Article

Morphology, phylogeny, host association and geography of fungi associated with plants of Annonaceae, Apocynaceae and Magnoliaceae

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Abstract

This paper elaborates the advances made in the study of morphology, phylogeny, host association and geography of novel and interesting fungi in China and Thailand. We documented saprobic microfungi from dead twigs of different plant hosts from Annonaceae (*Anomianthus dulcis*, *Cananga odorata* and *Desmos chinensis*), Apocynaceae (*Alstonia scholaris*) and Magnoliaceae (*Magnolia champaca*, *M. garrettii* and *M. liliifera*) in Yunnan Province, China and northern Thailand. Descriptions, illustrations and discussions on the familial placement of taxa are given based on phylogeny and morphological data. One new genus *Muriformispora* in Neohendersoniaceae (Dothideomycetes) and twelve new species, *Acrocalymma magnoliae*, *Diaporthe chiangmaiensis*, *Fuscostagonospora magnoliae*, *Gyrothrix anomianthi*, *Hermatomyces anomianthi*, *Muriformispora magnoliae*, *Neomassaria alstoniae*, *N. thailandica*, *Neoroussoella thailandica*, *Peroneutypa anomianthi*, *Pseudochaetosphaeronema magnoliae* and *Torula canangae* are introduced. An amended account of *Hermatomyces* is provided to include the sexual morph of the genus. New host records or new country records are provided for *Acrocalymma pterocarpi*, *A. walkeri*, *Amphisphaeria micheliae*, *Angustimassarina populi*, *Aurantiascoma minimum*, *Diaporthe musigena*, *D. pterocarpi*, *Eutypella citricola*, *Gyrothrix oleae*, *Hermatomyces sphaericus*, *Lasiodiplodia crassispora*, *L. exigua*, *L. ponkanicola*, *L. pseudotheobromae*, *L. thailandica*, *L. theobromae*, *Magnibotryascoma kunmingense*, *Memnoniella ellipsoidea*, *Melomastia clematidis*,

M. thamplaensis, *Neoroussoella entadae*, *Nectria pseudotrichia*, *Nigrograna thymi*, *Periconia byssoides*, *P. pseudobyssoides*, *Phaeosphaeria sinensis*, *Pseudopithomyces chartarum*, *Pseudofusicoccum adansoniae*, *Rhytidhysteron neorufulum*, *Setoapiospora thailandica* and *Xenoroussoella triseptata*.

Keywords – 12 new species – Ascomycota – Dothideomycetes – Multi-locus phylogeny – Sordariomycetes – Systematics

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Introduction

    Fungi are diverse and ubiquitous in terrestrial, freshwater and marine ecosystems and form an integral component of life's genetic diversity (Hyde et al. 2020b, Lücking et al. 2020). They are a heterogeneous group of organisms that show great variation in morphology, reproduction, life cycles and modes of dispersal (Promputtha et al. 2007, Lofgren et al. 2018). In general, microfungi can be found as the asexual morphs that produce conidia on conidiophores and the sexual morph produces a closed structure known as ascoma (sporocarps or fruit bodies) that protect asci and ascospores and use a variety of ways to release spores (Money 2016). These sporulating fungi produce numerous sexual and asexual spores and take advantage of multiple abiotic vectors (wind and precipitation) and biotic vectors such as plants (seeds and senesced leaves) and animals (fur, feathers, and gut microbiomes). In many cases, humans also facilitate successful dispersal into new habitats (Golan & Pringle 2017).

    Fungi are an essential component in the most ecosystems and play key roles as decomposers, mutualists, and pathogens (Schmit & Mueller 2007). The majority of fungi are decomposers, while some are partners in lichens and mycorrhizal symbioses, and some are pathogens of plants and animals (particularly invertebrates). Fungal decomposers grow not only on woody and other plant tissues but also on herbivore dung (Money 2016). Fungal decomposers maintain ecological balance by recycling nutrients and degrading organic matter (lignocellulose) in wood and leaves (Bucher et al. 2004, Hyde et al. 2018). The decomposition of organic materials maintains the balance between soil carbon storage and CO_2 emission into the atmosphere and increases the availability of mineral nutrients in the soil that can be utilized for plant growth (van der Wal et al. 2013). In addition, fungi are widely utilized for antibiotics, enzymes, food production, and the pharmaceutical industry. In addition, they function as agents for biological control of a wide range of plant pathogens, crop pests and bioremediation of chemical spills (Lodge 1997, Lücking et al. 2020, Thambugala et al. 2020).

    A study by Hawksworth & Lucking (2017) emended the global fungal species richness of 1.5 million to an updated range of 2.2 to 3.8 million. Hyde et al. (2020) discussed the various data that is lacking and needed to estimate fungal numbers which have ranged from 0.5 to 13.2 million species. Hyde et al. (2018, 2020) suggested that poorly studied countries and hosts, or understudied habitats or niches, harbour diverse fungal species that will lead to the discovery novel taxa (Hyde et al. 2018, 2020). Microfungi show a higher degree of diversity where numerous novel species have been discovered in tropical and sub-tropical regions. These regions facilitate fungal infections because they have good biotic and abiotic factors such as highly diverse host plants and microhabitats that drive a higher degree of biodiversity (Piepenbring et al. 2011, Guzman & Heil 2014). Saprobic fungi can be found in four phyla namely, Ascomycota, Basidiomycota, Chytridiomycota and Zygomycota (van der Wal et al. 2013). Zygomycota consists of over 1000 described species and the Mucoromycotina includes approximately 300 described species that are recognized as opportunistic saprotrophs (van der Wal et al. 2013). Chytridiomycota is generally considered as an aquatic fungal group. However, it was identified that those saprobic chytrids fungi are present in non-vegetated, high-elevation soils (van der Wal et al. 2013). Basidiomycota consists of approximately 40 000 described species (He et al. 2022) and among them the majority of saprobic basidiomycetes are found in the subphylum Agaricomycotina (van der Wal et al. 2013). Ascomycota is the largest phylum of fungi comprising more than 33,000 named species and numerous undescribed fungi (Money 2016). In this study, we focus mainly on two classes of Ascomycota *viz.* Dothideomycetes and Sordariomycetes. Dothideomycetes is the largest class and most ecologically diverse group of fungi consisting of endophytes, epiphytes, saprobes, human and plant pathogens, lichens, and lichenicolous taxa (Hongsanan et al. 2020a). They are characterized by bitunicate asci with fissitunicate dehiscence and they occur on a broad range of hosts in aquatic

and terrestrial habitats (Hongsanan et al. 2020a). The second-largest class is Sordariomycetes comprising a diverse range of taxa (Maharachchikumbura et al. 2015, 2016). They are characterized by perithecial ascomata and inoperculate unitunicate or non-fissitunicate asci (Maharachchikumbura et al. 2015, 2016, Hyde et al. 2020b).

Taxonomy is crucial to understanding life's diversity through exploring and discovering fungi in nature (Hibbett 2016). Nomenclature promotes universally accepted scientific names that reflect relationships between species and thereby strengthen communication among scientists and the public (Hibbett 2016). The taxonomy of microorganisms especially fungi is challenging due to their extreme diversity in terms of morphological features, nutritional modes and asexual-sexual fungal morphs (Hibbett 2016). In the early nomenclature, fungal names often related to their host plants on which the holotype was collected. For example, *Pestalotiopsis* species were named based on host plants names (Maharachchikumbura et al. 2014). However, many scientists argued that *Pestalotiopsis* species are generally not host-specific as they probably have a wide range of hosts and substrates (Jeewon et al. 2004, Lee et al. 2006). This indicates that many traditional host-based *Pestalotiopsis* species might be spurious (Maharachchikumbura et al. 2014). Similarly, most *Aplosporella* species have been described based on their host occurrence, however, presently available data suggested that the majority of these species are not host-specific (Damm et al. 2007). Therefore, it is suggested to employ phenotypic analyses coupled with phylogenetic analyses to delimitate species boundaries (Maharachchikumbura et al. 2014, 2021). However, it is essential to report host association and geographic distribution of fungi for the better understanding of the fungi and their interactions with natural environment. This study aims to investigate saprobic microfungi from dead twigs of different plant hosts from Annonaceae, Apocynaceae and Magnoliaceae in northern Thailand and Yunnan Province, China. We describe novel and existing fungi in China and Thailand based on both morphology and multi-locus phylogeny.

Materials & Methods

Dead twigs attached to different host plants were collected in this study. The host plant species were selected according to a selection design (Fig. 1). We selected three plant species from family 2 (order 1) and one plant genus from family 1 (order 1) in Thailand according to the design. Then, we selected one plant species from family 3 which belong to a different order (order 2) in Thailand. In addition, we selected the same plant genus from family 1 (order 1) in China (not included in Figure 1).

According to the above design we selected *Anomianthus dulcis*, *Cananga odorata*, *Desmos chinensis* from Annonaceae (Magnoliales) and *Magnolia* sp. from Magnoliaceae (Magnoliales) in Thailand. Further, we selected *Alstonia scholaris* from Apocynaceae (Gentianales) in Thailand. In addition, we selected *Magnolia* sp. from Magnoliaceae (Magnoliales) in China. The isolated fungal species are given in the Table 1.

The study area of northern Thailand has the average annual temperature ranges between 20 and 34°C. The rainy season is from May to October, with average annual rainfall ranging between 600 and >1000 mm (Arunrat et al. 2021). The study area of Yunnan, China has annual average temperature of 6.90–27.10°C and the wet season is from May to October with average annual rainfall ranging 560.00–2300.00 mm (Yang et al. 2019a). Micro-morphological characteristics were examined with an OLYMPUS SZ61 compound microscope while the images were recorded with a Canon EOS 600D digital camera mounted to a Nikon ECLIPSE 80i compound microscope. All microscopic measurements were made with the Tarosoft (R) image framework v. 0.9.0.7 and images were further processed with Adobe Photoshop CS3 Extended version. Pure cultures were obtained by single spore isolation as outlined by Senanayake et al. (2020). Germinating ascospores were transferred aseptically to potato dextrose agar (PDA) and culture characteristics, such as growth rate and colony characteristics, were determined from cultures grown on PDA at room temperature (25°C) for one week.

The specimens cited in this paper were deposited at the Mae Fah Luang University Herbarium (Herb. MFLU), Chiang Rai, Thailand. The living fungal cultures recovered in this study

were deposited at the Mae Fah Luang University Culture Collection (MFLUCC), Thailand and Kunming Institute of Botany Culture Collection (KUMCC), China. Faces of Fungi numbers and Index Fungorum numbers were registered as described in Jayasiri et al. (2015) and Index Fungorum (2022), respectively. Recent publications that were used to introduce new species were mentioned in the relevant notes of result section.
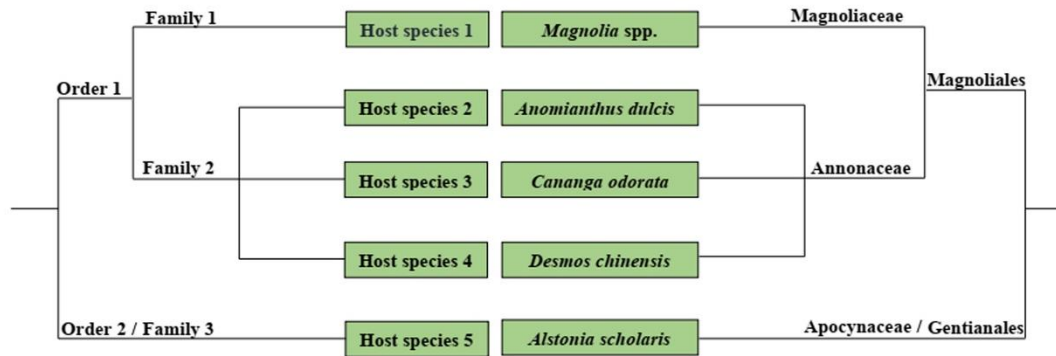

Figure 1 – Host plant species used in this study.

DNA extraction and PCR amplification

One-week old pure cultures on PDA were used for DNA extraction (Dissanayake et al. 2020). The mycelia were scraped off from pure cultures and genomic DNA was extracted using Biospin fungus genomic DNA kit (BioFlux®, P.R. China) following the manufacturer's protocol. DNA was kept at 4 °C for the DNA amplification of genes and maintained at –20 °C for long term storage.

Polymerase chain reaction (PCR) was used to amplify the internal transcribed spacers (ITS) and partial gene regions of 28S ribosomal RNA (LSU), 18S ribosomal RNA (SSU), RNA polymerase II second largest subunit (RPB2), β-tubulin (*tub2*), actin (ACT), glyceraldehyde-3-phosphate dehydrogenase (GADPH), chitin synthase 1 (CHS–1), calmodulin (CAL) and translation elongation factor 1–alpha (*tef*1) where appropriate using primers as in de Silva et al. (2021). The final volume of the PCR reaction was 25 μl, containing 1 μl of DNA template, 1 μl of each forward and reward primers, 12.5 μl of 2×Easy Taq PCR SuperMix (a mixture of *EasyTaq* TM DNA Polymerase, dNTPs, and optimized buffer, Beijing TransGen Biotech Co., Ltd., Beijing, P.R. China) and 9.5 μl of ddH2O. Amplification of gene regions were performed following Li et al. (2020a) for ITS, LSU, SSU, *tef*1, RPB2, *tub2*, Gomes et al. (2013) for CAL and Weir et al. (2012) for ACT, GADPH, CHS–1. PCR purification and sequencing of amplified PCR products were done by Shanghai Sangon Biological Engineering Technology & Services Co., Ltd, P.R. China.

Newly generated nucleotide sequences were deposited in the GenBank and the accession numbers were mentioned in relevant entries. Sequences of the individual loci were aligned with MAFFT v. 7 online version (Yamada et al. 2016) using default settings. BioEdit v. 7.0.5.2 (Hall 1999) software was used to refine the alignments manually where necessary and to exclude incomplete portions at the ends of the sequences before the analyses.

Phylogenetic analyses

Maximum likelihood analysis was performed in RAxML GUI v. 1.3 (Silvestro & Michalak 2012) and maximum parsimony analysis was done in PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2002). Evolutionary models for phylogenetic analyses were selected independently for each locus using MrModeltest v. 3.7 (Posada & Crandall 1998) under the Akaike Information Criterion (AIC). Parameters for maximum likelihood were set to rapid bootstrapping with 1000 replicates and the GTR + GAMMA model of nucleotide substitution. Bayesian analysis was conducted in MrBayes v. 3.1.2 (Huelsenbeck & Ronqvist 2001). Parameters

of Bayesian analysis include markov chains that were run for 1000000 generations, trees were sampled at every 100th generation (printfreq = 100), leading to 10000 trees. Among these trees, 20% of the initial trees were discarded and the remaining trees were used to evaluate posterior probabilities (PP) in the majority rule consensus tree. Parameters for maximum likelihood were set to rapid bootstrapping with 1000 replicates using the GTR + GAMMA model of nucleotide substitution. Maximum parsimony was run with the heuristic search option, random taxon addition, tree bisection-reconnection (TBR) for the branch swapping algorithm and 1000 random sequence additions, with maxtrees set at 1000. Gaps were treated as missing data. Tree Length [TL], Consistency Index [CI], Retention Index [RI], Relative Consistency Index [RC] and Homoplasy Index [HI] were calculated for the most parsimonious tree. Phylograms were visualized with FigTree v1.4.0 (Rambaut 2012) and annotated in Microsoft PowerPoint (2010). We conducted different analyses to obtain phylogenetic support and discussed results in respective entries.

Table 1 Fungal species isolated and identified in this study.

				Fungal Species	Host plant species				
					Magnolia	*Anomianthus dulcis*	*Cananga odorata*	*Desmos chinensis*	*Alstonia scholaris*
Dothideomycetes	Hysteriales	Hysteriaceae	*Rhytidhysteron*	*Rhytidhysteron neorufulum*	NI260[CH] NI287[TH]				
	Pleosporales	Acrocalymmaceae	*Acrocalymma*	*Acrocalymma pterocarpi* *Acrocalymma magnoliae* *Acrocalymma walkeri*	NI175[CH] NI209[TH] NI214[TH]	AND31[TH]			
		Amorosiaceae	*Angustimassarina*	*Angustimassarina populi* *Angustimassarina populi*	NI283[TH] NI286[TH]				
		Didymosphaeriaceae	*Pseudopithomyces*	*Pseudopithomyces chartarum*		AND22b[TH]			
		Fuscostagonosporaceae	*Fuscostagonospora*	*Fuscostagonospora magnoliae*	NI284[TH] NI285[TH]				
		Hermatomycetaceae	*Hermatomyces*	*Hermatomyces sphaericus*		AND5[TH]			AS16A[TH] AS16B[TH]
				Hermatomyces anomianthi		AND23[TH]			
		Macrodiplodiopsidaceae	*Pseudochaetosphaeronema*	*Pseudochaetosphaeronema magnoliae*	NI167[CH] NI197[TH]				
		Neohendersoniaceae	*Muriformispora*	*Muriformispora magnoliae*	NI261[CH]				
		Neomassariaceae	*Neomassaria*	*Neomassaria alstoniae* *Neomassaria thailandica*		AND4[TH]			AS14[TH]
		Nigrogranaceae	*Nigrograna*	*Nigrograna thymi*	NI269[CH]				
		Periconiaceae	*Periconia*	*Periconia byssoides* *Periconia pseudobyssoides*	NI273[CH]		CO10[TH]		
		Phaeosphaeriaceae	*Phaeosphaeria*	*Phaeosphaeria sinensis*	NI166[CH]				
		Roussoellaceae	*Neoroussoella*	*Neoroussoella entadae* *Neoroussoella thailandica*	NI213[TH] NI258[TH]				

Table 1 Continued.

				Fungal Species	Host plant species				
					Magnolia	*Anomianthus dulcis*	*Cananga odorata*	*Desmos chinensis*	*Alstonia scholaris*
			Xenoroussoella	*Xenoroussoella triseptata*		AND11b^TH		DC9^TH	
		Teichosporaceae	*Magnibotryascoma*	*Magnibotryascoma kunmingense*	NI196^TH				
			Aurantiascoma	*Aurantiascoma minimum*	NI194^TH				
		Torulaceae	*Torula*	*Torula canangae*			CO1^TH		
Dothideomycetes orders *incertae sedis*	Botryosphaeriales	Botryosphaeriaceae	*Lasiodiplodia*	*Lasiodiplodia theobromae*	NI302^TH NI306^TH	AND13^TH			
				Lasiodiplodia microconidia		AND1^TH			
				Lasiodiplodia swieteniae	NI300^TH				
				Lasiodiplodia pseudotheobromae	NI325^TH		CO6^TH	DC7^TH	
				Lasiodiplodia aquilariae	NI305^TH				
				Lasiodiplodia pyriformis	NI326^TH				
		Phyllostictaceae	*Pseudofusicoccum*	*Pseudofusicoccum adansoniae*	NI320^TH	AND32^TH			AS15^TH
	Dyfrolomycetales	Pleurotremataceae	*Dyfrolomyces*	*Dyfrolomyces thamplaensis*		AND9^TH AND12^TH			
			Melomastia	*Melomastia clematidis*			CO12^TH		
	Muyocopronales	Muyocopronaceae	*Setoapiospora*	*Setoapiospora thailandica*		AND3^TH			
Sordariomycetes Subclass Diaporthomycetidae	Diaporthales	Diaporthaceae	*Diaporthe*	*Diaporthe musigena*	NI304^TH				
				Diaporthe pterocarpi					AS3^TH AS17^TH AS19^TH
				Diaporthe chiangmaiensis	NI207b^TH GMT8^TH				
Subclass Hypocreomycetidae	Hypocreales	Nectriaceae	*Nectria*	*Nectria pseudotrichia*		AND25^TH			
		Stachybotryaceae	*Memnoniella*	*Memnoniella ellipsoidea*			CO2^TH		
Subclass Xylariomycetidae	Amphisphaeriales	Amphisphaeriaceae	*Amphisphaeria*	*Amphisphaeria micheliae*					AS12a^TH
	Xylariales	Diatrypaceae	*Eutypella*	*Eutypella citricola*	NI329^TH				
			Peroneutypa	*Peroneutypa anomianthi*		AND6^TH			
	Xylariales Incertae sedis		*Gyrothrix*	*Gyrothrix oleae*				DC8^TH	
				Gyrothrix anomianthi		AND20^TH			

^CH = Specimens collected in China

^TH = Specimens collected in Thailand

Results

Class Dothideomycetes O.E. Erikss. & Winka
Subclass Pleosporomycetidae Schoch et al.
Hysteriales Lindau.
Hysteriaceae Chevall.

Hysteriaceae was established by Chevallier (1826) as 'Hysterineae'. Members of this family are characterized by having immersed to superficial, carbonaceous to coriaceous, navicular, hysterothecium, characteristically dehiscing by an invaginated slit or sulcus, bitunicate asci and hyaline to pigmented, one to multi-septate, or muriform ascospores (Hyde et al. 2013, Thambugala et al. 2016, Jayasiri et al. 2018). Nine genera are accepted in this family, *Gloniopsis*, *Graphyllium*, *Hysterium*, *Hysterobrevium*, *Hysterodifractum*, *Oedohysterium*, *Ostreichnion*, *Psiloglonium* and *Rhytidhysteron* (Hongsanan et al. 2020a).

Rhytidhysteron Speg.

Rhytidhysteron was introduced by Spegazzini (1881) to accommodate *R. brasiliense* and *R. viride*. Clements & Shear (1931) designated *R. brasiliense* as the type species. *Rhytidhysteron* species are characterized by closed and navicular ascomata, later opening by a longitudinal slit to become irregularly apothecioid at maturity and heavily pigmented, with thick-walled ascospores (Bohm et al. 2009, Thambugala et al. 2016, Hongsanan et al. 2020a). This genus has wide distribution of endophytes, saprobes and weak pathogens (Hyde et al. 2013, Kumar et al. 2019). In this study, we report on a new host record of *Rhytidhysteron neorufulum* from *Magnolia* sp. in China and Thailand.

Rhytidhysteron neorufulum Thambug. & K.D. Hyde, Cryptog. Mycol. 37(1): 110 (2016)

Fig. 3

Index Fungorum number: IF 551865, Faces of Fungi number: FoF 01840

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 900–1400 μm long, 450–600 μm high, 700–750 μm diam. ($\bar{x}$ = 1200 × 550 × 730 μm, n = 10), apothecioid, solitary to aggregated, superficial, black, coriaceous, elliptic or irregular in shape, with lenticular or irregular opening when wet, not striate, black or yellow at the center, when dry folded at the margin, forming an elongate slit. *Exciple* 90–110 μm wide, composed of dark brown to black, thick-walled cells of *textura angularis*. *Hamathecium* comprising 1.5–2.5 μm wide, dense, septate pseudoparaphyses, forming epithecium above the asci, enclosed in a gelatinous matrix. *Asci* 160–200 × 9–16 μm ($\bar{x}$ = 180 × 12 μm, n = 20), 8-spored, bitunicate, clavate to cylindrical, with a short, furcate pedicel, apically rounded, without a distinct ocular chamber. *Ascospores* 28–36 × 9 –12 μm ($\bar{x}$ = 30 × 11 μm, n = 40), uni-seriate, slightly overlapping, ellipsoidal to fusiform, slightly rounded or pointed at both ends, 1–3-septate, constricted at the septa, yellowish when immature, reddish-brown to brown when mature, without a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin undulate, dense, slightly raised, yellowish brown at the margin, brown in the centre; reverse: pale brown at the margin, dark brown in the centre.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI260 (MFLU 18-2644), living culture, MFLUCC 19-0035; Thailand, Chiang Rai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 9 January 2019, N. I. de Silva, NI287 (MFLU 21-0248), living culture, MFLUCC 21-0179.

Known hosts and distribution – On dead stems, dead wood of unidentified plant in Chiang Rai, Chiang Mai Provinces Thailand (Thambugala et al. 2016), dead twigs attached to *Magnolia* sp. in China and Thailand (this study).

GenBank numbers – (NI260): LSU: OK655812, ITS: OL413432, SSU: OL331091, *tef1*: OM117545, (NI287): LSU: OK655813, ITS: OL413433, SSU: OL331092.
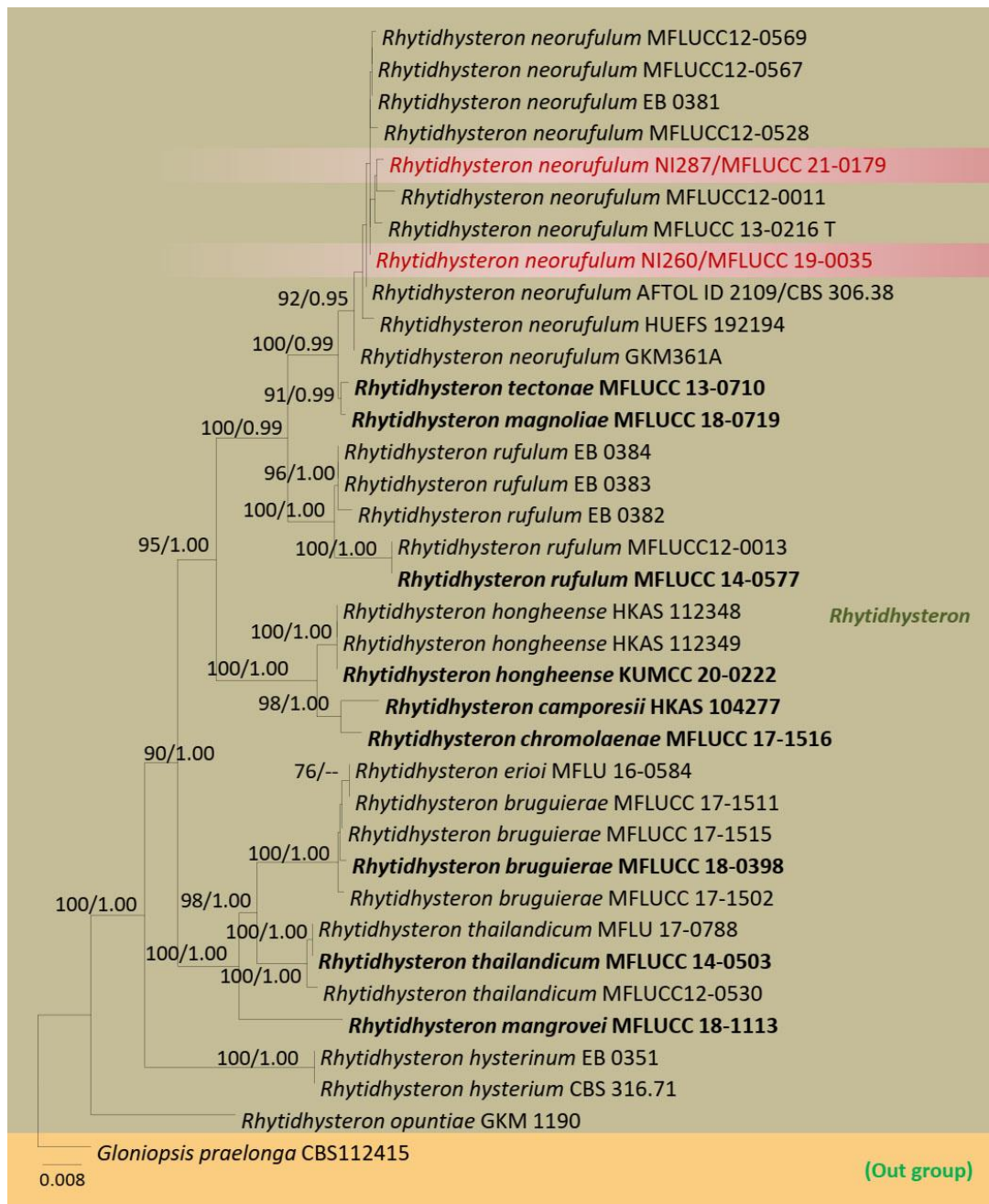
Figure 2 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, SSU and *tef1* sequence data. Related sequences of *Rhytidhysteron* were obtained from Wanasinghe et al. (2020). Thirty-six strains are included in the combined gene analyses comprising 3390 characters after alignment (950 characters for LSU, 1000 characters for SSU, 580 characters for ITS, 860 characters for *tef1*). *Gloniopsis praelonga* (CBS112415) is used as outgroup taxon. The best RAxML tree with a final likelihood value of -8813.420544 is presented. The matrix had 620 distinct alignment patterns, with 27.77% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red. Type and ex-type strains are in **black bold**.

Notes – *Rhytidhysteron neorufulum* was introduced by Thambugala et al. (2016) from decaying wood in Thailand. The morphological characteristics of our collection (MFLU 18-2644) tally well with *R. neorufulum* (MFLUCC 13-0316) in having superficial, black, coriaceous, elliptic or irregular shaped hysterothecia, clavate to cylindrical asci (185–220 × 9.5–13 μm *vs* 160–200 × 9 –16 μm) and ellipsoidal to fusiform, 1–3-septate, reddish-brown to brown ascospores (27–34 × 7 –

965

10.6 μm *vs* 28–36 × 9 –12 μm) (Thambugala et al. 2016). According to our combined multi-gene (LSU, ITS, SSU and t*ef1*) phylogenetic analyses, our collection nested with *R. neorufulum* isolates in a well-supported clade (92% ML, 0.95 BYPP). This is the first record of *R. neorufulum* on *Magnolia* species.
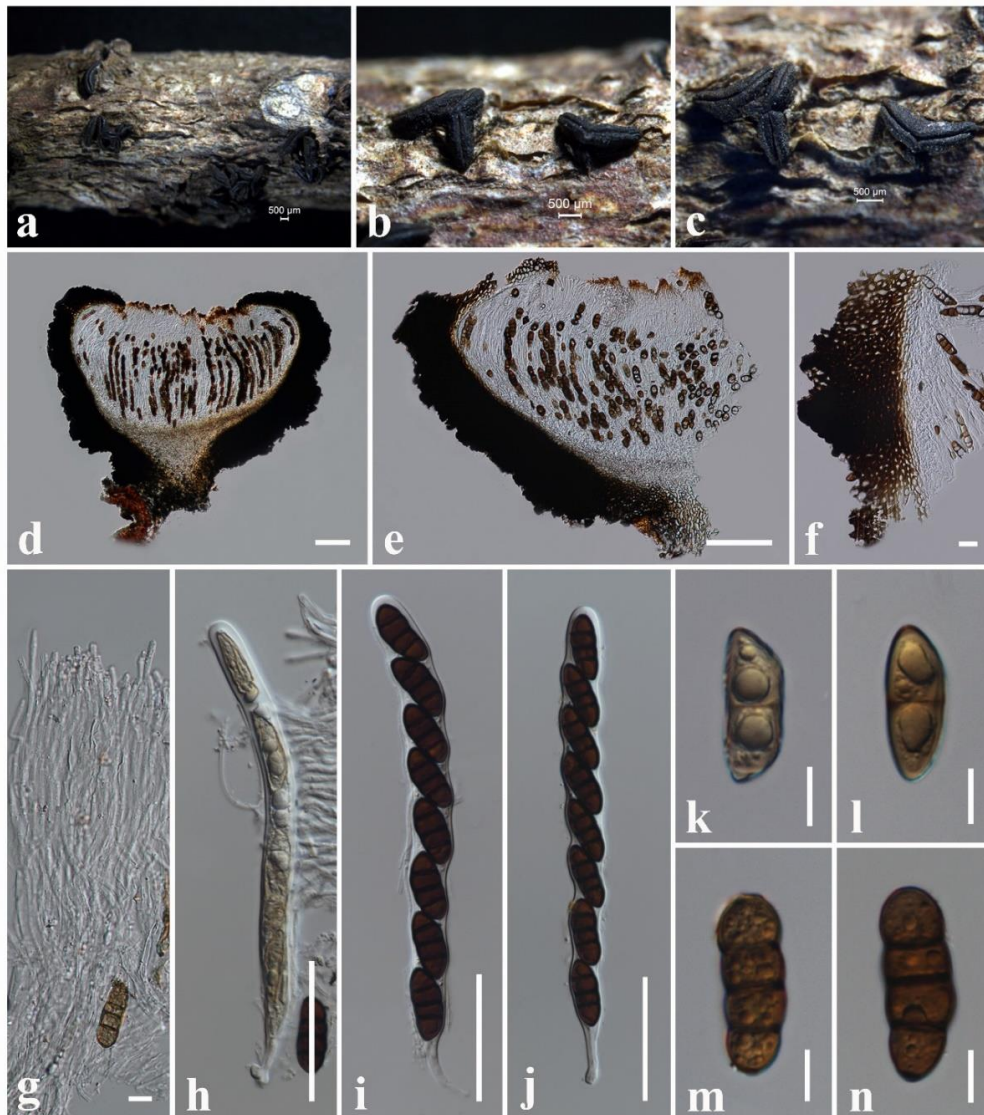

Figure 3 – *Rhytidhysteron neorufulum* (MFLU 18-2644). a The specimen. b, c Appearance of ascomata on the host surface. d, e Vertical sections through ascomata. f Exciple. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a–c = 500 μm, d, e = 100 μm, f = 20 μm, g, k–n = 10 μm, h–j = 50 μm.

