Hyde 1994)
O. oedema	Cocos nucifera	Pupa New Guinea	(Hyde 1994)
O. opaca	Rhopalostylis sapida	New Zeland	(Hyde 1994)
O. oraniopsidis	On fronds of Oraniopsis appendiculata	Queensland	(Fröhlich and Hyde 1994)
O. palmicola	On dead leaves of *Elaeis guineensis*	Thailand	(Konta et al. 2016)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. parvula	On wilting leaves of *Pandanus tectorius*	France, Tubuai	(Huguenin 1964)
O. pandani	On dead leaves of *Pandanus*	Philippines	(Petrak 1952)
O. pandanicola	On leaf of *Licuala ramsayi*	Queensland	(Fröhlich and Hyde 1994)
O. parasitica	On dead petioles of *Orania*	Philippines	(Petrak and Deighton 1952)
O. perangusta	On dead petiole of *Licuala*	Brunei	(Fröhlich and Hyde 2000)
O. pertusarioides	On branches	São Paulo	(Rehm 1907)
O. phoenicis	On rachis of *Phoenix paludosa*	Thailand	(Hyde et al. 2020)
O. poliothea	On stems of Palmae	Venezuela	(Sydow 1930)
O. pusillispora	On dead frond of Licuala	Brunei	(Fröhlich and Hyde 2000)
O. ragae	In freshwater swamp on rotten petiole of Palmae	Irian Jaya	(Hyde 1994)
O. rattanica	On dead rachis of *Daemonorops margaritae*	Hong Kong	(Fröhlich and Hyde 2000)
O. rattanicola	On dead stem of Calamus tetradactylus	Hong Kong	(Fröhlich and Hyde 2000)
O. rhapidicola	On petiole of Rhapis excelsa: Thailand	−	(Konta et al. 2016)
O. rhopalostylidis	On leaf midrib of Rhopalostylis sapida	New Zealand	(Samuels and Rossmann 1987)

Table 3.7 (continued)

Species	Host/Substrate	Location	Reference
O. rimicolla	On dead rattan of *Calamus pogonacanthus*	Brunei	(Fröhlich and Hyde 2000)
O. rubella	On trunk of dead Calamus	Queensland	(Hyde 1993)
O. sabalensis	On Sabal (palm))	Georgia, USA	(Petrak 1952)
O. saltuensis	On dead terrestrial frond of Livistona	Papua New Guinea	(Hyde 1994)
O. selenosporellae	On leaf midrib of Rhopalostylis sapida	New Zealand	(Samuels and Rossmann 1987)
O. tayabensis	On dead stems of Calamus	Philippines	(Trotter 1928)
O. uniseriata	On dead rattan of Calamus radicalis	Queensland	(Fröhlich and Hyde 2000)
O. wallichianensis	On decaying fronds of Wallichia siamensis	Thailand	(Hidayat et al. 2006)

Oxydothis narathiwatensis O. Karimi & K.D. Hyde, sp. nov. Figure 3.58

Index Fungorum: IF902133; Facesoffungi Number: FoF16036

Etymology – The epithet "*narathiwatensis*" refers to Narathiwat Province, where the holotype was collected

Holotype – MFLU 24-0044

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Sexual morph: *Ascomata* 170–320 μm diam., ($\bar{x}$ = 250 μm diam., n = 15), mostly in small groups, immersed, erumpent, with the non-blistering area on the host, subglobose or pyriform. *Peridium* 17–30 μm ($\bar{x}$ = 22 μm, n = 10), thick, dark brown to black, *textura angularis*. *Paraphyses* 40–80 × 3–6 μm ($\bar{x}$ = 62 × 4 μm, n = 20), cylindrical, fragmented, hyaline, branched or non-branched. *Asci* 171–257 × 7–11 μm ($\bar{x}$ = 225 × 9 μm, n = 20), 8-spored,

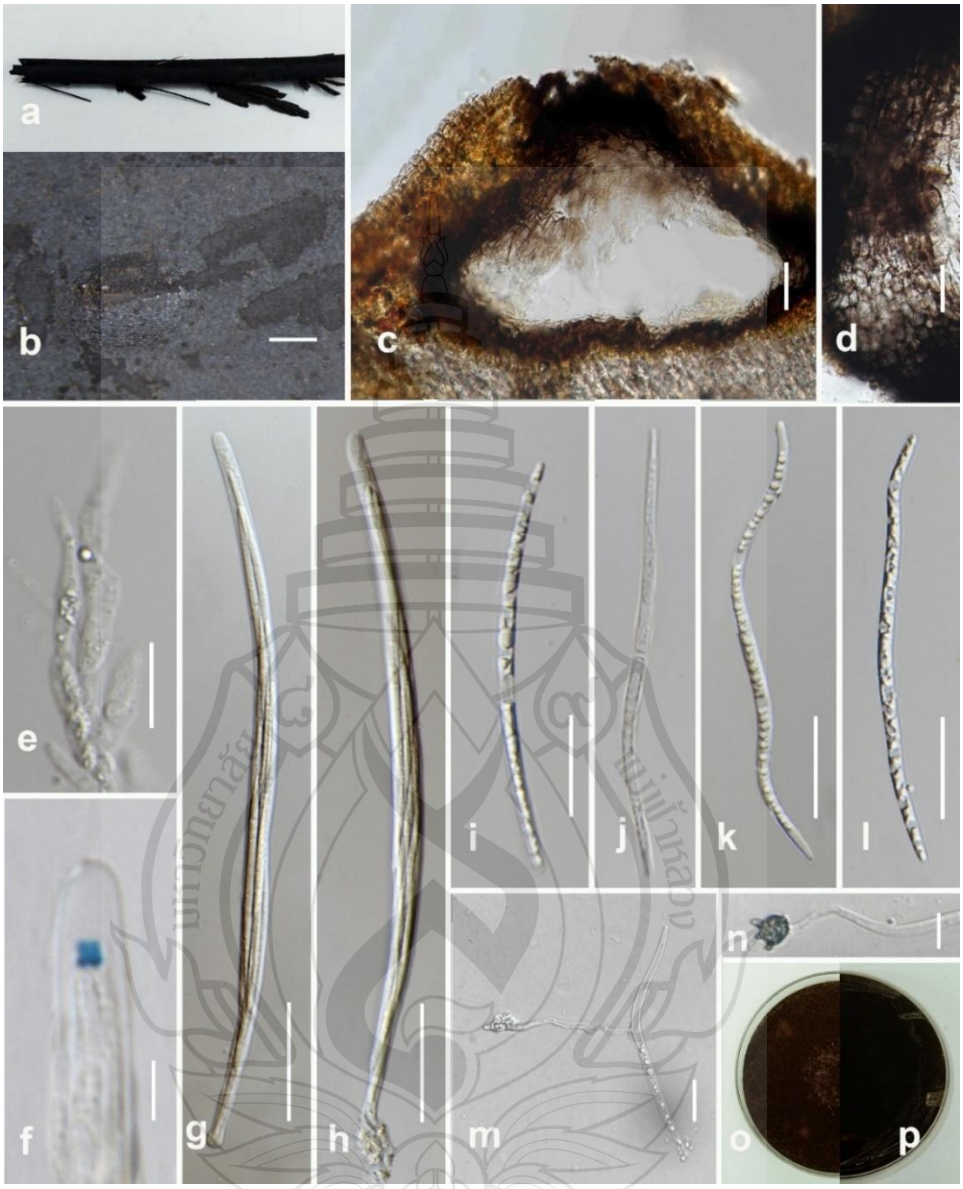
cylindrical, unitunicate, short pedicellate, smooth-walled, with a J+, wedge-shaped, subapical ring. *Ascospores* 95–121 × 3–5 µm ($\overline{x}$ = 110 × 4 µm, n = 20), 2–3-seriate, hyaline, filiform, straight, curved or flexuous, rounded ends, centrally uniseptate, guttulate with smooth walls. *Appressoria* 10–20 × 9–10 µm ($\overline{x}$ = 13 × 9.5 µm, n = 10), irregular, hyaline to green, thick-walled, verrucose. Asexual morph: Undetermined.

Culture characters – Colonies on PDA, reaching 55 mm in diameter after 30 days at 25–27 °C, under dark conditions, medium dense, mycelium superficial to immersed, circular, flat, raised in the center with aerial mycelium, dull surface, entire edge, velvety, without pigment diffusion and sporulation, dark brown on the top and reverse-side black.

Material examined – Thailand, Narathiwat, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta* (Arecaceae), 3 August 2023, O. Karimi, 19-W (MFLU 24-0044, holotype); Ex-type living culture MFLUCC 24-0085.

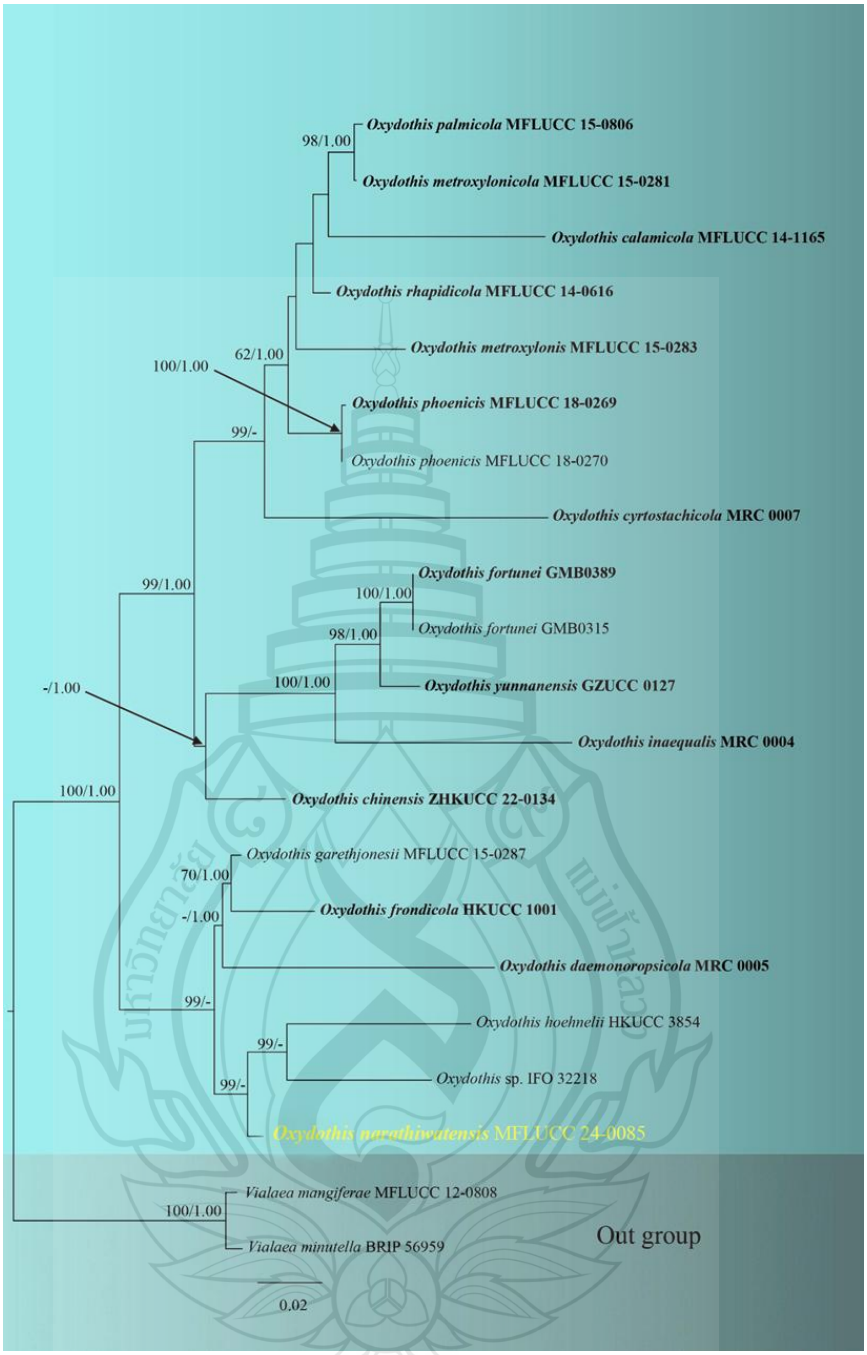
Notes – Morphologically, *Oxydothis narathiwatensis* (MFLU 24-0044) shares similar characteristics with *O. gigantea* (BRIP 21921) and *O. maquilingiana* (3975) in having cylindrical asci with J+, wedge-shaped, subapical ring and filiform ascospores (Hyde 1994b). However, *O. narathiwatensis* (MFLU 24-0044) differs from *O. gigantea* (BRIP 21921) in having longer and narrower asci (171–257 × 7–11 µm vs. 240 × 20 µm), and shorter and narrower ascospore (95–121 × 3–5 µm vs. 100–150 × 6.5–7.5 µm). *Oxydothis narathiwatensis* (MFLU 24-0044) differs from *O. maquilingiana* (3975) in having longer and narrower asci (171–257 × 7–11 µm vs. 140–150 × 12–14 µm), longer and narrower ascospore (95–121 × 3–5 µm vs. 85–95 × 5–6 µm) and longer ascal ring (1.5–5 × 1–3 µm vs. 2.6–3.5 × 1.6–2.4 µm). However, due to the lack of sequence data for *O. gigantea* and *O. maquilingiana*, a phylogenetic comparison with *O. narathiwatensis* was not possible. Phylogenetically, *O. narathiwatensis* (MFLUCC 24-0085) formed a robust subclade (100% ML) basal to *O. hoehnelii* (KDH 1837). Morphologically, *O. narathiwatensis* differs from *O. hoehnelii* in having shorter and narrower asci (171–257 × 7–11 µm vs. 250–290 × 12–14 µm), fusiform ascospores against filiform ascospores in *O. narathiwatensis* (MFLU 24-0044) and longer and narrower ascospores (95– 121 × 3–5 µm vs. 72–86 × 7–10 µm). The result of the pairwise homoplasy index (PHI) test revealed no significant recombination (Φw = 0.4) between *O. narathiwatensis* (MFLUCC 24-0085) and its closely related species (Figure

3.59). Therefore, we introduced *Oxydothis narathiwatensis* (MFLU 24-0044) as a novel species based on morphological evidence and phylogenetic analyses (Figure 3.59).



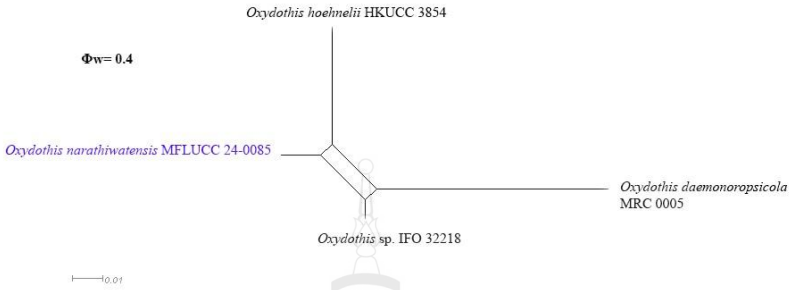
Note a host substrate b close up of ascomata c section of ascoma d peridium e paraphyses f j+ reaction of apical ring in Melzer's reagent g, h asci i–l ascospores m germinating ascospore n appressoria o, p colony on PDA after two weeks. Scale bars: 500 µm (b); 50 µm (c, d, g, h); 20 µm (e, m); 5 µm (f); 25 µm (i–l); 10 µm (n).

Figure 3.57 *Oxydothis narathiwatensis* (MFLU 24-0044, holotype)



Note Maximum likelihood bootstrap support (MLBS) values equal to or higher than 60%, and the Bayesian posterior probability (BYPP) equal to or greater than 0.95 are given near the nodes. The ex-types are in bold. The new sequence is shown in yellow font. The tree is rooted with *Vialaea mangiferae* and *Vialaea minutella*.

Figure 3.58 RAxML tree is based on the analysis of a combined dataset of ITS, LSU, and SSU sequence data of *Oxydothis*



Note The PHI test was constructed using the combined ITS, LSU, and SSU sequence data of closely related taxa. The PHI test (Φw) < 0.05 indicates significant recombination within the dataset. The newly identified taxon is represented in blue.

Figure 3.59 The split diagram resulting from the pairwise homoplasy index (PHI) test

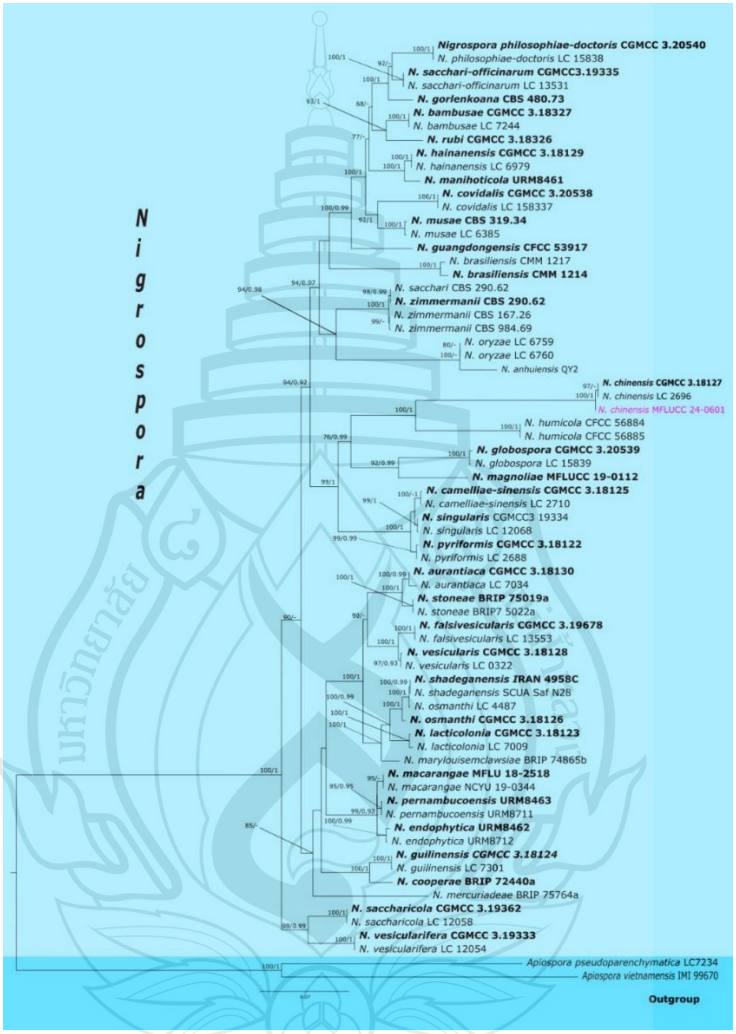
Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, Sydowia 50 (1): 23 (1998)

Hyde et al. (1998) established *Apiosporaceae* to include *Appendicospora*, *Arthrinium* (=*Apiospora*), *Dictyoarthrinium*, *Endocalyx*, and *Spegazzinia*. Currently, the family comprises four accepted genera: *Apiospora* (100 species), *Arthrinium* (30 species), *Dictyoarthrinium* (10 species), and *Nigrospora* (35 species) (Hyde et al. 2024; Tian et al. 2024; Samarakoon et al. 2024). Members of this family reported as saprobes, pathogens, or endophytes, associated with various hosts and habitats (Crous and Groenewald 2013; Hyde et al. 2020).

Nigrospora Zimm., Centralbl. Bakteriol. Parasitenk. 8: 220 (1902)

Nigrospora (*Ni.*), was introduced by Zimmerman (1902) to accommodate its type species, *Ni. panici*, which was reported from dead leaves of *Panicum amphibium*. *Nigrospora* comprises 46 species (Species Fungorum, accessed December 2024) and has been reported as saprobes, endophytes, and pathogens in plants and humans (Liu et al. 2021; Takayama et al. 2024; Zou et al. 2024). The genus is characterised by spherical to subspherical conidiogenous cells and globose to subglobose black conidia (Wang et

al. 2017). Wang et al. (2017) introduced 12 new species based on morphology and phylogeny and placed the genus in *Apiosporaceae* (*Xylariales*). To date, no species of this genus have been reported from peat swamp forests. In this study, we found *Ni. chinensis* on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated phylogeny for the genus is shown in Figure 3.61.



Note *Apiospora vietnamensis* (IMI 99670), and *A. pseudoparenchymatica* (LC7234) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.60 Phylogram generated from the ML analysis based on the combined ITS, *tef-1α* and *tub2* sequence data of *Nigrospora*

Nigrospora chinensis Mei Wang & L. Cai, Persoonia 39: 129 (2017) Figure 3.62

Index Fungorum number: IF820732; Facesoffungi number: FoF 09446

Associated with leaf spots on *Eleiodoxa conferta*. Asexual morph: *Hyphae* 1–3.7 μm ($\overline{x}$ = 2 μm, n = 40) wide, hyaline to brown, septate, branched, smooth, thick wall. *Conidiophores* 16–26 × 2–3.5 μm ($\overline{x}$ = 20 × 2.5 μm, n = 20), micronematous, hyaline to pale brown, smooth, branched, straight or flexuous, frequently reduced to conidiogenous cells. *Conidiogenous cells* 8–11 (–15) × 2–7 μm ($\overline{x}$ = 10 × 4 μm, n = 20), monoblastic, determinate, solitary, ampulliform, sub cylindrical or irregular, hyaline to pale brown. *Conidia* globose or subglobose 7–11.5 μm ($\overline{x}$ = 10 μm, n = 40) diam., to ellipsoidal (11–12.5 × 7–9 μm) ($\overline{x}$ = 11.5 × 8.5 μm, n = 25), solitary, aseptate, smooth, pale brown, dark brown to black. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 5.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, flat, felted, entire edge, surface and reverse white.

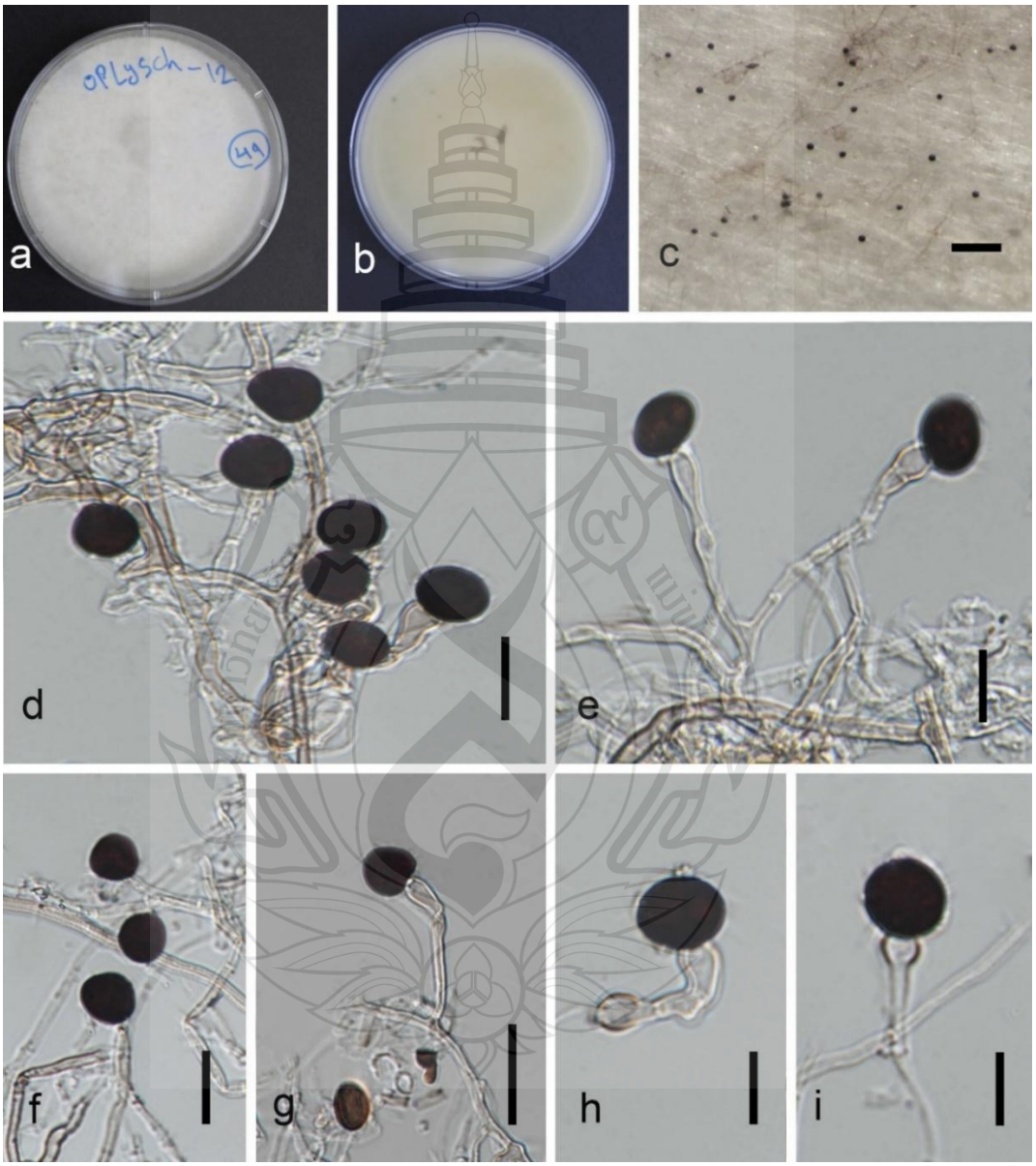
Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, leaf spots on *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 324 (MFLU 24-0516); living culture MFLUCC 24-0601.

Known host – *Aucuba japonica* (Wang et al. 2017), *Camellia oleifera* (Qin et al. 2021), *Camellia sinensis* (Wang et al. 2017), *Castanopsis* sp. (Wang et al. 2017), *Eleiodoxa conferta* (This study), *Ginkgo biloba* (Lee et al. 2019), *Lindera aggregate* (Wang et al. 2017), *Machilus duthiei* (Wang et al. 2017), *Magnolia candolli* (de Silva et al. 2021), *Musa* ×*paradisiaca* (Wang et al. 2017), *Osmanthus* sp. (Wang et al. 2017), *Smilax ocreata* (Wang et al. 2017), Tobacco (*Nicotiana tabacum*) (Zhong et al. 2022).

Known distribution – China (Wang et al. 2017; Qin et al. 2021; Ma et al. 2022; Zhong et al. 2022), Republic of Korea (Lee et al. 2019), Thailand (Ma et al. 2022; This study).

Notes – In the multi-gene phylogeny, our strain clustered with *Nigrospora chinensis* (CGMCC3.18127) with 100% ML and 1.00 PP statistical support. Morphologically, our collection shares similar characteristics with *Ni. chinensis* (CGMCC3.18127) in having hyaline, smooth, branched, septate hyphae, monoblastic, determinate, solitary, ampulliform conidiogenous cells, globose or subglobose,

aseptate, smooth conidia. Therefore, we identified our strain (MFLU24-0516) as *Ni. chinensis* based on morphology and phylogenetic data. We report our strain (MFLU24-0516) as a new host record of *Ni. chinensis* on *Eleiodoxa conferta* from Thailand. Additionally, we document *Ni. chinensis* as a new habitat record from the peat swamp forest.



Note a, b Surface and reverse view of the culture on the PDA. d–i Conidiophores, conidiogenous cells and conidia. Scale bars: c = 50 μm, d, g = 15 μm, e, f, i, h = 10 μm.

Figure 3.61 *Nigrospora chinensis* (MFLU 24-0516, new host and habitat record)

Xylariales Nannf

Xylariales is one of the largest orders in *Ascomycota*, introduced by Nannfeldt (1932), and belongs to the subclass *Xylariomycetidae* and class *Sordariomycetes* (Hyde et al. 2020a). Many *Xylariales* produce conspicuous fruiting bodies (stromata) and are known as "macromycetes" (Helaly et al. 2018). *Xylariales* members are characterized by perithecial stromata, usually dark-colored and thick-walled ascomata with true paraphyses, periphysate and papillate ostioles, eight-spored unitunicate asci, often with amyloid apical rings and apical J+ apparatus and pigmented ascospores (Maharachchikumbura et al. 2016; Hyde et al. 2020a).

Xylariales consists of coprophilous saprobes, pathogens and endophytic fungi. Saprotrophs generally occur on wood and other plant debris. Wood decomposers are important for forest ecosystems (Stadler 2011; Hyde et al. 2020b). Members in *Xylariales* are known as soft-rot fungi, while also grouped as the white-rot fungi because of their ability to degrade lignin (Raju et al. 2022). Some species are important plant pathogens in terrestrial habitats such as *Biscogniauxia* (Nugent 2005), *Dematophora* (Wittstein et al. 2020), *Entoleuca* (Ostry and Anderson 2009), *Hypoxylon* (Stadler 2011) and *Kretzschmaria* (da Luz Morales et al. 2021). Also, some species of *Xylariales* are endophytes, acting as mycobionts (lignicolous) and endolichenic (U'Ren et al. 2016; Oh et al. 2020; Dissanayake et al. 2021). Moreover, some species are typically encountered on dung or related to insect vectors (Stadler 2011; Pažoutová et al. 2013; Wendt et al. 2018).

Some *Xylariales* species, especially endophytes as well as lignicolous and endolichenic, were reported as secondary metabolites producers (Calcott et al. 2018; Oh et al. 2020; Becker and Stadler 2021). These secondary metabolites have shown antibacterial, antifungal, cytotoxic, antimalarial, anti-inflammatory, anti-neuroinflammatory, immunosuppressive and herbicidal activities and are used in medicine and agriculture (Biasetto et al. 2019; Chen et al. 2019; Intaraudom et al. 2019; Wang et al. 2019; Chen et al. 2020a, b; Noppawan et al. 2020; Wittstein et al. 2020; Patjana et al. 2021;). Franco et al. (2022) reported that diverse secondary metabolite gene clusters that may facilitate symbiosis with phylogenetically diverse hosts.

