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ARTICLE

Peat swamp *Ascomycota* associated with palms (*Arecaceae*) from Narathiwat, Thailand

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Abstract

Peat swamp forests are critical ecosystems that serve as significant carbon stores. However, they are increasingly threatened by deforestation and land-use changes. The peat swamp forests in Narathiwat, southern Thailand, represent the last remaining primary peat swamp ecosystems in the country, yet studies on microfungi in these habitats remain limited and mostly lack molecular data. This study focuses on identifying and characterizing fungi associated with palms, particularly *Eleiodoxa conferta*, in the peat swamp forests of Narathiwat, Thailand. Based on detailed morphological comparisons and multi-gene phylogenetic studies, we introduce one new genus, *Narathiwatomyces*, along with 25 new species, viz., *Cancellidium narathiwatense, Chaetosphaeria narathiwatensis, Chloridium narathiwatense, Conioscypha narathiwatensis, Daldinia narathiwatensis, Gongromerizella palmicola, Helicoma narathiwatense, H. eleiodoxae, Javarisimilis narathiwatensis, Lentistoma narathiwatense, Longivarius narathiwatensis, Narathiwatomyces confertae, Nawawia narathiwatensis, Neohelicosporium narathiwatense, Ne. arecacearum, Neoleptodontidium narathiwatense, Pseudosaprodesmium narathiwatense, Savoryella narathiwatensis, Stanjehughesia narathiwatensis, Strossmayeria narathiwatensis, Tamhinispora narathiwatensis, Terriera narathiwatensis, Tubeufia narathiwatensis, Vamsapriya narathiwatensis* and *Yunnanomyces narathiwatensis.* Furthermore, we report 16 new records based on host, geographical, or habitat associations. These include 11 previously described species — *Ernakulamia cochinensis, Lasiodiplodia brasiliensis, La. theobromae, Linocarpon appendiculatum, Longicorpus striataspora, Megacapitula villosa, Neohelicosporium fusisporum, Nigrospora chinensis, Polyancora globosa, Pseudodactylaria longidenticulata, Trichoderma virens* — as well as *Conioscypha narathiwatensis, Longivarius narathiwatensis, Neoleptodontidium narathiwatense, Terriera narathiwatensis,* and *Vamsapriya narathiwatensis,* which represent the first records of their respective genera on the host family *Arecaceae*. Each taxon is provided with detailed descriptions and illustrations, along with a concise summary for each family and genus. This study enhances our understanding of fungal diversity in peat swamp forests and validates the identification of species introduced in previous studies, which relied solely on morphological analysis. By incorporating molecular data, it ensures more accurate taxonomic placement.

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INTRODUCTION

Fungi, a diverse group of organisms, occur in various types of environments, including terrestrial (Phukhamsakda et al. 2020, Zhang et al. 2024a), freshwater (Hyde et al. 2021, Wang et al. 2024), and marine (Jones et al. 2019, Gao et al. 2024) environments. They play crucial roles in ecosystem functioning as decomposers, mutualists, and pathogens (Bhunjun et al. 2022, Niego et al. 2023a, Hyde et al. 2024). 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, Niego et al. 2023b).

Ascomycota, the largest phylum within the fungal kingdom, thrives in diverse habitats and on various substrates, including human and animal, plant, 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 for their ecological importance and vital role in global trade, with examples of palm-associated fungal genera presented in Table 1.

Arecaceae, commonly known as palm trees, includes approximately 2,600 species within 181 genera distributed globally, mostly in tropical and subtropical regions (Baker & Dransfield 2016). The relationship between palm trees and fungi involves multiple roles, including those of decomposers, endophytes, pathogens, and symbionts (Taylor et al. 1999, Konta et al. 2016a, b, c), with an estimate of over 76,000 fungal species from different habitats (Pereira & Phillips 2023). Peat swamp forests have a remarkable palm diversity (Pinnoi et al. 2006, Pinruan et al. 2007), 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). 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 (UNEP 2022).

Peat swamp forests are important ecosystems for providing food and shelter for animals and birds (Minayeva & Sirin 2012, Bonn et al. 2016). Local communities rely on and are deeply connected to peat swamps for their livelihoods, engaging in activities such as beekeeping, fishery, timber harvesting, using medicinal plants, crafting with peat and vegetation, and promoting ecotourism (Gearey & Fyfe 2016, Crump 2017). Thailand's peat swamp forests have a high plant diversity, with over 470 species across 109 families (Nuyim 2005). Narathiwat Province is home to Thailand's last primary peat swamp forest (Nuyim 2005), with native palm species such as *Calamus caesius* (*Ca.*)*, Ca. concinnus, Ca. melanochaetes, Caryota mitis, Cyrtostachys renda, Eleiodoxa conferta* (*El.*)*, Eugeissona tristis, Korthalsia laciniosa, Licuala paludosa, Livistona saribus, Nenga pumila, Oncosperma tigillarium, Pinanga glaucescens,* and *P. riparia* (POWO 2024).

Table 1 Examples of fungal genera associated with palms.

Fungal Genera	Palm Genera	Location	Nutritional Mode	References
Oxydothis	*Archontophoenix*	Australia	Saprobes	Hyde (1993b), Fröhlich & Hyde (1994)
	Licuala	Thailand		Liu et al. (2015)
		Brunei		Fröhlich & Hyde (2000)
		Philippines		Hyde (1993a)
		Malaysia		Hyde (1994)
	Calamus	Brunei		Fröhlich & Hyde (2000)
		Philippines		Sydow & Sydow (1917)
		Thailand		Konta et al. (2016)
		Australia		Hyde (1994)
Linocarpon	*Nypa*	Malaysia	Saprobes	Hyde & Alias (1999)
		Brunei, Philippines		Hyde (1988b)
	Arenga	Thailand		Konta et al. (2017)
	Licuala	Australia		Hyde (1997)
		Malaysia		
		Thailand		Pinnoi et al. (2006), Pinruan et al. (2007), Zhang et al. (2024a)
Neolinocarpon	*Arenga*	Thailand		Konta et al. (2017)
	Calamus	Australia		Hyde et al. (1998)
		Brunei		
Astrosphaeriella	*Eleiodoxa*	Thailand	Saprobes	Pinnoi et al. (2006)
Canalisporium	*Licuala*	Thailand	Saprobes	Pinruan et al. (2007)

Fungal Genera	Palm Genera	Location	Nutritional Mode	References
Phruensis	*Licuala*	Thailand	Saprobes	Pinruan et al. (2004)

The peat swamp forest represents an endangered ecosystem, yet its microbial diversity, particularly fungal communities, remains insufficiently explored, with studies mostly confined to Thailand. Previous research on fungi in Thailand's peat swamp forests has been limited, with findings indicating *Pleosporales*, *Xylariales*, and *Chaetosphaeriales* as the dominant orders within the phylum *Ascomycota* (Pinnoi et al. 2003a, b, 2004, 2006, 2009, 2010, Pinruan et al. 2004a, b, c, 2007, 2010a, b, 2014). However, many fungal taxa from these earlier studies lack molecular data. To address this knowledge gap, we investigated the fungal communities associated with palms in Narathiwat's peat swamp forest ecosystem, with a particular emphasis on *Eleiodoxa conferta* and other native species. The known and newly identified fungal species are documented with detailed illustrations, comprehensive morphological descriptions, and phylogenetic analyses.

MATERIALS AND METHODS

Sample collection, morphological study, and isolation

Submerged and dead palm materials, primarily from *Eleiodoxa conferta* and occasionally from *Caryota mitis*, *Cyrtostachys renda*, were collected during 2022–2023 from the Princess Sirindhorn Wildlife Sanctuary, a peat swamp forest in Narathiwat Province, Thailand. Small pieces of the collected samples were analysed with a Motic SMZ 168 Series microscope (Motic Asia, Kowloon, Hong Kong) and isolated into axenic cultures using the single spore isolation (Senanayake et al. 2020) on PDA (potato dextrose agar; 39 g in 1,000 mL distilled water, Microbiology, Darmstadt, Germany) supplemented with 0.5 g/L streptomycin. Germinating spores were transferred to fresh PDA and incubated at 25 ± 1 °C in dark for two weeks. 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 stored in the Mae Fah Luang University Culture Collection (MFLUCC), while the herbarium specimens were placed in the Mae Fah Luang University Herbarium (MFLU). Facesoffungi (FoF) and Index Fungorum numbers were assigned according to the methods outlined by Jayasiri et al. (2015) and the Index Fungorum (http://www.indexfungorum.org), respectively.

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 Biospin Fungus Genomic DNA Extraction Kit (BioFlux, P.R. China), following the manufacturer's standard procedure. Polymerase chain reactions (PCR) were performed using the primers and conditions listed in Table 2. The PCR products were visualized on 1% agarose gels stained with 4S Green Stain and sequenced at SolGent Co., Ltd. (South Korea).

Sequence alignment and phylogenetic analyses

The sequences of seven genomic loci including the internal transcribed spacer regions (ITS), nuclear large subunit rDNA (LSU), nuclear small subunit rDNA (SSU), mitochondrial small subunit rDNA (mtSSU), RNA polymerase II subunit 2 (*rpb2*), translation elongation factor 1-alpha (*tef1-α*), and β-tubulin (*tub2*) were assembled using SeqMan v7.1.0 and identified through BLASTn searches against NCBI's GenBank. Related taxa were retrieved from GenBank and prior publications. Alignments were conducted using MAFFT v.7 (http://mafft.cbrc.jp/alignment/server/index.html, Katoh et al. 2019) and trimmed using trimAl v1.4 (Capella-Gutiérrez et al. 2009), with datasets combined in SequenceMatrix v1.9. Maximum likelihood (ML) analyses were conducted in RAxMLHPC2 on XSEDE (Stamatakis 2014) under the GTRCAT model with 1,000 bootstrap replicates via the CIPRES platform (Miller et al. 2010). Bayesian inference (BI) was performed in

MrBayes v3.2.6 using optimal models selected by jModelTest2 under AIC criteria. Phylogenetic trees were visualized with FigTree v1.4.0 (Rambaut 2009) and finalized in Inkscape v.1.2.2. Newly produced sequences were deposited in the GenBank (https://www.ncbi.nlm.nih.gov/).

Table 2 Gene regions, primers, and PCR conditions used in this study.

Gene Regions	Primer	PCR condition					Reference
			35 cycles				
		Initial Denaturation	Denaturation	Annealing	Extension	Final extension	
ITS	ITS5/ ITS4	94 °C, 3 min	94 °C, 45 sec	53 °C, 55 sec	72 °C, 2 min	72 °C, 10 min	White et al. (1990)
LSU	LR0R/LR 5	94 °C, 5 min	94 °C, 30 sec	55 °C, 50 sec			Vilgalys & Hester (1990), Rehner & Samuels (1994)
SSU	NS1/NS4	94 °C, 3 min	94 °C, 30 sec	52 °C, 45 sec			White et al. (1990)
mtSSU	mrSSU1/ mrSSU3R						Zoller et al. 1999
tef1-α	728F/986 R	94 °C, 3 min	94 °C, 30 sec	58 °C, 50 sec			Carbone & Kohn (1999)
	983F/2218 R						Rehner (2001)
	728F/LLE rev						Liu et al. (1999), Carbone & Kohn (1999
rpb2	fRPB2-5f/ fRPB2-7cR	95 °C, 5 min	95 °C, 1 min	52 °C, 1 min			Liu et al. (1999)
tub2	Bt2a/ Bt2b	94 °C, 3 min	94 °C, 30 sec	58 °C, 50 sec	72 °C, 1 min		Glass & Donaldson (1995)
	T1/T22			58 °C, 55 sec			O'Donnell & Cigelnik (1997)

ITS: Internal transcribed spacer regions, LSU: Nuclear large subunit rDNA, SSU: Nuclear small subunit rDNA, mtSSU: Mitochondrial small subunit rDNA, *tef1-α*: Translation elongation factor 1-alpha; *rpb2*: RNA polymerase II subunit 2; *tub2*: β-tubulin.

RESULTS

The classification follows the latest outline of fungi and fungus-like organisms (Hyde et al. 2024)

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. 2018, Wanasinghe et al. 2018, 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. 2024a). Members of *Astrosphaeriellaceae* have been reported as saprobic or parasitic on palms, bamboo, *Quercus* species, or robust grasses (Zhang et al. 2024a). The sexual morph is characterized 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 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. 2020). An updated phylogenetic tree for the family is shown in Fig. 1.

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

Zhang et al. (2024a) 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. Fig. 2

Index Fungorum number: IF903514; Facesoffungi number: FoF17517

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

Holotype – MFLU 24-0484

Saprobic on submerged, decaying rachis of *Eleiodoxa conferta*. **Asexual morph**: Not observed. **Sexual morph**: *Ascomata* 350–600 µm diam., ($\overline{x}$ = 503 µm, n = 15), scattered or in small groups, superficial, hemispherical, carbonaceous, gray 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.

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 *J. palmarum* isolates

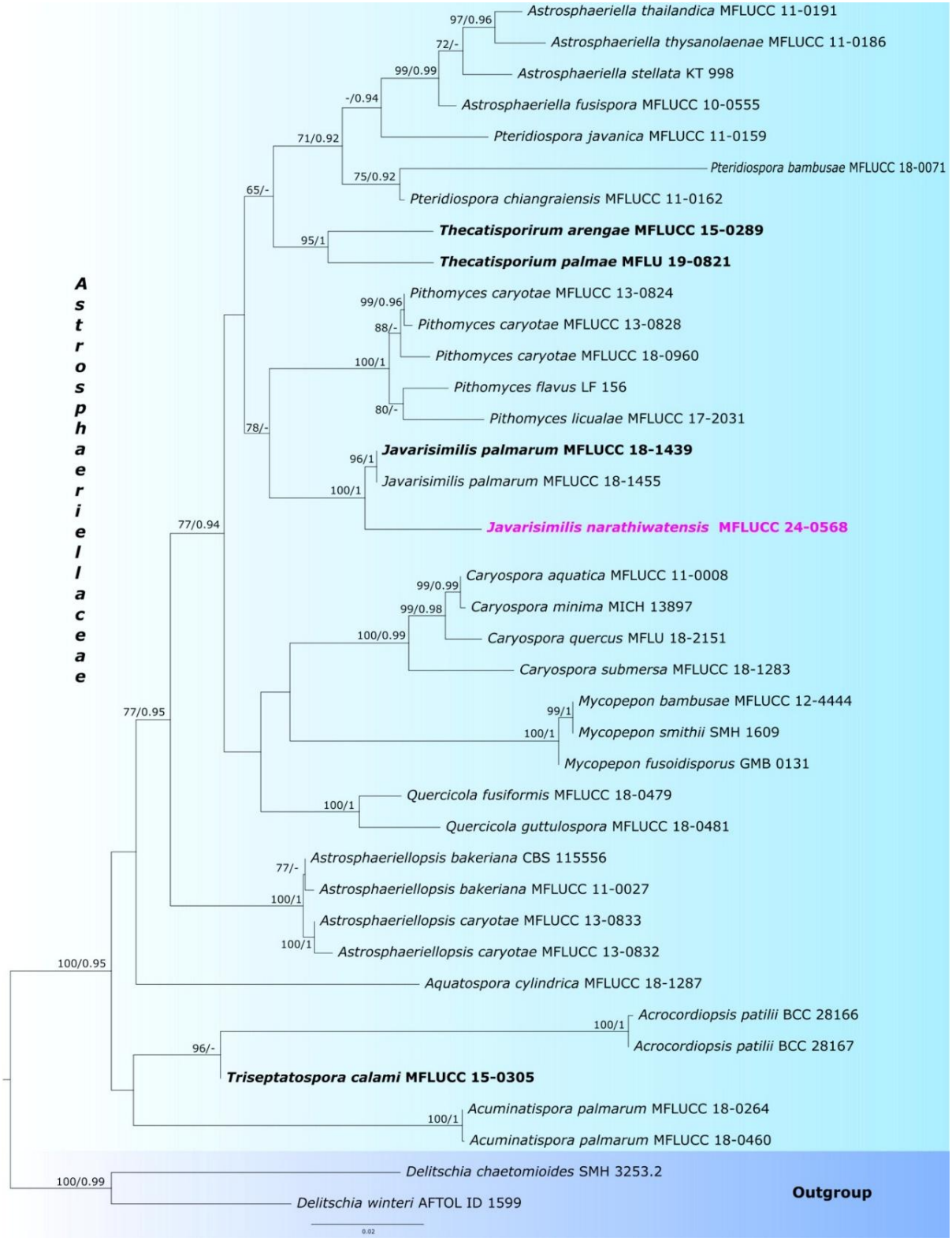

Figure 1 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU and *tef-1α* sequences. The analysis includes 60 strains; total characters: 2815 (LSU: 846, SSU: 1039, *tef-1α*: 930). *Delitschia chaetomioides* (SMH 3253.2), and *D. winteri* (AFTOL-ID 1599) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -11198.122 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 3.03273, AT = 1.00000, CG = 1.00000, CT = 10.39679, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

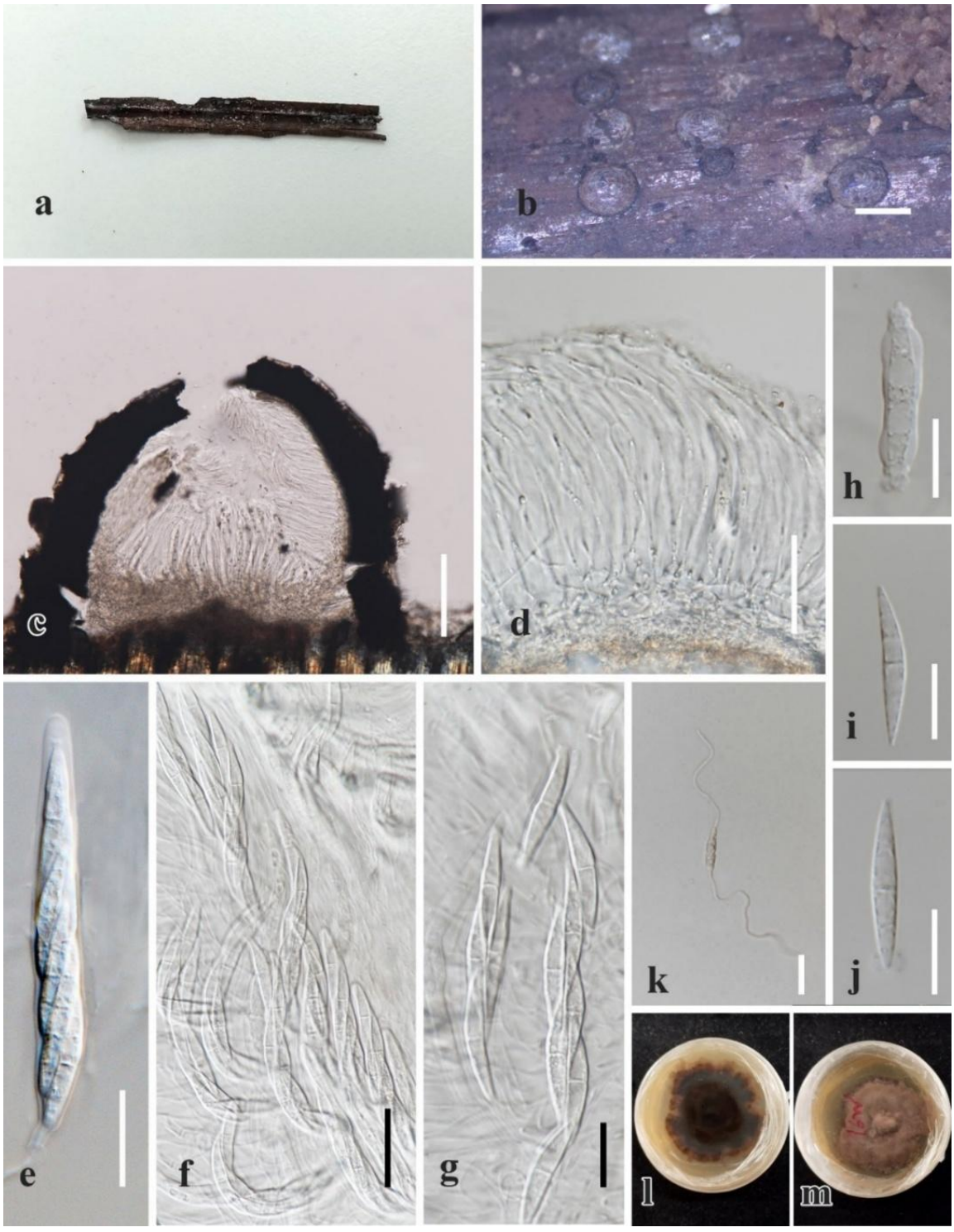

Figure 2 – *Javarisimilis narathiwatensis* (MFLU 24-0484, holotype). a Host. b Appearance of ascomata on the substrate. c Vertical section of the ascoma. d Trabeculate pseudoparaphyses. e–g Asci. h–j Ascospores. k A germinated ascospore. l, m Colonies on the PDA. Scale bars: b = 500 µm, c = 100 µm, d = 40 µm, e, f, k = 30 µm, g–j = 15 µm.

MFLUCC 18-1439 (ex-type) and MFLUCC 18-1455 with 100% ML, 1.00 PP statistical support in the combined phylogenetic analyses (Fig. 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. 2024a). 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 distinct morphological characters and phylogenetic evidence.

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 & 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* are reported as saprobes on stems, bark or twigs of various woody and herbaceous plants in both terrestrial and aquatic environments (Mapook et al. 2020). The sexual morph is characterized by having superficial or semi-immersed to densely erumpent, globose to subglobose, dark-brown to black and carbonaceous ascomata, with an elongate, often slit-like ostiole, with a peridium of thin-walled and lightly pigmented cells of *textura prismatica*, and long, hyaline, septate, anastomosing and branched 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 subglobose, semi-immersed, uni-loculate or rarely bi-loculate, 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 phylogenetic tree for the family is shown in Fig. 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*, 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, Hashimoto et al. 2018, Dong et al. 2020, Pem et al. 2024, Hyde 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.

Lentistoma narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 4

Index Fungorum number: IF903515; Facesoffungi number: FoF17518

Etymology – The epithet "narathiwatense" refers to Narathiwat Province where the holotype was collected.

Holotype – MFLU 24-0485

Saprobic on the submerged rachis of *Eleiodoxa conferta*. **Asexual morph**: Not observed. **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 ($\bar{x}$ = 17 µm, n = 20), comprising of carbonaceous, *textura prismatica* to *textura angularis* cells. *Pseudoparaphyses* 1.6–3 µm wide ($\bar{x}$ = 2.3 µm, n = 40), numerous, distantly septate, branched, hypha-like, hyaline. *Asci* 85–108 × 10−16.6 ($\bar{x}$ = 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 ($\bar{x}$ = 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.

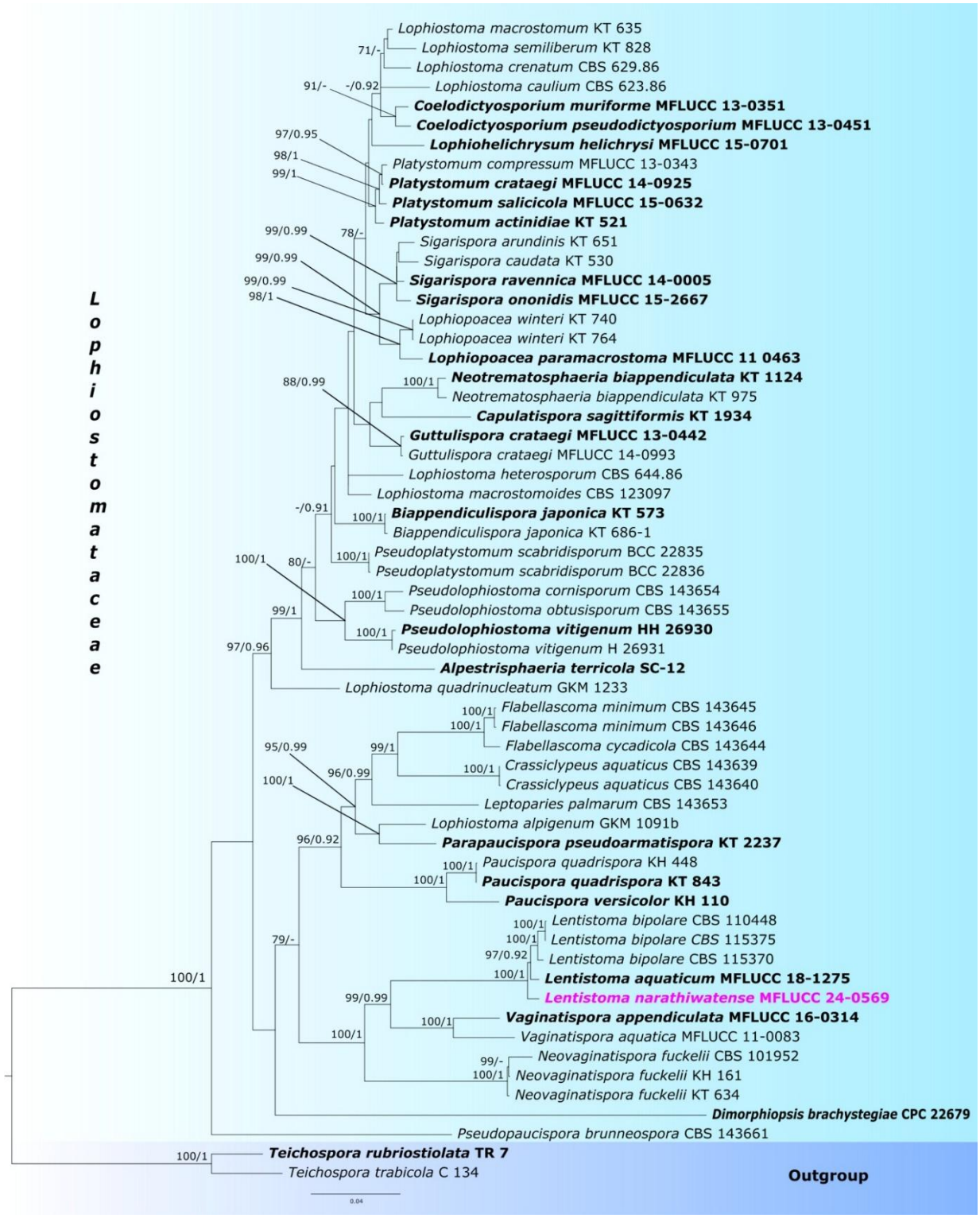

Figure 3 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU, ITS, *tef-1α* and *rpb2* sequences. The analysis includes 60 strains; total characters: 4713 (LSU: 1257, SSU: 983, ITS: 523, *tef-1α*: 925, *rpb2*: 1025). *Teichospora rubriostiolata* (TR 7) and *T. trabicola* (C 134) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -26309.200 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.36168, AG = 3.99173 5, AT = 1.00000, CG = 1.36168, CT = 7.78689, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian

analysis. 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.

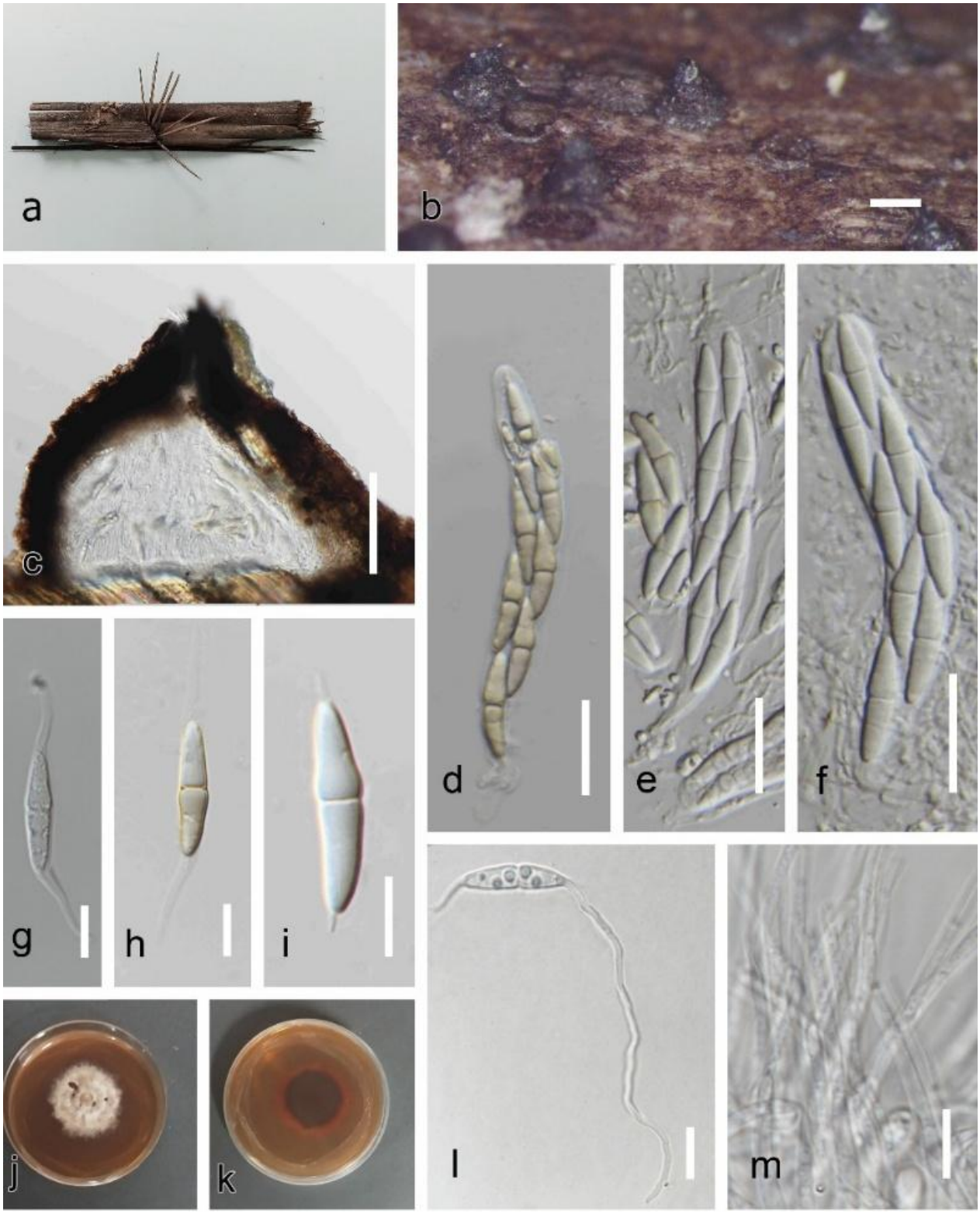

Figure 4 – *Lentistoma narathiwatense* (MFLU 24-0485, holotype). a Host. b Appearance of ascomata on the host substrate. c A vertical section of an ascoma. d–f Asci. g–i Ascospores. j, k Colonies on the PDA. l Germinated ascospore. m Pseudoparaphyses. Scale bars: b = 200 µm, c = 100 µm, d–f = 25 µm, g–i, m = 10 µm.

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 gray with white center and margin, reverse grayish orange with yellowish center 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 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* (Fig. 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). Based on a pairwise comparison of ITS, LSU, *tef-1α* and SSU nucleotides, *Le. narathiwatense* (MFLU 24-0485) differs from *Le. aquaticum* (MFLUCC 18-1275) in 4.9% (30/607 bp, excluding gaps) in the ITS, 0.35% (3/852 bp, excluding gaps) in the LSU, 0.84% (7/864 bp, excluding gaps) in *tef-1α* and without differences in SSU. The *rpb2* region of our strain cannot be compared with *Le. aquaticum* (MFLUCC 18-1275), as it is unavailable for *Le. aquaticum* (MFLUCC 18-1275). *Lentistoma narathiwatense* (MFLU 24-0485) differs from *Le. bipolare* (CBS 115370) in 5.4% (33/610 bp, excluding gaps) in the ITS, 0.70% (6/852 bp, excluding gaps) in the LSU, 1.6% (13/791 bp, excluding gaps) in *rpb2*, 1.12% (10/886 bp, without including gaps) in *tef-1α* and without differences in SSU. Therefore, we introduce *Le. narathiwatense* as a novel species based on morphological and phylogenetic evidence.

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

Zhang et al. (2019a) 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, 2019a). Species in *Striatiguttulaceae* are saprobic on palm hosts in mangrove habitats. The sexual morph is characterized 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. 2019a). An updated phylogenetic tree for the family is shown in Fig. 5.

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

Longicorpus (*L.*), was introduced by Zhang et al. (2019a), 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.

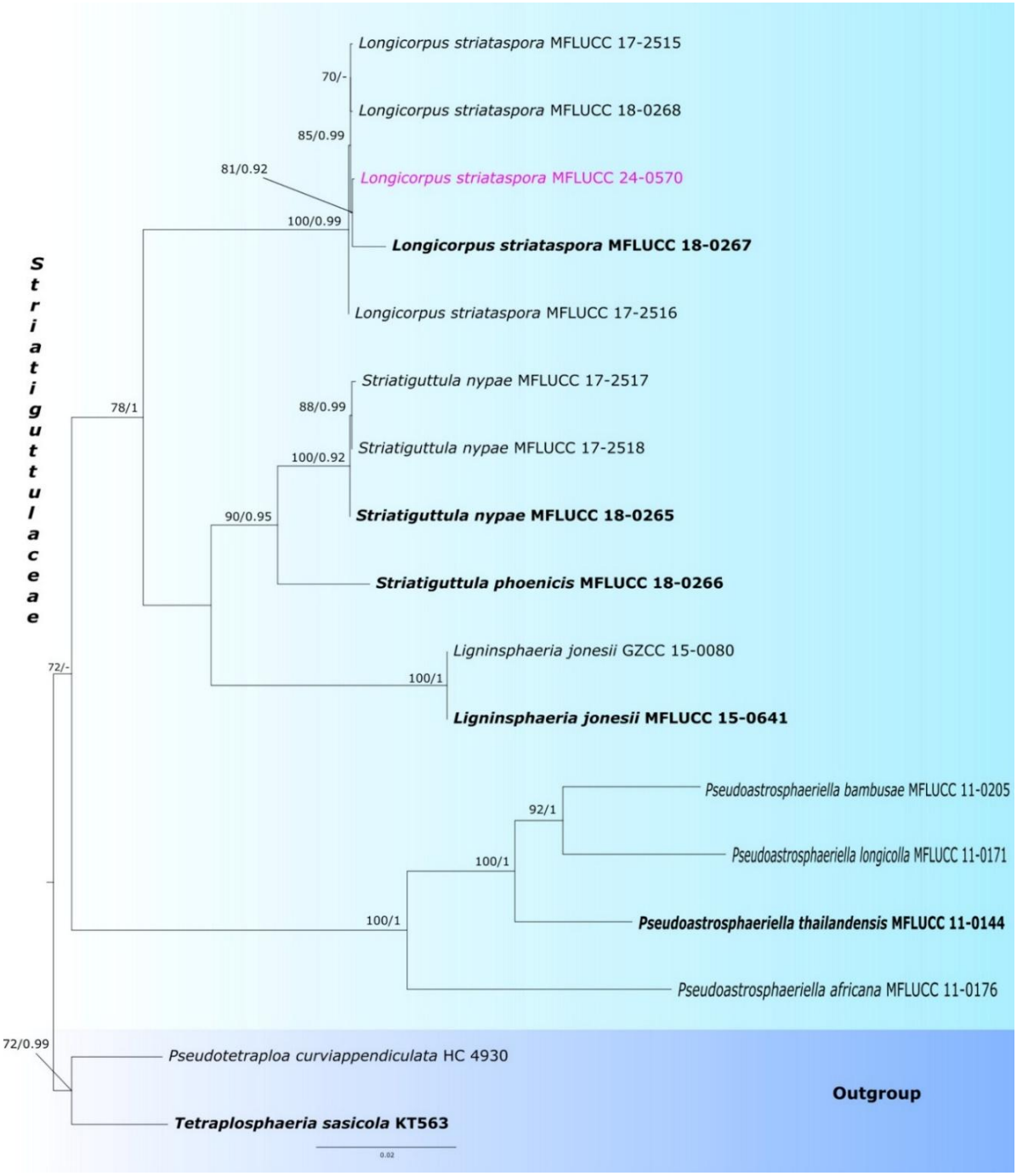

Figure 5 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU, *tef-1α* and *rpb2* sequences. The analysis includes 17 strains; total characters: 3695 (LSU: 846, SSU: 1023, *tef-1α*: 925, *rpb2*: 901). *Pseudotetraploa curviappendiculata* (HC 4930) and *Tetraplosphaeria sasicola* (KT563) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -9210.943 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.57574, AT = 1.00000, CG = 1.00000, CT = 6.17351, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Longicorpus striataspora (K.D. Hyde) S.N. Zhang, K.D. Hyde & J.K. Liu (2019) Fig. 6
Index Fungorum number: IF838919; Facesoffungi number: FoF05037
Saprobic on the submerged rachis of *Eleiodoxa conferta*. **Asexual morph**: Not observed.

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.

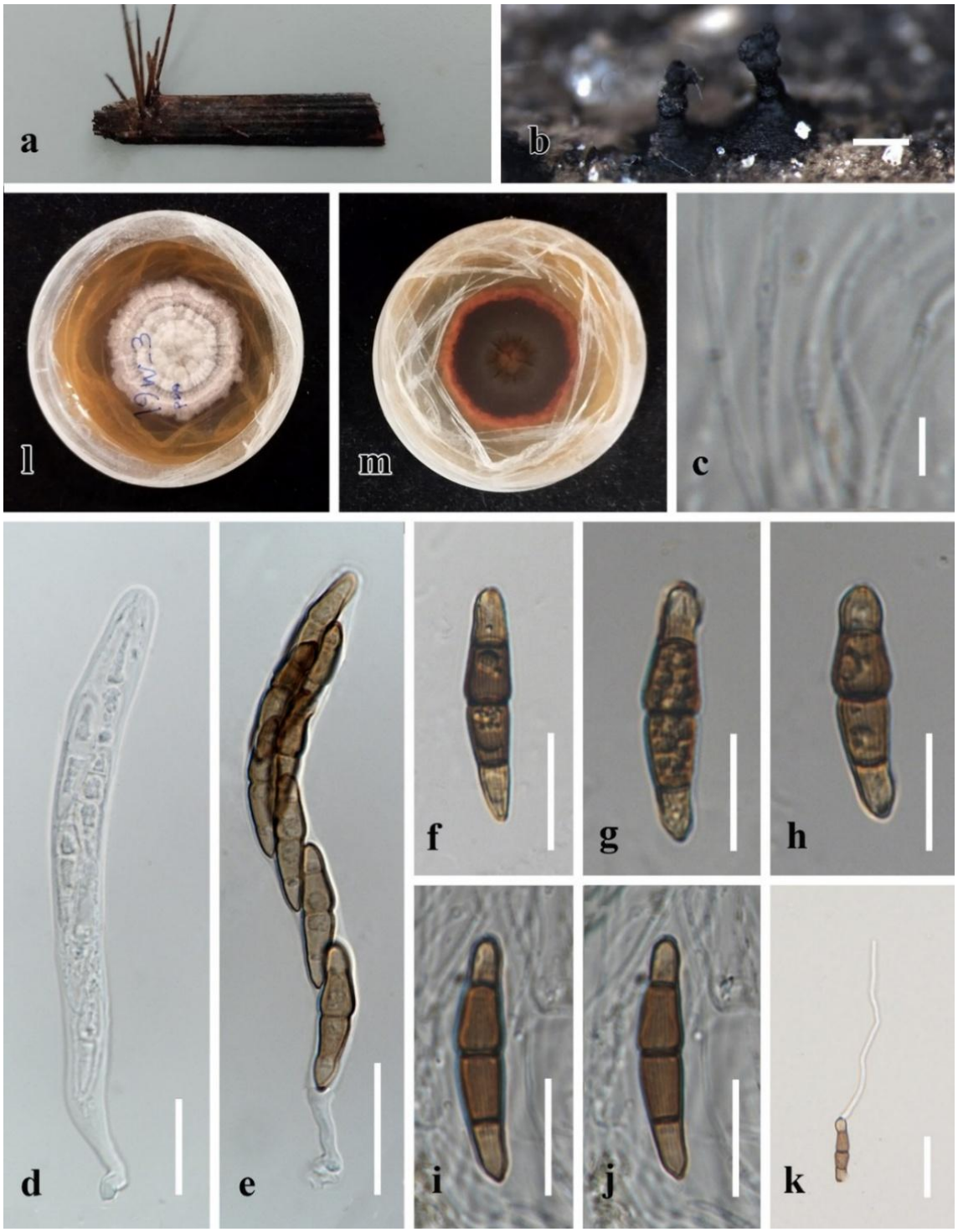

Figure 6 – *Longicorpus striataspora* (MFLU 24-0486, a new host and habitat record). a Host. b Appearance of ascomata on natural substrate. c Pseudoparaphyses. d, e Asci. f–j Ascospores. k Germinated ascospore. l, m Colonies on the PDA. Scale bars: b = 250 μm, c = 5 μm, d = 20 μm, e, k = 30 μm, f–j= 15 μm.