Pleosporales Luttr. ex M.E. Barr
Acrocalymmaceae Crous & Trakun.

This family was introduced by Trakunyingcharoen et al. (2014) to accommodate *Acrocalymma* as the type genus. In this study, we follow the recent treatment for Acrocalymmaceae in Hongsanan et al. (2020a) and Tennakoon et al. (2021).

Acrocalymma Alcorn & J.A.G. Irwin

Alcorn & Irwin (1987) introduced *Acrocalymma* to accommodate the root pathogen *A. medicaginis* on *Medicago* in Australia. There are eleven *Acrocalymma* epithets in Species Fungorum (2022).
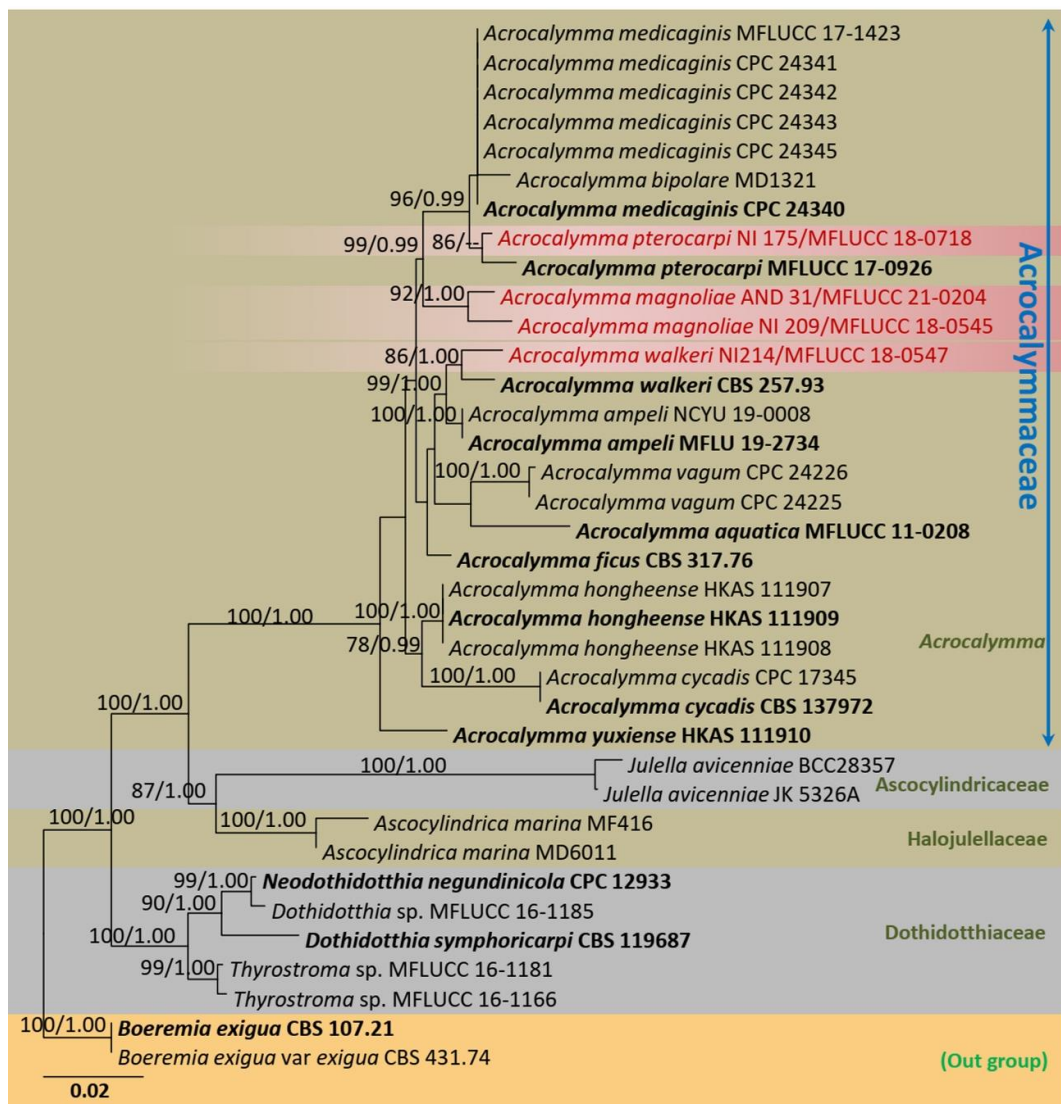
Figure 4 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU and ITS sequence data. Related sequences of *Acrocalymma* were obtained from Tennakoon et al. (2021). Thirty-six strains are included in the combined gene analyses comprising 2420 characters after alignment (880 characters for LSU, 1000 characters for SSU, 540 characters for ITS). *Boeremia exgua* (CBS 107.21) and *B. exigua* var *exigua* (CBS 431.74) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -7640.126204 is presented. The matrix had 535 distinct alignment patterns, with 38.35% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Acrocalymma magnoliae N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 5

Index Fungorum number: IF 559515, Faces of Fungi number: FoF 10713

Etymology – Name reflects the host genus *Magnolia*, from which the new species was isolated.

Holotype – MFLU 18-1306

Saprobic on dead twigs attached to *Magnolia lilifera*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 135–160 × 200–230 µm ($\bar{x}$ = 145 × 215 µm, n = 10), sub-globose, dark brown or black, semi-immersed to erumpent, solitary, scattered without ostiole. *Conidiomatal wall* 20–35 µm wide, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, cells in the inner layer lightly pigmented, arranged in a *textura*

angularis, in the outer layer, darker, fusing cells and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–12 × 3–7 μm ($\bar{x}$ = 10 × 5 μm, n = 10), phialidic, hyaline, smooth, ampulliform to doliiform, proliferating with visible periclinal thickening at apex. *Conidia* 22–30 × 5–7 μm ($\bar{x}$ = 26 × 6 μm, n = 40), hyaline, cylindrical to fusoid, smooth, guttulate, thin-walled, straight, apex obtuse, unicellular, 2–3 pseudosepta present with flaring mucoid. Apical appendage visible in water mounts.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, cottony to fairy fluffy appearance, white at the margin, olivaceous green in the centre; reverse: cream at the margin, greyish green in the centre.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 15 November 2017, N. I. de Silva, NI209 (MFLU 18-1306, holotype), ex-type living culture, MFLUCC 18-0545, Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND31 (MFLU 21-0206), living culture, MFLUCC 21-0204.

GenBank numbers – (NI209): LSU: OK655819, SSU: OL331094, ITS: OL413439, (AND31): LSU: OK655820, SSU: OL331095, ITS: OL413440.
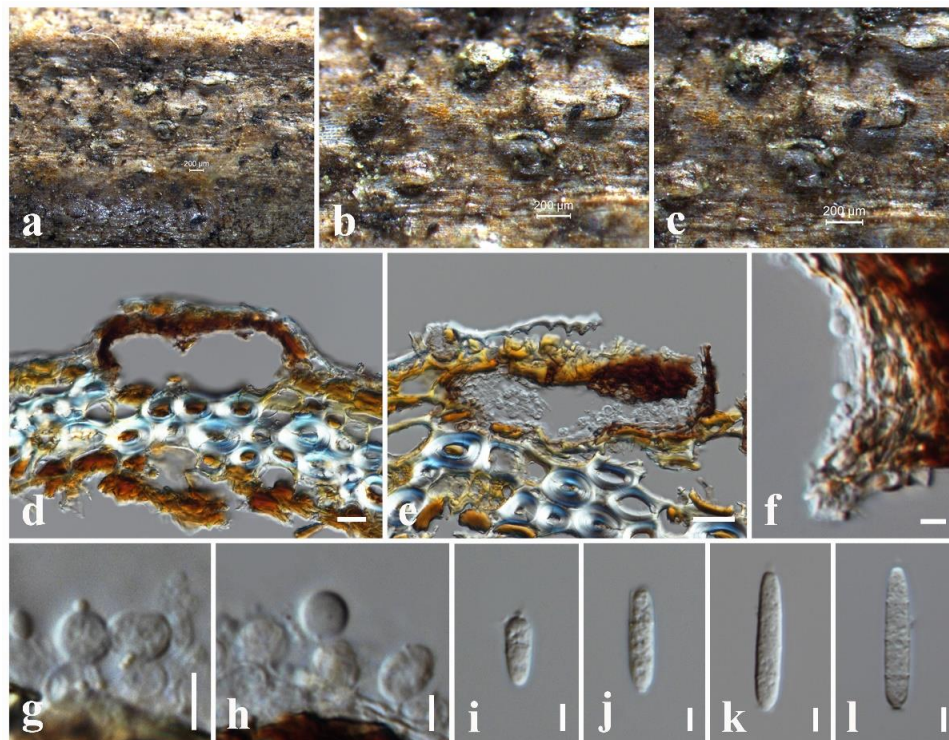

Figure 5 – *Acrocalymma magnoliae* (MFLU 18-1306, holotype). a–c Appearance of immersed conidiomata on substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g, h Conidiogenous cells. i–l Conidia. Scale bars: a–c = 200 μm, d, e = 20 μm, f–l = 5 μm.

Notes – The morphology of our collection (MFLU 18-1306 and MFLU 21-0206) tally with it being an *Acrocalymma* species in having globose, semi-immersed to immersed, ostiolate conidiomata, ampulliform to doliiform, hyaline conidiogenous cells and hyaline, smooth, guttulate, cylindrical to fusoid, unicellular conidia (Trakunyingcharoen et al. 2014, Jayasiri et al. 2019, tennakoon et al. 2021). Multi-gene phylogeny indicates that our collection groups independently, sister to the clade containing *Acrocalymma bipolare*, *A. medicaginis* and *A. pterocarpi* with 99% ML, 0.99 BYPP supports (Fig. 4). *Acrocalymma magnoliae* is differ from *A. bipolare*, *A. medicaginis*, *A. pterocarpi* considering their morphology. *Acrocalymma magnoliae* has (22–30 × 5–7) μm conidia with inconspicuous apical appendage. *Acrocalymma bipolare* has (9–12 × 3–5)

µm conidia with apical and lower appendages (Dong et al. 2020). *Acrocalymma medicaginis* has (11–21 × 3.5–5) µm conidia with helmet-shaped apical appendages (Alcorn & Irwin 1987). A morphological comparison between *Acrocalymma magnoliae* and *A. pterocarpi* cannot be made because the latter is only known for its sexual morph characteristics (Jayasiri et al. 2019). It is interesting to note that this is the first *Acrocalymma* record from *Magnolia* species (Table 2).

Table 2 Comparison of habitats and localities of *Acrocalymma* spp.

Species	Host	Locality	Reference
Acrocalymma ampeli (Asexual morph)	*Ficus ampelas*	Taiwan	Tennakoon et al. (2021)
Acrocalymma aquatica (Asexual morph)	Submerged wood in a freshwater stream	Thailand	Zhang et al. (2012b)
Acrocalymma bipolare (Asexual morph)	On submerged wood	Egypt	Dong et al. (2020)
Acrocalymma cycadis (Asexual morph)	*Cycas calcicola*	Australia	Crous et al. (2014)
Acrocalymma fici (Asexual morph)	*Ficus* sp.	India	Trakunyingcharoen et al. (2014)
Acrocalymma magnoliae (Asexual morph)	**Magnolia sp. Anomianthus dulcis**	**Thailand**	**This study**
Acrocalymma medicaginis (Asexual morph)	*Medicago sativa*	Australia	Alcorn & Irwin (1987)
Acrocalymma pterocarpi (Sexual morph)	*Pterocarpus indicus*	Thailand	Jayasiri et al. (2019)
Acrocalymma vagum (Asexual morph)	*Amaranthusm* sp., *Citrullus lanatus*, *Cucumis melo*, *C. sativus*, *Cucurbita* rootstock, *Vitis vinifera*	Spain, USA	Trakunyingcharoen et al. (2014)
Acrocalymma walkeri (Sexual morph)	*Medicago sativa*	Australia	Trakunyingcharoen et al. (2014)
Acrocalymma yuxiense (Asexual morph)	On dead leaves of *Quercus*	China	Mortimer et al. (2021)

Acrocalymma pterocarpi Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 20 (2019)

Fig. 6

Index Fungorum number: IF 555528, Faces of Fungi number: FoF 05228

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 130–150 µm high, 180–200 µm diam. ($\overline{x}$ = 145 × 190 µm, n = 10), scattered, erumpent to nearly superficial, with basal wall remaining immersed in host tissue, globose to subglobose, dark brown to black, ostiolate with minute papilla. *Peridium* 12–20 µm wide ($\overline{x}$ = 14 µm, n = 10), composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, inner cells hyaline to lightly pigmented, arranged in a *textura angularis*, outer cells, darker, fusing and indistinguishable from the host tissues. *Hamathecium* composed of 1–2 µm wide, numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 50–75 × 5–7 µm ($\overline{x}$ = 65 × 6 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, furcate pedicel, apically rounded with a small ocular chamber. *Ascospores* 10–13 × 2–4 µm ($\overline{x}$ = 12 × 3 µm, n = 30), obliquely biseriate, hyaline, fusiform, 1–3-septate, with narrowly rounded ends with mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: circular, margin undulate, dense, slightly raised, cottony to fluffy appearance, white; reverse: cream at the margin, orangish brown in the centre.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI175 (MFLU 18-1034), living culture, MFLUCC 18-0718.

Known hosts and distribution – On a fallen pod of *Pterocarpus indicus* in Thailand (Jayasiri et al. 2019), dead twigs attached to the *Magnolia* sp. in China (this study).

GenBank numbers – LSU: OK655818, SSU: OL331093, ITS: OL413438.

Notes – *Acrocalymma pterocarpi* was introduced by Jayasiri et al. (2019) from a fallen pod of *Pterocarpus indicus* in Thailand. The morphological characteristics of our collection (MFLUCC 18-0718) resemble *A. pterocarpi* (MFLUCC 17-0926) in having erumpent to nearly superficial, globose to subglobose, dark brown to black conidiomata, cylindrical asci (50–75 × 5–7 µm *vs* 65–75 × 7–12 µm) and hyaline, fusiform, 1–3-septate ascospores (10–13 × 2–4 µm *vs* 17–21 × 3–5 µm) (Jayasiri et al. 2019). According to the multi-gene phylogeny herein, our collection (MFLUCC 18-0718) was nested with *A. pterocarpi* (MFLUCC 17-0926) with 86% ML support. Therefore, we introduce our collection as a new host record of *A. pterocarpi* from *Magnolia* sp. in China.
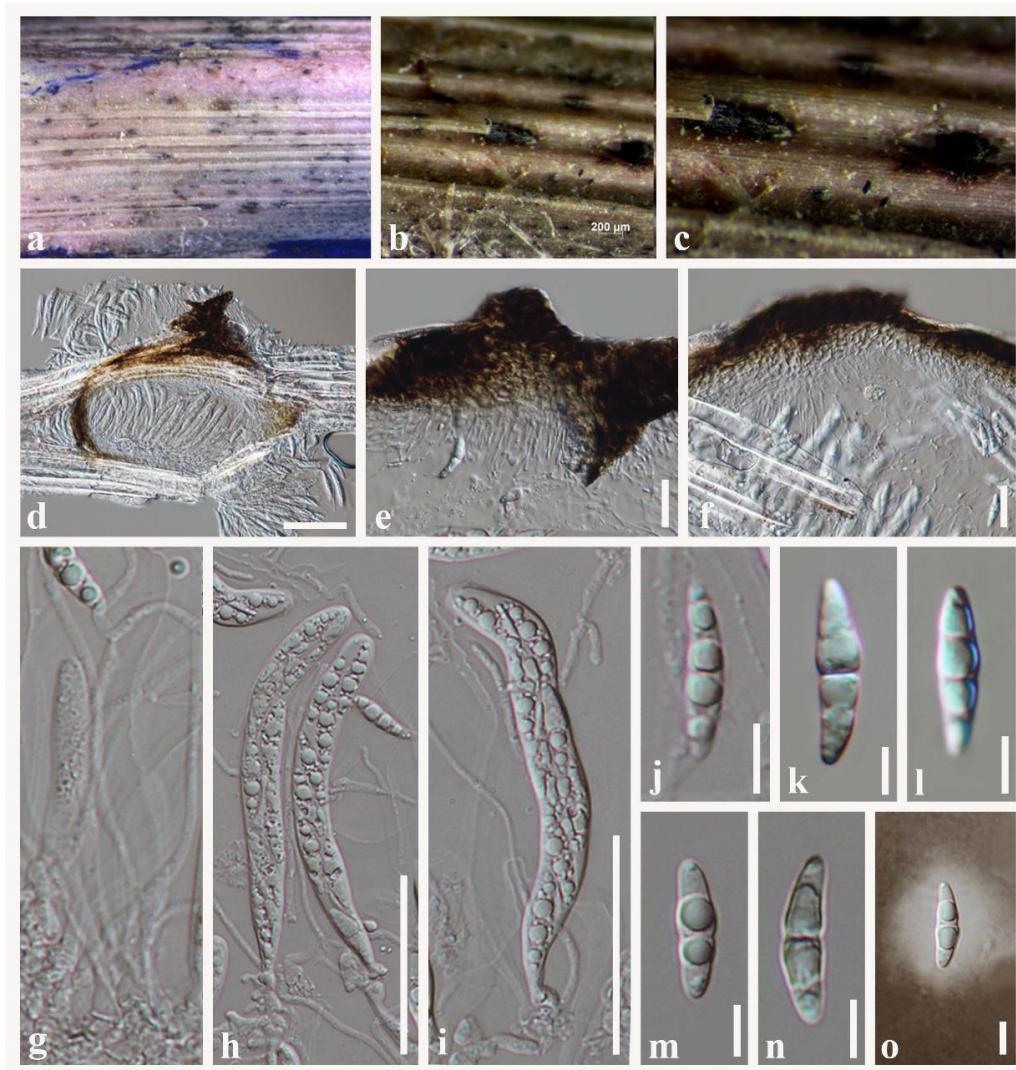

Figure 6 – *Acrocalymma pterocarpi* (MFLU 18-1034). a–c Appearance of ascomata on host surface. d Vertical sections through ascomata. e, f Peridium. g Pseudoparaphyses with young asci. h, i Asci. j–n Ascospores. g Ascospore stained with Indian ink. Scale bars: d = 80 µm, e, f = 20 µm, h, i = 30 µm, i–o = 5 µm.

Acrocalymma walkeri (Shoemaker, C.E. Babc. & J.A.G. Irwin) Crous & Trakun., IMA Fungus 5(2): 407 (2014)   Fig. 7

Index Fungorum number: IF 810840, Faces of Fungi number: FoF 12929

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 180–220 µm high, 155–170 µm diam. ($\bar{x}$ = 200 × 165 µm, n = 10), scattered, immersed to erumpent, globose or

subglobose, dark brown to black, elongated neck, with minute papilla, ostiolate. *Peridium* 10–15 μm wide ($\bar{x}$ = 12 μm, n = 10), composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, cells towards the inside hyaline to lightly pigmented, arranged in a *textura angularis*, at the outside, darker, fusing and indistinguishable from the host tissues. *Hamathecium* composed of 1–2 μm wide, numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 60–95 × 7–10 μm ($\bar{x}$ = 80 × 8.5 μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, furcate pedicel, and with a small ocular chamber. *Ascospores* 16–20 × 3–5 μm ($\bar{x}$ = 18 × 4 μm, n = 30), obliquely biseriate, hyaline, fusiform with acute ends, 1-septate, constricted at the septum, upper cell slightly wider than lower cell, smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 22 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, cottony to fairy fluffy appearance, white at the margin, light grey in the centre; reverse: cream at the margin, grey in the centre.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 15 November 2017, N. I. de Silva, NI214 (MFLU 18-1311), living culture, MFLUCC 18-0547.
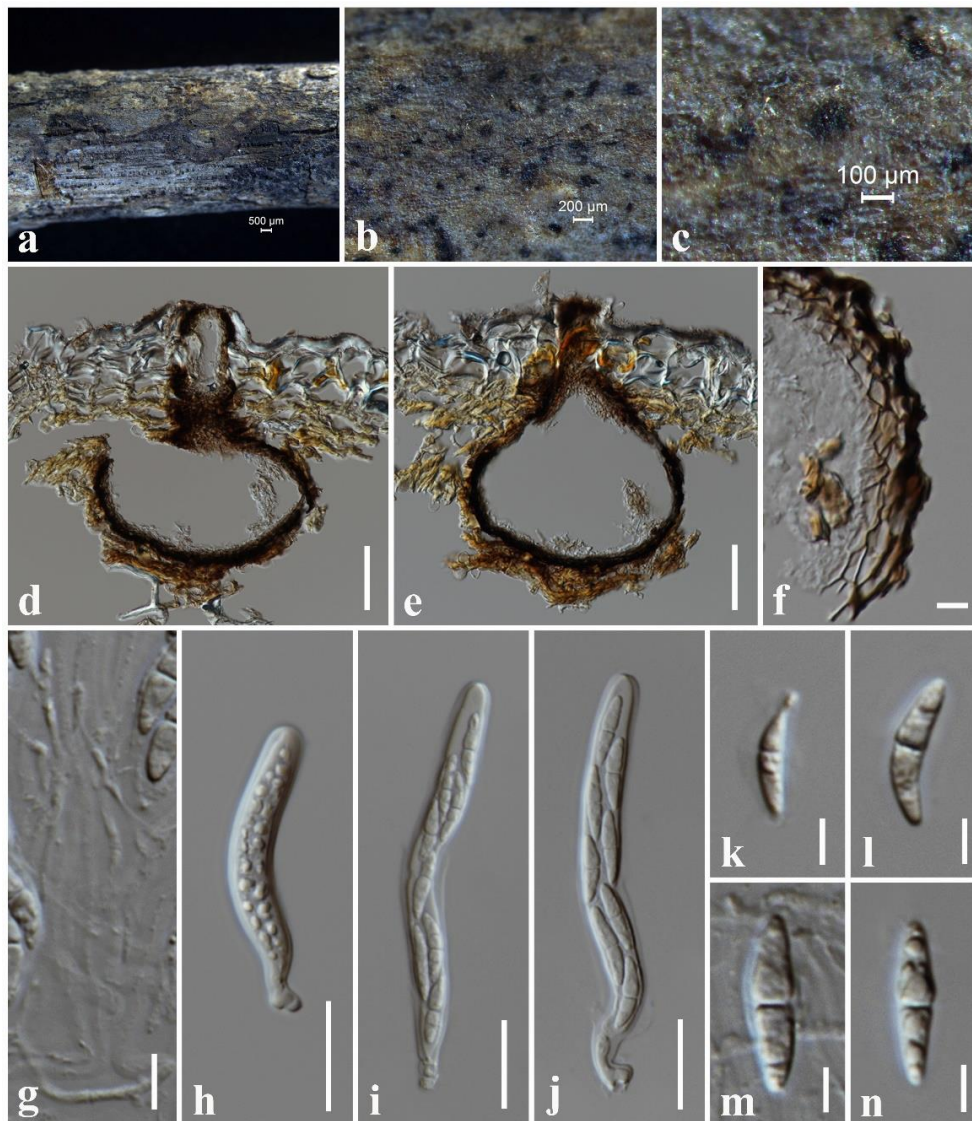

Figure 7 – *Acrocalymma walkeri* (MFLU 18-1311). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci.

k–n Ascospores. Scale bars: a = 500 μm, b = 200 μm, c = 100 μm, d, e = 50 μm, f = 5 μm, h–j = 20 μm, k–n = 5 μm.

Known hosts and distribution – *Medicago sativa* in Australia (Shoemaker et al. 1991), dead twigs attached to *Magnolia* sp. in Thailand (this study).

GenBank numbers – LSU: OK655821, ITS: OL413441.

Notes – The morphological characteristics of our collection (MFLUCC 18-0547) resembles *Acrocalymma walkeri* in having immersed to erumpent, globose or subglobose, dark brown to black ascomata (180–220 × 155–170 μm *vs* 160–180 μm diam.), cylindrical asci (60–95 × 7–10 μm *vs* 50–80 × 8–11 μm) and hyaline, fusiform, 1-septate ascospores (16–20 × 3–5 μm *vs* 19–22 × 4.5–5.5 μm) (Shoemaker et al. 1991). Multi-gene phylogeny also indicates that our collection (MFLUCC 18-0547) nested with *A. walkeri* with 86% ML, 1.00 BYPP support (Fig. 4). Therefore, based on both morphology and phylogeny evidence, we report our collection as a new host record of *A. walker* from *Magnolia* species in Thailand.

Amorosiaceae Thambug. & K.D. Hyde

Amorosiaceae was introduced by Thambugala et al. (2015), to include *Amorosia* as the type genus. Amorosiaceae members can be distinguished from their phylogenetically closely related families (i.e., Lophiostomataceae, Teichosporaceae, Sporormiaceae) from their hyphomycete asexual morphs (elongate-clavate, uni- to multi-septate conidia) (Thambugala et al. 2015, Honsanan et al. 2020). The sexual morphs of Amorosiaceae have immersed to semi-immersed ascomata with crest-like, papillate ostiole and hyaline, 1–3-septate ascospores with mucilaginous sheath (Thambugala et al. 2015). Four genera are accepted in this family, *viz. Alfoldia*, *Amorosia*, *Amorocoelophoma* and *Angustimassarina* (Honsanan et al. 2020).
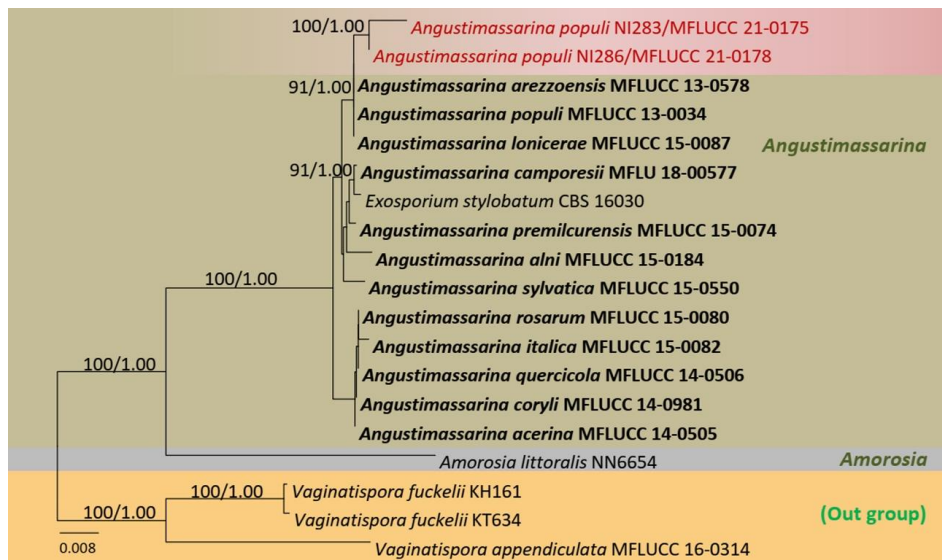

Figure 8 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, ITS and *tef1* sequence data. Related sequences of *Angustimassarina* and some other strains of Pleosporales were obtained from Hyde et al. (2020). Nineteen strains are included in the combined gene analyses comprising 3250 characters after alignment (840 characters for LSU, 970 characters for SSU, 500 characters for ITS and 940 characters for *tef1*). *Vaginatispora appendiculate* (MFLUCC 16-0314) and *V. fuckelii* (KT634, KH161) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -7732.858499 is presented. The matrix had 422 distinct alignment patterns, with 25.24% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Angustimassarina Thambug., Kaz. Tanaka & K.D. Hyde

Angustimassarina was introduced by Thambugala et al. (2015) to accommodate *A. populi* as the generic type. *Angustimassarina* members have uniloculate ascomata with a pore-like opening or that open through the cracks of the host surface and fusiform to cylindrical or ellipsoidal-fusiform, septate, hyaline ascospores, becoming ocher brown at maturity (Thambugala et al. 2015, Hyde et al. 2019). The asexual morph of this genus comprises micronematous to semi-macronematous, pale brown conidiophores, integrated, terminal, holoblastic, short-cylindrical to elongate-cylindrical, conidiogenous cells and solitary, elongate-clavate, pale to dark brown, 1–3-septate, conidia (Thambugala et al. 2015). Twelve *Angustimassarina* epithets are listed in Index Fungorum (2022).

Angustimassarina populi Thambug. & K.D. Hyde, in Thambugala et al., Fungal Divers.: 10.1007/s13225-015-0348-3, [56] (2015)   Fig. 9

Index Fungorum number: IF 551279, Faces of Fungi number: FoF 01086

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 200–230 μm high × 230–260 μm diam. ($\bar{x} = 220 \times 240$ μm, n = 10), uniloculate, scattered, immersed, erumpent, dark brown to black, globose to subglobose. *Ostiole* 50–70 μm wide, in the centre without a papilla. *Peridium* 35–45 μm wide, composed of several layers of dark brown to lightly pigmented cells of *textura angularis*, fusing at the outside with the host tissues. *Hamathecium* comprising 1.5–2 μm wide, septate, unbranched, cellular, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–95 × 9–11 μm ($\bar{x} = 80 \times 10$ μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with short pedicel, rounded at the apex. *Ascospores* 19–23 × 3–5 μm ($\bar{x} = 21 \times 4$ μm, n = 40), bi-seriate, hyaline, fusiform, 1– septate with 2 pseudosepta, deeply constricted at the septum, widest at the centre and tapering toward the ends, straight, smooth-walled, guttulate, surrounded by a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin undulate, dense, slightly raised, velvety appearance, brown at the margin, yellowish brown in the centre; reverse: pale brown at the margin, dark brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 9 January 2019, N. I. de Silva, NI283 (MFLU 21-0209), living culture, MFLUCC 21-0175, NI286 (MFLU 21-0208), living culture, MFLUCC 21-0178.