Research showed that secondary metabolite production in these taxa is unique or specific for certain groups, and secondary metabolite profiles were demonstrated as

important species-specific characters and have phylogenetic significance (Stadler 2011). Therefore, metabolite profiles are used as an additional tool to support classical morphology and molecular phylogenetic approaches (Helaly et al. 2018). Polyphasic studies using chemotaxonomic, molecular phylogenetics and morphological data have led to numerous changes in the classification of *Xylariales*.

Presently, *Xylariales* comprises 22 families and over 2,400 species assigned to 194 genera (Wendt et al. 2018; Voglmayr et al. 2019; Hyde et al. 2020a, 2020b; Sun et al. 2021; Hernãndez-Restrepo et al. 2022; Sugita et al. 2022; Wijayawardene et al. 2022). However, the xylariaceous taxa have shown a polyphyletic topology and require further verification (Wendt et al. 2018; Konta et al. 2020).

Nannfeldt (1932) established *Xylariales* in *Sordariomycetes*. Xylariaceous taxa have been recognized to comprise a homogenous evolutionary lineage based on its ascal and ascospore morphology (Rogers 1979), which was later accommodated as the only order in the subclass *Xylariomycetidae*, introduced by Eriksson and Winka (1997). Initially, *Xylariales* was classified mainly based on morphology (Müller et al. 1962; Wehmeyer 1975; Barr 1990). With the adoption of molecular technologies for species identifications, the *Xylariales* classification changed drastically (Eriksson et al. 2003; Smith et al. 2003). Smith et al. (2003) introduced seven families in this order based on LSU and SSU rDNA phylogeny, while Lumbsch and Huhndorf (2010) accepted six families, and Senanayake et al. (2015) resurrected *Amphisphaeriales* in *Xylariomycetidae* using ITS and LSU phylogeny and accepted six families for *Amphisphaeriales* and eleven for *Xylariales*, together with morphological evidence. However, Maharachchikumbura et al. (2016) considered *Amphisphaeriales* as a synonym of *Xylariales* because of the poor phylogenetic support in the LSU, SSU, TEF and RPB2-based phylogeny. Also, they synonymized *Graphostromataceae* with *Xylariaceae* and accepted 22 families for *Xylariales* (Maharachchikumbura et al. 2016). Simultaneously, Jaklitsch et al. (2016) transferred *Requienellaceae* to *Xylariales* based on morphology and ITS and LSU-based phylogeny, which previously was classified in *Melanommatales* in the class *Loculoascomycetes* (Liew et al. 2000). Subsequently, Perera et al. (2017) introduced *Delonicicolales* to accommodate *Delonicicolaceae* in *Xylariomycetidae* as the third order, using morphology and LSU, SSU and RPB2-based

phylogeny. Later, *Clypeophysalosporaceae* was introduced into *Xylariales* based on ITS and LSU data (Giraldo et al. 2017).

Xylariaceae was divided into two major sections (*Xylarioideae* and *Hypoxyloideae* subfamilies), based on their respective asexual morphs, the genera related to *Xylaria* with geniculosporium-like asexual morphs and the genera related to *Hypoxylon* with nodulisporium-like asexual morphs (Daranagama et al. 2015; Maharachchikumbura et al. 2015, 2016; Senanayake et al. 2015). Later, Wendt et al. (2018) introduced *Xylarioideae* and *Hypoxyloideae* subfamilies in separate families. Hyde et al. (2020b) revised the families of *Sordariomycetes* using morphology and multigene analysis (LSU, ITS, RPB2 and TEF1 sequence data) and accepted 15 families. Marasinghe et al. (2019) transferred *Iodosphaeriaceae* from *Amphisphaeriaceae* to the *Xylariales* with *Iodosphaeria* as the type genus. In subsequent studies, several new families were introduced using the morphological data and phylogenetic analysis, such as *Barrmaeliaceae* (Voglmayr et al. 2019), *Hypoxylaceae* (Wendt et al. 2018), *Fasciatisporaceae* (Hyde et al. 2020a), *Spirodecosporaceae* (Sugita et al. 2022), and *Vamsapriyaceae* (Sun et al. 2021). Sun et al. (2021) introduced two genera *Podosporium* and *Tretophragmia* into the novel family *Vamsapriyaceae*. Wijayawardene et al. (2022) listed 20 families under *Xylariales*. The genera *Circinotrichum*, *Gyrothrix* and *Vermiculariopsiella* had a complex taxonomy and have generally been confused in the past. Both *Circinotrichum* and *Gyrothrix* have polyblastic conidiogenous cells, while *Vermiculariopsiella* has phialidic conidiogenous cells. The *Circinotrichum* produces simple setae, *Gyrothrix* produces branched setae and *Vermiculariopsiella* produces both simple and branched setae (Hernãndez-Restrepo et al. 2022). Morphological and phylogenetic analyses based on the ITS, LSU, and RPB2 sequences showed that *Circinotrichum* and *Gyrothrix* are polyphyletic and placed in *Coniocessiaceae* and *Gyrothricaceae*, respectively. The *Gyrothricaceae* was introduced to accommodate *Gyrothrix*, *Xenoanthostomella*, and the newly introduced *Neogyrothrix, Pseudocircinotrichum* and *Pseudoceratocladium.* The new genus *Pirozynskiomyces* was introduced into *Coniocessiaceae* (Hernãndez-Restrepo et al. 2022). The genus *Vermiculariopsiella* is emended to include species with setose sporodochia with simple setae, which belongs to order *Vermiculariopsiellales* and the family *Vermiculariopsiellaceae*. Also,

Vermiculariopsis is resurrected and includes setose fungi (Hernãndez-Restrepo et al. 2022), while Crous et al. (2018) suggested to retain *Vermiculariopsis* as the older name over *Vermiculariopsiella*.

Hernãndez-Restrepo et al. (2022) resurrected the genus *Peglionia* in the family *Microdochiaceae.* Cedeño-Sanchez et al. (2023a) considered the *Barrmaeliaceae* synonymous with *Induratiaceae* and accommodated the genera *Emarcea* and *Muscodor* in the *Xylariaceae*. Also, the new genus *Parahypoxylon* was introduced using a polyphasic approach, considering morphology, multigene phylogeny and chemotaxonomy (Cedeño-Sanchez et al. 2023b). *Alloeutypa* was introduced into *Diatrypaceae* using morphological features and molecular evidence (Ma et al. 2023). Therefore, *Xylariales* comprises 21 families as mentioned in the introduction (Wendt et al. 2018; Voglmayr et al. 2019; Hyde et al. 2020a, 2020b; Sun et al. 2021; Hernãndez-Restrepo et al. 2022; Sugita et al. 2022; Wijayawardene et al. 2022).

Xylariales taxa produce both conspicuous and inconspicuous stromata, of which many are "macromycetes" and produce conspicuous fruiting bodies (Helaly et al. 2018). Stromata are variable in size and shape, and are mostly dark (Hyde et al. 2020b). *Clypeosphaeriaceae* taxa produce a pseudoclypeus, which is black and comprises both host and fungal tissues (Hyde et al. 2020b). Metabolite profiles of stromata are often complementary to those of mycelial cultures (Helaly et al. 2018). Most *Xylariales* have a persistent hamathecium. Ascomata are usually perithecial, dark-colored and thick-walled with true paraphyses and periphysate ostioles. However, ascomata color is variable and is seen as whitish, greyish to black. The interior of ascomata is sometimes zonate or filled with a liquid, as in the family *Hypoxylaceae*. Paraphyses develop from a hymenial layer, which is apically free (Barr 1990, Hawksworth et al. 1995). Asci are mostly unitunicate and eight-spored with a J+ apical ring when stained in the Melzer's reagent or with apical thickening. Sometimes asci are with J- or J+ apparatus, such as in *Barrmaeliaceae*, *Clypeosphaeriaceae*, *Diatrypaceae*, and *Hypoxylaceae*. Asci of some taxa turn slightly reddish in Congo Red as in *Requienellaceae*. The ascospores are usually pigmented, 1–2-celled, and often with germ slits (Maharachchikumbura et al. 2016; Hyde et al. 2020a). Anamorphs of *Xylariales* taxa are mostly hyphomycetous, with holoblastic conidial production (Rogers 1979; Whalley 1996), some are coelomycetous, as *Diatrypaceae* (Konta et al. 2020). Among these, are libertella-like,

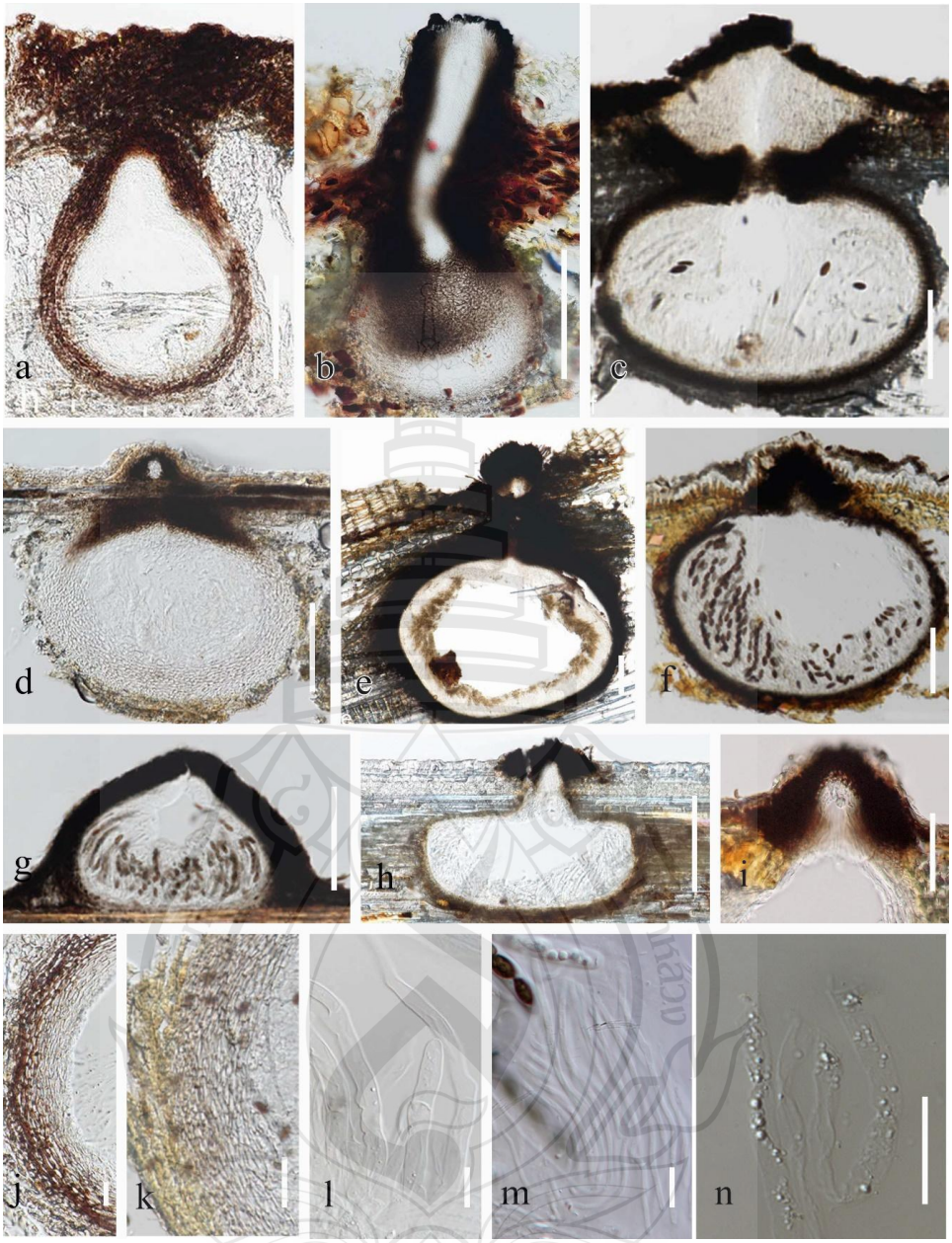
phomopsis-like, geniculosporium-like and nodulisporium-like anamorphs (Phookamsak et al. 2019; Dayarathne et al. 2020).

Sexual morph: *Stromata* are eustromatic or pseudostromatic, dark coloured, more or less well-developed, or sometimes reduced or lacking, variable in size, shape and colour, erect, glomerate, pulvinate, discoid, effused-pulvinate, hemispherical, spherical, peltate applanate or effuse-pulvinate, ostiolate, arising singly or aggregated into groups, with one to several ascomata, mostly with extractable stromal pigments, unipartite or bipartite, sometimes with carbonaceous outer layer. *Ascomata* are variable in size and shape, immersed to erumpent or superficial, perithecial, bottle-shaped, spherical, globose-subglobose, coriaceous or elongate cylindrical-pyriform, solitary or aggregated. *Ostioles* are inconspicuous or strongly erumpent, flattened or papillate to conical, umbilicate or at the same level as the stromal surface, with or without discs. *Paraphyses* are hyaline, filamentous, septate, embedded in a gelatinous matrix. *Asci* are 4–8-spored or sometimes polysporous, unitunicate, cylindrical to clavate to pyriform, fusiform or globose, pedicellate-apedicellate, apically rounded, with or without J+ or J-, apical ring stained in Melzer's reagent, or with apical thickening. *Ascospores* are unicellular or septate, uniseriate-biseriate, variously-shaped, sphaerical, ellipsoidal, subglobose, reniform, oval, straight, spiral or sigmoid, allantoid or ellipsoid, yellow to black, mostly dark, with or without germ slits or germ pores, sometimes surrounded by a gelatinous sheath. *Perispore* is dehiscent or lacking, smooth or with patterns. Asexual morph: hyphomycetous or coelomycetous, libertella-like, phomopsis-like, geniculosporium-like, nodulisporium-like, periconiella-like or xylocladium-like. *Conidiomata* are pycnidial, acervuli, sporodochial. *Conidiophores* are micronematous, macronematous, synnematous or sympodially proliferating, hyaline to light brown, smooth to finely verruculose, simple or branched. *Conidiogenous cells* are polyphialidic, polyblastic, sympodial, cylindrical, usually hyaline, one to several on each branch of the conidiophore, and have a swollen apex. *Conidia* are solitary, aggregating in slimy mass, unicellular or septate, hyaline to pale brown, with pointed ends, roughened or smooth, elongate fusiform, falcate, lunate, ellipsoidal, obclavate, clavate. *Chlamydospores* are present or absent (Wendt et al. 2018; Daranagama et al. 2018; Hyde et al. 2020b).

Note a Cross section through stroma in *Engleromyces goetzei*. b Cross section through stroma in *Annulohypoxylon truncatum*. c *Entonaema liquescens*. d, e *Hypoxylon fragiforme*. f Longitudinal section through ascomata of *Allocryptovalsa sichuanensis*. g Cross section through sroma in *Diatrype disciformis*. h *Camillea leprieurii*. i *Jackrogersella minutella*. j *Xylaria Karsticola*. k *Camillea tinctor*. Scale bars: a, b, c = 1000 μm, d, e = 2000 μm. f = 200 μm, g = 500 μm, h = 10 μm, i, h = 1000 μm.

Source Daranagama et al. (2017), Samarakoon et al. (2022), Karimi et al. (2023)

Figure 3.62 Stromatal morphology in *Xylariales*



Note a–i Ascomatal morphologies: a *Eutypa camelliae*. b *Melanostictus longiostiolatus*. c *Magnostiolata mucida*. d *Hypocopra zeae*. e *Peroneutypa leucaenae*. f *Occultitheca rosae*. g *Xenoanthostomella chromolaenae*. h *Vamsapriya mucosa*. i *Emarcea castanopsidicola*. j–k Peridium morphologies: j *Eutypa camelliae*. k *Hypocopra zeae*. l–n Paraphyses morphologies: l *Acrocordiella photiniicola*. m *Xylaria* sp. n *Jackrogersella minutella*. Scale bars: a, b = 200 µm, c−h = 200 µm, i = 50 µm, j, k = 20 µm, l−n= 10 µm.

Source Daranagama et al. (2017), Samarakoon et al. (2022), Karimi et al. (2023)

Figure 3.63 Ascomata, peridium and paraphyses morphology of *Xylariales*

Note a *Allocryptovalsa sichuanensis.* b *Acrocordiella photiniicola*. c *Nigropunctata bambusicola*. d *Magnostiolata mucida*. f *Neoanthostomella bambusicola*. g *Magnostiolata mucida*. h *Acrocordiella photiniicola*. i *Rosellinia markhamiae*. j *Nigropunctata bambusicola*. Scale bars: a, b, f, g, h = 20 μm, c, j = 10 μm, e, i = 50 μm.

Source Konta et al. (2016), Samarakoon et al. (2022)

Figure 3.64 Ascal morphology in *Xylariales*

Genera included in *Xylariales*

Anungitiomycetaceae Crous

Anungitiomyces Crous

Nothoramichloridium Crous

Strelitziomyces Crous

Barrmaeliaceae Voglmayr & Jaklitsch

Barrmaelia Rappaz.

Entosordaria (Sacc.) Höhn.

Induratia Samuels, E. Müll. & Petrini

Cainiaceae J.C. Krug

Alishanica Karun., C.H. Kuo & K.D. Hyde

Amphibambusa D.Q. Dai & K.D. Hyde

Arecophila K.D. Hyde

Atrotorquata Kohlm. & Volkm.-Kohlm.

Cainia Arx & E. Müll.

Endocalyx Berk. & Broome

Longiappendispora Mapook & K.D. Hyde

Paramphibambusa L.S. Han & D.Q. Dai

Seynesia Sacc.

Clypeosphaeriaceae G. Winter

Aquasphaeria K.D. Hyde

Apioclypea K.D. Hyde

Brunneiapiospora K.D. Hyde, J. Fröhl. & Joanne E. Taylor

Clypeosphaeria Fuckel

Crassoascus Checa, Barrasa & A.T. Martínez

Ommatomyces Kohlm., Volkm.-Kohlm. & O.E. Erikss

Palmaria K.D. Hyde, J. Fröhl. & Joanne E. Taylor

Coniocessiaceae Asgari & Zare

Coniocessia Dania García, Stchigel, D. Hawksw. & Guarro

Paraxylaria Wanas., E.B.G. Jones, Gafforov & K.D. Hyde

Pirozynskiomyces Hern.-Restr. & Crous

Pseudoconiocessia L. Lu & Tibpromma

Diatrypaceae Nitschke

Alloeutypa Hai X. Ma, Z.E. Yang & Yu Li

Allocryptovalsa Senwanna, Phook. & K.D. Hyde

Allodiatrype Konta & K.D. Hyde

Anthostoma Nitschke

Cryptosphaeria Ces & De Not.

Cryptovalsa Ces. & De Not. ex Fuckel

Diatrypasimilis J.J. Zhou & Kohlm.

Diatrype Fr.

Diatrypella (Ces. & De Not.) De Not. (= *Allodiatrypella* H.Y. Zhu & X.L. Fan, nom. invalid)

Echinomyces Rappaz

Endoxylina Romell

Eutypa Tul. & C. Tul.

Eutypella (Nitschke) Sacc.

Halocryptosphaeria Dayarath., Devadatha, V.V. Sarma & K.D. Hyde

Halocryptovalsa Dayar. & K.D. Hyde

Halodiatrype Dayar. & K.D. Hyde

Leptoperidia Rappaz

Libertella Desm.

Mangifericola E.F. Yang & Tibpromma

Melanostictus Samarak. & K.D. Hyde

Monosporascus Pollack & Uecker

Neoeutypella M. Raza, Q.J. Shang, Phookamsak & L. Cai

Paraeutypella L.S. Dissan., J.C. Kang, Wijayaw. & K.D. Hyde

Pedumispora K.D. Hyde & E.B.G. Jones

Peroneutypa Berl. (ca 30)

Pseudodiatrype S.H. Long & Q.R. Li

Pseudoeutypa S.N. Zhang & E.B.G. Jones

Quaternaria Tul. & C. Tul.

Rhizophila K.D. Hyde & E.B.G. Jones

Vasilyeva S.H. Long, Wijayaw. & Q.R. Li

Fasciatisporaceae S.N. Zhang, K.D. Hyde & J.K. Liu

Fasciatispora K.D. Hyde

Gyrotrichaceae Hern.-Restr. & Crous

Gyrothrix (Corda) Corda

Neogyrothrix Hern.-Restr. & Crous

Pseudoceratocladium Hern. -Restr. & Crous

Pseudocircinotrichum Hern. -Restr. & Crous

Xenoanthostomella Mapook & K.D. Hyde

Graphostromataceae M.E. Barr, J.D. Rogers & Y.M. Ju

Biscogniauxia Kuntze

Camillea Fr.

Graphostroma Piroz.

Obolarina Pouzar

Vivantia J.D. Rogers, Y.M. Ju & Cand.

Hansfordiaceae Crous

Hansfordia S. Hughes

Hypoxylaceae DC.

Annulohypoxylon Y.M. Ju, J.D. Rogers & H.M. Hsieh

Chlorostroma A.N. Mill., Lar.N. Vassiljeva & J.D. Rogers

Daldinia Ces. & De Not.

Durotheca Læssøe, Srikit., Luangsa-ard & M. Stadler

Entonaema Möller

Hypomontagnella Sir, L. Wendt & C. Lamb.

Hypoxylon Bull.

Jackrogersella L. Wendt, Kuhnert & M. Stadler

Parahypoxylon Cedeño-Sanchez, Charria-Girón & M. Stadler

Phylacia Lév.

Pyrenomyxa Morgan

Pyrenopolyporus Lloyd

Rhopalostroma D. Hawksw.

Rostrohypoxylon J. Fourn. & M. Stadler

Ruwenzoria J. Fourn., M. Stadler, Læssøe & Decock

Thamnomyces Ehrenb.

Theissenia Maubl.

Thuemenella Penz. & Sacc.

Lopadostomataceae Daranag. & K.D. Hyde

Creosphaeria Theiss.

Jumillera J.D. Rogers, Y.M. Ju & F. San Martín

Lopadostoma (Nitschke) Traverso

Whalleya J.D. Rogers, Y.M. Ju & F. San Martín

Microdochiaceae Hern.-Restr., Crous & J.Z. Groenew.

Idriella P.E. Nelson & S. Wilh. (= *Monographella* Petr.)

Macroidriella Z.X. Zhang, J.W. Xia & X.G. Zhang

Microdochium Syd.

Peglionia Goid.

Selenodriella R.F. Castañeda & W.B. Kendr

Xenoidriella Crous

Nothodactylariaceae Crous

Nothodactylaria Crous

Pallidoperidiaceae R. Sugita & Kaz. Tanaka

Amphigermslita R. Sugita & Kaz. Tanaka

Crassipseudostroma R. Sugita & Kaz. Tanaka

Minuticlypeus R. Sugita & Kaz. Tanaka

Pallidoperidium R. Sugita & Kaz. Tanaka

Polystigmataceae Höhn. ex Nannf.

Polystigma DC.

Requienellaceae Boise

Acrocordiella O.E. Erikss.

Lacrymospora Aptroot

Parapyrenis Aptroot

Requienella Fabre

Spirodecosporaceae R. Sugita & Kaz. Tanaka

Spirodecospora B.S. Lu, K.D. Hyde & W.H. Ho

Vamsapriyaceae Y.R. Sun, Yong Wang bis & K.D. Hyde

Diabolocovidia Crous

Didymobotryum Sacc.

Vamsapriya Gawas & Bhat

Paravamsapriya Samarak. & K.D. Hyde

Podosporium Schwein.

Tretophragmia Subram. & Natarajan

Xyladictyochaetaceae Crous & Hern.-Restr

Brachiampulla Réblová & Hern.-Restr.

Xyladictyochaeta Hern.-Restr., R.F. Castañeda & Gené

Xylariaceae Tul. & C. Tul. (= *Clypeosphaeriaceae* G. Winter; = *Induratiaceae* Samarak., *Thongbai*, K.D. Hyde & M. Stadler)

Abieticola Hyang B. Lee

Albicollum Voglmayr, J. Fourn., Tello & Jaklitsch

Amphirosellinia Y.M. Ju, J.D. Rogers, H.M. Hsieh & Lar.N. Vassiljeva

Anthostomelloides Tibpromma & K.D. Hyde

Astrocystis Berk. & Broome

Brunneiperidium Daranag., Camporesi & K.D. Hyde

Collodiscula I. Hino & Katum.

Coniolariella Dania García, Stchigel & Guarro

Emarcea Duong, Jeewon & K.D. Hyde

Engleromyces Henn.

Entalbostroma J.D. Rogers & P.R. Johnst.

Entoleuca Syd.

Halorosellinia Whalley, E.B.G. Jones, K.D. Hyde & Læssøe

Helicogermslita Lodha & D. Hawksw.

Hypocopra (Fr) J. Kickx f.

Hypocreodendron Henn.

Kretzschmaria Fr.

Kretzschmariella Viégas

Leprieuria Læssøe, J.D. Rogers & Whalley

Leptomassaria Petr.

Linosporopsis Voglmayr & Beenken

Linteromyces Crous

Lunatiannulus Daranag., Camporesi & K.D. Hyde

Muscodor Worapong, Strobel & W.M. Hess

Nemania Gray (= *Euepixylon* Füisting)

Neoxylaria Konta & K.D. Hyde

Nigropunctata Samarak. & K.D. Hyde

Oligostoma Voglmayr, J. Fourn. & Jaklitsch

Podosordaria Ellis & Holw.

Poronia Willd.

Rosellinia De Not.

Sarcoxylon Cooke

Spiririma Voglmayr, J. Fourn., Tello & Jaklitsch

Squamotubera Henn.

Stellatus J.F. Zhang & K.D. Hyde

Stilbohypoxylon Henn.

Virgaria Nees

Wawelia Namysl.

Xylaria Hill ex Schrank

Xylotumulus J.D. Rogers, Y.M. Ju & Hemmes

Zygosporiaceae J.F. Li, Phook. & K.D. Hyde

Ascotricha Berk.

Flosculomyces B. Sutton

Vesiculozygosporium Crous

Zygosporium Mont.

Xylariales genera *incertae* sedis

Adomia S. Schatz

Alloanthostomella Daranag., Camporesi & K.D. Hyde

Anthostomella Sacc.

Anungitea B. Sutton

Ascotrichella Valldos. & Guarro

Neobarrmaelia Crous

Basifimbria Subram. & Lodha

Bicellulospora W.L. Li, R.R. Liang & Jian K. Liu

Biporispora J.D. Rogers, Y.M. Ju & Cand.

Castellaniomyces Senan., Camporesi & K.D. Hyde

Catenuliconidia N.G. Liu & K.D. Hyde

Chaenocarpus Rebent.

Circinotrichum Nees

Cryptostroma P.H. Greg. & S. Waller

Cyanopulvis J. Fröhl. & K.D. Hyde

Diamantinia A.N. Mill., Læssøe & Huhndorf

Gigantospora B.S. Lu & K.D. Hyde

Guayaquilia R.F. Castañeda, Magdana, D. Sosa & Hern.-Restr.

Guestia G.J.D. Sm. & K.D. Hyde

Hadrotrichum Fuckel (15)

Haploanthostomella Konta & K.D. Hyde

Idriellopsis Hern.-Restr. & Crous

Kirstenboschia Quaedvl., Verkley & Crous

Lanceispora Nakagiri, Okane, Tad. Ito & Katum.

Lasiobertia Sivan.

Magnostiolata Samarak. & K.D. Hyde

Natonodosa Heredia, R.F. Castañeda & D.W. Li

Neoanthostomella D.Q. Dai & K.D. Hyde

Neoidriella Hern.-Restr. & Crous

Neoleptodontidium Crous & Jurjević

Neotrichosphaeria Crous & Carnegie

Nipicola K.D. Hyde

Occultitheca J.D. Rogers & Y.M. Ju

Ophiorosellinia J.D. Rogers, A. Hidalgo, F.A. Fernández & Huhndorf

Palmicola K.D. Hyde

Pandanicola K.D. Hyde

Paraidriella Hern.-Restr. & Crous

Paramphisphaeria F.A. Fernández, J.D. Rogers, Y.M. Ju, Huhndorf & L. Umaña

Paraphysalospora Crous

Paucithecium Lloyd

Pidoplitchkoviella Kiril.

Polyancora Voglmayr & Yule

Polyscytalum Riess

Poroleprieuria M.C. González, Hanlin, Ulloa & Elv. Aguirre

Pseudoanthostomella Daranag., Camporesi & K.D. Hyde

Pseudophloeospora Crous & R.G. Shivas

Pulmosphaeria Joanne E. Taylor, K.D. Hyde & E.B.G. Jones

Pyriformiascoma Daranag., Camporesi & K.D. Hyde

Roselymyces Fiuza, C.R. Silva, R.F. Castañeda & Gusmão

Sabalicola K.D. Hyde

Sporidesmina Subram. & Bhat

Striatodecospora D.Q. Zhou, K.D. Hyde & B.S. Lu

Stromatoneurospora S.C. Jong & E.E. Davis

Subanthostomella S.N. Zhang, K.D. Hyde & Jian K. Liu

Surculiseries Okane

Synnemadiella Crous & M.J. Wingf.

Tristratiperidium Daranag., Camporesi & K.D. Hyde

Xylocrea Möller

Yuea O.E. Erikss

Earlier *Xylariomycetidae* have evolved around 159 (124–193) MYA and the divergence between *Amphisphaeriales* and *Xylariales* occurred approximately 150.5 MYA during the rapid diversification in the early Mesozoic era (Samarakoon et al. 2022). The rapid diversification of angiosperms during the Cretaceous period likely influenced the diversification of xylarialean taxa, giving rise to several independent lineages (Samarakoon et al. 2022).