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 center, reverse grayish 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 1988a, Zhang et al. 2019a), *Phoenix paludosa* (Zhang et al. 2019a).

Known distribution – Brunei (Hyde 1988a), Thailand (Zhang et al. 2019a, 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 (Fig. 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. 2019a). 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.

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. (2023b) 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. 2024a). The family is characterized 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 phylogenetic tree for the family is shown in Fig. 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.

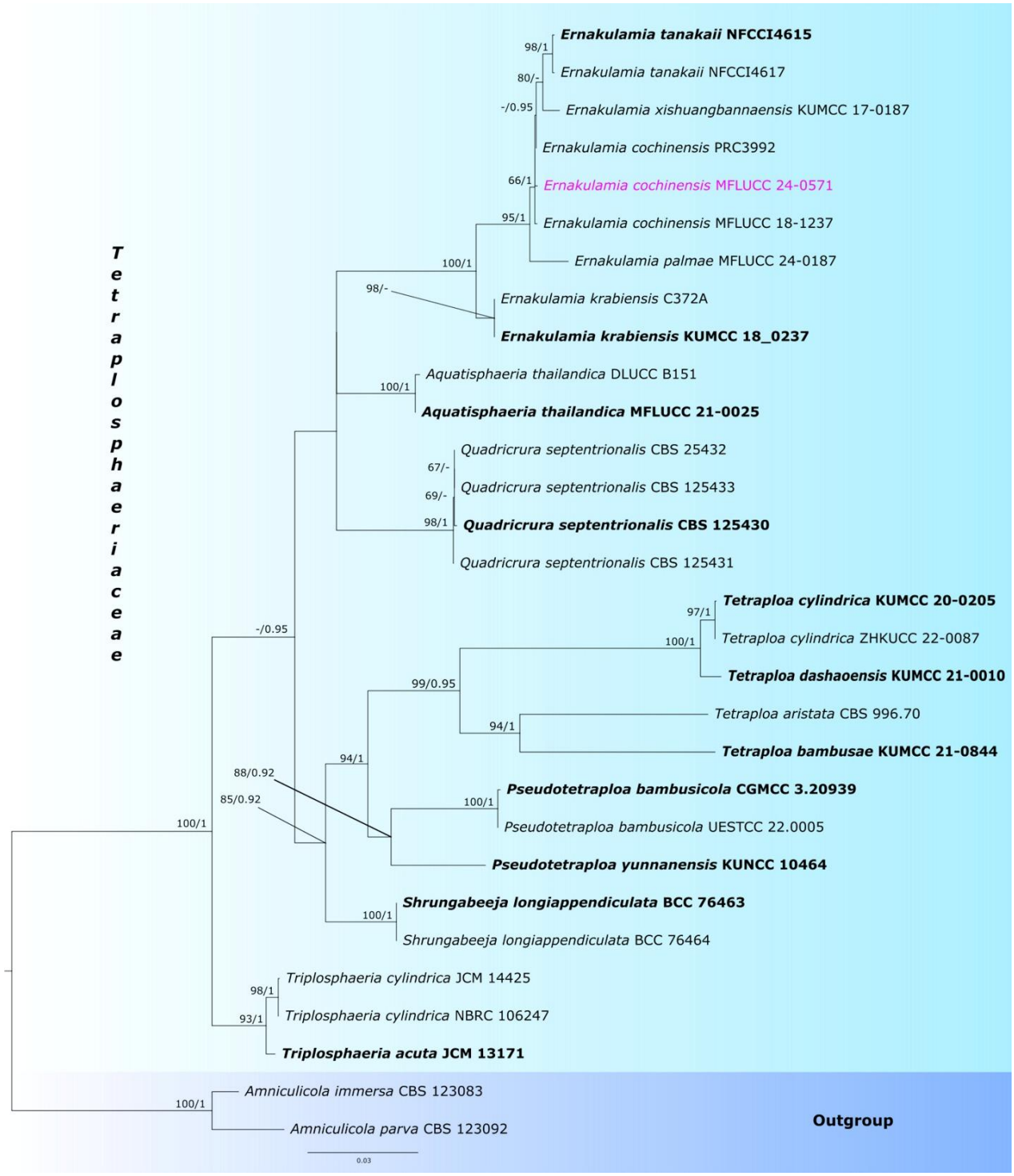

Figure 7 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, ITS, SSU, *tub2* and *tef-1α* sequences. The analysis includes 30 strains; total characters: 3306 (LSU: 860, ITS: 526, SSU: 990, *tub2*: 634, *tef-1α*: 296). *Amniculicola parva* (CBS 123092) and *A. immersa* (CBS 123083) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -12006.601 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.50537, AG = 2.65581, AT = 1.00000, CG = 1.50537, CT = 6.38812, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis.

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.

Ernakulamia cochinensis (Subram.) Subram., Kavaka 22/23: 67 (1996) [1994] Fig. 8

Index Fungorum number: IF374840; Facesoffungi number: FoF09277

Saprobic on the submerged petiole of *Cyrtostachys renda*. **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. **Sexual morph**: Not observed.

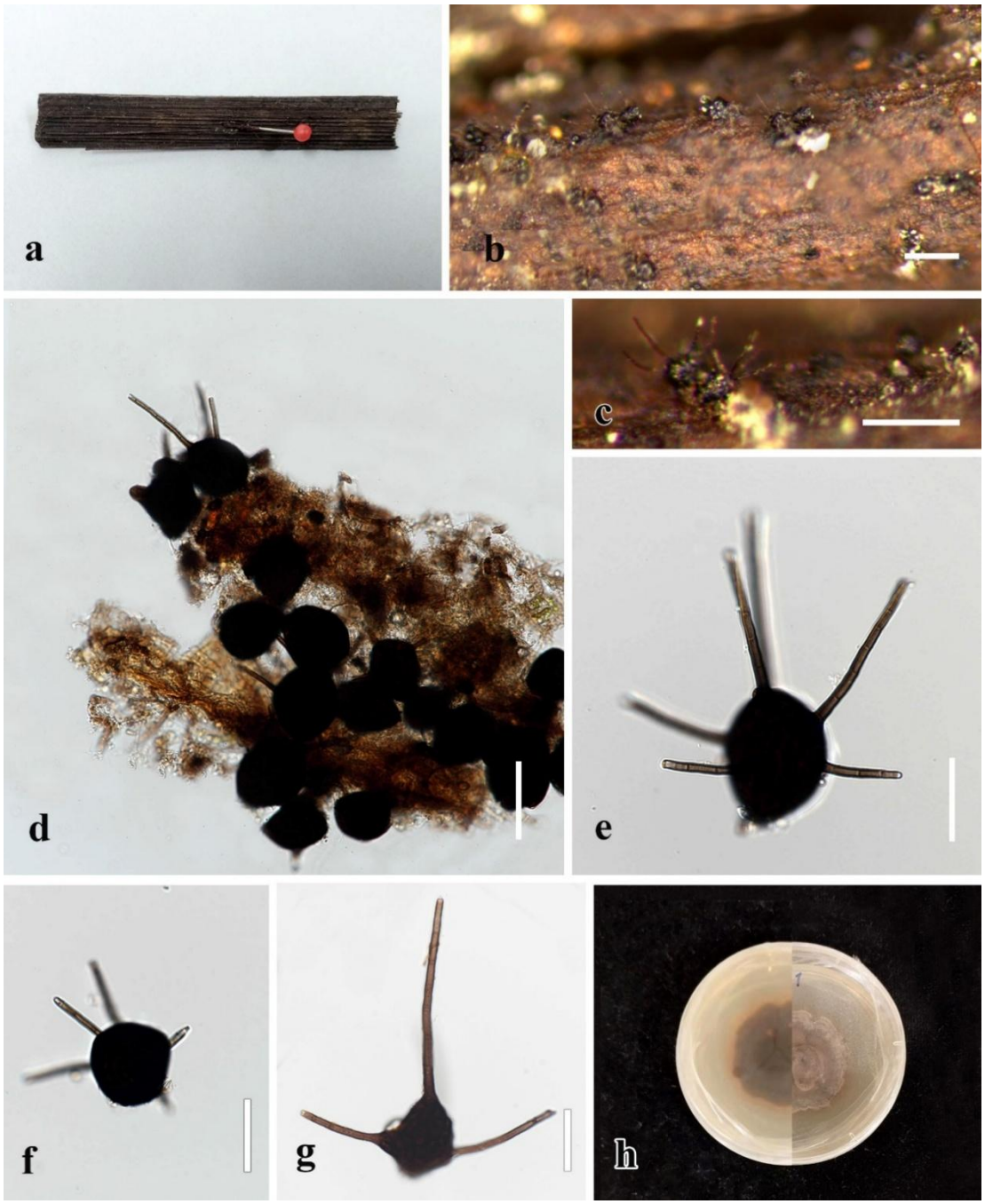

Figure 8 – *Ernakulamia cochinensis* (MFLU 24-0487, a new host and habitat record). a Host. b, c Colonies on the host. d–g Conidia. h Colonies on the PDA. Scale bars: b, c = 250 µm, d, e = 20 µm, g = 40 µm.

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, mycelium superficial to immersed, dull, surface grayish-brown with light gray 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, *rpb2* = PV340517, *tef-1α* = PV340483, *tub2* = PV477060.

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 (Fig. 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.

Megacapitulaceae Rajeshk., Sruthi OP, Hongsanan, Jeewon, Karuna & Harik., Kavaka 60(4): 6 (2024)

Megacapitulaceae was recently introduced by Rajeshkumar et al. (2024) to accommodate its type genus *Megacapitula*, which was formerly considered *incertae sedis* within *Pleosporales*. The authors designated a lectotype based on illustrations of the original material and provided a sequenced epitype. Their phylogenetic analysis, based on a combined dataset of LSU, SSU, ITS, *tef-1α*, and *rpb2*, revealed a distinct placement of the *Megacapitulaceae* clade within *Pleosporales*, closely related to *Phaeoseptaceae*. *Megacapitulaceae* is characterized by a hyphomycetous asexual morph, with micronematous to semi-macronematous conidiophores that are smooth, roughened, or verrucose; integrated conidiogenous cells; and holoblastic, solitary, muriform, pigmented conidia with apical hair-like appendages.

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* derived from a collection in 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) Fig. 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 gray 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 & Tzean 1993), decaying fronds of *Caryota urens* (Prabhugaonkar & Bhat 2011), *Eleiodoxa conferta* (This study), dead rachides of *Roystonea regia* (Zhang et al. 2024a).

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

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

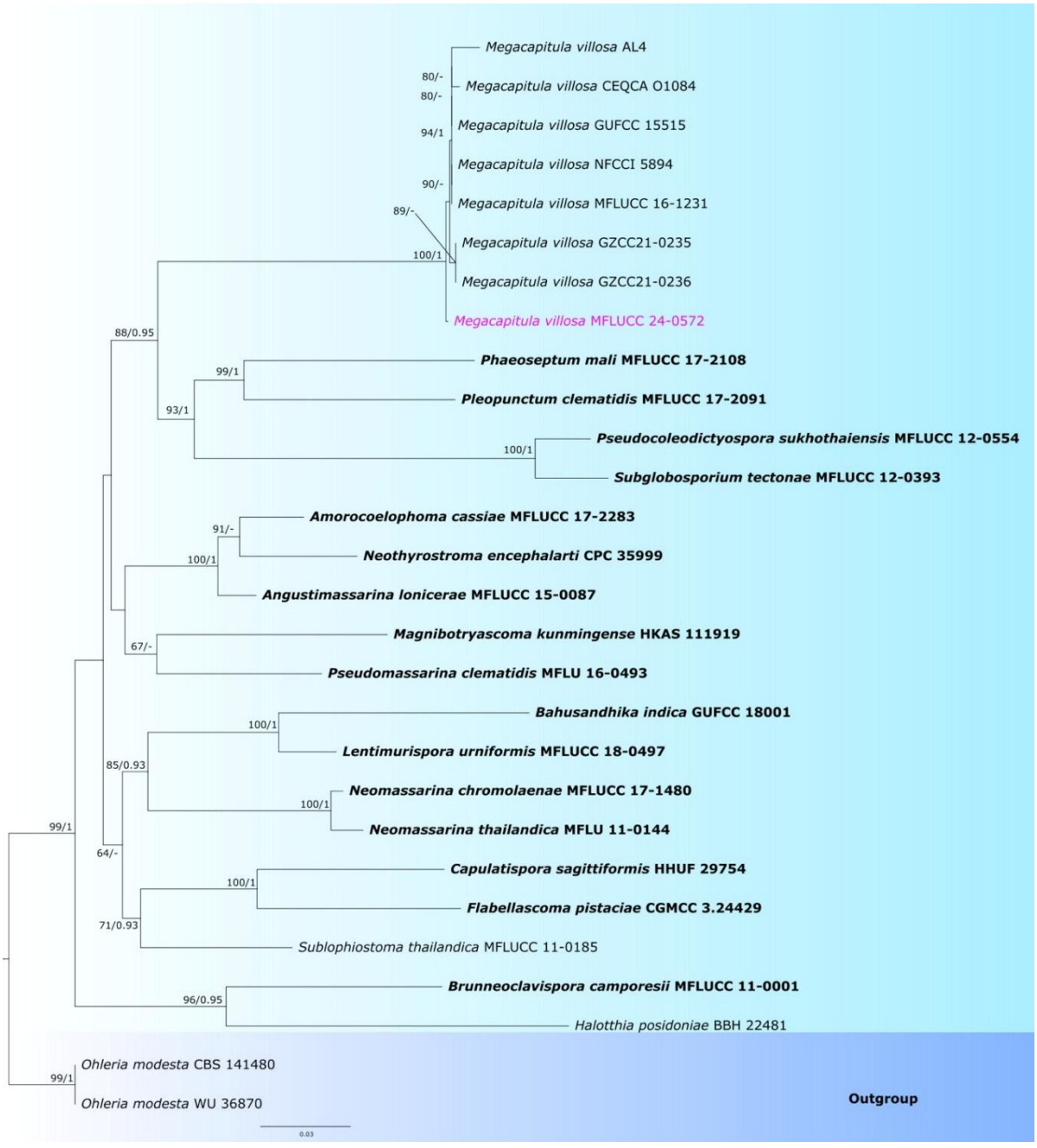

Figure 9 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, ITS, SSU and *tef-1α* sequences. The analysis includes 28 strains; total characters: 3325 (LSU: 864, ITS: 526, SSU: 1004, *tef-1α*: 928). *Hysterobrevium baoshanense* (MFLUCC 16-2162) and *H. karsti* (MFLU 18-2251) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -83065.128 is presented. Estimated base frequencies were as follows: A = 0.2386, C = 0.2588, G = 0.2727, T = 0.2299; substitution rates AC = 1.0000, AG = 2.1282, AT = 1.0000, CG = 1.0000, CT = 6.2404, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 60% 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.

Notes – We recognized 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 & 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 (Fig. 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 & 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.

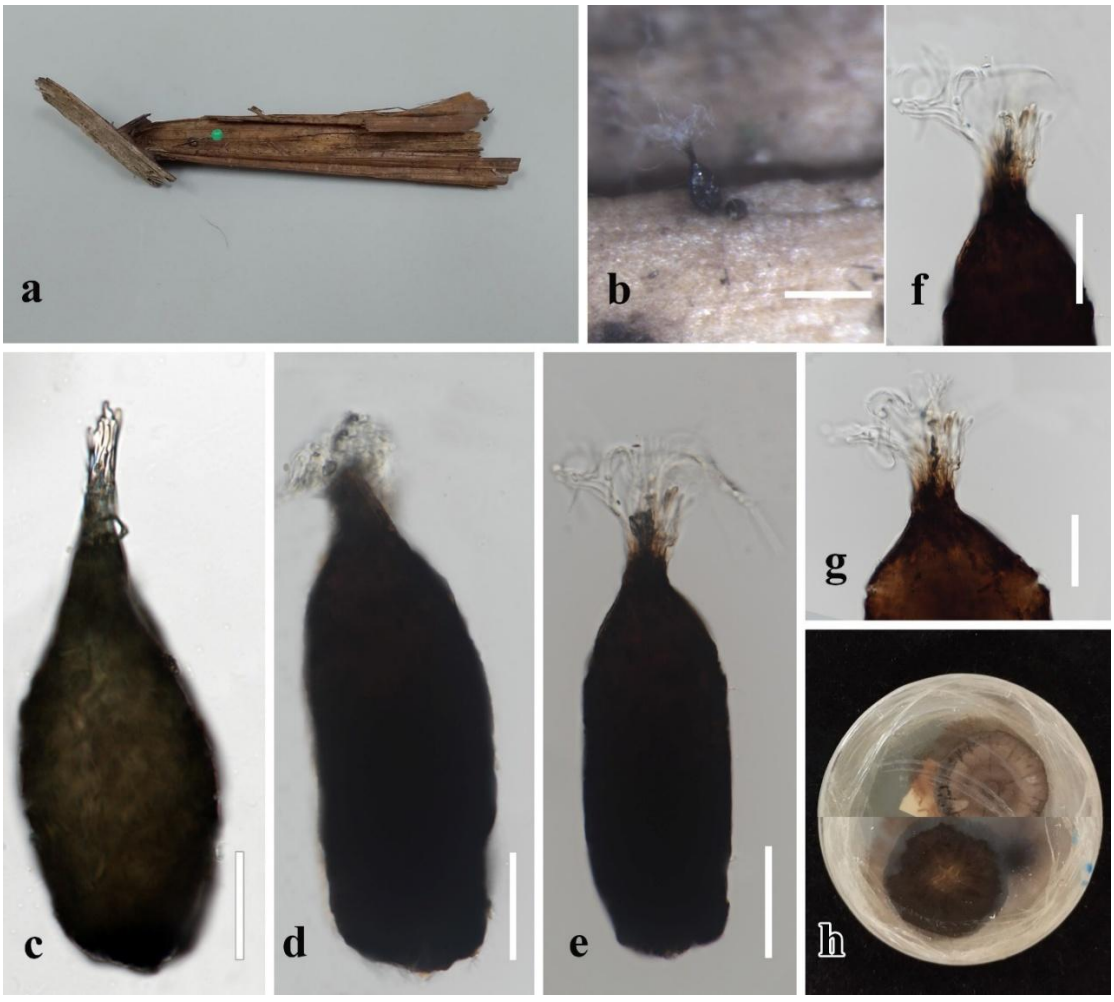

Figure 10 – *Megacapitula villosa* (MFLU 24-0488, a new host and habitat record). a Host. b Colonies on the host. c–g Conidia with appendages. h Colonies on the PDA. Scale bars: b = 250 μm, c = 35 μm, d, e = 40 μm, f, g = 35 μm.

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 characterized 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, *Narathiwatomyces* (*Nar.*), to accommodate *Nar. confertae*, based on morpho-phylogenetic analyses. An updated phylogenetic tree for the family is shown in Fig. 11.

Narathiwatomyces O. Karimi, R. Asghari & K.D. Hyde, gen. nov. Fig. 12

Index Fungorum number: IF903517; Facesoffungi number: FoF17520

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*. **Asexual morph**: Not observed. **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.

Notes – *Narathiwatomyces* has a single species, *Nar. confertae* (MFLUCC 24-0573), formed a 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 (Fig. 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, *Narathiwatomyces* 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*.

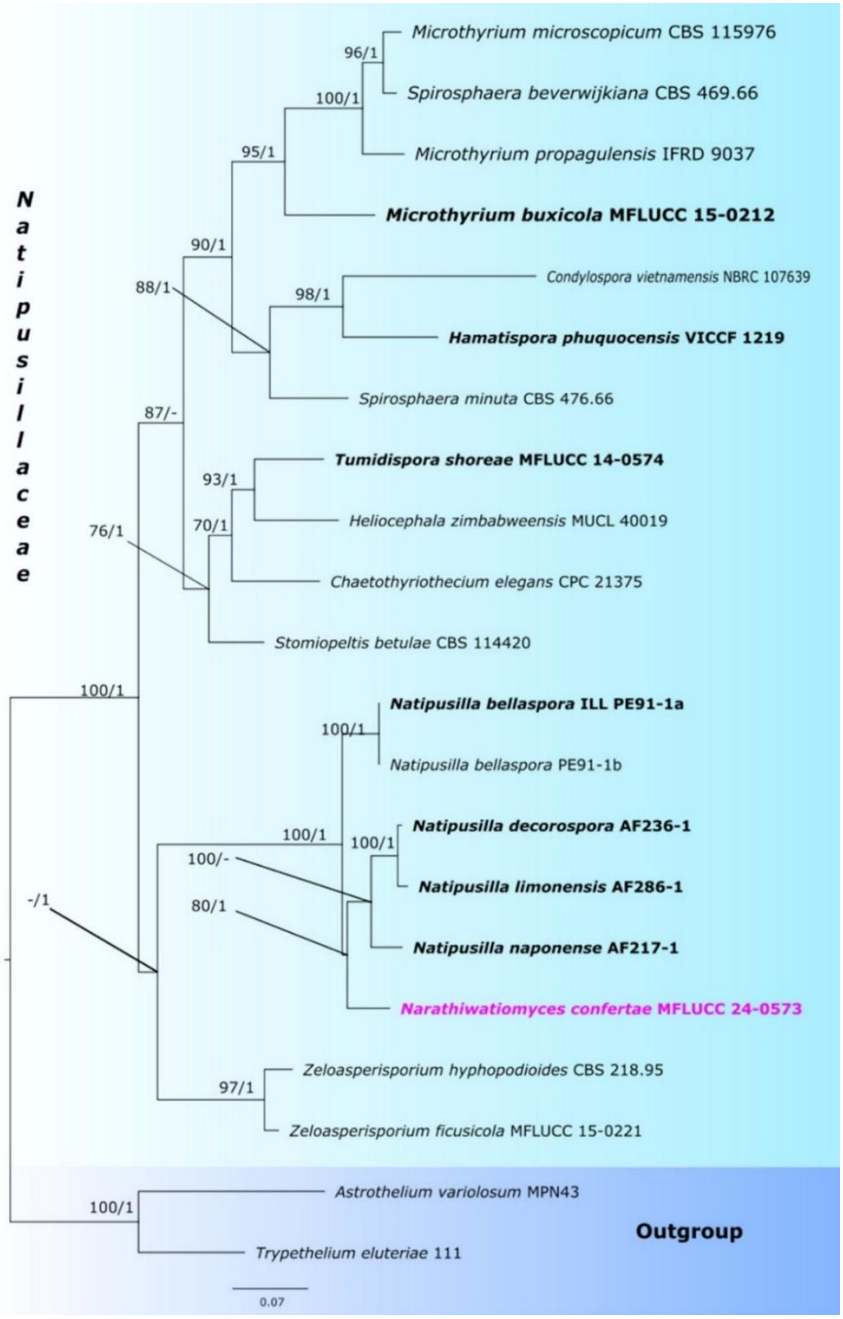

Figure 11 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU and SSU sequences. The analysis includes 21 strains; total characters: 1889 (LSU: 874, SSU: 1015). *Astrothellium variolosum* (MPN43), and *Trypethelium eluteriae* (111) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -15543.965 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 3.99173 5, AT = 1.00000, CG = 1.00000, CT = 5.46023, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Narathiwatomyces confertae O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 12

Index Fungorum number: IF903518; Facesoffungi number: FoF17521

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

Holotype – MFLU 24-0489

Saprobic on the submerged rachis of *Eleiodoxa conferta*. **Asexual morph**: Not observed. **Sexual morph**: *Ascomata* 200–280 µm ($\bar{x}$ = 250 µm, n = 10), hemispherical, superficial, scattered,

effused-pulvinate, umbonate, raised and mostly wrinkled at the center, 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.

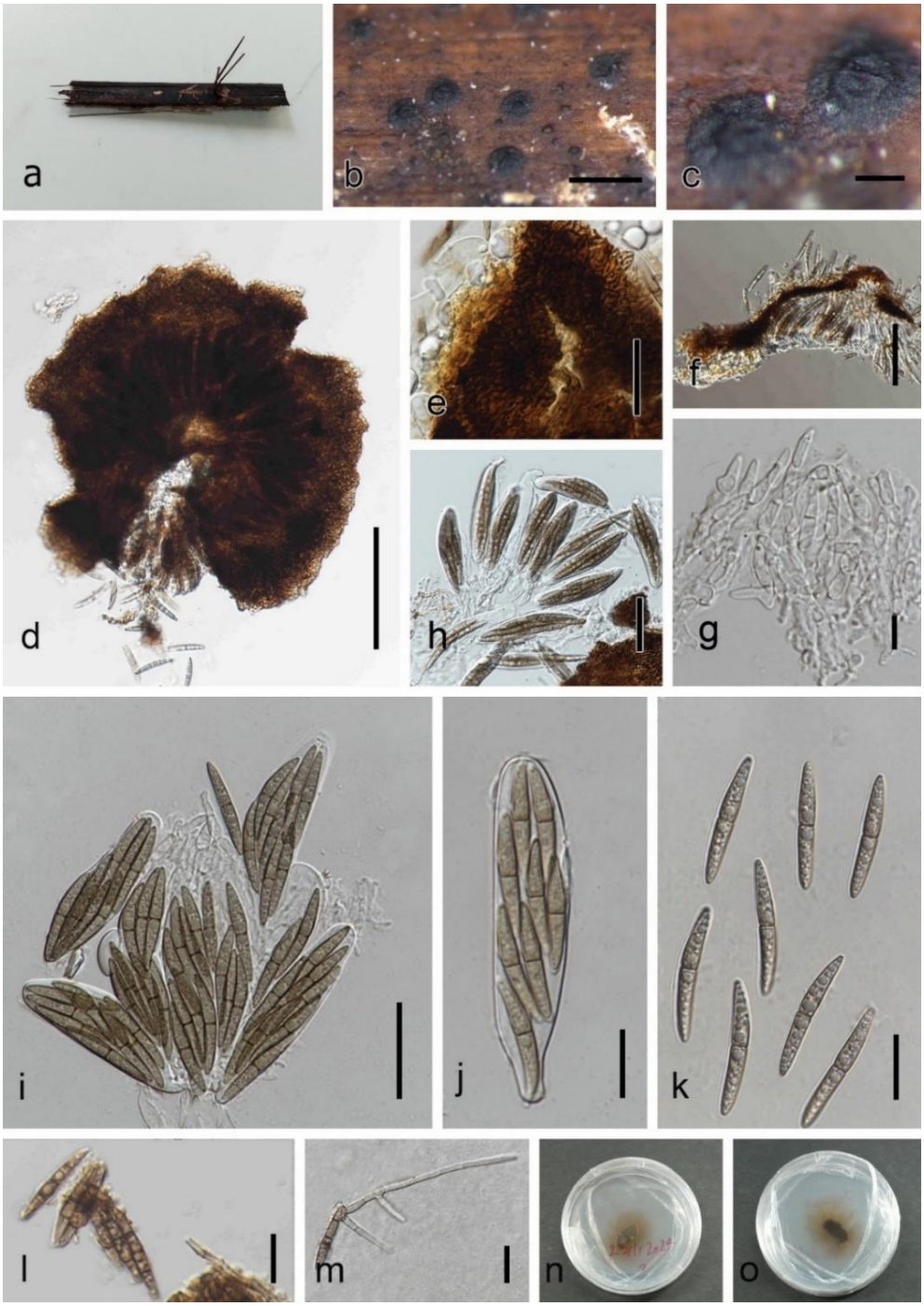

Figure 12 – *Narathiwatomyces confertae* (MFLU 24-0489, holotype). a Host. b, c Appearance of ascomata on the host substrate. d–f A section of the ascoma. g Pseudoparaphyses. h–j Asci. k, l Ascospores. m A germinated ascospore. n, o Colonies on the PDA. Scale bars: b = 500 µm, c–e = 100 µm, f = 50 µm, g = 6 µm, h, i = 30 µm, j–m = 15 µm.

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 grayish 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 – *Narathiwatomyces 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 (Fig. 11). *Nar. confertae* is introduced as a novel species and the sole species of *Narathiwatomyces* based on morphological and phylogenetic evidence. Detailed information is provided in the generic note of *Narathiwatomyces*.

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 & Kang 2020, Li et al. 2022, Ma et al. 2023, 2024). The sexual morph of *Tubeufiaceae* is characterized 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. 2007, Boonmee et al. 2014, Lu et al. 2018). In this study, we introduce six new species and report one new record from palm in the peat swamp forest of Narathiwat, Thailand. An updated phylogenetic tree for the order is shown in Fig. 13.

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

Corda (1837) 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 & 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, Pinuruan 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.

Helicoma narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 14

Index Fungorum number: IF903519; Facesoffungi number: FoF17522

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.

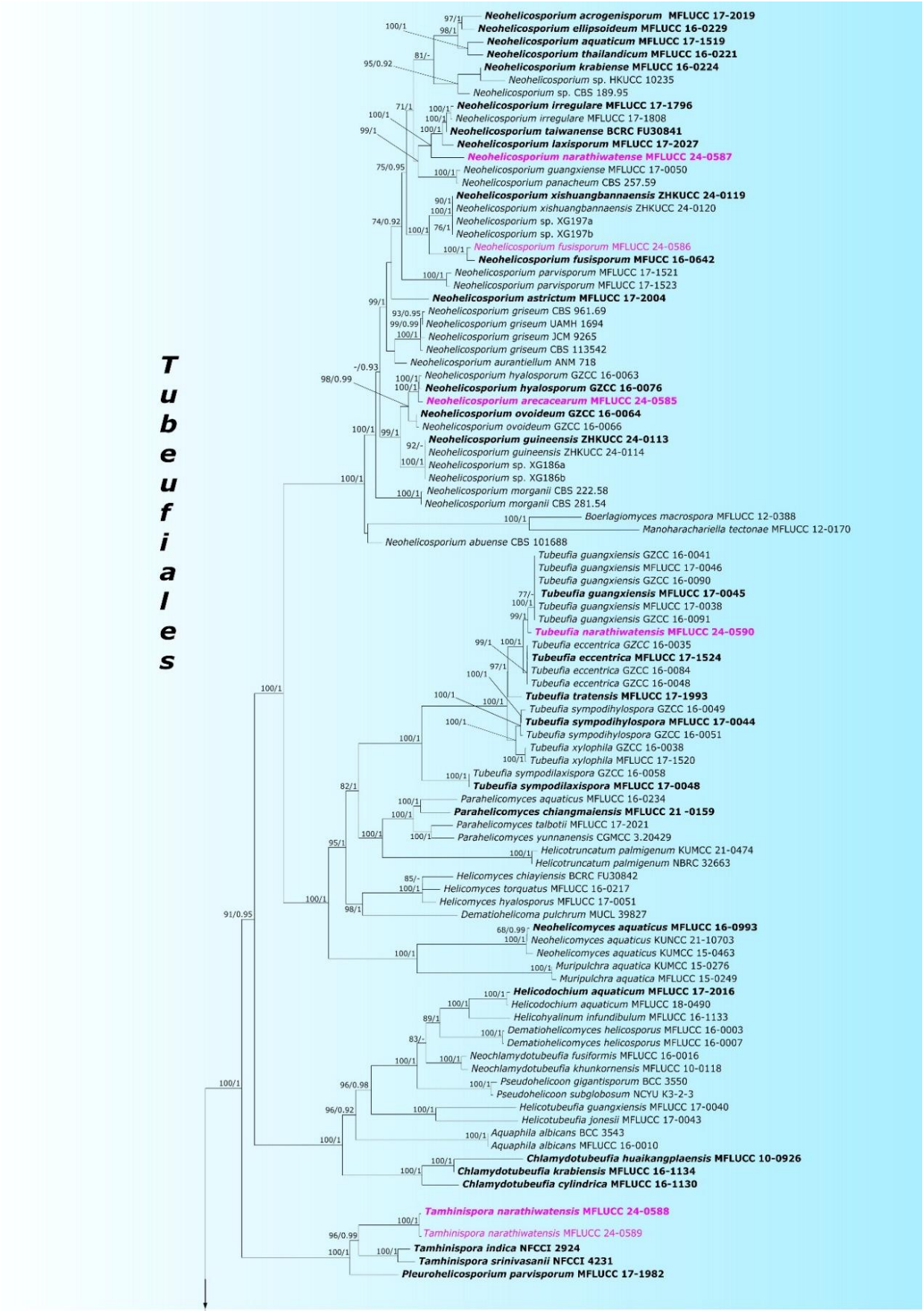

Figure 13 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, *rpb2* and *tef1-α* sequences. The analysis includes 161 strains; total characters: 3496 (ITS: 622, LSU: 919, *rpb2*: 1044, *tef1-α*: 911). *Botryosphaeria agaves* (MFLUCC 10-0051) and *B. dothidea* (CBS 115476) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -46070.174 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.05658, AG = 4.93071, AT = 1.83109, CG = 0.81107, CT = 9.11224, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. Strains of the newly described species are in purple, while type strains are in bold.

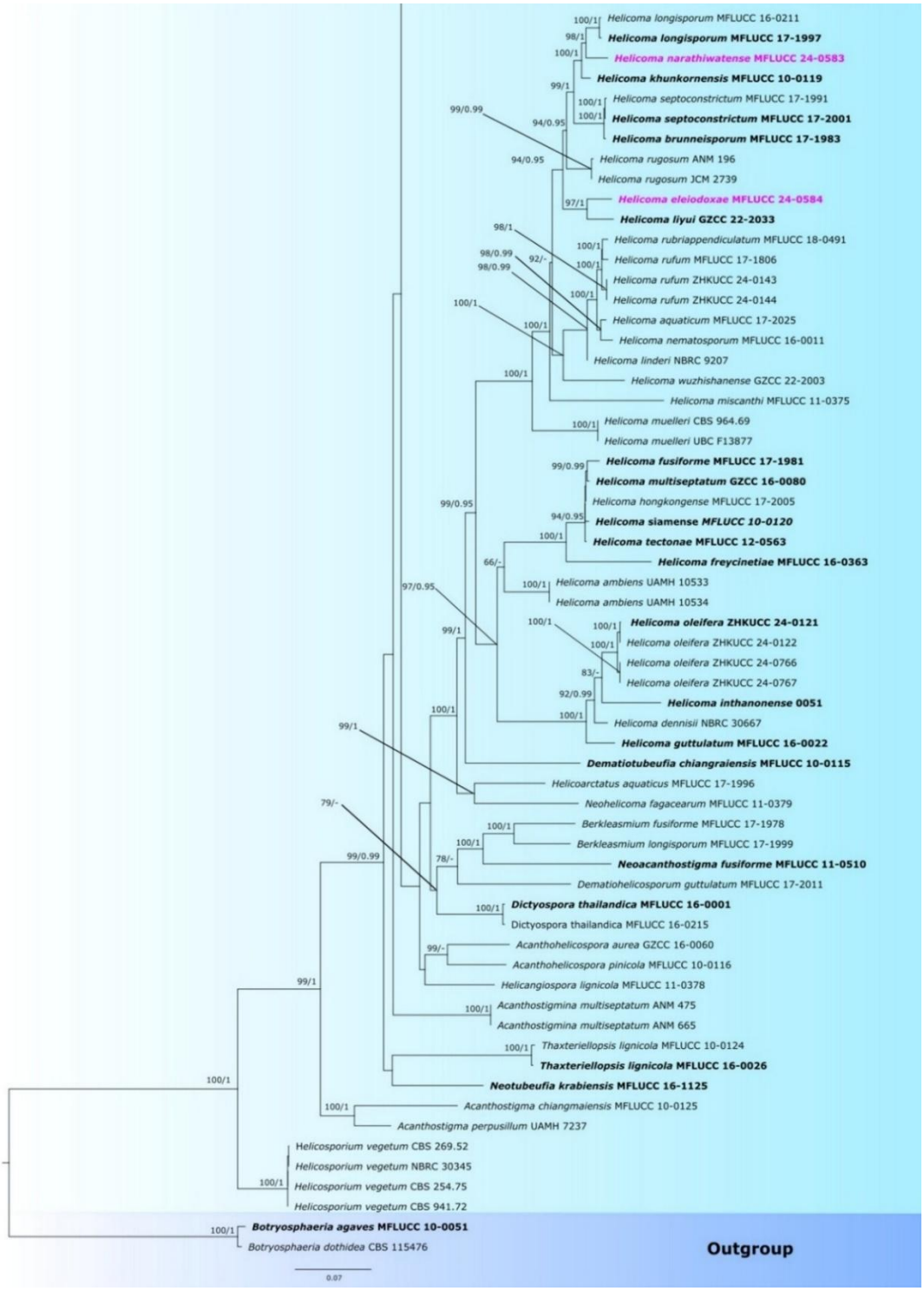

Figure 13 – Continued.

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.

Figure 14 – *Helicoma narathiwatense* (MFLU 24-0498, holotype). a Host. b Colonies on the natural substrate. c–e Conidiophores and conidiogenous cells. f–h Conidia. i A 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.

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* (Fig. 13), 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* (MFLUCC 10–0119), 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. Fig. 15

Index Fungorum number: IF903520; Facesoffungi number: FoF17523

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* 112–178 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.

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* (Fig. 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. (2018) 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. arecacearum* 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. An updated phylogenetic tree for the genus, including all species, has been constructed (Fig. 16).