Known hosts and distribution – On dead branches of *Populus* sp. in Italy (Thambugala et al. 2015), dead twigs of *Magnolia* sp. in Thailand (this study).

GenBank numbers – (NI283); LSU: OL813501, SSU: OL824797, ITS: OM212461; (NI286); LSU: OL813502, SSU: OL824798, ITS: OM212462.

Notes – Two new strains (MFLUCC 21-0175 and MFLUCC 21-0178) clustered with *Angustimassarina arezzoensis*, *A. lonicerae* and *A. populi* in the phylogeny of combined LSU, SSU, ITS and *tef1* sequence data (Fig. 8). The phylogenetic analyses of combined LSU, SSU, ITS and *tef1* sequence data were not provided good separation among the new strains, *A. arezzoensis*, *A. lonicerae* and *A. populi*. It would be necessary to use additional protein-coding genes in the phylogenetic analyses for good resolution of these taxa in future.

The morphological characteristics of the new collection (MFLU 21-0209) fit well with *A. populi* in having immersed to erumpent, black, globose to subglobose, uniloculate ascomata, cylindric-clavate, with short pedicellate asci and hyaline, fusiform, 1–3-septate ascospores (Thambugala et al. 2015). The new collection (MFLU 21-0209) also has a similar size range of asci and ascospores (Table 3). Therefore, we identified the new collection (MFLU 21-0209) as a new geographical and host record of *A. populi*.

Didymosphaeriaceae Munk

Munk (1953) introduced Didymosphaeriaceae and typified by *Didymosphaeria*. Members of this family are mainly saprobes, while other taxa are endophytes or pathogens in terrestrial and aquatic environments (Barr 2001, Zhang et al. 2012a, Ariyawansa et al. 2014, Wanasinghe et al.

2016). Ariyawansa et al. (2014) and Wanasinghe et al. (2016) conducted comprehensive phylogenetic and morphological analyses for Didymosphaeriaceae to resolve the species and generic boundaries of the family.

Table 3 Synopsis of recorded *Angustimassarina* species.

Taxa	Ascomata (μm)	Peridium (μm)	Asci (μm)	Ascospores (μm)	References
A. acerina	200–350 × 164–183	15–26	92–105 × 7.5–8.6	21–23 × 4.1–4.6	Thambugala et al. (2015)
A. alni	160–250 × 130–200	28–44	71–89 × 8–10	19–22 × 3–4	Tibpromma et al. (2017)
A. arezzoensis	169–234 × 166–245	22–41	67–95 × 10–15	19–21 × 5–6	Tibpromma et al. (2017)
A. coryli	150–250 × 500–750	15–25	70–100 × 10–15	20–25 × 5–8	Hyde et al. (2017)
A. italica	127–159 × 97–131	23–40	78–103 × 10–12	15–22 × 3–6	Tibpromma et al. (2017)
A. lonicerae	193–203 × 170–220	10–18	55–81 × 9–13	19–25 × 4–7	Tibpromma et al. (2017)
A. populi	125–175 × 100–120	14–32	80–95 × 9.5–13	19–22 × 3.2–5.5	Thambugala et al. (2015)
A. populi	**200–230 × 230–260**	**35–45**	**70–95 × 9–11**	**19–23 × 3–5**	**This study**
A. premilcurensis	231–238 × 290–311	20–30	64–93 × 11–15	19–23 × 4–7	Tibpromma et al. (2017)
A. quercicola	200–250 × 150–265	14–27	60–94 × 8.8–13	17–21 × 4–6	Thambugala et al. (2015)
A. rosarum	100–150 × 125–165	10–17	40–102 × 6–13	16–22 × 4–6	Wanasinghe et al. (2018)
A. sylvatica	180–260 × 150–200	8–12	95–110 × 8–12	21–25 × 4–5	Hyde et al. (2019)

Pseudopithomyces Ariyaw. & K.D. Hyde

Pseudopithomyces was introduced by Ariyawansa et al. (2015) with *P. chartarum* as the type species. Asexual morph is characterized by brown to black colonies on the host consisting of fusiform, verruculose dark conidia (Ariyawansa et al. 2015, Hyde et al. 2017, Wanasinghe et al. 2018, Jayasiri et al. 2019). *Pseudopithomyces* species are saprobic or parasitic on dead leaves, stems of plants and humans Ariyawansa et al. (2015). Index Fungorum (2022) lists 13 epithets of *Pseudopithomyces*.

Pseudopithomyces chartarum (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, Fungal Divers. 75: 64 (2015)   Fig. 11

Index Fungorum number: IF 551393, Faces of Fungi number: FoF 00938

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, dark brown to black. *Conidiophores* mononematous, micronematous, mostly intercalary, denticulate, aseptate. *Conidiogenous cells* mono or polyblastic, light brown, smooth, or denticulate with 2 μm broad conidial attachment. *Conidia* 23–26 × 11–15 μm ($\bar{x}$ = 25 × 13 μm, n = 30), brown, solitary, obovate to oblong, verruculose to spinulose, 3-transverse septa, with middle cells usually divided by 1–2 longitudinal septa, slightly constricted at the septa with rhexolytic secession.

Culture characteristics – Colonies on PDA reaching 50 mm diameter after 1 week at 25 °C, colonies from above: medium dense, circular, flat, surface slightly rough, entire edge, margin well-defined, cottony to fairly fluffy with sparse aspects, white; reverse: dark brown at the margin, cream in the centre.
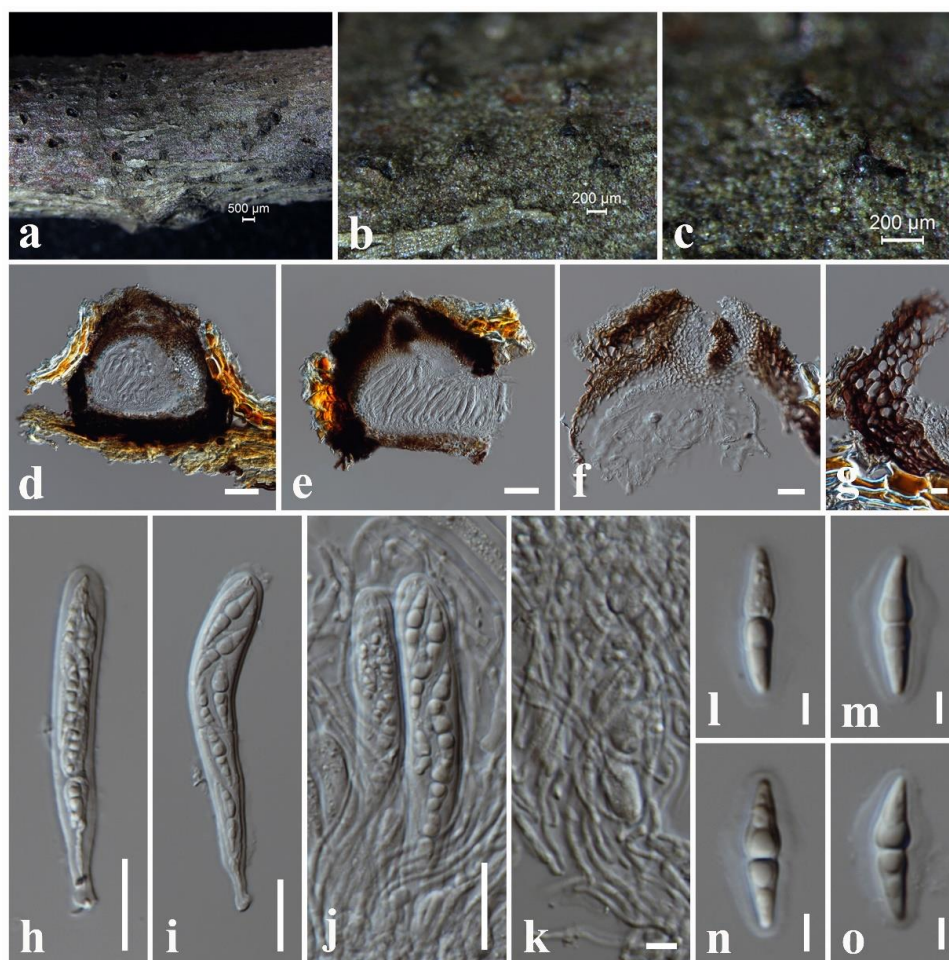
Figure 9 – *Angustimassarina populi* (MFLU 21-0209). a The specimen. b, c Appearance of ascomata on host surface. d, e Vertical sections through ascomata. f Vertical sections through ascomata showing neck region. g Peridium. h–j Asci. k Pseudoparaphyses. l–o Ascospores. Scale bars: a = 500 μm, b, c = 200 μm, d, e = 50 μm, f = 20 μm, g = 10 μm, h–j = 20 μm, k–n = 5 μm.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND22 (MFLU 21-0247), living culture, MFLUCC 21-0201.

Known hosts and distribution – Occurring on numerous host plants and distributed in different countries including decaying pods of *Radermachera sinica*, *Bauhinia* sp., *Leucaena* sp. in Thailand, decaying cone of *Magnolia grandiflora* in China (Jayasiri et al. 2019), stems of grass in China (Hyde et al. 2017), dead leaves of *Macaranga tanarius* in Taiwan Province of China (Tennakoon et al 2021), dead twigs attached to *Anomianthus dulcis* in Thailand (this study).

GenBank numbers – LSU: OK655822, SSU: OL331096, ITS: OL413442, *tef1*: OM471894.

Notes – The new collection (MFLU 21-0247) shares similar morphology with the type, *Pseudopithomyces chartarum* in having brown, solitary, verruculose conidia with 3 transverse and 1–2 longitudinal septa (Ellis 1960). The newly collected specimen overlaps in the size range of conidia (23–26 × 11–15 μm) with the type (18–29 × 10–17 μm) (Ellis 1960). Phylogenetic analyses of a combined LSU, SSU, ITS and *tef1*sequence data showed that the new strain clustered with the ex-type of *Ps*. *chartarum* (UTHSC 04-678) and other strains of *P*. *chartarum* (Fig. 10). However, *Ps*. *chartarum* has not been recorded from *Anomianthus dulcis* (Annonaceae) (Farr & Rossman 2022). In the present study, we report *P*. *chartarum* from *Anomianthus dulcis* for the first time.

Fuscostagonosporaceae Jayasiri, Camporesi & K.D. Hyde
This family was introduced by Hyde et al. (2017) to accommodate *Fuscostagonospora* as the

type genus. Fuscostagonosporaceae members are characterized by immersed, globose to subglobose ascomata, branched trabeculate pseudoparaphyses and narrowly fusiform, hyaline ascospores with a sheath (Hyde et al. 2017). In this study, we followed Hyde et al. (2020) as the latest treatment for this family.
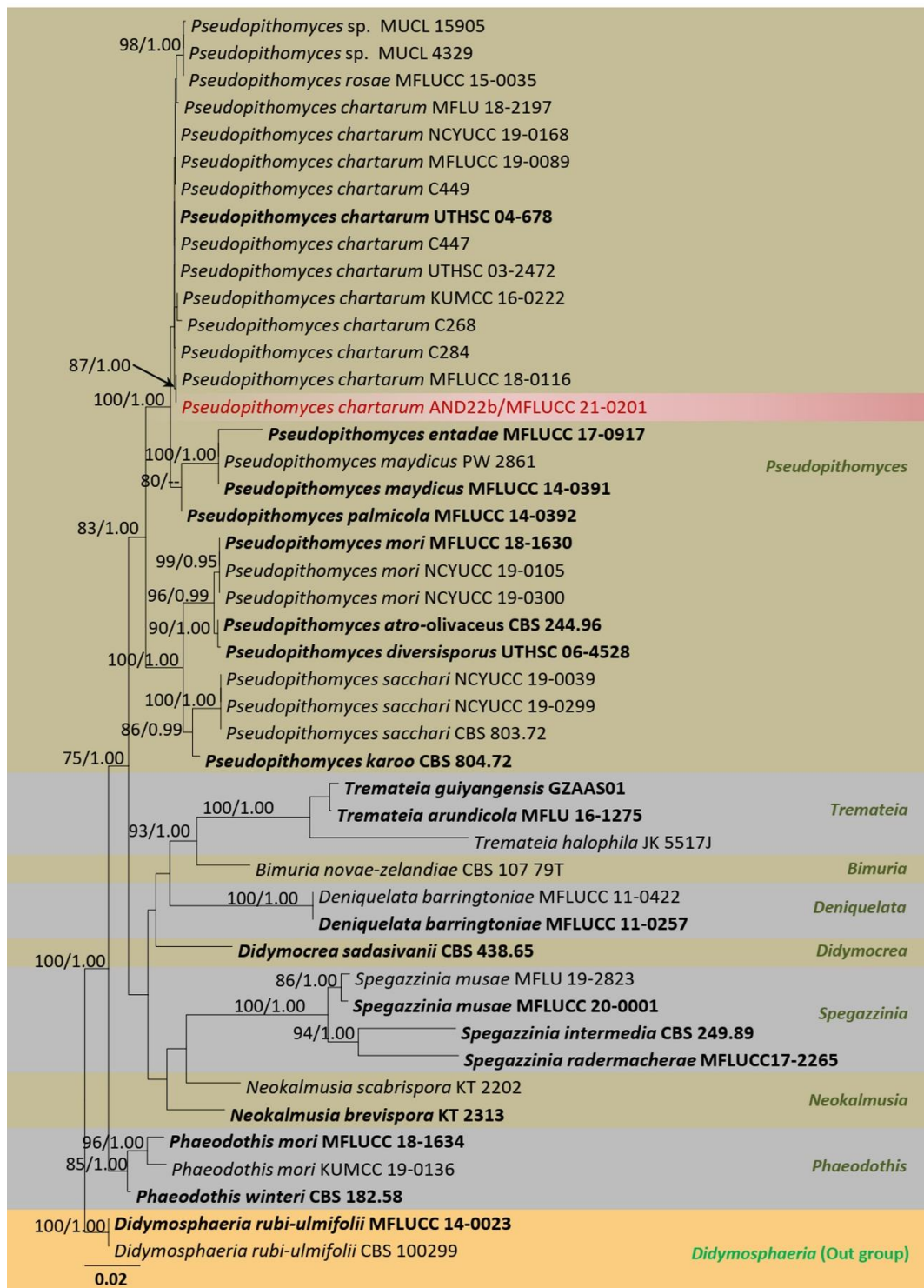

Figure 10 – Phylogram generated from maximum likelihood analysis of combined LSU SSU, ITS and *tef1*sequence data. Related sequences of *Pseudopithomyces* were obtained from Tennakoon et al. (2021). Forty-six strains are included in the combined gene analyses comprising 3110 characters after alignment (850 characters for LSU, 870 characters for SSU, 470 characters for ITS and 920 characters for *tef1*). Two strains of *Didymosphaeria rubi-ulmifolii* (CBS 100299 and MFLUCC 14-0023) are used as outgroup taxon. The best RAxML tree with a final likelihood value of -

10494.371749 is presented. The matrix had 748 distinct alignment patterns, with 30.82% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
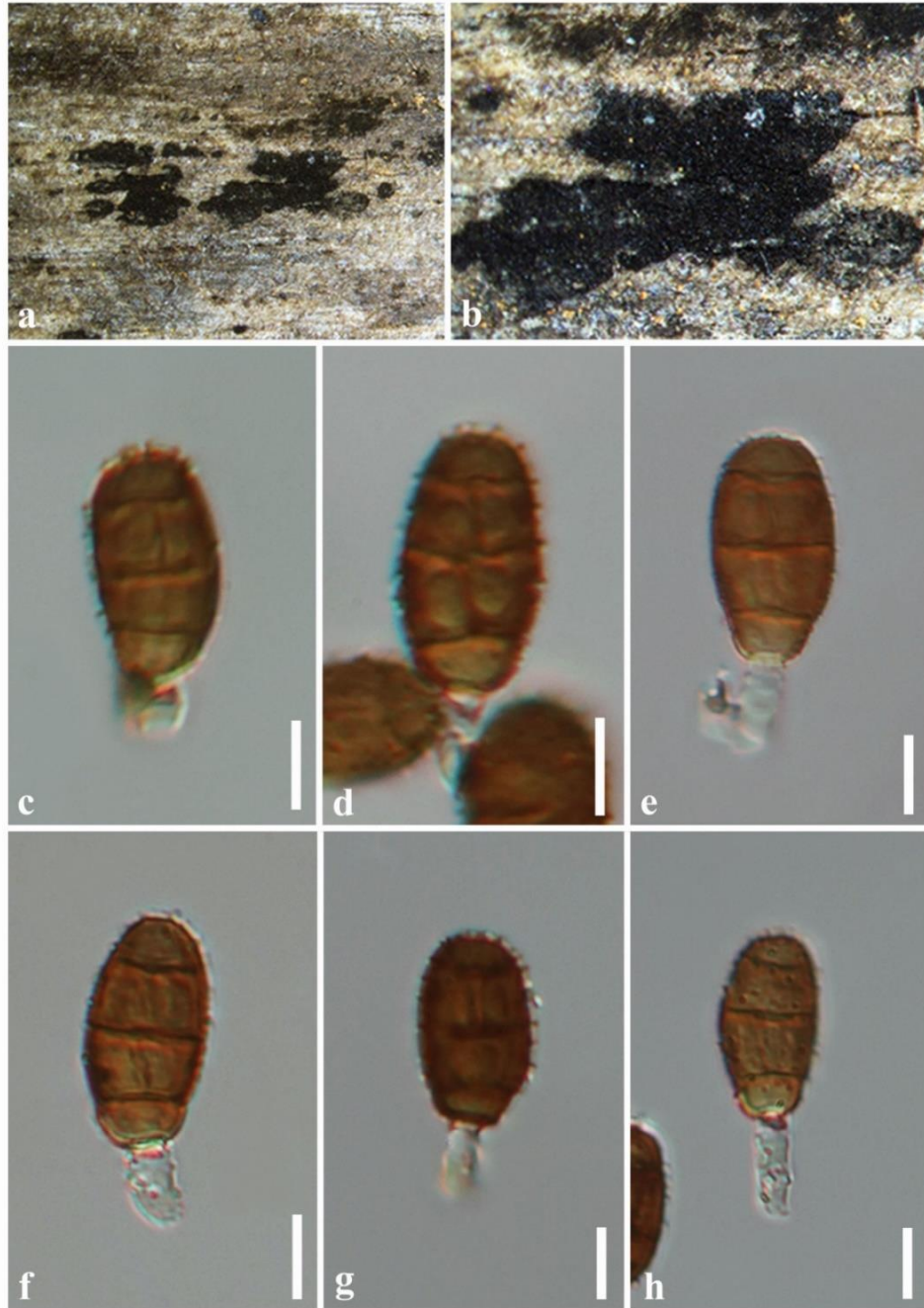

Figure 11 – *Pseudopithomyces chartarum* (MFLU 21-0247). a, b Appearance of colonies on substrate. c, d Conidia. e–h Conidia with conidiophores and conidiogenous cells. Scale bars: c–h = 10 μm.

Fuscostagonospora Kaz. Tanaka & K. Hiray.

Fuscostagonospora has four species, *viz. Fuscostagonospora banksiae*, *F. camporesii*, *F. cytisi* and *F. sasae* (Index Fungorum 2022). This genus was initially introduced by Tanaka et al. (2015), to accommodate a bambusicolous taxon, *F. sasae*. In this study, we introduce another species, *F. magnoliae* from Thailand.

Fuscostagonospora magnoliae N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 13

Index Fungorum number: IF 559516, Faces of Fungi number: FoF 10714

Etymology – Name reflects the host genus *Magnolia*, from which the new species was isolated.

Holotype – MFLU 21-0218

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: *Ascomata* 160–190 μm high × 165–180 μm diam. ($\overline{x} = 180 \times 170$ μm, n = 10), solitary, scattered to clustered, semi-immersed to erumpent, black spots on host surface globose to subglobose, glabrous, uni-loculate, ostiole central with minute papilla. *Peridium* 25–30 μm thin-walled with equal thickness, composed of several layers of lightly pigmented to light brown to dark brown, *textura angularis* cells, inner cells lighter, outer cells darker and fusing with the host tissues. *Hamathecium* composed of dense, broad, 1–2 μm wide, filamentous, cellular pseudoparaphyses, with indistinct septa, not constricted at the septa, anastomosing at the apex, embedded in a hyaline gelatinous matrix. *Asci* 50–75 × 5–8 μm ($\overline{x} = 70 \times 6$ μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, with furcate to obtuse end, apically rounded with well-developed ocular chamber. *Ascospores* 9–12 × 4–6 μm ($\overline{x} = 10 \times 5$ μm, n = 40), overlapping, 1-seriate, ellipsoid to obovoid, hyaline, aseptate when young, becoming 1-septate, straight to slightly curved, smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: pale brown, circular, entire margin, slightly raised, dense at the centre, dark brown at the margin; reverse: brown from the centre of the colony, dark brown at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia champaca* (Magnoliaceae), 9 January 2019, N. I. de Silva, NI284 (MFLU 21-0218, holotype), ex-type living culture, MFLUCC 21-0176, NI285 living culture, MFLUCC 21-0177.

GenBank numbers – (NI284); LSU: OL830819, ITS: OL966953, SSU: OL964387, (NI285); LSU: OL830820, ITS: OL966954, SSU: OL964388.

Notes – The morphological characteristics of *Fuscostagonospora magnoliae* resembles *F. camporesii* in having semi-immersed to erumpent, subglobose to globose ascomata, cylindric-clavate, short pedicellate asci and 1-septate, ellipsoid to obovoid ascospores (Hyde et al. 2020a). However, *F. magnoliae* can be distinguished from *F. camporesii* in having smaller asci (50–75 × 5–8 μm) and hyaline ascospores (9–12 × 4–6 μm), whereas *F. camporesii* has larger asci (80–90 × 8–9 μm) and light brown ascospores (13–15 × 6–6.5 μm) (Hyde et al. 2020a). According to the multi-gene phylogenetic analyses of a combined LSU, SSU, ITS and TEF1-α sequence dataset, *F. magnoliae* isolates nested sister to the *F. camporesii* with 83% ML and 0.99 BYPP supports (Fig. 12). A pairwise comparison of ITS sequence data between *F. magnoliae* (MFLUCC 21-0176) and *F. camporesii* (MFLUCC 16-0787) indicates 12 base pair (2.5%) differences across 480 nucleotides. A pairwise comparison of LSU sequence data between *F. magnoliae* (MFLUCC 21-0176) and *F. camporesii* (MFLUCC 16-0787) indicates 17 base pair (1.8%) differences across 900 nucleotides. A pairwise comparison of SSU sequence data between *F. magnoliae* (MFLUCC 21-0176) and *F. camporesii* (MFLUCC 16-0787) indicates 10 base pair (1%) differences across 1000 nucleotides.

Pleosporales Luttr. ex M.E. Barr
Hermatomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka

Hermatomycetaceae was informally proposed by Locquin (1984). Hermatomycetaceae was established by Hashimoto et al. (2017) with the type genus *Hermatomyces*, based on phylogeny of combined SSU, ITS, LSU, *tef1* and *rpb2* sequence data. The presence of the sporodochial conidiomata and the dimorphic conidia (lenticular and cylindrical forms) are two distinctive characteristics of the asexual morph (Hashimoto et al. 2017). Species of this family are saprobic on various plants (Hashimoto et al. 2017).
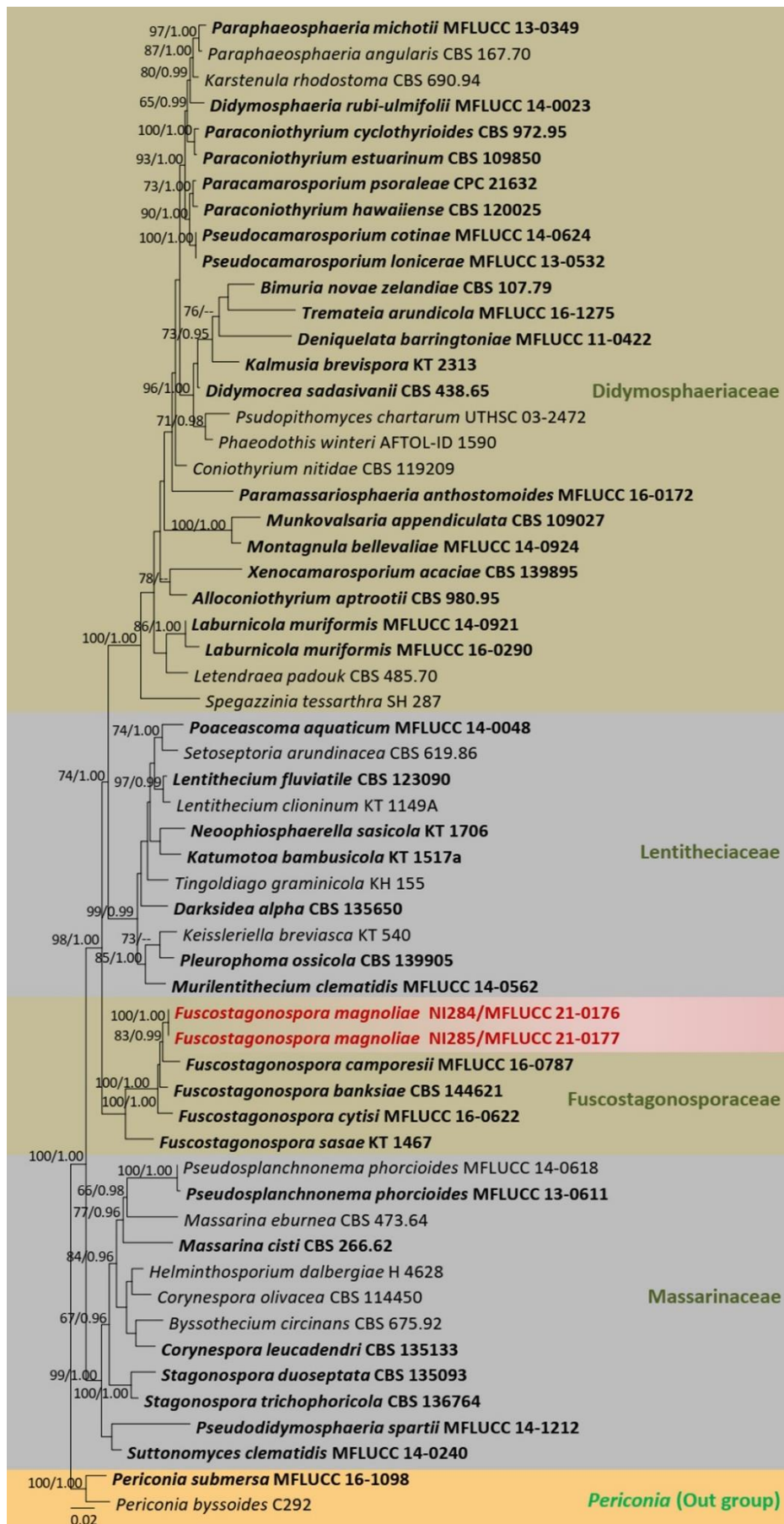
Figure 12 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, SSU and *tef1* sequence data. Related sequences of family Fuscostagonosporaceae and some other strains

of Pleosporales were obtained from Hyde et al. (2020). Fifty-eight strains are included in the combined gene analyses comprising 3230 characters after alignment (850 characters for LSU, 1000 characters for SSU, 480 characters for ITS and 900 characters for *tef1*). *Periconia byssoides* (C292) and *P. submerse* (MFLUCC 16-1098) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -18853.314671 is presented. The matrix had 1197 distinct alignment patterns, with 37.25% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
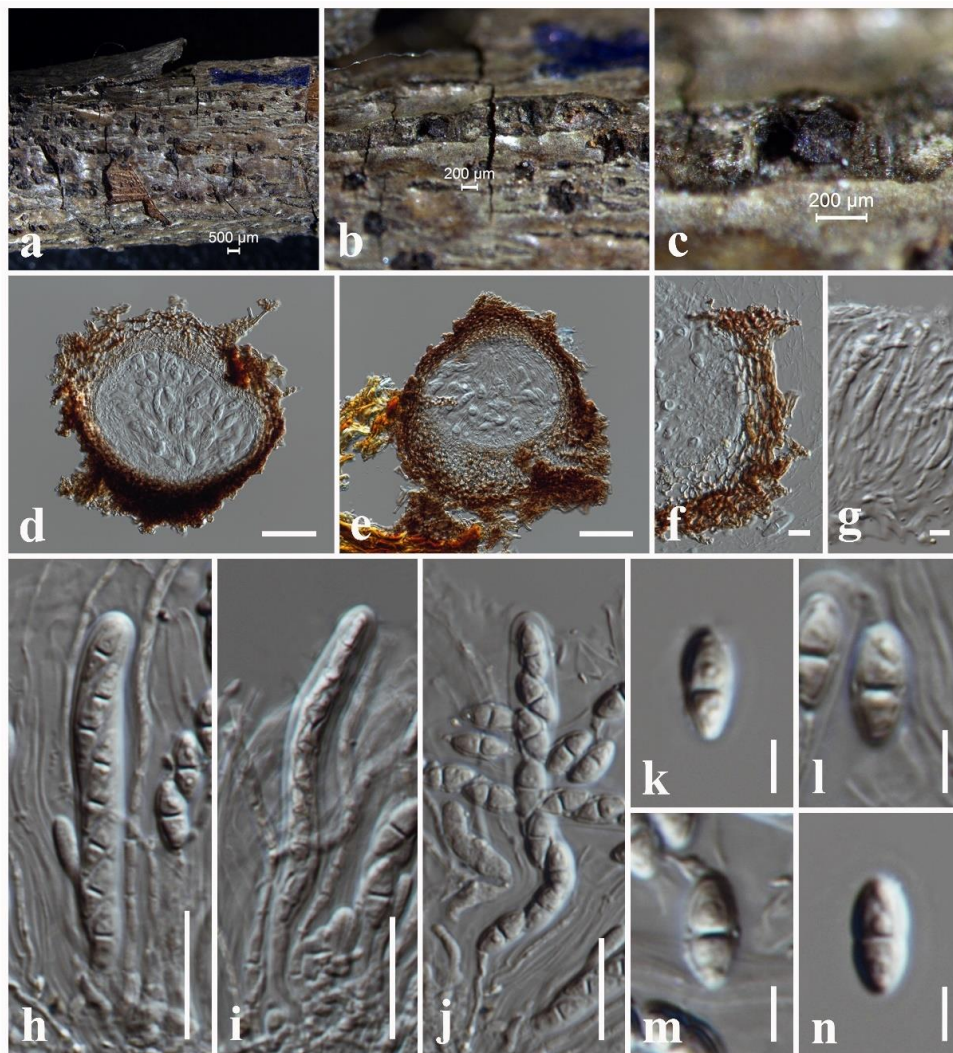

Figure 13 – *Fuscostagonospora magnoliae* (MFLU 21-0218, holotype). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a = 500 μm, b, c = 200 μm, d, e = 50 μm, f = 10 μm, g = 5 μm, h–j = 20 μm k–n = 5 μm.