Numerous researchers have postulated a hypothesis regarding the evolutionary transition of fungi from aquatic to terrestrial environments. According to this theory, fungal endophytes are believed to represent the ancestral lifestyle, which later underwent further evolution leading to the development of saprobes and pathogens (Krings et al. 2012; Lutzoni et al. 2018; Samarakoon et al. 2022). The transition from

an endophytic to a saprobic lifestyle is evident in certain *Xylariales* taxa, as observed in instances where they appear on freshly fallen branches as well as branches still attached to the host tree (Whalley 1996). Astromatic xylarialean taxa evolved from endophytes and further diversified into stromatic forms, adapting to various environmental conditions. It is also believed that the endophytes originate from spores that come from saprobes (Promputtha et al. 2007; Zhou et al. 2018). The spore origin of endophytes is supported by the substantial genetic diversity observed in *X. cubensis* endophytic isolates found on leaves of the Brazilian rainforest palm (Rodrigues et al. 1993). Some saprobic *Oxydothis* and *Linocarpon* taxa shown to produce hyaline appressoria (Konta et al. 2016, 2017), which is considered as the ancestral character of endophytic Ascomycota (Chethana et al. 2021a, b). Based on the evidence produced from previous research, it is suggested that early xylarialean fungi likely had an endophytic lifestyle, giving rise to simple anthostomella-like ascomata on the surface of the host (Rogers 2000; Phillips et al. 2019). Over time, other stromatic forms evolved as a response to different environmental conditions (Samarakoon et al. 2022). The development of stromatic structures may have been linked to successful parasitism and saprotrophism (Rogers 1979), with Samarakoon et al. (2022) proposing that stromata development might be related to moisture conservation. Furthermore, stromatic forms have been found to produce a variety of chemical compounds, as reported by Becker and Stadler (2021), which could serve the purpose of deterring insects. Samarakoon et al. (2022) further mentioned that these stromatic forms likely developed insecticidal chemicals as a means of protection against insects and other predators. Through ancestral character analysis, it has been revealed that the divergence of ascomata types predominantly occurred during the Cretaceous period, between 66 and 145 million years ago (Samarakoon et al. 2022).

According to Rogers (2000), it is suggested that truly xylariaceous fungi, characterized by aseptate ascospores with a germ slit, evolved from dark-colored fungi with one septate ascospores lacking a germ slit. Additionally, Samarakoon et al. (2022) proposed that an independent evolution may have occurred from aseptate to septate ascospores in response to rapid diversification (Samarakoon et al. 2022). Through ancestral character analysis, Samarakoon et al. (2022) stated that the ascospore germ slit appeared exclusively in *Xylariales* during the Cretaceous period, around 95 to 156

million years ago. Therefore, the genus *Collodiscula* with its two-celled ascospores was suggested as the primitive xylarialean taxon, and the genus *Astrocystis* was identified as its closest relative (Ju and Rogers 1990). According to the hypothesis of Samarakoon et al. (2022), the ancestral *Xylariomycetidae* probably featured astromatic, clypeate ascomata with aseptate, hyaline ascospores lacking a germ slit, which likely evolved through interactions with plant-fungal endophytes.

The taxonomic placements of many genera in *Xylariales* are controversial, and these taxa are considered genera *incertae sedis* due to uncertain morphologies (sexual or asexual) and lack of molecular data (Daranagama et al. 2018, Wendt et al. 2018, Hyde et al. 2020a). Wijayawardene et al. (2022) listed 57 genera under *Xylariales* genera *incertae sedis*, of which most of these genera have only a single collection.

Hypocopra species inhabit dung, while *Hypocopra zeae* is saprobic on a dead culm of *Zea mays* and is the only species described from plant substrates. This species is similar to xylariaceous taxa based on morphological characteristics such as immersed ascomata under a clypeus, septate, hyaline paraphyses, 8-spored, unitunicate, cylindrical asci with a J +, apical ring and uniseriate, brown ascospores with a short germ slit. Also, *H. zeae* is similar to *H. rostrata* (99%), *Podosordaria muli* (89%) and *Stromatoneurospora phoenix* (92%) using the LSU, ITS and *rpb*2 sequences (Samarakoon et al. 2022). Furthermore, there are few *Hypocopra* species and only *Stromatoneurospora phoenix* with molecular data (Becker et al. 2020b). Therefore, the phylogenetic placement could be altered with the investigation of new sequence data and more collections are needed (Samarakoon et al. 2022).

Hypoxylon, typified by *H. fragiforme*, is clustered in a relatively small clade with *H. howeanum*, *H. ticinense* and *H. rickii* in the recently established phylogenies (Wendt et al. 2018; Lambert et al. 2021), which shows that *Hypoxylon*, in the current sense, is heterogeneous and paraphyletic. Also, Song et al. (2022) reported that *Hypoxylon* is a polyphyletic genus using phylogenetic analyses. Also, their studies showed that the species of *Hypoxylon* were distributed in six separate clades, and any apparent correlation in morphological features with the distribution of species in the phylogenetic trees did not observe. Therefore, the phylogenetic tree showed that the classification of *Hypoxylon* is confusing. Also, they suggested that more collections, more gene sequences, new taxonomic features, and the application of polyphasic

taxonomic approaches using morphological (asexual and sexual), phylogenetic and chemotaxonomic data are needed in the further studies (Song et al. 2022). However, Wibberg et al. (2021) performed a phylogenomic analysis and provide a stable phylogeny for *Hypoxylaceae*, which can also be adapted for *Xylariales* in the future.

Ecological and economical roles: These taxa consist of coprophilous saprobes, lignicolous (mycobionts or lichen-forming fungi), endolichenic and endophytic fungi, which have potential ecological and industrial applications. Several taxa of *Xylariales*, such as *Daldinia*, *Euepixylon*, *Nemania*, *Hypocopra*, *Podosordaria*, *Poronia* and *Wawelia*, are important in forestry and plant ecology as wood decomposers (coprophilous saprobes) worldwide and are involved in the biodegradation of xenobiotics (Whalley 1996; Stadler 2011; Hyde et al. 2020b). These fungi mostly colonize dead and decaying wood of angiospermous plants and are considered soft-rot fungi mainly because of their ability to degrade lignin, and their ability to degrade cellulose has also been reported (Merrill et al. 1964; Wei et al. 1992). Some xylarialean taxa are mycobionts (lichen-forming fungi), such as *Acrocordiella*, *Burrowsia*, *Parapyrenis* and *Requienella*. These fungi play important roles in ecosystems, providing habitats and food for other animals (birds, ants, snails and mites), aiding soil formation and participating in nutrient cycling (Jackson 2015). They also include secondary metabolites producers (Calcott et al. 2018).

Several genera in *Xylariales* have shown high potential for producing bioactive secondary metabolites by endophytic, lichens and endolichenic fungi, which are used as pharmaceuticals and agrochemicals (Calcott et al. 2018; Oh et al. 2020; Becker and Stadler 2021). These beneficial compounds have shown antibacterial (Hein et al. 1998; Kralj et al. 2006; Arunrattiyakorn et al. 2018; Intaraudom et al. 2019; Liang et al. 2019; Wittstein et al. 2020), antifungal (Schneider et al. 1995, 1996; Burgess et al. 2017; Xu et al. 2017; Intaraudom et al. 2019), cytotoxic (McCloskey et al. 2017; Patjana et al. 2021; Wang et al. 2019; Noppawan et al. 2020), antimalarial (Intaraudom et al. 2019), anti-inflammatory (Arunrattiyakorn et al. 2018; Patjana et al. 2021; Chen et al. 2019), anti-neuroinflammatory (Chang et al. 2017; Patjana et al. 2021), immunosuppressive (Chen et al. 2020a, b), and herbicidal (Han et al. 2019; Biasetto et al. 2019) properties, and are used in medical and agriculture industries.

Several important plant parasites have been reported in this order, of which *Dematophora* is the most severe pathogen on trees or agricultural plants (Wittstein et al. 2020). Other pathogenic genera include *Biscogniauxia* (Nugent 2005), *Entoleuca* (Ostry and Anderson 2009), *Hypoxylon* (Stadler 2011) and *Kretzschmaria* (da Luz Morales et al. 2021). Therefore, genera of *Xylariales* are important in terms of their economic and environmental value due to their various lifestyles as saprobes, pathogens, endophytes and lichen-forming fungi (Hyde et al. 2020b).

Chemical diversity: Secondary metabolites are produced by many genera in *Xylariales* in their mycelial cultures and stromata. These compounds are categorized into cytochalasans (a class of hybrid polyketide non-ribosomal peptide), terpenoids, hybrid-terpenoids, non-ribosomal peptides, polyketides, benzenoids, lactones and azaphilones, and are used as pharmaceuticals and agrochemicals (Becker and Stadler 2021). Also, enzymes are essential for biotechnological applications. *Kretzschmaria zonata*, a plant pathogenic fungus, showed great potential for enzyme production. The fungus produced a wide variety of enzymes, such as xylanases, endoglucanases, pectinases, β-glucosidases and hemicellulases (da Luz Morales et al. 2021). Stadler (2011) reported that secondary metabolite production in xylarialean taxa was correlated with molecular data and demonstrated that secondary metabolite profiles are important species-specific characters and have phylogenetic significance. For example, azaphilone pigments are exclusively found in *Hypoxylaceae* (Cedeño-Sanchez et al. 2023a). Different secondary metabolites of this order and their bioactivities are summarized in Table 3.8.

Table 3.8 The secondary metabolites of *Xylariales* and their bioactivities.

Fungi	Chemical compounds	Class of chemical compounds	Bioactivity	Reference
Amphirosellinia nigrospora	Coriloxin	Cyclohexenone derivative	Antimicrobial	(Nguyen et al. 2019)
Annulohypoxylon sp.	Hypoxylide	Polyketide	Cytotoxic	(Liu et al. 2018)
	Viridistratins A–C	Benzenoid	Antimicrobial	(Becker et al. 2020a)
Biscogniauxia sp.	Nigriterpene A, 10 xylariterpenoid, Isocoumarin orthosporin, Daldinin C, 7'dechloro-5'-hydroxygriseofulvin, Daldinone D, Sch-642305, Curtachalasin A, Cytochalasin E, Epoxycytochalasins Z8, Z8 isomer, and Z17	Terpenoids and polyketide	Cytotoxic	(Pedra et al. 2023)
Daldinia sp.	Botryane-type sesquiterpenoids and Sacchalasins	Polyketide-nonribosomal Peptide	Anti-HIV	(Qin et al. 2006)
	Daldinin	Polyketide-nonribosomal Peptide	Cytotoxic	(Trung et al. 2019)
	Daldiquinone	Naphthoquinone	Cytotoxic	(Kamauchi et al. 2018)

Table 3.8 (Continued)

Fungi	Chemical compounds	Class of chemical compounds	Bioactivity	Reference
Hypoxylon sp.	Rickenyls A-E,	Terphenyl	Antimicrobial,	(Kuhnert et al. 2015)
	Fendlerinines A–D, Fendlerinines E–F	Terpenoid	antioxidative, cytotoxic	(Intaraudom et al.
	Fendlerals A-B and	Azaphilone	and Anti-malaria	2019)
	Hypoxyside	Diterpene	Antibacterial	(Becker et al. 2021)
	Hybridorubrins A-D	Benzenoid	Antiparasitic	(Bills et al. 2012)
	Nodulisporic acid	α-pyrones	Antimicrobial	(Becker et al. 2020a)
	Viridistratins A–C	Polyketide-nonribosomal	Cytotoxic	(Yuan et al. 2019)
	Hypotiens A –D	peptide	Antibacterial and	(Lambert et al. 2021)
	Pseudofuscochalasin A and daldinin F		Cytotoxic	
Muscodor albus	1-butanol, 3-methyl-, acetate	Ester	Antimicrobial	(Strobel et al. 2001)
Nemania sp.	Nemenonediol A and B, Botryane-type	Terpenoid	Cytotoxic	(Medina et al. 2019)
	sesquiterpenoids,		Antiplasmodial,	
	19,20-epoxycytochalasin C and D, and	Polyketide-nonribosomal	cytotoxic	(Kumarihamy et al.
	18-deoxy-19,20- epoxycytochalasin C	peptide	and antibacterial	2019)
Rosellinia sp.	Jammosporin A	Polyketide-nonribosomal	Cytotoxic	(Sharma et al. 2018)
		peptide		
	Cytochalasin E and $\Delta^{6,12}$-cytochalasin	Polyketide-nonribosomal	Cytotoxic	(Pourmoghaddam et al.
	E	peptide		2022)

Table 3.8 (Continued)

Fungi	Chemical compounds	Class of chemical compounds	Bioactivity	Reference
Stromatoneurospora phoenix	Phoenixilanes A-B and Punctaporonin B	Sesquiterpenoid	Cytotoxic (Phoenixilanes B)	(Becker et al. 2020b)
Xylaria sp.	Cytochalasin C and D	Polyketide-nonribosomal peptide	Herbicide, cytotoxic	(Biasetto et al. 2019)
	Cytochalasin P1		Cytotoxic	(Chen et al. 2017)
	Demethylincisterol A3 and chaxine C	Terpenoid	Cytotoxic	(McCloskey et al. 2017)
	Hydroxydecandrin G	Terpenoid	Herbicide	
	Nigriterpenes A–F	Terpenoid	Anti-neuroinflammatory	(Han et al. 2019)
	Xylareremophil	Terpenoid		(Chang et al. 2017)
	Xylarinoditerpenes A–R	Terpenoid	Antibacterial	(Liang et al. 2019)
	Xylarilongipins A-B	Terpenoid	Immunosuppressive	(Chen et al. 2020a)
	xylapeptide A–B	Cyclic pentapeptides	Immunosuppressive	(Chen et al. 2020b)
	E1011	Polyketides	Antibacterial	(Xu et al. 2017)
	Fimbriethers B, E and G	Benzenoid	Cytotoxic	(Ai et al. 2018)
	Xylarianin A	Oxydibenzenoid	Anti-inflammatory	(Chen et al. 2019)
	Penixylarins C	Benzenoid	Cytotoxic	(Zhang et al. 2018)
	Xylarodons A and B	Hexaketide	Antimicrobial	(Guo et al. 2019)
	β-mangostin	Xanthone	Cytotoxic	(Arunrattiyakorn et al. 2018)

Table 3.8 (Continued)

Fungi	Chemical compounds	Class of chemical compounds	Bioactivity	Reference
***Xylaria* sp.**	β-mangostin	Xanthone	Cytotoxic Anti-inflammatory,	(Arunrattiyakorn et al. 2018)
	6-ethyl-7,8-dihydroxy-4Hchromen-4-one and 3,4-dihydro-5,7,8-trihydroxy-3-methyl-isocoumarin	Polyketides	antibacterial, antimalarial, and antimycobacterial Anti-inflammatory	(Patjana et al. 2021)
	Xylariahgins A –F	Pyranone		(Chen et al. 2018)
	Xylaropyranones B -C	Pyranone		(Guo et al. 2018)
	Xylaridines A –B	Alkaloid	Cytotoxic	(Li et al. 2019a)
	Xylaridines C–D	Alkaloid	Cytotoxic Antimicrobial and Cytotoxic Antimicrobial and Cytotoxic	(Li et al. 2019b)

Some species of *Xylariales* are endolichenic fungi, which live in the lichen thallus (Arnold et al. 2009), and have high diversity in tropical or subtropical regions (Oh et al. 2020). Suryanarayanan (2017) suggested that endolichenic fungi influence the physiology of lichens and promote the biological function of host lichens in the ecosystems. While the relationship between endolichenic fungi and lichens is unclear (Suryanarayanan 2017), Oh et al. (2020) stated that the distribution pattern and biodiversity of endolichenic fungi are essential for understanding the ecology and physiology of lichens and the maintenance of ecosystem sustainability against global climate change. Therefore, they suggested analyzing various lichen species in more environments for more expansion of the diversity and ecology of endolichenic fungi (Oh et al. 2020).

Also, fossils can give complete information about evolution, but the fossil *Xylariales* are extremely rare. There is only a little information about fossils of *Xylariales*, which fruiting bodies and spores were found on the leaves of *Dacrycarpus* (Wu et al. 2020) and in ancient carbonized specimens (Surup et al. 2018). Studies of fossils will expand our understanding of the evolution of *Xylariales* in the future (Maslova et al. 2021). Schmitt et al. (2009) hypothesised that ancestral character state reconstruction can play a vital role in a better understanding of morphological character evolution. Many researchers studied the ancestral character state reconstruction in xylarialean taxa using morphological data of ascospores and appressoria (Chethana et al. 2021b), lifestyles and and geographical and host distributions (Píchová et al. 2018; Zhu et al. 2019). However, no information is available on the study of the ancestral character state reconstruction using molecular data (Samarakoon et al. 2022).

Samarakoon et al. (2022) stated that the pseudo-stromatic character found in some diatrypaceous fungi may have an intermediate astromatic and stromatic development and needs more characterizations to examine unknown sexual morphs. According to Samarakoon et al. (2022), the early *Ascomycota* likely have been endophytes and then evolved as saprobes, however, it is unknown how the endophytic species arise as saprobes. Many researchers reported evidence that it is possibly due to the spore origin of endophytes (Rodrigues et al. 1993) and wind-borne xylariaceous fungal spores (Ju et al. 2018). Therefore, Ju et al. (2018) suggested using the efficiency of modern molecular techniques for tracing infections and propagules.

Samarakoon et al. (2022) suggested introducing higher ranks for xylarioid taxa because the criteria for taxonomic classification were altered using molecular data. Therefore, it showed that stalk-like or well-developed stromata could not use to place all taxa in *Xylariales*. Also, the classification of xylarialean taxa will not be based on stromatic variations in the future, but it will be based on the type of ring, the colour of the ascospores, and the presence or absence and the type of germ slit. Daranagama et al. (2018) stated that *Xylaria* may comprise several thousands of species, which the majority didn't describe formally because this genus has never been subjected to a world monograph using modern methodology. Wibberg et al. (2021) sequenced the whole genomes of 13 members of *Hypoxylaceae* and addressed the issues of generic and species delimitation based on phylogenomic reconstructions using amino acid sequences and genomic comparisons. These methods can also be used to define family, generic and species delimitation in *Xylariales*. Therefore, future research can be focused on re-evaluating *Xylariales* using polyphyletic approaches, combining morphology, phylogenetics, phylogenomics and genomic comparisons to produce reliable and stable taxonomy for the order.

3.2.1 Notes on peat swamp *Xylariales* on palms

Allocryptovalsa Senwanna, Phookamsak & K.D. Hyde, Mycosphere 8 (10): 1839 (2017)

Allocryptovalsa is a saprobe genus belonging to *Diatrypaceae*, *Xylariales* (*Sordariomycetes*, *Ascomycota*) (Hyde et al. 2020). The genus was established by Senwanna (2017) from Thailand on *Hevea brasiliensis* to accommodate *A. polyspora* and two combined species: *A. cryptovalsoidea*, and *Allocryptovalsa rabenhorstii*, which were transferred from *Eutypella* and *Cryptovalsa* respectively. Based on Species Fungorum (2025) there are 9 accepted species in this genus with molecular data in the GenBank. The genus is characterized by perithecial, solitary to scattered, immersed to semi-immersed ascomata in host substrate, peridium composed of several cell layers of brown to black of textura angularis. Paraphyses are hyaline, unbranched, septate and slightly constricted at septa. Asci are polysporous, unitunicate, thin-walled, clavate to cylindric with a long pedicellate and J- subapical ring. Ascospores are crowded, hyaline to pale yellowish with oblong to allantoid shape. They are smooth-walled, guttules and

don’t have septa (Senwanna 2017). Konta et al. (2020) introduced *A. elaeidis* on dead petiole of *Elaeis guineensis* (Arecaceae) from Thailand.

Arecomyces K.D. Hyde, Sydowia 48 (2): 227 (1996)

Arecomyces introduced by Hyde (1996) to accommodate *Physalospora*-like species on palms. Based on Species Fungorum (2025) there are 10 accepted morphological species with no sequence data in GenBank. *Arecomyces* is a saprobic genus that typified by *Arecomyces frondicola*, which was collected on rachis of *Arenga undulatifolia* (Arecaceae) from Brunei. The genus is characterized by semi immersed to immersed ascomata, peridium comprising several layers, hyaline or brown, numerous, hypha-like, filamentous, irregular, septate paraphyses, cylindrical, pedicellate, thin-walled, unitunicate, 4-8 spore, uniseriate, ellipsoidal, hyaline ascospores. Hyde (1996) described *A. bruneiensis* on *Daemonorops* sp. from Brunei, *A. dicksonii* on rachis of *Oenocarpus* sp. from *Ecuador, A. epigeni* on *Eugeissona* sp., from *Australia, A. frondicola Arenga undulatifolia* from Brunei, *A. hedgerii* on rachis of *Oenocarpus* sp. from Ecuador, *A. sekoyae* on *Oenocarpus* sp. from *Ecuador, A. tetrasporus* on *Phytelephas* sp. from Ecuador and Hyde and Fröhlich (2003) described *A. calami* on dead rattan of *Calamus conirostris* from Brunei, Vitoria et al. (2011) *described A. attaleae* on dead rachis of *Attalea funifera* from Brazil.

Arecophila K.D. Hyde, Nova Hedwigia 63: 82 (1996)

Arecomyces introduced by Hyde (1996) to accommodate *Physalospora*-like species on palms. Based on Species Fungorum (2025) there are 10 accepted morphological species. *Arecomyces* is a saprobic genus that typified with *Arecomyces frondicola*, which was collected on rachis of *Arenga undulatifolia* (Arecaceae) from Brunei. The genus is characterized by semi immersed to immersed ascomata, hyaline or brown, numerous, hypha-like, filamentous, irregular, septate paraphyses, cylindrical, pedicellate, thin-walled, unitunicate asci and 4-8 spore, uniseriate, ellipsoidal, hyaline ascospores (Hyde 1996). Hyde (1996) described *A. bruneiensis* on *Daemonorops* sp. from Brunei, *A. dicksonii* on rachis of *Oenocarpus* sp. from *Ecuador, A. epigeni* on *Eugeissona* sp., from *Australia, A. frondicola Arenga undulatifolia from Brunei, A. hedgerii* on rachis of *Oenocarpus* sp. from Ecuador, *A. sekoyae* on *Oenocarpus* sp. from

Ecuador, A. tetrasporus on *Phytelephas* sp. from Ecuador and Hyde and Fröhlich (2003) described *A. calami* on dead rattan of *Calamus conirostris* from Brunei, Vitoria et al. (2011) *described A. attaleae* on dead rachis of *Attalea funifera* from Brazil.

Astrocystis Berk. & Broome, J. Linn. Soc., Bot. 14 (73 & 74): 123 (1875)

Astrocystis is a saprobic genus belonging to *Xylariaceae*, *Xylariales* (*Sordariomycetes*, *Ascomycota*) (Hyde et al. 2020). The genus was established by Berkeley and Broome (1875) on bamboo from the USA, with *A. mirabilis* as type species. The genus is characterized by having uni or pauciperitheicate stromata and unicellular ascospores with straight germslit (Berkeley and Broome 1875). In the asexual morph its developing within ectostromal perithecia, accompanied by conidiophores in sporodochia (Berkeley and Broome 1875; Petrini 2023). According to Species Fungorum (2025) there are 20 accepted species in this genus. *Astrocystis* species have been reported on Aceraceae including instances like *Astrocystis rachidis* on various hosts such as: *Astrocaryum* sp., *Calamus* sp., *Elaeis guineensis*, *Jessenia bataua*, *Korthalsia brassi*, *Mauritia flexuosa*, *Phytelephas* sp. and *Pinanga* sp. from diverse locations such as Ecuador, Australia, France, Malaysia, Ecuador, Papua New Guinea, Ecuador, Malaysia and *Astrocystis rudis* on *Korthalsia brassi* from Papua New Guinea, *Astrocystis ambigens* on *Daemonorops* sp., from Singapore, *Astrocystis eleiodoxae* on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand, *Astrocystis nypae* on *Nypa* sp. from Malaysia, *Astrocystis sinensis* on *Trachycarpus fortunei* from China and *Astrocystis palmarum* on fallen petioles of palm from Bermuda (Hughes 1953; Ju and Rogers 1994; Læssøe and Spooner 1994; Fröhlich and Hyde 2000; Smith and Hyde 2001; Taylor and Hyde 2003; Petrini 2003; Pinnoi et al. 2010; Daranagama et al. 2015; Li et al. 2016; Hyde et al. 2017; Wu et al. 2021).

Brunneiapiospora K.D. Hyde, J. Fröhl. & Joanne E. Taylor, Sydowia 50 (1): 40 (1998)

Brunneiapiospora introduced as new genus by Hyde et al. (1998) with *B. Javensis* as type species. Based on Species Fungorum (2025) there are nine accepted morphological species while molecular data is limited, only the Internal Transcribed Spacer (ITS) is available for an unnamed species identified as *Brunneiapiospora* sp.

HKUCC. *Brunneiapiospora* species are defined by their immersed, solitary, subglobose ascomata, featuring a peridium composed of several layers of compressed, brown-walled cells. Paraphyses are hypha-like, septate, and numerous. Asci are 8-spored, cylindrical, pedicellate, and possess thin walls. Ascospores are arranged either uniseriate or overlapping uniseriate, apiosporous, and exhibit a brown coloration (Hyde et al. 1998).

Hyde et al. (1998) described *Brunneiapiospora javensis* on rachis of *Calamus* sp. from Indonesia, *B. aequatoriensis* on dead trunk of *Geonoma* sp. from Ecuador, *B. australiensis* on base of dead flagella of *Calamus australis* from Australia, *B. daemonoropis* on dead rachis of *Daemonorops* sp. from Brunei, *B. deightoniella* on *Elaeis guineensis* from Sierra Leone, *B.* jesseniae on dead petiole of *Jessenia bataua* from Ecuador. Crous et al. (2012) described *B. austropalmicola* on *Rhopalostylis sapida* from New Zealand. Nadja et al. (2012) described *B. brasiliensis* on dead rachis of *Elaeis guineensis* from Brazil.

Endocalyx Berk. & Broome, Bot. J. Linn. Soc. 15: 84 (1877)

Endocalyx is a saprobic genus which mostly reported on Arecaceae (Berkeley and Broome 1877; Petch 1908; Okada and Tubaki 1984; Konta et al. 2021; Delgado et al. 2022; Senanayake et al. 2023). The genus was established by Petch (1908) to accommodate *E. thwaitesii*. There are 10 accepted species in this genus based on Species Fungorum (2025). Molecular data are available only for seven species. Aaexual morhp is coelomycetous, and chrachtrized by scattered, erect, cupulate tocylindrical conidiomata. Peridial wall are thick, comprising dark brown, thick-walled cells of textura angularis. Conidiophores are filiform, septate, meristematic, pale at the base and gradually turning brown apically towards the apex with holoblastic, integrated, determinate conidiogenous cells and solitary, unicellular, flattened, oval or slightly polygonal conidia (Petch 1908; Konta et al. 2021). Wijayawardene et al. (2020) placed *Endocalyx* in *Apiosporaceae* (*Amphisphaeriales*, *Sordariomycetes*) based on morphological characters. However, Konta et al. (2021) conducted a multi gene phylogenetic analyses using ITS, LSU, *rpb2*, and *tub2* as well as a single gene phylogenetic analyses (ITS) and transferd *Endocalyx* to *Cainiaceae* (*Xylariales*).

Endocalyx amarkantakensis, E. cinctus, E. indumentum, E. melanoxanthus, and *E. thwaitesii* have been documented on various palm hosts, including *Acrocomia mexicana, Archontophoenix alexandrae, Arenga engleri, Dypsis lutescens, Livistona chinensis, Oncosperma fasciculatum, Phoenix hanceana,* and *Trachycarpus fortunei*. These occurrences span across diverse countries, encompassing Australia, Ghana, Hong Kong, Japan, Malaysia, Mexico, Papua New Guinea, Seychelles, Singapore, and Sri Lanka (Petch 1908; Okada and Tubaki 1984; Heredia et al. 2000; Lu et al. 2000; Taylor and Hyde 2003; Kobayashi 2007; Konta et al. 2021; Senanayake et al. 2023).

Pemphidium Mont., Annales des Sciences Naturelles Botanique 14: 329 (1840)

Pemphidium is a saprobic ascomycete genus in *Amphisphaeriaceae* (*Amphisphaeriales, Sordariomycetes*) and comprises seven species (Index Fungorum 2024). *Pemphidium* was characterized by well-developed stromata, unitunicate, cylindrical asci, and hyaline, cylindrical to fusiform ascospores that are often unicellular. *Ascospores* possess appendages with or without mucilage at one or both ends. The anamorph of the genus has not been determined (Hyde 1993). The genus *Pemphidium* was introduced by Montagne (1840) to accommodate *P. nitidum,* a species on *Maximiliana regia* Martius (palm) with fusiform-acicular hyaline ascospores, fusiform-acicular unitunicate asci and darkened stroma. Subsequently, six new species (Welwitsch and Currey 1867; Berkeley and Broome 1870; Cesati 1879; Karsten 1973; Hennings 1903) and four species from other genera were placed in this genus (Saccardo 1883; Batista and Maia 1960). By reviewing the genus, Petrak (1953) accepted only *P. nitidum* and excluded other described species based on morphological features. Arx and Müller (1954) proposed *Astrosphaeriella*, *Merrilliopeltis*, *Seynesia* and *Steganopycnis* as synonyms of *Pemphidium*, but later kept it as a separate genus (Müller and Arx 1962). Hyde reviewed the genus, accepted *P. nitidum* as the type and added three new species (Hyde 1993, 1996). After that, Fröhlich and Hyde (2000) added two more species and provided a dichotomous key for the genus. *Pemphidium* resembles *Linocarpon*, but the asci of *Pemphidium* are longer and have a non-reflective subapical ring compared to *Linocarpon*. Ascospores of this genus differ in their appendage morphologies (Hyde 1993). *Pemphidium* was placed in the family *Amphisphaeriaceae* by Wehmeyer (1975) and was confirmed by Eriksson and Hawksworth (1991). All

Pemphidium species have been reported on palm hosts, and *P. zonatum* was also found on *strelitziaceae* (Hyde 1993). Members of this genus were collected from Australia, Brazil, Guyana, Indonesia and South America (Montagne 1840; Hyde 1993, 1996; Fröhlich and Hyde 2000).