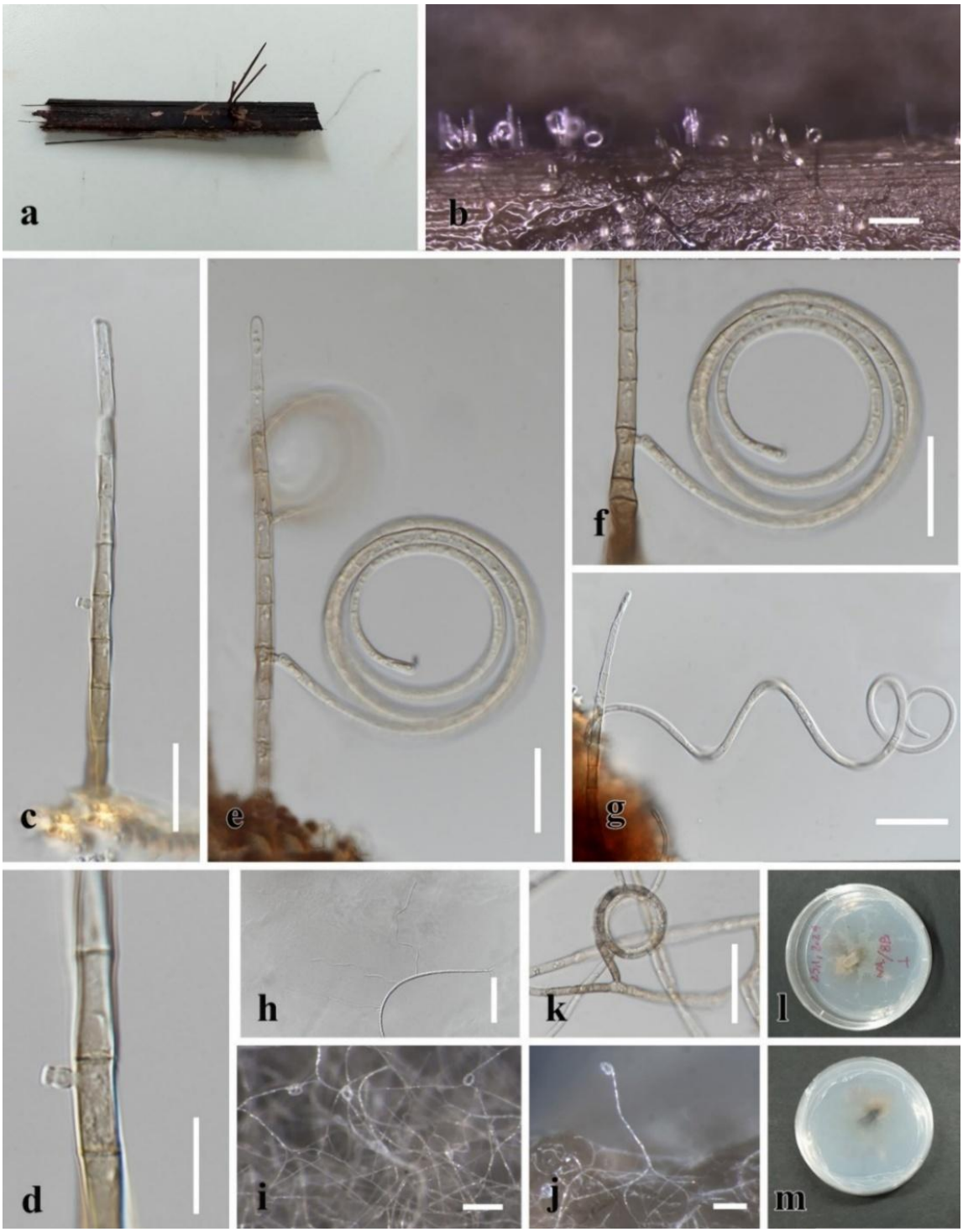

Figure 15 – *Helicoma eleiodoxae* (MFLU 24-0499, holotype). a Host. b Colonies on the natural substrate. c, d Conidiophores and conidiogenous cells. e–g Conidiophores, conidiogenous cells and conidia. h Germinated conidium. i–k Colonies in culture (water agar). m, l Upper surface and reverse overview of culture (WA). 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.

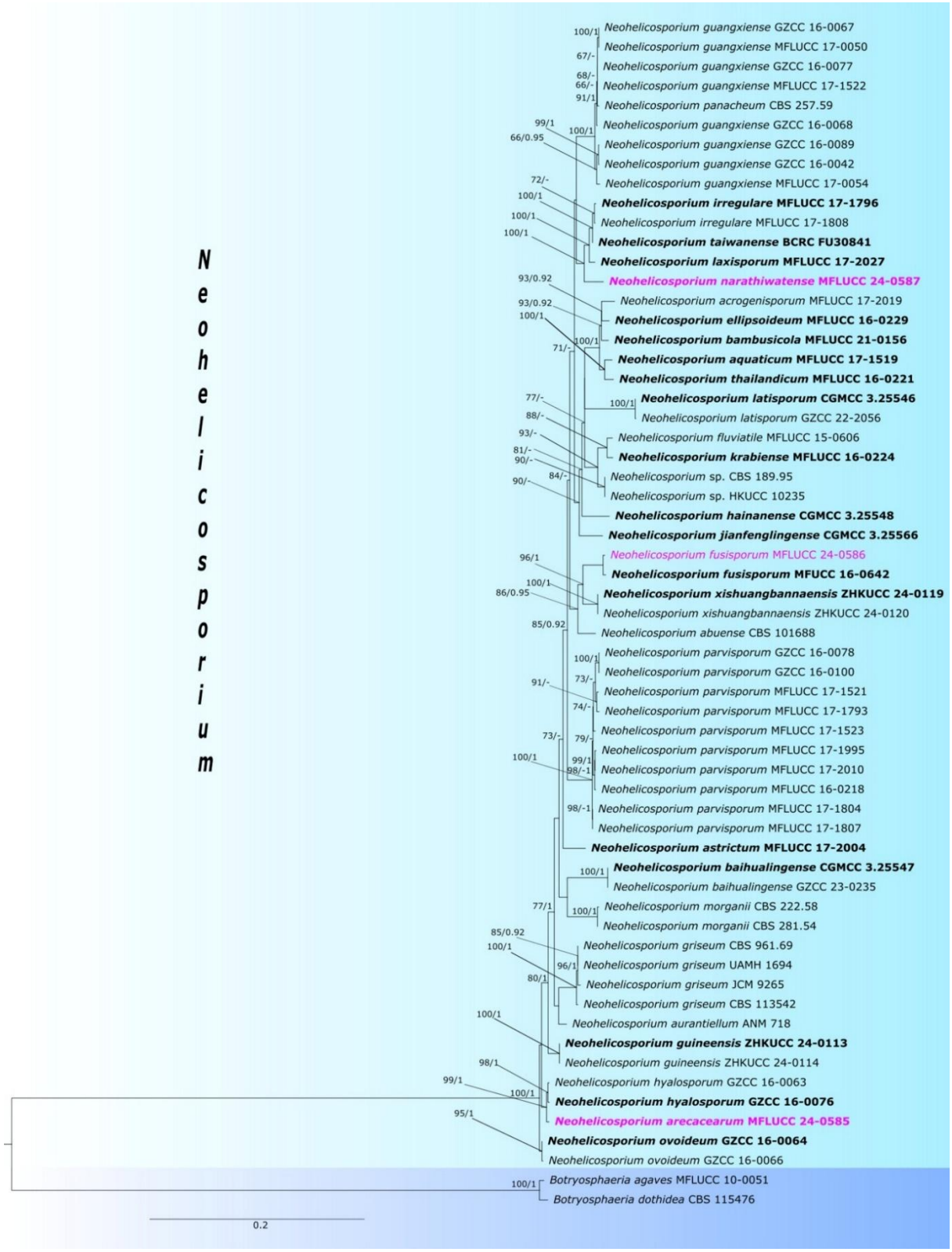

Figure 16 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, *rpb2* and *tef1-α* sequences. The analysis includes 59 strains; total characters: 3380 (ITS: 581, LSU: 842, *rpb2*: 1045, *tef1-α*: 912). *Botryosphaeria agaves* (MFLUCC 10-0051) and *B. dothidea* (CBS 115476) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -13720.438 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.54769, AG = 5.70062, AT = 1.54769, CG = 1.00000, CT = 17.42026, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis.

Bootstrap values for ML equal to or greater than 65% and BYPP values greater than 0.90 are labelled on the nodes. Strains of the newly described species are in purple, while type strains are in bold.

Neohelicosporium arecacearum O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 17

Index Fungorum number: IF903521; Facesoffungi number: FoF17524

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

Holotype – MFLU 24-0500

Saprobic on dead rachis of *Caryota mitis*. **Asexual morph**: Hyphomycetous, helicosporous. *Colonies* on 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.

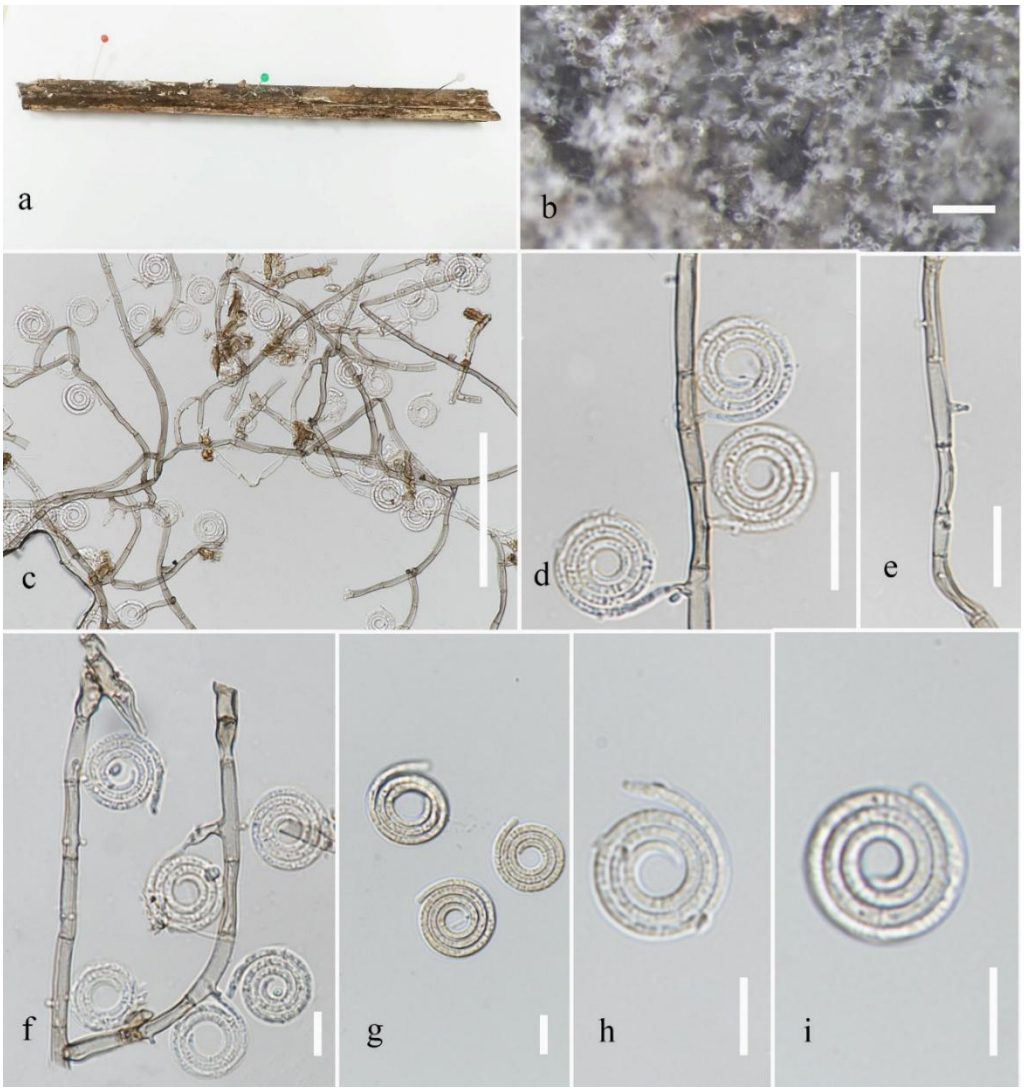

Figure 17 – *Neohelicosporium arecacearum* (MFLU 24-0500, holotype). a Host. b Colonies on the natural substrate. c–f Conidiophores, conidiogenous cells and conidia. g–i Conidia. Scale bars: b = 150 µm, c = 70 µm, d = 50 µm, e = 30 µm, f, i = 60 µm, g = 55 µm, h = 45 µm.

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 (Fig. 13). 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.

Neohelicosporium fusisporum Jayasiri & K.D. Hyde, Index Fungorum 352: 1 (2018) Fig. 18

Index Fungorum number: IF553637; Facesoffungi number: FoF03785

Saprobic on the submerged rachis of *Eleiodoxa conferta*. **Asexual morph**: Hyphomycetous, helicosporous. *Colonies* on the 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 grayish 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 (Fig. 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.

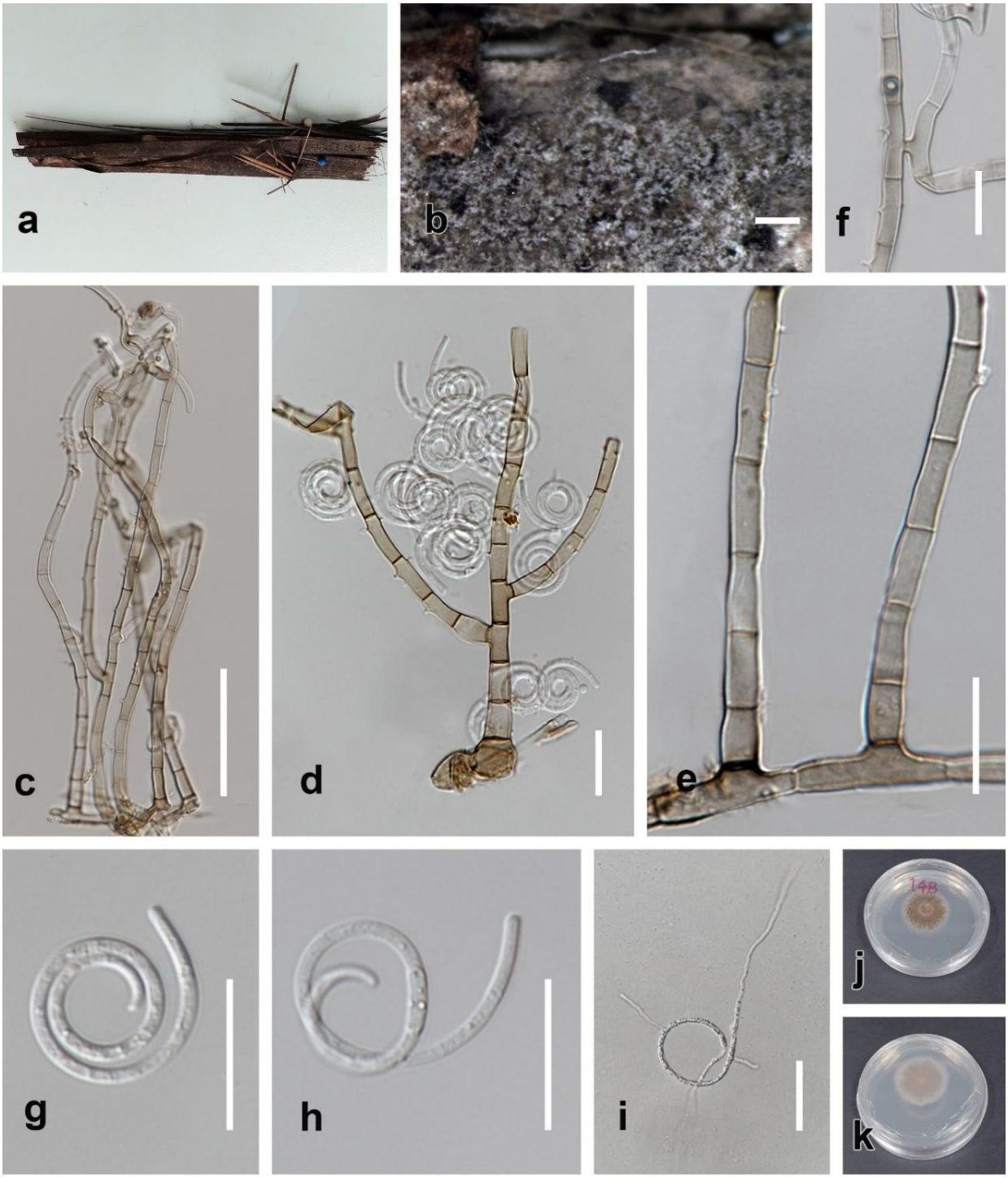

Figure 18 – *Neohelicosporium fusisporum* (MFLU 24-0501, a new host and habitat record). a Host. b Colonies on natural substrate. c, e, f Conidiophores and conidiogenous cells. d Conidiophores and conidia. g, h Conidia. i Germinated conidium. j, k Colonies on PDA. Scale bars: b = 200 µm, c = 50 µm, e, d, g, h = 20 µm, f = 15 µm, i, g = 40 µm.

Neohelicosporium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 19

Index Fungorum number: IF903522; Facesoffungi number: FoF17525

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 colored 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* (Fig. 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 & 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.

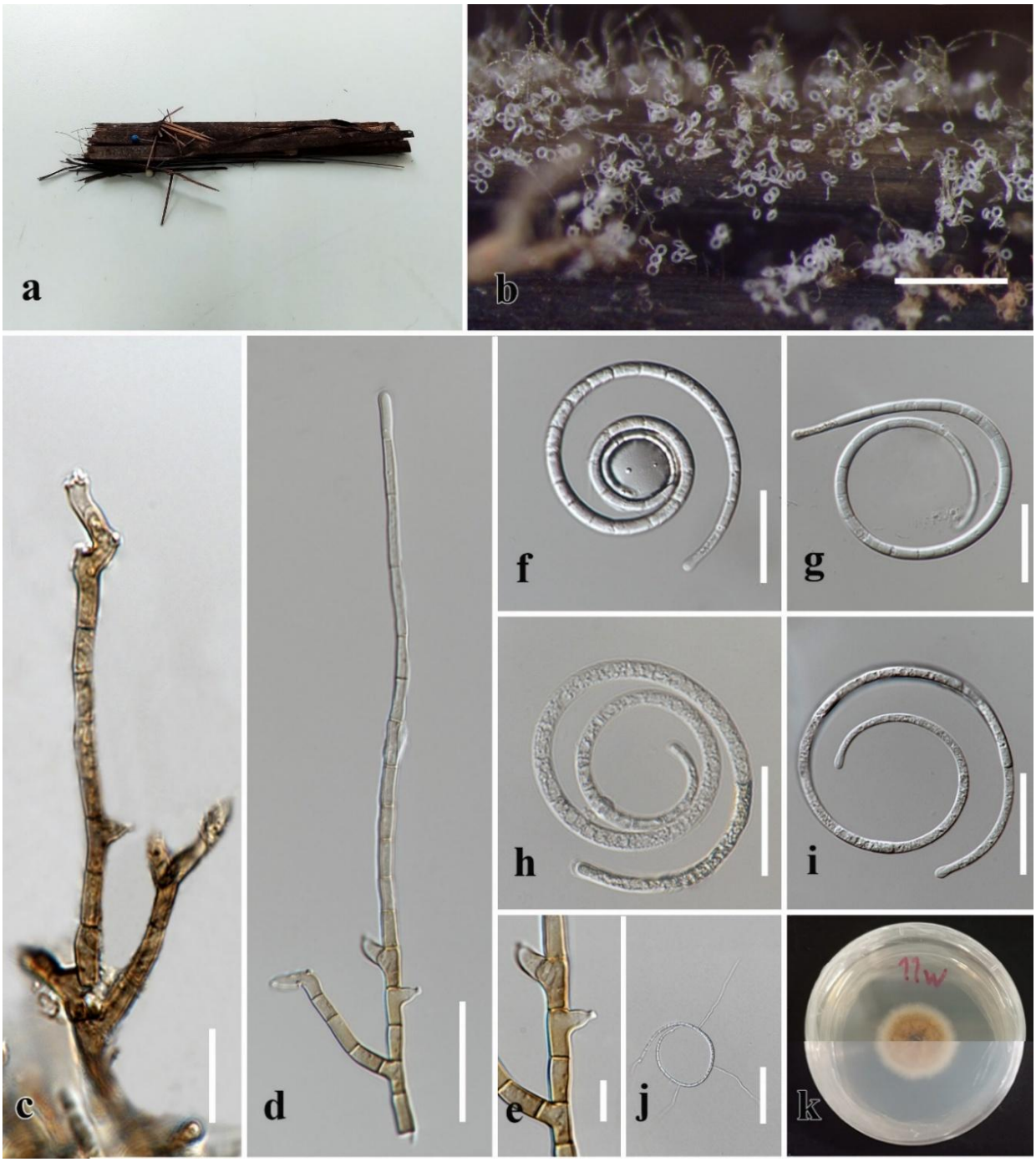

Figure 19 – *Neohelicosporium narathiwatense* (MFLU 24-0502, holotype). a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f–i Conidia. j Germinated conidium. k Colonies on the PDA. Scale bars: b = 400 µm, c= 20 µm, d = 40 µm, e = 10 µm, f, g = 30 µm, h, i = 25 µm, j = 100 µm.

Tamhinispora narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 20

Index Fungorum number: IF903523; Facesoffungi number: FoF17526

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.

Conidia 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 gray with white margin, from reverse gray 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.

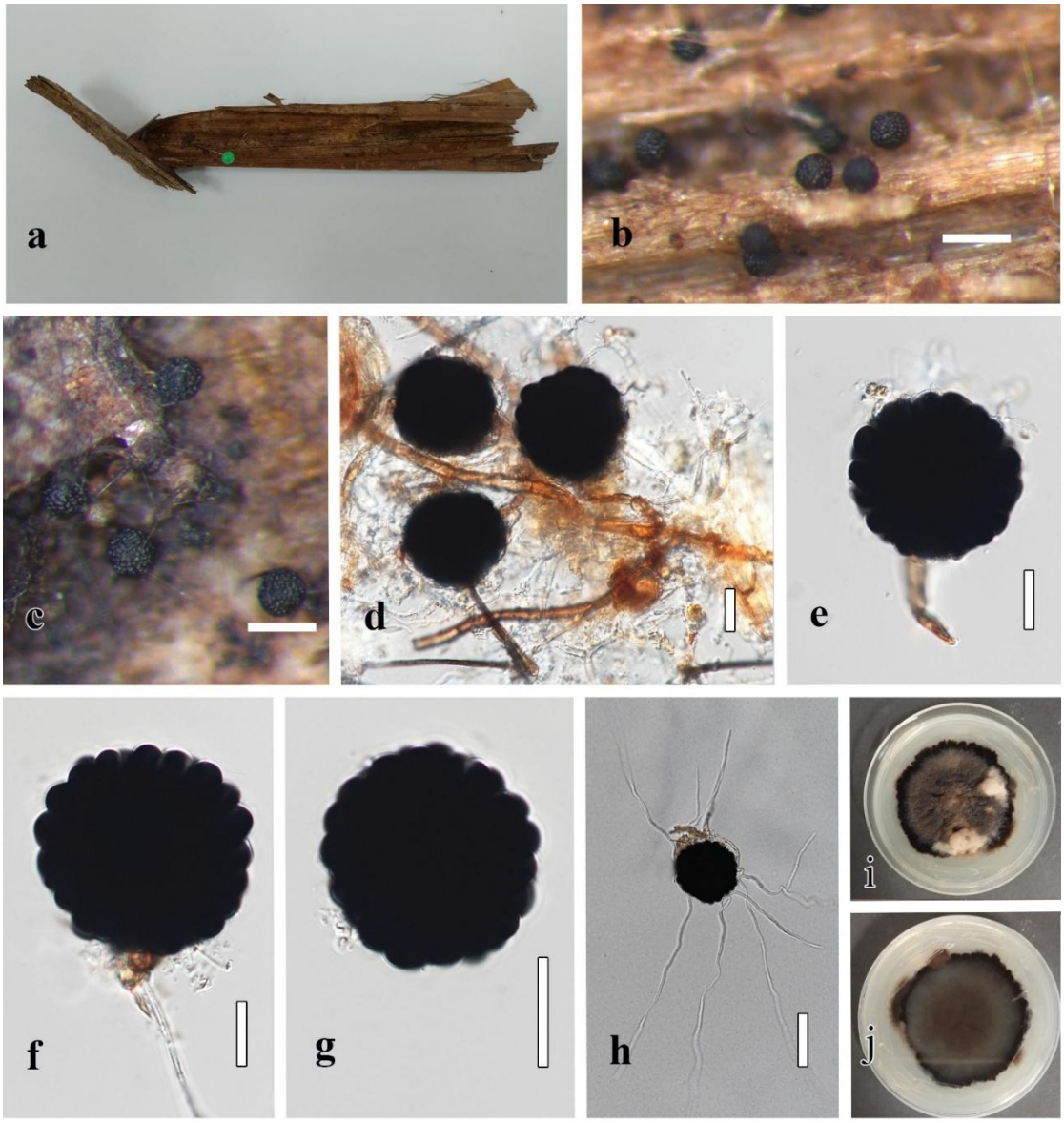

Figure 20 – *Tamhinispora narathiwatensis* (MFLU 24-0503, holotype). a Host. b, c Colonies on the host substrate. d–g Conidia. h A germinated conidium. i, j Colonies on the PDA. Scale bars: b, c = 100 µm, c = 50 µm, d, f = 20 µm, e, g = 25 µm, h = 30 µm.

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 statistical support in the combined phylogenetic analyses of ITS, LSU, *rpb2* and *tef-1α* (Fig. 13). Morphologically, our species is similar to *Ta. srinivasanii*, but it differs from *Ta. srinivasanii* (AMH 9942) in having globose to subglobose conidia, lacking appendages, in contrast to the ovoid or branched or Y-shaped conidia 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 & Sharma 2013). Therefore, based on morphological and phylogenetical evidence, we introduce *Ta. narathiwatensis* (MFLU 24-0503) as a novel species from peat swamp forests.

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. 2018, Dong et al. 2020). To date, one species of this genus (*Tu. claspisphaeria*) has been reported from peat swamp forests (Pinnoi et al. 2006, Pinuruan 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 (Fig. 21).

Tubeufia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 22

Index Fungorum number: IF903524; Facesoffungi number: FoF17527

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 whitish gray 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 support in the combined phylogenetic analysis of ITS, LSU, *rpb2* and *tef-1α* (Fig. 13). Morphologically, *Tu. narathiwatensis* is similar to *Tu. guangxiensis* (GZAAS 16–0042), however, 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.

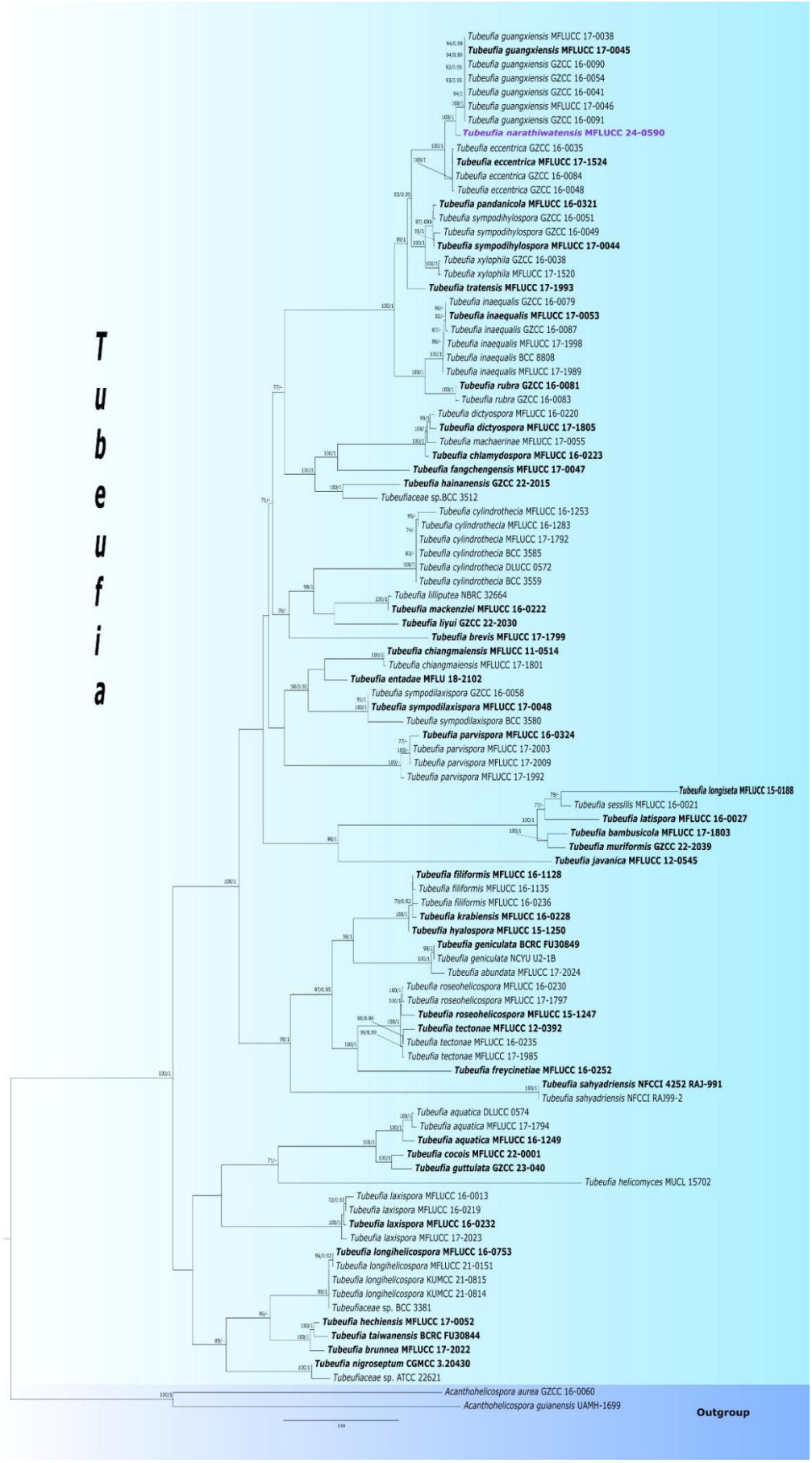

Figure 21 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, *rpb2* and *tef1-α* sequences. The analysis includes 99 strains; total characters: 3395 (ITS: 584, LSU: 854, *rpb2*: 912, *tef1-α*: 1045). *Acanthohelicospora aurea* (GZCC 16-0060) and *A. guianensis* (UAMH-1699) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -21076.381 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 11.17706, AG = 5.88680, AT = 2.36689, CG = 0.83311, CT = 9.66228, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 65% 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.

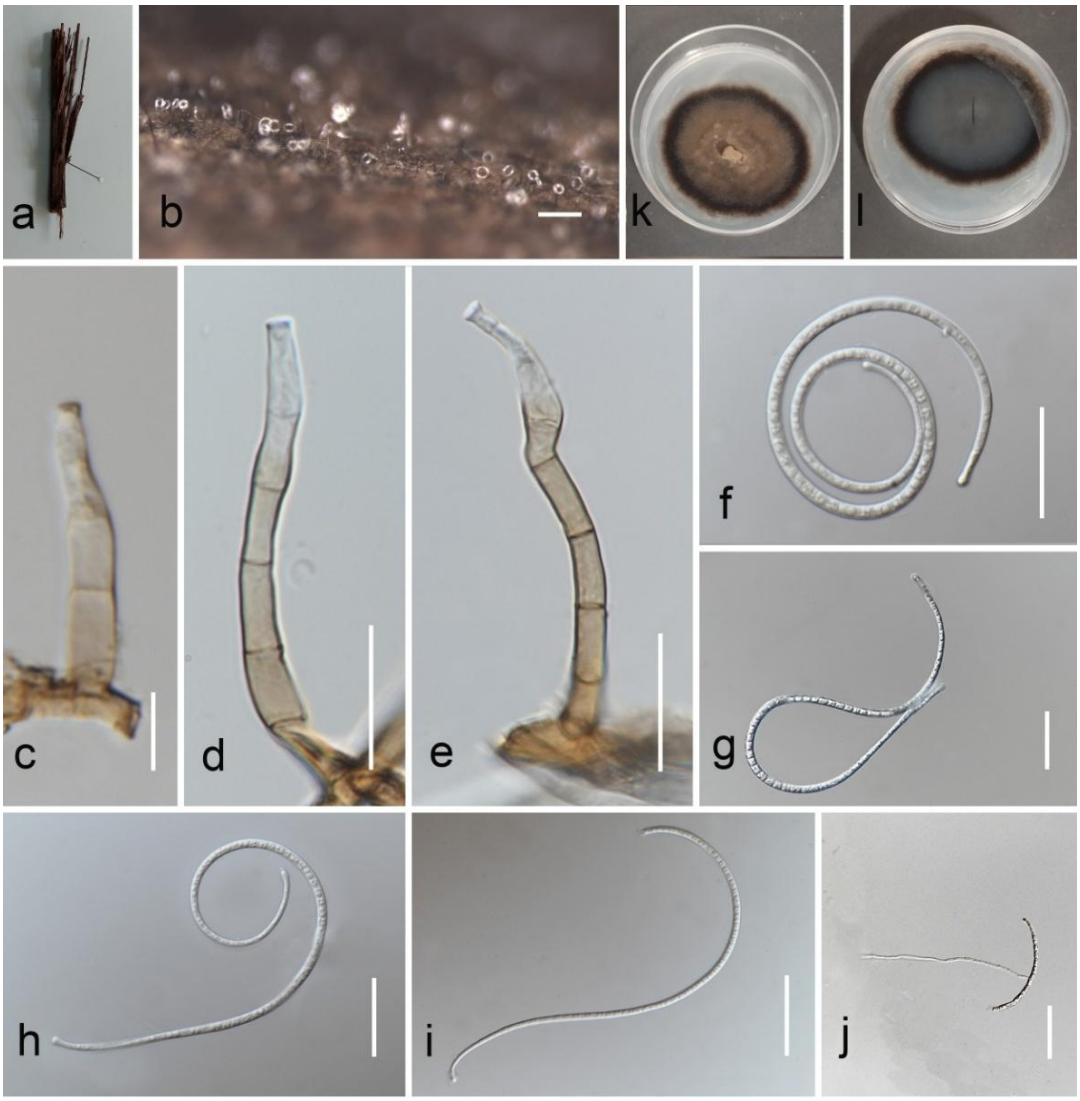

Figure 22 – *Tubeufia narathiwatensis* (MFLU 24-0505, holotype). a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f–i Conidia. j A germinated conidium. k, l Colonies on the PDA. Scale bars: b = 200 µm, c = 10 µm, d, e = 20 µm, f, g, h, j = 50 µm, i= 70 µm.

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*, *rpb1* and *rpb2* 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. 2024b). 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. 2024b). An updated phylogenetic tree for the family is shown in Fig. 23.

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. (2019c) 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. Fig. 24

Index Fungorum number: IF903525; Facesoffungi number: FoF17528

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*. **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. **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, lobate, medium dense, slightly raised, mycelium submerged in media at the margin, dull, felted, surface grayish brown, reverse dark brown to black.

Material examined – Thailand, Narathiwat, Princess Sirindhorn Wildlife Sanctuary, peat swamp forest, 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 *rpb2*. 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 (Fig. 23). 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. 2019c). *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. 2024b). Thus, we introduce *Y. narathiwatensis* as a novel species based on morphological and phylogenetic evidence.