Hermatomyces Speg.

The genus was erected by Spegazzini (1911) to accommodate *H. tucumanensis* as the type species. The asexual morph is characterized by sporodochial conidiomata and brown, muriform lenticular conidia or hyaline and cylindrical conidia (Hashimoto et al. 2017, Hyde et al 2019). Most of the species are saprobic on various plants of angiosperms and monocots, with a few rarely found on ferns (Castañeda-Ruiz & Heredia 2000) or gymnosperms (Mel'nik 2000, Hashimoto et al. 2017). These species have a worldwide distribution (Hashimoto et al. 2017).

Hermatomyces anomianthi N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 15

Index Fungorum number: IF 559517, Faces of Fungi number: FoF 10715

Etymology – Name reflects the host genus *Anomianthus*, from which the new species was isolated.

Holotype – MFLU 21-0221

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Ascomata* 150–220 μm high × 200–230 μm diam. ($\bar{x}$ = 180 × 220 μm, n = 10), dark brown to black, immersed, slightly erumpent, solitary to aggregated, scattered, appearing as black spots, with a poorly developed basal layer. *Ostiole* 40–70 μm wide, central. *Peridium* 15–25 μm wide, hyaline to light brown, comprising of thick-walled cells of *textura angularis* fusing and indistinguishable from the host tissues. *Hamathecium* comprising 1.4–2.5 μm wide, cylindrical to filiform, septate, pseudoparaphyses. *Asci* 75–110 × 19–24 μm ($\bar{x}$ = 100 × 21 μm, n = 20), 8-spored, bitunicate, cylindrical short, straight or slightly curved pedicellate. *Ascospores* 35–49 × 8–12 μm ($\bar{x}$ = 40 × 10 μm, n = 30), hyaline, broadly fusiform, 1-septate, constricted at the septum, widest at the centre and tapering towards ends, granular. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, surface smooth, velvety appearance, cream at the margin, pale brown in the centre; reverse: brown at the margin, dark brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND23 (MFLU 21-0221, holotype), ex-type living culture, MFLUCC 21-0202.

GenBank numbers – LSU: OK655817, ITS: OL413437, *tef1*: OM117546.

Notes – Our new isolate (MFLUCC 21-0202) groups with the ex-type strain of *Hermatomyces nabanheensis* (KUMCC 16-0149) and *H. turbinatus* (HKAS 112724) with 97% ML, 1.00 BYPP statistical support (Fig. 14). *Hermatomyces nabanheensis* was isolated on dead leaves of *Pandanus* sp. in China (Hyde et al. 2017) and *H. turbinatus* was isolated on woody litter of *Dipterocarpus* sp. in Thailand (Ren et al. 2021). Pairwise comparison of ITS sequence data between the new collection (MFLUCC 21-0202) and *H. nabanheensis* (KUMCC 16-0149) indicates 20 base pair (4%) differences across 500 nucleotides. Pairwise comparison of *tef1* sequence data between the new isolate (MFLUCC 21-0202) and *H. nabanheensis* indicates 29 base pair (3.11%) differences across 930 nucleotides. Pairwise comparison of ITS sequence data between the new collection (MFLUCC 21-0202) and *H. turbinatus* (HKAS 112724) indicates 30 base pair (6%) differences across 500 nucleotides. Pairwise comparison of *tef1* sequence data between the new isolate (MFLUCC 21-0202) and *H. turbinatus* (HKAS 112724) indicates 26 base pair (2.8%) differences across 930 nucleotides. Since our new collection is the sexual morph, we are unable to compare morphological differences with the type *H. nabanheensis* or *H. turbinatus*. We introduce our collection as the first sexual morph record of *Hermatomyces* and here we introduce *H. anomianthi* as a novel species.

Hermatomyces sphaericus (Sacc.) S. Hughes, Mycol. Pap. 50: 100 (1953)   Fig. 16

Index Fungorum number: IF 298410, Faces of Fungi number: FoF 05259

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: *Conidiomata* sporodochial, dark brown to black, circular or oval, pulvinate, often confluent, superficial, consisting of a well-developed, velvety, dense, thick, annular, dark brown sterile mycelial outer zone. *Mycelium* superficial, composed of a compact network of branched, septate, smooth or finely verrucose, thick-walled, brown hyphae. *Conidiophores* up to 35 μm long, 2-3 wide, micronematous, mononematous, cylindrical, pale brown, often corresponding to conidiogenous cells. *Conidia* one type, solitary, dry, lenticular. *Lenticular conidia* 23–29 × 22–27 μm ($\bar{x}$ = 27 × 25 μm, n = 30), globose, subglobose, muriform, smooth or verruculose, central cells brown, dark brown to blackish brown, sometimes all cells brown and muriform septation visible, outer ring of peripheral cells narrow or wide, pale brown to brown, often constricted at septa.
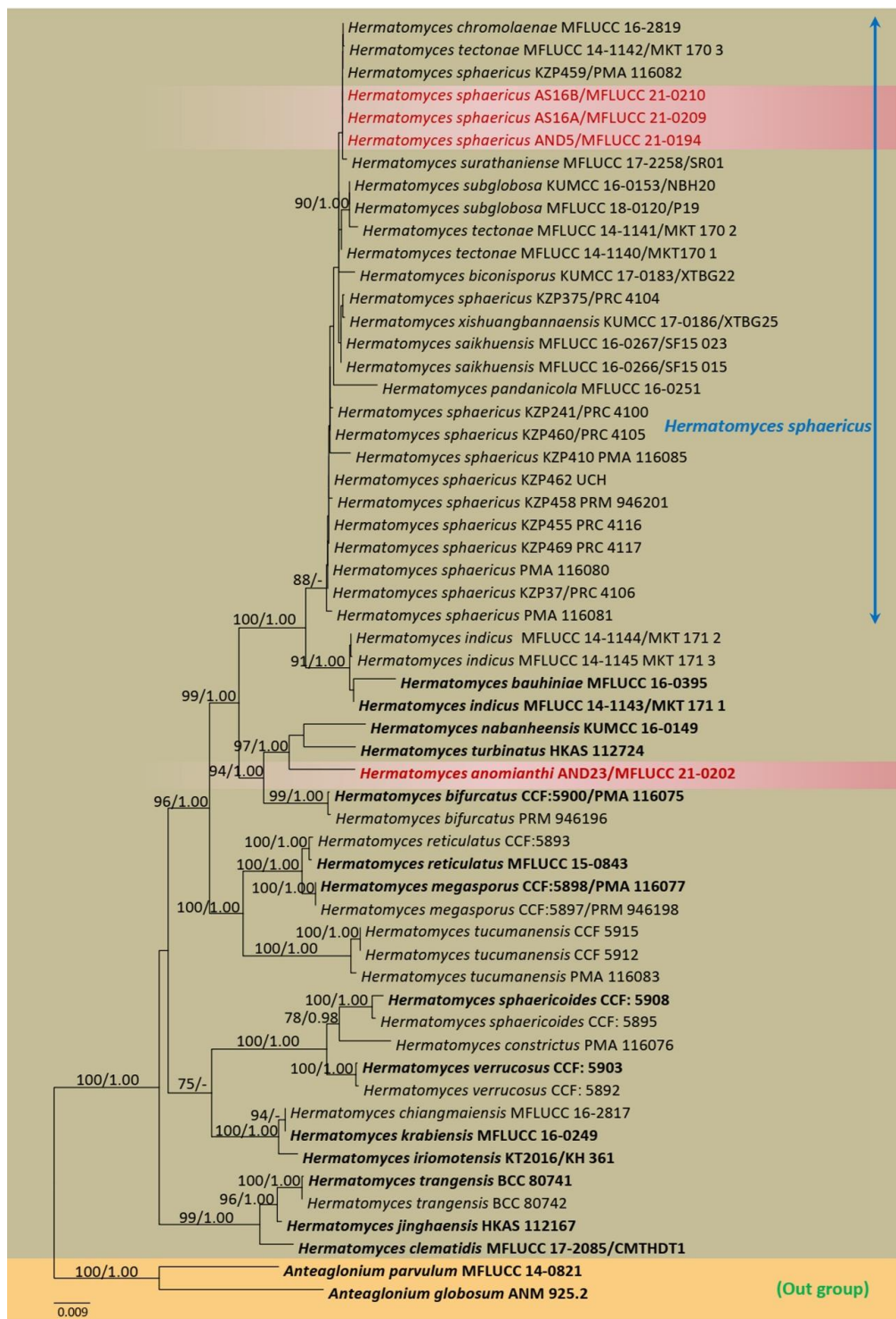
Figure 14 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, *tef1* and *rpb2* sequence data. Related sequences of *Hermatomyces* were obtained from Phukhamsakda et al. (2020). Fifty-five strains are included in the combined gene analyses comprising 3155 characters after alignment (825 characters for LSU, 500 characters for ITS, 930 characters for *tef1* and 900 characters for *rpb2*). *Anteaglonium globosum* (ANM 925.2) and *A. parvulum* (MFLUCC 14-0821) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -10621.809312 is presented. The matrix had 809 distinct alignment patterns, with 29.14% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, surface smooth, white at the margin, pale brown in the centre; reverse: cream at the margin, brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND5 (MFLU 21-0222), living culture, MFLUCC 21-0194; *ibid*., dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS16A (MFLU 21-0223), living culture, MFLUCC 21-0209, AS16B living culture, MFLUCC 21-0210.
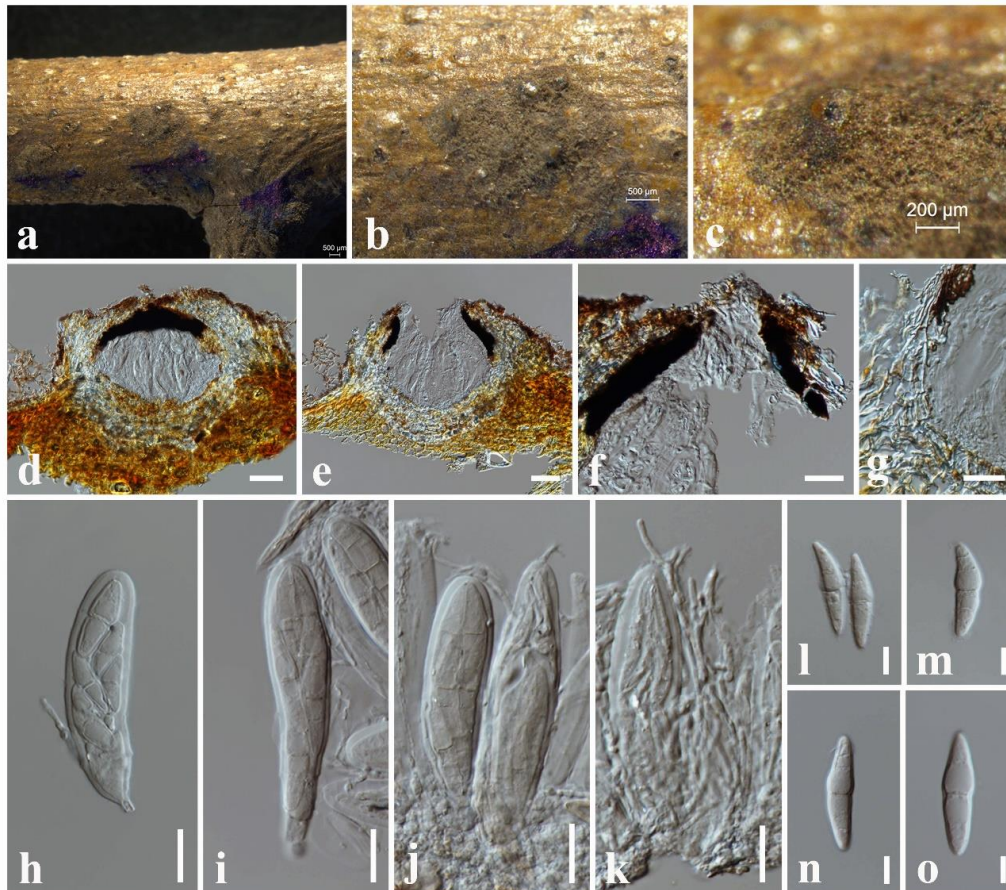

Figure 15 – *Hermatomyces anomianthi* (MFLU 21-0221, holotype). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Apex of ascoma. g Peridium. h–j Asci. k Pseudoparaphyses with asci. l–o Ascospores. Scale bars: b = 500 µm, c = 200 µm, d–k = 20 µm, l–o = 10 µm.

Known hosts and distribution – *Hermatomyces sphaericus* occurring on numerous host plants and distributed in worldwide including from on decorticated branches of *Barleria cristata* (Acanthaceae) in Philipines (Saccardo 1917), on the bark of *Albizia gummifera* (Mimosaceae), *Averrhoa carambola* (Oxalidaceae), *Theobroma cacao* (Sterculidaceae), and rachides of leaves of *Elais guineensis* (Arecaceae) collected in Ghana (Koukol et al. 2018), on fallen twigs and branches of angiosperms and on a palm petiole in Mexico (Heredia et al. 1997), on dead branches of *Rauvolfia vomitoria* (Apocynaceae) and dead wood of *Tectona grandis* (Lamiaceae) in China (Zhang et al. 2009), on dry thin branches of *Larix sibirica* (Pinaceae) in Russia (Mel'nik 2000), dead twigs attached to *Anomianthus dulcis* in Thailand (this study).

GenBank numbers – (AND5): LSU: OK655814, ITS: OL413434, (AS16A): LSU: OK655815, ITS: OL413435, *tef1*: OM117547, (AS16B): LSU: OK655816, ITS: OL413436, *tef1*: OM117548.

Notes – The type of *Hermatomyces sphaericus* (as *Stemphylium sphaericum*) was described on decorticated branches of *Barleria cristata* (Acanthaceae) in the Philippines (Saccardo 1917). Hughes (1953) synonymized *Stemphylium sphaericum* as *Hermatomyces sphaericus*. The phylogenetic treatment of Phukhamsakda et al. (2020) was followed for *Hermatomyces sphaericus* in this study. During our investigations of fungi on different host trees, three strains with brown, globose, subglobose, muriform lenticular conidia were isolated from dead twigs attached to the host plant of *Anomianthus dulcis* (Annonaceae) and *Alstonia scholaris* (Apocynaceae) in Thailand. We recognized these three strains belong to *Hermatomyces sphaericus* based on morphology and phylogeny of combined LSU, ITS, *tef1* and *rpb2* sequence data (Fig. 14). Thus, new collections are reported as new host records of *Anomianthus dulcis* (Annonaceae) and *Alstonia scholaris* (Apocynaceae) in Thailand herein.
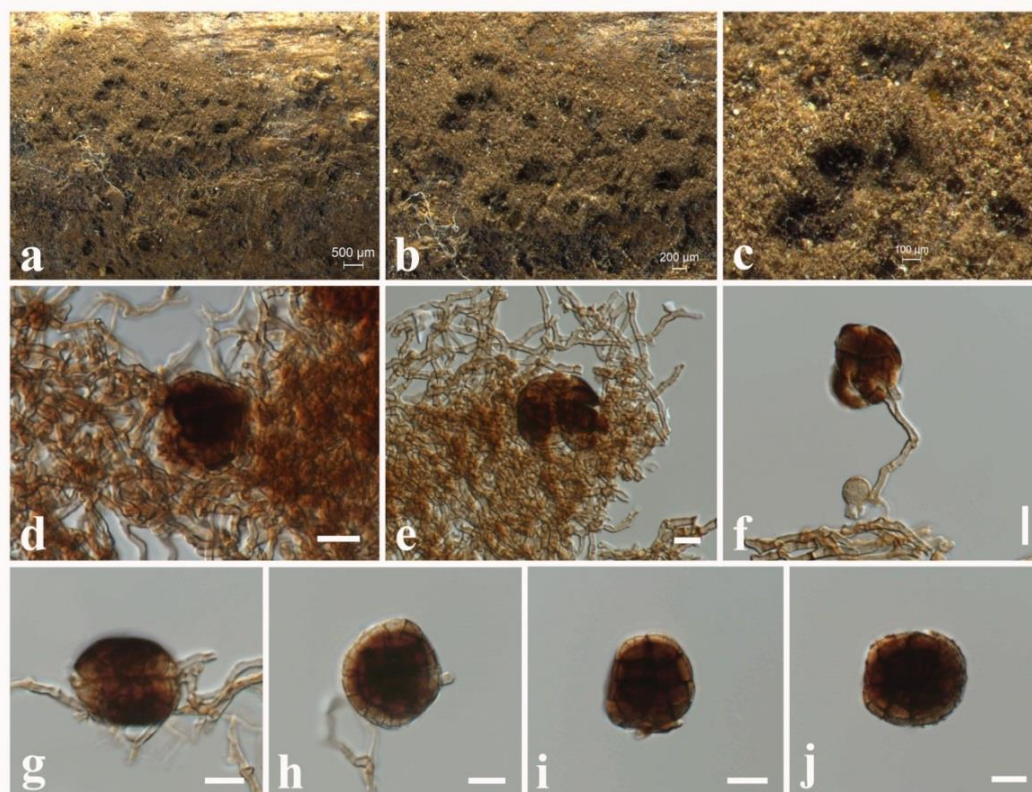

Figure 16 – *Hermatomyces sphaericus* (MFLU 21-0222). a–c Colonies on substrate. d, e Conidia with mycelia. f Conidiophore with conidia. g–j Conidia. Scale bars: a = 500 μm, b = 200 μm, c = 100 μm, d–j = 10 μm.

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous

Macrodiplodiopsidaceae was introduced by Crous et al. (2015) with *Macrodiplodiopsis* Petr. as the type genus. Two genera are accepted in this family, *viz. Macrodiplodiopsis* and *Pseudochaetosphaeronema* (Hongsanan et al. 2020a). In this study, we follow Hongsanan et al. (2020a) as the latest treatment for Macrodiplodiopsidaceae.

Pseudochaetosphaeronema Punith.

Pseudochaetosphaeronema was introduced by Punithalingam (1979) to accomodate *P. larense* as the type species. *Pseudochaetosphaeronema* members can found as saprobes in both terrestrial and aquatic habitats, as well as some can be human pathogens (Zhang et al. 2012a, Hongsanan et al. 2020a). Seven *Pseudochaetosphaeronema* species are listed in Index Fungorum (2022), such as P. *ginkgonis*, *P. kunmingense*, *P. larense*, *P. martinelli*, *P. pandanicola* and *P. siamense*. In this study, we introduce a new species, *Pseudochaetosphaeronema magnoliae*.
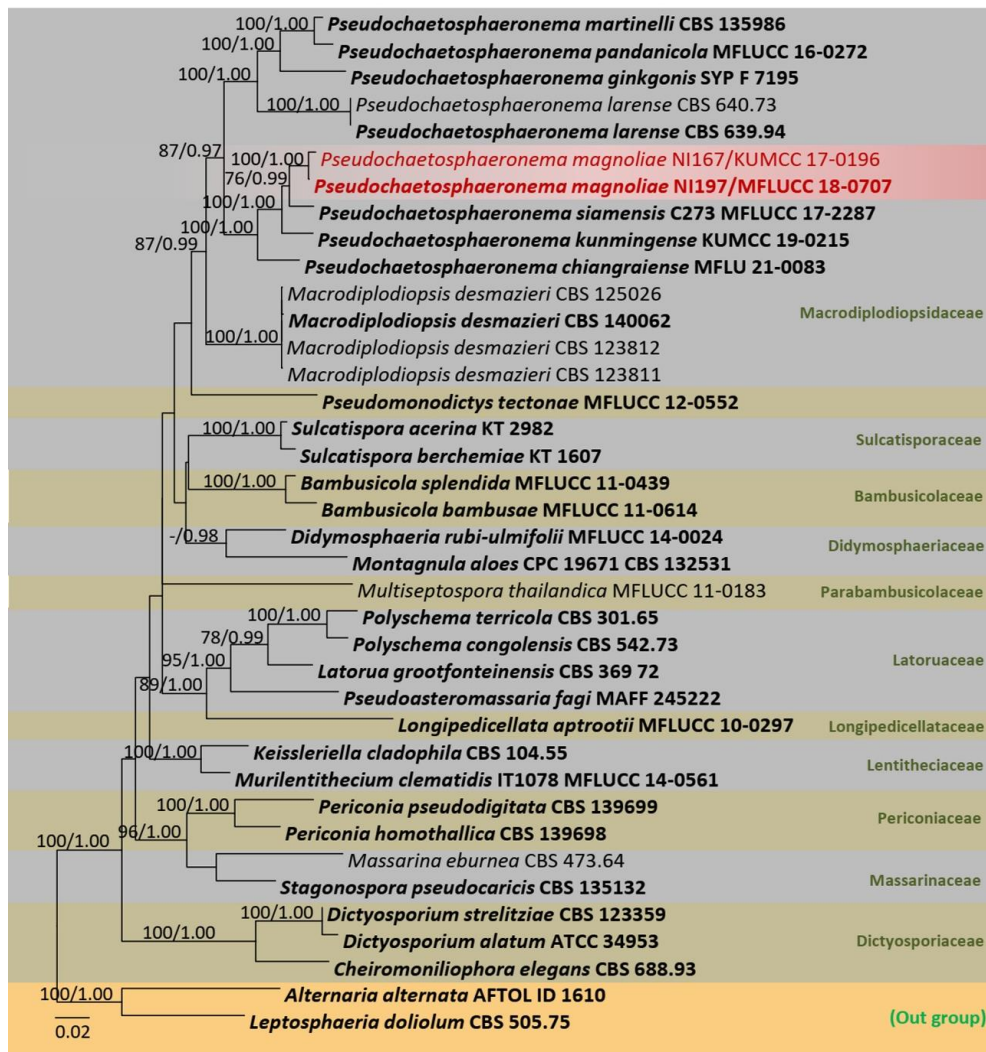
Figure 17 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, ITS and *tef1* sequence data. Related sequences of Macrodiplodiopsidaceae and some other strains of Pleosporales were obtained from Hyde et al. (2020). Thirty-seven strains are included in the combined gene analyses comprising 3330 characters after alignment (890 characters for LSU, 1000 characters for SSU, 850 characters for ITS and 890 characters for *tef1*). *Alternaria alternata* (AFTOL-ID 1610), *Leptosphaeria doliolum* (CBS 505.75) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -18358.033323 is presented. The matrix had 1177 distinct alignment patterns, with 31.02% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Pseudochaetosphaeronema magnoliae N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.

Fig. 18

Index Fungorum number: IF 559518, Faces of Fungi number: FoF 10716

Etymology – Name reflects the host genus *Magnolia*, from which the new species was isolated.

Holotype – MFLU 18-1296

Saprobic on dead twigs attached to *Magnolia candolli*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 160–190 × 150–180 µm ($\bar{x}$ = 170 × 165 µm, n = 10), solitary, globose to subglobose, dark brown to black, immersed to erumpent, solitary, unilocular, ostiolate. *Conidiomatal wall* 15–20 µm wide, composed of several layers of small, flattened, brown to dark

brown pseudoparenchymatous cells, cells towards the inside lightly pigmented, arranged in a *textura angularis*, at the outside, darker, fusing and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 × 2.5–3.5 µm ($\bar{x}$ = 4.6 × 3.2 µm, n = 20), produced from inner stromatic tissue, monophialidic, cylindrical or ampulliform, integrated, hyaline, smooth-walled. *Conidia* 12–18 × 2–3.5 µm ($\bar{x}$ = 14 × 3 µm, n = 40), hyaline, cylindrical to fusoid, solitary, smooth, thin-walled, straight, apex obtuse, unicellular, without mucilaginous sheath.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, white at the margin, light brown in the centre; reverse: cream at the margin, dark brown in the centre.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 13 September 2017, N. I. de Silva, NI197 (MFLU 18-1296, holotype), ex-type living culture, MFLUCC 18-0707, China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI167 (MFLU 18-1028), living culture, KUMCC 17-0196.

GenBank numbers – (NI197); LSU: OL813497, SSU: OL824793, ITS: OM212457, *tef1*: ON203109, (NI167); LSU: OL813498, SSU: OL824794, ITS: OM212458, *tef1*: ON203110.

Notes – According to the multi-gene phylogeny, *Pseudochaetosphaeronema magnoliae* clustered with *P. kunmingense* and *P. siamense* with 100% ML and 1.00 BYPP support (Fig. 17). *Pseudochaetosphaeronema magnoliae* can be distinguished from *P. kunmingense* in having smaller conidiomata (160–190 × 150–180 µm *vs* 180–250 µm diam.) and hyaline, aseptate conidia (12–18 × 2–3.5 µm), whereas *P. kunmingense* has light brown, 3-septate conidia (10–15 × 4–6 µm) (Hyde et al. 2020a). In addition, *P. magnoliae* differs from *P. siamense* by distinct size differences of conidiomata (160–190 × 150–180 µm *vs* 85–100 × 80–90 µm), conidiogenous cells (4–5 × 2.5–3.5 µm *vs* 8–17 × 1–2.5 µm) and conidia (12–18 × 2–3.5 µm *vs* 3–5 × 2.5–3 µm) (Jayasiri et al. 2019). It is interesting to note that *Pseudochaetosphaeronema magnoliae* was recorded from both China and Thailand in *Magnolia candolli*.

Neohendersoniaceae A. Giraldo & Crous

Giraldo et al. (2017) introduced Neohendersoniaceae to accommodate a monotypic genus *Neohendersonia* typified by *N. kickxii*. Species of this family are endophytes or saprobic on plants, and human pathogens (Tanaka et al. 2017, Hongsanan et al. 2020a). The family is characterized by having immersed, globose to depressed globose, ostiolate ascomata, bitunicate asci, 2-seriate, broadly fusiform, 1- or multi-septate, hyaline ascospore (Hongsanan et al. 2020a). The asexual morph is characterized by having, immersed, globose to collabent conidiomata, discrete, determinate or indeterminate conidiogenous cells and obovoid, cylindrical, clavate or fusiform, distoseptate or euseptate conidia (Giraldo et al. 2017).

Amarenographium solium grouped within Neohendersoniaceae in our phylogeny and also in previous studies (Tanaka et al. 2017, Devadatha et al. 2020). However, species of *Amarenographium* is polyphyletic, and therefore, the family placement of *Amarenographium sensu stricto* remains unresolved (Tanaka et al. 2017). Neohendersoniaceae comprises five genera, *Brevicollum*, *Crassiparies*, *Medicopsis*, *Neohendersonia* and *Neomedicopsis* (Tanaka et al. 2017, Devadatha et al. 2020, Hongsanan et al. 2020a).

Muriformispora N.I. de Silva, S. Lumyong & K.D. Hyde, gen. nov.

Index Fungorum number: IF 900049, Facesoffungi number: FoF 13097
Etymology – Referring to the muriform ascospores.

Saprobic on dead twigs attach to *Magnolia* sp. Sexual morph: *Ascomata* black, globose to subglobose, solitary, scattered, immersed to slightly erumpent, uni-loculate, forming black spots on host surface, ostiolate. *Ostiole* central. *Peridium* composed of several layers of hyaline, light brown to dark brown, *textura angularis* cells. *Hamathecium* composed of dense, filamentous, cellular pseudoparaphyses, with indistinct septa. *Asci* 8-spored, bitunicate, fissitunicate, pyriform,

pedicellate, with furcate to obtuse end, apically rounded. *Ascospores* overlapping, 1-3-seriate, broadly ellipsoidal, muriform, 4–5 transverse septa and 2–3 longitudinal septa with apex rounded and basal end acute or truncate, at first hyaline becoming olivaceous-brown at maturity, constricted at the central septum and slightly at the other septa, with guttules in almost every cell, smooth-walled. Asexual morph: Not observed.
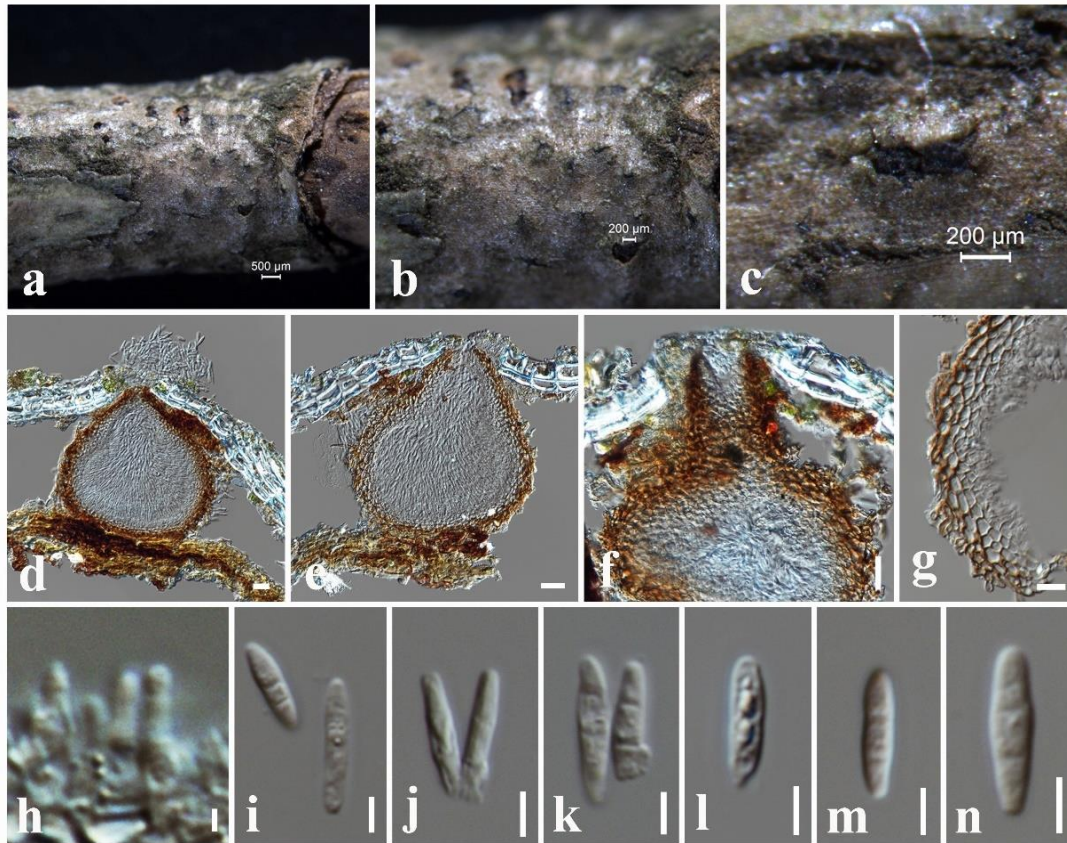

Figure 18 – *Pseudochaetosphaeronema magnoliae* (MFLU 18-1296, holotype). a The specimen. b, c Appearance of immersed conidiomata on substrate. d, e Vertical sections through conidiomata. f Vertical sections through conidioma and neck region. g Conidiomatal wall. h Conidiogenous cells. i–n Conidia. Scale bars: a = 500 μm, b, c = 200 μm, d–f = 20 μm, g = 10 μm, h = 2 μm, i–n = 5 μm.