Table 3.9 World distribution of *Pemphidium* species.

Species	Host/Substrate	Country	References
Pemphidium australiense	dead rattan of *Calamus australis*	Australia, Queensland	(Fröhlich and Hyde 2000)
P. bomulense	leaves of Berlinia	Tanzania	(Hennings 1904)
P. calamicola	stems of *Calamus*	Australia, Queensland	(Hyde 1996)
P. nitidum	the cortex of rachids of *Maximiliana regia* Martius and *strelitziaceae*	Brazil	(Montagne 1840) (Hyde 1993)
P. palmicola	frond of *Palmae*	Indonesia, Java	(Hyde 1996)
P. rattanicola	dead rattan of *Calamus moti*	Australia, Queensland	(Fröhlich and Hyde 2000)
P. zonatum	Palm rachids	Brazil	(Hyde 1993)

Palmicola K.D. Hyde, Sydowia 45(1): 15 (1993)

Palmicola K.D. Hyde, a genus with scolecospores in *Xylariales* (*Sordariomycetes, Ascomycota*), was typified with *Palmicola archontophoenicis*, and the family which it belongs to has been uncertain (Lumbsch and Huhndorf 2007; Wijayawardene et al. 2021). The genus was characterized by numerous ascomata clustered around a central pore and cylindrical, unitunicate asci with a J-refractive subapical ring (Hyde 1993). The ascospores are filiform, hyaline, septate or aseptate

and often have mucilaginous apical appendages (Hyde 1993; Goh and Hyde 1996), except for *P. australiensis* (Fröhlich and Hyde 2000).

Hyde (1993) first described *Palmicola* on the rachis of *Archontophoenix alexandrae* (Arecaceae) from Australia and discussed how it differs from other scolecosporous ascomycete taxa, such as *Ophioceras* Sacc. and *Linocarpon* Syd. & P. Syd. Hyde (1993) placed this genus in the family *Lasiosphaeriaceae*, which was confirmed by Eriksson and Hawksworth (1994). Goh and Hyde (1996) described the second species, *P. filiformis*, from *Jessenia bataua* in Ecuador, showing that the genus is widespread. Four species of *Palmicola* have been reported to date, viz., *P. archontophoenicis*, *P. australiensis*, *P. bipolaris*, and *P. filiformis* (Index Fungorum 2025) and all of them reported on palm host (Hyde 1993; Goh and Hyde 1996; Fröhlich and Hyde 2000; Taylor and Hyde 2003). *Palmicola* species differ in the morphology of their ascomata and ascospores and lack mucilaginous pads.

Table 3.10 World distribution of *Palmicola* species.

Species	Host/Substrate	Country	References
Palmicola archontophoenicis	fallen rachid of *Archontophoenix alexandrae*	Australia, Queensland	(Hyde 1993)
P. australiensis	dead petiole of *Licuala ramsayi*	Australia, Queensland	(Fröhlich and Hyde 2000)
P. bipolaris	dead petiole of *Archontophoenix alexandrae*	Australia, Queensland	(Taylor and Hyde 2003)
P. filiformis	dead rachis of Jessenia bataua	Ecuador	(Goh and Hyde 1996)

Hypoxylaceae DC., Flore française, Ed. 3 2: 280 (1805)

The family *Hypoxylaceae* was formally validated by Wendt et al. (2018) within the *Xylariales* based on multi-locus phylogenetic analyses, morphological characteristics, and chemotaxonomy. Currently, 18 accepted genera are included in this family: *Annulohypoxylon, Chlorostroma, Daldinia, Durotheca, Entonaema, Hypomontagnella, Hypoxylon, Jackrogersella, Parahypoxylon, Phylacia, Pyrenomyxa,*

Pyrenopolyporus, *Rhopalostroma*, *Rostrohypoxylon*, *Ruwenzoria*, *Theissenia*, and *Thuemenella* (Hyde et al. 2024). Members of *Hypoxylaceae* are primarily saprobic on plant material, while many species also function as endophytes, and some are associated with insect vectors (Wendt et al. 2018). An updated phylogeny for the family is shown in Figure 3.55.

Daldinia Ces. & De Not., Comment. Soc. Crittog. Ital. 1 (4): 197 (1863)

Daldinia (*D.*), introduced by Cesati and De Notaris (1863), is one of the largest genera in *Hypoxylaceae*, comprising approximately 60 species (Hyde et al. 2024). The genus is primarily characterised by well-defined concentric zones in the stromatal interior (Stadler 2014). It has been studied in three major monographs by Child (1932), Ju et al. (1997), and Stadler (2014). Stadler (2014) revisited the genus using a polyphasic approach that incorporated morphology, phylogeny, and chemical profiles, demonstrating the distinction of *Daldinia* from *Annulohypoxylon* and *Hypoxylon*. The classification of *Daldinia* as a distinct genus within *Hypoxylaceae* was further confirmed by Wendt et al. (2018) and Wibberg et al. (2021). Yi et al. (2024) identified 94 *Daldinia* strains from diseased and decayed leaves, introduced seven new species, and proposed that, although these species are mostly hosted by dicots, they do not show host specificity. To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *D. narathiwatensis* as a novel species found on *Eleiodoxa conferta* in the peat swamp forest of Narathiwat, Thailand.

Daldinia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.67

Index Fungorum number: IF903552; Facesoffungi number: FoF 17542

Etymology – The epithet “narathiwatensis” refers to Narathiwat, the region from where the fungus was collected

Holotype – MFLU 24-0517

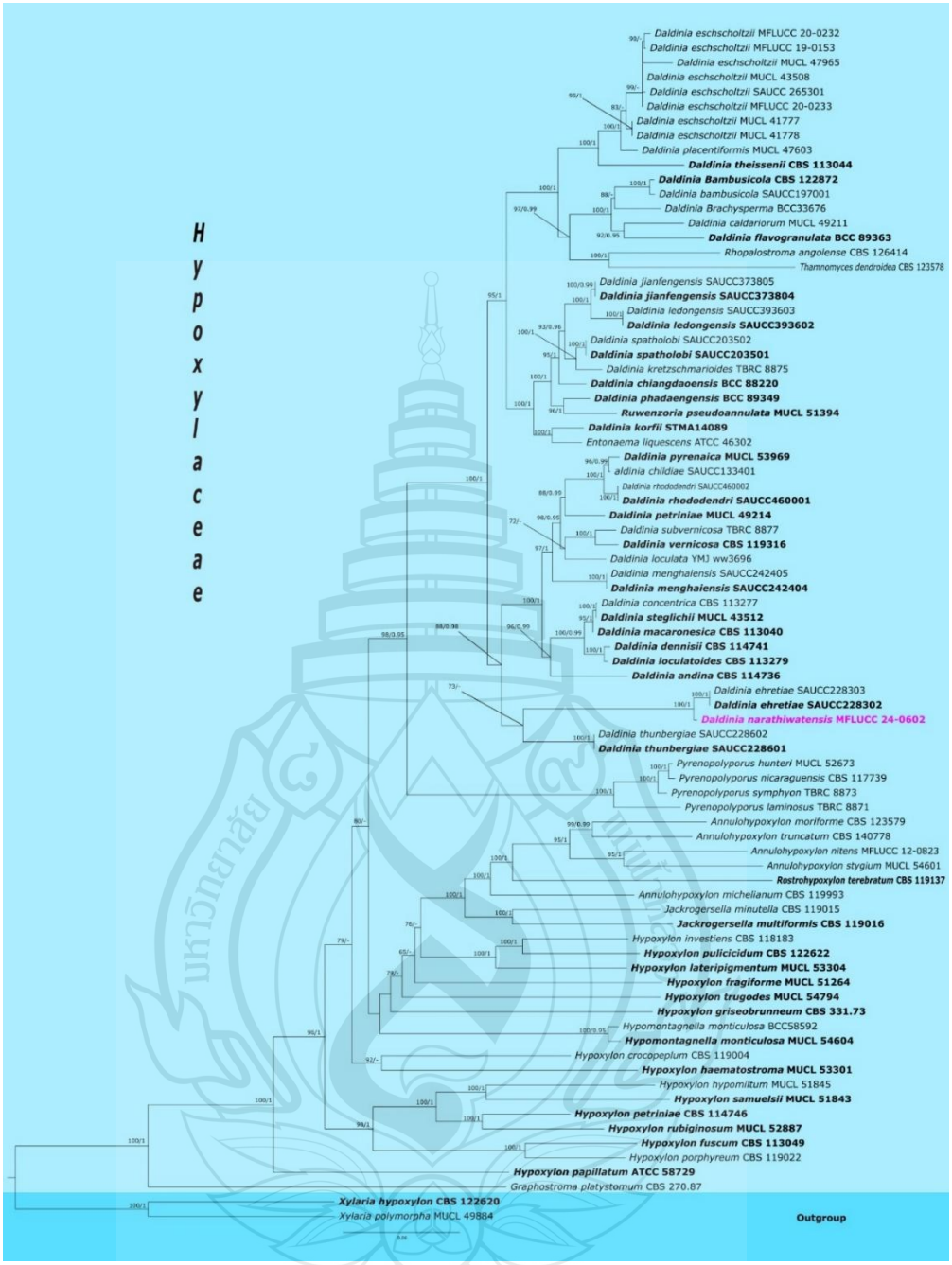
Associated with leaf spot on *Eleiodoxa conferta*. **Asexual morph**: Hyphomycetous. *Mycelium* 2–6 µm wide ($\bar{x}$ = 4 µm, n = 20), septate, branched, thick-walled, verrucose, pale brown to dark brown. *Conidiophores* 120–255.5 × 2.5–8 µm ($\bar{x}$ = 181 × 3.5 µm, n = 30), virgaria-like, micronematous, mononematous, branched,

septate, straight or flexuous, brown, verrucose, thick-walled. *Conidiogenous cells* 9–70 × 2–4.7 µm ($\bar{x}$ = 30 × 3 µm, n = 30), polyblastic, cylindrical, terminal or intercalary, thick-walled. *Conidia* 4–8.8 × 2.5–4.3 µm ($\bar{x}$ = 7 × 3.4 µm, n = 30), ovoid, aseptate, pale brown to brown, smooth, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 6 cm diam. after 10 days at room temperature (25–28 °C). Colony circular, medium dense, slightly raised, dull, entire edge, without pigment diffusion and sporulated after 25 days, surface grey, reverse black.

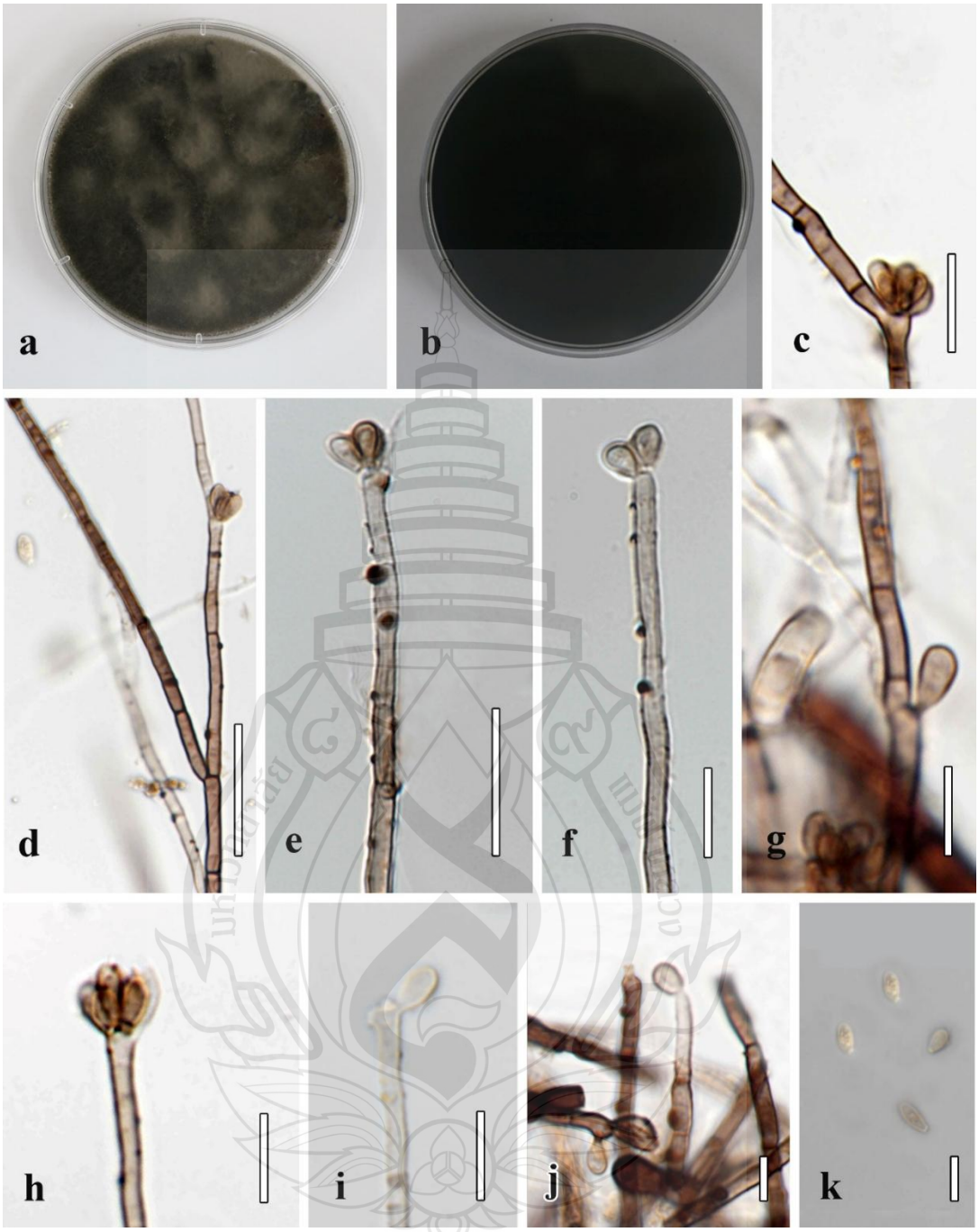
Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on leaf spots of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 207 (MFLU 24-0517, holotype); ex-type living culture MFLUCC 24-0602.

Notes – Phylogenetically, our strain (MFLUCC 24-0602) clustered separately from *Daldinia ehretiae* (SAUCC228302, SAUCC228303) with 100% ML and 1.00 PP statistical support in the combined phylogenetic analyses using ITS, LSU, *rpb2* and *tub2* sequence data (Figure 3.66). Morphologically, *D. narathiwatensis* (MFLU 24-0517) is similar to *D. ehretiae* (HMAS352914), but it can easily be distinguished by having septate hyphae, septate and brown conidiophores, longer and wider conidiophores (120–255.5 × 2.5–8 µm vs. 100–210 × 3.1–4.3 µm), and brown, larger conidiogenous cells (9−70 µm vs. 16.8–24.5 µm), and ovoid, brown conidia, in contrast to aseptate hyphae, aseptate, hyaline conidiophores, hyaline conidiogenous cells, and ellipsoid or cylindrical, hyaline conidia in *D. ehretiae* (HMAS352914) (Yin et al. 2024). Based on the pairwise comparison of *rpb2* and *tub2*, our strain (MFLUCC 24-0602) differs from *D. ehretiae* (HMAS352914) by 1.7% (17/1000 bp, excluded gaps) in *rpb2*, 2.63% (19/722 bp, excluded gaps) in *tub2* and 0.6% (3/550 bp, excluded gaps) in the ITS. Therefore, we introduce *D. narathiwatensis* (MFLU 24-0517) as a novel species based on morphological and phylogenetic evidence.



Note *Xylaria polymorpha* (MUCL 49884), and *X. hypoxylon* (CBS 122620) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.65 Phylogram generated from the ML analysis based on the combined ITS, LSU, *rpb2* and *tub2* sequence data of *Hypoxylaceae*



Note a, b Colonies on the PDA, above (a), and below (b). c–k Conidiophores, conidiogenous cells and conidia. Scale bars: c = 15 µm, d = 30 µm, e = 20 µm, f–i = 10 µm, j–k = 5 µm.

Figure 3.66 *Daldinia narathiwatensis* (MFLU 24-0517, holotype)

Diatrypaceae Nitschke, Pyrenomycetes Germanici 1: 62 (1867)

Allodiatrype Konta & K.D. Hyde, Mycosphere 11 (1): 247 (2020)

Konta et al. (2020) described *Allodiatrype* as a novel genus in the order *Xylariales* based on morphological and phylogenetic data (ITS-*tub*2). *Allodiatrype* is a saprobic genus that typified by *A. arengae*, which was collected on *Arenga pinnata* (Arecaceae) from Thailand. Based on Species Fungorum (2024) there are 7 accepted species in this genus with molecular data in the GenBank. The genus is characterized by stromata that are scattered or clustered, emerging irregularly with either circular or orbicular shapes and a convex surface. The ostiole, opening through the host bark, appears as black spots. Ascomata are perithecial, immersed, and brown, forming in aggregated clusters. Peridium comprises an outer layer of yellow-brown, composed of thick-walled cells arranged in a textura angularis. Paraphyses are septate and hyaline. *Asci* are unitunicate, 8-spored, elongated, narrow, and cylindrical. Ascospores are arranged in a series, hyaline, allantoid, unicellular, and have a thin and smooth wall. Asexual morph: Undetermined. Konta et al. (2020) described *A. arengae* on petiole *Arenga pinnata* (Arecaceae) and *A. elaeidicola*, *A. elaeidis* on petiole *Elaeis guineensis* (Arecaceae) from Thailand. Afsahri et al. (2023) introduced *A. dalbergiae* on woody litter of *Dalbergia cana* in Thailand and *A. eleiodoxae* on *Eleiodoxa* sp. in Narathiwat, Thailand.

Allodiatrype eleiodoxae N. Afshari and S. Lumyong, sp. nov. Figure 3.67

Index Fungorum number: IF901105; Faces of fungi number: FoF14766.

Etymology – Epithet refers to the host genus "*Eleiodoxa*"

Holotype – MFLU 23-0357

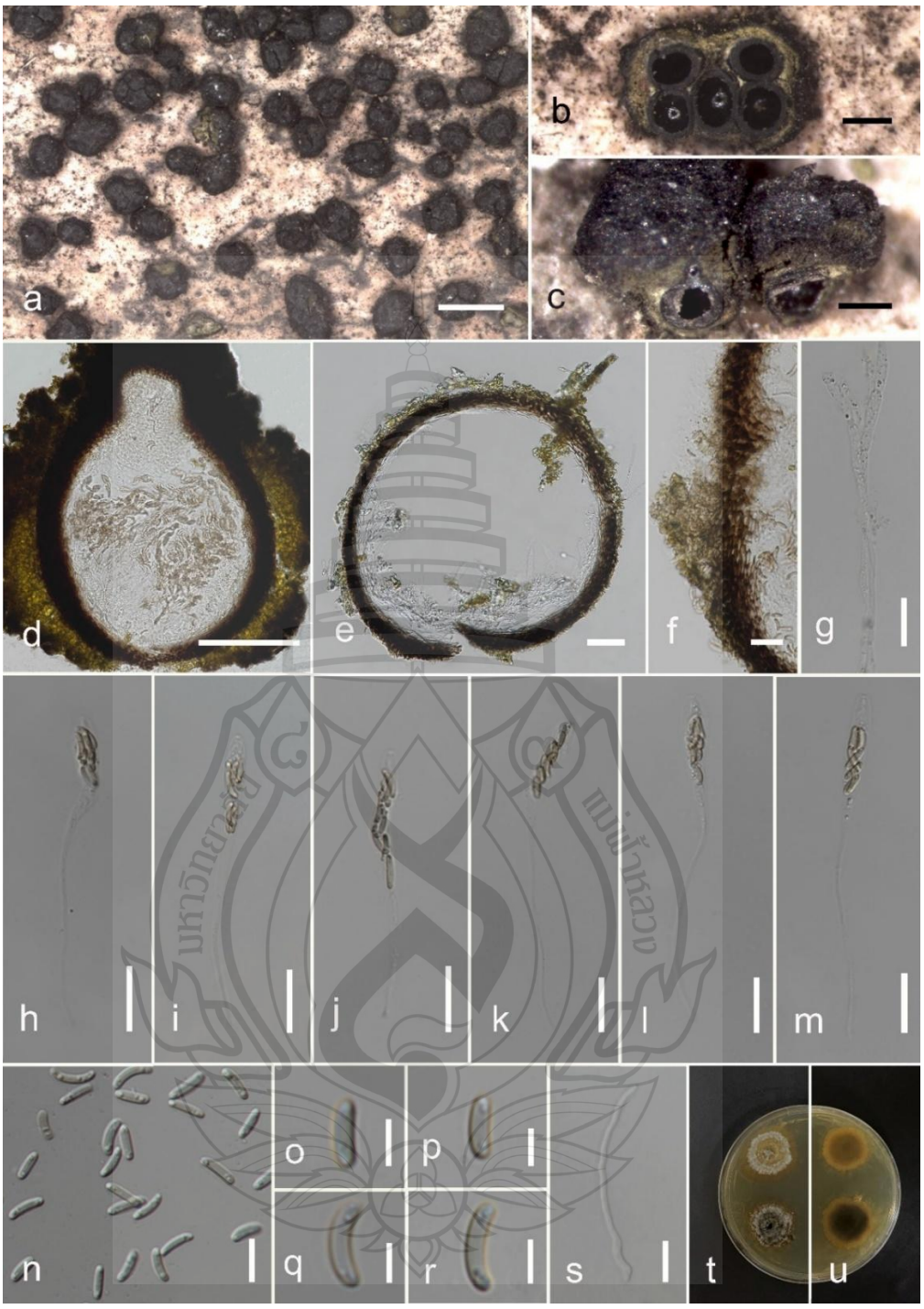
Saprobic on *Eleiodoxa* sp. (*Arecaceae*) woody litter. Sexual morph: *Stromata* 1.1 0.8 × 1–2.7 mm ($\bar{x}$ = 0.9 × 0.77 mm, n = 10), well-developed interior, superficial, scattered or rarely gregarious on host, comprising black outer layer with smooth or tightly packed, thin parenchymatous cell layer and greenish yellow inner layer with loosely packed parenchymatous cells, with umbilicate ostioles opening to surface of stroma as black spots. *Ascomata* (excluding necks) 195–450 × 170–300(–405) µm ($\bar{x}$ = 288 × 329 µm, n = 10), perithecial with groups of 2–5 perithecia immersed in a single stroma, globose–subglobose, black–dark brown, with ostiol. Ostiolar necks 100–150 ×

50–120 µm ($\bar{x}$ = 140 × 110 µm, n = 10), emerging separately, immersed in stromata's outer layer, cylindrical, sulcate, periphysate. *Peridium* 17–25 µm wide ($\bar{x}$ = 21 µm, n = 30), composed of two sections, outer section comprising dark brown, tightly packed cells, arranged in textura angularis, inner layer comprising hyaline cells of textura angularis. *Hamathecium* comprising 3.5–6 µm wide ($\bar{x}$ = 4.8 µm, n = 20) septate, constricted at the septa, wider and flat at the apex, guttulate paraphyses. *Asci* 65–118 × 5.7–9 µm ($\bar{x}$ = 92 × 7.5 µm, n = 25), eight-spored, unitunicate, clavate, with long, thin-walled pedicel, upper portion wide, flattened in apex, with J-apical apparatus. *Ascospores* 7–10 × 2.2–3.3 µm ($\bar{x}$ = 9 × 2.8 µm, n = 30), unicellular, overlapping, hyaline–pale yellow, allantoid–cylindrical or elongate allantoid, with small, 2–3 guttulate at both ends, smooth-walled. Asexual morph: Not observed.

Culture characters – Ascospores germinated on PDA within 24 h, and germ tubes were produced from both end cells. Colonies on PDA, reaching 5 cm diam. after one week at room temperature (25–28 °C). Colony flat, effuse in the center, dense radially fimbriate towards the periphery, from upper surface white to grey, from reverse dark brown or brown at centre becoming radiantly pale brown to the edge. Yellowish brown pigmentation produced on PDA medium at maturity.

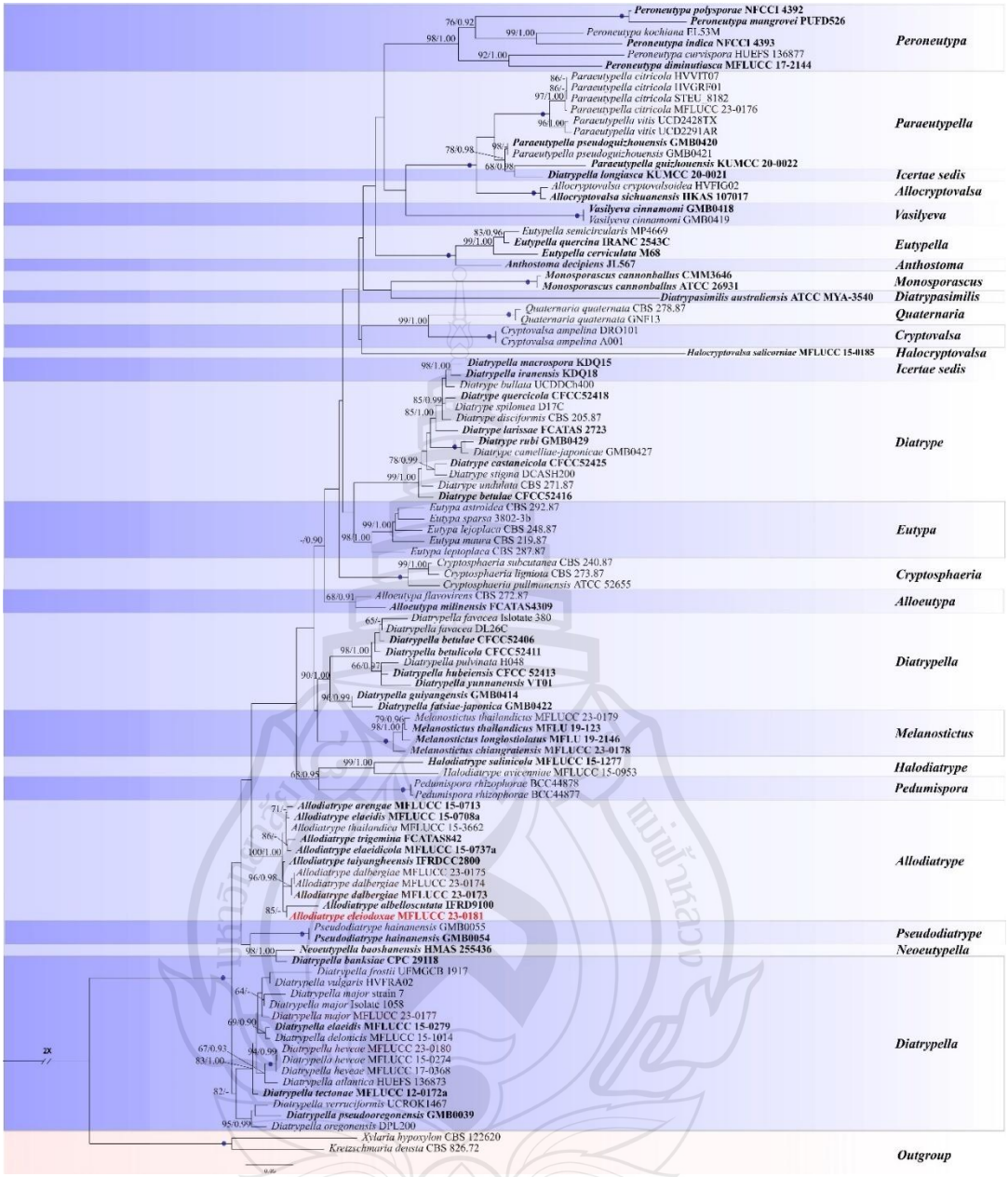
Material examined – Thailand, Narathiwat Province, Yi-ngo District, peat swamp forest, on dead wood of Eleiodoxa sp., 6 April 2022, O. Karimi, 71-Y (MFLU 23-0357, holotype); ex-type living culture MFLUCC 23-0181.

Notes – Based on the phylogram generated from ITS/*tub*2 sequence data, *A. eleiodoxae* (MFLUCC 23-0181) clustered with *A. albelloscutata* (IFRD9100) (85% ML). They have 10/554 bp (1.8%) ITS nucleotide differences. There is a significant difference between the branch length in the phylogenetic tree and the single ITS gene tree. *Allodiatrype eleiodoxae* (MFLU 23-0357) differs from *A. albelloscutata* (IFRD9100) in larger stromata with 2–5 ascomata, whereas IFRD9100 has 5–11 ascomata (Konta et al. 2020). Also, the asci and peridium dimension is considerably larger (Konta et al. 2020). However, these two species have no significant differences in the size and shape of ascospores. Our species was isolated on *Eleiodoxa* sp. from a peat swamp forest in southern Thailand, whereas *A. albelloscutata* (IFRD9100) was from an unidentified host in a terrestrial habitat in China (Li et al. 2022).



Note a Close-up of stromata on Eleiodoxa sp. woody litter. b Transverse section of stroma. c Longitudinal section of stroma. d, e Vertical section through ascoma. f Section of peridium. g Paraphyses. h–m Asci. n–r Ascospores. s A germinated ascospore. t, u Colony on PDA. Scale bars: a = 1 mm, b, c = 200 µm, d = 100 µm, e = 50 µm, f–m, s = 20 µm, n = 10 µm, o–r = 10 µm.