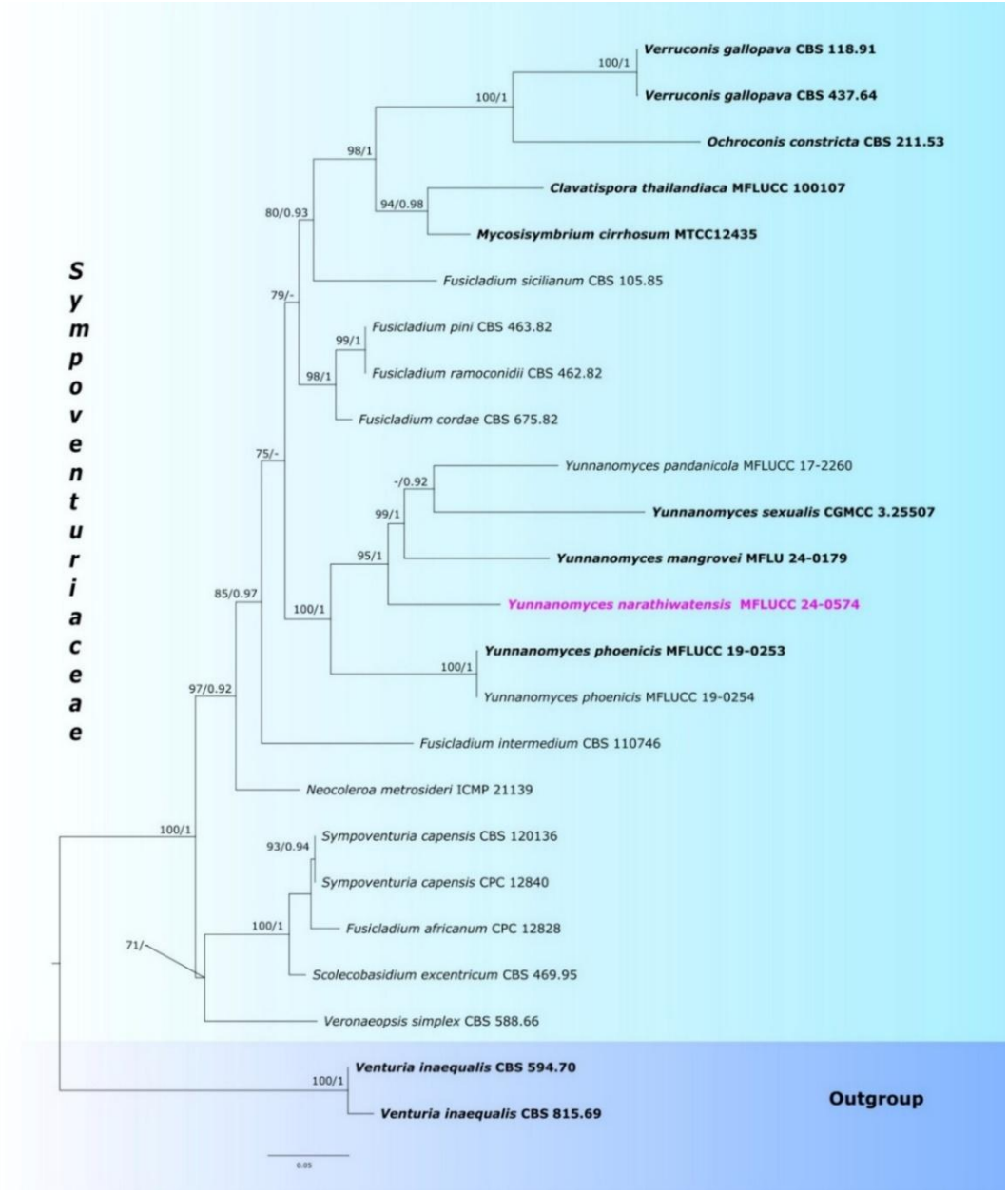

Figure 23 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU and *rpb2* sequences. The analysis includes 26 strains; total characters: 3014 (LSU: 860, SSU: 1033, *rpb2*: 1121). The tree is rooted to *Venturia inaequalis* (CBS 594.70, CBS 815.69). The best-scoring RAxML tree with a final likelihood value of -14797.123 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.97064, AT = 1.00000, CG = 1.00000, CT = 4.70218, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

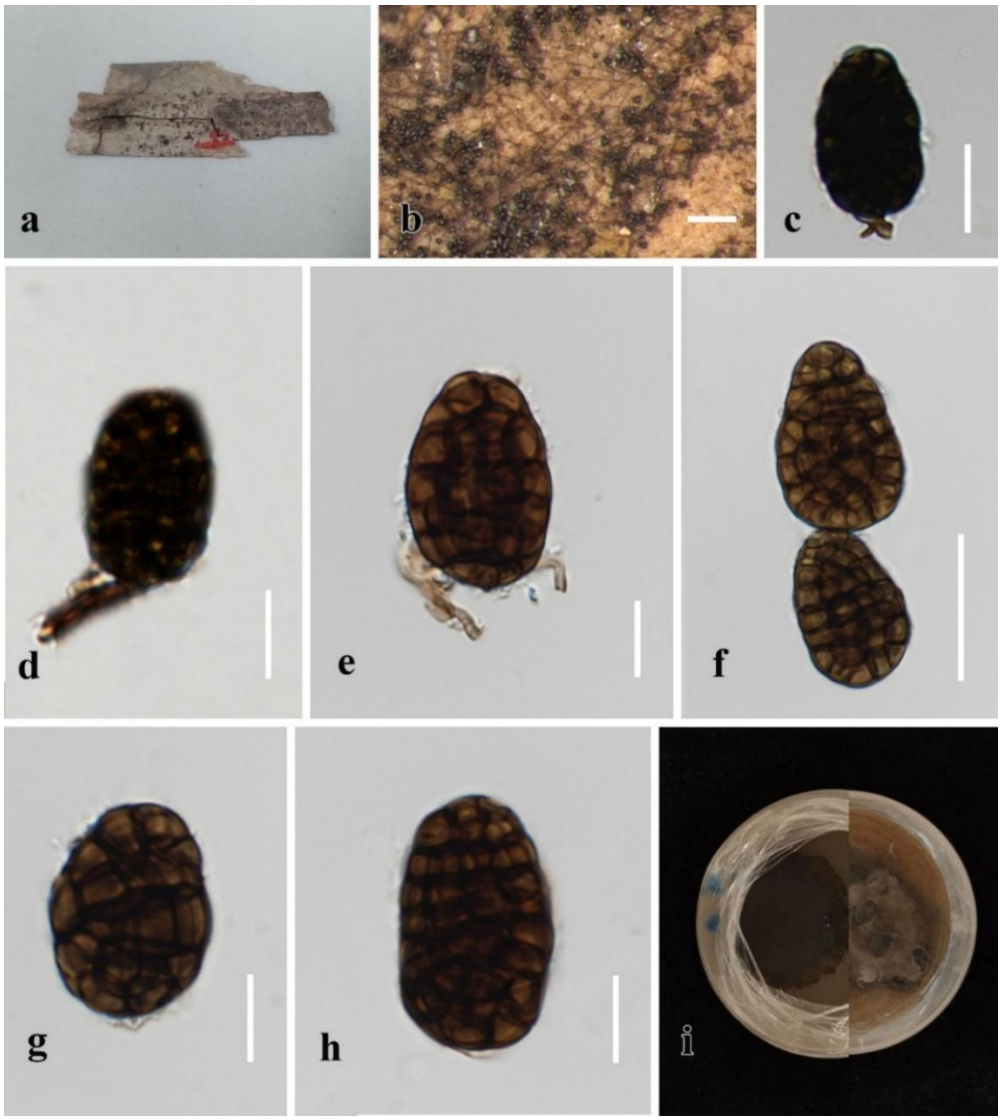

Figure 24 – *Yunnanomyces narathiwatensis* (MFLU 24-0490, holotype). a Host. b Colonies on the host. c, d Conidiogenous cells and developing conidia. e–h Conidia. i Culture characters on the PDA. Scale bars: b = 250 μm, c, d = 15 μm, e, g, h = 10 μm, f = 25 μm.

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. 2023, 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, Samarakoon et al. 2024, Tian 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 phylogenetic tree for the genus *Lasiodiplodia* is shown in Fig. 25.

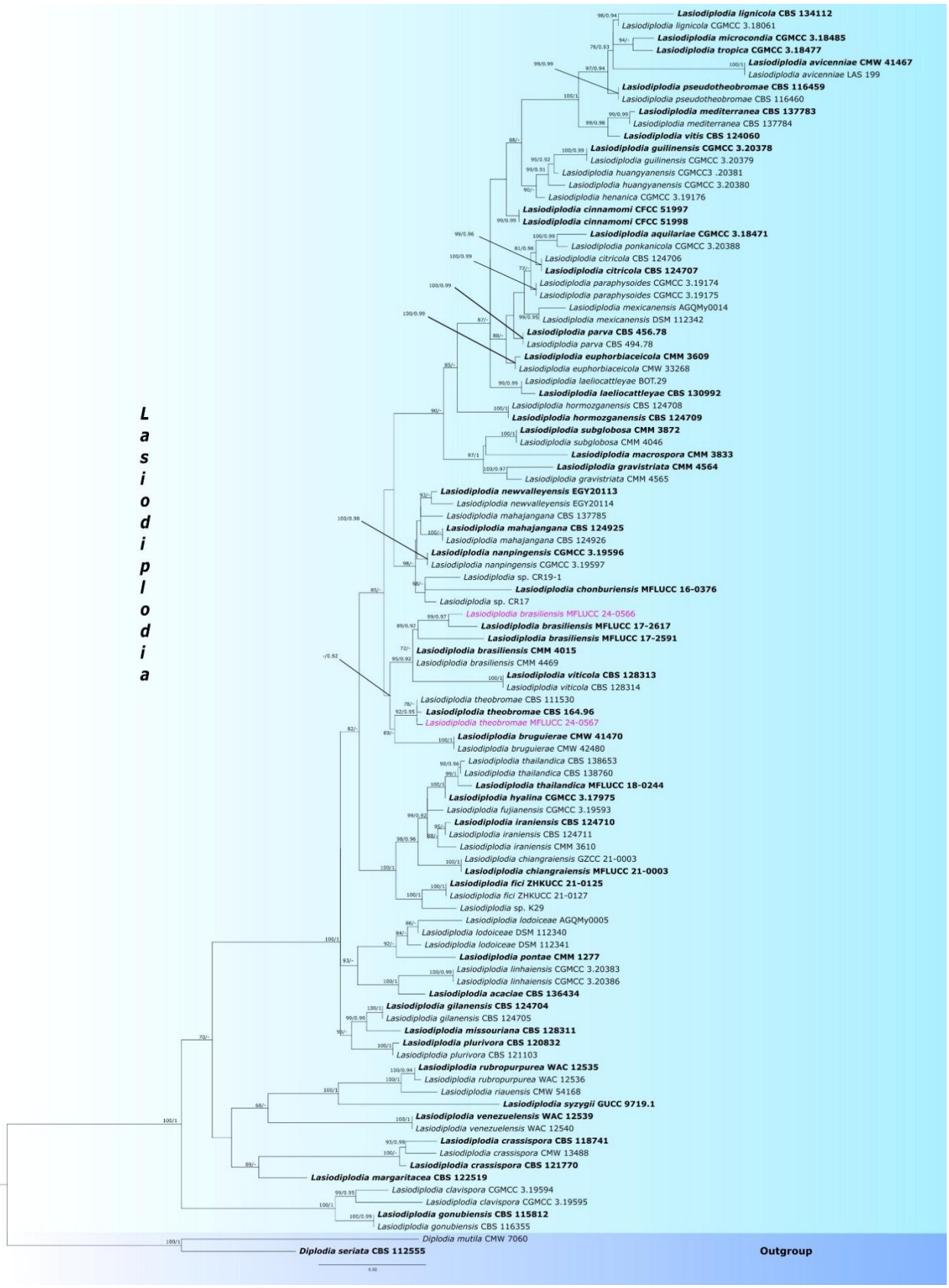

Figure 25 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, *tef1-α* and *tub2* sequences. The analysis includes 102 strains; total characters: 1200 (ITS: 494, *tef1-α*: 305, *tub2*: 401). *Diplodia seriata* (CBS 112555) and *D. mutila* (CMW 7060) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -6211.464 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.94872, AT = 1.00000, CG = 1.00000, CT = 5.73009, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Lasiodiplodia brasiliensis M.S.B. Netto et al., Fungal Diversity 67: 134 (2014) Fig. 26

Index Fungorum number: IF812566; Facesoffungi number: FoF 14085

Saprobic on a dead leaflet of *Cyrtostachys renda*. **Asexual morph**: *Pycnidia* 610–720 × 200–340 µm ($\bar{x}$ = 700 × 315.5 µm, n = 7), immersed, scattered to gregarious, dark brown. *Pycnidial wall* 50–76 µm wide, composed of several layers of brown to dark brown, thick-walled 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 ($\bar{x}$ = 15 × 3.5 µm, n = 20), cylindrical, annellidic, smooth, thick-walled. *Conidia* 22–29 × 11.2–14.5 µm ($\bar{x}$ = 27 × 13 µm, n = 20), subglobose to oval, guttulate, hyaline, aseptate. **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 mycelium, 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 & 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 (Fig. 25). Nucleotide comparisons showed that our strain (MFLUCC 24-0566) has similar ITS and *tef-1α* sequences with *La. brasiliensis*. 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 µm) and larger conidia (22–29 × 11.2–14.5 µm vs. 20–25 × 10–14 µm). 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.

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909) Fig. 27

Index Fungorum number: IF188476; Facesoffungi number: FoF00167

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 brown to dark brown, thick-walled 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 mycelium, dull, entire edge,

without pigment diffusion, surface brownish gray 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 & 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.

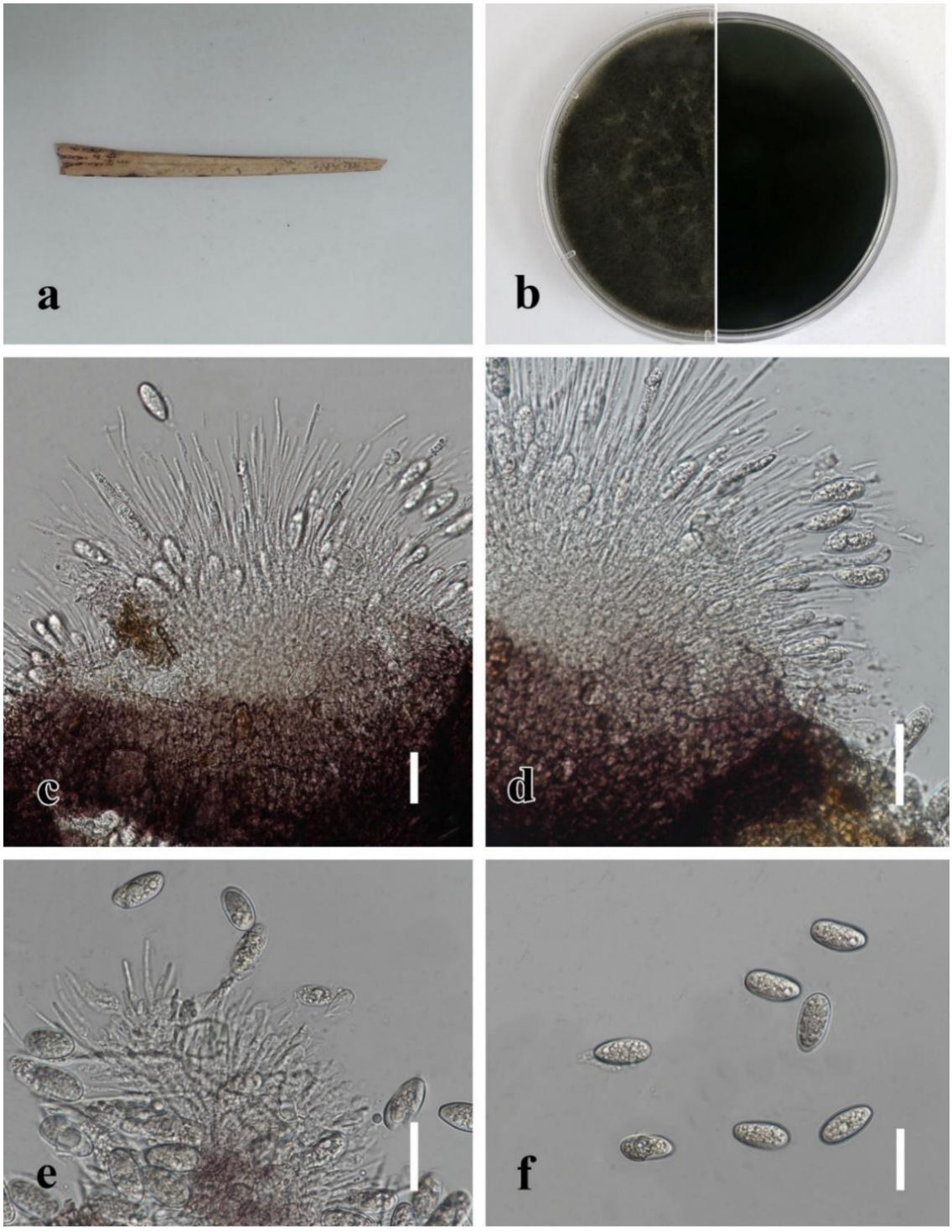

Figure 26 – *Lasiodiplodia brasiliensis* (MFLU 24-0482, new host record). a Host. b Colonies on the PDA. c–e Conidiogenous cells, paraphyses and conidia. f Conidia. Scale bars: c, e = 30 µm, d = 40 µm, f = 25 µm.

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 (Fig. 25). Nucleotide comparisons showed that our strain (MFLUCC 24-0567) has similar ITS sequences to *La. theobromae* (CBS 164.96), and the *tef-1α* sequence shows two bp differences. Morphologically, our strain (MFLUCC 24-0567) is similar to the neotype (MBT176098) (Alves et al. 2008). Therefore, we identified our strain as *La. theobromae* based on phylogenetic analyses and morphological characters. We report our strain as a new host record of *La. theobromae* on *Cyrtostachys renda* from Thailand.

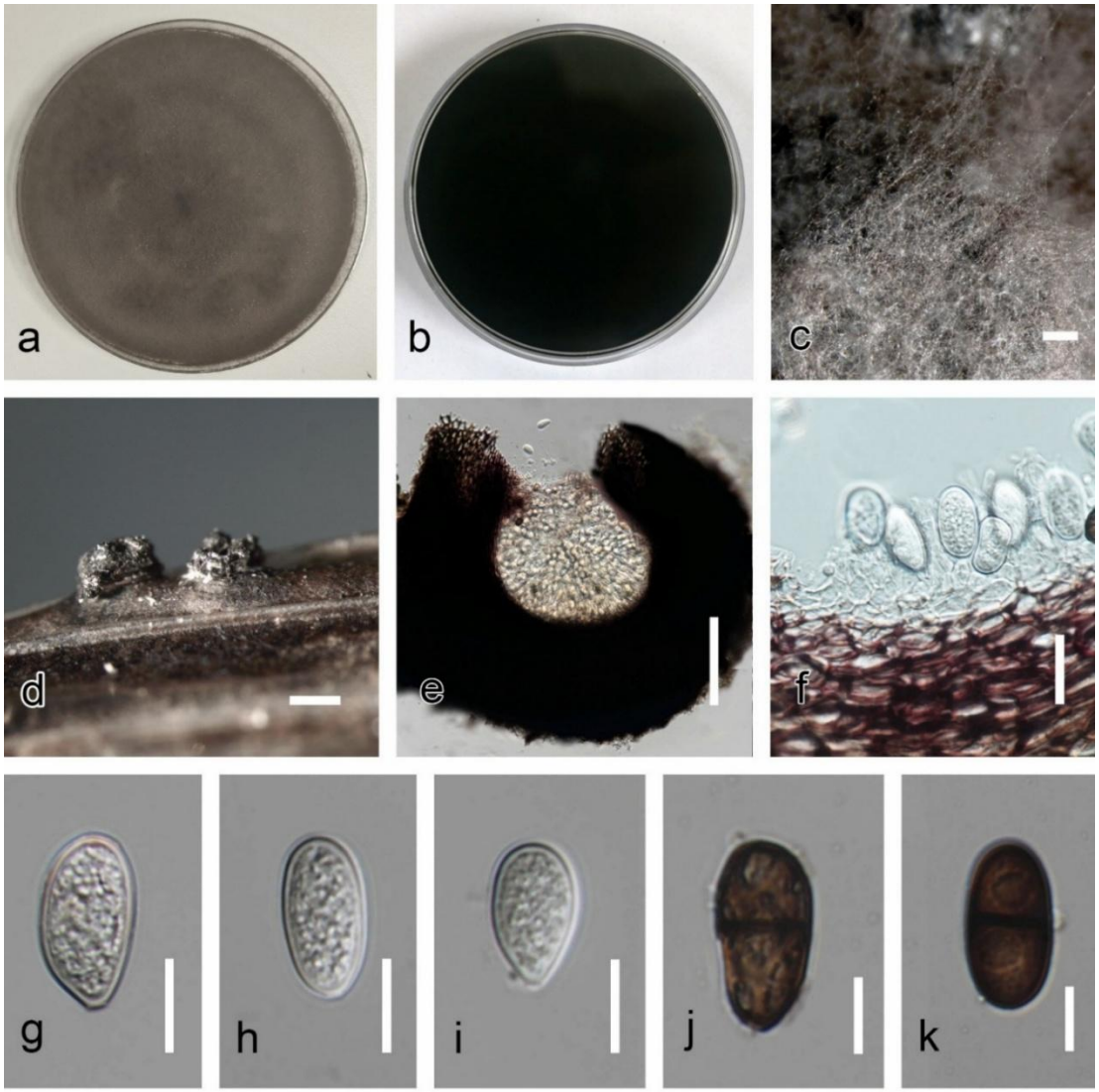

Figure 27 – *Lasiodiplodia theobromae* (MFLUCC 24-0567, new host record). a, b Colonies on the PDA, above (a), and below (b). c, d Aerial mycelium and conidiomata in culture. e Vertical section through a conidioma. f Conidiomatal wall. g–i Immature conidia. j, k Mature conidia. Scale bars: c = 1 mm, d = 750 µm, e = 25 µm, f = 15 µm, g–k = 10 µm.

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 & Korf 1990, Fröhlich & 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 Fig. 28.

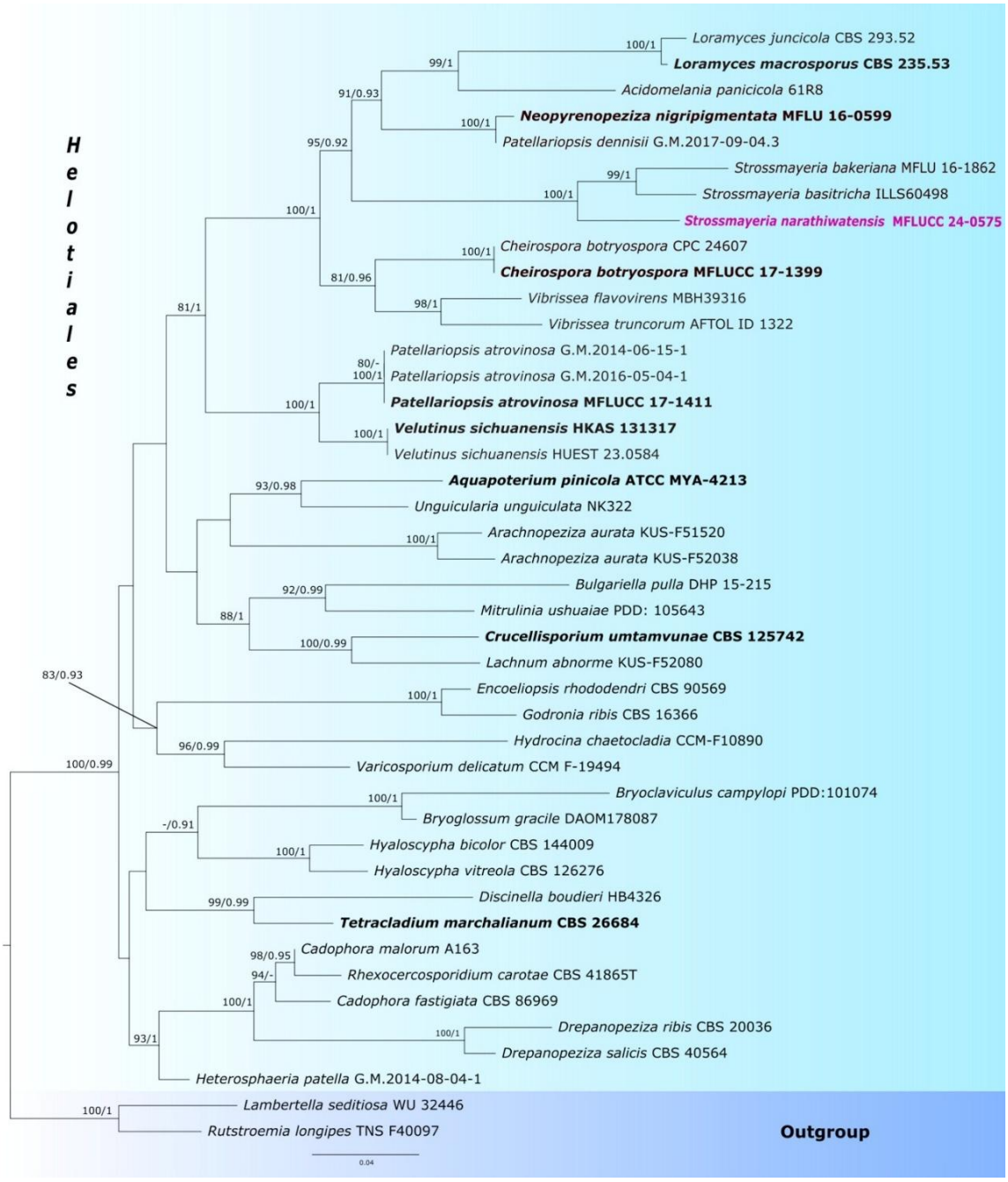

Figure 28 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU and ITS sequences. The analysis includes 43 strains; total characters: 1430 (LSU: 885, ITS: 545). *Lamertella seditiosa* (WU-32446) and *Rutsroemia longipes* (TNS F40097) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -11733.349 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.42800, AG = 2.69025, AT = 1.42800, CG = 1.00000, CT = 5.22489, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Strossmayeria narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 29

Index Fungorum number: IF903526; Facesoffungi number: FoF17529

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*. **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. **Sexual morph**: Not observed.

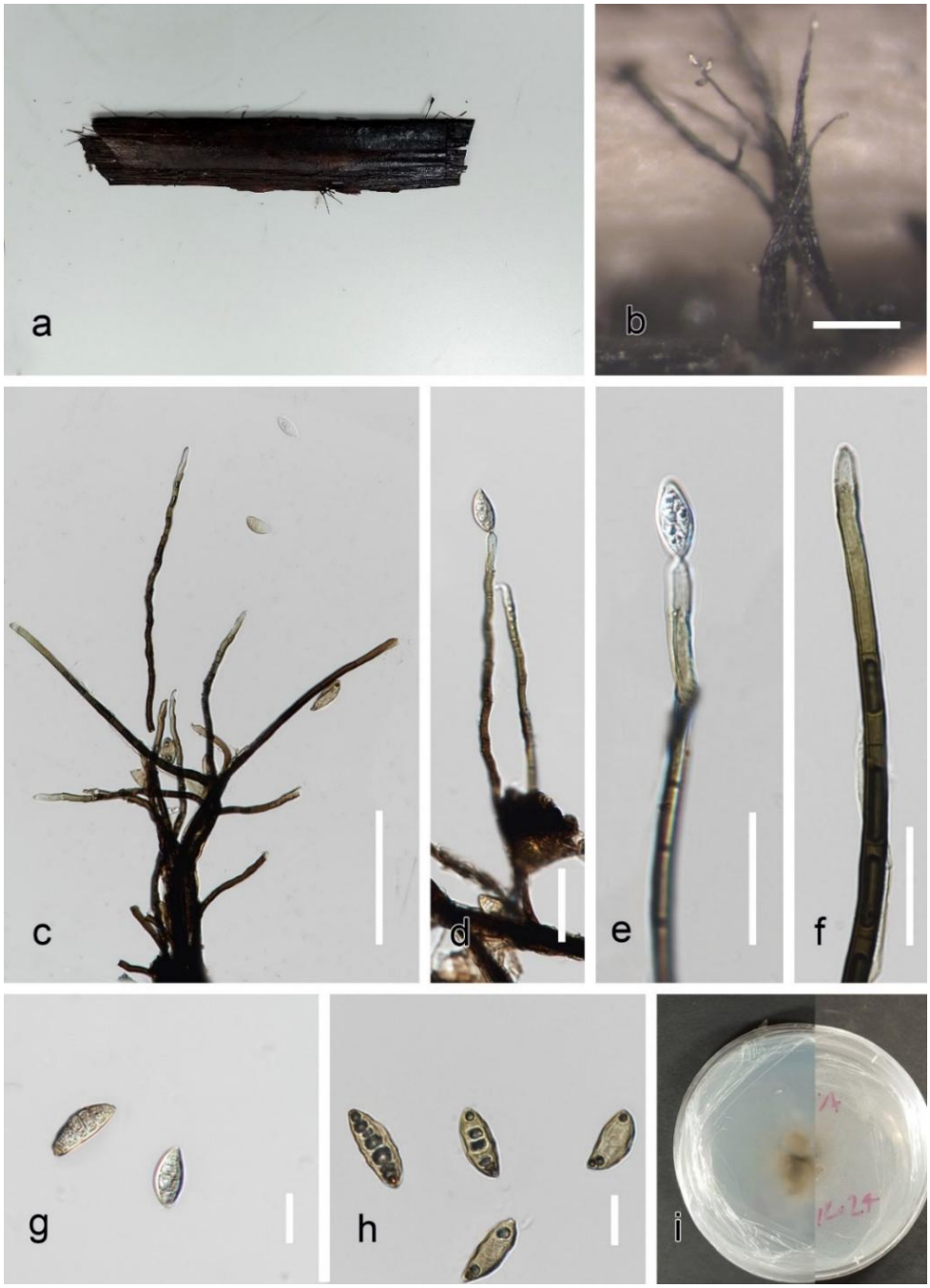

Figure 29 – *Strossmayeria narathiwatensis* (MFLU 24-0491, holotype). a Host. b Colonies on the host substrate. c–f Conidiophores, conidiogenous cells and conidia. g, h Conidia. i Colonies on the CMA. Scale bars: b, c = 100 μm, d = 40 μm, e, f = 30 μm, g, h = 15 μm.

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 (Fig. 28), 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 from *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.

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 & Eriksson (1986). Sexual morph is characterized 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 & 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 Fig. 30.

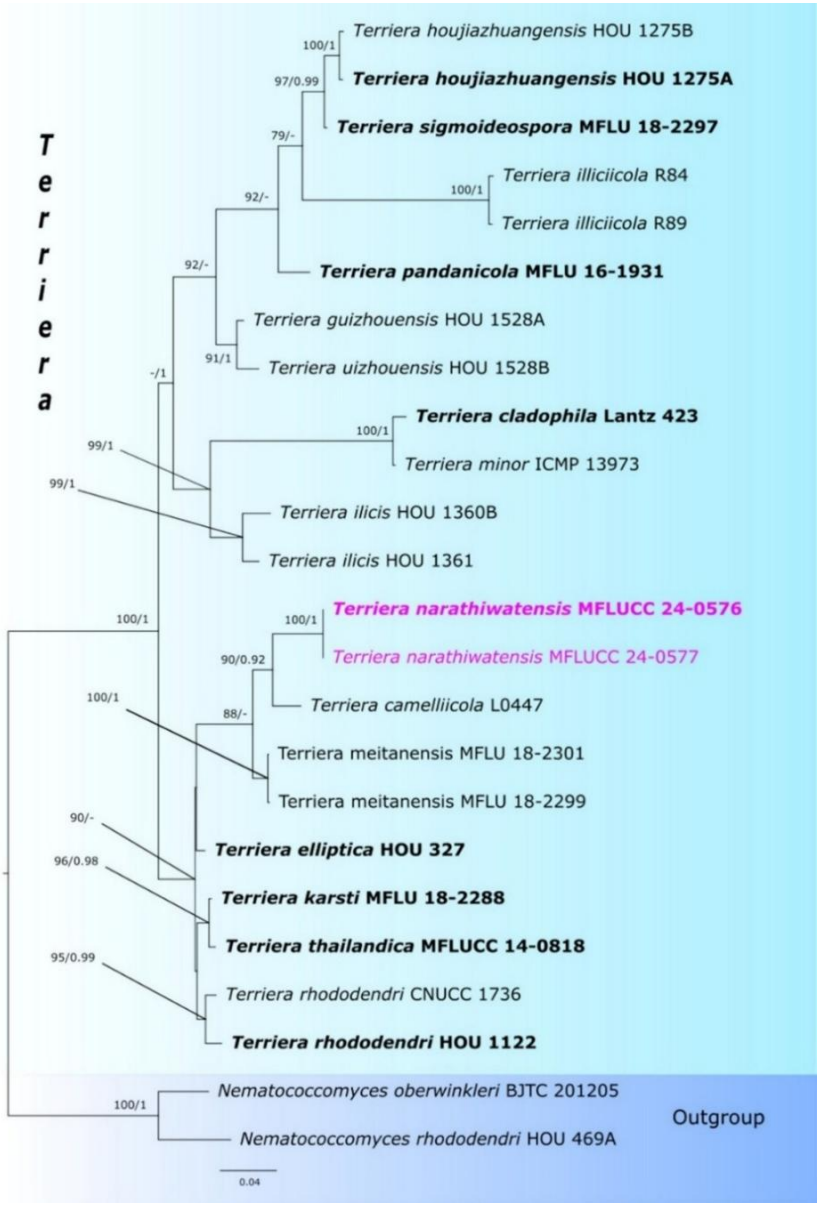

Figure 30 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, ITS and mtSSU sequences. The analysis includes 24 strains; total characters: 1430 (LSU: 1193, ITS: 771, mtSSU: 873). *Nematococcomyces oberwinkleri* (BJTC 201205) and *N. rhododendri* (HOU 469A) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -11966.072 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.31099, AT = 1.00000, CG = 1.00000, CT = 3.08817, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The strains from the current study are in purple, while the type strains are in bold.

Terriera narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 31

Index Fungorum number: IF903527; Facesoffungi number: FoF17530

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*. **Asexual morph**: Not observed. **Sexual morph**: *Ascomata* 430–1100 × 70–250 µm ($\bar{x}$ = 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 ($\bar{x}$ = 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 ($\bar{x}$ = 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 ($\bar{x}$ = 29 µm, n = 10), composed of thick-walled, brown, *textura prismatica* to *textura angularis* or *textura globosa* cells. *Subhymenium* 5.5–11 µm wide ($\bar{x}$ = 8 µm, n = 15), hyaline, *textura angularis* to *textura intricata*, thin-walled cells. *Paraphyses* 68–88 × 0.9–2.2 µm ($\bar{x}$ = 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 ($\bar{x}$ = 80 × 5.7 µm, n = 25), cylindrical, short-stalked, flattened apex, thin-walled. *Ascospores* 48–53 × 2.3–2.7 µm ($\bar{x}$ = 50 × 2.5 µm, n = 30), fascicle, filiform, slightly tapering towards the ends, hyaline, guttulate, aseptate, straight or slightly curved, lacking a gelatinous sheath.

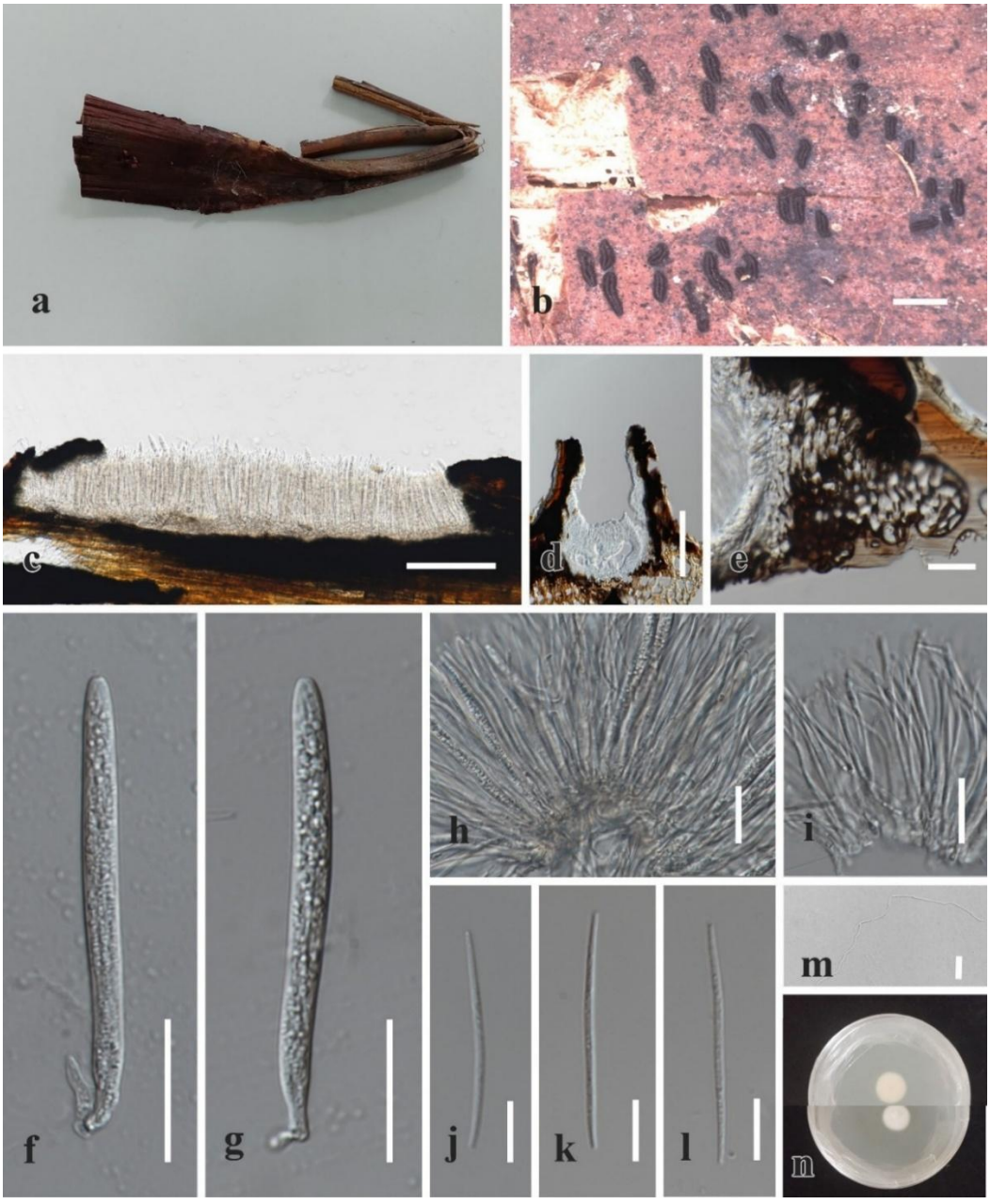

Figure 31 – *Terriera narathiwatensis* (MFLU 24-0492, holotype). a Host. b Appearance of apothecia on the host substrate. c Horizontal section through an apothecium. d Vertical section through an apothecium. e Triangular space in the section between the covering stroma and basal stroma. f, g Asci. h, 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

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 (Fig. 30). 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 & 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.

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. (1998) introduced *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 *rpb2* 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. 1998, Hyde et al. 1999, Ranghoo et al. 2001, Campbell & Shearer 2004, Fryar & 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 characterized 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 Fig. 32.

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. (2021) 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 *rpb2*. 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.

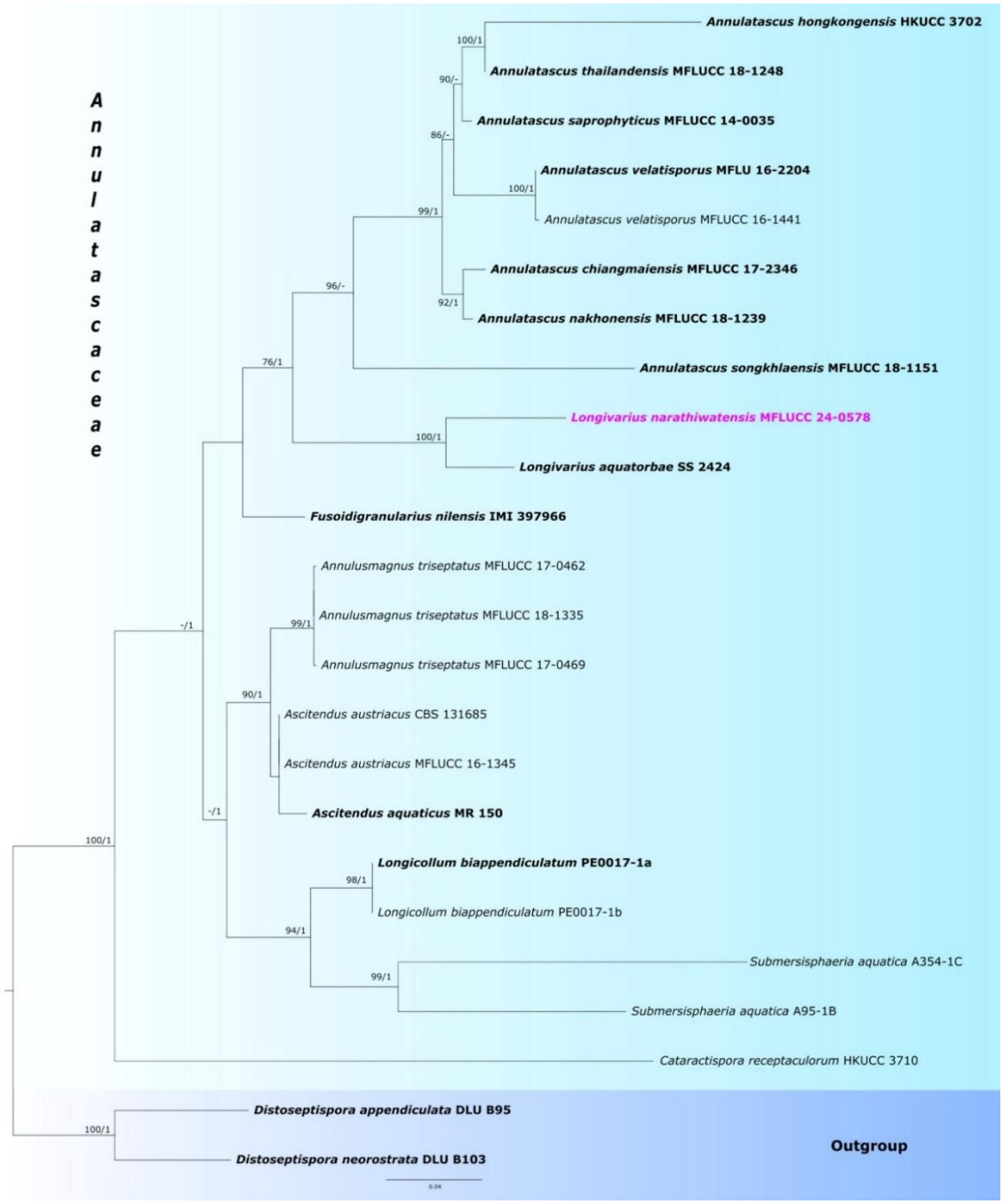

Figure 32 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU and ITS sequences. The analysis includes 24 strains; total characters: 1434 (LSU: 868, ITS: 566). *Distoseptispora appendiculata* (B95), and *D. neorostrata* (B103) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -6990.385 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 1.60674, AT = 1.00000, CG = 1.00000, CT = 4.33822, GT = 1.00000. The tree

topology of the ML analysis is similar to the Bayesian analysis. 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.