Muriformispora magnoliae N.I. de Silva, S. Lumyong & K.D. Hyde, sp.nov.   Fig. 20

Index Fungorum number: IF 900050, Faces of Fungi number: FoF 13098

Etymology – Name reflects the host genus *Magnolia*, from which the new species was isolated.

Holotype – MFLU 18-2645.

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 170–220 μm high × 200–260 μm diam. ($\bar{x} = 200 \times 240$ μm, n = 10), black, globose to subglobose, solitary, scattered, immersed to slightly erumpent, forming black spots on host surface, uni-loculate, ostiolate. *Ostiole* 50–70 μm wide, central. *Peridium* 14–28 μm, composed of several layers of hyaline, light brown to dark brown cells of *textura angularis*. *Hamathecium* composed of dense, 1.5–2 μm wide, filamentous, cellular pseudoparaphyses, with indistinct septa. *Asci* 80–95 × 25–30 μm ($\bar{x} = 85 \times 28$ μm, n = 20), 8-spored, bitunicate, fissitunicate, pyriform, pedicellate, with furcate to obtuse end, apically rounded. *Ascospores* 19–24 × 8–12 μm ($\bar{x} = 22 \times 10$ μm, n = 30), overlapping, 1-3-seriate, broadly ellipsoidal, muriform, 4–5 transverse septa and 2–3 longitudinal septa with apex rounded and basal end acute or truncate, at first hyaline becoming olivaceous-brown at maturity, constricted

at the central septum and slightly at the other septa, with guttules in almost every cell, smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: olivaceous green, circular, flat, edge entire, margin well-defined, cottony to fairly fluffy with sparse aspects, white at the margin; reverse: grey from the centre of the colony, cream at margin.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to the *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI261 (MFLU 18-2645, holotype), ex-type living culture, MFLUCC 19-0036.

GenBank numbers – (NI261); LSU: OL813499, SSU: OL824795, ITS: OM212459, *tef1*: ON303277, *rpb2*: ON502385, (NI261D); LSU: OL813500, SSU: OL824796, ITS: OM212460, *tef1*: ON303278.

Notes – The present phylogenetic analyses indicate that *Muriformispora* (*Muriformispora magnoliae*), constitutes a monophyletic clade distinctly separated from five genera, *Brevicollum*, *Crassiparies*, *Medicopsis*, *Neohendersonia* and *Neomedicopsis* in Neohendersoniaceae with 99% ML and 0.99 BYPP support (Fig. 19). *Neohendersonia* (Wijayawardene et al. 2016) and *Neomedicopsis* (Crous et al. 2019a) are known from their asexual morph characteristics. Based on morphological characteristics of sexual morphs within species representing Neohendersoniaceae, the new genus (*Muriformispora*) is distinct from *Brevicollum*, *Crassiparies* and *Medicopsis* in having broadly ellipsoidal, muriform ascospores (de Gruyter et al. 2012, Tanaka et al. 2017). *Muriformispora* also has pyriform, pedicellate, apically rounded asci, with furcate to obtuse end, apically rounded asci whereas *Brevicollum*, *Crassiparies* and *Medicopsis* have cylindrical or clavate asci (de Gruyter et al. 2012, Tanaka et al. 2017). In addition, ascomata structures of *Brevicollum*, *Crassiparies* and *Medicopsis* are different from *Muriformispora*. *Medicopsis* has stromata with poorly developed interior, immersed to erumpent from the bark with an ostiolar canal, circular to irregular in shape containing globose to subglobose, ostiolate, perithecia (de Gruyter et al. 2012). *Brevicollum* has scattered, sometimes 2–3 grouped, immersed, erumpent at ostiolar neck, globose to depressed globose ascomata (Tanaka et al. 2017). *Crassiparies* has scattered, immersed, erumpent at the ostiolar neck, subglobose, ostiolate ascomata (Tanaka et al. 2017). The new genus has black, globose to subglobose, uni-loculate, solitary, scattered, immersed to semi-immersed, ostiolate ascomata with black spots on the host surface. Based on morphological differences among other reported sexual morphs in Neohendersoniaceae and the phylogenetic analyses, we placed *Muriformispora* in the family Neohendersoniaceae. However, further collections are needed for the expansion of this genus.

Neomassariaceae Ariyawansa, Jaklitsch & Voglmayr

Neomassariaceae was introduced by Ariyawansa et al. (2018) to place the *Neomassaria* as the type genus. The members of Neomassariaceae differ from Massariaceae species in having small globose to subglobose ascomata, small asci lacking a refractive ring and small, hyaline, 1-septate ascospores (Ariyawansa et al. 2018, Hongsanan et al. 2020a).

Neomassaria Mapook, Camporesi & K.D. Hyde

Neomassaria was introduced as a monotypic genus based on multi-gene phylogeny and morphological characteristics (Ariyawansa et al. 2018). Two *Neomassaria* species are listed in Index Fungorum (2022), *viz. N. fabacearum* and *N. formosana*. In this study, we introduce two new *Neomassaria* species *viz. N. alstoniae* and *N. thailandica*.

Neomassaria alstoniae N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 22
Index Fungorum number: IF 559519, Faces of Fungi number: FoF 10717

Etymology – Name reflects the host genus *Alstonia*, from which the new species was isolated.
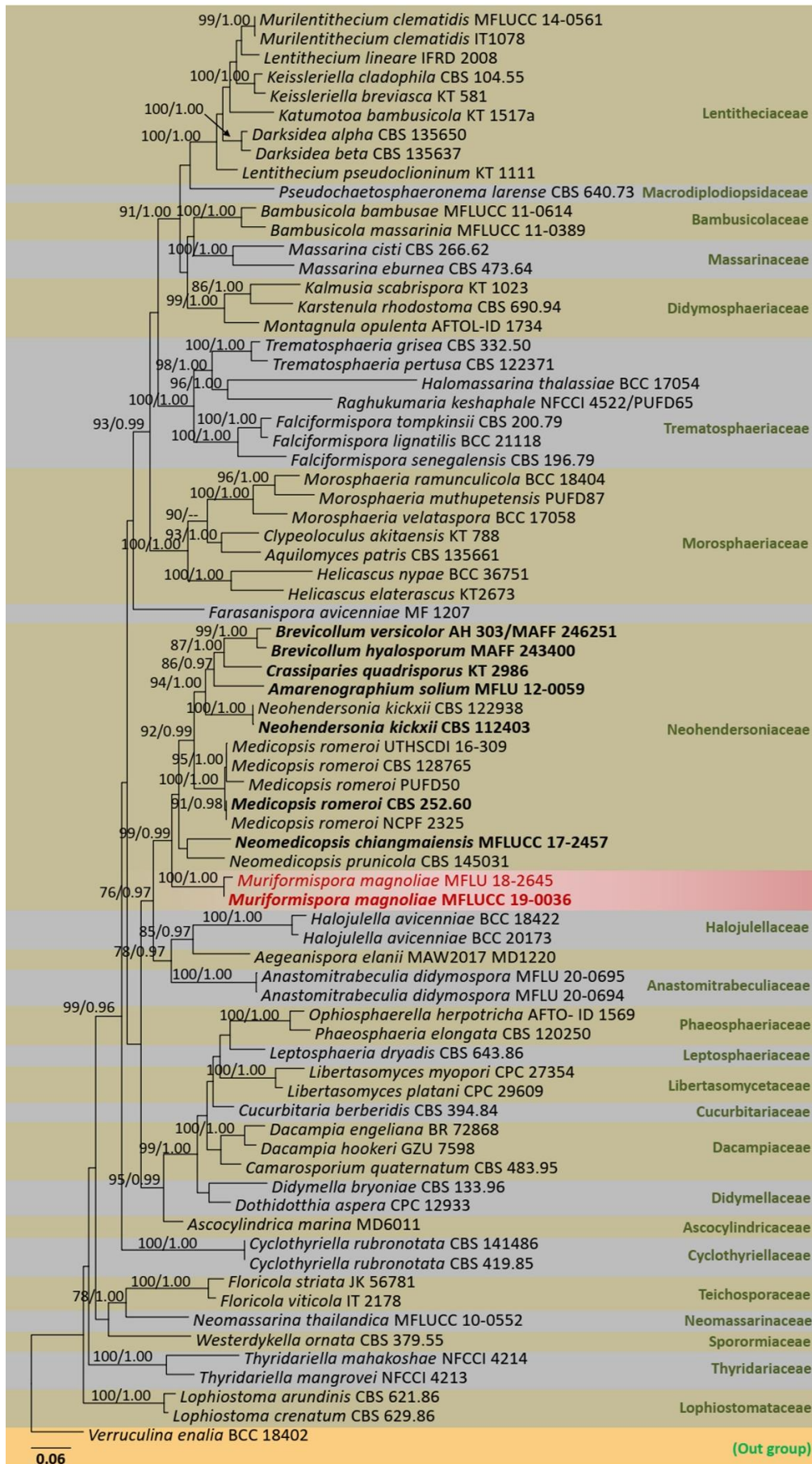
Holotype – MFLU 21-0238.

Figure 19 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, ITS, *tef1* and *rpb2* sequence data. Related sequences of Neohendersoniaceae and some other strains of

Pleosporales were obtained from Devadatha et al. (2020). Seventy-five strains are included in the combined gene analyses comprising 4100 characters after alignment (900 characters for LSU, 970 characters for SSU, 480 characters for ITS, 900 characters for *tef1* and 850 characters for *rpb2*). *Verruculina enalia* (BCC 18402) is used as outgroup taxon. The best RAxML tree with a final likelihood value of -45735.366656 is presented. The matrix had 2261 distinct alignment patterns, with 39.56% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
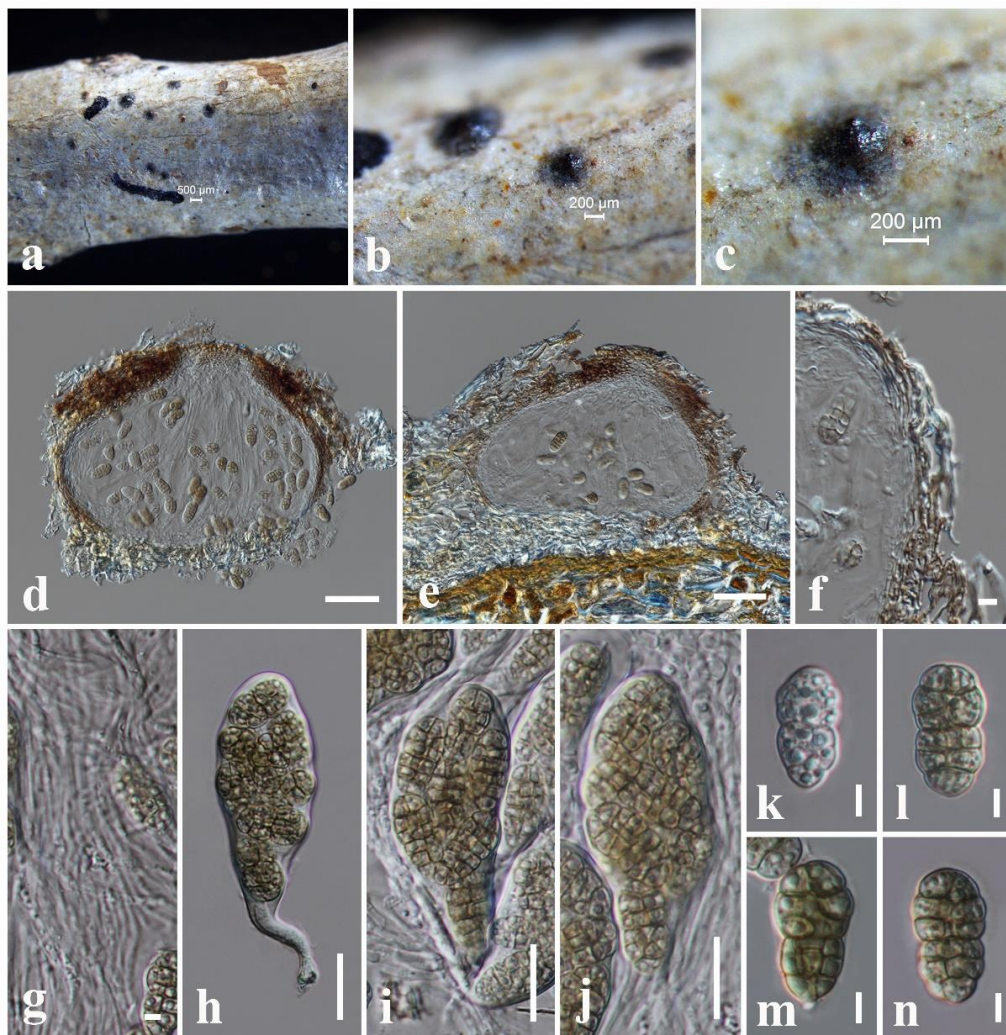

Figure 20 – *Muriformispora magnoliae* (MFLU 18-2645, holotype). a The specimen. b, c Appearance of ascomata on the host surface. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a = 500 μm, b, c = 200 μm, d, e = 50 μm, f, g, k–n = 5 μm, h–j = 20 μm.

Saprobic on dead twigs attached to *Alstonia scholaris*. Sexual morph: *Ascomata* 170–300 μm high × 300–350 μm diam. ($\bar{x}$ = 250 × 320 μm, n = 10), solitary or scattered, coriaceous, immersed to slightly erumpent, visible as black dots on the host surface, unilocular, globose to subglobose, brown to dark brown. *Ostiole* central. *Peridium* 20–36 μm wide, comprising light brown cells of *textura angularis*, inner cells hyaline to lightly pigmented, fusing at the outside indistinguishable from the host tissues. *Hamathecium* comprising 1–2 μm wide, cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 80–100 × 12–18 μm ($\bar{x}$ = 92 × 16 μm, n = 20), 8-spored, bitunicate, oblong to cylindrical, short pedicellate, with ocular chamber. *Ascospores* 20–24 × 7–10

μm ($\overline{x}$ = 22 × 8.5 μm, n = 30), overlapping 1–2-seriate, hyaline, ellipsoid to fusiform, 1-septate, constricted at the septum, without a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 12 mm diameter after 1 week at 25 °C, colonies from above: white, irregular, undulate margin, flat, slightly raised, fluffy appearance, cream at the margin; reverse: brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS14 (MFLU 21-0238, holotype), ex-type living culture, MFLUCC 21-0213.

GenBank numbers – LSU: OL457711, SSU: OL764416.

Notes – *Neomassaria alstoniae* was collected from dead twigs of *Alstonia scholaris* in Thailand. According to the multi-gene phylogeny, *N. alstoniae* forms a sister lineage to *N. formosana* with 94% ML and 1.00 BYPP support (Fig. 21). *Neomassaria formosana* can be distinguished from *N. alstoniae* in having a distinct neck in ascomata and periphyses (Ariyawansa et al. 2018). *Neomassaria formosana* was introduced by Ariyawansa et al. (2018) from a dead stem of *Rhododendron* species in Taiwan Province of China. Additional morphological differences of reported *Neomassaria* are mentioned in Table 4.

Neomassaria thailandica N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 23

Index Fungorum number: IF 559520, Faces of Fungi number: FoF 10718

Etymology: The epithet '*thailandica*' refers to the country (Thailand) where the type specimen was collected.

Holotype: MFLU 21-0239.

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Ascomata* 170–200 μm high × 200–280 μm diam. ($\overline{x}$ = 190 × 250 μm, n = 10), solitary or scattered, coriaceous, immersed to slightly erumpent, visible as black dots on the host surface, unilocular or bilocular, globose to subglobose, brown to dark brown. *Ostiole* central. *Peridium* 12–20 μm wide, comprising light brown cells of *textura angularis*, inner cells hyaline, fusing at the outside indistinguishable from the host tissues. *Hamathecium* comprising 1–2 μm wide, cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 80–120 × 14–22 μm ($\overline{x}$ = 95 × 18 μm, n = 20), 8-spored, bitunicate, oblong to cylindrical, short pedicellate, with ocular chamber. *Ascospores* 20–28 × 6–9 μm ($\overline{x}$ = 26 × 8 μm, n = 30), overlapping 1–2-seriate, hyaline, ellipsoid to fusiform, 1-septate, constricted at the septum, without a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 17 mm diameter after 1 week at 25 °C, colonies from above: grey, circular, undulate margin, flat, slightly raised, white at the margin; reverse: greyish brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs of *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND4 (MFLU 21-0239, holotype), ex-type living culture, MFLUCC 21-0193.

GenBank numbers – LSU: OL457712, SSU: OL700224, *tef1*: ON032376.

Notes – The morphological characteristics of our collection fit well with *Neomassaria* species in having immersed to erumpent, coriaceous, globose to subglobose ascomata, oblong to cylindrical asci and hyaline, ellipsoid to fusiform, 1-septate ascospores (Hyde et al. 2016, Ariyawansa et al. 2018, Hongsanan et al. 2020a). Multi-gene phylogeny indicates that our collection constitutes an independent lineage between *Neomassaria alstoniae* and *N. fabacearum* with 99% ML and 1.00 BYPP support (Fig. 21). Their morphological differences are mentioned in Table 4. A comparison of 902 nucleotides across the *tef1* gene region of *Neomassaria thailandica* and *N. fabacearum* shows 39 base pair differences (4.32%).

Nigrogranaceae Jaklitsch & Voglmayr

Jaklitsch & Voglmayr (2016) established Nigrogranaceae in Pleosporales to accommodate *Nigrograna* based on phylogeny and morphology. Members of this family are characterized by immersed-erumpent to superficial ascomata, papillate to cylindrical ostiolar necks, clavate,

bitunicate, fissitunicate asci, fusoid to narrowly ellipsoid 1–3-euseptate and pale to chocolate brown ascospores (Jaklitsch & Voglmayr 2016).
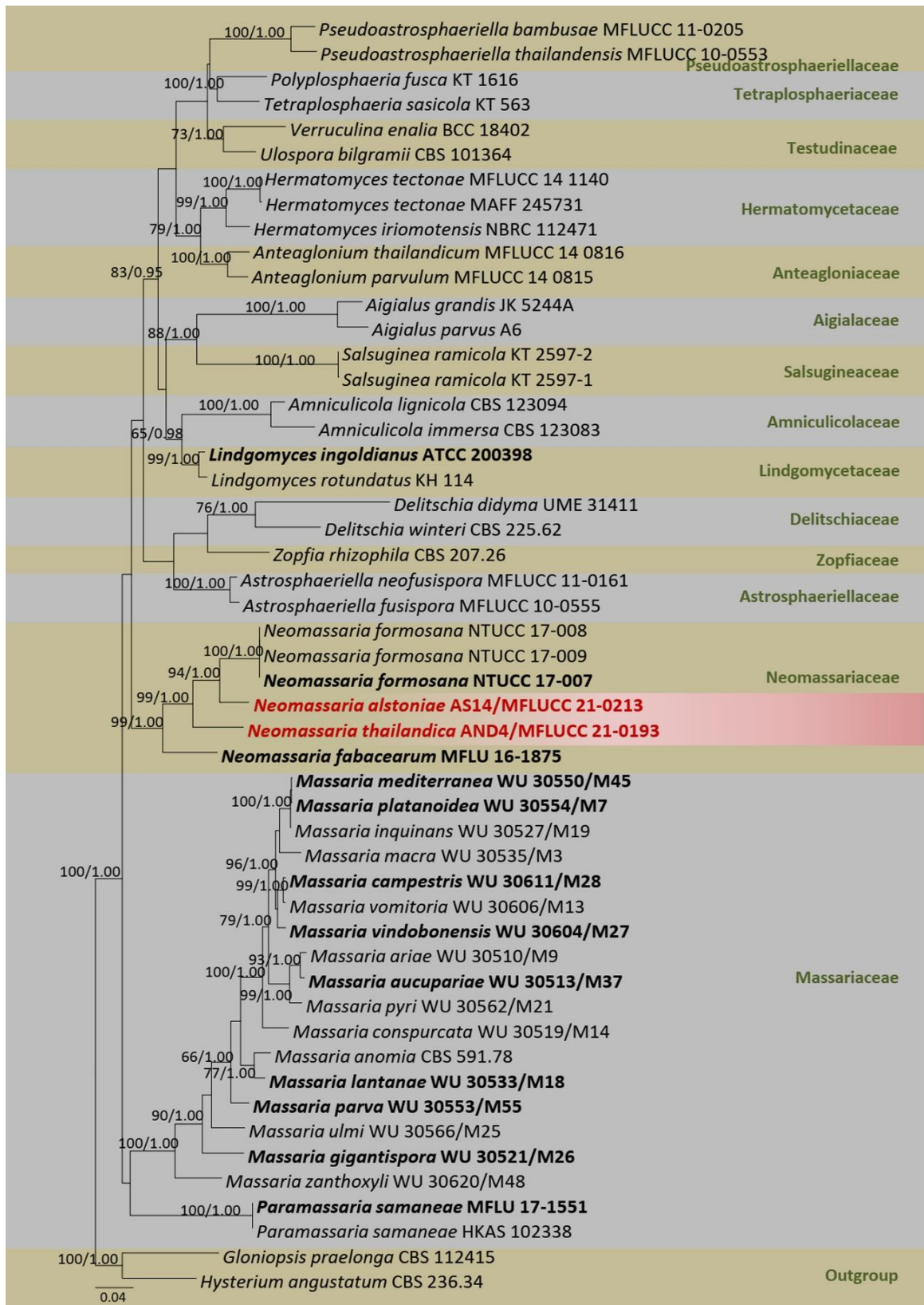

Figure 21 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, *tef1* and *rpb2* sequence data. Related sequences of Neomassariaceae and several closely related families in Pleosporales were obtained from Ariyawansa et al. (2018) and Hyde et al. (2019). Fifty-one strains are included in the combined gene analyses comprising 3550 characters after alignment (880

characters for LSU, 800 characters for SSU, 900 characters for *tef1* and 970 characters for *rpb2*). *Gloniopsis praelonga* (CBS 112415), *Hysterium angustatum* (CBS 236.34) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -26276.529060 is presented. The matrix had 1648 distinct alignment patterns, with 32.32% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
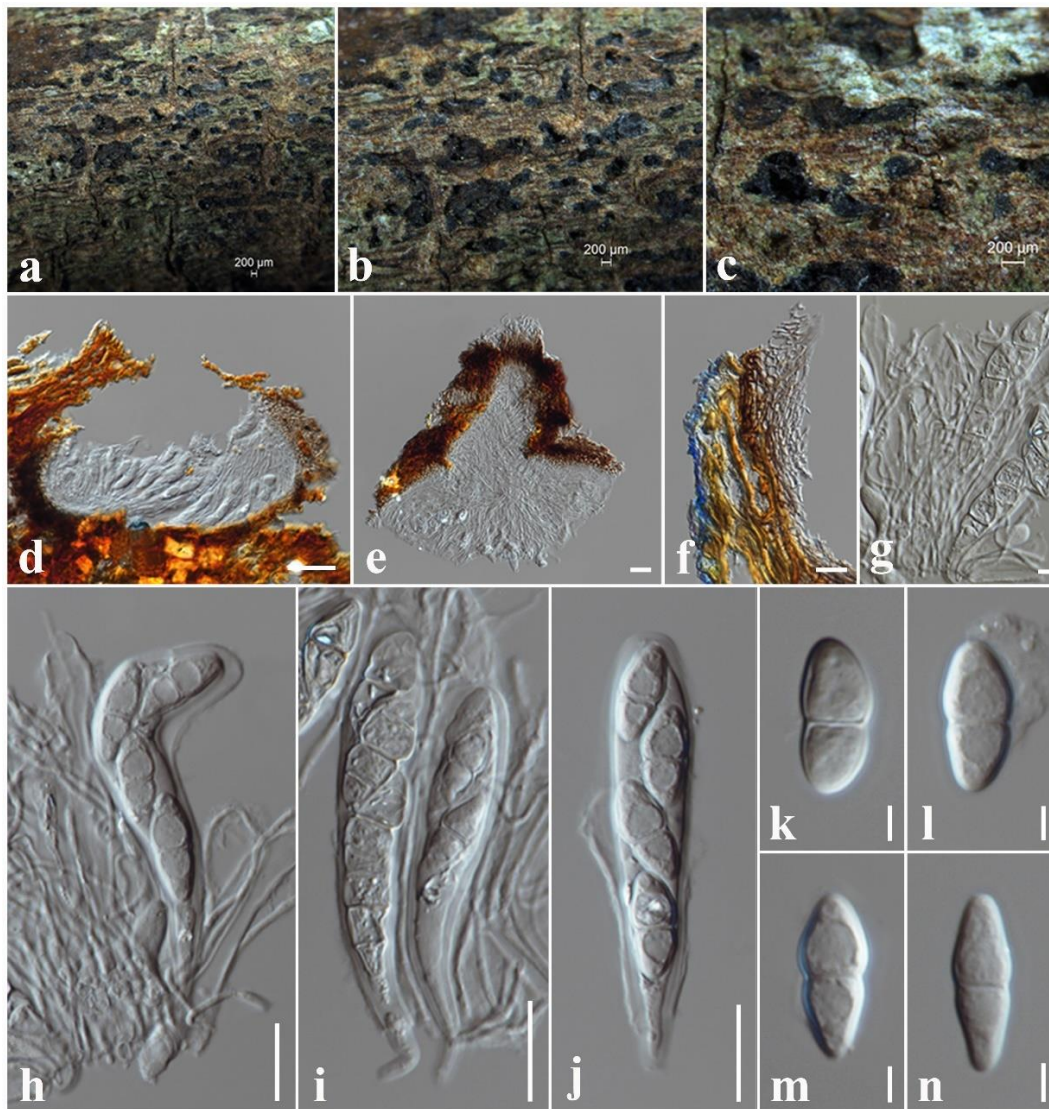

Figure 22 – *Neomassaria alstoniae* (MFLU 21-0238, holotype). a–c Appearance of ascomata on substrate. d Vertical section through ascoma. e Vertical section through neck region. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a–c = 200 μm, d = 50 μm, e, f = 20 μm, g = 5 μm, h–j = 20 μm, k–n = 5 μm.

Nigrograna Gruyter, Verkley & Crous

    Nigrograna is characterized by depressed globose to globose, immersed to erumpent, less commonly superficial ascomata, papillate ostiolar necks, clavate, bitunicate, fissitunicate asci and fusoid to narrowly ellipsoid, 1–3-euseptate, pale to chocolate brown ascospores (Jaklitsch & Voglmayr 2016). The asexual morph is characterized by pycnidial conidiomata, oblong, cylindrical or allantoid, sometimes ellipsoid, hyaline, 1-celled, smooth conidia (de Gruyter et al. 2012, Jaklitsch & Voglmayr 2016). *Nigrograna* species exhibit diverse fungal life-styles in nature as saprobic, endophytic and fungicolous in plant hosts while one was a human pathogen (de Gruyter et

al. 2012, Kolarik et al. 2016, Jaklitsch & Voglmayr 2016, Hyde et al. 2017, Tibpromma et al. 2017, Zhao et al. 2018).
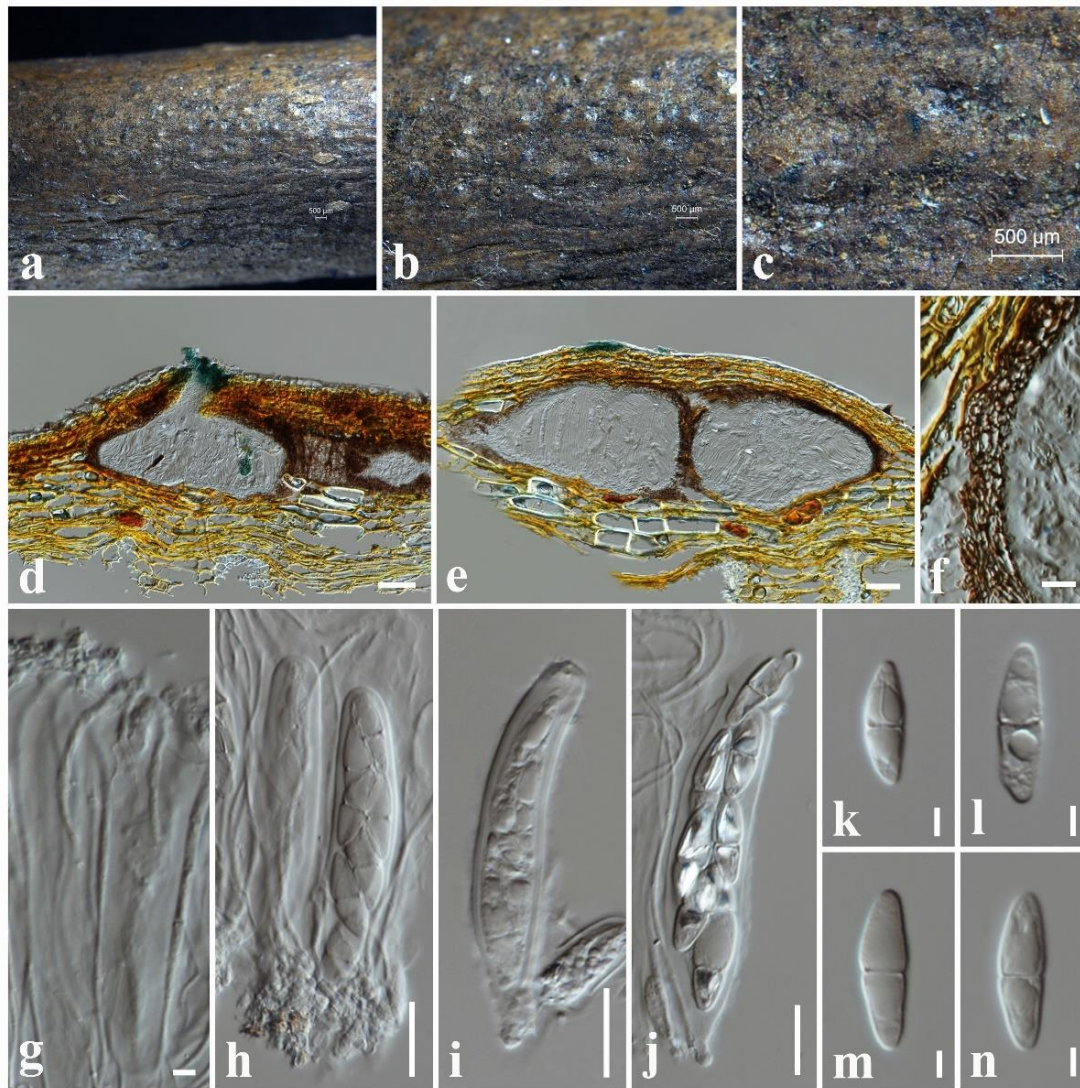

Figure 23 – *Neomassaria thailandica* (MFLU 21-0239, holotype). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a–c = 500 μm, d, e = 50 μm, f = 10 μm, g, k–n = 5 μm, h–j = 20 μm.