Figure 3.67 *Allodiatrype eleiodoxae* (MFLU 23-0357, holotype)



Note Branch supports of maximum-likelihood (ML) values and Bayesian posterior probability values (BPP) are indicated at the nodes (ML ≥ 60%, left/ BPP ≥ 0.90, right); the tree is rooted with *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122620). Branches with 100% ML/1.00 BPP are shown with a blue dot. Ex-type strains are in black bold. Taxa originating from this study are demonstrated in red.

Figure 3.68 Phylogram generated from maximum-likelihood phylogram analyses of selected taxa in *Diatrypaceae* family based on ITS and *tub*2 matrix

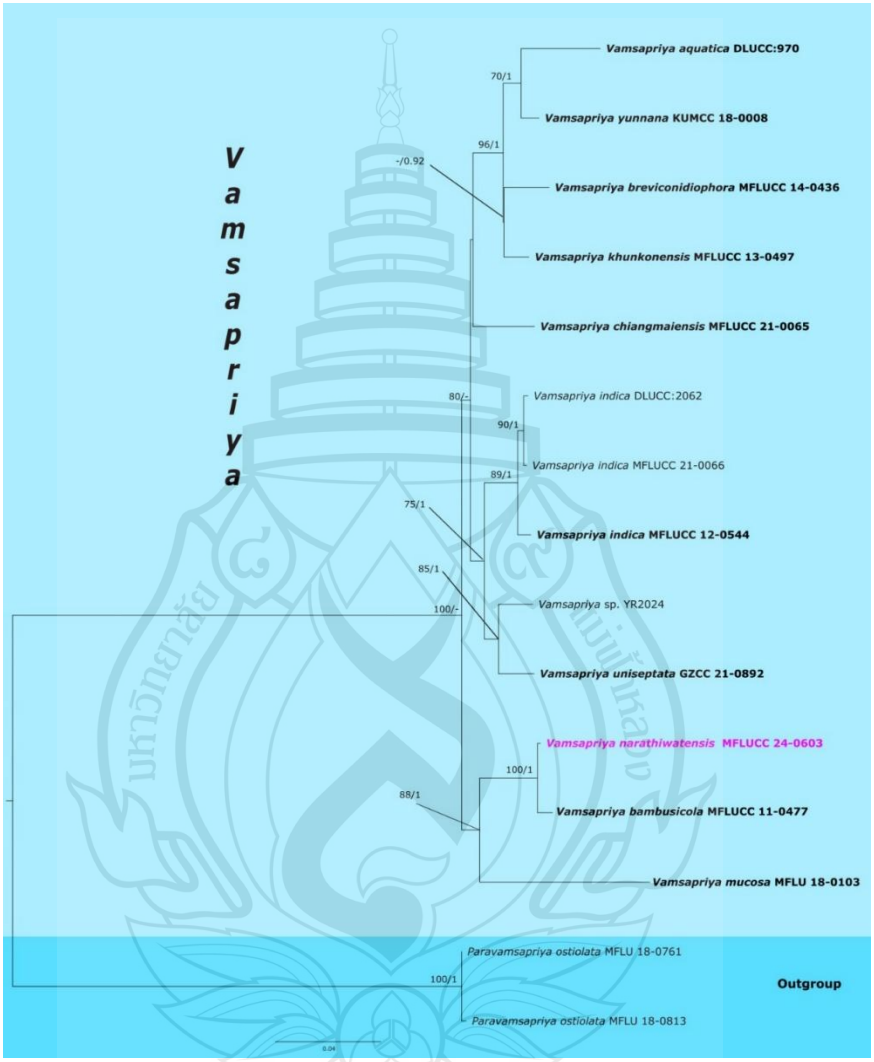
Vamsapriyaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, Journal of Fungi 7 (11, no. 891): 7 (2021)

Vamsapriyaceae was established by Sun et al. (2021) to accommodate the genus *Vamsapriya* (*V.*), originally introduced by Gawas and Bhat (2005), based on the combined phylogenetic analyses of LSU, *rpb2*, *tub2*, and ITS sequence data. Currently, the family comprises six genera: *Diabolocovidia*, *Didymobotryum*, *Vamsapriya*, *Paravamsapriya*, *Podosporium*, and *Tretophragmia* (Saccardo 1886; Gawas and Bhat 2005; Crous et al. 2020; Sun et al. 2021; Samarakoon et al. 2022). Members of *Vamsapriyaceae* are predominantly saprobes found on woody substrates in tropical and subtropical regions (Saccardo 1886; Gawas and Bhat 2005; Crous et al. 2020; Sun et al. 2021; Samarakoon et al. 2022). The sexual morph is characterised by immersed, subglobose, black, ostiolate ascomata with a thin-walled, brown peridium. Paraphyses are hyaline and septate. Asci are eight-spored, unitunicate, cylindrical, and short-pedicellate with a J+ apical ring. Ascospores are apiosporous, fusiform to broad fusiform, and hyaline. The asexual morph is effuse, black, and velvety on natural substrates. It may or may not form synnemata. If present, synnemata are erect, rigid, dark brown, and composed of compact parallel conidiophores. Conidiophores are mono- or polytretic, terminal, clavate to cylindrical, and brown. Conidiogenous cells are similar in morphology, and conidia are catenate or solitary, acrogenous, pigmented, multiform, and septate. Without synnemata, the asexual morph features monoblastic, subcylindrical to clavate conidiogenous cells, and conidia are catenated, acrogenous, brown, ellipsoid to obovoid, thin-walled, and aseptate (Crous et al. 2020; Sun et al. 2021).

Vamsapriya Gawas & Bhat, Mycotaxon 94: 150 (2006)

Gawas and Bhat (2005) introduced *Vamsapriya*, with *V. indica* as the type species. Initially placed in *Xylariaceae* (Hyde et al. 2020), *Vamsapriya* was later reassigned to the newly established family *Vamsapriyaceae* by Sun et al. (2021) based on the combined phylogenetic analyses of LSU, *rpb2*, *tub2*, and ITS sequences, along with morphological characteristics. Currently, 12 *Vamsapriya* species are listed in Index Fungorum (2024). Species of *Vamsapriya* are primarily reported from China and Thailand, where they occur in both aquatic and terrestrial habitats (Dai et al. 2014; Jiang

et al. 2018; Sun et al. 2021; Samarakoon et al. 2022). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *V. narathiwatensis* as a novel species on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated tree for the genus is given in Figure 3.70.



Note *Paravamsapriya ostiolata* (MFLU 18-0761), and *P. ostiolata* (MFLU 18-0813) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolate of the current study is in purple, while the type strains are in bold.

Figure 3.69 Phylogram generated from the ML analysis based on the combined LSU, *rpb2*, *tub2*, and ITS sequence data of *Vamsapriya*

Vamsapriya narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.71

Index Fungorum number: IF903553; Facesoffungi number: FoF 17543

Etymology – The epithet "narathiwatensis" refers to Narathiwat, the region from where the fungus was collected

Holotype – MFLU 24-0518

Saprobic on the submerged rachis of *Eleiodoxa conferta*. **Sexual morph**: Not observed. Asexual morph: Hyphomycetous. *Colonies* on the host scattered or sometimes gregarious, brown. *Mycelium* mostly immersed, composed of branched, septate, brown hyphae. *Conidiophores* synnematous, macronematous, erect, straight or curved, brown to dark brown, cylindrical. *Synnemata* 400–650 µm long, 6.4–16.2 µm wide in the middle, 10.4–20.6 µm wide at the base, erect, dark brown to black, composed of parallel conidiophores which are compact or have distance in some parts. *Conidiogenous cells* 6.5–20 × 3.5–4 ($\overline{x}$ = 11.5 × 4 µm, n = 20), monotretic, integrated, terminal, cylindrical to clavate, brown. *Conidia* 16–47.5 × 6–9.5 µm ($\overline{x}$ = 34 × 7.5 µm, n = 20), cylindrical to obclavate, verrucose, mostly with a large guttule in the apical cells, brown whit 3–6 septa, constricted at septa.

Culture characteristics – Colonies on the PDA reaching 4 cm diam. after 14 days at room temperature (25–28 °C). Colony irregular, convex, fluffy, smooth, surface white with a brownish orange centre, reverse greyish yellow with a whitish margin and brown centre.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, S5PP3N4SBAN (MFLU 24-0518, holotype); ex-type living culture MFLUCC 24-0603.

GenBank numbers – MFLUCC 24-0603: ITS = PV271902, LSU = PV271941, *rpb2* = PV340532.

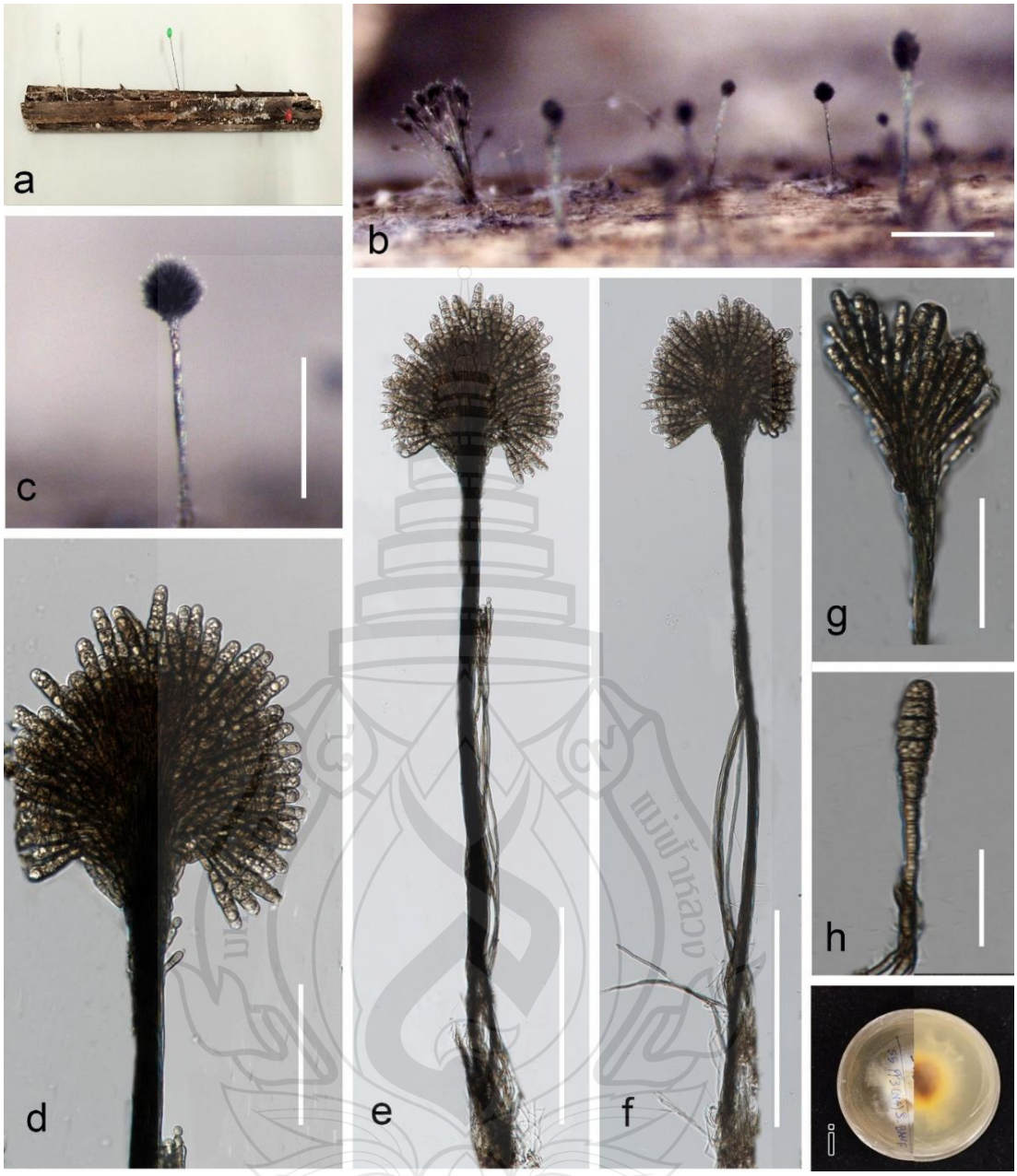
Notes – Our strain (MFLUCC 24-0603) clustered with *Vamsapriya bambusicola* (MFLU 13-0368) with 100% ML and 1.00 PP statistical support in the combined phylogenetic tree (Figure 3.57). Morphologically, our species is similar to *V. bambusicola* (MFLU 13-0368), but it can be easily distinguished by the absence of small circular colonies on the substrate, which are present in the latter. Additionally, it

lacks rigid synnemata, which are shorter (400–650 μm vs. 1100–1400 μm) and narrower at both the middle (6.4–16.2 μm vs. 25–35 μm) and base (10.4–20.6 μm vs. 80–200 μm). Furthermore, it has longer conidiogenous cells (6.5–20 μm vs. 6.5–12.5 μm) and obclavate, verrucose conidia, in contrast to the smooth, cylindrical conidia of *V. bambusicola* (MFLU 13-0368). Based on a pairwise comparison, *V. narathiwatensis* differs from *V. bambusicola* (MFLU 13-0368) by 2.4% (12/499 bp, excluded gaps) in the ITS, 1% (7/750 bp, excluded gaps) in *rpb2* and 0.4% (3/880 bp, excluded gaps) in LSU. Thus, we introduce *V. narathiwatensis* (MFLU 24-0518) as a novel species based on morphological and phylogenetic evidence.

Xylariales genera *incertae sedis*

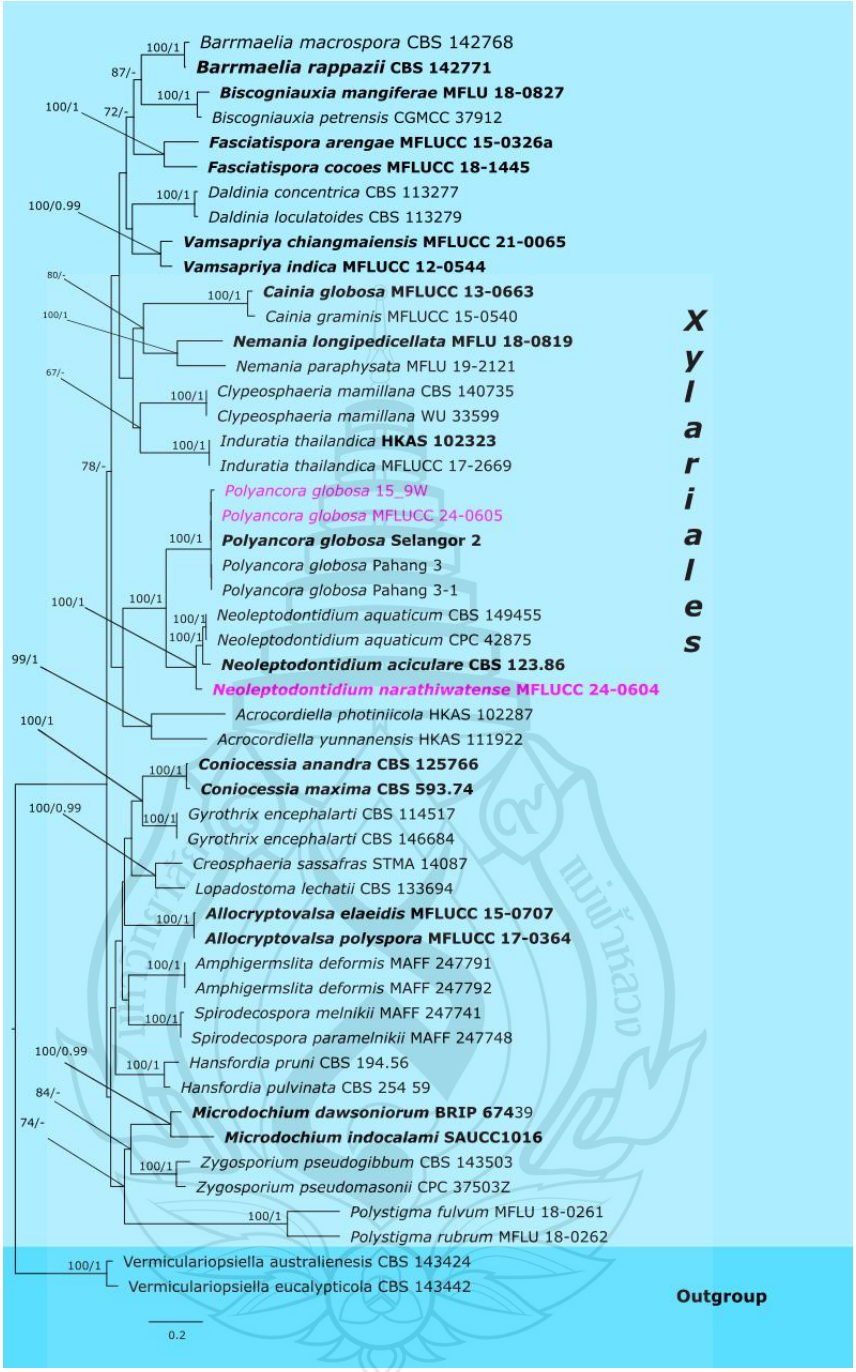
Neoleptodontidium Crous & Jurjević, Fungal Syst. Evol. 11: 135 (2023)

Crous et al. (2023) established a new genus, *Neoleptodontidium* (*N.*), within *Xylariales incertae sedis* to accommodate two species: *N. aquaticum* as the type species, and *N. aciculare* (≡ *Leptodontidium aciculare* V. Rao & de Hoog), which was transferred from *Leptodontidium* based on combined phylogenetic analyses of ITS-SSU sequences and morphology. Currently, there are only two species of *Neoleptodontidium* listed in Index Fungorum (2024). *Neoleptodontidium aquaticum* was isolated from hydroponic water in the USA (Crous et al. 2023), and *N. aciculare* was isolated from rotten wood in India (Rao and de Hoog 1986). To date, no species of this genus have been reported from peat swamp forests. In this study, we introduce *N. narathiwatense* as a novel species on the submerged rachis of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand. An updated tree for the order is given in Figure 3.72



Note a Host. b Colonies on the host substrate. c–f Conidiophores and conidia. g, h Conidiogenous cells and developing conidia. i Colonies on the PDA. Scale bars: b = 400 μm, c = 200 μm, d, g = 50 μm, e, f = 150 μm, h = 20 μm.

Figure 3.70 *Vamsapriya narathiwatensis* (MFLU 24-0518, holotype)



Note *Vermiculariopsiella australienesis* (CBS 141499, CBS 141500, CBS 143424), and *V. eucalypticola* (CBS 143442, CBS 146091) were used as the outgroup taxa. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The isolates of the current study are in purple, while the type strains are in bold.

Figure 3.71 Phylogram generated from the ML analysis based on the combinedLSU, *rpb2*, *tub2*, and ITS sequence data of *Xylariales*

Neoleptodontidium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Figure 3.73

Index Fungorum number: IF903554; Facesoffungi number: FoF 17544

Etymology – The epithet "narathiwatense" refers to Narathiwat, the region from where the holotype was collected

Holotype – MFLU 24-0519

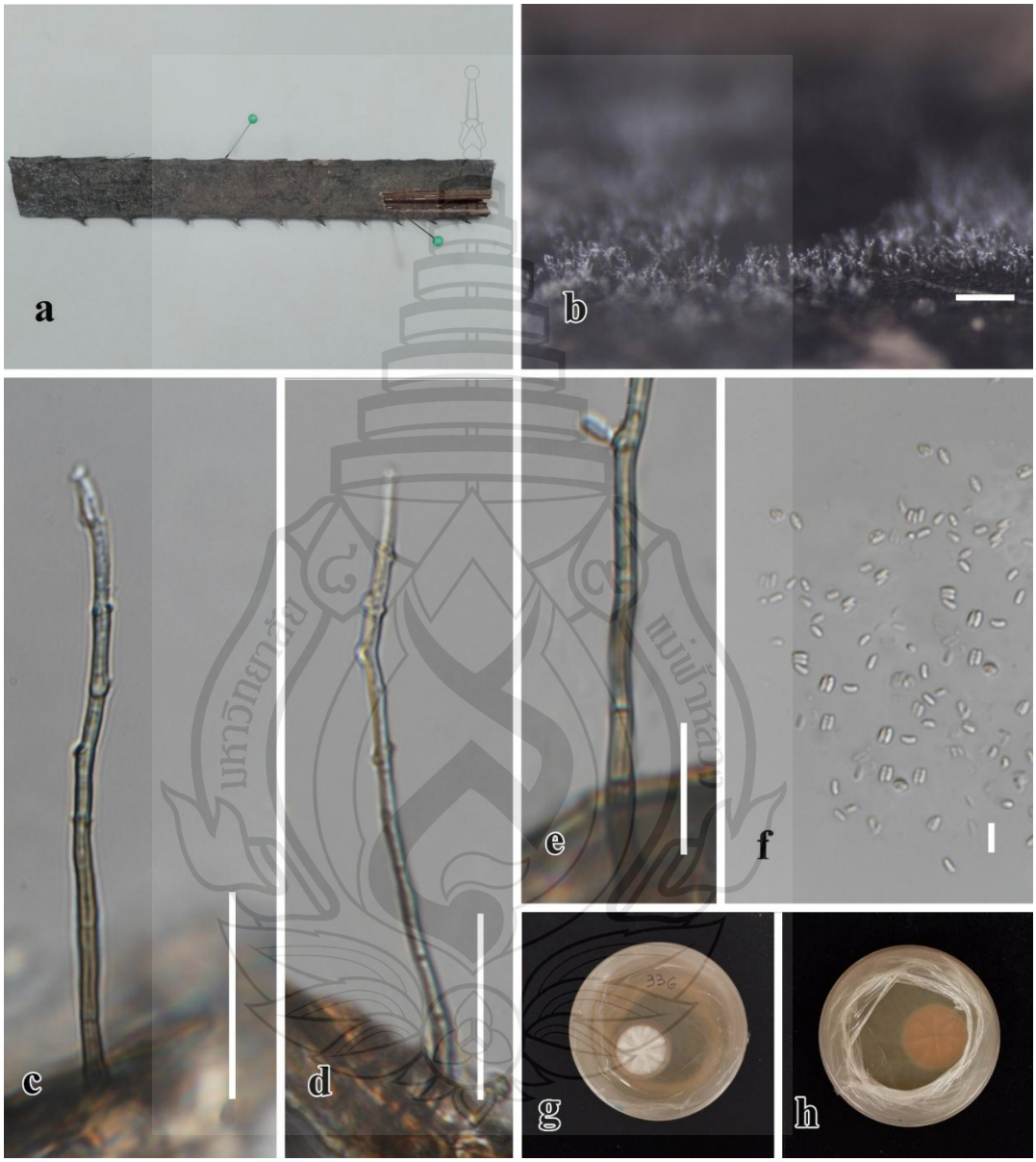
Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on natural host effuse, gregarious, white, glistening. *Conidiophores* 60–82 × 1.2–2.2 μm ($\overline{x}$ = 71.7 × 1.8 μm, n = 20), macronematous, mononematous, solitary or in small groups, unbranched, septate, erect, straight or curved toward the apex, cylindrical, smooth, thin-walled, brown, paler towards the apex. *Conidiogenous cells* 10.5–43 × 2–2.5 μm ($\overline{x}$ = 30 × 2 μm, n = 20), phialidic, cylindrical, integrated with short denticles, terminal and lateral, smooth, thin-walled, pale brown, subhyaline towards the apex. *Conidia* 2.6–4.2 × 1.1–1.9 μm ($\overline{x}$ = 3.3 × 1.6 μm, n = 30), aggregating in mucoid mass, cylindrical to subcylindrical, sometimes reniform, aseptate, hyaline, smooth, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 2.8 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, medium dense, dull, slightly raised, entire edge, surface whitish grey with pale brown margin and reverse soot brown.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta*, 4 August 2023, O. Karimi, 33G (MFLU 24-0519, holotype); ex-type living culture MFLUCC 24-0604.

Notes – Phylogenetically, *Neoleptodontidium narathiwatense* (MFLUCC 24-0604) formed a distinct clade from *N. aciculare* (CBS 12386) and *N. aquaticum* (CBS 149455, CPC 42875), with 100% ML, 1.00 PP statistical support in the combined phylogenetic analyses (Figure 3.59). Morphologically, it is similar to *N. aciculare* (CBS-H 3858), but it differs in having longer conidiophores (60–82 μm vs. 15–30 μm) and lacks rejuvenation through terminal phialides, which form new phialides above older ones (Rao and Hoog 1986; Crous et al. 2023). A pairwise comparison of ITS sequences revealed that our strain differs from *N. aciculare* (CBS-H 3858) by 4.8%

(23/500 bp, without including gaps). The sequences for *rpb2* and *tub2* of *N. narathiwatense* were not comparable with *N. aciculare*, as these markers are unavailable for *N. aciculare* (CBS-H 3858). Therefore, we introduce *N. narathiwatense* (MFLU 24-0519) as novel species based on morphological and phylogenetic evidence.



Note a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f Conidia. g, h Colonies on the PDA. Scale bars: b = 20 μm, c–e = 25 μm, f = 5 μm.

Figure 3.72 *Neoleptodontidium narathiwatense* (MFLU 24-0519, holotype)

Polyancora Voglmayr & C. Yule, Mycological Research 110 (10): 1247 (2006)

Voglmayr and Yule (2006) established *Polyancora* (*Po.*), as a new genus to accommodate *Po. globosa*, which was originally found on submerged leaves and twigs in tropical peat swamp forests in Peninsular Malaysia within *Xylariales*. Currently, only one species of this genus is listed in Index Fungorum (Hyde et al. 2024). Although there is one report of this species as an endophyte, the results are doubtful as it relied solely on the 18S rRNA sequence without morphological data. In the phylogenetic tree, the endophytic strain formed a separate clade from the type species of *Po. globosa*, raising questions on the identification of the species (Netala et al. 2016). Since the discovery of the type species in 2006, no further reports of this genus have been made from peat swamp habitats worldwide or from other habitats. In this study, we report *Po. globosa* on submerged rachides of *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand, and provide *rpb2* and *tef-1α* sequences of this genus for the first time.

Polyancora globosa Voglmayr & Yule. Figure 3.74

Index Fungorum number: IF500736; Facesoffungi number: FoF 17545

Saprobic on the submerged rachis of *Eleiodoxa conferta*. Asexual morph: Hyphomycetous. *Colonies* on the host effuse, scattered or in small groups, whitish grey. *Mycelium* mostly immersed, composed thick-walled, brown to dark brown hyphae. *Conidiophores* 200–350 × 1.2–2.2 μm ($\overline{x}$ = 283.5 × 6.2 μm, n = 15), macronematous, mononematous, unbranched, septate, straight or slightly curved at the apex, thick-walled, smooth, brown to dark brown at base, hyaline to subhyaline toward the apex. *Conidiogenous cells* 10–15 × 2.5–4 μm, integrated, holoblastic, terminal. *Conidia* 50–56 μm diam. ($\overline{x}$ = 54 μm, n = 20), composed of chains of globose to subglobose cells 6–8 μm wide ($\overline{x}$ = 6.7 μm, n = 20), which branch repeatedly in a centrifugal manner, the outer globose cells bear 2–5 cylindrical, radially oriented cells with 9–13 μm long ($\overline{x}$ = 11.2 μm, n = 20), and 1–2 μm wide ($\overline{x}$ = 1.2 μm, n = 20), which at the tip of these cells, 2–6 branches arise at right angles from the cylindrical cells, hyaline to subhyaline, thin-walled. Sexual morph: Not observed.

Culture characteristics – Colonies on the PDA reaching 5.5 cm diam. after 14 days at room temperature (25–28 °C). Colony circular, dense, dull, slightly raised, entire edge, surface olive brownish and reverse brown.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, on the submerged rachis of *Eleiodoxa conferta,* 4 August 2023, O. Karimi, 18B (MFLU 24-0520); living culture MFLUCC 24-0605.

Known host – *Eleiodoxa conferta* (This study).

Known distribution – Malaysia (Voglmayr and Yule 2006), Thailand (This study).

GenBank numbers – MFLUCC 24-0605: ITS = PV271903, LSU = PV271942, *rpb2* = PV340533, *tef-1α* = PV340506.