Longivarius narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 33

Index Fungorum number: IF903530; Facesoffungi number: FoF17531

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*. **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. **Sexual morph**: Not observed.

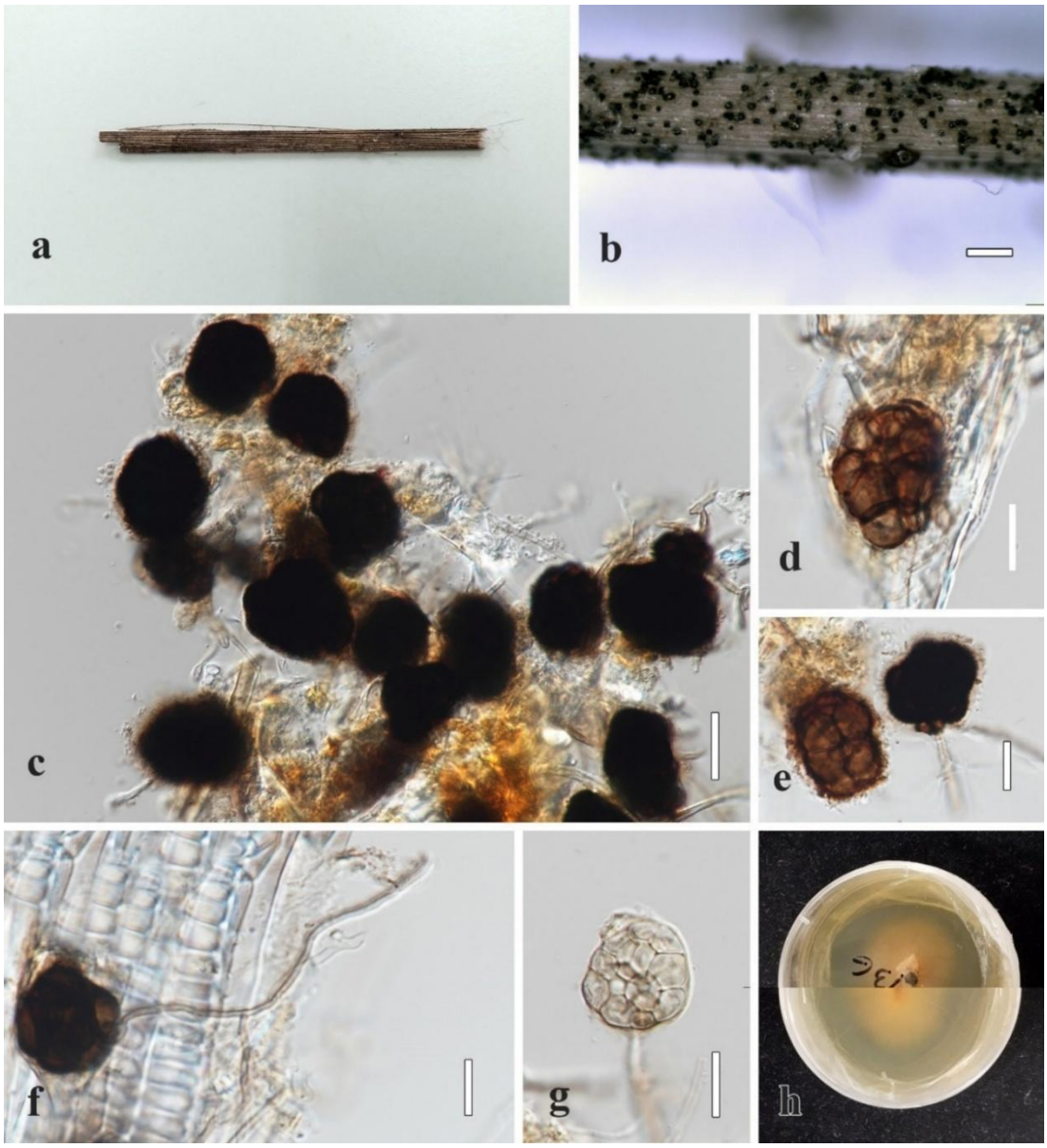

Figure 33 – *Longivarius narathiwatensis* (MFLU 24-0494, holotype). a Host. b Colonies on the host substrate. c–g Conidia, conidiophores and conidiogenous cells. h Colonies on the PDA. Scale bars: b = 200 μm, c = 25 μm, e, f = 15 μm, g = 10 μm.

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 grayish 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 (Fig. 32), 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* (MFLUCC 24-0578) differs from *Lo. aquatorbae* (SS 2424) by 3.3% (33/995 bp, excluding gaps), and ITS, SSU and *rpb2* 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 & 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 characterized 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, Pinuruan 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 Fig. 34.

Cancellidium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 35

Index Fungorum number: IF903541; Facesoffungi number: FoF17532

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***. 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. **Sexual morph**: Not observed.

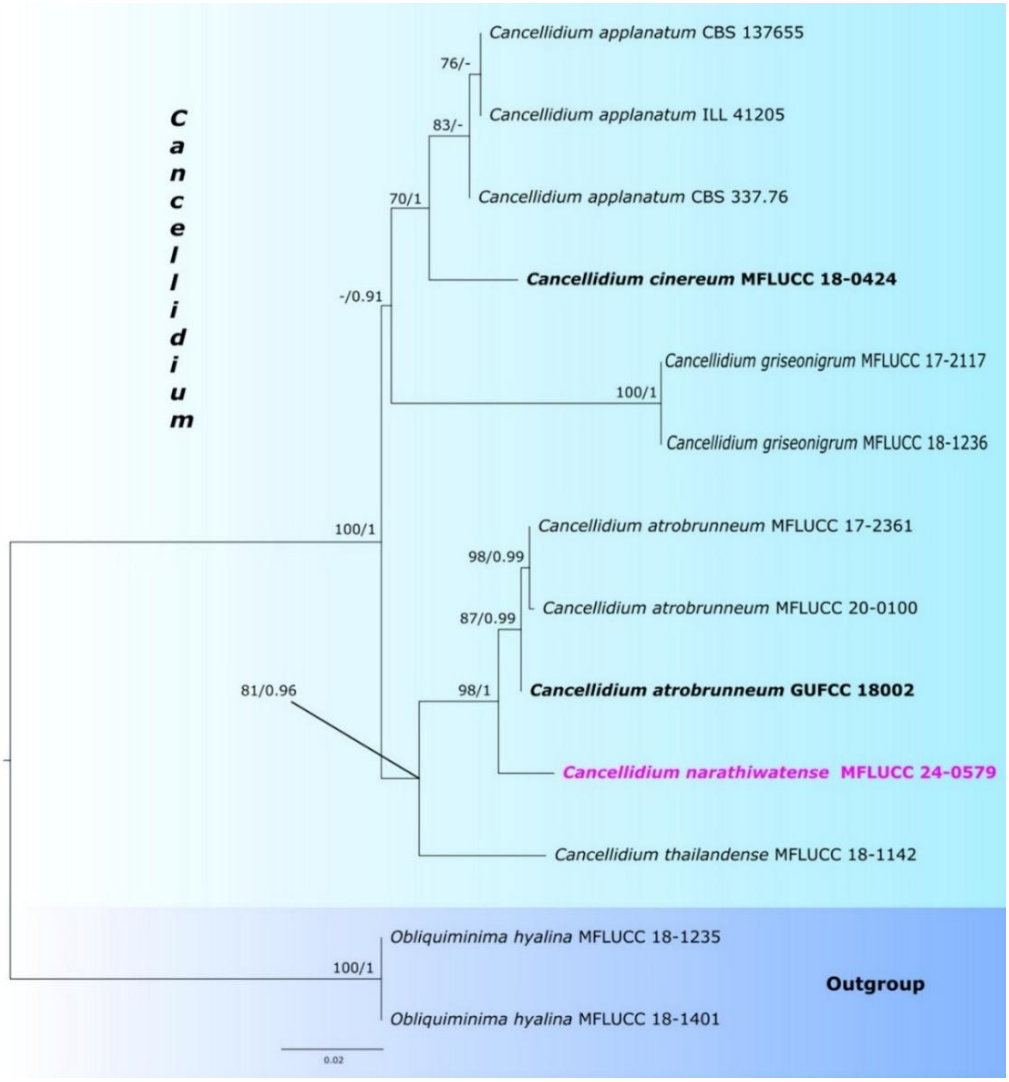

Figure 34 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU, *tef-1α* and *rpb2* sequences. The analysis includes 17 strains; total characters: 3695 (LSU: 846, SSU: 1023, *tef-1α*: 925, *rpb2*: 901). *Pseudotetraploa curviappendiculata* (HC 4930) and *Tetraplosphaeria sasicola* (KT563) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -9210.943 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.57574, AT = 1.00000, CG = 1.00000, CT = 6.17351, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

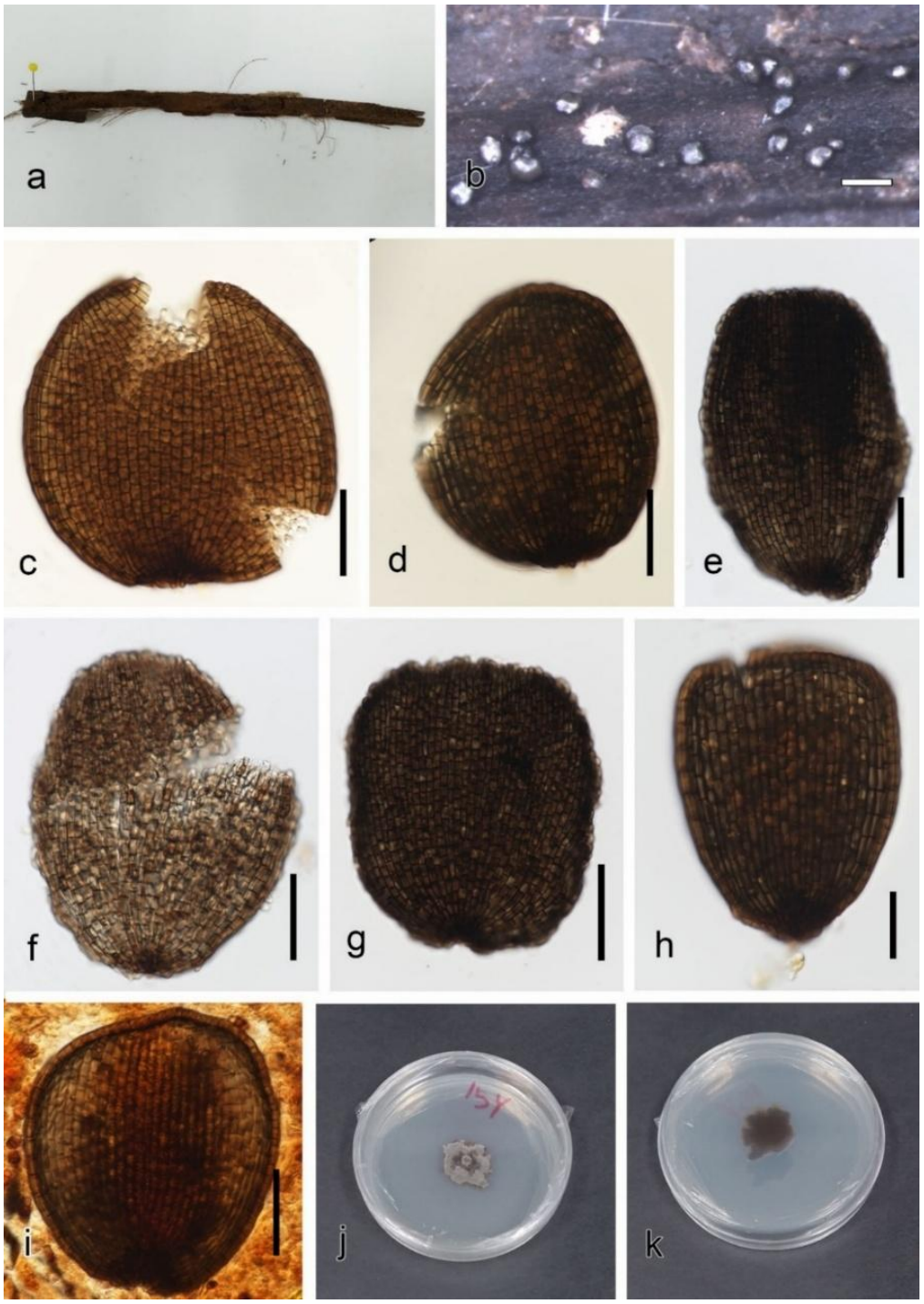

Figure 35 – *Cancellidium narathiwatense* (MFLU 24-0521, holotype). a Host. b Colonies on the host substrate. c–g, i Conidia. h Conidiogenous cell and conidium. j, k Colonies on PDA. Scale bars: b = 200 µm, c–f, i = 50 µm, g = 60 µm, h = 40 µm.

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 gray, reverse black with olive gray 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 subclade to *Cancellidium atrobrunneum* (MFLUCC 20-0100), with 98% ML and 1.00 PP statistical support (Fig. 34). It separated from *Ca. thailandense* (MFLUCC 18-1142) by 81% ML and 0.96 PP statistical support (Fig. 34). 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) (Hyde et al. 2021). 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) (Dong et al. 2021). Based on a pairwise comparison of ITS and LSU nucleotides, *Ca. narathiwatense* (MFLUCC 24-0579) differs from *Ca. atrobrunneum* (GUFCC 18002) by 3.5% (17/517 bp) in the ITS, and 0.12% (1/811 bp) in LSU, without including gaps. The *rpb2* and *tef-1α* regions of our strain cannot be compared with *Ca. atrobrunneum* (GUFCC 18002), as they are unavailable for *Ca. atrobrunneum* (GUFCC 18002). Therefore, we introduce *Ca. narathiwatense* (MFLU 24-0521) as a novel species based on morphological and phylogenetic evidence.

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 1951, Munk 1957, Gäumann 1964, Kreisel 1969, Rogerson 1970, 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 characterized 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 Fig. 36.

Trichoderma virens (J.Miller, Giddens & Foster) von Arx, Beih. Nova Hedwigia 87: 288. 1987 Fig. 37

Index Fungorum number: IF128198; Facesoffungi number: FoF17532

Saprobic on 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.

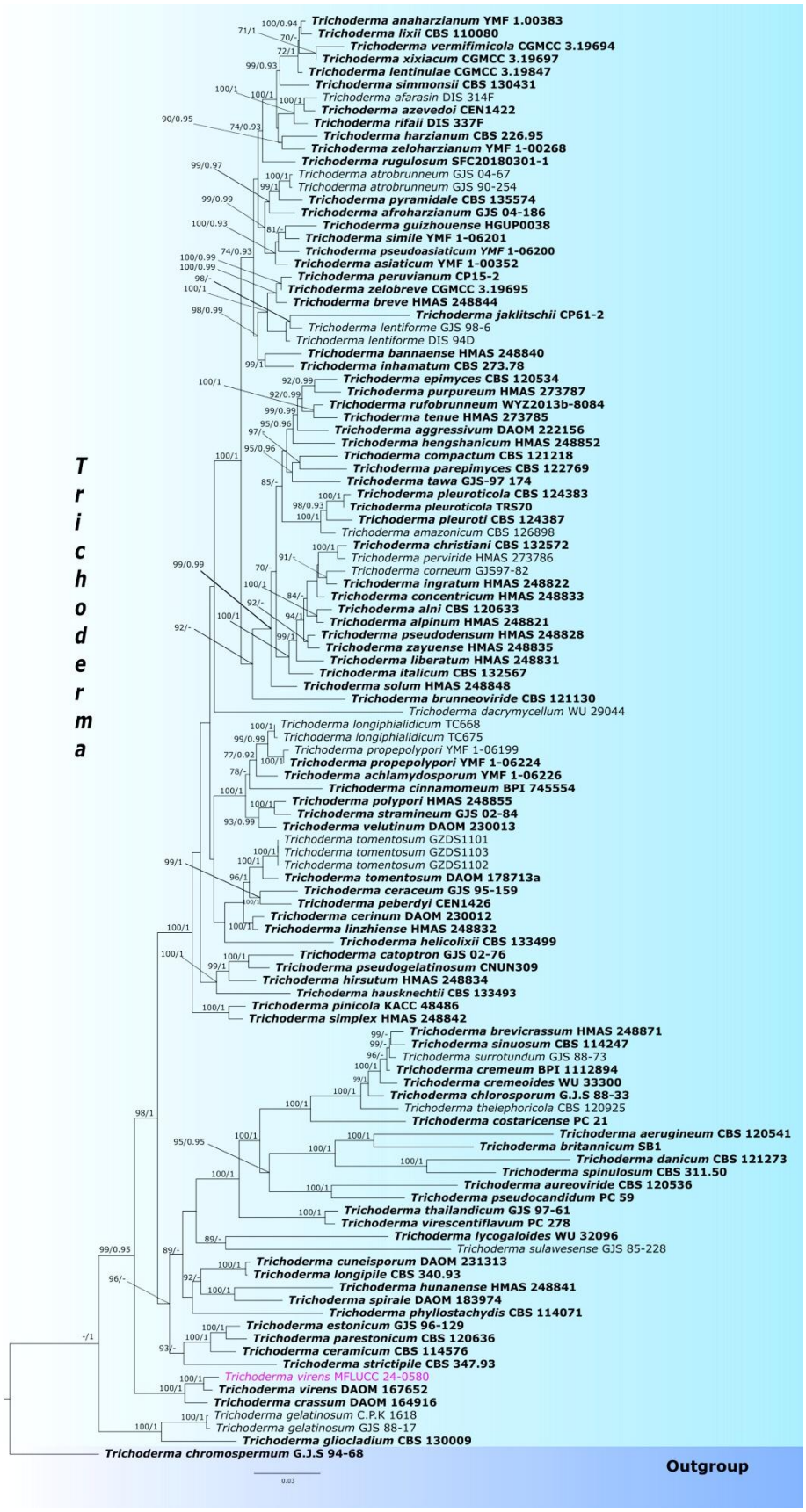

Figure 36 – Phylogram of maximum likelihood phylogenetic analysis based on combined *tef-1α*, *rpb2* and ITS sequences. The analysis includes 115 strains; total characters: 2910 (*tef-1α*: 1252, *rpb2*: 1067, ITS: 591). *Trichoderma chromospermum* (G.J.S. 94-68) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -31954.291 is presented. Estimated base frequencies were as follows; A = 0.233, C = 0.285, G = 0.250, T = 0.232; substitution rates AC = 1.15554, AG = 4.39610, AT = 1.15554, CG = 1.00000, CT = 6.29872, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

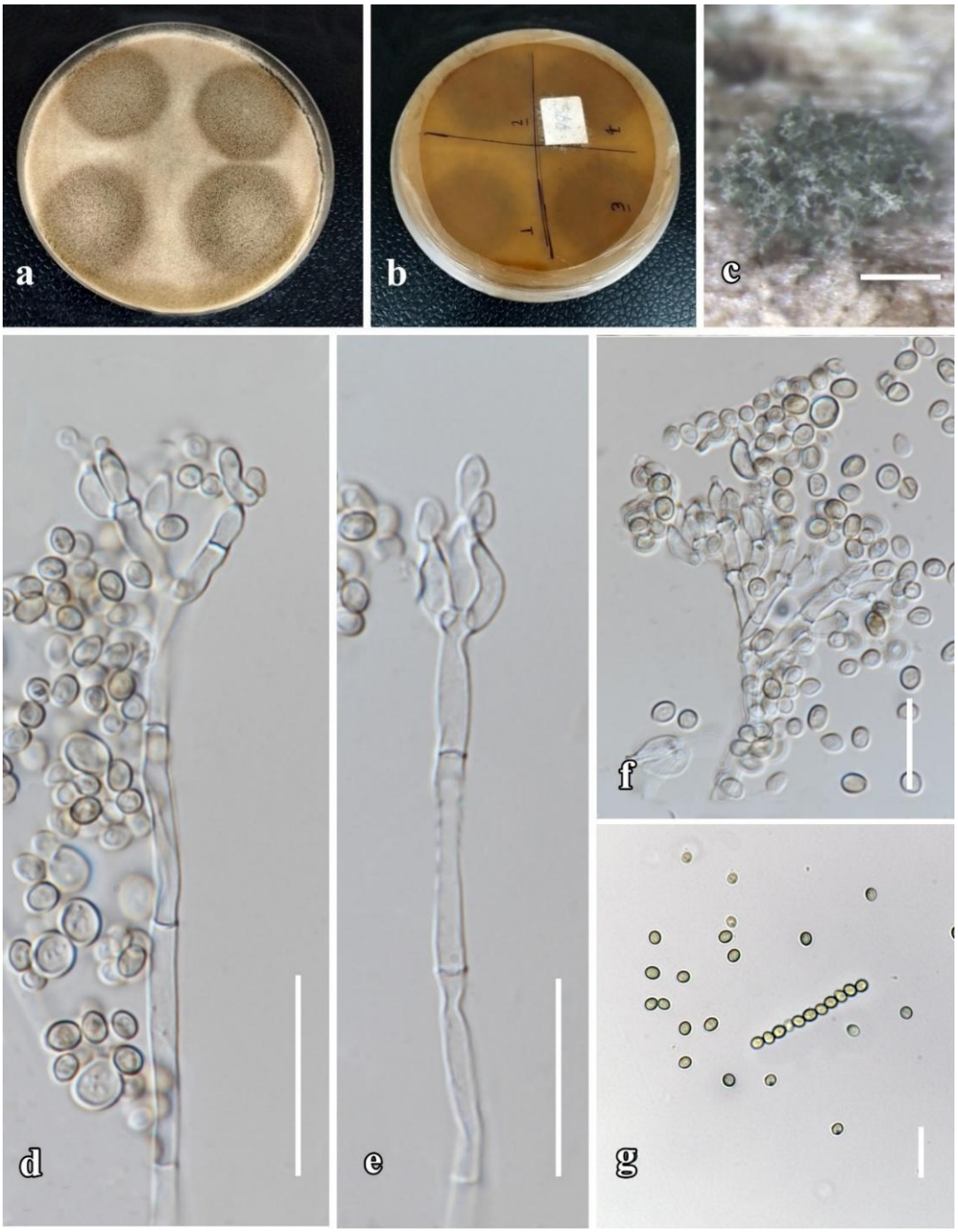

Figure 37 – *Trichoderma virens* (MFLU 24-0495, new host and habitat record). a, b Upper surface and reverse overview of the culture on the PDA. c Colonies on the host substrate. d–f Conidiophores and conidiogenous cells. g Conidia. Scale bars: c = 200 µm, d = 25 µm, e = 20 µm, f = 15 µm, g = 15 µm.

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 center, reverse dull yellow with a dull green center.

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 & 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 – Brazil (Hanada et al. 2010), Canada (Kindermann et al. 1998), Germany (Tokumasu et al. 1994), India (Nagaraja & Krishnappa 2009), Malaysia (Liu 1977), New Zealand (Kindermann et al. 1998), Peru (Chaverri et al. 2011), Poland (Przybyl 2002, Mulenko et al. 2008), Thailand (This study), USA (Zabel et al. 1985, Nelson et al. 1987).

GenBank numbers – MFLUCC 24-0580: ITS = PV271886, *rpb2* = PV340528, *tef-1α* = PV477059.

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 (Fig. 36). Morphologically, our strain resembles *T. virens* in having similar conidiophores, phialides, and conidia with almost identical sizes (Kubicek & Harman 1998). Based on a pairwise comparison of ITS, *rpb2* and *tef-1α* nucleotides, *T. virens* (MFLU 24-0495) differs from *T. virens* (DAOM 167652) by 0.85% (5/582 bp) in the ITS, and 0.66% (6/903 bp) in *rpb2*, and 0.32% (2/615 bp) in the *tef-1α*, without including gaps. Thus, we identified our strain (MFLU 24-0495) as *T. virens* based on phylogenetic analyses and morphological characters. We report our strain (MFLU 24-0495) 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 *tef-1α*) and accepted *Vanakripa* as the second genus in *Conioscyphaceae*. The family now includes *Conioscypha* and *Vanakripa* (Hyde et al. 2024, Yu et al. 2024a, b). 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 morph is characterised by micronematous, mononematous, hyaline conidiophores, blastic, cyathiform to doliiform conidiogenous cells, and brown or black, aseptate conidia (Réblová et al. 2016).

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

Höhnel (1904) 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. 2019, 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 Fig. 38.

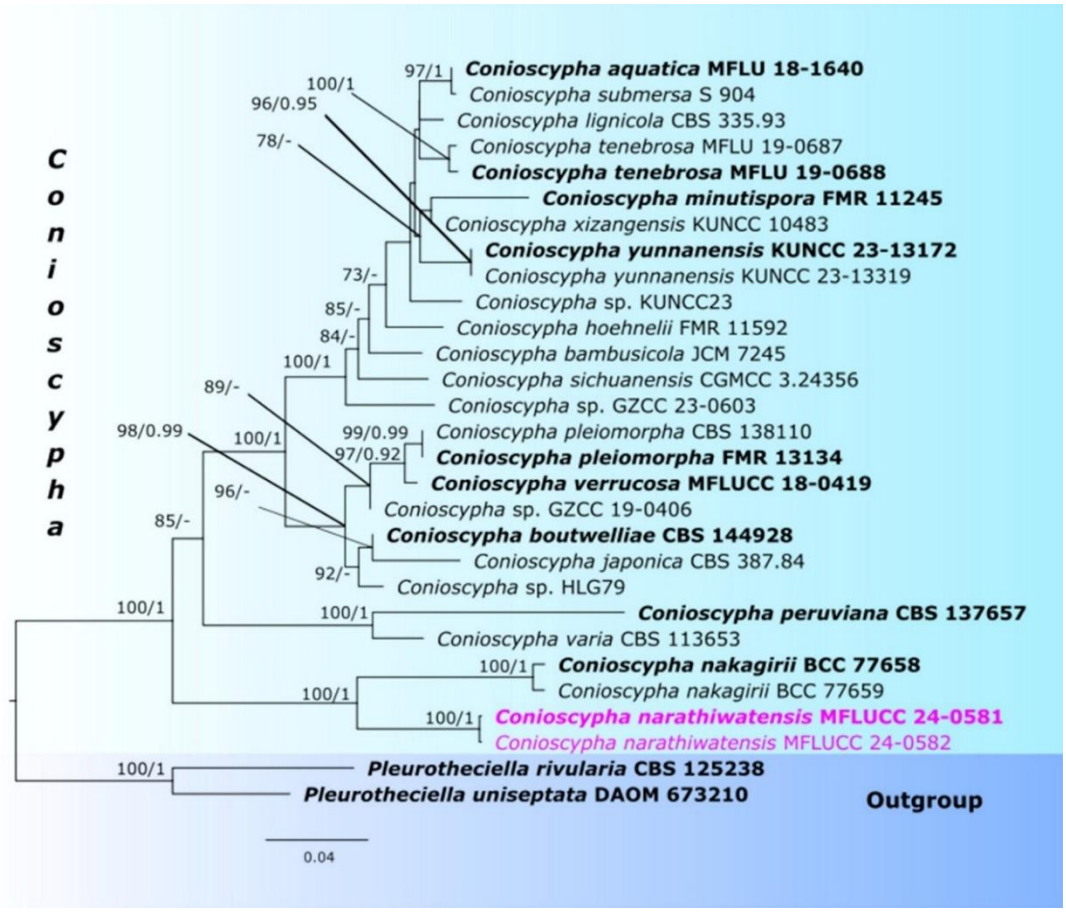

Figure 38 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, SSU and *rpb2* sequences. The analysis includes 29 strains; total characters: 3705 (ITS: 664, LSU: 923, SSU: 1041, *rpb2*: 1077). *Pleurotheciella rivularia* (CBS 125238) and *Pleurotheciella uniseptata* (DAOM 673210) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -20645.091 is presented. Estimated base frequencies were as follows; A = 0.239, C = 0.266, G = 0.293, T = 0.203; substitution rates AC = 1.00000, AG = 2.97064, AT = 1.00000, CG = 1.00000, CT = 5.61198, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Conioscypha narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 39

Index Fungorum number: IF903542; Facesoffungi number: FoF17533

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*. **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 ($\bar{x}$ = 36 × 36.5 µm, n = 20), solitary, turbinate to pyriform, black, smooth-walled, aseptate, rounded at the apex, rounded to truncate at the base. **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, medium dense, flat, mycelium superficial to immersed, dull, entire edge, radially furrowed, felted, surface medium gray with a whitish margin, reverse light gray 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, *rpb2* = PV340534.

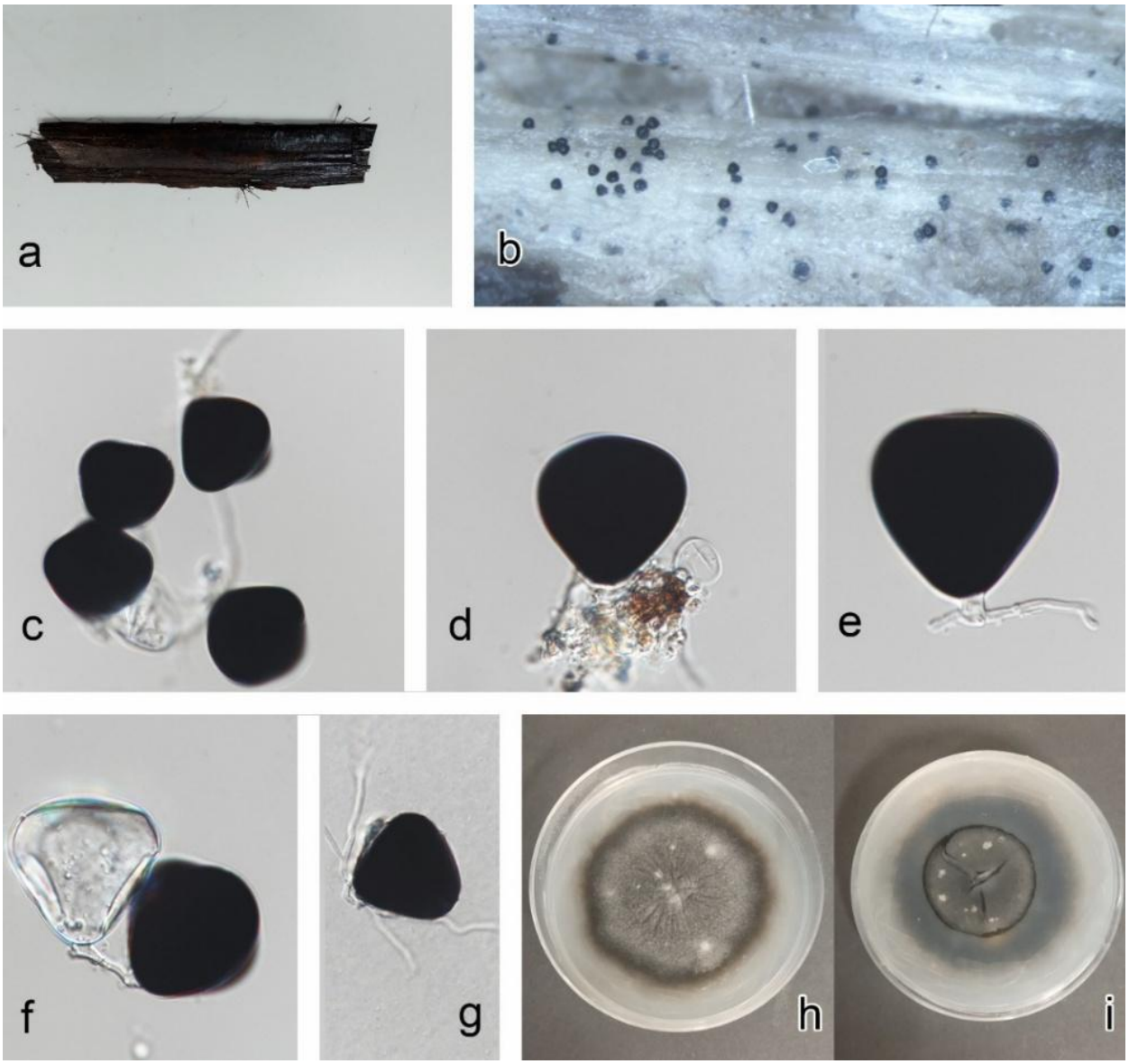

Figure 39 – *Conioscypha narathiwatensis* (MFLU 24-0496, holotype). a Host. b Colonies on the host. c Conidiophores and conidia. d–f Conidiogenous cells and developing conidia. g A germinated conidium. h, i Culture characters on the PDA. Scale bars: b = 200 µm, c = 35 µm, d, f = 20 µm, e = 25 µm, g = 30 µm.

Notes – Phylogenetically, our strain (MFLUCC 24-0581) clustered separately from *Conioscypha nakagirii* (BBH40587) with 100% ML and 1.00 PP statistical support in the combined phylogenetic tree of ITS, LSU, SSU and *rpb2* (Fig. 38). 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.

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 (Réblová et al. 2016, Sun et al. 2017, Dong et al. 2021). The sexual morph is characterized 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 characterized 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 (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 Fig. 40.

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.

Pseudosaprodesmium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 41

Index Fungorum number: IF903544; Facesoffungi number: FoF17533

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.

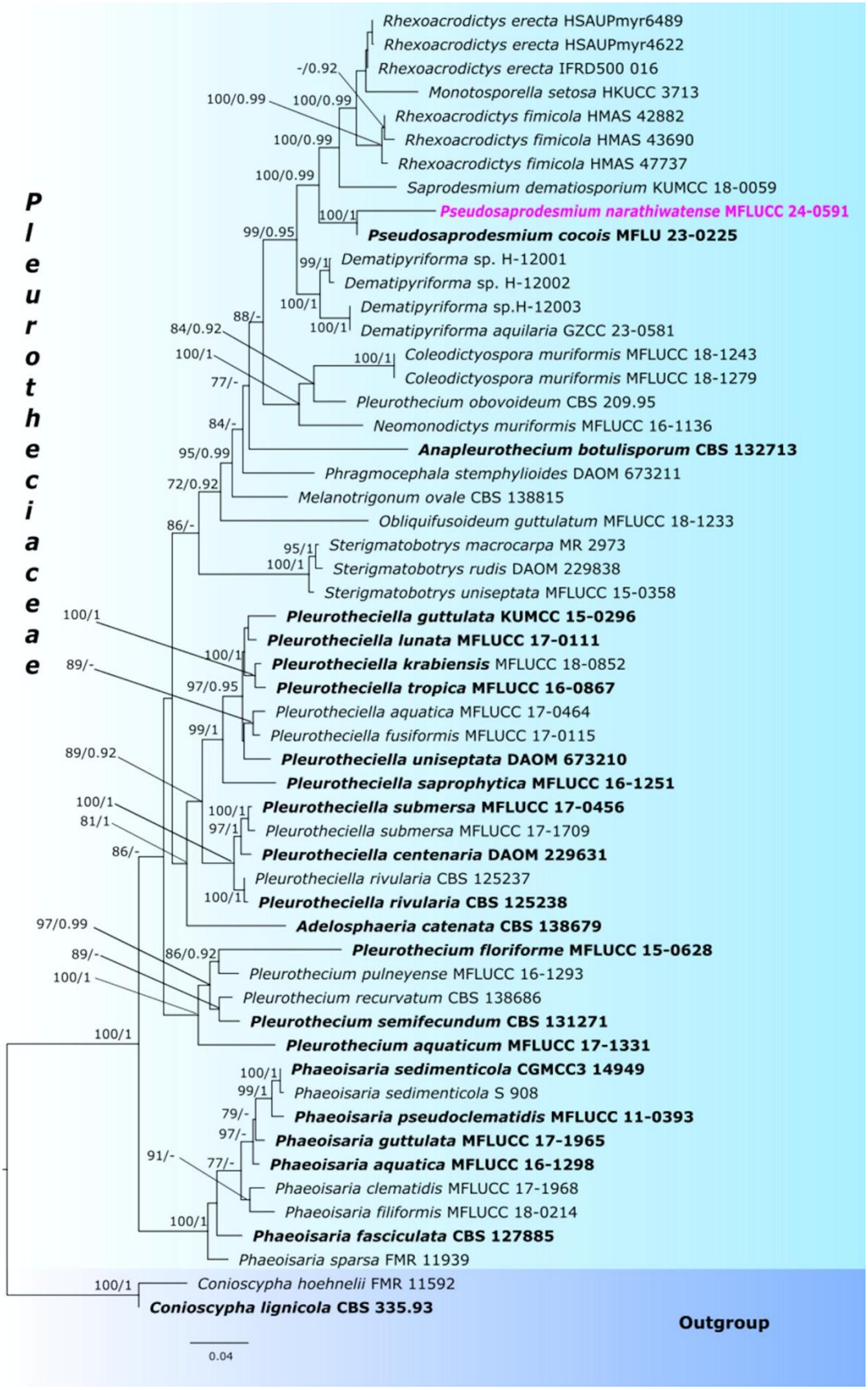

Figure 40 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, and SSU sequences. The analysis includes 17 strains; total characters: 2420 (ITS: 574, LSU: 861, SSU: 985). *Conioscypha hoehnelii* (FMR 11592), and *C. lignicola* (CBS 335.93) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -14889.527 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution

rates AC = 1.76003, AG = 3.16953, AT = 1.76003, CG = 1.00000, CT = 7.33453, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

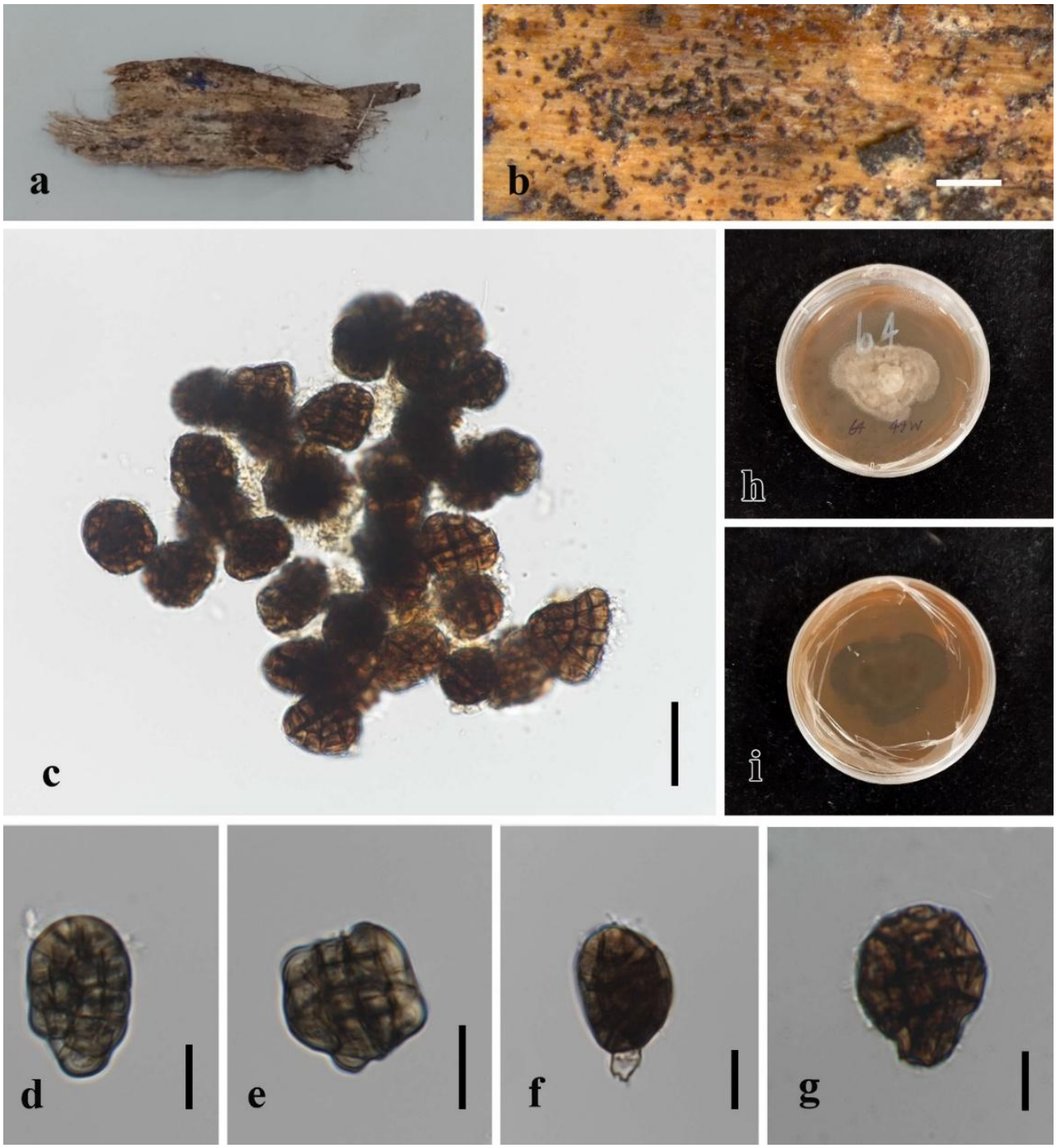

Figure 41 – *Pseudosaprodesmium narathiwatense* (MFLU 24-0506, holotype). a Host. b Colonies on the host substrate. c–g Conidia and conidiogenous cells. h, i Colonies on the PDA. Scale bars: b = 1000 µm, c = 25 µm, d = 15 µm, e, f = 20 µm, g = 10 µm.