Table 4 Synopsis of recorded *Neomassaria* species.

| Taxa	Ascomata (μm)	Peridium (μm)	Asci (μm)	Ascospores (μm)	Host	Country	References
N. alstoniae	**170–300 × 300–350**	**20–36**	**80–100 × 12–18**	**20–24 × 7–10**	**Alstonia scholaris**	**Thailand**	**This study**
N. fabacearum	200–220 × 130–150	10–20	65–75 × 10–15	18–20 × 5–6	*Hippocrepis emerus*	Italy	Hyde et al. (2016)
N. formosana	100–200 × 100–370	13–40	80–125 × 14–17	20–30 × 3–7	*Rhododendron*	Taiwan	Ariyawansa et al. (2018)
N. thailandica	**170–200 × 200–280**	**12–20**	**80–120 × 14–22**	**20–28 × 6–9**	**Anomianthus dulcis**	**Thailand**	**This study**
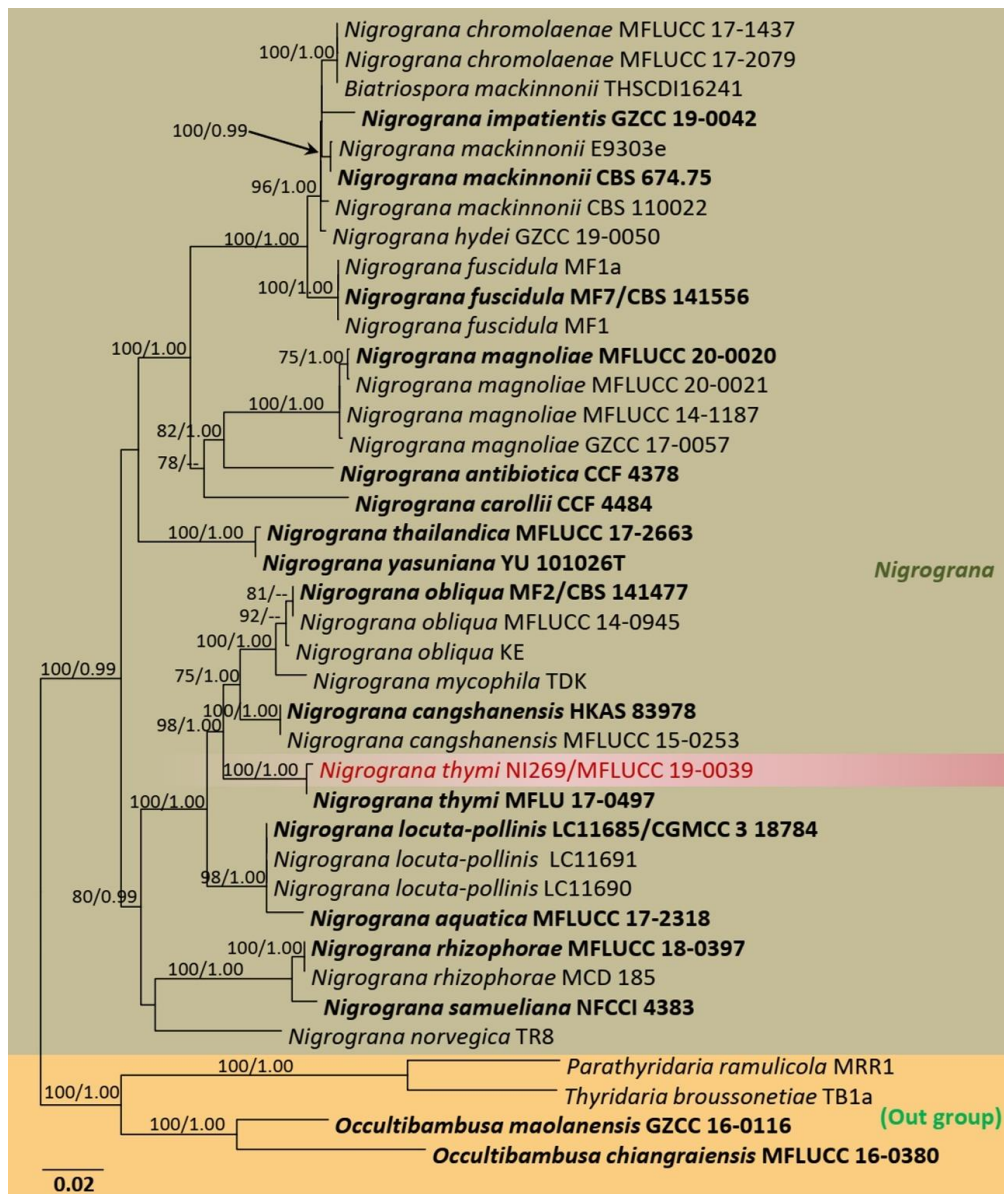
Figure 24 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, *tef1* and *rpb2* sequence data. Related sequences of *Nigrograna* were obtained from Wanasinghe et al. (2020). Thirty-nine strains are included in the combined gene analyses comprising 3580 characters after alignment (800 characters for LSU, 1000 characters for SSU, 880 characters for *tef1* and 900 characters for *rpb2*). *Occultibambusa chiangraiensis* (MFLUCC 16-0380), *O. maolanensis* (GZCC 16-0116), *Parathyridaria ramulicola* (MRR1) and *Thyridaria broussonetiae* (TB1a) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -15101.125007 is presented. The matrix had 965 distinct alignment patterns, with 28.81% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Nigrograna thymi Mapook, Camporesi & K.D. Hyde, Fungal Diversity 87: 68 (2017)   Fig. 25
          Index Fungorum number: IF 552958, Faces of Fungi number: FoF 03119

Saprobic on dead twigs attached to *Magnolia grandiflora*. Sexual morph: *Ascomata* 200–250 µm high, 250–350 µm diam. ($\bar{x} = 220 \times 310$ µm, n = 10), semi-immersed to slightly erumpent, solitary, globose to sub-globose, dark brown. *Neck* 120–300 µm high, visible on erumpent host surface. *Peridium* 30–40 µm wide, comprising inner light brown *textura angularis* cells and outer

brown *textura angularis* cells. *Hamathecium* comprising 1–2 µm wide, cylindrical to filiform, septate, hyaline pseudoparaphyses. *Asci* 35–46 × 6–9 µm ($\bar{x}$ = 42 × 8 µm, n = 25), 8-spored, bitunicate, fissitunicate, clavate, apex rounded with a short pedicel. *Ascospores* 10–14 × 2–5 µm ($\bar{x}$ = 12 × 3.5 µm, n = 30), overlapping, 1–2-seriate, broadly fusiform, 3-septate, hyaline when immature and brown at maturity and widest at the middle cell. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diam. after 1 week at 25 °C, colonies from above: brown, circular, flat, edge entire, margin well-defined, cottony to fairly fluffy with sparse aspects, dark brown at the margin; reverse: dark brown from the centre of the colony, light brown at margin.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia grandiflora* (Magnoliaceae), 26 April 2017, N. I. de Silva, NI269 (MFLU 18–2648), living culture, MFLUCC 19–0039.

GenBank numbers – LSU: MN075269, SSU: MN075271, ITS: MN075272, *tef1*: MN095405.

Known hosts and distribution – On dead aerial stem of *Thymus oenipontanus* in Italy (Hyde et al. 2017), dead twigs attached to *Magnolia grandiflora* in China (this study).

Notes – The new isolate of *Nigrograna thymi* (MFLUCC 19–0039) resembles the sexual morph of this genus in having similar asci and ascospore morphology and clustered with the type *N. thymi* (MFLU 17–0497) with high statistical support (100% ML, 1.00 PP). The new isolate has some morphological differences, such as shorter asci (35–46 µm) and shorter ascospores (10–14 µm), whereas *N. thymi* (MFLU 17–0497) has 90–98 µm asci and (24–26 µm) ascospores (Hyde et al. 2017). The new isolate has 3-septate ascospores and the type *N. thymi* has 4–5-septate ascospores (Hyde et al. 2017). A comparison of the total length of 488bp of ITS sequences revealed one insertion of 'T' at the 477th position of the new isolate (MFLUCC 19–0039). A comparison of the total length of 900 bp of *tef1* sequences revealed no base pair difference between the type *N. thymi* and the new isolate (MFLUCC 19–0039). Therefore, it is considered a new host record of *N. thymi* from *Magnolia grandiflora* in Yunnan, China, giving priority to the phylogeny and sequence data comparison.

Periconiaceae (Sacc.) Nann.

Nannizzi (1934) introduced Periconiaceae to accommodate *Periconia* as the type genus. Previously, this family has long been accommodated in Massarinaceae, but subsequently Tanaka et al. (2015) erected Periconiaceae as a distinct family based on phylogeny. Phukhamsakda et al. (2016) showed that this family diverged in the late Cretaceous period (around 70 Mya). We follow the latest treatment and updated accounts of Periconiaceae in Hongsanan et al. (2020a).

Periconia Tode

Tode (1791) introduced *Periconia*, typified by *P. lichenoides*. *Periconia* members are currently known as hyphomycetes and are characterized by having macronematous, unbranched to branched, stiff, light to dark brown conidiophores with a spherical apex, monoblastic or polyblastic, discrete conidiogenous cells and verruculose or echinulate, pale to dark brown, unicellular which are catenate, usually sphaerical to subsphaerical conidia (Thambugala et al. 2017, Phookamsak et al. 2019, Hongsanan et al. 2020a). There are 114 accepted *Periconia* species in Species Fungorum (2022). In this study, we introduce two new host records of *Periconia*.

Periconia byssoides Pers., Syn. meth. fung. (Göttingen) 2: 686 (1801)   Fig. 27
Index Fungorum number: IF 144538, Faces of Fungi number: FoF 09319

Saprobic on dead twigs attached to *Cananga odorata*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on substrate numerous, effuse, dark brown to black, floccose. *Conidiophores* 230–250 × 13–17 µm ($\bar{x}$ = 240 × 15 µm, n = 10), macronematous, mononematous, unbranched, erect, straight or slightly flexuous, single, light brown to dark brown, septate, thick-walled. *Conidiogenous cells* polyblastic, discrete. *Conidia* 10–12 × 10–13 µm ($\bar{x}$ = 11 × 12 µm, n = 30), solitary, subglobose to globose, light brown to dark brown, finely verruculose, aseptate.

Culture characteristics – Colonies on PDA reaching 35 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, fairy fluffy appearance, cream; reverse: pale brown.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Cananga odorata* (Annonaceae), 2 January 2019, N. I. de Silva, CO10 (MFLU 21-0241), living culture, MFLUCC 21-0173.

Known hosts and distribution – On dead leaves of *Ficus altissima*, *F. virens* and *F. benjamina* in Thailand (Wang et al. 2008), on decaying pod of *Peltophorum* sp. in Thailand (Jayasiri et al. 2019), on decaying cone of *Magnolia grandiflora* in Thailand (Jayasiri et al. 2019), on dead leaves of *Macaranga tanarius* in Taiwan Province of China (Tennakoon et al. 2021), dead twigs of *Cananga odorata* in Thailand (this study).

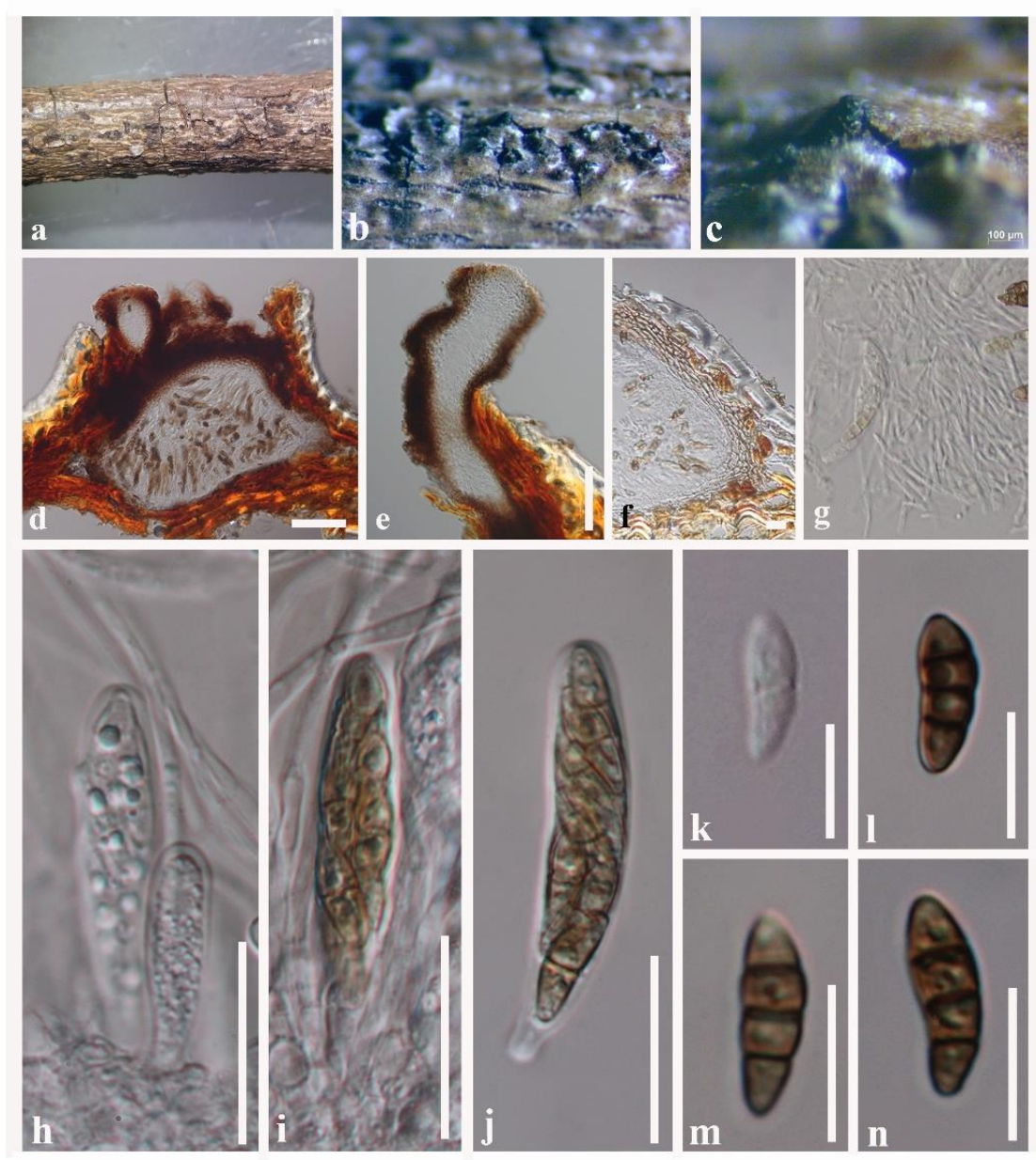GenBank numbers – ITS: OL966948, LSU: OL830814, *tef1*: ON032377.

Figure 25 – *Nigrograna thymi* (MFLU 18–2648) a The specimen. b, c Appearance of ascomata on host surface. d Vertical section through ascoma. e Neck. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Immature and mature ascospores. Scale bars: d, e = 80 μm, f = 10 μm, h–j = 20 μm, k–n = 10 μm.
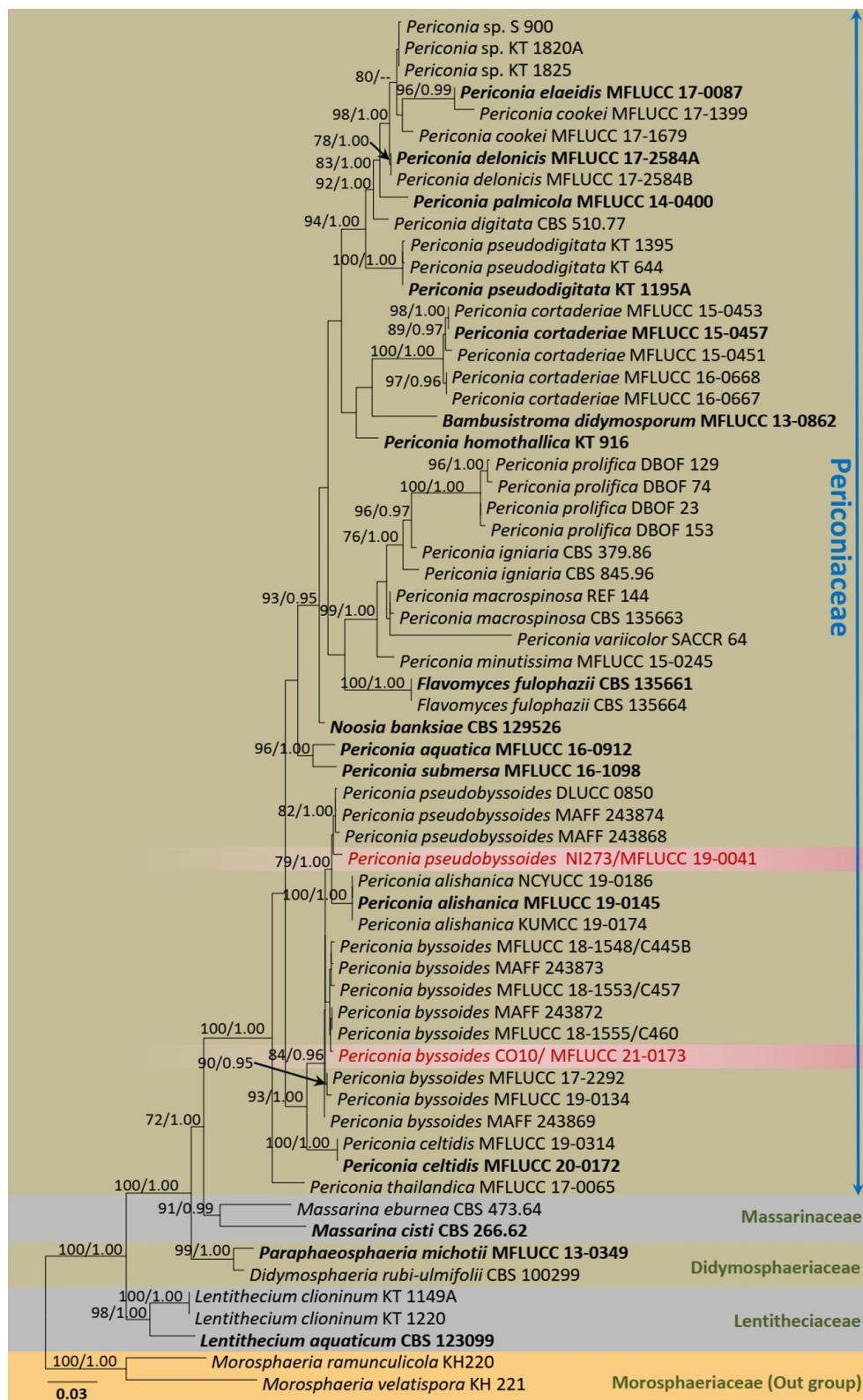
Figure 26 – Phylogram generated from maximum likelihood analysis of combined ITS, LSU and *tef1* sequence data. Related sequences of *Periconia* were obtained from Tennakoon et al. (2021). Sixty-three strains are included in the combined gene analyses comprising 2350 characters after alignment (530 characters for ITS, 820 characters for LSU and 1000 characters for *tef1*). *Morosphaeria ramunculicola* (KH220), *M. velatispora* (KH221) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -12084.936218 is presented. The matrix had 799 distinct alignment patterns, with 26.64% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or

greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red. Type and ex-type strains are in **black bold**.

Notes – The morphological characteristics of our collection resembles *Periconia byssoides* in having macronematous, mononematous, unbranched, erect, light brown to dark brown conidiophores and globose to subglobose, light brown to dark brown, verruculose, aseptate conidia (Persoon 1801, Jayasiri et al. 2019, Tennakoon et al. 2021). Multi-gene phylogeny also indicates that our collection clusters with other *Periconia byssoides* isolates in 84% ML, 0.96 BYPP supported clade (Fig. 26). Therefore, we report our collection as a new host record of *Periconia byssoides* from *Cananga odorata* in Thailand. *Periconia byssoides* seems to have a diverse distribution from various host species (Wang et al. 2008, Jayasiri et al. 2019, Tennakoon et al. 2021).
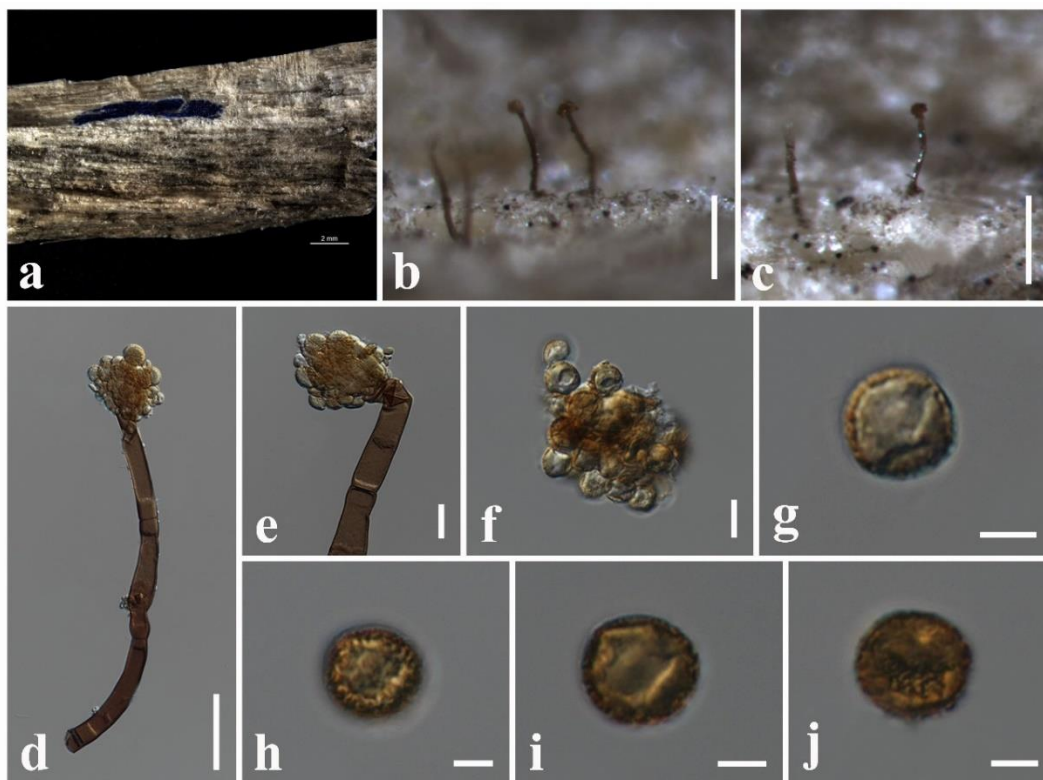

Figure 27 – *Periconia byssoides* (MFLU 21-0241) a The specimen. b, c Appearance of colonies on substrate. d Conidiophore with conidia. e Part of conidiophore with conidia. f Conidiogenesis cells and conidia. g–j Conidia. Scale bars: a = 2 mm, b, c = 0.2 mm, d = 50 μm, e = 20 μm, f = 10 μm, g–j = 5 μm.

Periconia pseudobyssoides Markovsk. & A. Kačergius, Mycol. Progr. 13(2): 293 (2013) [2014]

Fig. 28

Index Fungorum number: IF 804763, Faces of Fungi number: FoF 03857

Saprobic on dead twigs attach to *Magnolia* sp. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on substrate numerous, effuse, dark brown to black, floccose. *Conidiophores* 350–370 × 22–25 μm ($\bar{x}$ = 360 × 23 μm, n = 10), macronematous, mononematous, unbranched, erect, straight or slightly flexuous, single, light brown to dark brown, septate, thick-walled. *Conidiogenous cells* polyblastic, discrete. *Conidia* 10–15 × 10–15 μm ($\bar{x}$ = 14 × 14 μm, n = 30), solitary, globose, light brown to dark brown, finely verruculose, aseptate.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, fairy fluffy appearance, cream; reverse: pale brown.
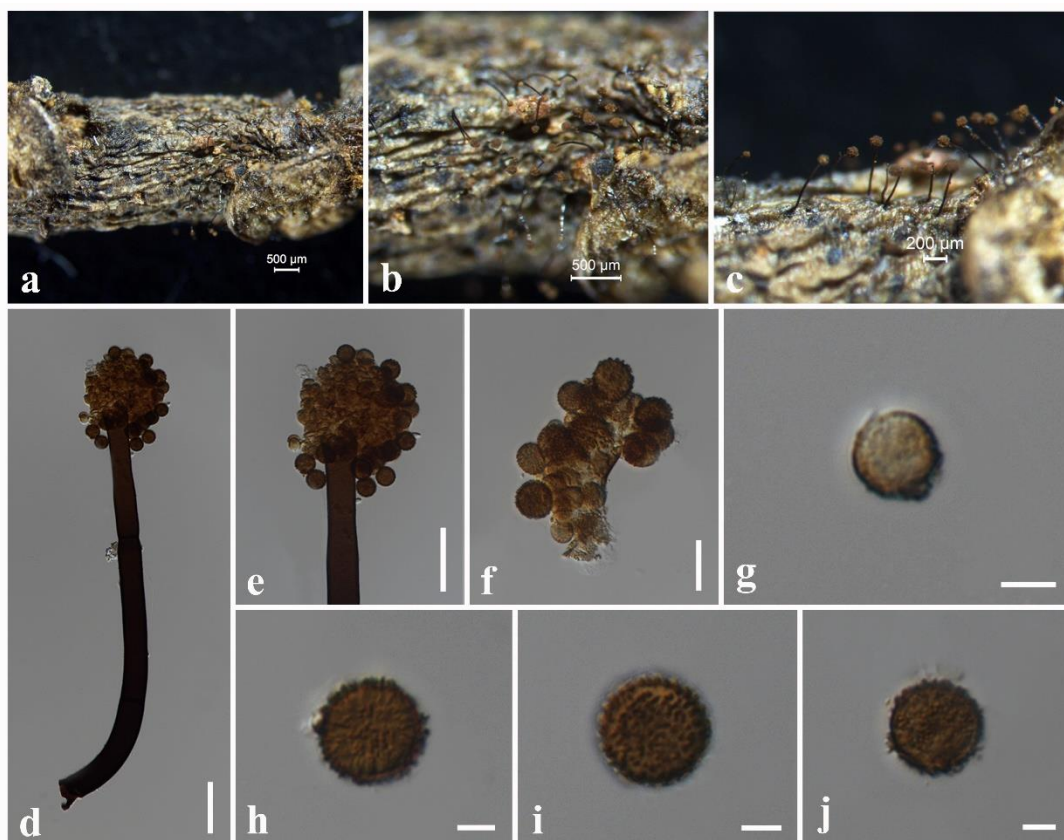
Figure 28 – *Periconia pseudobyssoides* (MFLU 18-2651). a The specimen. b, c Appearance of colonies on substrate. d Conidiophore with conidia. e Part of conidiophore with conidia. f Conidiogenesis cells and conidia. g–j Conidia. Scale bars: a, b = 500 μm, c = 200 μm, d = 50 μm, e, f = 20 μm, g–j = 5 μm.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI273 (MFLU 18-2651), living culture, MFLUCC 19-0041.

Known hosts and distribution – On dead stalks of *Heracleum sosnowskyi* in Lithuania (Markovskaja & Kačergius 2014), dead twigs of *Magnolia* sp. in China (this study).

GenBank numbers – ITS: OL966949, LSU: OL830815, *tef1*: ON032378.

Notes – *Periconia pseudobyssoides* was introduced by Markovskaja & Kačergius (2014) from dead stalks of *Heracleum sosnowskyi* in Lithuania. The morphology of our collection (MFLU 18-2651) shares similarities with *Periconia pseudobyssoides* in having macronematous, mononematous, unbranched, light brown to dark brown, septate conidiophores and globose, light brown to dark brown, aseptate conidia (10–15 × 10–15 μm *vs* 15–17 μm diam.) (Markovskaja & Kačergius 2014). Multi-gene phylogeny also indicates that our collection clusters with other *Periconia pseudobyssoides* isolates with 82% ML, 1.00 BYPP support (Fig. 26). Therefore, we introduce our collection as a new host record of *Periconia pseudobyssoides* from dead twigs of *Magnolia* sp. in Thailand.

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae is one of the species-rich families in Pleosporales and includes species that inhabit a wide range of ecosystems (Phookamsak et al. 2014, Tennakoon et al. 2020). This family was introduced by Barr (2002) which is characterized by immersed to superficial, globose to subglobose ascomata, short papilla, bitunicate asci and hyaline, yellowish or brown, fusiform to ellipsoidal, filiform, or muriform, septate ascospores. There are more than 70 genera are accommodated in this family (Hongsanan et al. 2020a).
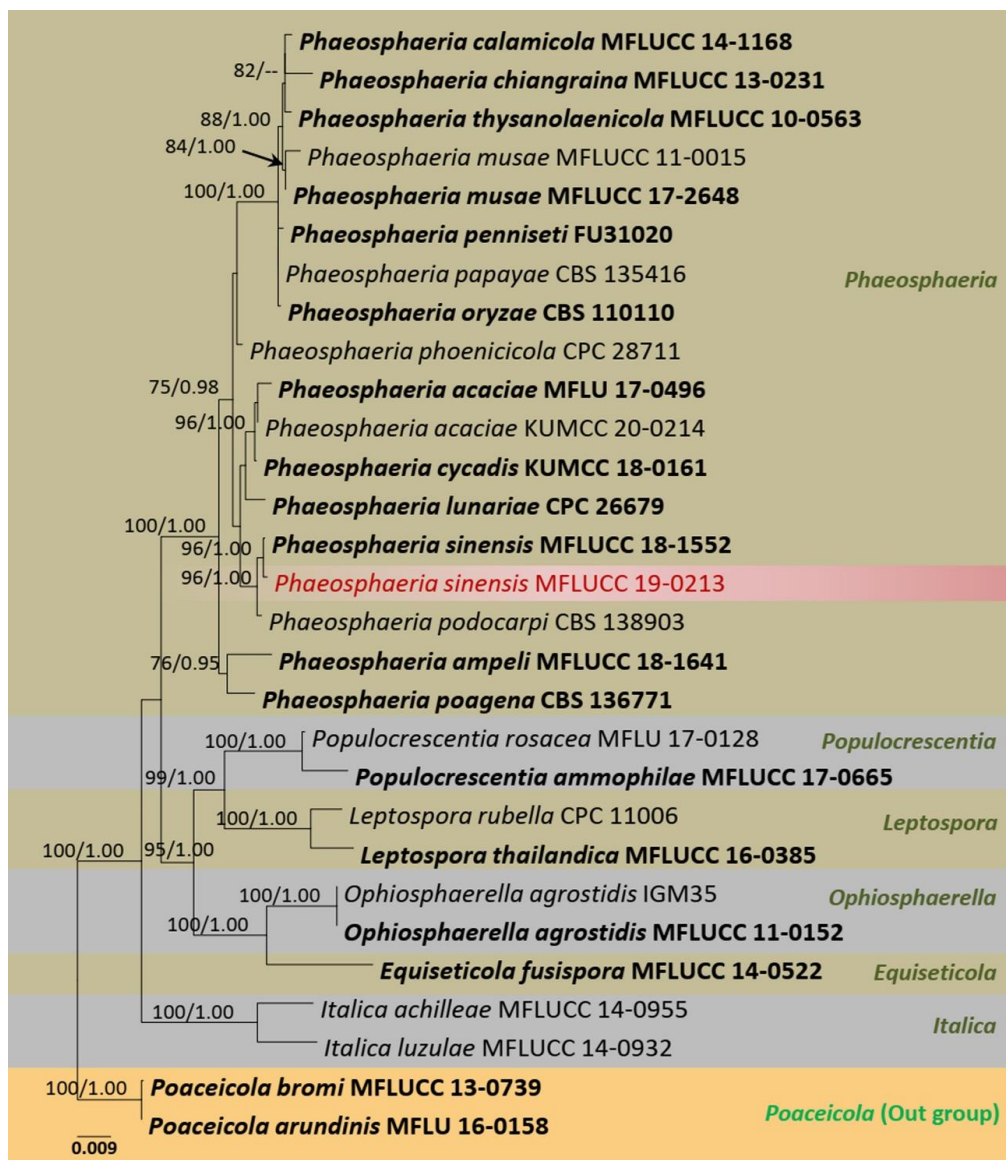
Figure 29 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, ITS and *tef1* sequence data. Related sequences of *Phaeosphaeria* and some other strains of Phaeosphaeriaceae were obtained from Liao et al. (2021). Twenty-nine strains are included in the combined gene analyses comprising 2870 characters after alignment (800 characters for LSU, 950 characters for SSU, 520 characters for ITS and 600 characters for *tef1*). *Poaceicola arundinis* (MFLU 16-0158) and *P. bromi* MFLUCC 13-0739 are used as outgroup taxa. The best RAxML tree with a final likelihood value of -8242.237617 is presented. The matrix had 469 distinct alignment patterns, with 22.59% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Phaeosphaeria I. Miyake

Phaeosphaeria was introduced by Miyake (1909) to accommodate *P. oryzae* as the type species. *Phaeosphaeria* species seem to have cosmopolitan in distribution since they have been recorded from both temperate and tropical countries (i.e., China, Germany, Italy, Japan, Taiwan, Thailand, USA) (Hyde et al. 2013, Hongsanan et al. 2020a, Phookamsak et al. 2014, Tennakoon et al. 2020). There are 219 epithets for *Phaeosphaeria* in Index Fungorum (2021). We follow the latest treatment and updated account of *Phaeosphaeria* in Tennakoon et al. (2019) and Zhang et al. (2019).