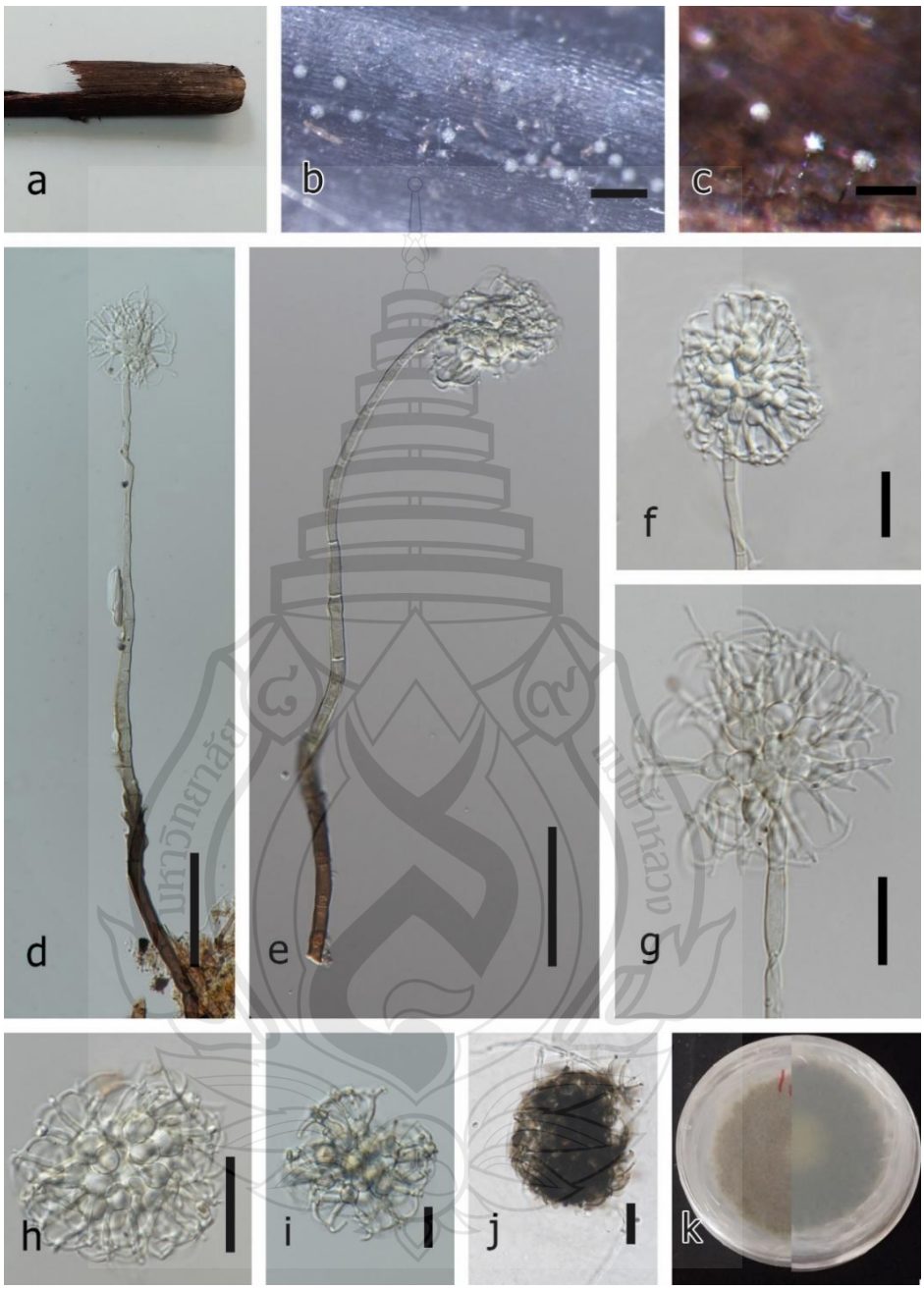
Notes – Phylogenetically, our strain (MFLU 24-0520) clustered with *Polyancora globosa* strains (Selangor 2, Pahang 3, Pahang 3-1) with 100% ML and 1.00 PP statical support (Figure 3.59). Morphologically, our strain (MFLU 24-0520) resembles *Po. globosa* (WU 26489) in having macronematous, mononematous, unbranched, septate conidiophores, integrated, holoblastic, terminal conidiogenous cells and acrogenous, multicellular, globose conidia (Voglmayr and Yule 2006). Therefore, we identified our strain (MFLU 24-0520) as *Po. globosa* based on morphological characters and phylogenetic analyses. We report our strain (MFLU 24-0520) as a new host and geographical record of *Po. globosa* on *Eleiodoxa conferta* from the peat swamp forest in Narathiwat, Thailand.

Sordariomycetes genera *incertae sedis*

Flammispora U. Pinruan, J. Sakayaroj, K.D. Hyde & E.B.G. Jones, Studies in Mycology 50 (2): 384 (2004)

Flammispora is a saprobic genus, which was described by Pinruan et al. (2004) as freshwater ascomycetes on submerged leaves of *Licuala longecalycata* from peat swamp forest in Narathiwat, Thailand. There are only two accepted species in this genus based on Species Fungorum (2024) with available sequence data for one species in the GenBank. The genus characterized by having immersed or semi-immersed, coriaceous, ostiolate, solitary ascomata, 8-spored, unitunicate, clavate to cylindrical clavate, pedicellate asci, biseriate, fusiform, hyaline, septate ascospores. Pinruan et al. (2004) introduced *Flammispora bioteca* as a new species on *Licuala longecalycata* based on morphological evidence and single phylogenetic analysis using partial SSU rDNA. Raja and Shearer (2008) identified the second species within this genus, which was found on

submerged decorticated woody debris in a lake located in Ocala National Forest, Florida, using morphological characteristics.



Note a Host. b, c Colonies on the host substrate. d, e Conidiophores. f, g Conidiogenous cells and conidia. h, i Conidia. j A germinated conidium. k Colonies on the PDA. Scale bars: b = 200 μm, c = 125 μm, d–e = 60 μm, f–i = 15 μm.

Figure 3.73 *Polyancora globosa* (MFLU 24-0520, a new host and geographical record)

Ungerminated fungal isolates identified based solely on morphology

Several fungal genera were observed but did not successfully germinate in culture. These genera were identified based on their morphological characteristics and are listed in Table 3.11. Their classification was determined through microscopic examination and taxonomic comparison.

Table 3.11 Fungal taxa that have not been identified to the species level. These include taxa identified solely on morphology and fungi that did not germinate on the media

No.	Genera name	Family	Order	Class	Host
1	*Paravamsapriya* sp.	*Vamsapriyaceae*	*Xylariales*	*Sordariomycetes*	*Eleiodoxa conferta*
2	*Sporoschisma* sp.	*Chaetosphaeriaceae*	*Chaetosphaeriales*	*Sordariomycetes*	*E. conferta*
3	*Bactrodesmium* sp.	*Savoryellaceae*	*Savoryellales*	*Sordariomycetes*	*E. conferta*
4	*Cheiromyceopsis* sp.	-	-	*Ascomycota genera incertae sedis*	*E. conferta*
5	*Linocarpon* sp.	*Linocarpaceae*	*Chaetosphaeriales*	*Sordariomycetes*	*Cyrtostachys renda*
6	*Oxydothis* sp.	*Oxydothidaceae*	*Amphisphaeriales*	*Sordariomycetes*	*C. renda*
7	*Lasiodiplodia* sp.	*Botryosphaeriaceae*	*Botryosphaeriales*	*Dothideomycetes orders incertae sedis*	*C. renda*
8	*Berkleasmium* sp.	*Tubeufiaceae*	*Tubeufiales*	*Dothideomycetes*	*Licuala paludosa*
9	*Sporidesmium* sp.	*Sporidesmiaceae*	*Sporidesmiales*	*Sordariomycetes*	*E. conferta*
10	*Chloridium* sp.	*Chaetosphaeriaceae*	*Chaetosphaeriales*	*Sordariomycetes*	*E. conferta*

3.3 Discussion

The peat swamp fungi identified in this study belong to *Ascomycota*, distributed across three classes, including *Sordariomycetes* (65%), *Dothidiomycetes* (32%) and *Leotiomycetes* (3%) (Figure 3.74). The recorded taxa were distributed across 19 orders, with *Chaetosphaeriales Tubeufiales*, *Xylariales*, and *Pleosporales* being the dominant orders (Figure 75). Our findings align with the results of previous studies on peat

swamp forests in Narathiwat (Pinnoi et al. 2006; Pinruan et al. 2007). However, although numerous species in those studies were classified under undetermined orders, *Pleosporales*, *Xylariales*, *Tubeufiales* and *Chaetosphaeriales* were identified as the dominant orders, respectively.

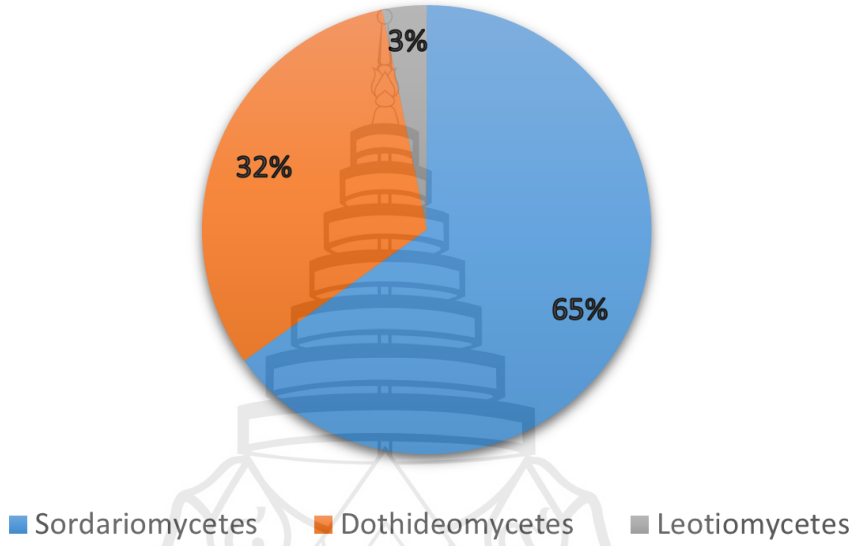


Figure 3.74 Distribution of peat swamp *Ascomycota* in three classes

The recorded species are distributed among 26 families, with 16 of them in *Sordariomycetes*, 10 in *Dothideomycetes* and one in *Leotiomycetes*. *Tubeufiaceae* is the largest family, followed by *Chaetosphaeriaceae*, *Linocarpaceae* and *Distoseptisporaceae* (Figure 76).

Chloridium, *Tamhinispora*, *Distoseptispora*, *Linocarpon*, and *Oxydothis* were frequently observed genera, indicating the ability of these fungi to colonise palm substrates in peat swamp forests. Some genera from this research have been recorded in freshwater habitats for the first time, including *Javarisimilis*, *Tamhinispora*, *Strossmayeria*, and *Pseudosaprodesmium*, demonstrating the rich biodiversity of peat swamp forests. Additionally, this ecosystem may provide a unique environment for certain fungi; for example, we found *Polyancora globosa*, which has only been recorded from peat swamp forests (Voglmayr and Yule 2006). This result underscores the importance of conserving this environment.

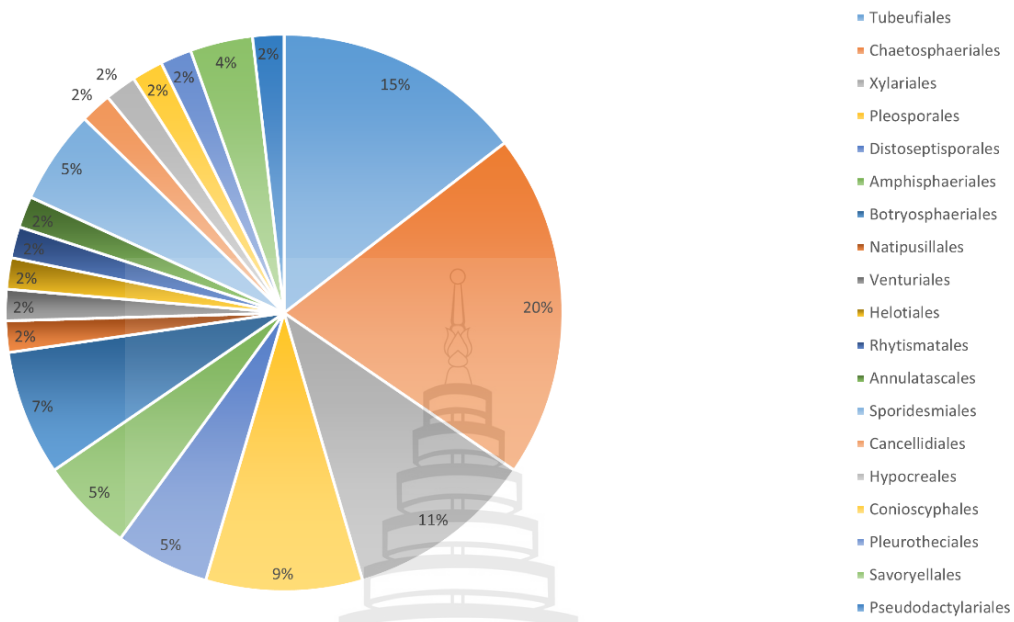


Figure 3.75 Distribution of peat swamp *Asomycota* in 19 orders

We investigated the fungal presence on *Eleiodoxa conferta*, *Cyrtostachys renda*, *Eugeissona tristis*, *Livistona saribus*, *Licuala paludosa*, and *Caryota mitis*. As the focus of the research was on *Eleiodoxa conferta*, most species were recorded on this host, accounting for about 80%.

Pinnoi et al. (2006) recorded the abundance of fungi on different parts of *Eleiodoxa conferta*, reporting mostly on petioles (53%), followed by rachides, and leaves. However, our study showed the highest fungal presence on rachides (73%), followed by leaves and petioles. The greater abundance of fungi on petioles and rachides might be attributed to their higher nutrient content, resulting from thicker cell walls and the abundance of sclerenchyma associated with vascular bundles. Pinnoi et al. (2006) suggested that another reason for the higher fungal presence on petioles could be their higher water content, as petioles are often submerged or in contact with the water surface. In contrast, in our study, we mostly recorded fungi on rachides as we primarily collected submerged plant material, ensuring that all parts were equally exposed to water, which provided suitable conditions for fungal growth and colonisation.

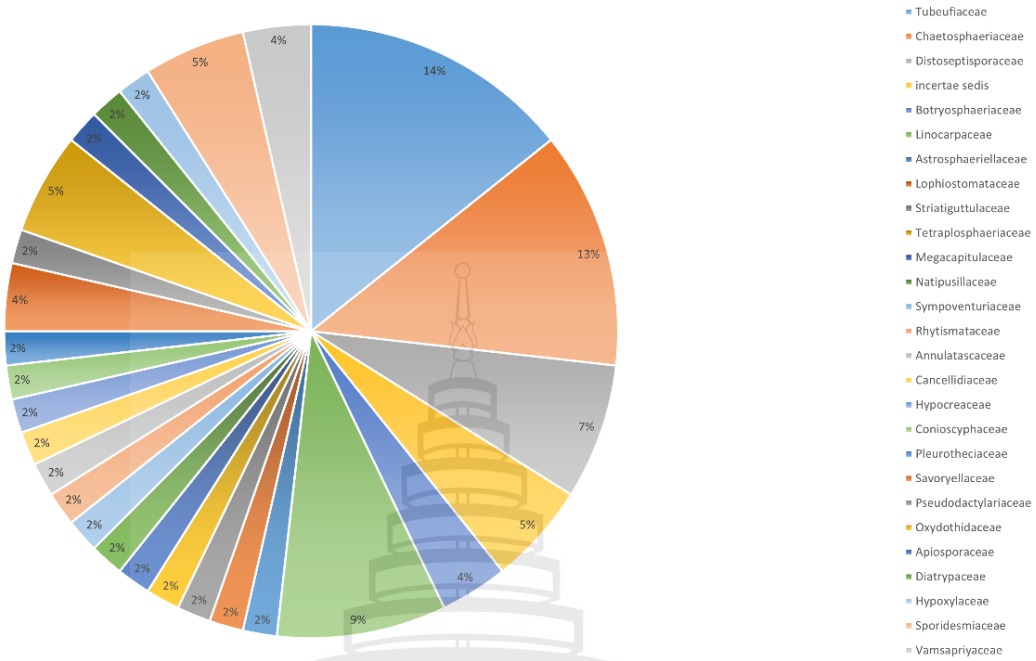


Figure 3.76 Distribution of peat swamp *Asomycota* in 26 families

When comparing our results with the previous study by Pinnoi et al. (2006) on *Eleiodoxa conferta*, we identified 10 overlapping genera: *Cancellidium, Chloridium, Helicoma, Lasiodiplodia, Lentistoma, Linocarpon, Nawawia, Oxydothis, Trichoderma* and *Tubeufiai*. However, due to numerous taxonomic changes in generic classifications since that study, there might be additional overlaps. For instance, they recorded Sporidesmium-like genera, but with the availability of sequence data, these genera were later divided into different taxa, such as *Distoseptispora* (Su et al. 2016), of which we have introduced three new species (*D. arecacearum, D. eleiodoxae, D. narathiwatensis*). Another example is their report of undetermined species of *Annulatascus*, some of which were later transferred to other genera, including *Longivarius* (Dong et al. 2021a), which we have also reported in our research (*Lo. narathiwatensis*). This finding highlights the importance of molecular knowledge in accurate fungal classification, enabling a more comprehensive investigation of fungal composition across different hosts and habitats.

CHAPTER 4

OVERALL CONCLUSIONS

4.1 Conclusion

Peat swamp forests are endangered, unique habitats found in only a few regions globally, providing various ecosystem services. Human activities threaten this productive ecosystem, as many of them lead to degradation (Jackson et al. 2009). Therefore, it is crucial to study and preserve the biodiversity of the organisms inhabiting these ecosystems. Fungi, essential decomposers in peat swamp forests, have been poorly studied. A few studies in Thailand have shown the fungal species richness of Narathiwat peat swamp forests. However, the recorded taxa are mostly identified using morphological characteristics, and many are identified only at the genus level (Pinruan et al. 2002; 2004a, 2004b; 2007; 2008; 2010a, 2010b; Pinnoi et al. 2003a, 2003b; 2004; 2006; 2009; 2010). This limitation highlights the need for incorporating molecular data for more accurate classification. Therefore, incorporating molecular data is necessary to classify fungi accurately. Based on the need to study the fungal community of peat swamp forests and provide molecular data for their taxonomy, this research was conducted. The study focused on investigating saprobic fungi inhabiting *Eleiodoxa conferta* (Arecaceae) from 2022 to 2024. This research specifically investigates various aspects of the taxonomy, phylogeny, and ecological relationships of fungi associated with native Thai palms from the peat swamp forest in Narathiwat, Thailand. This chapter aims to summarize all the data collected in the preceding chapters. The exploration of peat swamp fungi from Thailand, led to the discovery of both novel and known fungal taxa. From this research, we introduced one new family, one new genus and 31 new species and 25 new host, geographical and habitat records based on morphology and phylogeny. Some of these findings have already been published and some are awaiting further confirmation. These fungi belong to the following groups: Class *Dothidiomycetes: Botryosphaeriales* (*Botryosphaeriaceae*: *Lasiodiplodia brasiliensis, L. theobromae*), *Pleosporales* (*Astrosphaeriellaceae: Javarisimilis*

narathiwatensis, Lophiostomataceae: Lentistoma narathiwatense, Striatiguttulaceae: Longicorpus striataspora, Tetraplosphaeriaceae: *Ernakulamia cochinensis, Megacapitulaceae: Megacapitula villosa*), *Natipusillales (Natipusillaceae: Narathiwatiomyces confertae*), *Tubeufiales* (*Tubeufiaceae: Helicoma narathiwatense, Helicoma eleiodoxae, Neohelicosporium arecaceus, Neohelicosporium fusisporum, Neohelicosporium narathiwatense, Tamhinispora narathiwatensis, Tubeufia narathiwatensis*), *Venturiales* (*Sympoventuriaceae: Yunnanomyces narathiwatensis*), Class *Leotiomycetes: Helotiales genera incertae sedis* (*Strossmayeria narathiwatensi*s) *Rhytismatales* (*Rhytismataceae*: *Terriera narathiwatensis*), Class *Sordariomycetes: Annulatascales* (*Annulatascaceae: Longivarius narathiwatensis*), *Cancellidiales* (*Cancellidiaceae: Cancellidium narathiwatense*), *Distoseptisporales* (*Distoseptisporaceae*: *Distoseptispora arecacearum, D. eleiodoxae, D. narathiwatensis*), *Hypocreales* (*Hypocreaceae*: *Trichoderma virens*), *Microascales* (*Microascaceae*: *Petriella thailandica*), *Conioscyphales* (Conioscyphaceae: Conioscypha narathiwatensis), *Pleurotheciales* (*Pleurotheciaceae*: *Pseudosaprodesmium narathiwatense*), *Savoryellales* (*Savoryellaceae: Savoryella narathiwatensis*), *Chaetosphaeriales* (*Chaetosphaeriaceae*: *Chaetosphaeria narathiwatensis, Ch. palmicola, Chloridium narathiwatense, Nawawia narathiwatensis, Stanjehughesia narathiwatensis, Linocarpaceae*: *Linocarpon appendiculatum, Linocarpon narathiwatense*), *Pseudodactylariales* (*Pseudodactylariaceae*: *Pseudodactylaria longidenticulata*), *Amphisphaeriales* (*Oxydothidaceae*: *Oxydothis narathiwatensis*, *Apiosporaceae*: *Nigrospora chinensis*), *Xylariales* (*Diatrypaceae: Allodiatrype eleiodoxae, Hypoxylaceae: Annulohypoxylon thailandicum, Daldinia narathiwatensis, D. eschscholtzii, Hypoxylon hypomiltum, Jackrogersella minutella, Vamsapriyaceae: Vamsapriya narathiwatensis, Xylariaceae: Xylaria apiculate, X. bawanglingensis, X. grammica, X. karsticola, X. longipes, Neoleptodontidium narathiwatense,* and *Polyancora globosa*).

Our findings align with previous studies on peat swamp forests in Narathiwat (Pinnoi et al. 2006; Pinruan et al. 2007). However, although numerous species in those studies were classified under undetermined taxa, our study provides further taxonomic resolution. For example, our fungal collection from this habitat is predominantly composed of *Chaetosphaeriales, Tubeufiales, Xylariales,* and *Pleosporales,* which

were also the dominant orders reported in previous studies. As our study focuses on *Eleiodoxa conferta*, we identified ten overlapping genera when compared to previous studies on this host (Pinnoi et al. 2006). However, since those studies relied solely on morphological characteristics, many fungal taxa were only identified at the genus level. By incorporating molecular data, our study provides a more accurate identification and classification of peat swamp forest fungi, contributing to a better understanding of its fungal community.

In this study, taxa from *Xylariales* were identified as one of the dominant orders in the peat swamp forest. Additionally, we documented collections from palms and other hosts belonging to this order. As *Xylariales* are well known for their metabolite activity, this study expands the understanding of this group by providing notes on the order and its families, along with the introduction of four new species and ten new records. Our findings highlight the adaptability of this group to various habitats, including terrestrial and freshwater environments, across a wide range of hosts.

Furthermore, this study enhances the understanding of microfungi in Thailand by providing additional morphological and phylogenetic evidence for their taxonomic placement. The fungal specimens obtained have been deposited in herbarium and culture collections, serving as valuable resources for future research in fungal taxonomy and the exploration of their biomaterial properties.

4.2 Research Advantages

This study offers several important advancements in the understanding of fungi in peat swamp ecosystems. First, it provided a more accurate identification and classification of *Ascomycota* from peat swamp forests by utilizing a polyphasic approach that combines morphology and phylogenetic analyses. Additionally, sequence data were provided to address the limitations of previous studies on peat swamp fungi in Thailand, particularly for fungi associated with *Eleiodoxa conferta*, helping to establish more accurate taxonomic placements. The identification of a new family, genus, and numerous species expands the current taxonomic framework of fungi in these ecosystems. Moreover, the discovery of novel fungi in peat swamp forests emphasizes the importance of these habitats and highlights the potential for further

exploration, underscoring the need for conservation efforts to protect these unique environments. The deposition of various fungal isolates in herbarium and culture collections ensures their preservation for future studies. Finally, this research contributes to expanding the knowledge of *Xylariales* diversity in Thailand, with findings published in international journals, fostering broader recognition and understanding of this group.

4.3 Future Work

4.3.1 Investigate peat swamp fungi including endophytes and pathogens, along with further studies on saprobes, to understand their lifestyles and ecological roles.

4.3.2 To date, all fungal studies from peat swamp forests have relied on culture-dependent methods, which consider only fungi capable of growing on artificial media. However, to achieve a comprehensive understanding of the fungal community, it is essential to study both culturable and non-culturable fungal groups. Integrating culture-independent methods with traditional culture-dependent techniques is crucial for obtaining a more comprehensive understanding of fungal diversity. This combined approach facilitates the discovery of species that are challenging to identify using conventional methods alone.

4.3.3 Explore the potential of peat swamp Ascomycota in pharmaceutical and agricultural applications, such as developing natural antimicrobial or antifungal compounds.

4.3.4 Investigate the seasonal variation of fungal populations in peat swamp forests to examine the role of environmental factors (e.g., temperature, humidity, water level) in shaping fungal communities in this ecosystem.

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APPENDIX A

PUBLICATIONS

Asian Journal of Mycology 5(2): 187–201 (2022) ISSN 2651-1339
www.asianjournalofmycology.org **Article**
Doi 10.5943/ajom/5/2/8

Taxonomy and phylogenetic appraisal of *Hypomyces iranica* sp. nov. (*Hypocreaceae*, *Hypocreales*)

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Karimi O, Rathnayaka AR, Gajanayake AJ, Farias ARG, Mamarabadi M, Chethana KWT 2022 – Taxonomy and phylogenetic appraisal of *Hypomyces iranica* sp. nov. (*Hypocreaceae*, *Hypocreales*). Asian Journal of Mycology 5(2), 187–201, Doi 10.5943/ajom/5/2/8

Abstract

Hypomyces is an important genus of fungicolous fungi associated with different ascomycetes and basidiomycetes. Numerous researchers have conducted morphological and molecular studies on this genus. In this study, we collected submerged branches of *Fagus* sp. from Mazandaran Province in Iran, from which a fungal isolate was obtained. Morphology coupled with maximum likelihood and Bayesian inference analyses of the combined ITS, LSU, and *rpb2* sequence data showed it is a novel taxon (*Hypomyces iranica*). The morphology of the newly described species is compared with its sister taxa, and a comprehensive description and micrographs are provided.

Keywords – 1 new species – Mazandaran – morphology – multilocus phylogeny – saprobes

Introduction

Hypomyces (Fr.) Tul. & C. Tul is an important genus in *Hypocreaceae* (*Hypocreales*) (Yu et al. 2020). The genus was introduced as a subgenus of *Hypocrea* Fr. and elevated to a genus with *H. lactifluorum* (Schwein.) Tul. & C. Tul. as the type species (Tulasne & Tulasne 1860). The first detailed taxonomic study of this group was carried out by Arnold (1971), who distinguished *Hypomyces* from the related genera *Arachnocrea*, *Apiocrea*, and *Peckiella*. Several asexual morphs (Arnold 1969, 1970, Põldmaa 2000, Zare & Games 2016) of *Hypomyces* were reported, mostly cladobotryum-like asexual morph with verticillate conidiophores and conidia produced in a basipetal succession. The sexual morph name is predominant over the asexual name. Thus, the International Code of Nomenclature for algae, fungi, and plants (ICN) recommended *Hypomyces* over *Cladobotyrum* (McNeill et al. 2012; Rossman et al. 2013, Hyde et al. 2020). Following Arnolds' classification for *Hypomyces* (1971), subsequent comprehensive taxonomic studies were conducted on classifying this genus (Rogerson & Samuels 1985, 1989, 1993, 1994, Põldmaa 1996, 2000, 2003, 2011, Põldmaa et al. 1997, 1999). The members of this genus are distributed in different regions, *i.e.,* Australia, Asia, Europe, and North America (Zeng & Zhuang 2016, Lechat et al. 2017, Zare & Gams 2016, Rogerson & Samuels 1989), and currently, 118 *Hypomyces* species are listed in the Index fungorum (2022).

Host range and morphological diversity are key determinants of *Hypomyces* (Kim et al. 2017). It is characterized by perithecia in a concolorous subiculum with brightly or lightly colored,

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Article

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ISSN 1179-3163 (online edition)

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Two new records of *Xylariales* species from Northern Thailand

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Abstract

Xylariales members have conspicuous to inconspicuous perithecia with unitunicate asci. The most known species are endophytes and saprobes, known to produce secondary metabolites with fundamental importance in the pharmaceutical and chemical industries. The current study collected samples from decaying barks of *Quercus kingiana* at Doi Inthanon National Park, Thailand. Based on morphological features coupled with combined gene analyses of ITS, LSU, *rpb2* and *tub2* sequence data, the isolates were identified as *Xylaria karsticola* and *Jackrogersella minutella*, belonging to *Xylariaceae* and *Hypoxylaceae*, respectively. This study provides the first geographical records of *X. karsticola* and *J. minutella* in Thailand and the first records of these species on *Quercus kingiana*.

Keywords: Doi Inthanon national park, fungal diversity, morphology, multigene phylogeny, *Sordariomycetes*, taxonomy

Introduction

Xylariales (*Ascomycota*) was circumscribed by Nannfeldt (1932), and since then, members of this order have been traditionally described based on morphological characters (Munk 1953, Hawksworth *et al.* 1995). A significant study for establishing boundaries for taxa in this order was conducted by Smith *et al.* (2003), who accepted seven families based on morpho and molecular data. Subsequently, it was subjected to several revisions based on a morpho-molecular approach (Kang *et al.* 1998, 2002, Kirk *et al.* 2008, Lumbsch & Huhndorf 2010, Senanayake *et al.* 2015, Samarakoon *et al.* 2016, Voglmayr *et al.* 2018, Wendt *et al.* 2018, Hyde *et al.* 2020, Samarakoon *et al.* 2020, Hernández-Restrepo *et al.* 2022). Due to the complex nature of these taxa, most of the current taxonomic studies involving *Xylariales* employ morphological, multigene phylogenetic, chemotaxonomic, and genomic and comparative genomic approaches (Chethana *et al.* 2021, Wibberg *et al.* 2021, Samarakoon *et al.* 2022). Currently, 22 families are accepted under *Xylariales* (Hernández-Restrepo *et al.* 2022, Sugita *et al.* 2022), with species found worldwide as saprobes, pathogens and endophytes; however, the tropics and subtropics have the most remarkable diversity (Dayarathne *et al.* 2017, Li *et al.* 2017, Ma *et al.* 2018, Cedeño-Sanchez *et al.* 2020, Perera *et al.* 2020, Ma 2022). *Xylariales* species produce a wide range of secondary metabolites belonging to various biosynthetic families, including dihydroisocoumarins, punctaporonins, cytochalasins, butyrolactones, and succinic acid derivatives. Hence chemotaxonomy is frequently used in taxonomic studies to identify *Xylariales* species (Whalley & Edwards 1995, Becker & Stadler 2021).