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 gray, 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 (Fig. 40), 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 not provided 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.

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 *Savoryellaceae* was established by Jaklitsch & 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* (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) recognized *Neoascotaiwania* as a distinct genus and placed it in *Savoryellaceae*. The family now includes six genera: *Ascotaiwania*, *Ascothailandia*, *Bactrodesmium*, *Canalisporium*, *Dematiosporium*, and *Neoascotaiwania* (Réblová et al. 2020). The sexual morph of *Savoryellaceae* is characterized 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 bactrodesmium-like, monodictys-like, monotosporella-like, and trichocladium-like morphs (Ranghoo & Hyde 1998, Hernández-Restrepo et al. 2017). An updated phylogeny for the family is shown in Fig. 42.

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

Jones & Eaton (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 & 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 & 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.

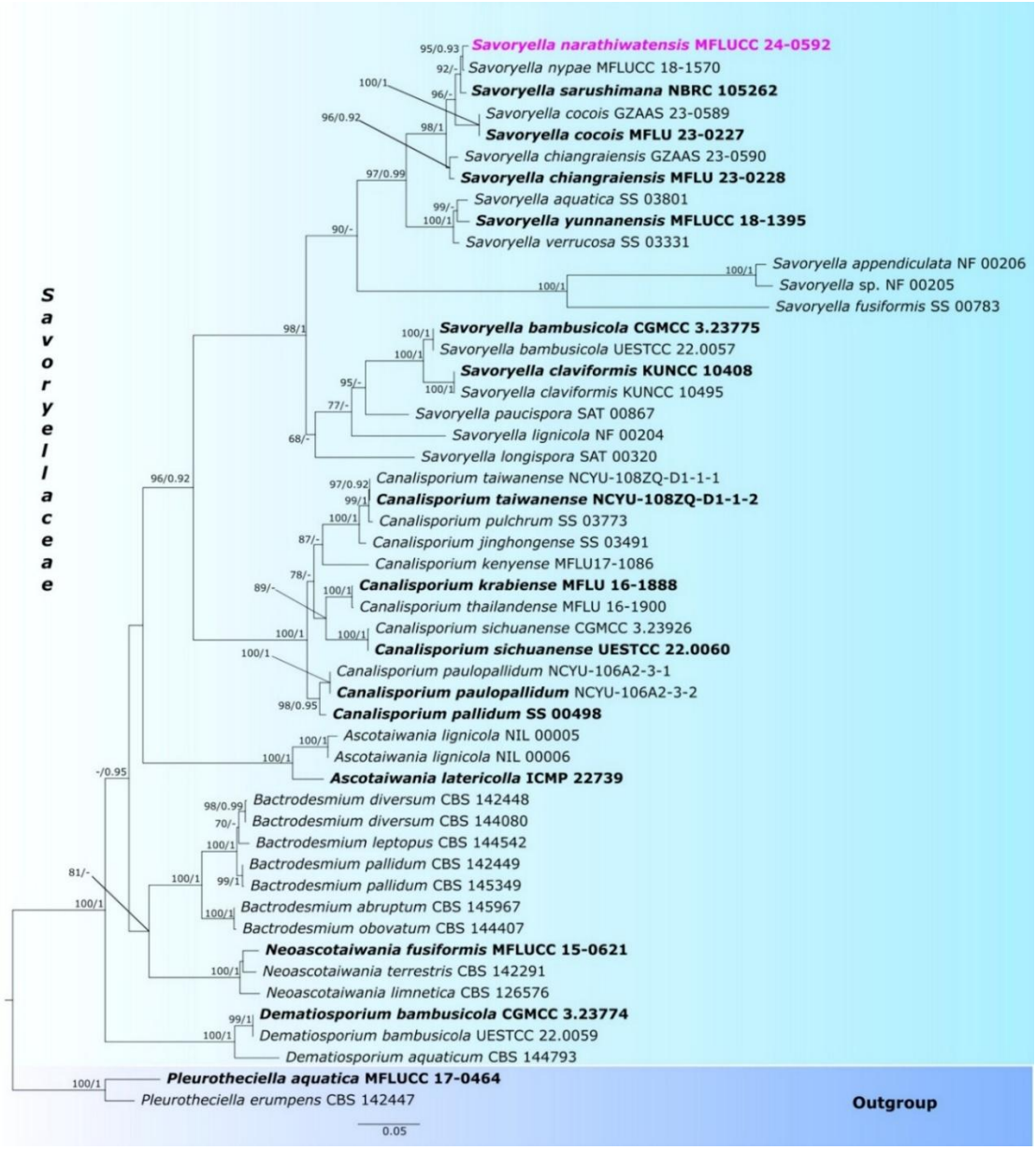

Figure 42 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, SSU and ITS sequences. The analysis includes 50 strains; total characters: 2464 (LSU: 864, SSU: 1010, ITS: 590). *Pleurotheciella aquatica* (MFLUCC 17-0464) and *Pleurotheciella erumpens* (CBS 142447) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -16926.104278 is presented. Estimated base frequencies were as follows; A = 0.2251, C = 0.2727, G = 0.3056, T = 0.1966; substitution rates AC = 1.7900, AG = 2.8101, AT = 1.7900, CG = 1.00000, CT = 6.7965, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Savoryella narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 43

Index Fungorum number: IF903545; Facesoffungi number: FoF17534

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, acrogenous, proliferating to develop new conidia, rounded, flattened or pointed at the apex, straight or slightly curved, thick-walled, conidial wall smooth or slightly rough, 1–5-septate, thick septa, dividing the conidium into unequal cells, the apical cell brown or pale brown, mostly being the largest, with pale brown to subhyaline basal cell.

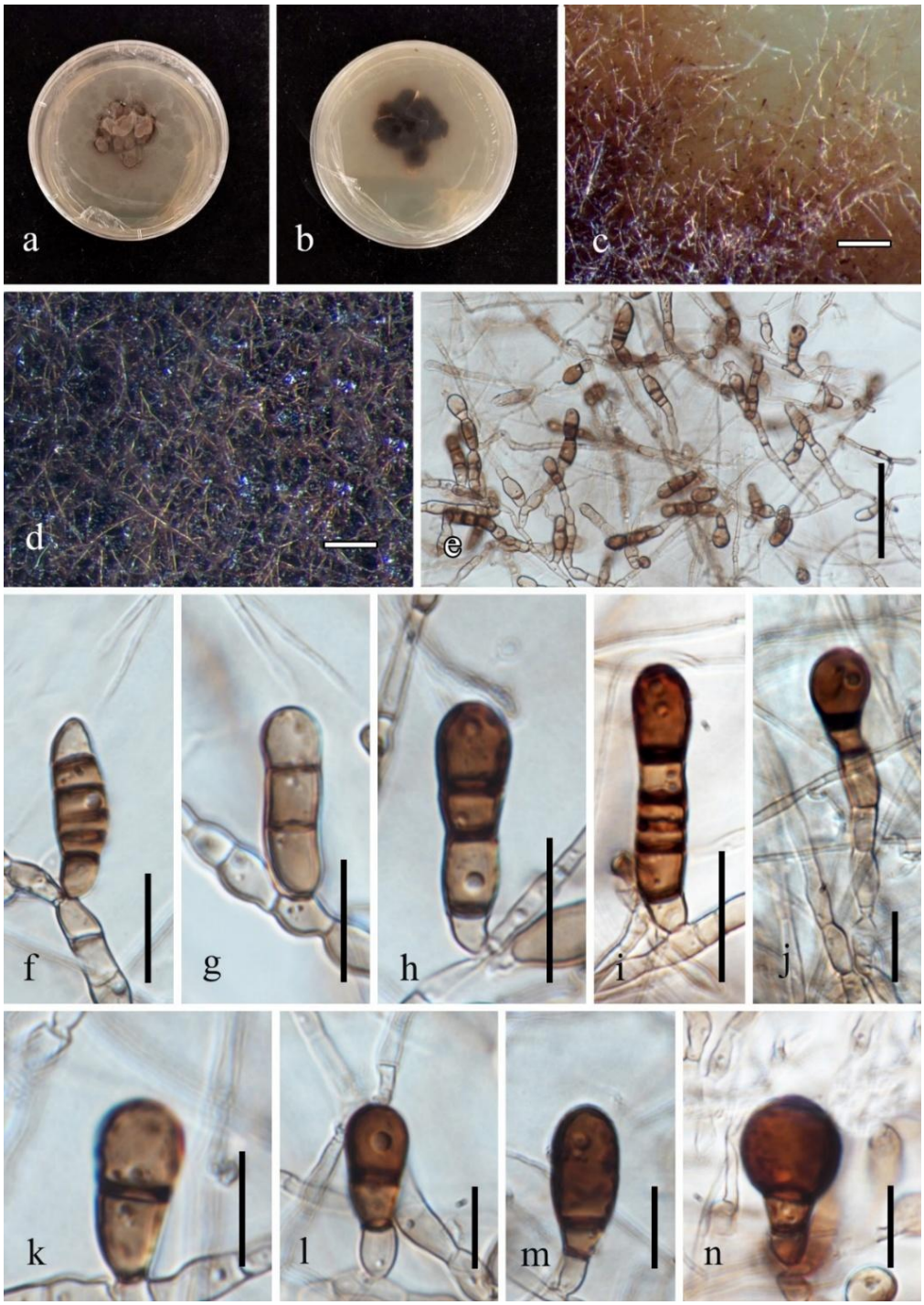

Figure 43 – *Savoryella narathiwatensis* (MFLUCC 24-0592, ex-type). a, b Culture characters on the PDA (a = from above, b = from down). c–d Mycelium on the PDA. e Conidiophores and conidia in the pure culture. f–n Sporulating conidia in the culture. Scale bars: c, d = 250 μm, e = 35 μm, f–i = 15 μm, j–m = 10 μm.

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, mycelium 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. Additional sequences: ITS = PV271891, LSU = PV271930, SSU = PV263320.

Notes – Phylogenetically, *Savoryella narathiwatensis* (MFLUCC 24-0592) clustered with *Sa. nypae* (MFLUCC 18-1570) with 95% ML and 0.93 PP statistical support (Fig. 42). Morphologically, *Sa. narathiwatensis* 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, acrogenous, proliferating conidia with rough wall despite the globose to subglobose smooth-walled conidia in *Sa. nypae* without proliferating (Zhang et al. 2019b). 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. The BLAST result of the SSU sequence from our collection of *Sa. narathiwatensis* (MFLUCC 24-0592) did not show close identity to *Savoryella*. To confirm whether this was due to contamination or a sequencing error, PCR amplification and sequencing were repeated, but the results remained consistent with the initial outcome. Due to the doubtful nature of the SSU sequence, we did not include it for *Sa. narathiwatensis* (MFLUCC 24-0592) in our phylogenetic analysis. Despite the close relationship observed in the phylogenetic tree (Fig. 44), we introduce *S. narathiwatensis* as a novel species based on ITS base pair differences and distinct morphological characteristics.

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. 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 *Chaetosphaeriaceae* (Locquin 1984, Réblová 1999, Maharachchikumbura et al. 2016, Lin et al. 2019, Zheng et al. 2020). Wu & 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 & Nekvindová (2023) examined species within *Chloridium sensu lato*, introducing six new genera: *Caliciastrum*, *Caligospora*, *Capillisphaeria*, *Geniculoseta*, *Papillospora*, and *Spicatispora*. The sexual morph of *Chaetosphaeriaceae* 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 have 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. 2020). An updated phylogeny for the selected genera in *Chaetosphaeriaceae* and *Linocarpaceae* in *Chaetosphaeriales* is shown in Fig. 44.

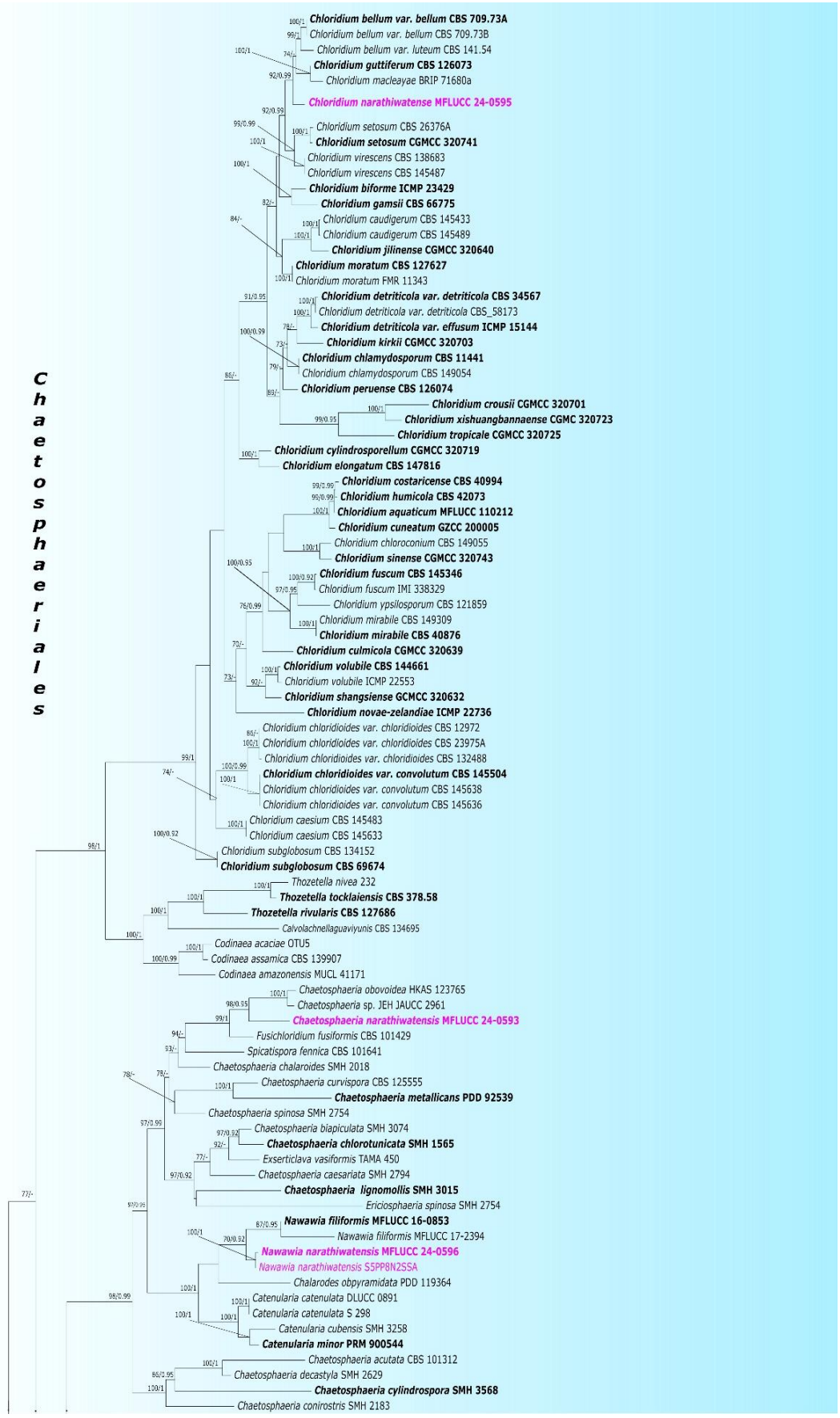

Figure 44 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU and *tef-1α* sequences. The analysis includes 148 strains; total characters: 2495 (ITS: 492, LSU: 1062, *tef-1α*: 941). *Phyllachora graminis* (TH544) and *Ph. sandiensis* (IFRD 9446) were used as the

outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -32658.691 is presented. Estimated base frequencies were as follows; A = 0.228, C = 0.279, G = 0.293, T = 0.201; substitution rates AC = 1.19170, AG = 1.72366, AT = 1.19170, CG = 1.00000, CT = 5.80328, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

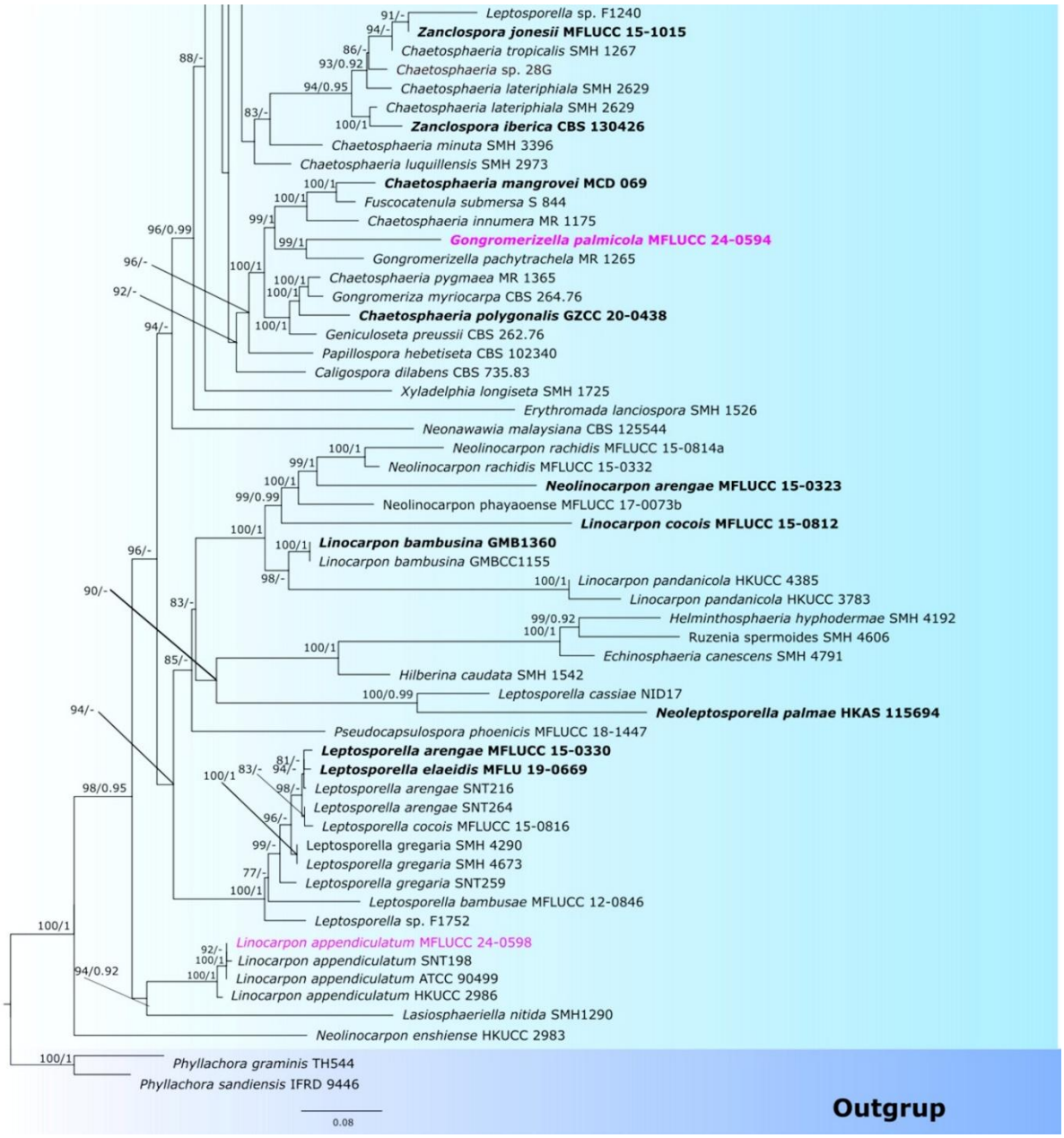

Fig. 44 - Continued

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

Tulasne & Tulasne (1863) introduced *Chaetosphaeria* (*Cha.*), as a new genus, with *Cha. innumera* as the type species. *Chaetosphaeria* species have a worldwide distribution and are commonly reported as saprobes on decaying plant material in terrestrial and freshwater habitats (Booth 1957, Sarbhoy & Varshney 1971, Kirk & Spooner 1984, Dennis 1986, McKenzie et al. 1992, Eriksson & Yue 1998, Lu et al. 2000, Irsenaite & Treigiene 2001, Fernández et al. 2006, Chlebicki & Chmiel 2006, Atkinson et al. 2007, Kobayashi 2007, Nasr et al. 2018, Hyde et al. 2024). To date,

only one unidentified *Chaetosphaeria* taxon has been reported from peat swamp forests (Pinruan et al. 2007). In this study, we describe *Cha. narathiwatensis* as a novel taxon.

Chaetosphaeria narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 45

Index Fungorum number: IF903546; Facesoffungi number: FoF17535

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, brown, thick-walled, 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. *tub2* = PV477061.

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* (Fig. 44). 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.

Gongromerizella Réblová, Stud. Mycol. 103: 199 (2022)

Réblová et al. (2022) introduced the genus *Gongromerizella* to accommodate three species with chloridium-like asexual morphs: *G. lignicola* (Basionym: *Bisporomyces lignicola*), *G. pachytrachela* (Basionym: *Chl. pachytrachelum*), and *G. pini* (Basionym: *Chl. pini*). *Gongromerizella silvana* was subsequently introduced as the fourth species by Réblová et al. (2023).

Gongromerizella palmicola O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 46

Index Fungorum number: IF904130; 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 gray 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, *Gongromerizella palmicola* (MFLUCC 24-0594) clustered with *G. pachytrachela* (MR 1265), with 99% ML and 1.00 PP statistical support in the phylogenetic tree (Fig. 44). Morphologically, *G. palmicola* differs from asexual morph of *G. pachytrachela* 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 *G. pachytrachela* (Gams & Holubová-Jechová 1976). Based on the pairwise comparison of ITS and LSU sequences, *G. palmicola* (MFLUCC 24-0594) differs from *G. pachytrachela* (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 *G. pachytrachela* (MR 1265). Therefore, we introduce *G. palmicola* as a novel species based on morphological and phylogenetic evidence.

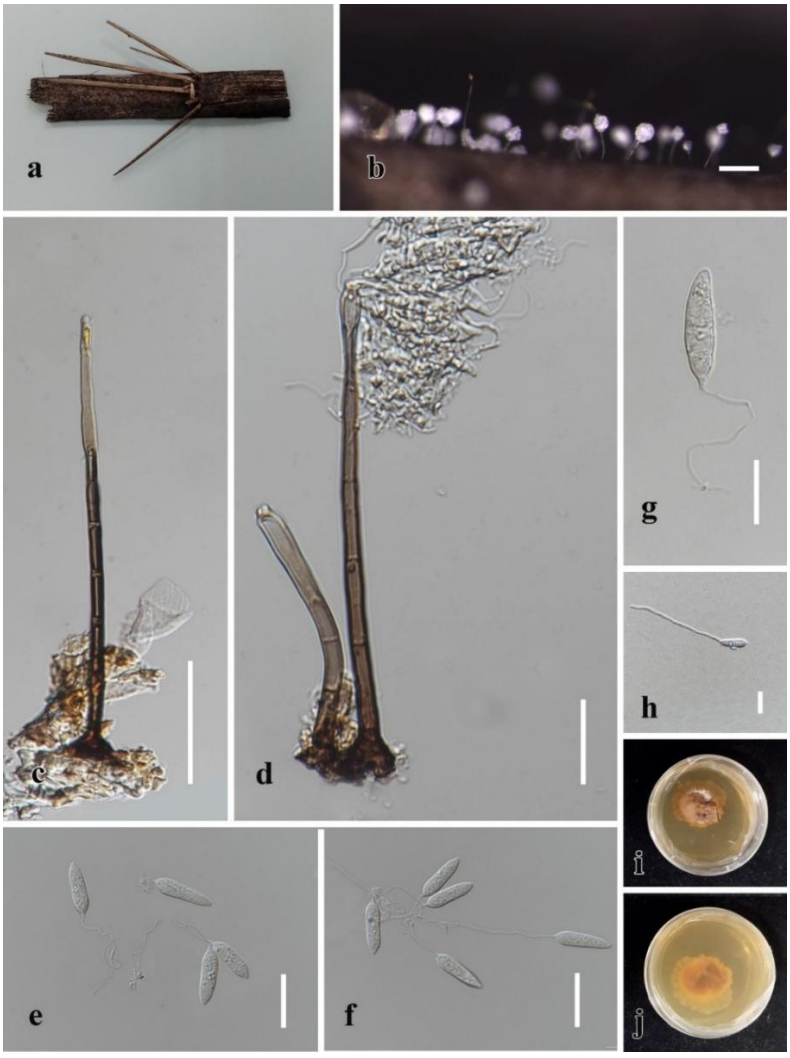

Figure 45 – *Chaetosphaeria narathiwatensis* (MFLU 24-0508, holotype). a Host. b Colonies on the host substrate. c, d Conidiophores and conidiogenous cells. e–g Conidia. h A germinated conidium. i, j Colonies on the PDA. Scale bars: b = 100 µm, c = 50 µm, d, h = 20 µm, e, f = 25 µm.

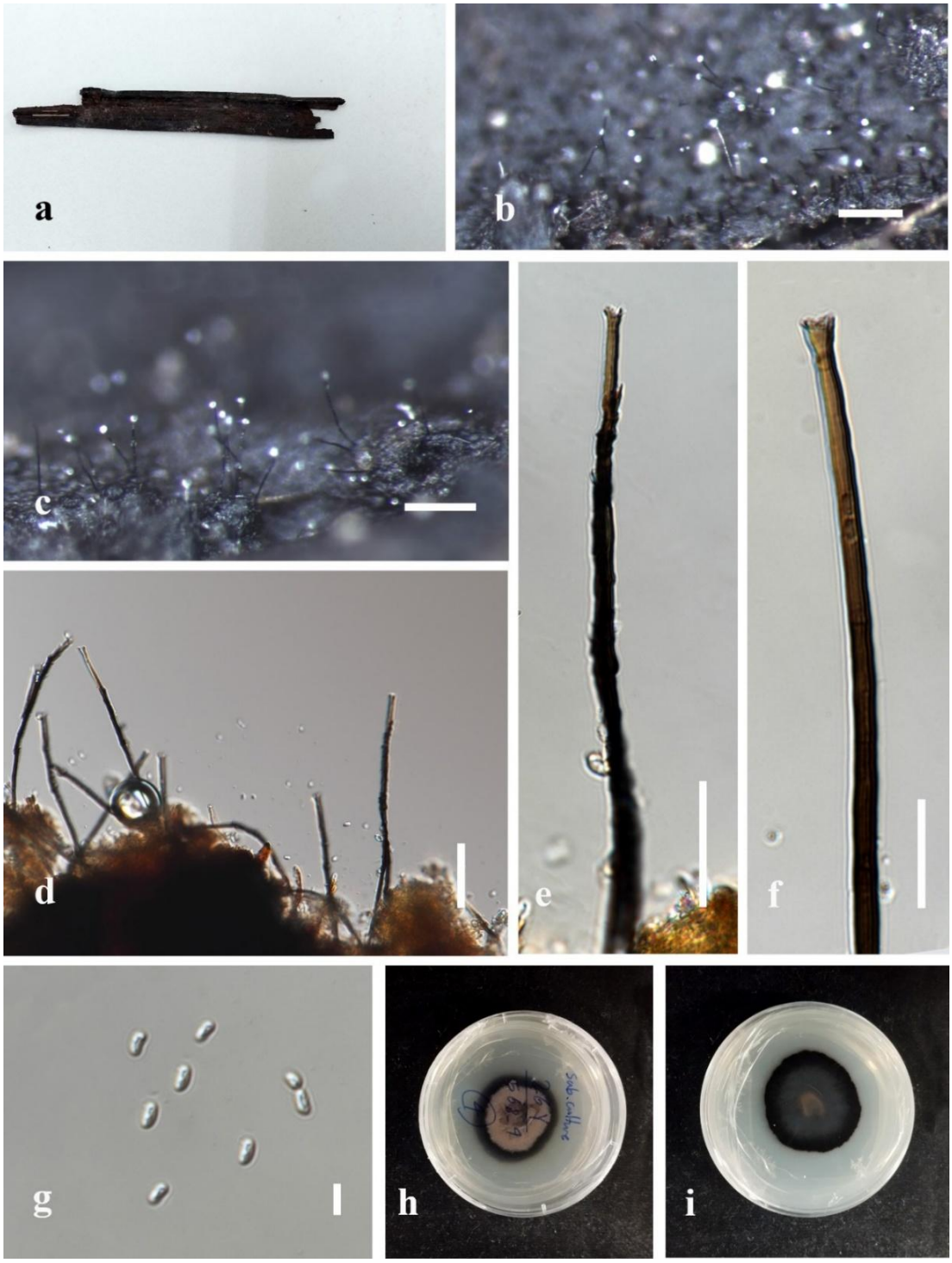

Figure 46 – *Gongromerizella palmicola* (MFLU 24-0509, holotype). a Host. b, c Colonies on the host substrate. d–f Conidiophores and conidiogenous cells. g Conidia. h, i Colonies on the PDA. Scale bars: b, c = 250 µm, d = 40 µm, e = 25 µm, f = 15 µm, g = 5 µm.

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. Fig. 47

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, hyaline to pale brown, septate, branched, smooth, thin-walled. *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 in center 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, *tub2* = PV477062.

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 (Fig. 44). 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 & 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.

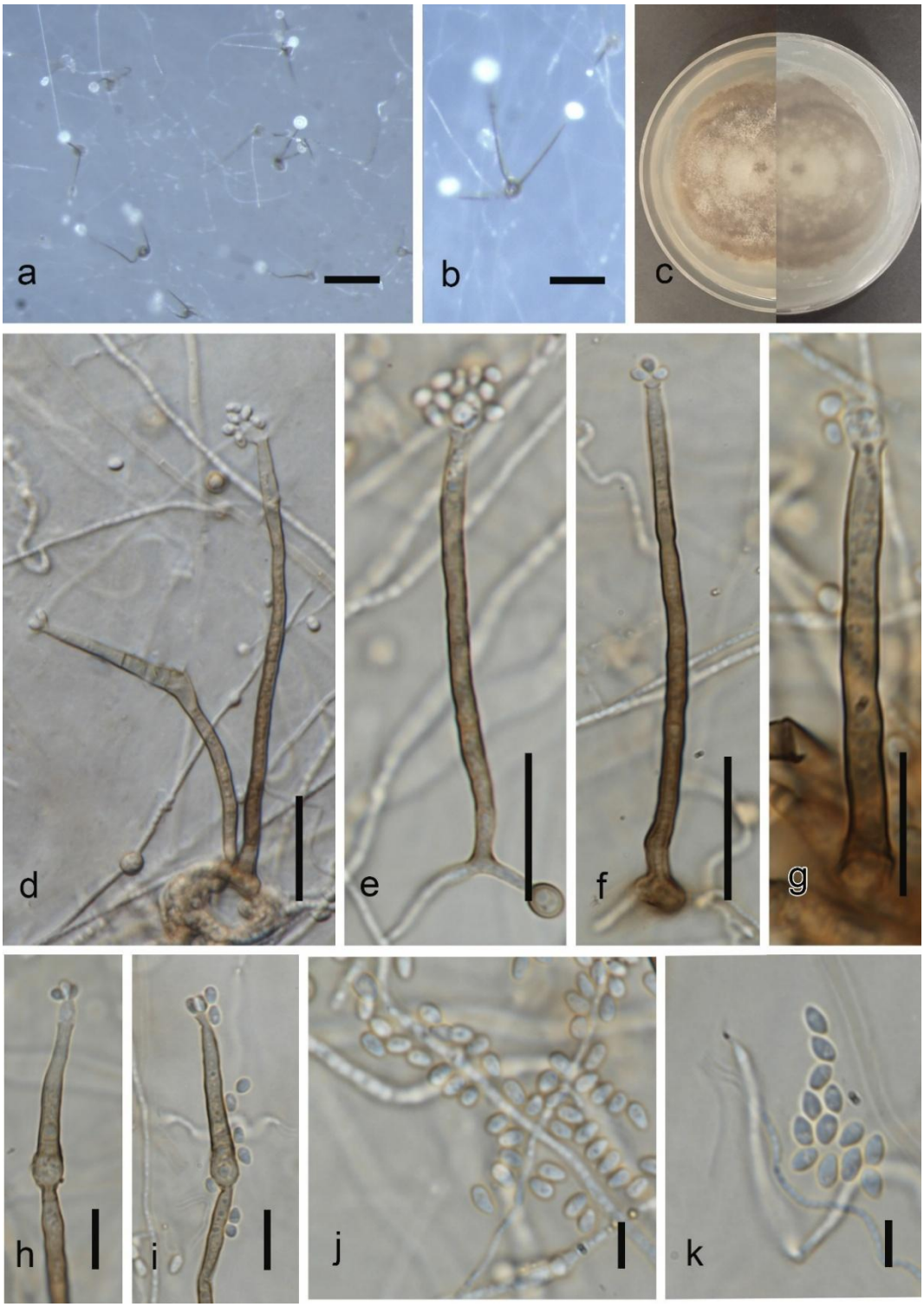

Figure 47 – *Chloridium narathiwatense* (MFLUCC 24-0595, ex-type). a, b Colonies on the CMA. c Surface and reverse overview of the culture. d–i Conidiophores and conidiogenous cells. j, k Conidia. Scale bars: a, b =100 µm, d–g = 20 µm, h, i = 10 µm, j, k = 5 µm.

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 & 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. Fig. 48

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 gray.

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; Additional sequences: ITS = PV271896, LSU = PV271935.

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 (Fig. 44). 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.

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. 2024a), *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 Fig. 49.

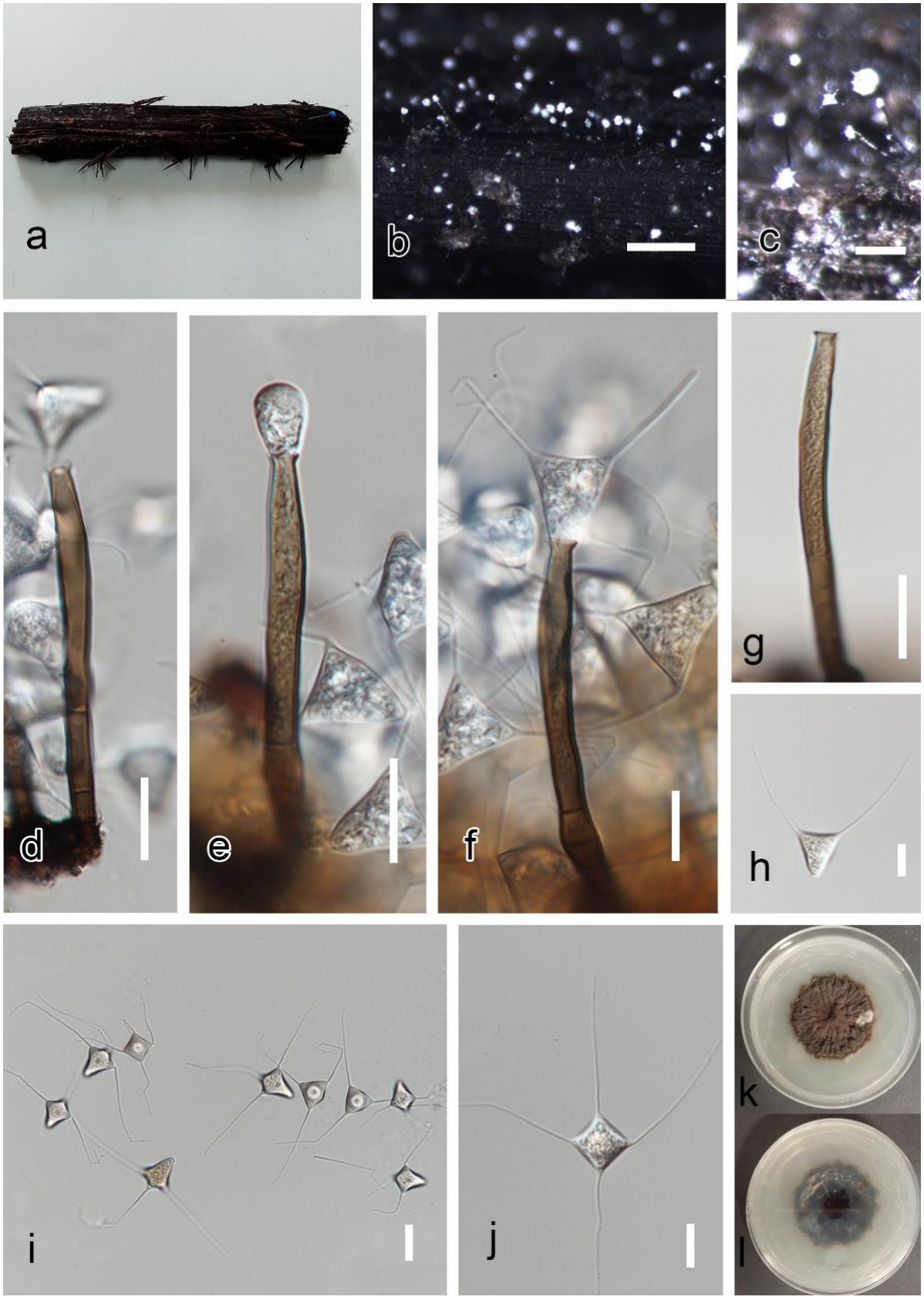

Figure 48 – *Nawawia narathiwatensis* (MFLU 24-0511, holotype). a Host. b, c Colonies on the host substrate. d–g Conidiophores and conidiogenous cells. h–j Conidia. k, l Colonies on the PDA. Scale bars: b = 200 µm, c = 100 µm, d, e, g, i–j = 20 µm, f, h = 15 µm.