Phaeosphaeria sinensis Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 96 (2019)

Fig. 30

Index Fungorum number: IF 555564, Faces of Fungi number: FoF 05270

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 90–110 µm high × 100–130 µm diam. ($\bar{x} = 100 \times 120$ µm, n = 10), pycnidial, immersed to erumpent, brown to black, globose to subglobose, solitary. *Conidiomatal wall* equal thickness thin-walled, composed of several layers of lightly pigmented to dark brown, *textura angularis* cells, inner cells hyaline, outer cells darker and fusing with the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 2–3 µm ($\bar{x} = 5 \times 2.4$ µm, n = 20), phialidic, ampulliform, lining the inner cavity, hyaline, smooth. *Conidia* 8–11 × 2–4 µm ($\bar{x} = 10 \times 3$ µm, n = 30), light brown, fusiform with rounded ends, 1-septate, guttulate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: brown, circular, edge entire, margin well-defined, cottony to fairly fluffy with sparse aspects; reverse: dark brown.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 27 March 2017, N. I. de Silva, NI166 (MFLU 18-1027), living culture, MFLUCC 19-0213, KUMCC 17-0195.

Known hosts and distribution – On decaying pod of *Wisteria* sp. in China (Jayasiri et al. 2019) and on dead twigs attached to *Magnolia* sp. in China (this study).

GenBank numbers – LSU: OL813496, SSU: OL824792, ITS: OM212456, *tef1*: ON203111.

Notes – *Phaeosphaeria sinensis* was introduced by Jayasiri et al. (2019) from a decaying pod of *Wisteria* sp. in China. The morphology of our collection (MFLUCC 19-0213) fits well with the *Phaeosphaeria sinensis* (MFLUCC 18–1552) in having immersed to erumpent, brown to black, globose to subglobose conidiomata, phialidic, ampulliform conidiogenous cells and light brown, fusiform conidia (Jayasiri et al. 2019). The phylogeny also indicates that our collection (MFLUCC 19-0213) nested with *Phaeosphaeria sinensis* (MFLUCC 18–1552) with 96% ML and 1.00 BYPP support (Fig. 29). Therefore, we report our collection (MFLUCC 19-0213) as a new host record of *Phaeosphaeria sinensis* from *Magnolia* sp. in China.

Roussoellaceae Liu, Phookamsak, Dai & K.D. Hyde

This family was introduced by Liu et al. (2014) to accommodate *Roussoella* with *R. nitidula* as the type species. Initially, three genera were accommodated in this family *viz. Neoroussoella*, *Roussoella* and *Roussoellopsis* (Liu et al. 2014). Jaklitsch & Voglmayr (2016) synonymized this family under Thyridariaceae based on phylogeny data, but subsequently Tibpromma et al. (2017) argued that Roussoellaceae and Thyridariaceae were separate families in Pleosporales. This family is now recognized as a well-resolved family in Pleosporales (Hongsanan et al. 2020a). Twelve genera are accommodated in this family (Hongsanan et al. 2020a, Mapook et al. 2020).

Neoroussoella Liu et al.

Neoroussoella was introduced by Liu et al. (2014) to include *N. bambusae,* which was collected from dead branch of *Bambusa* sp. in Thailand. *Neoroussoella* species can be distinguished from *Roussoella* species in having uni-locolate ascomata and its coelomycetous asexual morph forming hyaline to pale brown, smooth-walled conidia (Liu et al. 2014, Jayasiri et al. 2019). Eleven *Neoroussoella* epithets listed in Index Fungorum (2022).

Neoroussoella entadae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 105 (2019)

Fig. 32

Index Fungorum number: IF 555568, Faces of Fungi number: FoF 05275

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: Not observed. Asexual morph: Coelomycetes. *Conidiomata* 130–230 µm high × 150–170 µm diam. ($\bar{x} = 180 \times 160$ µm, n = 10), pycnidial, solitary to gregarious, unilocular, brown to black, immersed, becoming erumpent

at maturity, ostiolate. *Ostiole* papillate, central, circular. *Conidiomatal wall* 8–14 µm wide, composed of thick-walled, dark brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 20), phialidic, ampulliform to cylindrical, hyaline, smooth-walled. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 40), initially hyaline, becoming pale brown when mature, oblong to ovoid, straight, both ends broadly rounded, aseptate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: cream, circular, flat, slightly raised, dense at the centre, white at the margin; reverse: brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 15 November 2017, N. I. de Silva, NI213 (MFLU 18-1310), living culture, MFLUCC 18-0546.

Known hosts and distribution – On decaying pods of *Entada phaseoloides* and *Leucaena* sp. in Thailand (Jayasiri et al. 2019), dead twigs attached to *Magnolia candolli* in Thailand (this study).

GenBank numbers – LSU: OL457703, SSU: OL700217, ITS: OL703580, *tef1*: OM505027.

Notes – *Neoroussoella entadae* was introduced by Jayasiri et al. (2019) from decaying pods of *Entada phaseoloides* and *Leucaena* sp. in Thailand. The morphology of our collection resembles *Neoroussoella entadae* in having immersed to erumpent, ostiolate conidiomata, ampulliform to cylindrical, hyaline conidiogenous cells and hyaline to pale brown, oblong to ovoid conidia (Jayasiri et al. 2019). Multi-gene phylogeny also indicates that our collection clusters with *Neoroussoella entadae* isolates (MFLUCC 18-0243, MFLUCC 15-0098, MFLUCC 17-0920) in a 92% ML, 0.99 BYPP supported clade (Fig. 31). Therefore, based on both morphology and phylogeny evidence, we introduce our collection as a new host record of *Neoroussoella entadae* from *Magnolia candolli* in Thailand.
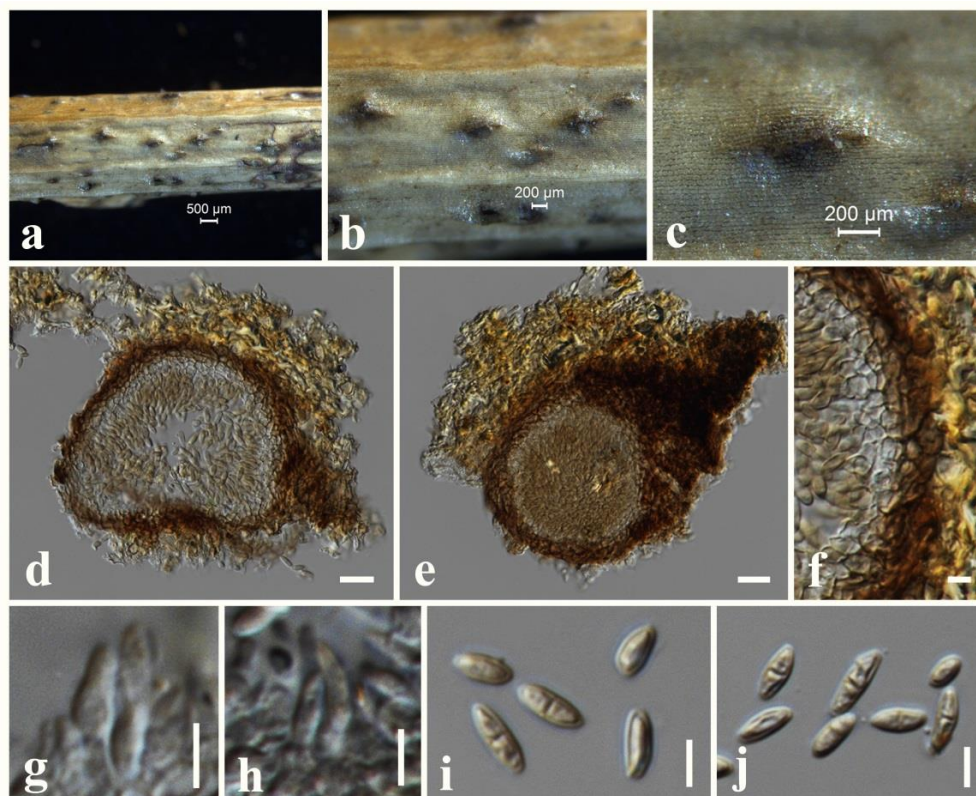

Figure 30 – *Phaeosphaeria sinensis* (MFLU 18-1027). a–c Appearance of conidiomata on substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g, h Conidiogenous cells. i, j Conidia. Scale bars: a = 500 µm, b, c = 200 µm, d, e = 20 µm, f–j = 5 µm.
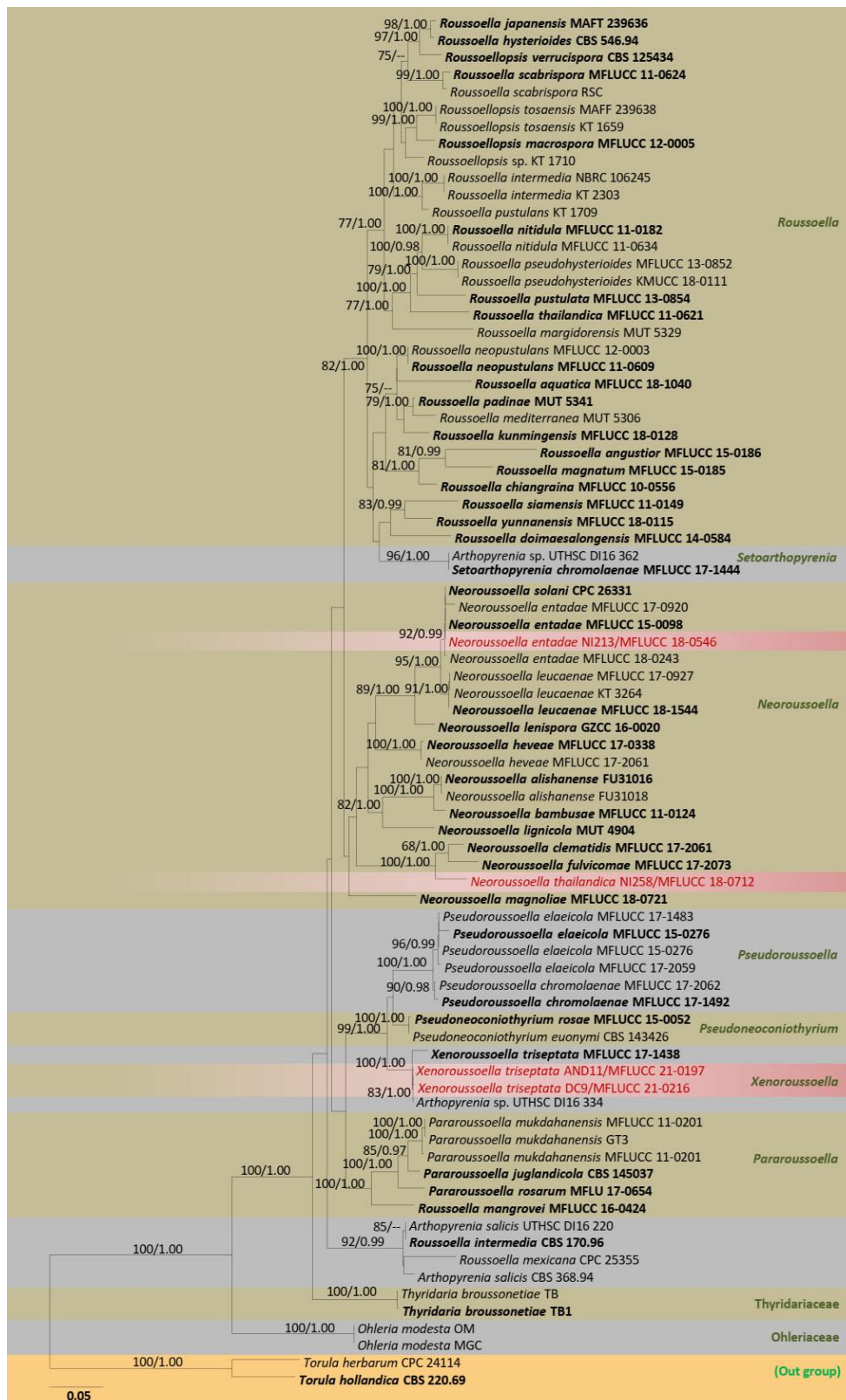
Figure 31 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, *tef1*, *rpb2* and SSU sequence data. Related sequences of family Roussoellaceae were obtained from Phukhamsakda et al. (2020). Eighty strains are included in the combined gene analyses comprising 4200 characters after alignment (800 characters for LSU, 500 characters for ITS, 900 characters for *tef1*, 1000 characters for *rpb2* and 1000 characters for SSU). *Torula herbarum* (CPC 24114) and *T. hollandica* (CBS 220.69) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -31556.109275 is presented. The matrix had 1645 distinct alignment patterns, with 41.53%

undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
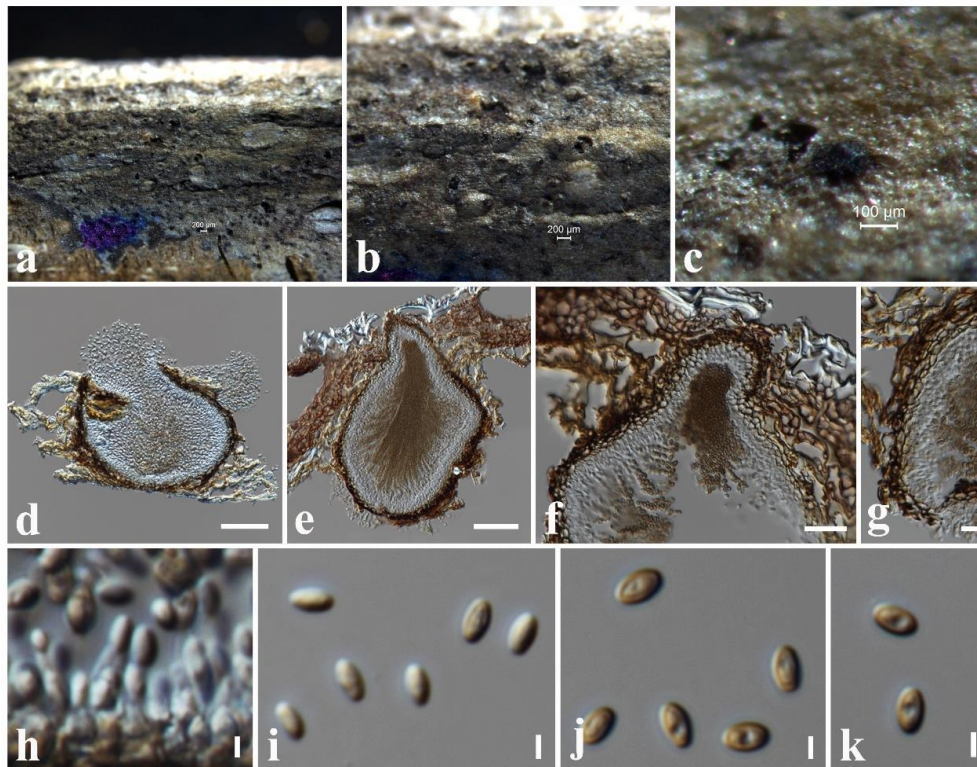

Figure 32 – *Neoroussoella entadae* (MFLU 18-1310). a–c Appearance of conidiomata on substrate. d, e Vertical sections through conidiomata. f Neck region. g Conidiomatal wall. h Conidiogenous cells. i–k Conidia. Scale bars: b = 200 μm, c = 100 μm, d, e = 50 μm, f = 20 μm, g = 10 μm, h–k = 2 μm.

Neoroussoella thailandica N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 33

Index Fungorum number: IF 559521, Faces of Fungi number: FoF 10719

Etymology: The epithet '*thailandica*' referring to the country (Thailand) where the specimen was collected.

Holotype: MFLU 18-1323

Saprobic on dead twigs attach to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: Coelomycetes. *Conidiomata* 130–190 μm high × 80–150 μm diam. ($\bar{x} = 160 \times 120$ μm, n = 10), pycnidial, immersed to erumpent, solitary to gregarious, unilocular, brown to black, ostiolate. *Ostiole* papillate, central, circular. *Conidiomatal wall* 8–12 μm wide, composed of thick-walled, dark brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 1–3 μm ($\bar{x} = 4 \times 2$ μm, n = 20), phialidic, ampulliform to cylindrical, hyaline, smooth-walled. *Conidia* 3–5 × 2–3 μm ($\bar{x} = 4 \times 2.3$ μm, n = 40), initially hyaline, becoming pale brown when mature, oblong to ovoid, straight, both ends broadly rounded, aseptate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: grey, circular, flat, slightly raised, dense at the centre, white at the margin; reverse: brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 8 February 2018, N. I. de Silva, NI258 (MFLU 18-1323, holotype), living culture, MFLUCC 18-0712.
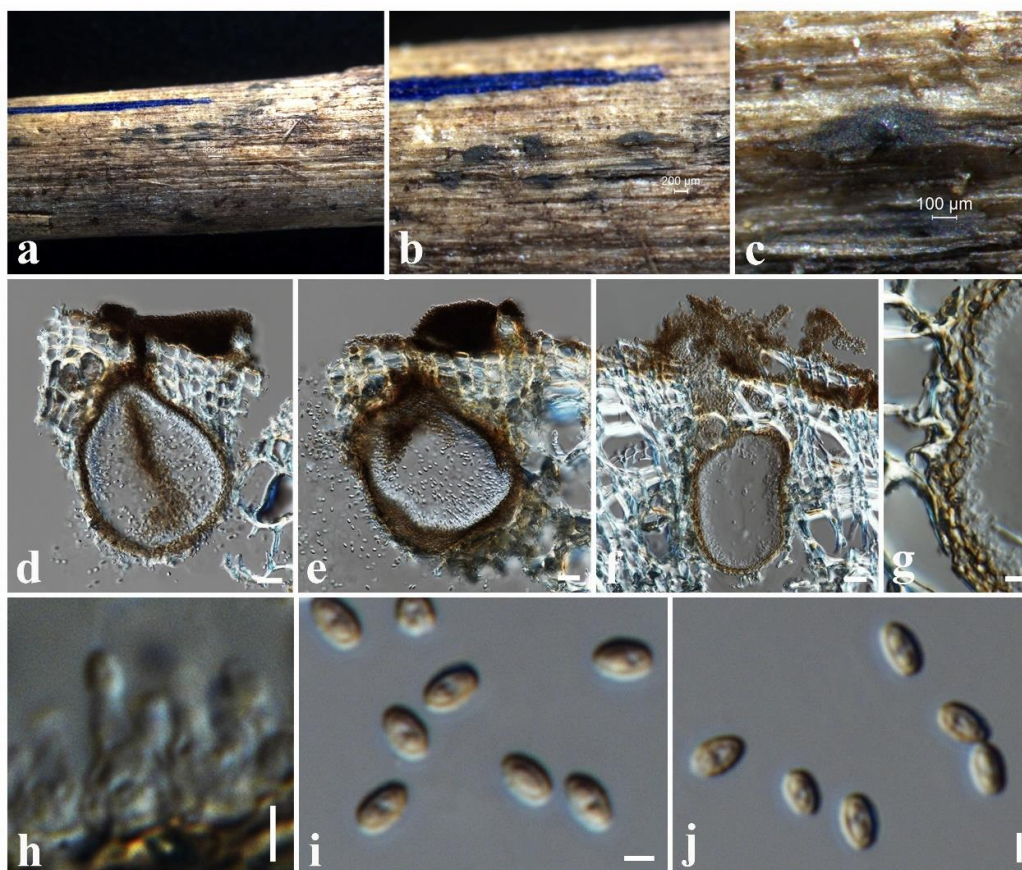
Figure 33 – *Neoroussoella thailandica* (MFLU 18-1323, holotype). a The specimen. b, c Appearance of conidiomata on substrate. d–f Vertical sections through conidiomata. g Conidiomatal wall. h Conidiogenous cells. i, j Conidia. Scale bars: b = 200 µm, c = 100 µm, d–f = 20 µm, g = 5 µm, h–j = 2 µm.

GenBank numbers – LSU: OL457704, SSU: OL764415, ITS: OL703581, *tef1*: OM505028, *rpb2*: ON502386.

Notes – According to the multi-gene phylogeny (LSU, SSU, ITS, *tef1* and *rpb2*), *Neoroussoella thailandica* (MFLUCC 18-0712) constitutes an independent lineage sister to a subclade containing *N. clematidis* and *N. fulvicomae* with 100% ML and 1.00 BYPP support (Fig. 31). *Neoroussoella thailandica* can be distinguished from *N. fulvicomae* in having thick conidiomatal wall (8–12 µm *vs* 12–18 µm) and phylogeny evidence (Phukhamsakda et al. 2020). A comparison of the 505 nucleotides across the ITS (+5.8S) gene region of *Neoroussoella fulvicomae* and *N. thailandica* (MFLUCC 18-0712) shows 24 base pair differences (4.75%). In addition, there are 21 base pair differences between *Neoroussoella clematidis* and *N. thailandica* (MFLUCC 18-0712). However, we are unable to compare the morphological differences with *Neoroussoella clematidis*, since it has only sexual morph (Phukhamsakda et al. 2020).

Xenoroussoella Mapook & K.D. Hyde

Mapook et al. (2020) introduced *Xenoroussoella* to accommodate *X. triseptata* which was collected from *Chromolaena odorata* in Thailand. *Xenoroussoella* members are characterized by immersed, solitary, globose to subglobose ascomata, with protruding ostiolar neck, cylindricclavate to clavate asci, and brown to dark brown, ellipsoid to obovoid, 3-septate ascospores (Mapook et al. 2020). This is a monotypic genus (Index Fungorum 2022).

Xenoroussoella triseptata Mapook & K.D. Hyde, Fungal Diversity 101: 95 (2020)   Fig. 34

Index Fungorum number: IF 557368, Faces of Fungi number: FoF 07823

Saprobic on dead twigs attach to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: Coelomycetes. *Conidiomata* 90–125 μm high × 90–135 μm diam. ($\bar{x} = 110 \times 120$ μm, n = 10), pycnidial, solitary to gregarious, uni- or multi-locular, dark brown to black, immersed, becoming erumpent at maturity, ostiole not clear. *Conidiomatal wall* 10–15 μm wide, composed of thick-walled, dark brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 2–3 μm ($\bar{x} = 4 \times 2.4$ μm, n = 20), phialidic, ampulliform to cylindrical, hyaline, smooth-walled. *Conidia* 3–5 × 2–3 μm ($\bar{x} = 3.7 \times 2.6$ μm, n = 40), initially hyaline, becoming pale brown when mature, oblong to ovoid, straight, both ends broadly rounded, aseptate, smooth-walled.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: white, circular, dense, fluffy appearance, slightly raised at the centre; reverse: brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND11 (MFLU 21-0251), living culture, MFLUCC 21-0197, *Desmos chinensis* (Annonaceae), 8 March 2019, N. I. de Silva, DC9 (MFLU 21-0252), living culture, MFLUCC 21-0216.

Known hosts and distribution – On dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020), dead twigs attached to *Anomianthus dulcis* and *Desmos chinensis* in Thailand (this study).

GenBank numbers – (AND11): LSU: OL457705, SSU: OL700218, ITS: OL703582, (DC9): LSU: OL457706, SSU: OL700219, ITS: OL703583, *tef1*: OM471893.

Notes – According to the multi-gene phylogeny, our collection (AND11 and DC9) nested in a 100 % ML and 1.00 BYPP supported clade containing *Xenoroussoella triseptata* (MFLUCC 17-1438) and *Arthopyrenia* sp. (UTHSC: DI16-334) (Fig. 31). The sexual morph of *X. triseptata* was introduced by Mapook et al. (2020) from *Chromolaena odorata* in Thailand. However, we could not compare the morphological characteristics with *X. triseptata* (MFLUCC 17-1438), since it lacks asexual morph record. A comparison of the 538 nucleotides across the ITS (+5.8S) gene region of *X. triseptata* (MFLUCC 17-1438) and our collection shows 3 base pair differences. In addition, we could not compare the morphological differences with *Arthopyrenia* sp. (UTHSC: DI16-334), since it was not properly introduced. Therefore, we introduce our collection as an asexual morph of *Xenoroussoella triseptata*.

Teichosporaceae M.E. Barr

Based on morphological characteristics, Barr (2002) introduced *Teichosporaceae* to accommodate *Teichospora* as the type genus. This family is considered a species rich family in *Pleosporales*, whose members are morphologically, ecologically and phylogenetically diverse (Barr 2002, Hongsanan et al. 2020a, Tennakoon et al. 2021). Twelve genera are accepted in *Teichosporaceae*, *viz.* *Asymmetrispora*, *Aurantiascoma*, *Chaetomastia*, *Floricola*, *Loculohypoxylon*, *Magnibotryascoma*, *Misturatosphaeria*, *Pseudoaurantiascoma*, *Pseudomisturatosphaeria*, *Ramusculicola*, *Sinodidymella* and *Teichospora* (Hongsanan et al. 2020a, Tennakoon et al. 2021). In this study, we followed Hongsanan et al. (2020a) and Tennakoon et al. (2021) as the recent treatments of this family.

Aurantiascoma Thambug. & K.D. Hyde

Thambugala et al. (2015) introduced *Aurantiascoma* to accommodate *A. minimum* as the type species, which was previously known as *Misturatosphaeria minima* (Mugambi and Huhndorf 2009). Jaklitsch et al. (2016) synonymized *Aurantiascoma* under *Teichospora* and erected *Misturatosphaeria minima* as *T. parva*. Recently, Tennakoon et al. (2021) resurrected *Aurantiascoma* as a separate genus as mentioned by Thambugala et al. (2015). Three species are recorded in Index Fungorum (2022), namely, *Aurantiascoma minimum*, *A. nephelii* and *A. quercus*.
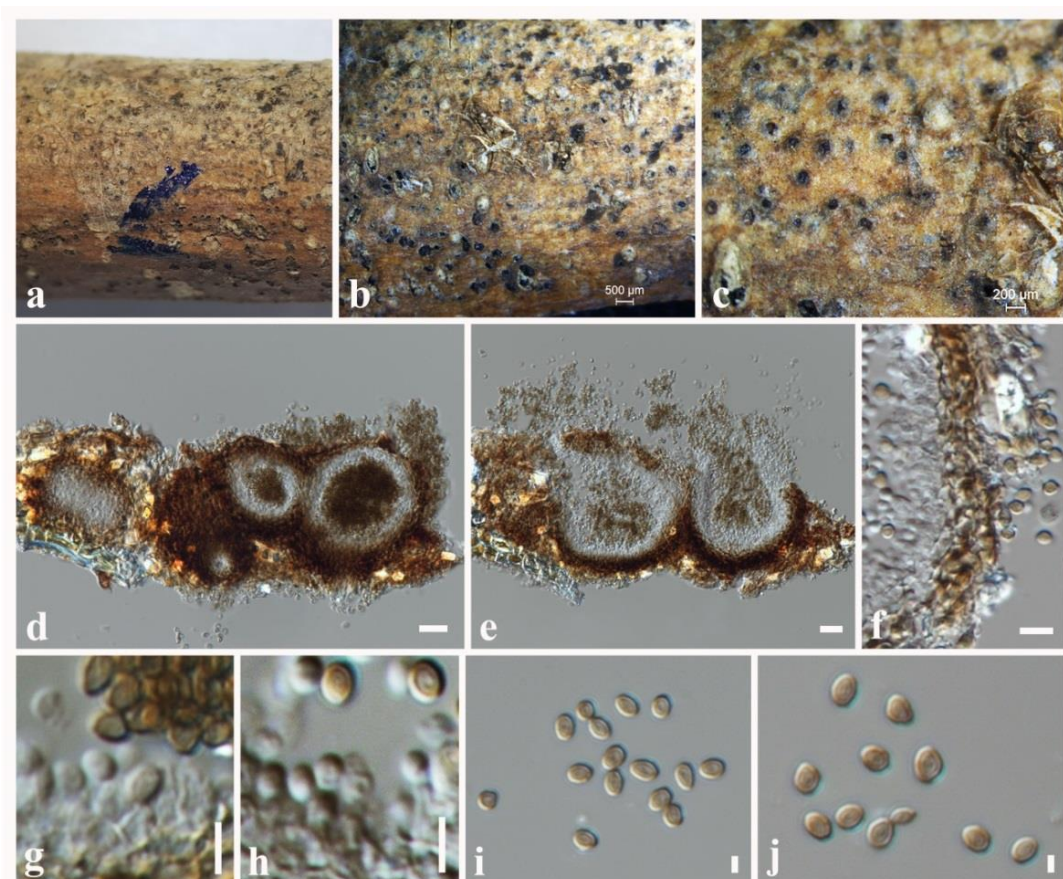
Figure 34 – *Xenoroussoella triseptata* (MFLU 21-0251). a–c Appearance of conidiomata on substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g, h Conidiogenous cells. i, j Conidia. Scale bars: b = 500 μm, c = 200 μm, d, e = 20 μm, f = 10 μm, g, h = 5 μm, i, j = 2 μm.