Xylariaceae comprises species with conspicuous and inconspicuous, superficial or immersed stromata, cylindrical asci, 8-spored asci, mostly pigmented ascospores and geniculosporium-like asexual morphs (Ju & Rogers 1996, Stadler *et al.* 2013, Konta *et al.* 2020, Samarakoon *et al.* 2022). *Xylaria* is the largest genus of *Xylariaceae* (almost 600 species), with *X. hypoxylon* as the type species (Peršoh *et al.* 2009, Wijayawardene *et al.* 2022).

Most hypoxylaceous fungi are essential for forest ecosystems and play a significant ecological role in carbon circulation (Rogers 2000). *Hypoxylaceae* in *Xylariales* comprises important genera (e.g. *Annulohypoxylon* and *Jackrogersella*). *Jackrogersella* was segregated from *Annulohypoxylon* by Wendt *et al.* (2018), based on multigene

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DOI: 10.3897/mycokeys.102.112815

Research Article

Morphology and multigene phylogeny reveal three new species of *Distoseptispora* (Distoseptisporales, Distoseptisporaceae) on palms (Arecaceae) from peatswamp areas in southern Thailand

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Abstract

Peatswamp forest is a unique habitat that supports high biodiversity, particularly fungal diversity. The current study collected submerged and dead plant parts from *Eleiodoxa conferta*, *Eugeissona tristis* and *Licuala paludosa* from a peatswamp forest in Narathiwat Province, Thailand. Morphological features coupled with multigene phylogenetic analyses of ITS, LSU, *rpb2* and *tef1-α* sequence data identified our isolates as new *Distoseptispora* species (viz. *D. arecacearum* **sp. nov.**, *D. eleiodoxae* **sp. nov.** and *D. narathiwatensis* **sp. nov.**). Morphological descriptions, illustrations and notes are provided.

Key words: asexual morph, molecular phylogeny, novel taxa, saprobic fungi, Sordariomycetes, taxonomy

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Introduction

Most peatswamp forests can be found in tropical rainforests where peat is submerged for most of the year and characterised by low nutrient contents and high acidity due to lack of fully decomposed plant materials (Page et al. 1999, 2011; Jackson et al. 2009; Lampela et al. 2016; Ratnayake 2020). Peatswamp forests are unique ecosystems due to their high species diversity and significant role in maintaining a stable global climate. They function as carbon sinks, storing twice as much carbon as all global forest biomass (Hakim et al. 2017; Fujimoto et al. 2019; Shuhada et al. 2020). Beyond carbon storage, peatlands offer valuable benefits. They play vital roles in the water cycle, storing and filtering water and mitigating floods by slowing peak flows. Home to diverse plants and animals, these wetlands support millions of people. Additionally, they hold archaeological relics and provide insights into past environmental conditions

MycoKeys

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DOI: 10.3897/mycokeys.107.127749

Research Article

Novel discoveries of Xylariomycetidae (Ascomycota) taxa from peat swamp forests and other terrestrial habitats in Thailand

Omid Karimi[1,2], Naghmeh Afshari[2,3], Raheleh Asghari[1,2], Qirui Li[4,5], K. W. Thilini Chethana[1,2], Kevin D. Hyde[1,2,6], Fatimah O. Alotibi[6]

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Abstract

In a comprehensive survey of fungi conducted in the northern (Chiang Rai Province) and southern (Narathiwat Province) regions of Thailand, several xylariales-like specimens were discovered. Through the integration of molecular phylogeny and morphological analyses, one previously undocumented taxon, *Oxydothis narathiwatensis* **sp. nov.**, was identified, along with *Xylaria bawanglingensis* and *Hypoxylon hypomiltum* as new host and geographical records from *Afzelia xylocarpa*, and *Dalbergia cana*, respectively. In addition, *Annulohypoxylon thailandicum* was identified as a new host record from *Swietenia macrophylla* in Thailand. The morphological characters, including ascomata, asci, and ascospores, were compared with known *Oxydothis*, *Xylaria*, *Hypoxylon*, and *Annulohypoxylon* species. Multi-locus phylogenetic analyses based on ITS, LSU, and SSU (for Oxydothidaceae), ITS, *rpb2*, *tub2*, and *act* (for Xylariaceae), and ITS, LSU, *rpb2*, and *tub2* (for Hypoxylaceae) gene regions were carried out to refine the taxonomic classifications of these specimens further. This research contributes to understanding fungal diversity in these ecologically significant regions, highlighting insights into the relationships among xylariales-like species.

Key words: Fungal diversity, multi-gene phylogeny, novel species, Sordariomycetes, taxonomy

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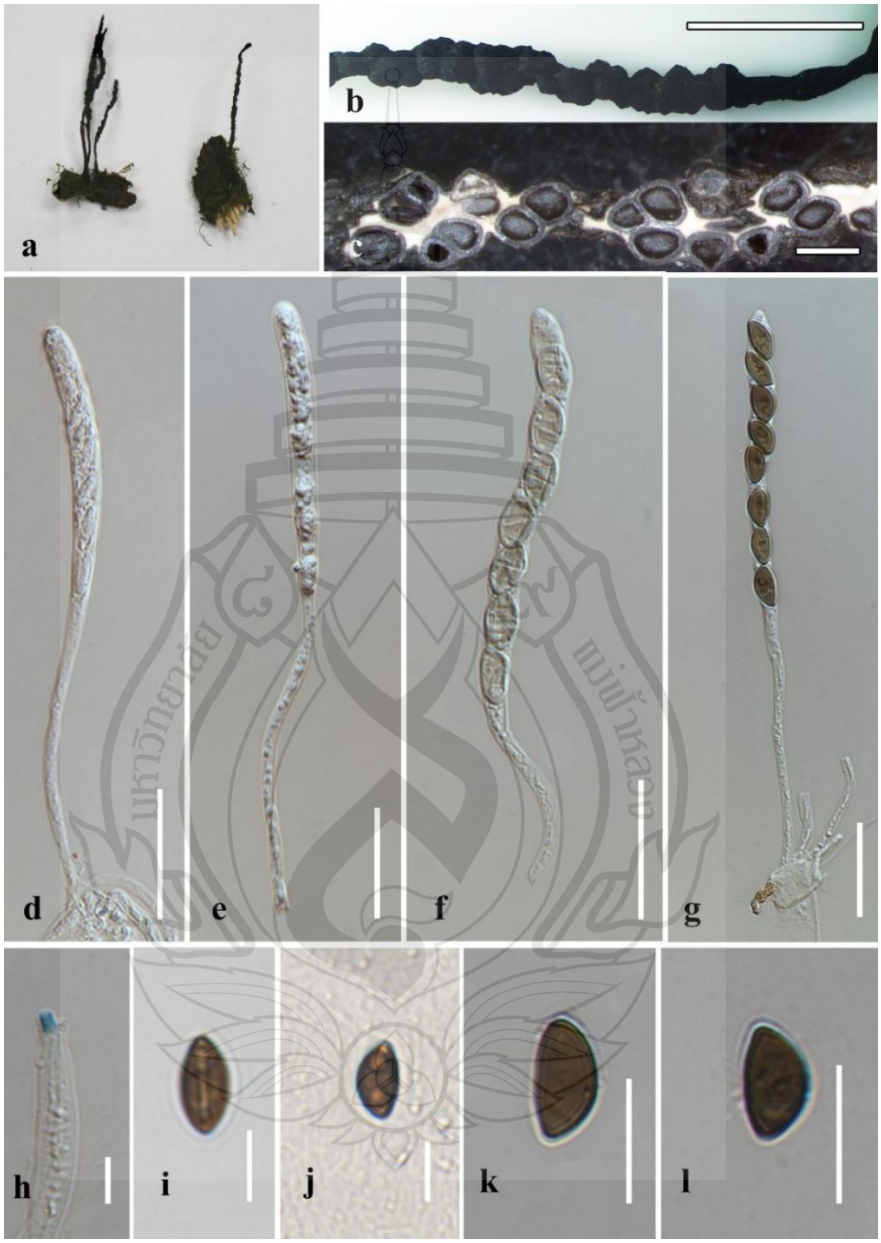
Introduction

Xylariomycetidae, introduced by Eriksson and Winka (1997), is one of the largest subclasses in Ascomycota and belongs to the class Sordariomycetes (Hyde et al. 2020a). This subclass encompasses three orders and more than 35 families (Wijayawardene et al. 2022). Among these, Xylariaceae and Hypoxylaceae stand out as two particularly significant families (Wendt et al. 2018; Voglmayr et al. 2019; Hyde et al. 2020a, 2020b; Sun et al. 2021; Hernãndez-Restrepo et

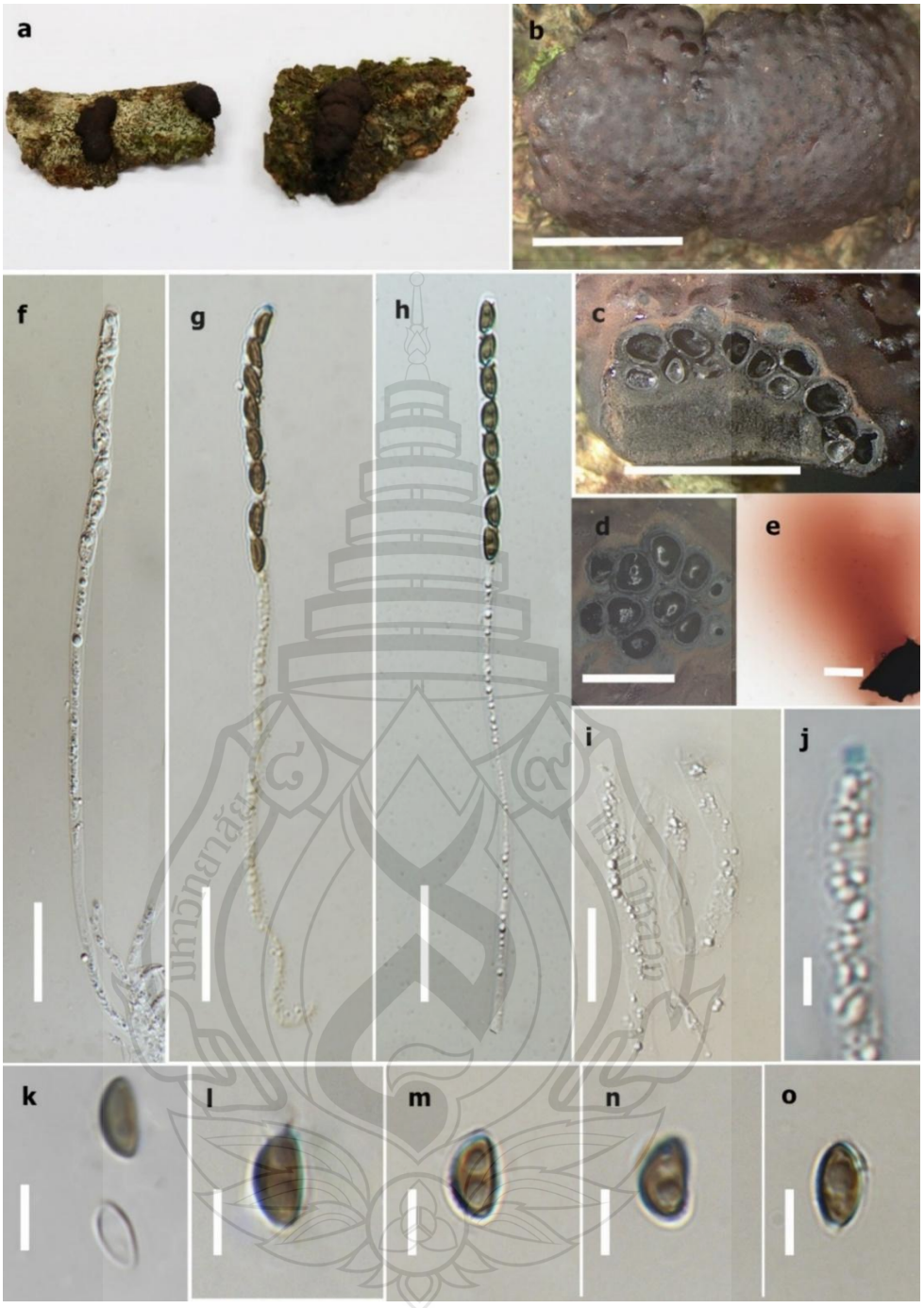
APPENDIX B

XYLARIALES TAXA ASSOCIATE WITH NON-PALM HOSTS



Note a, b Stromata. c Section through the stroma. d–g Asci. h Apical ring stained in Melzer reagent. i–l Ascospores. Scale bars: b = 1 mm, c = 500 µm, d–f = 20 µm, h = 5 µm, i–l = 10 µm

Figure B1 *Xylaria karsticola* (MFLU23-0049, new host and geographical record)

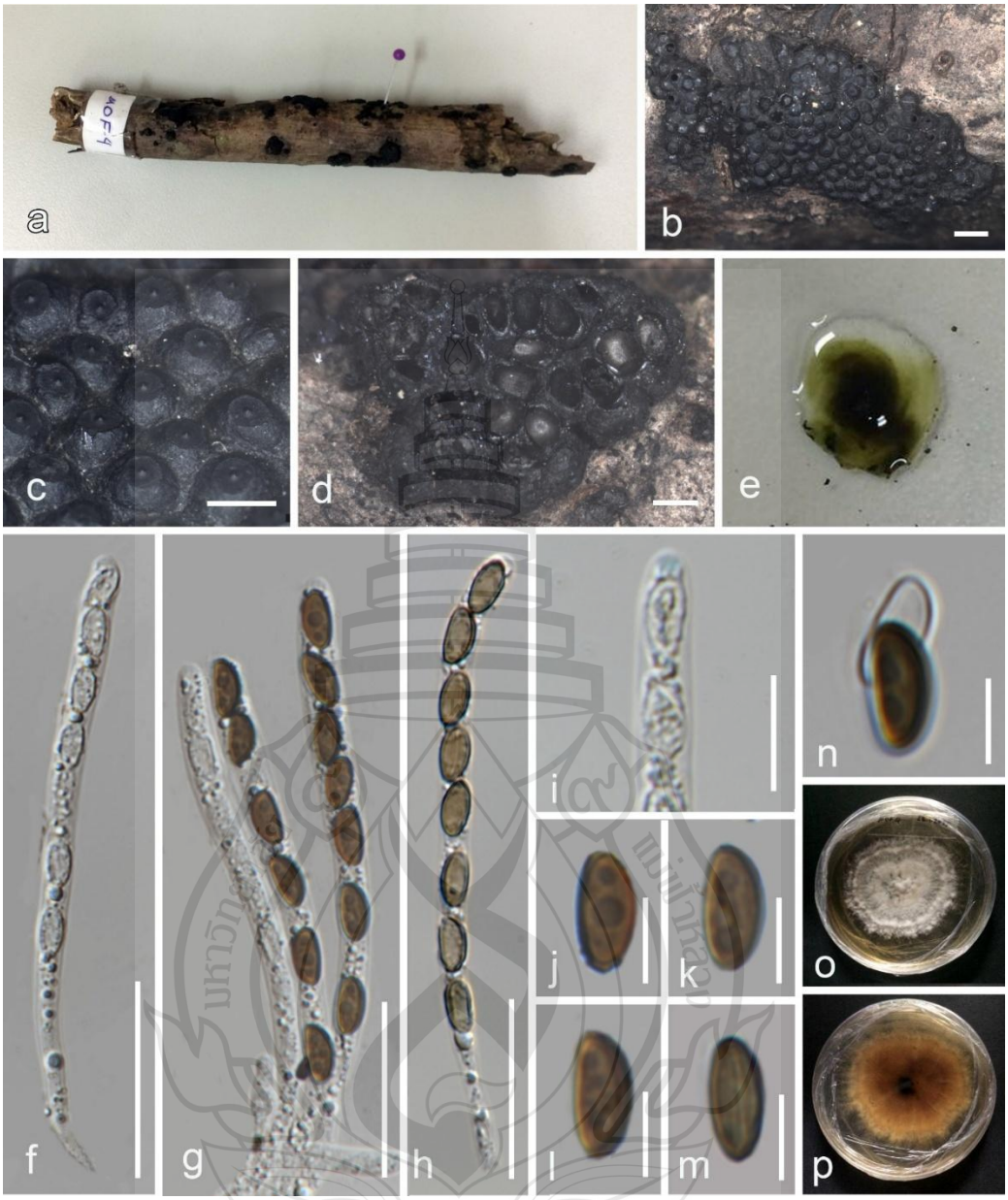


Note a, b Stromata. c, d Sections of an ascoma. e KOH-extractable pigments. f–h Asci. i Paraphyses. j Apical ring stained in Melzer reagent. k Perispore. i–o Ascospores. Scale bars: b, c = 1 mm, d = 500 µm, e = 300 µm, f–i =20 µm, j–o = 5 µm.

Figure B2 *Jackrogersella minutella* (MFLU23-0051, new host and geographical record)

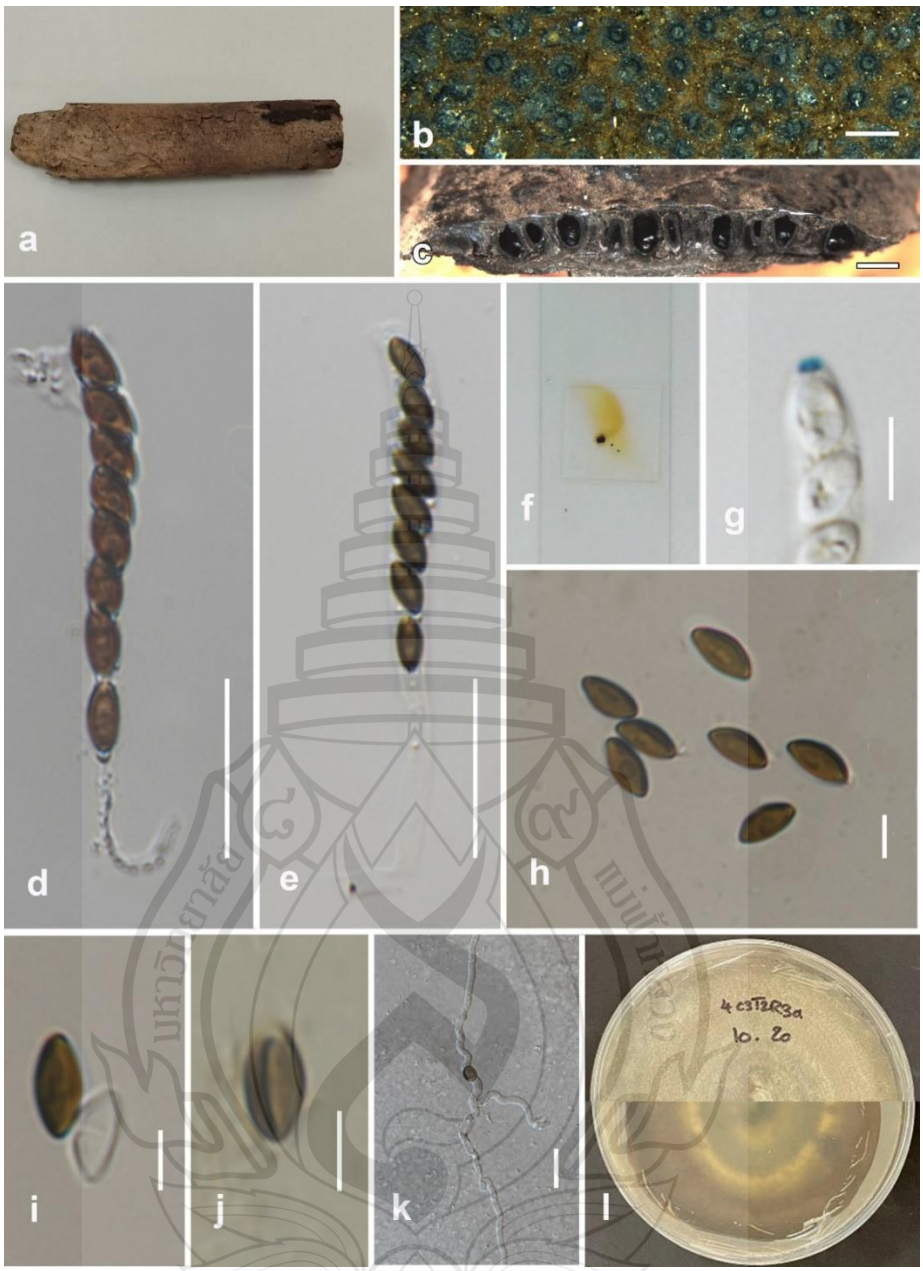
Note a stromata on host b, c stromata d longitudinal section through the stroma e–h asci i paraphyses j apical ring bluing in Melzer's reagent k, l ascospores m upper view and reverse view of the one-week-old colony on PDA. Scale bars: 1 mm (b, d); 20 µm (e–g); 70 µm (h); 20 µm (i); 5 µm (j); 10 µm (k, l).

Figure B3 *Xylaria bawanglingensis* (MFLU 24-0018, new host and geographical record)



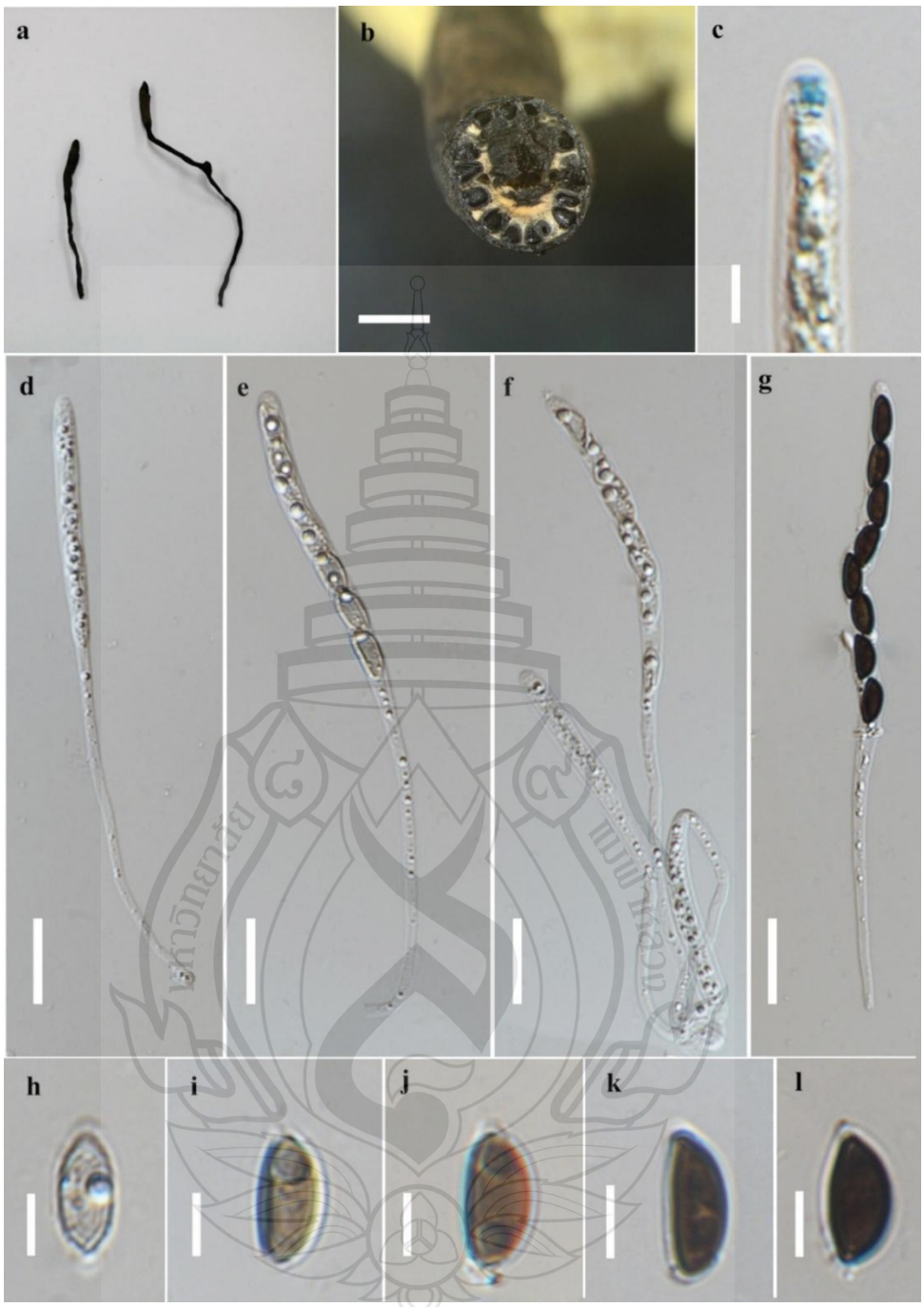
Note a host b stromatal habit on host c ostioles with ostiolar discs d stromata in horizontal section showing perithecia e pigments in KOH f–h asci i ascal apical apparatus in Melzer's reagent j–m ascospores o, p colonies on PDA after two weeks. Scale bars: 1 mm (b); 500 µm (c, d); 30 µm (f–h); 10 µm (i); 5 µm (j–m).

Figure B4 *Annulohypoxylon thailandicum* (MFLU 24-0019, new host record)



Note a host b stromatal habit on host c stromata in vertical section showing perithecia d, e asci f pigments in KOH g ascal apical apparatus in Melzer's reagent h-i ascospore (i ascospore with perispore j ascospore with germ slit) k germinated ascospore l colony on PDA after three weeks. Scale bars: 500 µm (b, c); 20 µm (d, e); 5 µm (g-j); 10 µm (k).

Figure B5 *Hypoxylon hypomiltum* (MFLU 24-0043, new host and geographical record)



Note a Stromata habit. b Section of ascoma. c Apical ring. d-g Asci. h-l Ascospores. Scale bars: b= 1 mm, c= 5 µm, d-g= 20 µm, h-l= 5 µm.