Stanjehughesia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 50

Index Fungorum number: IF903550; Facesoffungi number: FoF17539

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 ($\overline{x}$ = 12.9 × 5 µm, n = 20), monoblastic, terminal, solitary or caespitose, erect, 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 ($\overline{x}$ = 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 grayish 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, *tub2* = PV477063, *tef-1α* = PV340502.

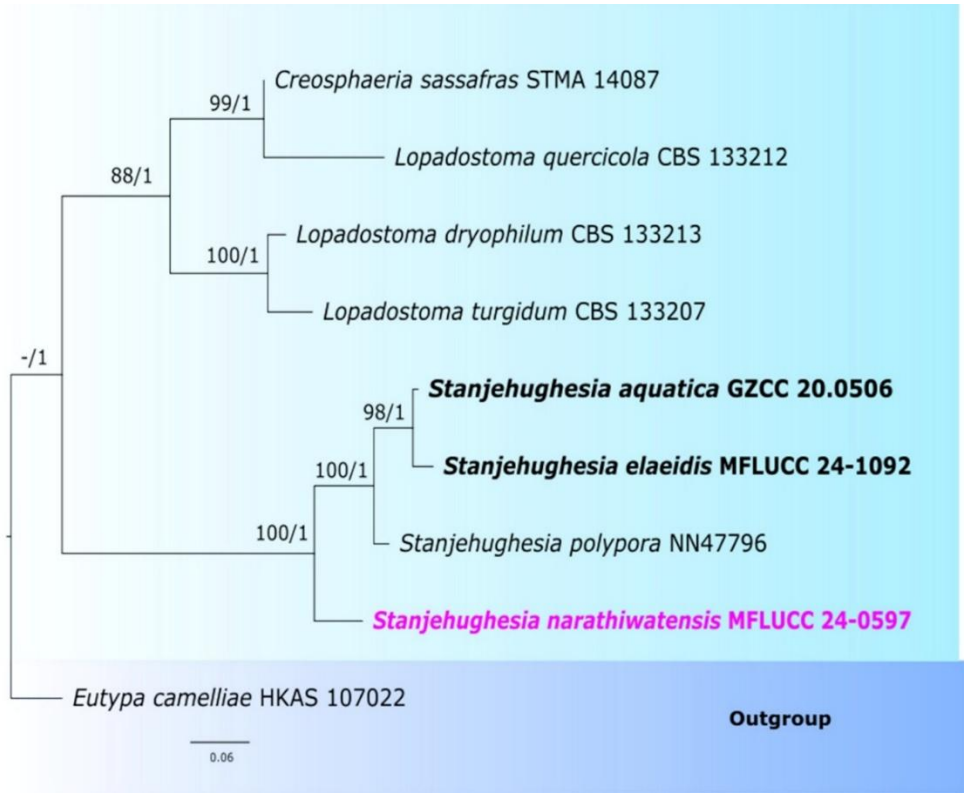

Figure 49 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, ITS, SSU, *tef-1α, rpb2* and *tub2* sequences. The analysis includes nine strains; total characters: 5233 (LSU: 850, ITS: 588, SSU: 1007, *tef-1α*: 929, *rpb2*: 1064, *tub2*: 795). *Eutypa camelliae* (HKAS 107022) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -15433.942 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.55110, AT = 1.00000, CG = 1.00000, CT

= 5.43662, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

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 (Fig. 49). 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. 2024a). Therefore, we introduce *S. narathiwatensis* as a novel species, based on morphological and phylogenetic evidence.

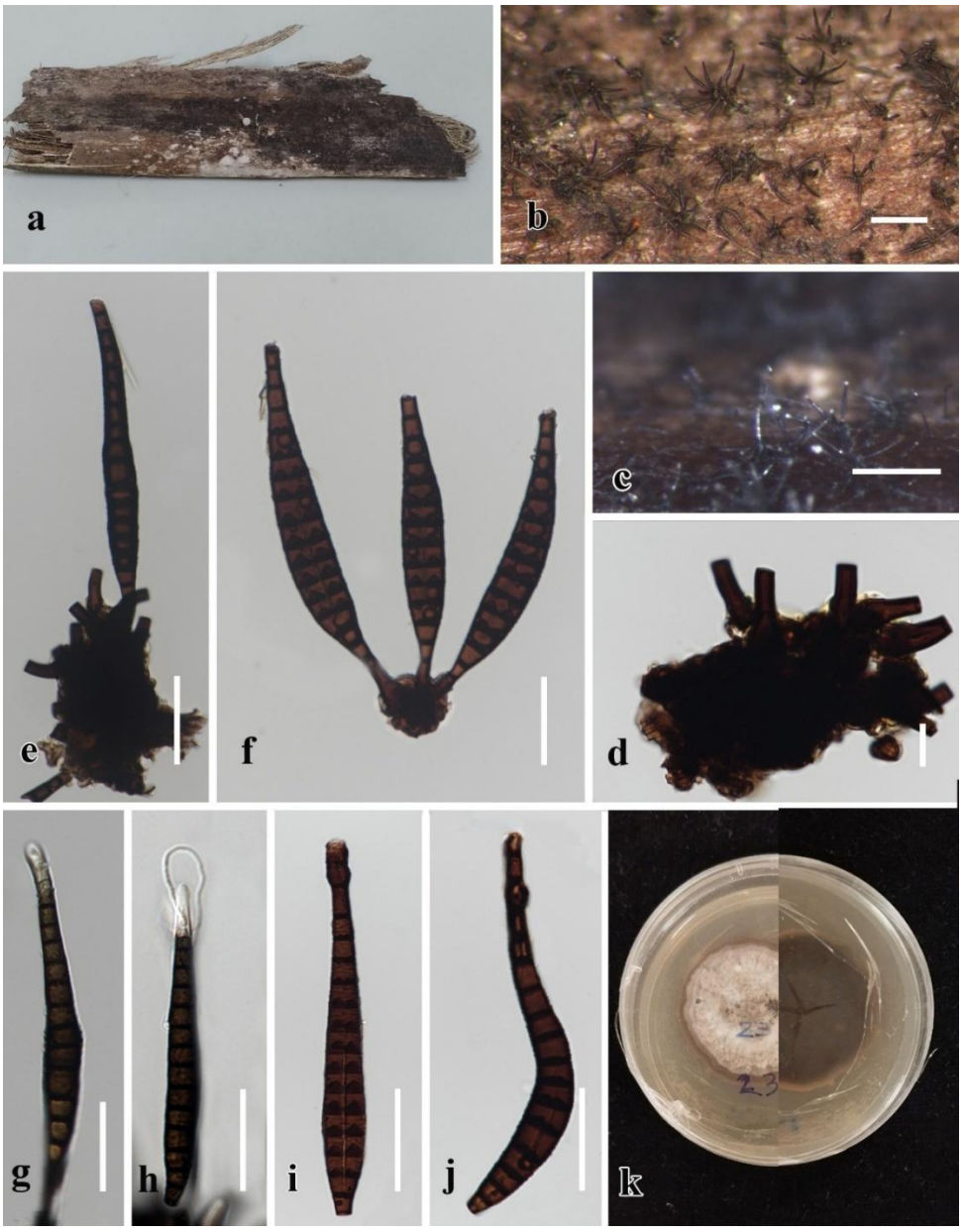

Figure 50 – *Stanjehughesia narathiwatensis* (MFLU 24-0512, holotype). a Host. b, c Colonies on the host substrate. d Conidiogenous cells. e, f Conidiogenous cells and conidia. g–k Conidia. l Colonies on the PDA. Scale bars: b = 500 μm, c = 250 μm, d = 10 μm, e, f, h–j = 30 μm, g = 20 μm

Linocarpaceae Konta & K.D. Hyde, Mycosphere 8 (10): 1962 (2017)

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* (*Li*.) 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. 2023a, 2024a, 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 (1992) from the cultures of *Li. appendiculatum* and *Li. elaeidis* (Konta et al. 2017, Zhang et al. 2023a).

Linocarpon Syd. & P. Syd., Ann. Mycol. 15 (3/4): 210 (1917)

Linocarpon was introduced by Sydow & Sydow (1917) and typified by *Li. pandani*. Currently, there are 45 accepted *Linocarpon* species listed in Species Fungorum (2024). *Linocarpon* is a saprobic genus found on plant materials (Konta et al. 2017). Most *Linocarpon* species have been collected from hosts in the families *Pandanaceae* and *Arecaceae*. However, *Linocarpon* has also been reported from other hosts, including *Zingiberaceae*, *Poaceae*, *Fabaceae*, *Fagaceae*, *Euphorbiaceae*, and *Smilacaceae* (Sydow & Sydow 1917, Petrak 1952, Petrak & Deighton 1952, Hansford 1954, Petrak 1956, Schrantz 1960, Turner 1971, Pirozynski 1972, Liu 1977, Barr 1978, Sivanesan & Hsieh 1989, Hyde 1992, Hyde 1997, 1988b, Dulymamode et al. 1998, Hsieh et al. 1998, Hyde & Alias 1999, Fröhlich & Hyde 2000, Lu et al. 2000, Zhuang 2001, Taylor & Hyde 2003, Huhndorf et al. 2004, Miller & Huhndorf 2005, Pinruan et al. 2007, Konta et al. 2017). *Linocarpon* species have been recorded from various locations worldwide, including Australia, Brazil, Brunei, China, Ecuador, India, Malaysia, Mauritius, Papua New Guinea, Thailand, Tanzania, the Philippines, Sierra Leone, Indonesia, and the United States (Hyde 1992, Hyde 1997, 1988b, Konta et al. 2017, Konta et al. 2023). To date, three species of this genus (*Li. elaeidis, Li. livistonae, Li. pandani*) have been reported from peat swamp forests (Pinnoi et al. 2006, Pinuruan et al. 2007). In this study, we report *Li. appendiculatum* as a new record from the peat swamp forest in Narathiwat, Thailand.

Linocarpon appendiculatum K.D. Hyde, Transactions of the Mycological Society of Japan 29: 339 (1989) Fig. 51

Index Fungorum number: IF135907; Facesoffungi number: FoF17540

Saprobic on the submerged rachis of *Cyrtostachys renda*. **Sexual morph**: *Ascomata* 350–420 μm × 110–130 μm ($\overline{x}$ = 327 × 82 μm, n = 15), superficial, solitary or aggregated, black, dome-shaped, raised, lenticular and with a central ostiole. *Peridium* 10–15 μm wide ($\overline{x}$ = 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 ($\overline{x}$ = 3 μm, n = 30), straight or flexuous, septate, hypha-like, hyaline. *Asci* 100–148 × 7–9 ($\overline{x}$ = 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 ($\overline{x}$ = 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 1988b), *Cyrtostachys renda* (This study).

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

GenBank numbers – MFLUCC 24-0598: LSU = PV271937, *tef-1α* = PV340503.

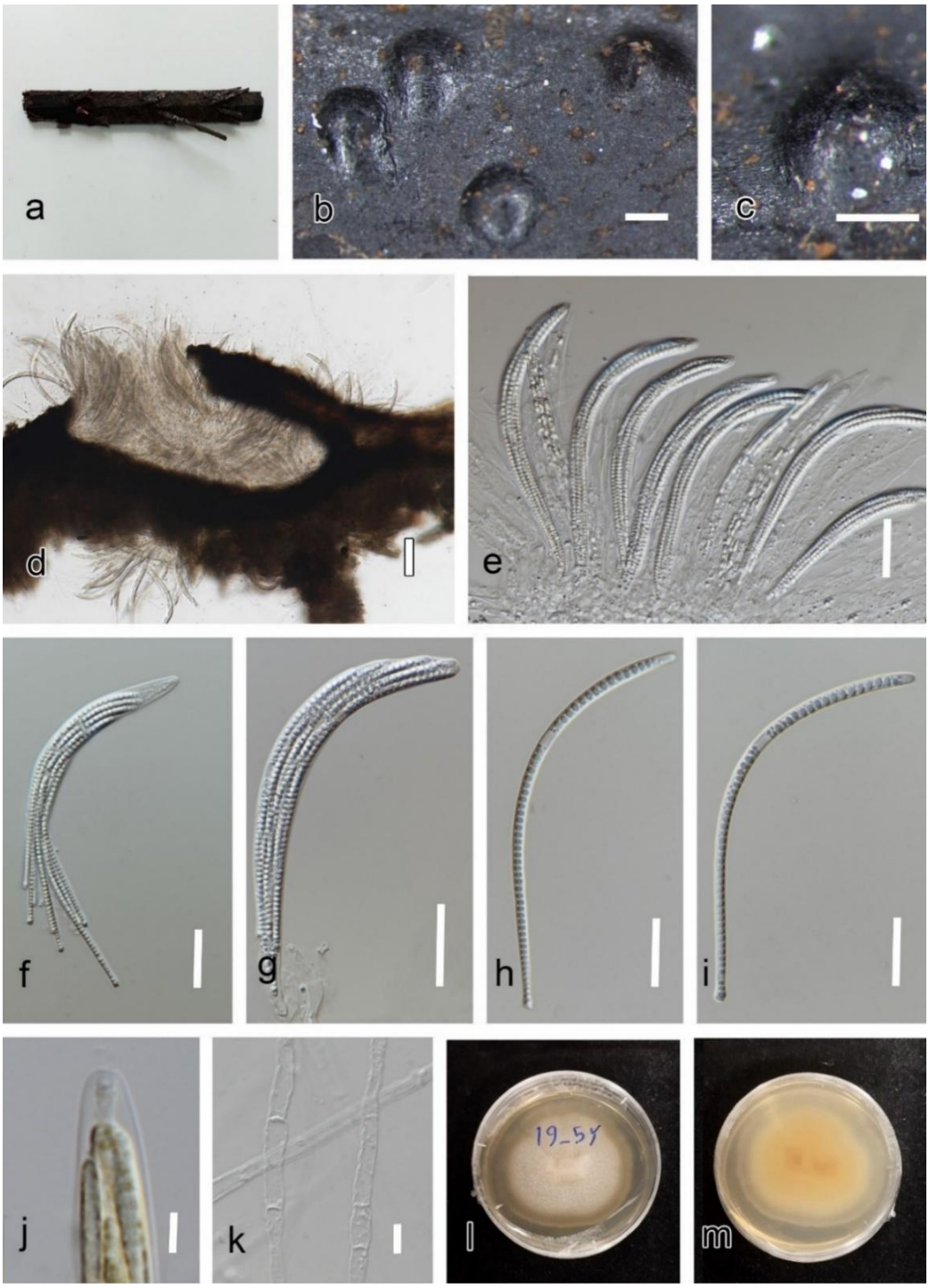

Figure 51 – *Linocarpon appendiculatum* (MFLU 24-0513, new host record). a Host. b, c Colonies on the host substrate. d A vertical section through an ascoma. e–g Asci. h, i Ascospore j The apex of

ascus stained in the Melzer's reagent. k Paraphyses. l, m Colonies on the PDA. Scale bars: b, c = 250 μm, d = 80 μm, e–g = 35 μm, h, i = 25 μm, j, k = 5 μm.

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 (MFLU 24-0513) as *Li. appendiculatum* based on phylogenetic analyses and morphological characters. We report our strain (MFLU 24-0513) as a new host record of *Li. appendiculatum* on *Cyrtostachys renda* from the peat swamp forest in Thailand.

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 characterized 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 Fig. 52.

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. 2020, Lu et al. 2020, Bao et al. 2021, 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 *Pseudodactylaria* 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.

Pseudodactylaria longidenticulata Jing Yang, E.B.G. Jones & K.D. Hyde, Fungal Diversity 119: 166 (2023) Fig. 53

Index Fungorum number: IF559823; Facesoffungi number: FoF12834

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, cylindrical, straight or slightly flexuous, 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, mycelium 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.

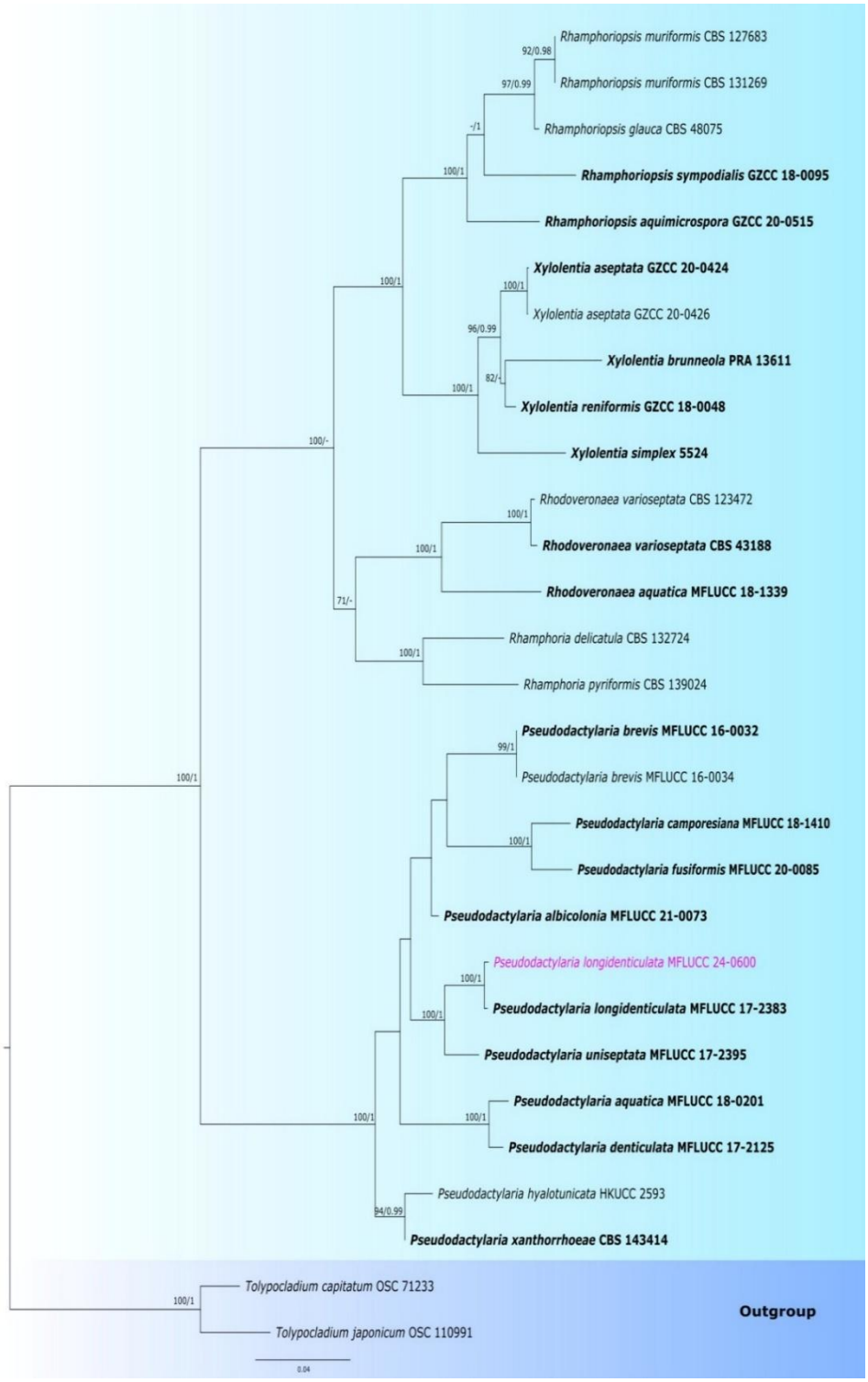

Figure 52 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, ITS, SSU, *tef-1α* and *rpb2* sequences. The analysis includes 29 strains; total characters: 4337 (LSU: 852, ITS: 526, SSU: 1003, *tef-1α*: 907, *rpb2*: 1049). *Tolypocladium capitatum* (OSC 71233) and *Tolypocladium japonicum* (OSC 110991) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -19148.987 is presented. Estimated base frequencies were as follows; A = 0.247, C = 0.253, G = 0.280, T = 0.220; substitution rates AC = 1.29148, AG = 2.16424, AT = 1.00000, CG = 1.29148, CT = 6.13607, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

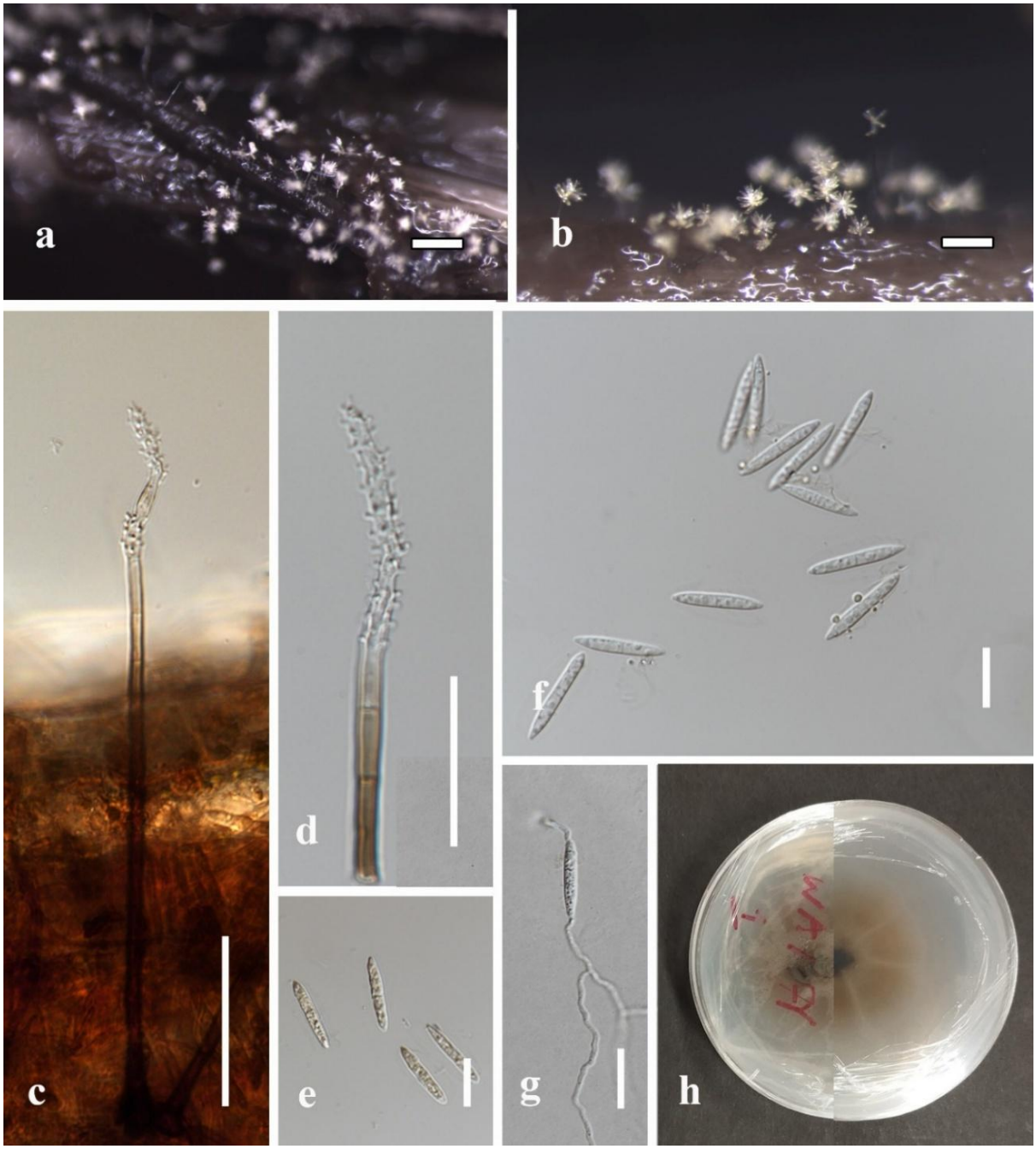

Figure 53 – *Pseudodactylaria longidenticulata* (MFLU 24-0515, new host and habitat record). a, b Colonies on the host substrate. c, d Conidiophores and conidiogenous cells. e, f Conidia. g A germinated conidium. h Colonies on the PDA. Scale bars: a, b = 100 µm, c = 50 µm, d = 30 µm, e = 15 µm, f, g = 15 µm.

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 (Fig. 52). 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. Although our strain differs from *Ps. longidenticulata* (MFLU 22-0075) in the size of conidiophores, conidiogenous cells, and conidia, it is closely related based on molecular data. 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.

Subclass ***Xylariomycetidae*** O.E. Erikss. & Winka, Myconet 1: 12 (1997)
Amphisphaeriales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 177 (1986)
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 three accepted genera: *Apiospora* (100 species), *Arthrinium* (30 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 & 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 characterized 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*). Recently, new *Nigrospora* species have been introduced from various substrates, including soil (Zhang et al. 2024c), *Spinifex sericeus* and *Chromolaena odorata* (Tan & Shivas 2024), *Citrus grandis* (Manawasinghe et al. 2024), *Juglans regia* (Zou et al. 2024) and oak species (Bashiri & Abdollahzadeh 2024). 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 Fig. 54.

Nigrospora chinensis Mei Wang & L. Cai, Persoonia 39: 129 (2017) Fig. 55

Index Fungorum number: IF820732; Facesoffungi number: FoF09446

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.

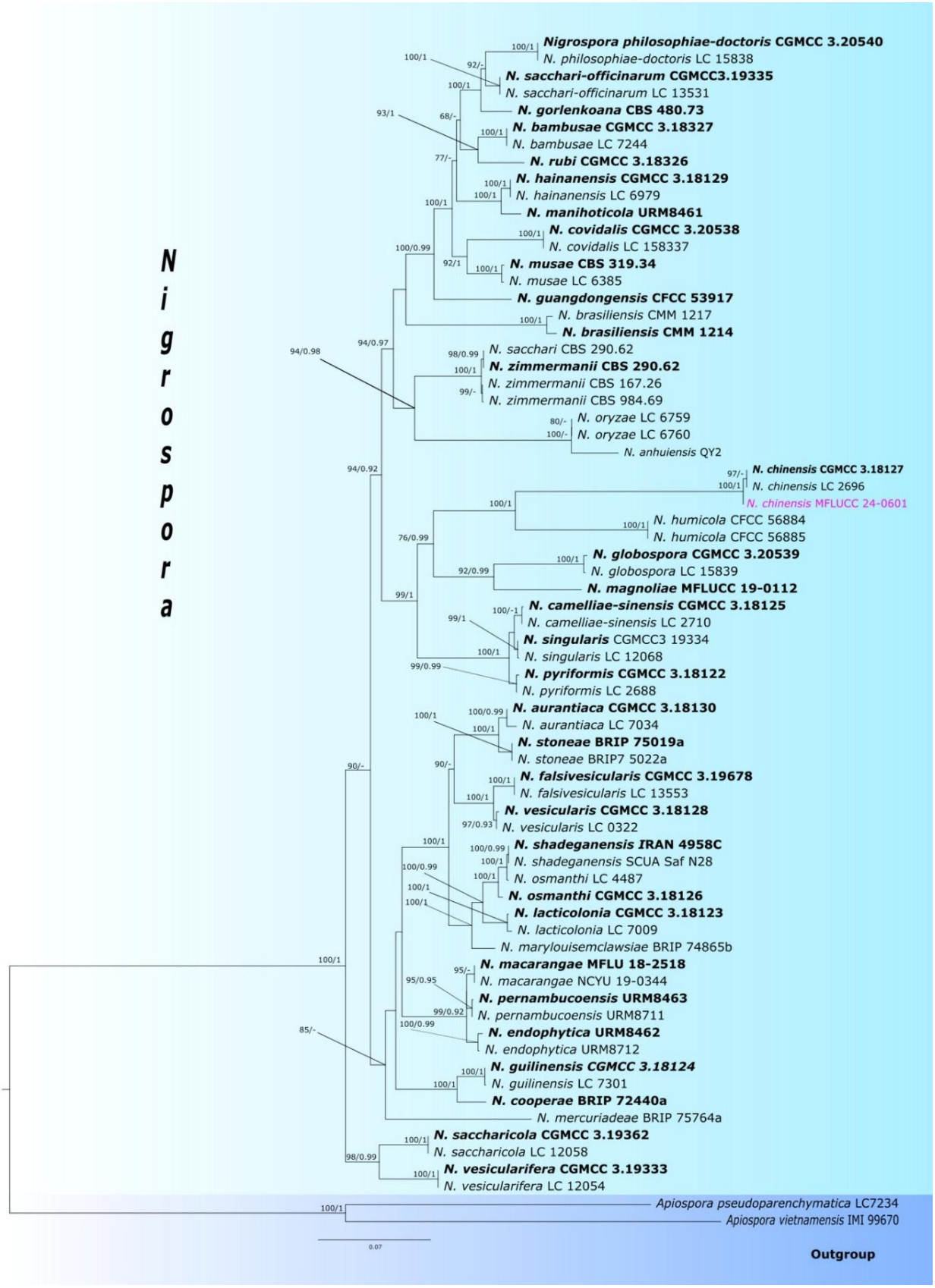

Figure 54 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, *tef-1α* and *tub2* sequences. The analysis includes 70 strains; total characters: 1430 (ITS: 533, *tef-1α*: 488, *tub2*: 409). *Apiospora vietnamensis* (IMI 99670), and *A. pseudoparenchymatica* (LC7234) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -12135.243 is presented. Estimated base frequencies were as follows; A = 0.215, C = 0.303, G = 0.243, T = 0.239; substitution rates AC = 1.00000, AG = 2.99812, AT = 1.00000, CG = 1.00000, CT = 4.59153, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

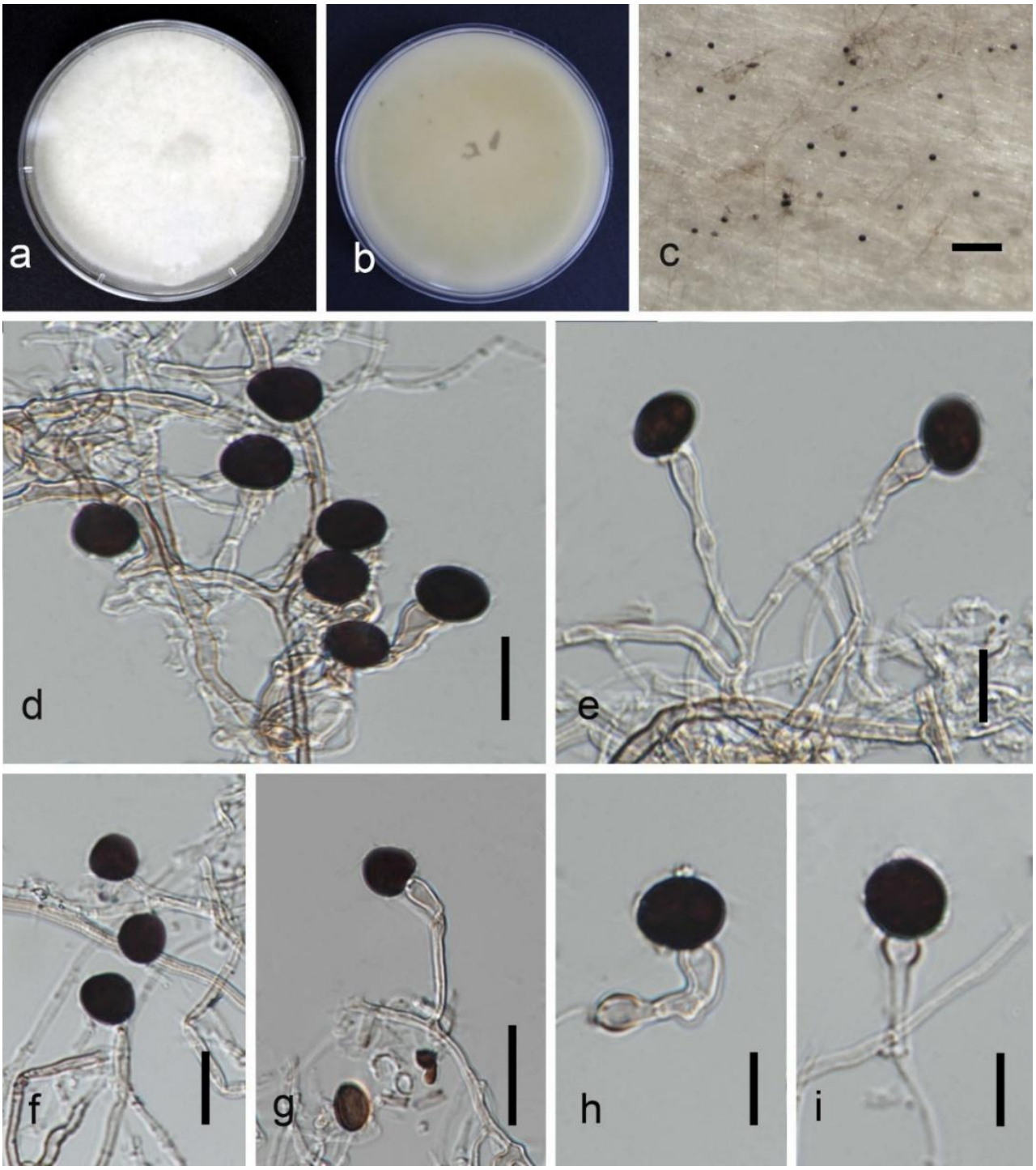

Figure 55 – *Nigrospora chinensis* (MFLUCC 24-0601, a new host and habitat record). a, b Surface and reverse view of the culture on the PDA. c Colony in culture. d–i Conidiophores, conidiogenous cells and conidia. Scale bars: c = 50 μm, d, g = 15 μm, e, f, i, h = 10 μm.

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), *Nicotiana tabacum* (Zhong et al. 2022), *Osmanthus* sp. (Wang et al. 2017), and *Smilax ocreata* (Wang et al. 2017).

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).

GenBank numbers – MFLUCC 24-0601: ITS = PV271900, *tub2* = PV477064.

Notes – In the multi-gene phylogeny, our strain (MFLUCC 24-0601) 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 as *Ni. chinensis* based on morphology and phylogenetic data. We report our strain 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.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis Ser. IV. 8 (2): 66 (1932)
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 *Daldinia* and its related taxa is shown in Fig. 56.

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

Daldinia 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 characterized by well-defined concentric zones in the stromatal interior (Stadler et al. 2014). It has been studied in three major monographs by Child (1932), Ju et al. (1997), and Stadler et al. (2014). Stadler et al. (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). Yin 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.

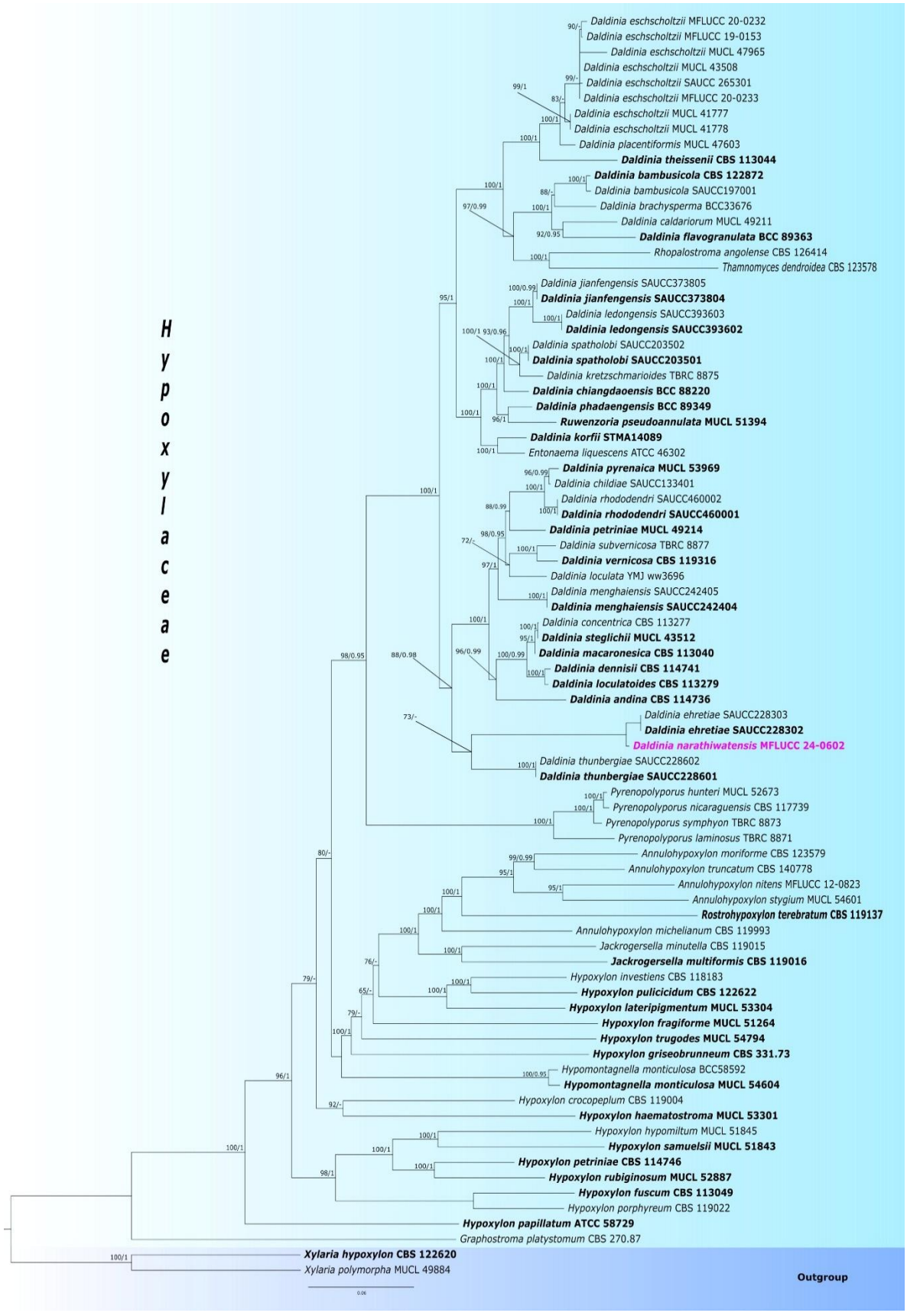

Figure 56 – Phylogram of maximum likelihood phylogenetic analysis based on combined ITS, LSU, *rpb2* and *tub2* sequences. The analysis includes 82 strains; total characters: 4145 (ITS: 552, LSU:

1288, *rpb2*: 934, *tub2*: 1371). *Xylaria polymorpha* (MUCL 49884), and *X. hypoxylon* (CBS 122620) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -56127.124 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.27936, AG = 4.24735, AT = 1.27936, CG = 1.00000, CT = 6.59339, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Daldinia narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 57

Index Fungorum number: IF903552; Facesoffungi number: FoF17542

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* 120–265.5 × 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.

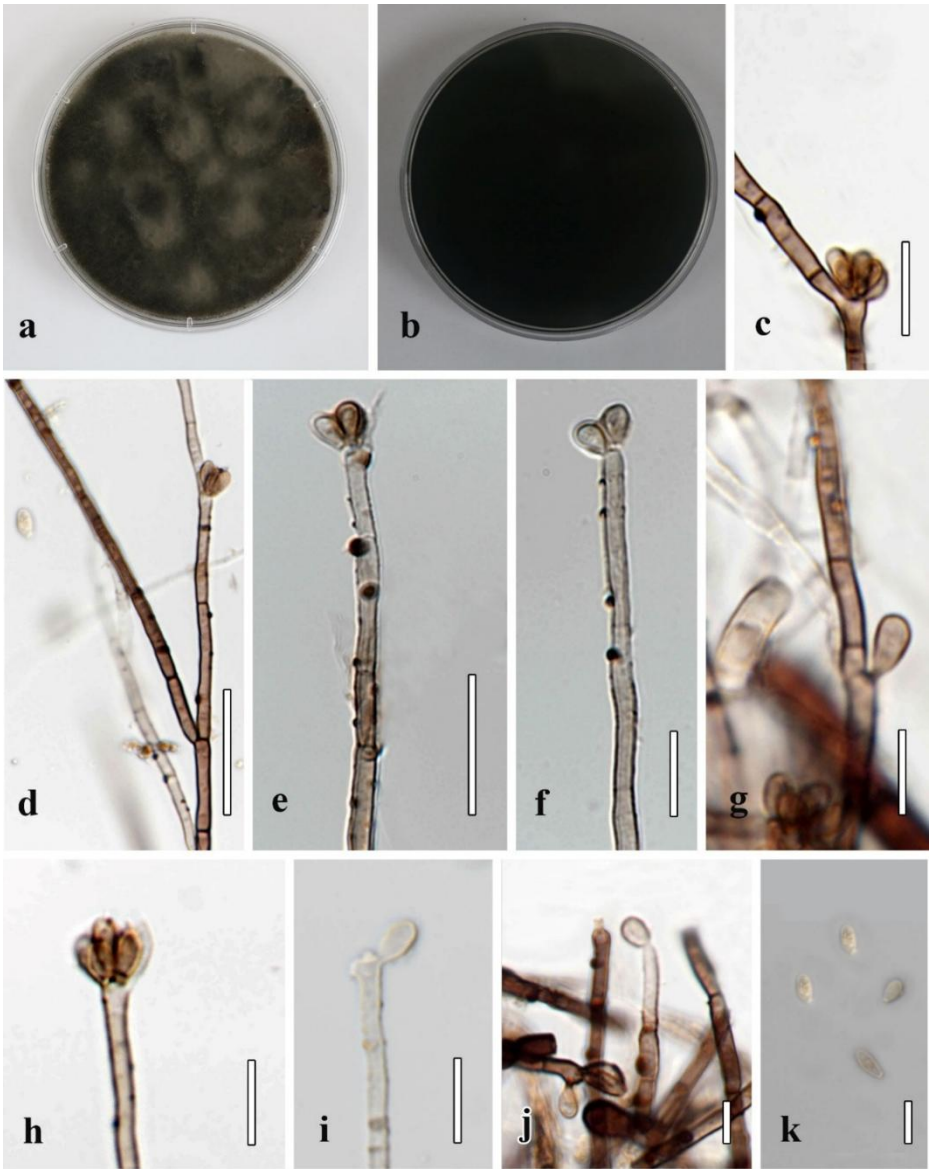

Figure 57 – *Daldinia narathiwatensis* (MFLUCC 24-0602, ex-type). a, b Colonies on the PDA, above (a), and below (b). c–k Conidiophores, conidiogenous cells and conidia. Scale bars: c = 15 μm, d = 30 μm, e = 20 μm, f–i = 10 μm, j–k = 5 μm.

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, sporulated after 25 days, surface gray, 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).

GenBank numbers – MFLUCC 24-0602: ITS = PV271901, *rpb2* = PV340531, *tub2* = PV477065.

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 (Fig. 56). Morphologically, *D. narathiwatensis* is similar to *D. ehretiae* (HMAS352914), but it can easily be distinguished by having septate hyphae, septate and brown conidiophores, longer and wider conidiophores (120–265.5 × 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, tub2* and ITS, 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* as a novel species based on morphological and phylogenetic evidence.

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 & 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 & 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 & Bhat 2005, Crous et al. 2020, Sun et al. 2021, Samarakoon et al. 2022). The sexual morph is characterized 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 phylogenetic tree for the genus is given in Fig. 58.

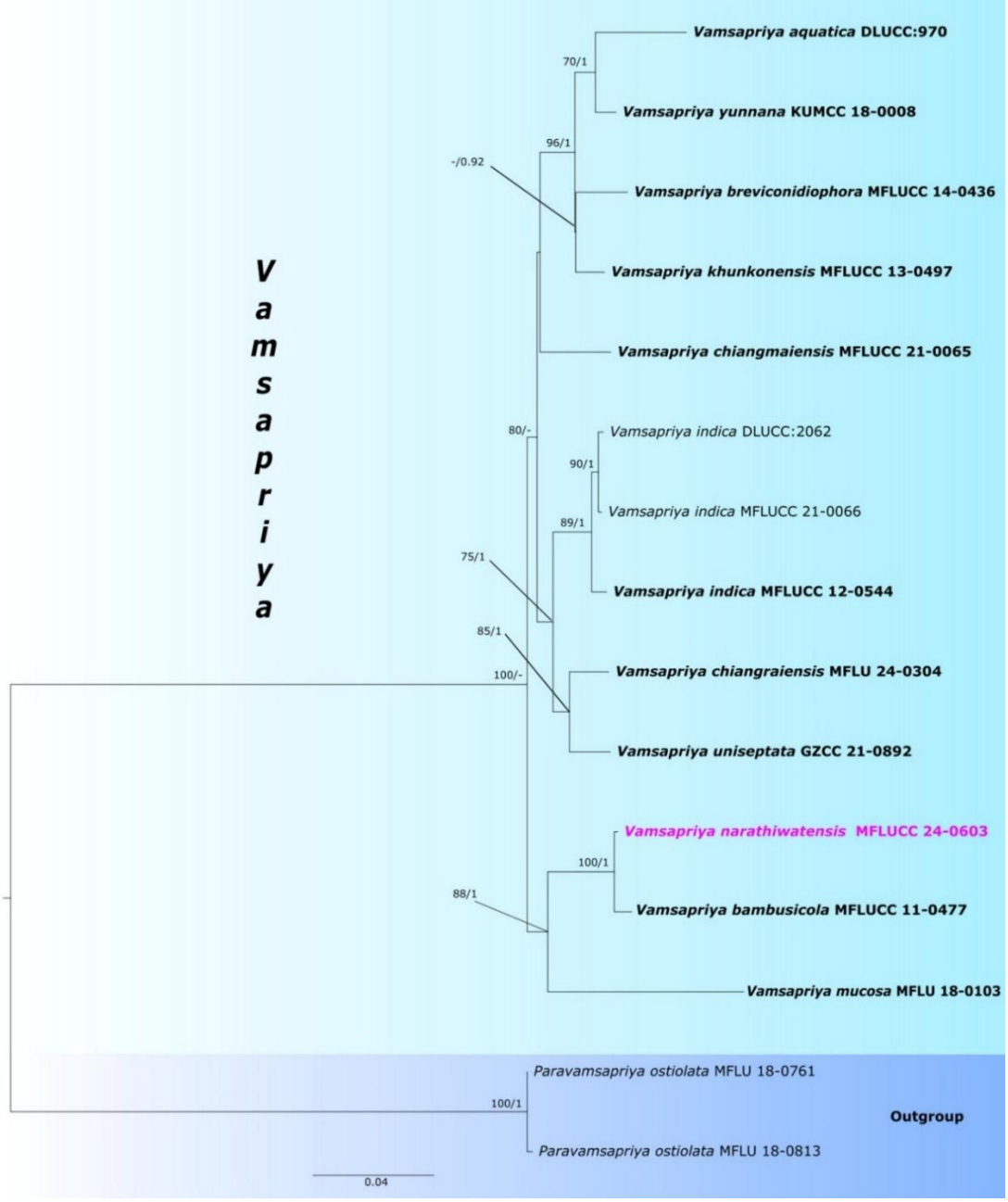

Figure 58 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, *rpb2, tub2,* and ITS sequences. The analysis includes 15 strains; total characters: 3604 (LSU: 839, *rpb2*: 1076, *tub2*: 1095, ITS: 594). *Paravamsapriya ostiolata* (MFLU 18-0761), and *P. ostiolata* (MFLU 18-0813) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -9046.404 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.91486, AT = 1.00000, CG = 1.00000, CT = 6.17351, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

Vamsapriya narathiwatensis O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 59

Index Fungorum number: IF903553; Facesoffungi number: FoF17543

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*. **Asexual morph**: Hyphomycetous. *Colonies* on the host scattered or sometimes gregarious, brown. *Mycelium* mostly immersed, composed of septate, branched, 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 ($\bar{x}$ = 11.5 × 4 µm, n = 20), monotretic, integrated, terminal, cylindrical to clavate, brown. *Conidia* 16–47.5 × 6–9.5 µm ($\bar{x}$ = 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. **Sexual morph**: Not observed.

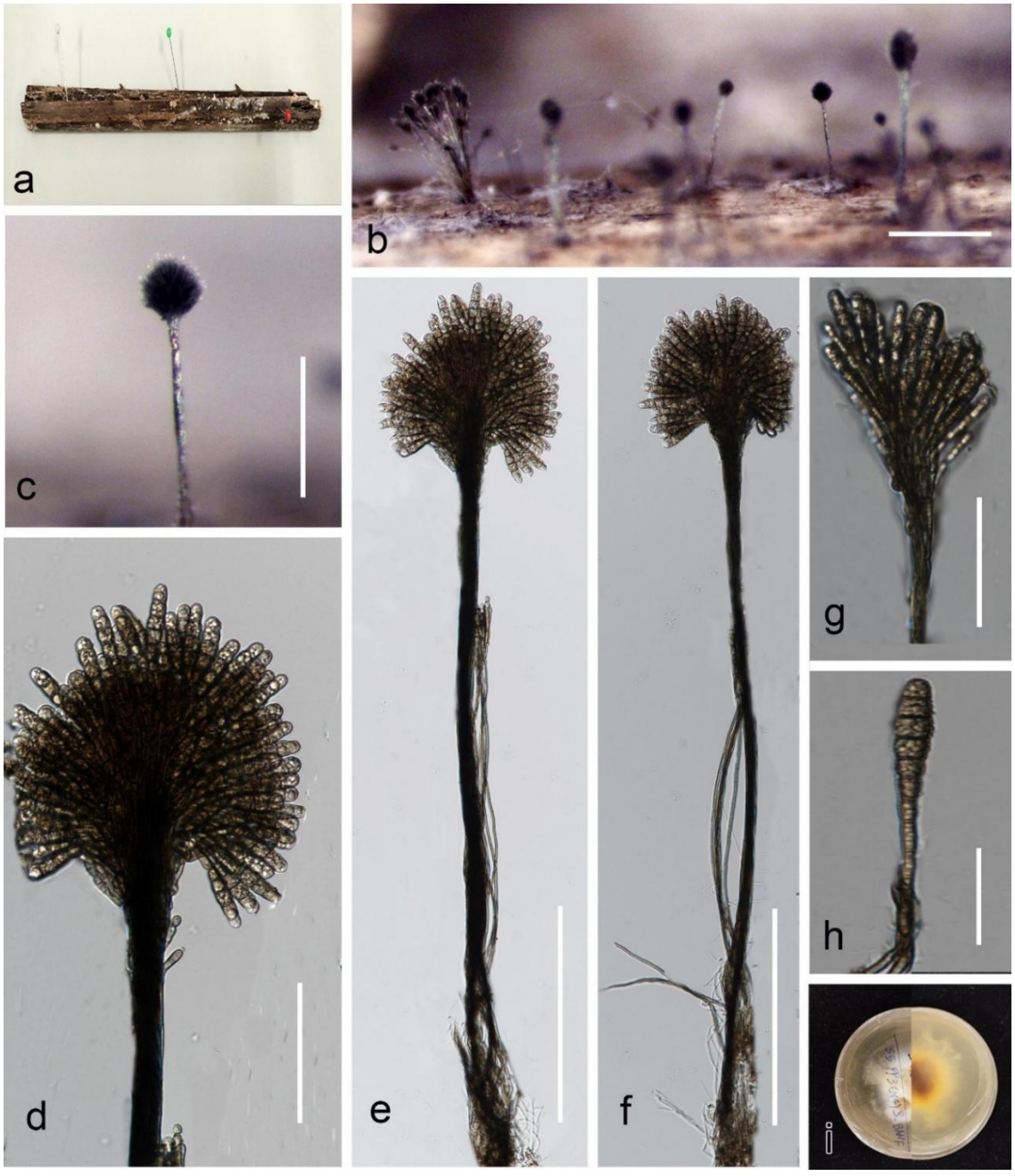

Figure 59 – *Vamsapriya narathiwatensis* (MFLU 24-0518, holotype). a Host. b Colonies on the host substrate. c–f Conidiophores and conidia. g, h Conidiogenous cells and developing conidia. i Colonies on the PDA. Scale bars: b = 400 μm, c = 200 μm, d, g = 50 μm, e, f = 150 μm, h = 20 μm.

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 center, reverse grayish yellow with a whitish margin and brown center.

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 =PV952911, LSU = PV952913, *rpb2* = PV955011.

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 (Fig. 58). 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* genera *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 & 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 Fig. 60.

Neoleptodontidium narathiwatense O. Karimi, R. Asghari & K.D. Hyde, sp. nov. Fig. 61

Index Fungorum number: IF903554; Facesoffungi number: FoF17544

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 gray 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.

GenBank numbers – MFLUCC 24-0604: ITS = PV271902, LSU = PV271941, *rpb2* = PV635145, *tub2* = PV635146. Additional sequences: ITS = PV483412, *rpb2* = PV340532, *tub2* = PV477066

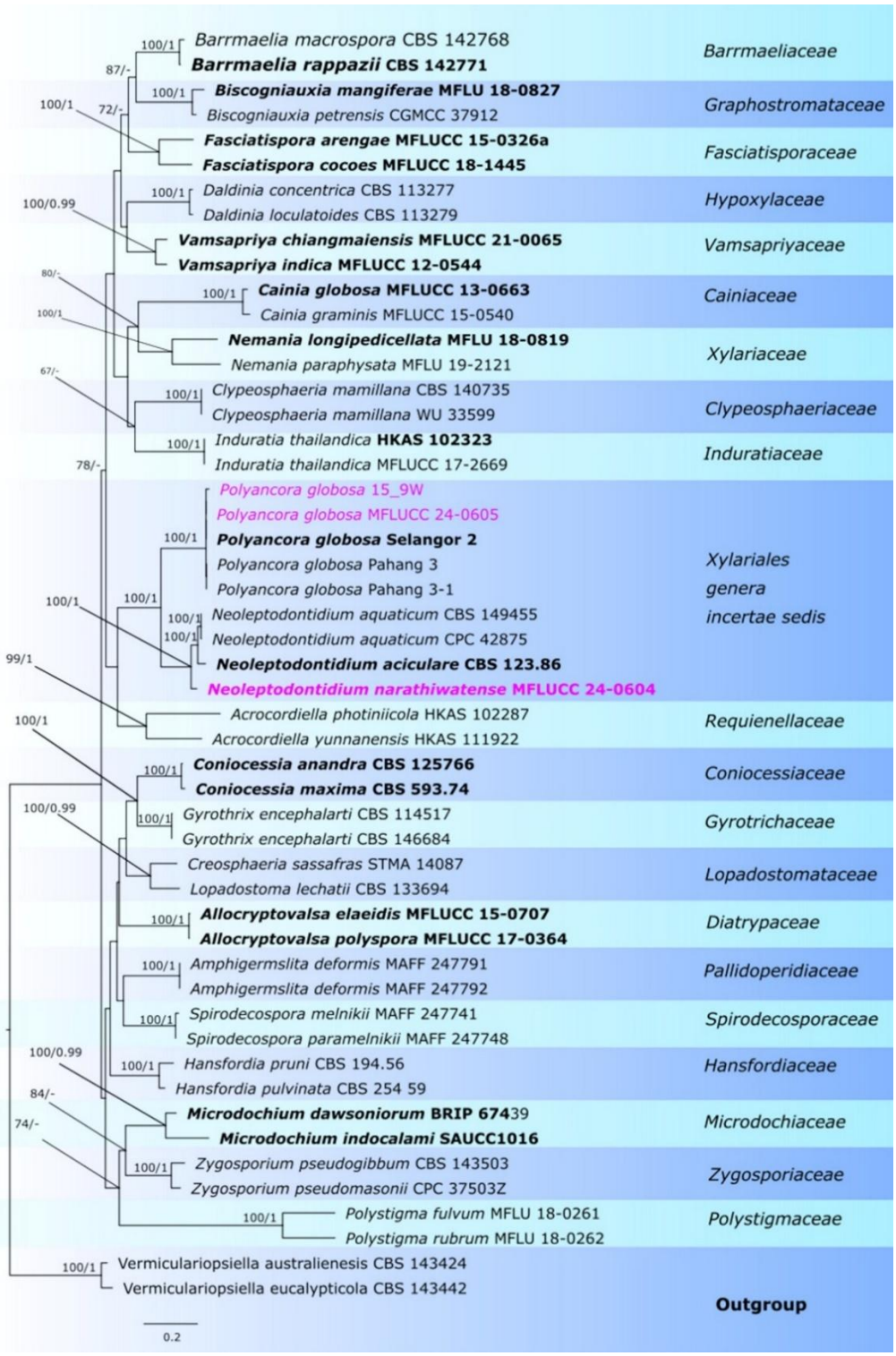

Figure 60 – Phylogram of maximum likelihood phylogenetic analysis based on combined LSU, *rpb2, tub2,* and ITS sequences. The analysis includes 51 strains; total characters: 3409 (LSU: 859, *rpb2*: 1020, *tub2*: 982, ITS: 548). *Vermiculariopsiella australienesis* (CBS 143424), and *V. eucalypticola* (CBS 143442) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -90626.770 is presented. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.32926, AG = 3.32712, AT = 1.32926, CG = 1.00000, CT = 5.67904, GT = 1.00000. The tree topology of the ML analysis is similar to the Bayesian analysis. 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.

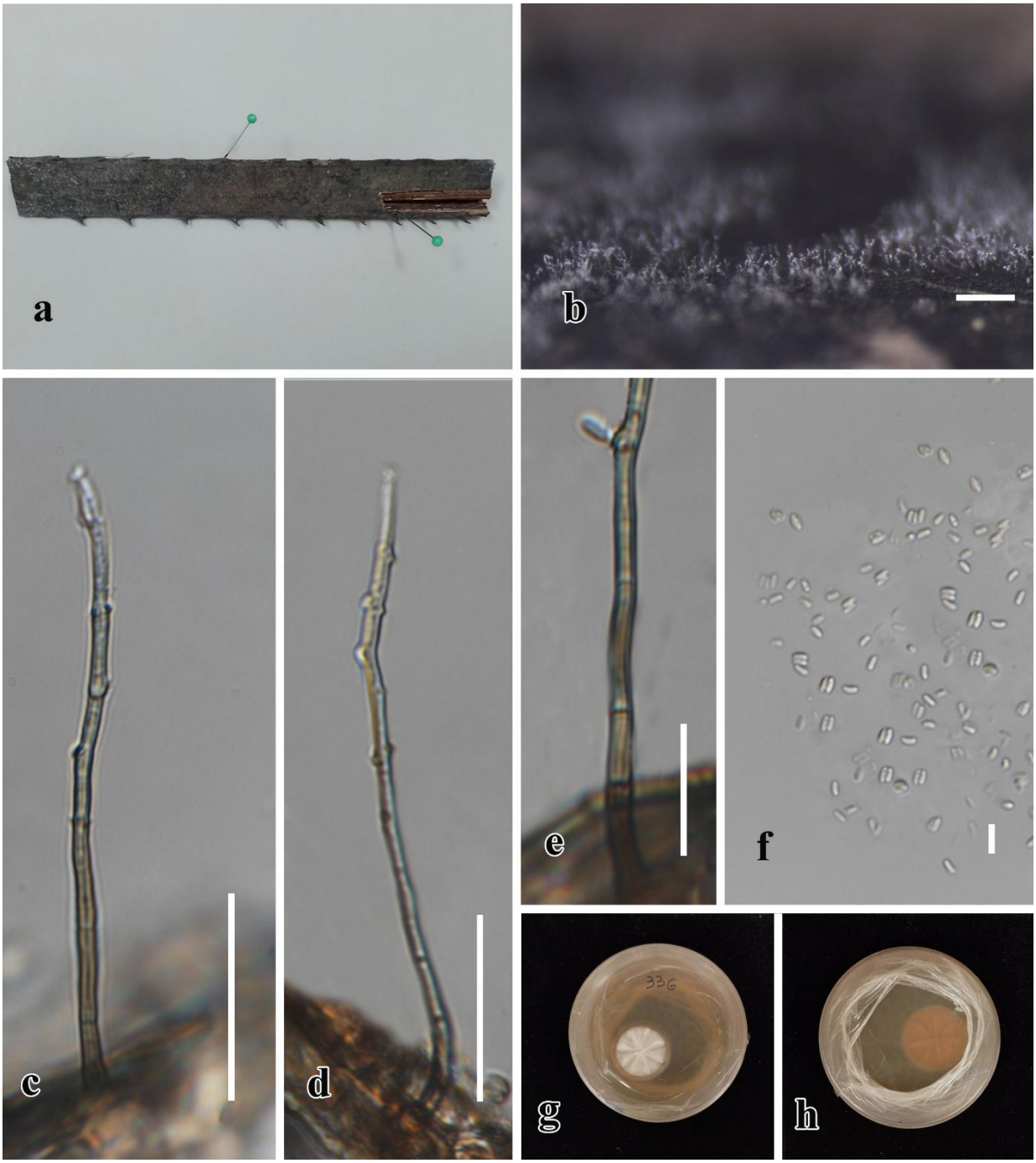

Figure 61 – *Neoleptodontidium narathiwatense* (MFLU 24-0519, holotype). a Host. b Colonies on the host substrate. c–e Conidiophores and conidiogenous cells. f Conidia. g, h Colonies on the PDA. Scale bars: b = 20 µm, c–e = 25 µm, f = 5 µm.

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 (Fig. 60). 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 & 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 a novel species based on morphological and phylogenetic evidence.

Polyancora Voglmayr & C. Yule, Mycological Research 110 (10): 1247 (2006)

Voglmayr & 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, Mycol. Res. 110 (10): 1247 (2006) Fig. 62

Index Fungorum number: IF500736; Facesoffungi number: FoF17545

Saprobic on the submerged petiole of *Eleiodoxa conferta*. **Asexual morph:** Hyphomycetous. *Colonies* on the host effuse, scattered or in small groups, whitish gray. *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 petiole 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 & 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 (Fig. 60). 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 & 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.

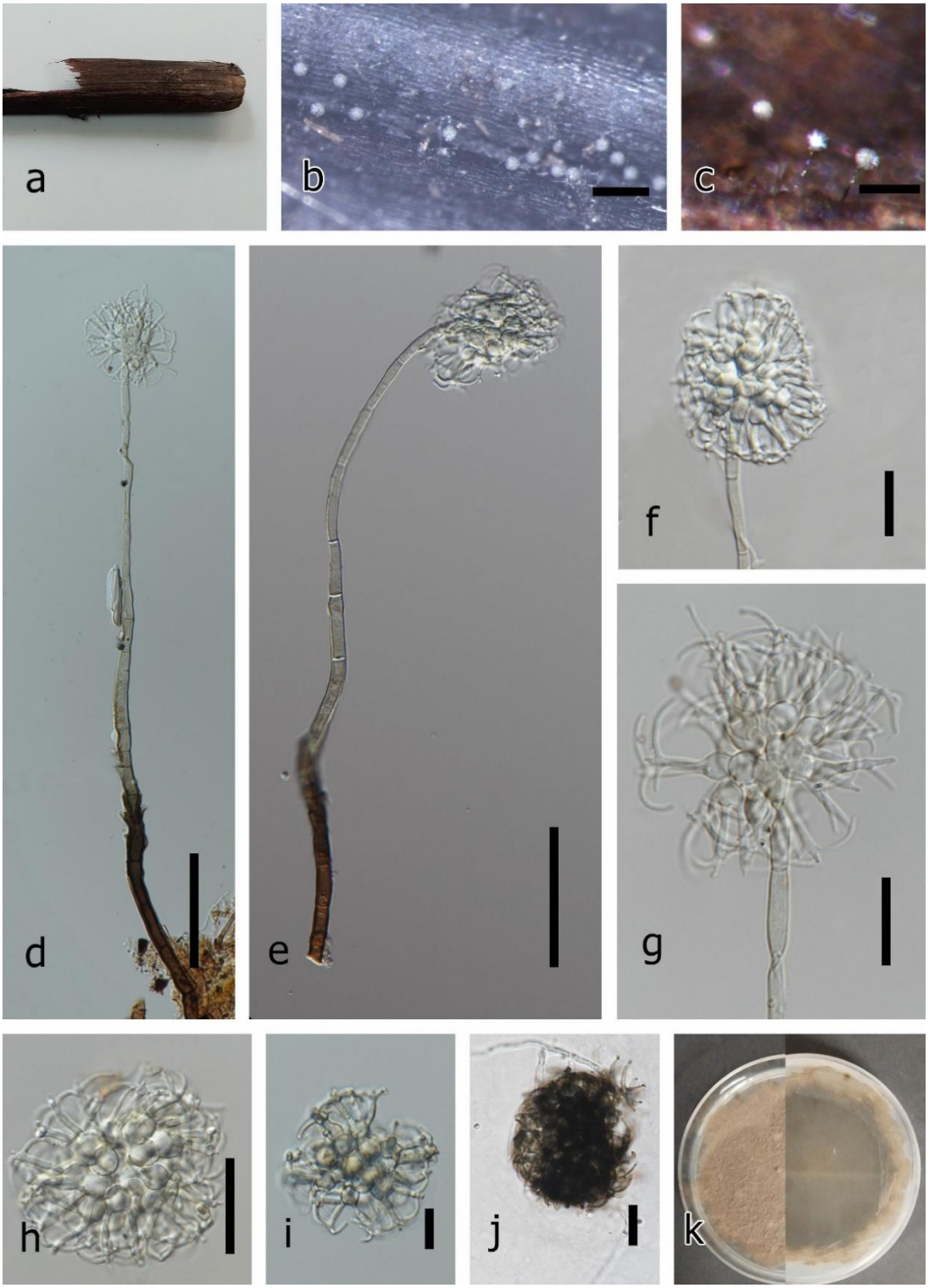

Figure 62 – *Polyancora globosa* (MFLU 24-0520, a new host and geographical record). a Host. b, c Colonies on the host substrate. d, e Conidiophores. f, g Conidiogenous cells and conidia. h, i Conidia. j A germinated conidium. k Colonies on the PDA. Scale bars: b = 200 µm, c = 125 µm, d–e = 60 µm, f–i = 15 µm.

Distribution of Peat Swamp *Asomycota*

Based on our fungal collection from the peat swamp habitat, we present the distribution of peat swamp *Ascomycota* across various classes (Fig. 63), orders (Fig. 64), and families (Fig. 65) (Karimi et al. 2024a, b, this study). The peat swamp fungi identified in this study belong to *Ascomycota*, distributed across three classes, including *Sordariomycetes* (57%), *Dothidiomycetes* (38%) and *Leotiomycetes* (5%) (Fig. 63).

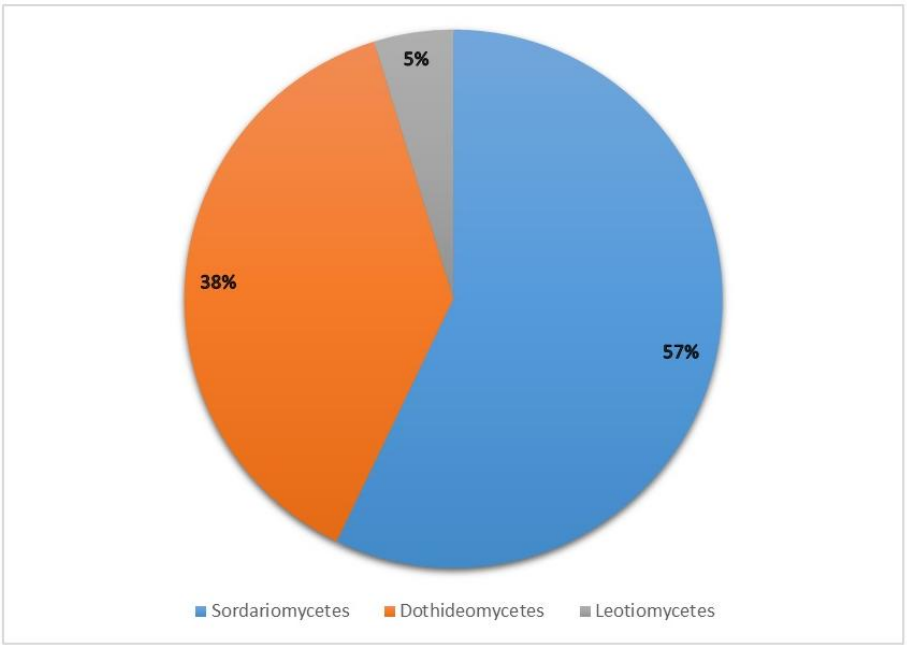

Figure 63 – Distribution of peat swamp *Ascomycota* in three classes.

The recorded taxa were distributed across 18 orders, with *Tubeufiales*, *Chaetosphaeriales*, *Xylariales*, and *Pleosporales* being the dominant orders (Fig. 64).

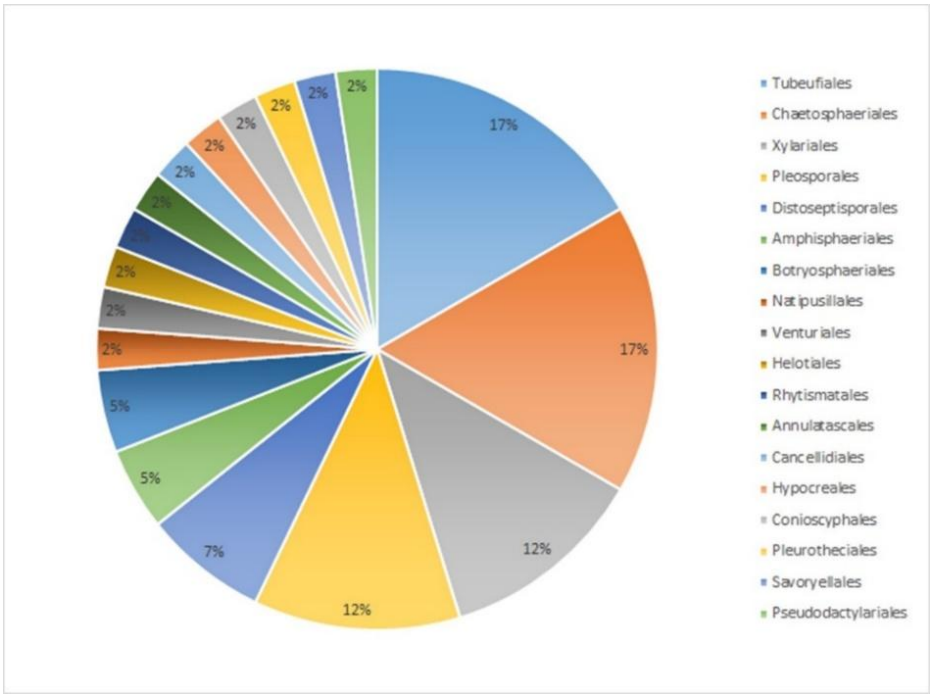

Figure 64 – Distribution of peat swamp *Ascomycota* in 18 orders.

The recorded species are distributed among 25 families, with 15 of them in *Sordariomycetes*, nine in *Dothideomycetes* and one in *Leotiomycetes*. *Tubeufiaceae* is the largest family, followed by *Chaetosphaeriaceae* and *Distoseptisporaceae* (Fig. 65).

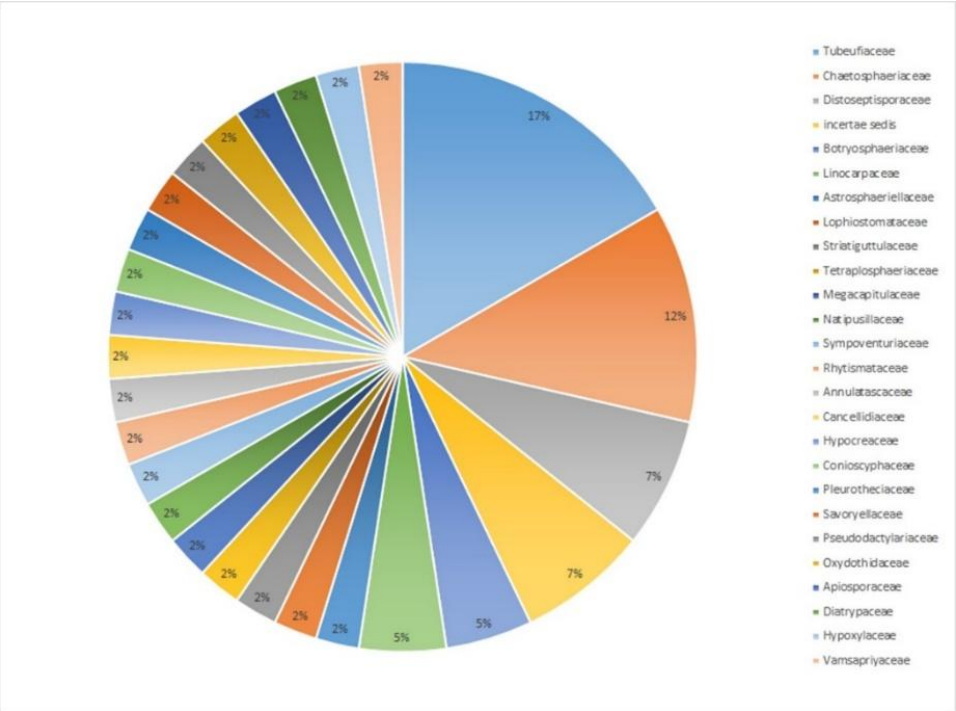

Figure 65 – Distribution of peat swamp *Ascomycota* in 25 families.

DISCUSSION

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, b, 2007, 2008, 2010a, b, Pinnoi et al. 2003a, b, 2004, 2006, 2009, 2010). 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.

From this research, we introduced one new genus, 25 new species and 16 new hosts, geographical and habitat records based on morphology and phylogeny. The identified fungal taxa belong to *Ascomycota*, mosthly distributed within *Tubeufiales*, *Chaetosphaeriales*, *Xylariales*, and *Pleosporales*. 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.

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 & Yule 2006). This result underscores the importance of conserving this environment.

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.

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*) (Karimi et al. 2024a). Another example is their report of undetermined species of *Annulatascus*, some of which were later transferred to other genera, including *Longivarius* (Dong et al. 2021), 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.

In this study, we describe 25 novel species and whenever possible, we included additional isolates to support the introduction of new species. Introducing a novel species based on multiple collections, isolates, or specimens can reduce errors in isolation or sequencing, supply more fungal material for preservation, and offer stronger evidence for taxonomic placement, especially in cryptic fungal groups. Additionally, it provides more information to investigate interspecies variation. However, recollecting the same species or obtaining additional isolates is not always feasible, particularly in habitats such as peat swamp forests, where waterlogged conditions make sampling difficult. Although additional specimens strengthen the description of a new species, the use of a single specimen is not prohibited by the *International Code of Nomenclature for algae, fungi, and plants* (Turland et al. 2018). Introducing a new species based on a single collection, specimen, or isolate is common in fungal taxonomy, especially in understudied locations or among poorly known fungal groups. Avoiding the description of such taxa can result in the loss of important taxonomic information and hinder conservation efforts (Cazabonne et al. 2024). For example, the marine fungus *Lulworthia fundyensis* was introduced from a single specimen based on molecular data, despite limited morphological information (Crous et al. 2022).

As previously mentioned, peat swamp forests are endangered ecosystems threatened by global warming and human activities. In this study, we aim to generate sequence data for accurate fungal identification and contribute to the conservation of fungal taxa before shifts in community composition or possible extinction occur. Waiting for more specimens or isolates is time-consuming and may hinder conservation efforts for microorganisms in such habitats, which are sometimes home to rare species like *Polyancora globosa*. In our study, we followed an approach combining sufficient morphological evidence with multigene phylogenetic analysis (Chethana et al. 2021). As the sequencing results aligned with morphological observations, we interpret this as evidence of correct isolation. In several species, sporulation occurred in culture, which further confirmed morphological

features. Additionally, all sequenced gene regions yielded consistent results, indicating accurate sequencing. Cazabonne et al. (2024) argue that species descriptions can be validly based on a holotype alone, even without additional specimens or isolates, and suggest that the drawbacks of publishing single-specimen species are outweighed by the risks of withholding data. Waiting for more material should not delay taxonomic progress. In cases where a new species was described from a single isolate, we provided sufficient supporting evidence rather than delaying publication in anticipation of additional material. This approach contributes to the documentation, conservation, and preservation of fungal taxa in peat swamp forests. Furthermore, both the specimens and cultures are deposited in collections for future study if needed.

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