Figure B6 *Xylaria grammica* (MFLU23-0073, new host record)

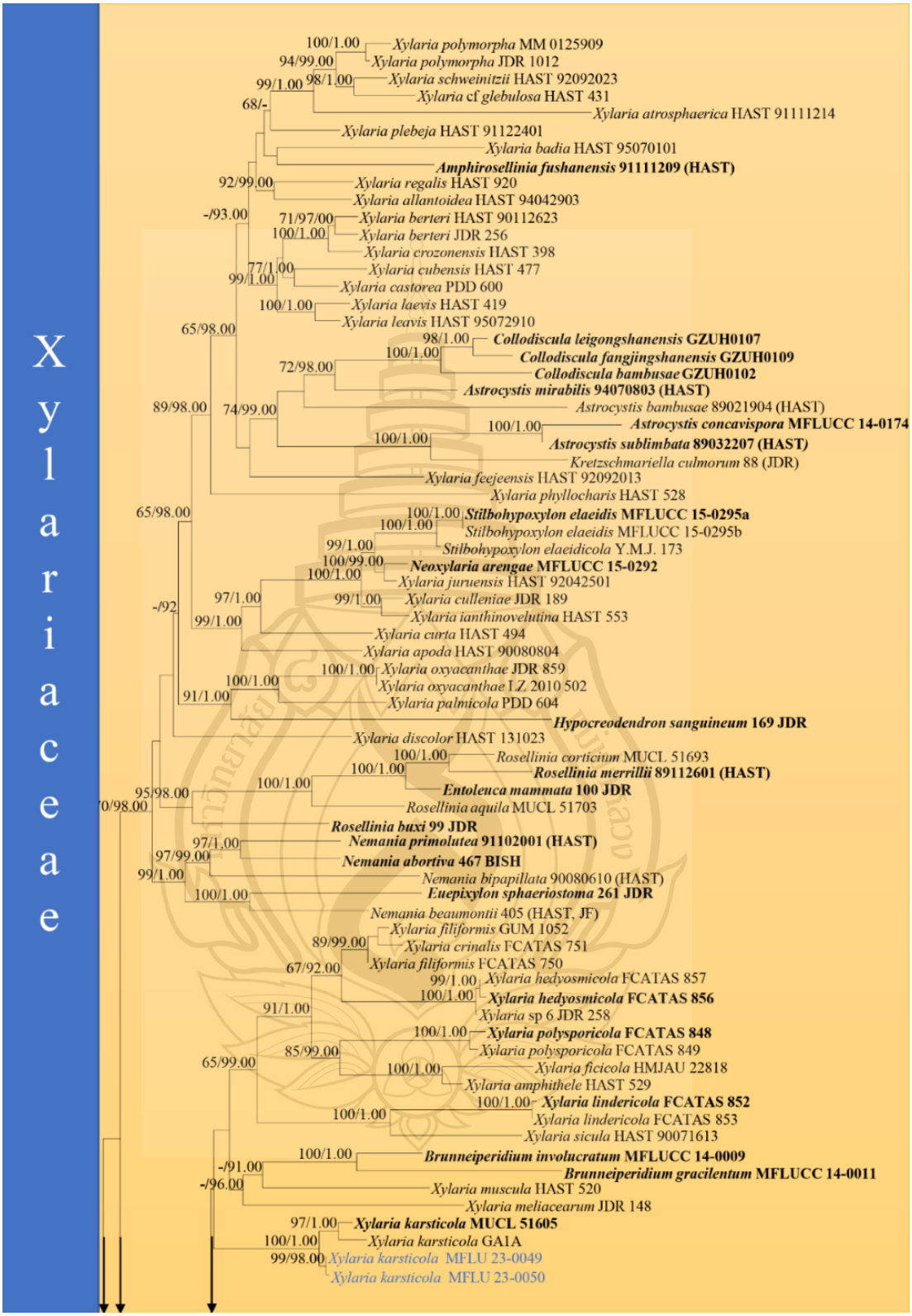
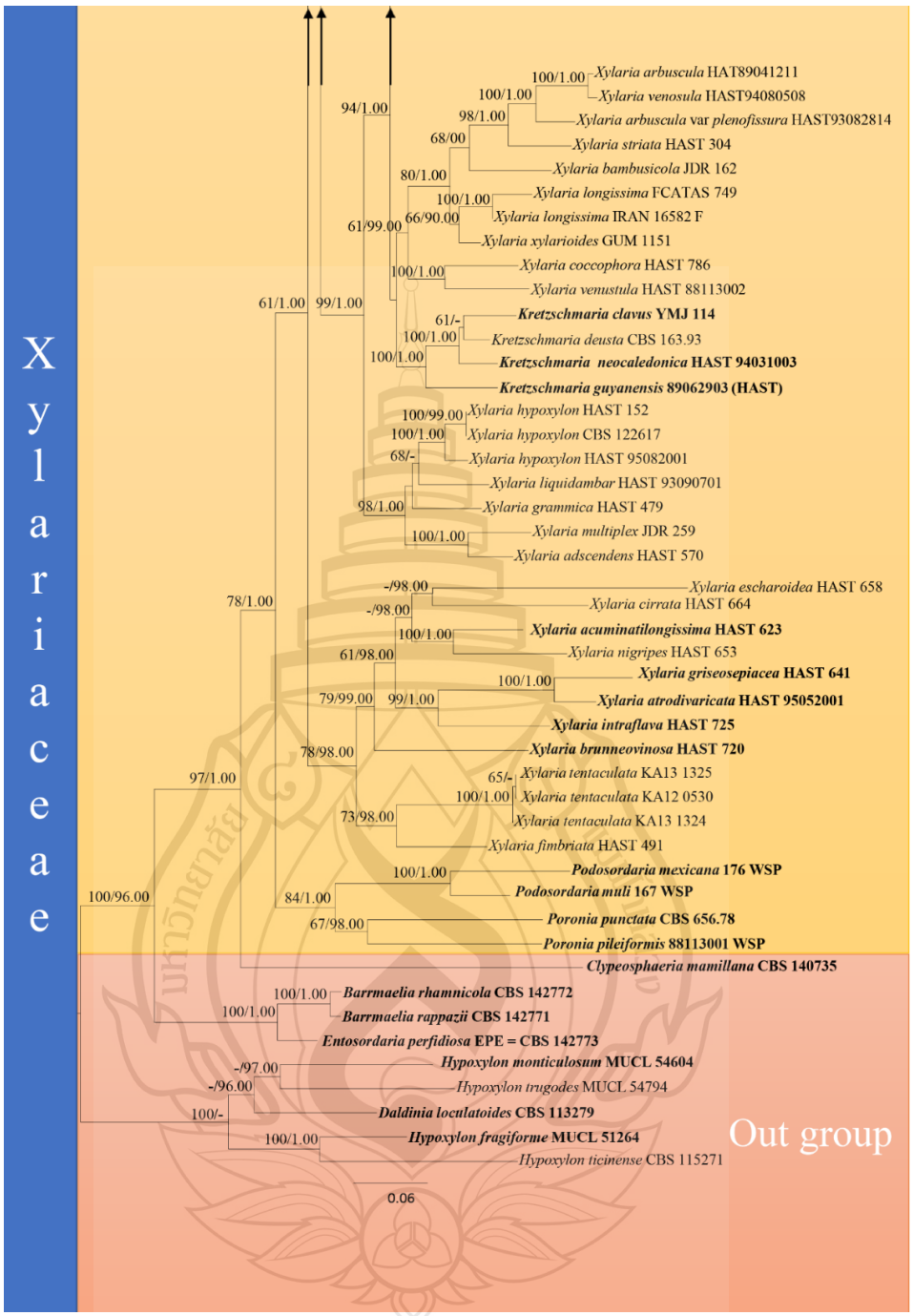
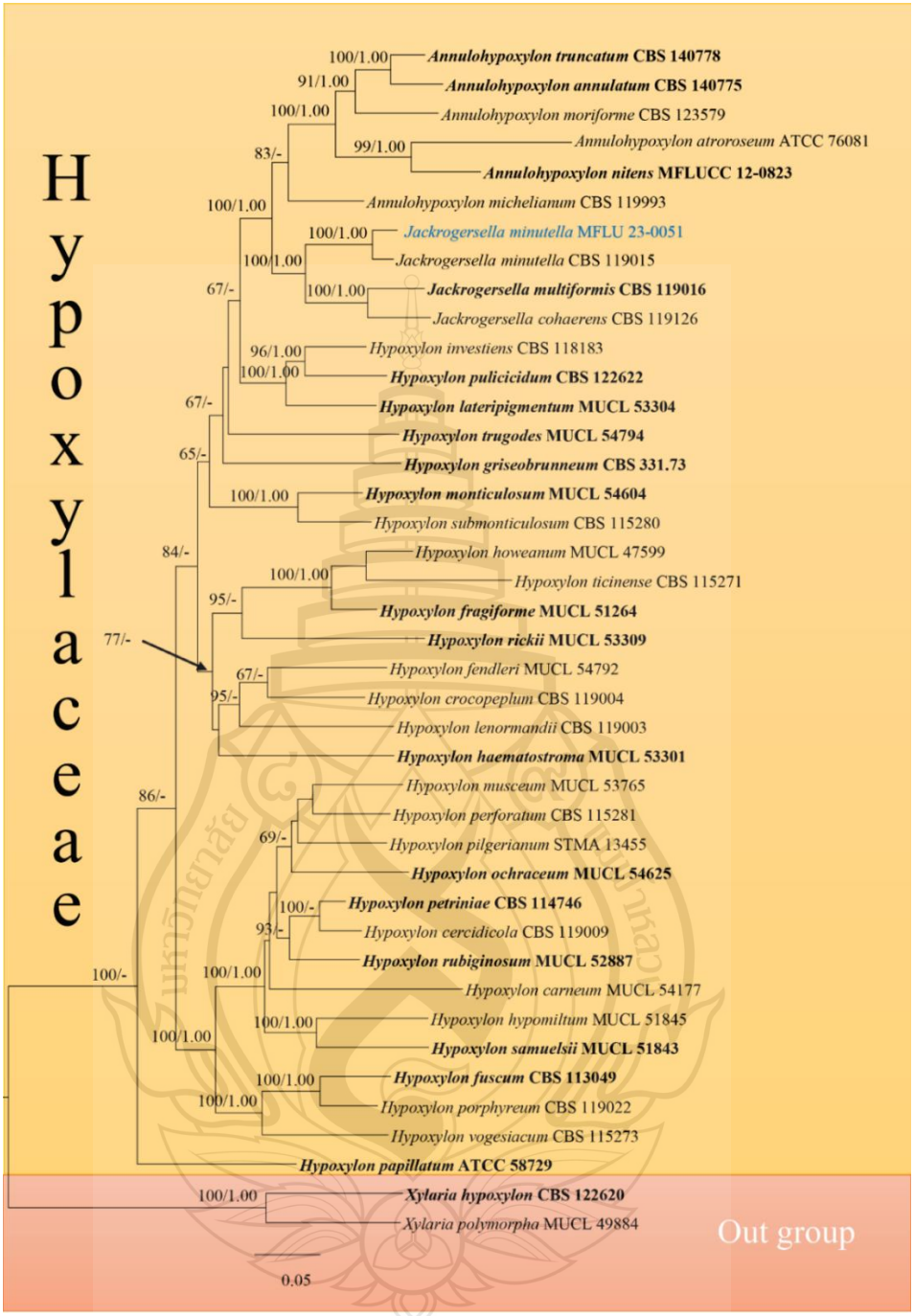


Figure B7 Phylogram generated from maximum likelihood analysis based on combined ITS, *rpb2*, and *tub2* sequence data of the *Xylariaceae*



Note Maximum likelihood bootstrap support values greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.95 are given near nodes, respectively. The newly generated sequences are indicated in blue. All the type specimens are in bold.

Figure B7 (continued)



Note Maximum likelihood bootstrap values greater than or equal to 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree was rooted with *Xylaria hypoxylon* (CBS 122620) and *Xylaria polymorpha* (MUCL 49884). The newly generated sequence is indicated in blue. All the type specimens are in bold.

Figure B8 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, and *tub2* sequence data of *Hypoxylaceae* taxa

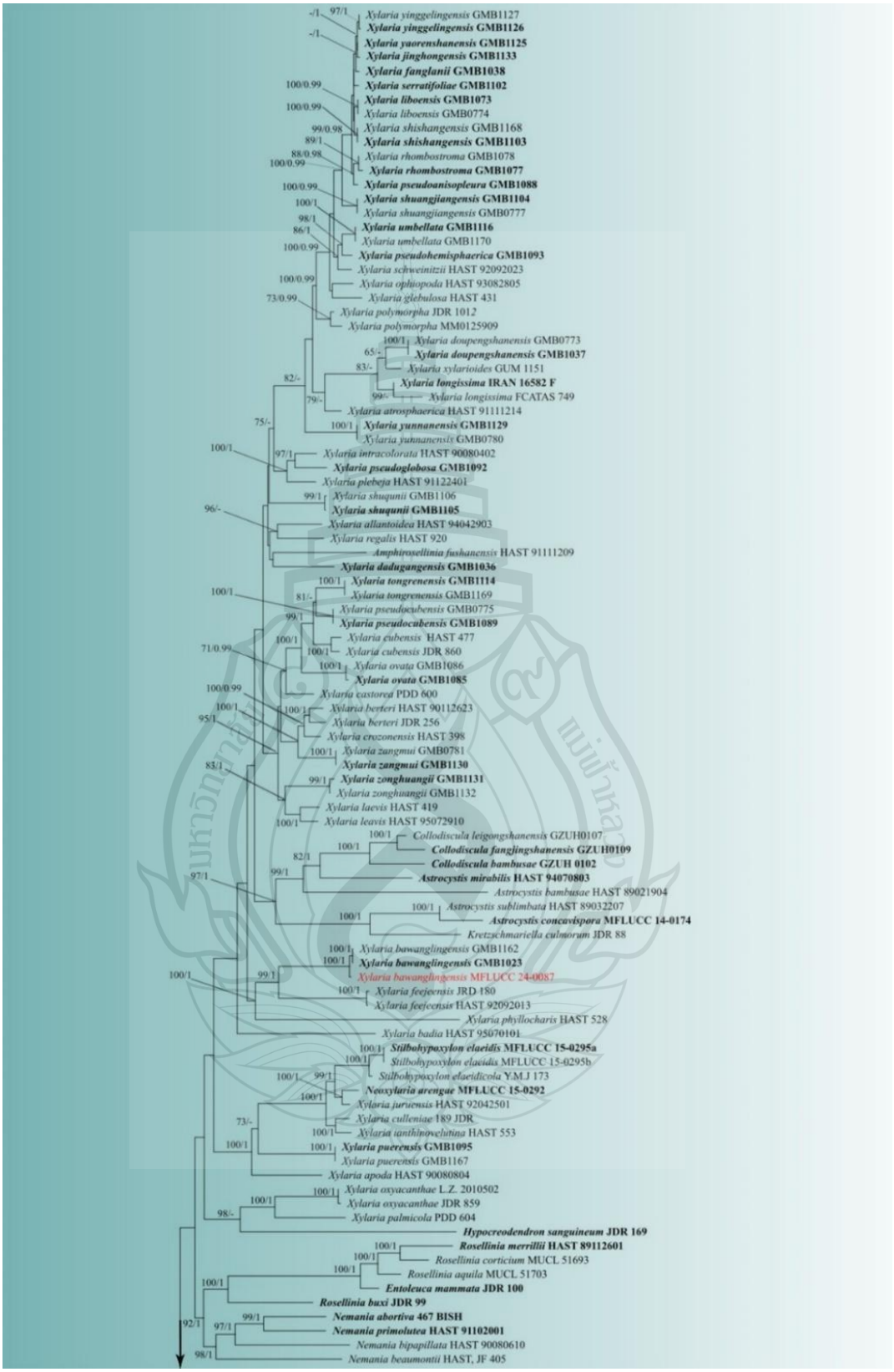
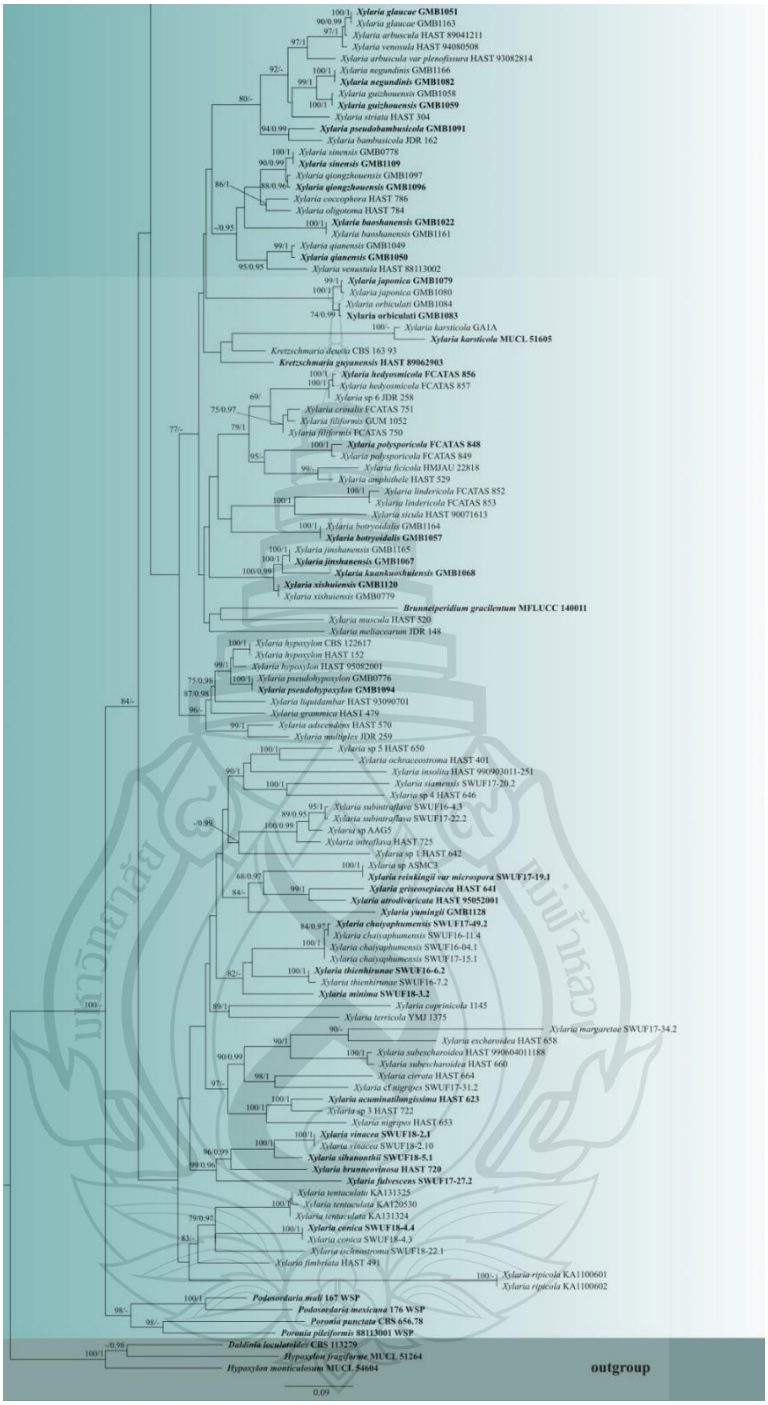


Figure B9 RAxML tree based on the analysis of a combined ITS, *rpb2*, *tub2*, and *act* dataset



Note ML bootstrap supports (MLBS) equal to or higher than 65% and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given near the nodes. Newly generated isolate of the current study is in red, and ex-types are in bold. The tree is rooted to *Daldinia loculatoides*, *Hypoxylon fragiforme* and *Hypoxylon monticulosum*.

Figure B9 (continued)

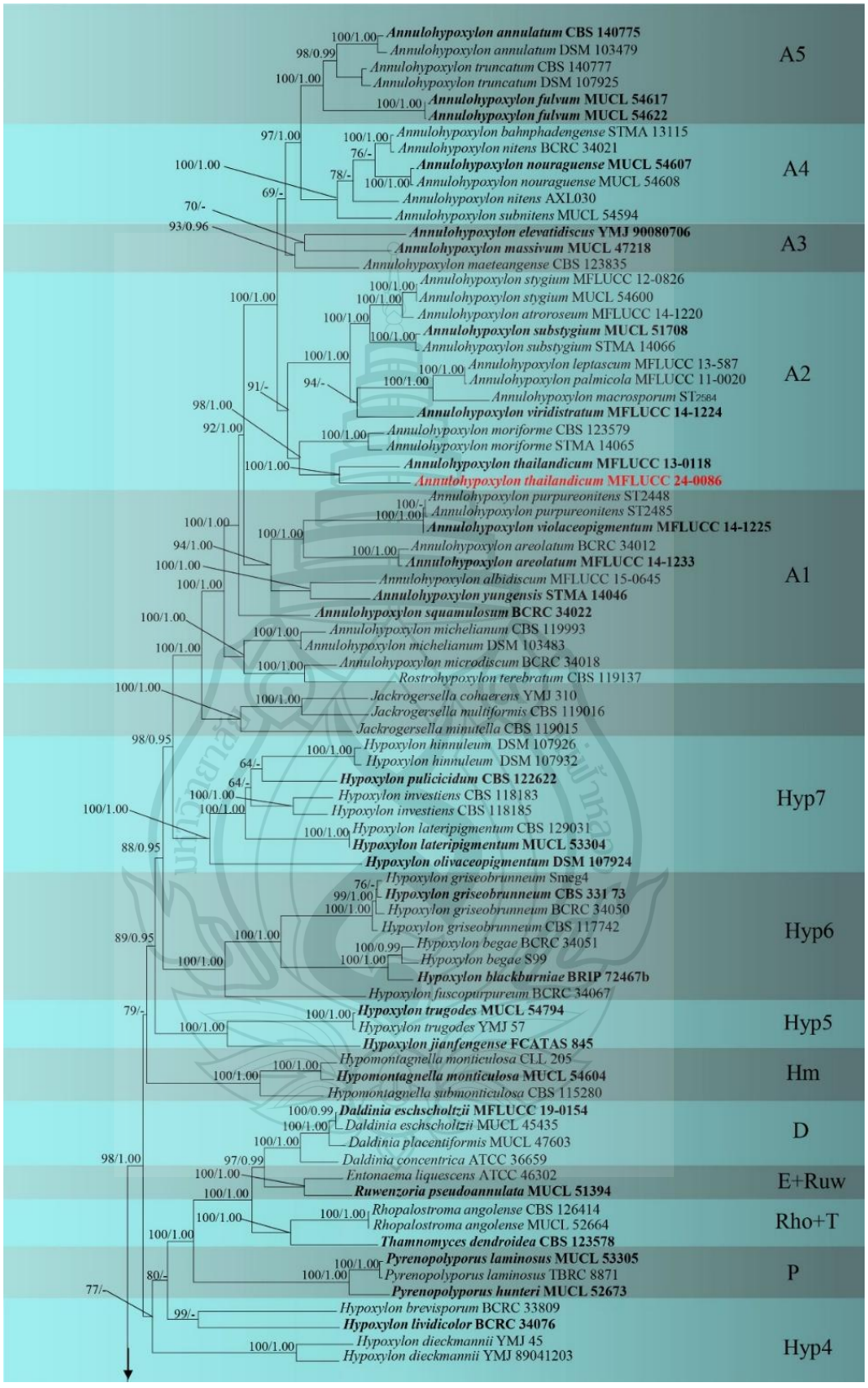
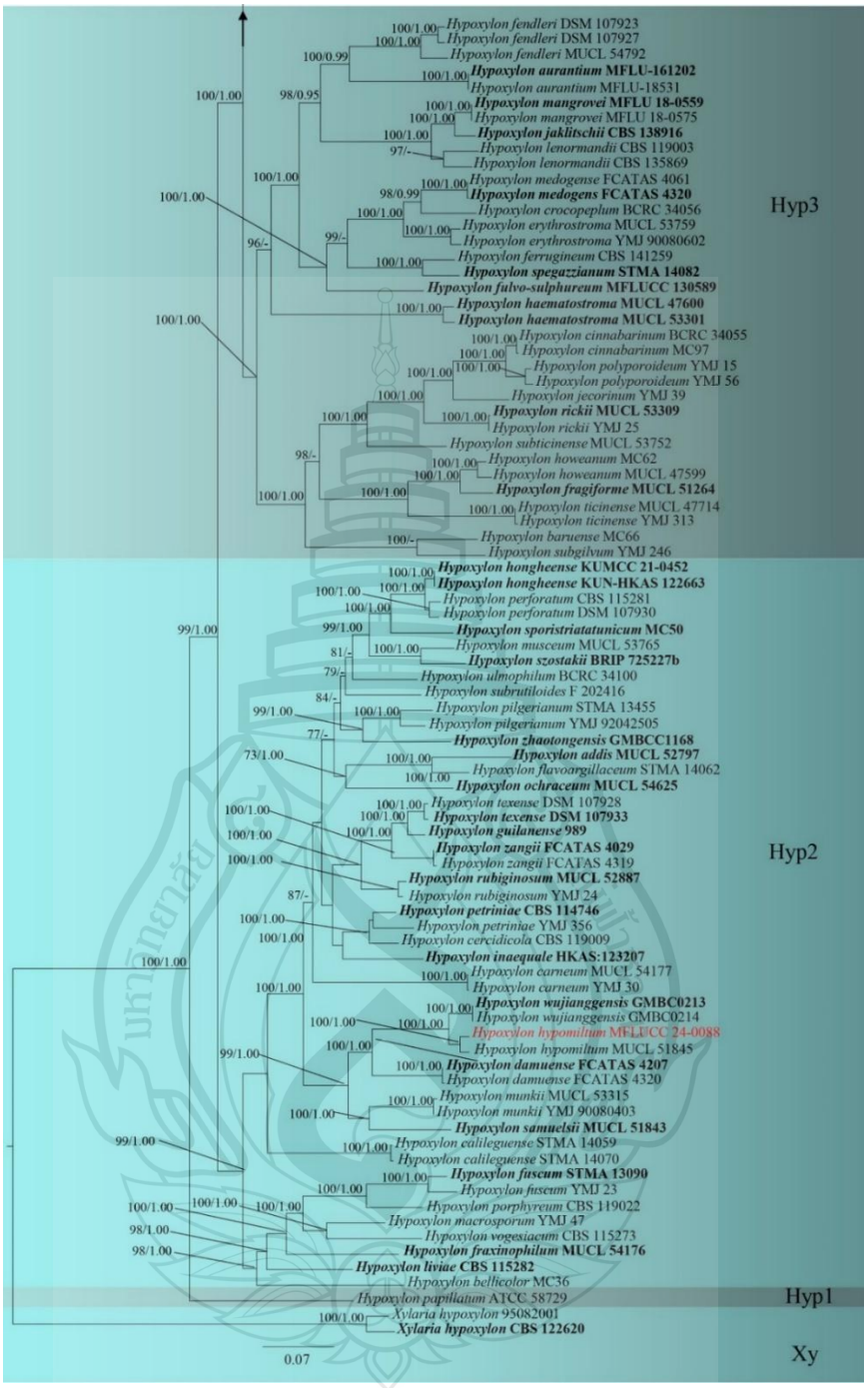
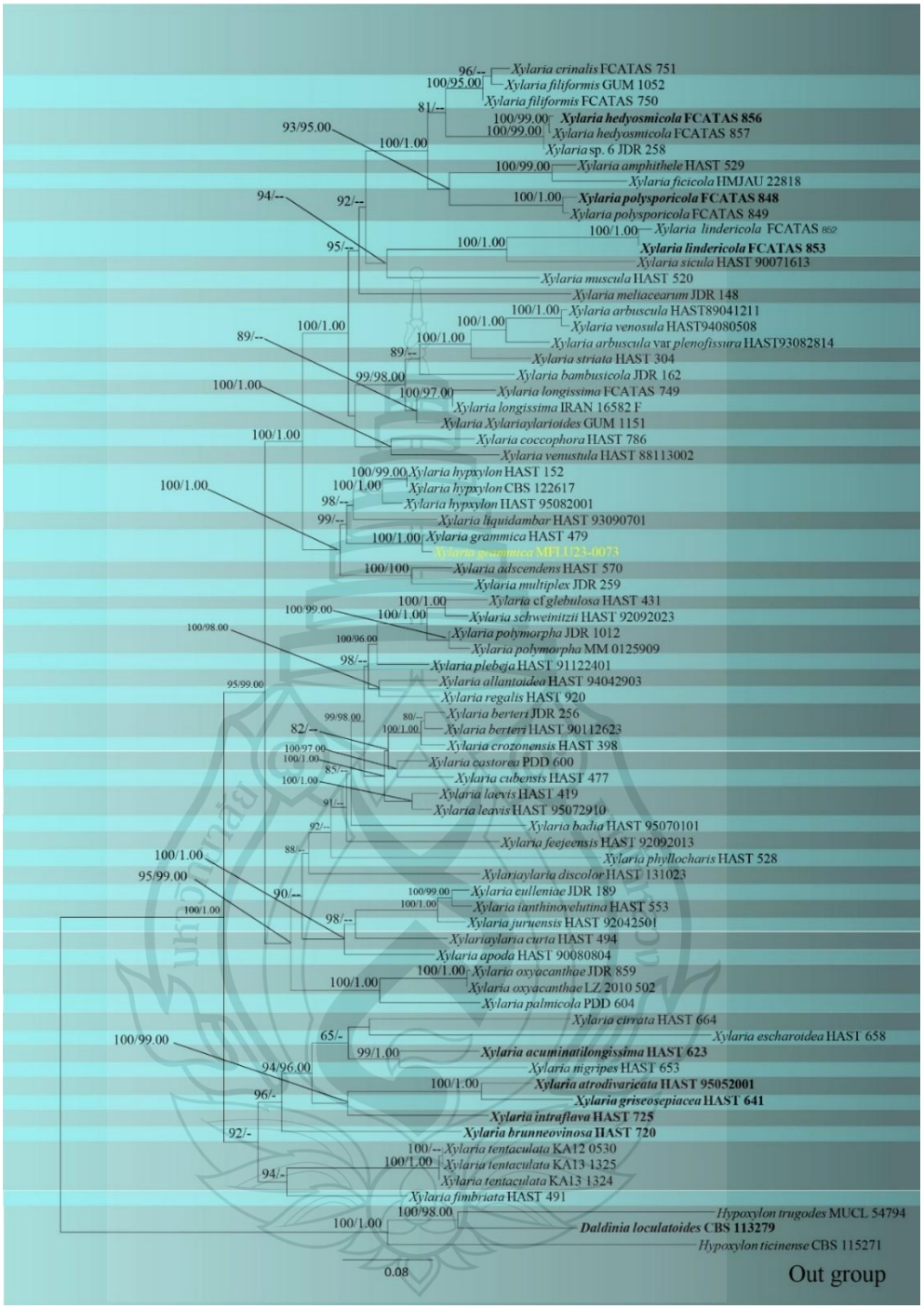


Figure B10 RAxML tree based on the analysis of the combined ITS, LSU, *rpb2*, and *tub2* dataset



Note ML bootstrap supports (MLBS) equal to or higher than 65%, and the Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are given near the nodes. The ex-types are in bold. The two new sequences are shown in red font.

Figure B10 (continued)



Note Maximum likelihood bootstrap support values greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.95 are given near nodes, respectively. All the type specimens are in bold. The newly generated sequences are indicated in yellow.

Figure B11 Phylogram generated from maximum likelihood analysis based on combined ITS, *rpb2*, and *tub2* sequence data of the *Xylariaceae*

APPENDIX C

CHEMICAL REAGENTS AND MEDIA

Potassium hydroxide (KOH) used in the rehydration of dried specimens. 5% aqueous solution.

Lactoglycerol used for mounting semi-permanent slides: Lactic acid 10 ml, Glycerol 10 ml, Distilled water 10 ml. Mix 10 ml lactic acid, 10 ml glycerol, and add 10 ml distilled water.

Lactic acid for preserving fungal structures and for getting a true color image of the fungal spore and structures without staining. This is helpful for some of the pigmented organisms. 85% Lactic acid 100 ml.

Lactophenol-Cotton Blue used to highlight fungal structures for viewing with the compound light microscope. Cotton blue is the most popular stain for observing pseudoparaphyses, septa or ascus walls. This gives excellent clarity and is also suitable for most fungal groups: Phenol (crystals) 20 g, Lactic acid 16 ml, Glycerol 31 ml. Dissolve phenol in distilled water, add lactic acid, glycerol and 0.05 g of Poirrier's (cotton) blue or acid fuchsin.

Melzer's Reagent as the general mounting medium that clears the material somewhat and allows particularly a brilliant resolution under the microscope, and usedfor identification of ascomycete fungi. Amyloid reaction of asci changed to blue or heavily purple colors. Chloral hydrate 100 g, Potassium iodide 5 g, Iodine 1.5 g, Distilled water 100 ml.

Malt Extract Agar (MEA) used for fungal culturing:Agar 15 g, Peptone 0.78 g, Glycerol 2.35 g, Dextrin 2.75 g, Maltose, Technical 12.75 g. Suspend 33.6 g of malt extract agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the power and bring volume to 1000 ml. Autoclave at 121 ℃ for 15 minutes

Potato Dextrose Agar (PDA) used for fungal culturing. Potato starch (from infusion) 4 g, Dextrose 20 g, Agar 15 g. Suspend 39 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to

completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121 ℃ for 15 minutes.

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2014 Master of Science
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