Aurantiascoma minimum (Mugambi, A.N. Mill. & Huhndorf) Thambug. & K.D. Hyde, Fungal Divers 74: 249 (2015)   Fig. 36

Index Fungorum number: IF 144538, Faces of Fungi number: FoF 09627

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Ascomata* 200–270 μm high × 240–300 μm diam. ($\overline{x}$ = 240 × 260 μm, n = 10), dark brown to black, solitary or scattered, gregarious, unilocular, semi-immersed, papilla usually erumpent, globose to subglobose, ostiolate. *Peridium* 35–65 μm wide, 2-layered, with outer layer composed of light brown to brown cells of *textura angularis*, lined with a hyaline inner layer, fusing at the outside with the host tissues. *Hamathecium* comprising 1.3–2.4 μm wide, numerous, filamentous, indistinct septate, cellular pseudoparaphyses, anastomosing at the apex, embedded in a gelatinous matrix. *Asci* 50–75 × 6–8.5 μm ($\overline{x}$ = 62 × 8 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 15–22× 3–5 μm ($\overline{x}$ = 18 × 4 μm, n = 30), overlapping, 1–2-seriate, hyaline, fusiform to cylindrical or fusiform, usually 1–3-septate, mostly 1-septate, constricted at the septa, surrounded by a thin mucilaginous sheath, filled with guttules when immature. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: pale brown, circular, slightly raised, dense at the centre, cream at the margin; reverse: pale brown from the centre of the colony, white at margin.

Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 13 September 2017, N. I. de Silva, NI194 (MFLU 18-1294), living culture, MFLUCC 18-0709.
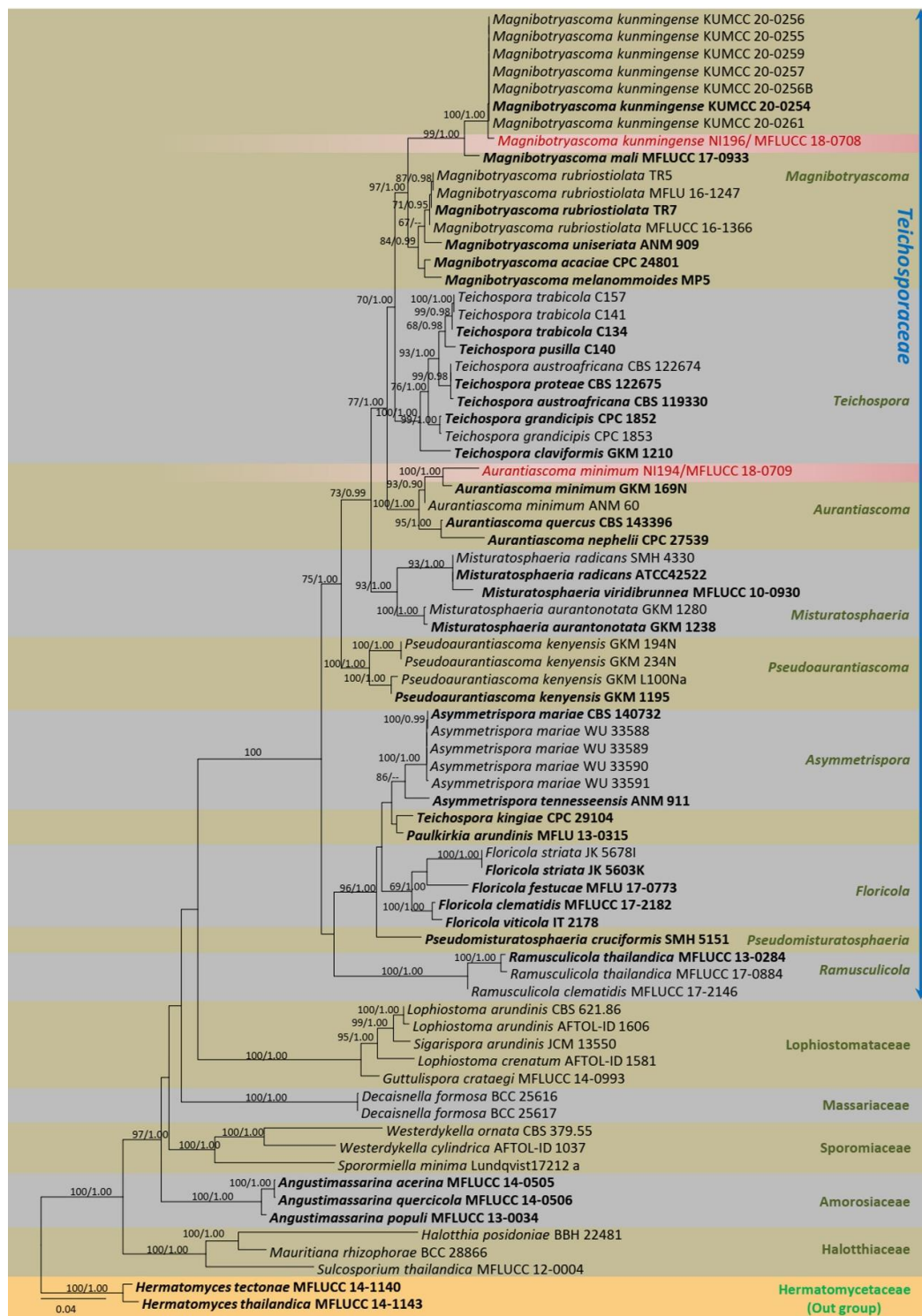
Figure 35 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, SSU, *tef1* and *rpb2* sequence data. Related sequences of family Teichosporaceae were obtained from Tennakoon et al. (2021). Seventy-five strains are included in the combined gene analyses comprising 4210 characters after alignment (890 characters for LSU, 500 characters for ITS, 1000 characters for SSU, 920 characters for *tef1*, 900 characters for *rpb2*). *Hermatomyces tectonae* (MFLUCC 14-1140) and *H. thailandica* (MFLUCC 14-1143) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -24837.502877 is presented. The matrix had 1680 distinct alignment patterns, with 43.35 % undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
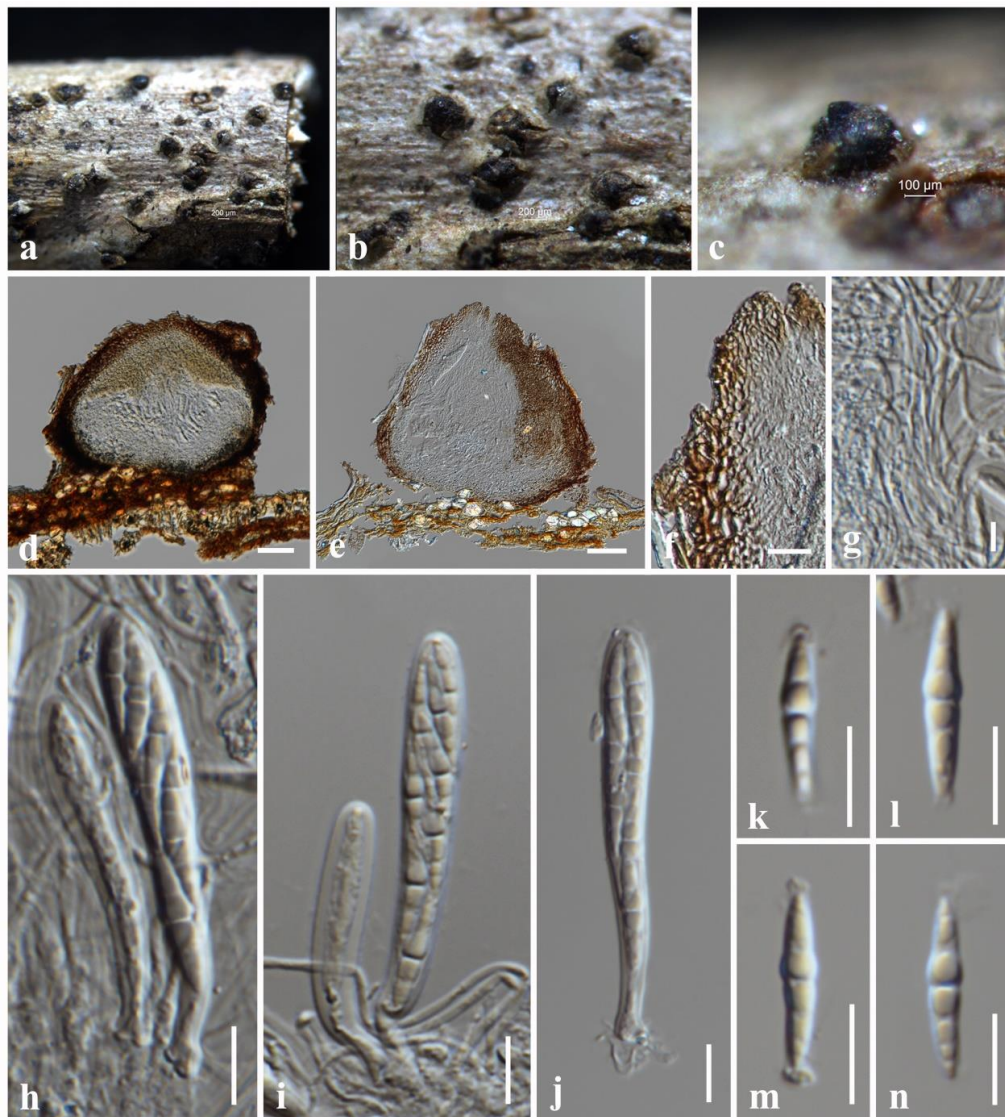
Figure 36 – *Aurantiascoma minimum* (MFLU 18-1294). a Specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: c = 100 μm, d, e = 50 μm, f, h–n = 10 μm, g = 5 μm.

Known hosts and distribution – On unidentified woody branches in Kenya and USA (Mugambi & Huhndorf 2009), dead twigs attached to *Magnolia* sp. in Thailand (this study).

GenBank numbers – LSU: OL830818, ITS: OL966952, SSU: OL964386, *tef1*: ON165232.

Notes – As morphological characteristics examined largely overlapped with *Aurantiascoma minimum*, we report our collection as a new host record of *A. minimum* from *Magnolia* sp. in Thailand. In particular, both isolates have semi-immersed to erumpent, globose to subglobose ascomata, cylindrical, short pedicellate asci and hyaline, fusiform to cylindrical, mostly 1-septate ascospores (Mugambi & Huhndorf 2009). Multi-locus phylogeny also indicates that our collection nests with *A. minimum* (GKM 169N) with strong statistical support (100% ML, 1.00 BYPP) (Fig. 35).

Magnibotryascoma Thambug. & K.D. Hyde

Magnibotryascoma was introduced by Thambugala et al. (2015), to accommodate *M. uniseriatum* as the type species, which was previously known as *Misturatosphaeria uniseriata* (Mugambi & Huhndorf 2009). *Magnibotryascoma* species have a cosmopolitan distribution as woody-based saprobes on *Clematis vitalba*, *Malus halliana*, *Ribes sanguineum*, *Robinia pseudoacacia*, *Salix* sp., and *Vaccinium myrtillus* from Belgium, China, Germany, Norway and the

United Kingdom (Jaklitsch et al. 2016, Hyde et al. 2017, Phukhamsakda et al. 2020, Mortimer et al. 2021). The sexual morph of *Magnibotryascoma* is characterized by erumpent to superficial ascomata lacking a subiculum and fusiform to elliptical and guttulate ascospores and the asexual morph has pycnidial conidiomata featuring aseptate and brown conidia (Jaklitsch et al. 2016, Hyde et al. 2017, Phukhamsakda et al. 2020, Tennakoon et al. 2021). There are four *Magnibotryascoma* species in Index Fungorum (2022).

Magnibotryascoma kunmingense Mortimer, Front. Microbiol.: 9 (2021) Fig. 37
   Index Fungorum number: IF 144538, Faces of Fungi number: FoF 10662
   Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: Not observed. Asexual morph: coelomycetous, *Conidiomata* 100–130 µm high × 115–140 µm diam. ($\bar{x} = 120 \times 130$ µm, n = 10), pycnidial, solitary, aggregated, uniloculate, semi-immersed to erumpent, globose to subglobose, coriaceous, dark brown to brown, papillate, with a central ostiole. *Conidiomatal wall* 15–23 µm wide, thick, 2-layered, with outer layer composed of light brown to brown cells of *textura angularis*, lined with a hyaline inner layer bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 3–4 µm ($\bar{x} = 4.5 \times 3.5$ µm, n = 20), enteroblastic, annellidic, discrete, cylindrical to oblong, hyaline, arising from the inner layer of pycnidium wall. *Conidia* 3–5 × 2.5–4 µm ($\bar{x} = 4.5 \times 3$ µm, n = 30), subglobose, oval, guttulate, hyaline when immature, pale brown at maturity, aseptate, smooth-walled.
   Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: cream, circular, flat, slightly raised, dense, white at the margin; reverse: pale brown from the centre of the colony, white at margin.
   Material examined – Thailand, Chiang Mai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 13 September 2017, N. I. de Silva, NI196 (MFLU 18-1295), living culture, MFLUCC 18-0708.
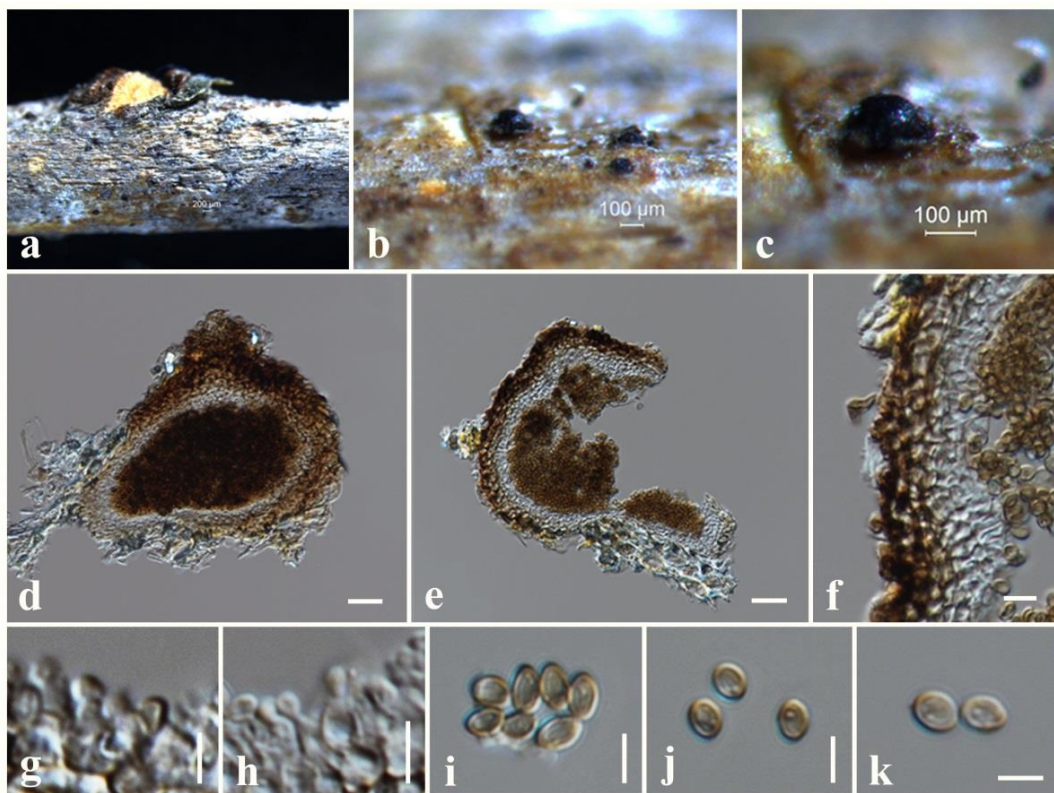

Figure 37 – *Magnibotryascoma kunmingense* (MFLU 18-1295). a Specimen. b, c Appearance of conidiomata on substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g, h Conidiogenous cells. i–k Conidia. Scale bars: b, c = 100 µm, d, e = 20 µm, f–k = 5 µm.

Known hosts and distribution – On dead twigs of *Machilus yunnanensis* and *Acer cappadocicum* in China (Mortimer et al. 2021), dead twigs attached to *Magnolia* sp. in Thailand (this study).

GenBank numbers – LSU: OL830817, ITS: OL966951, SSU: OL964385, *tef1*: ON165231.

Notes – Morphologically our collection (MFLU 18-1295) resembles *Magnibotryascoma kunmingense* in having semi-immersed to erumpent, globose to subglobose conidiomata, cylindrical to oblong, hyaline conidiogenous cells and subglobose, oval, pale brown, aseptate conidia (Mortimer et al. 2021). In phylogeny, our collection was nested within other *M. kunmingense* isolates in a well-supported clade (100% ML, 1.00 BYPP). Therefore, we introduce our collection as a new host record of *M. kunmingense* from *Magnolia* sp. in Thailand.

Torulaceae Corda

Sturm (1829) introduced Torulaceae within Pleosporales and typified by *Torula*. The asexual state of the family is hyphomycetous and characterized by erect micro- or macronematous conidiophores, doliiform to ellipsoid or clavate conidiogenous cells and brown, subcylindrical, phragmosporous dry, smooth to verrucose conidia produced in branched chains (Crous et al. 2015, Li et al. 2017, Tennakoon et al. 2021). Members of this family are mainly saprobes in terrestrial and freshwater habitats (Hongsanan et al. 2020a). Six genera are accepted in Torulaceae, namely *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides* and *Torula* (Hongsanan et al. 2020a).

Torula Pers.

Torula was erected by Persoon (1794) with the type *T. herbarum*. These species commonly inhabit terrestrial and aquatic habitats in temperate to tropical regions as saprobes (Li et al. 2020b). The asexual morph of the genus is characterized by terminal or lateral, monoblastic or polyblastic conidiogenous cells and dark brown, cylindrical to subcylindrical, solitary to catenate, acrogenous, simple, phragmosporous, septate conidia (Crane & Miller 2016, Li et al. 2017, 2020b). There are 541 *Torula* species epithets in Index Fungorum (2022).

Torula canangae N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 39
Index Fungorum number: IF 559523, Faces of Fungi number: FoF 10720

Etymology – Name reflects the host genus *Cananga*, from which the new species was isolated.

Holotype – MFLU 21-0250

Saprobic on dead twigs attach to *Cananga odorata*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse on host, black, powdery. *Mycelium* partly immersed to superficial on the substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* indistinct. *Conidiogenous cells* 3–4 × 3.5–5 μm ($\bar{x}$ = 3.4 × 4.2 μm, n = 10), light brown, ellipsoid to coronal, polyblastic, terminal, smooth to minutely verruculose, thick-walled. *Conidia* 10–18 × 4–6 μm ($\bar{x}$ = 16 × 5 μm, n = 30), light brown to dark brown, subcylindrical, catenate, acrogenous, phragmosporous, smooth to distinctly verrucose, 2–4-septate, rounded at apex, slightly constricted at some septa.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: white, circular, flat, slightly raised, fluffy appearance at the centre, cream at the margin; reverse: pale brown from the centre of the colony, white at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Cananga odorata* (Annonaceae), 2 January 2019, N. I. de Silva, CO1 (MFLU 21-0250, holotype), ex-type living culture, MFLUCC 21-0169.

GenBank numbers – LSU: OL830816, *tef1*: ON032379, ITS: OL966950.

Notes – Phylogeny based on combined LSU, SSU, *tef1*, *rpb2* and ITS sequence data (Fig. 38) indicates that a new strain (MFLUCC 21-0169) which shares similar morphological characteristics of *Torula* constitutes a strongly supported distinct lineage in a clade comprising *T. chiangmaiensis*,

T. hollandica, *T. pluriseptata*, *T. polyseptata* and *T. thailandica* with 92% ML, 1.00 BYPP statistical support. The new strain (MFLUCC 21-0169) has smaller conidia length (considering average conidial length) and lesser number of conidial septa than phylogenetically closely related *T. chiangmaiensis*, *T. polyseptata* and *T. thailandica* (Table 5). Considering morpho-molecular data, we conclude that *Torula canangae* is a novel species.
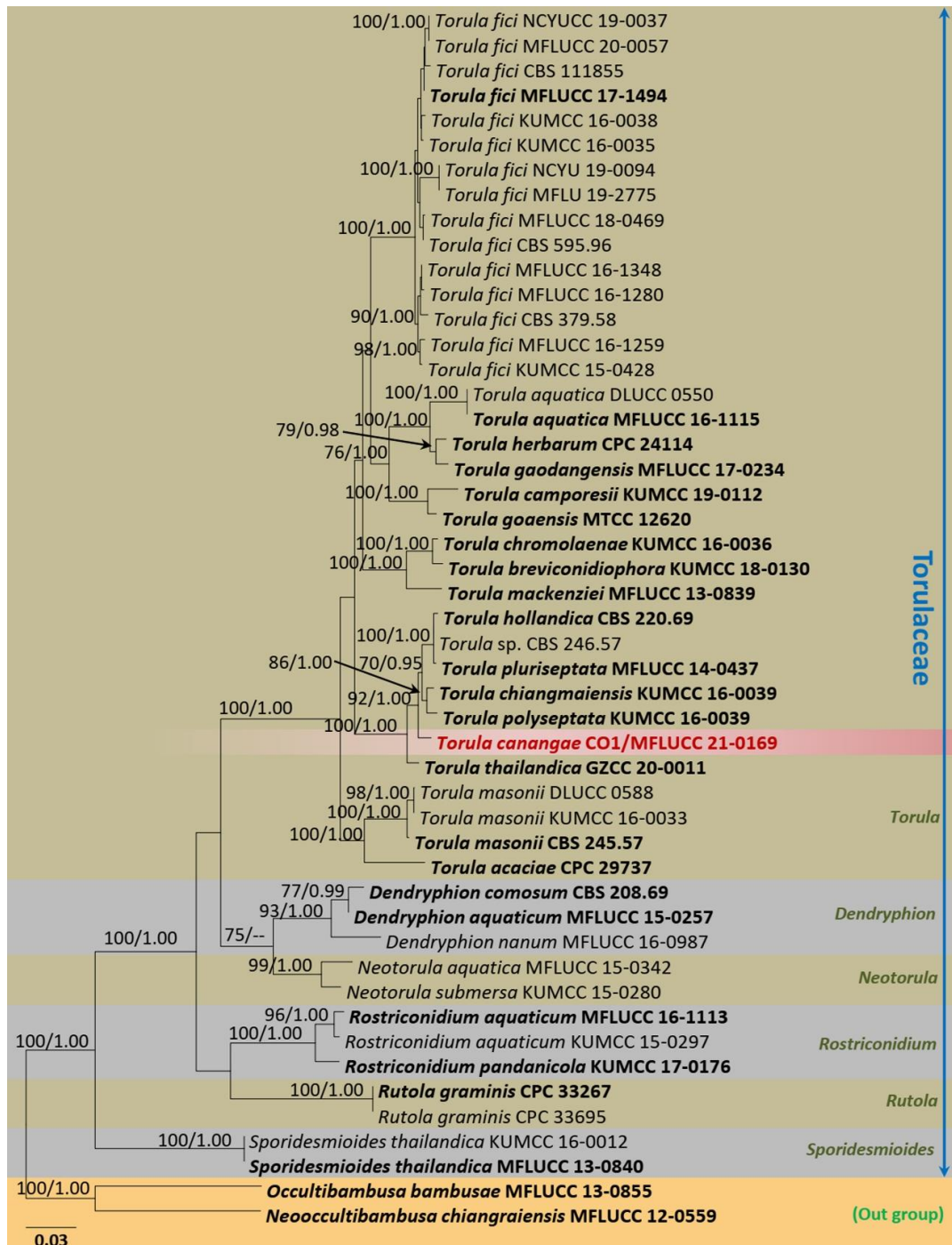

Figure 38 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU, *tef1*, *rpb2* and ITS sequence data. Related sequences of Torulaceae were obtained from Tennakoon et al. (2021). Forty-nine strains are included in the combined gene analyses comprising 3880 characters after alignment (890 characters for LSU, 800 characters for SSU, 860 characters for *tef1*, 850 characters for *rpb2* and 480 characters for ITS). *Neoccucurbitaria chiangraiensis* (MFLUCC 12-0559) and *Occultibambusa bambusae* (MFLUCC 13-0855) are used as outgroup taxon. The best RAxML tree with a final likelihood value of -19475.286794 is presented. The matrix had 1406

distinct alignment patterns, with 40.28% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
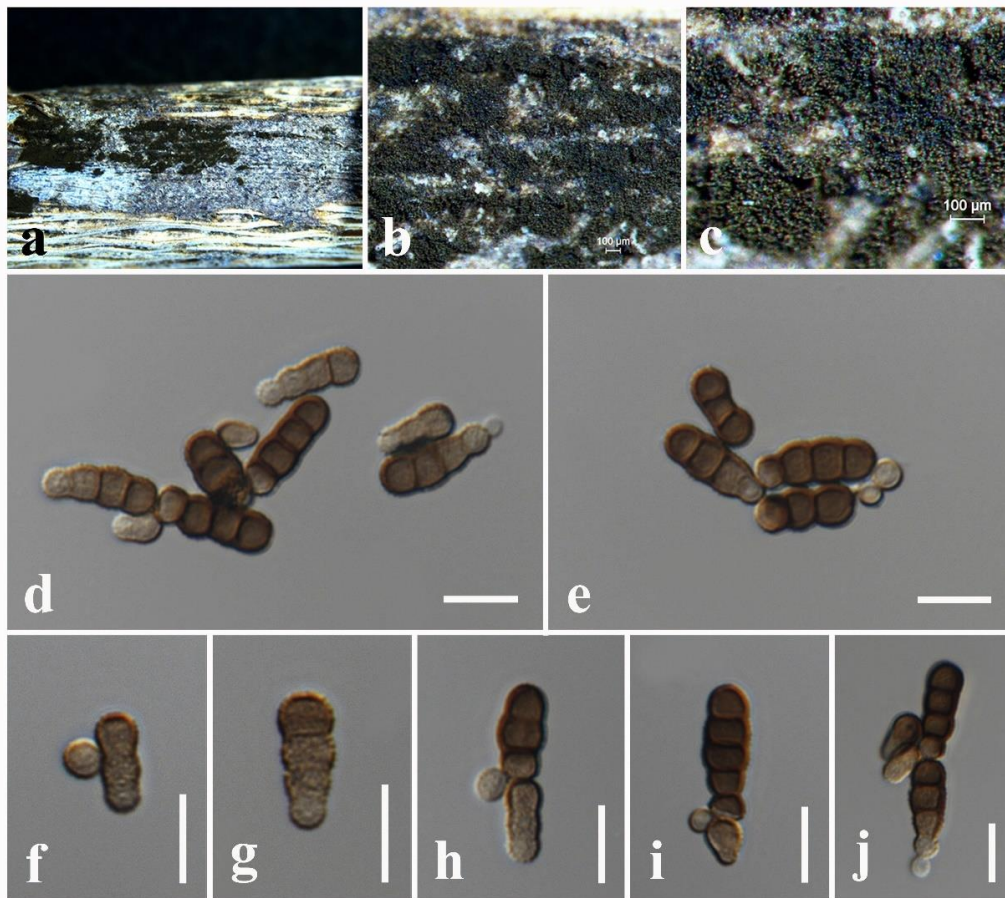

Figure 39 – *Torula canangae* (MFLU 21-0250, holotype). a–c Appearance of colonies on substrate. d–j Conidia with conidiogenous cells. Scale bars: b, c = 100 μm, d–j = 10 μm.

Table 5 Conidial dimensions and number of septa of *T. canangae* and closely related species.

Torula species	Conidia dimensions (μm)	Number of conidial septa	Substrate/host	Reference
T. canangae	16 × 5	2–4	dead twigs of *Cananga odorata*	This study
T. chiangmaiensis	59.6 × 6.6	4–12	Branch of dead herbaceous plant	Li et al. (2017)
T. hollandica	21–26 × 6–7	4	On *Delphinium* sp.	Crous et al (2015)
T. pluriseptata	30.5 × 4.1	3–10	Dead branch of *Clematis vitalba*	Li et al. (2017)
T. polyseptata	19.3 × 5.5	2–8	On submerged decaying wood	Hyde et al. (2019)
T. thailandica	18.1 × 5.6	2–8	On decaying wood	Hongsanan et al. (2020a)

Dothideomycetes order *incertae sedis*
Botryosphaeriales C.L. Schoch et al.
Botryosphaeriaceae Theiss. & Syd.

Botryosphaeriaceae was introduced by Theisen and Sydow (1918) who included three genera namely *Botryosphaeria*, *Phaeobotryon* and *Dibotryon*. Phillips et al. (2019) recognized 22 genera

within the family based on morphology of sexual morphs, phylogenetic relationships and evolutionary divergence times. This family includes pathogens, endophytes or saprobes, mainly on woody hosts that are widely distributed in different geographical and climatic areas of the world, except for the polar regions (Phillips et al. 2013). Pathogens cause various diseases such as shoot blights, stem cankers, fruit rots, dieback and gummosis in plants (Abdollahzadeh et al. 2010). The sexual morph is characterized by pseudothecial, uniloculate ascostromata comprising hyaline or pigmented, septate or not, fusoid to ellipsoid or ovoid ascospores (Phillips et al. 2019). The asexual morph is characterized by pycnidial conidiomata with hyaline or pigmented, aseptate, one or multi-septate, sometimes muriform, smooth or striate conidia (Phillips et al. 2019).

Lasiodiplodia Ellis & Everh.

Lasiodiplodia species are common in tropical and subtropical regions (Abdollahzadeh et al 2010). *Lasiodiplodia* was introduced by Ellis in 1894 with the type *L. tubericola* (Phillips et al. 2013). Clendenin (1896) described the genus. *Lasiodiplodia* species can be distinguished from other closely related genera by the presence of pycnidial paraphyses and longitudinal striations on mature brown conidia (Abdollahzadeh et al 2010). DNA sequence data have played a significant role in distinguishing species in *Lasiodiplodia* (Abdollahzadeh et al 2010, Phillips et al. 2019). Previously, combined ITS and *tef1* were used to identify phylogenetic relationships of species in *Lasiodiplodia* (Burgess et al. 2006, Phillips et al. 2013) while some studies have used combined ITS, LSU, *tef1*, *tub2* (Meng et al. 2021) or ITS, *tef1*, *tub2* and *rpb2* (Wang et al. 2019). The current phylogenetic analyses followed Zhang et al. (2021).

Lasiodiplodia crassispora T.I. Burgess & P.A. Barber, Mycologia 98(3): 425 (2006)   Fig. 41
        Index Fungorum number: IF 500235, Faces of Fungi number: FoF 0662
        Saprobic on dead twigs attached to *Magnolia lilifera*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 190–220 μm high × 180–230 μm diam. ($\bar{x} = 200 \times 215$ μm, n = 10), pycnidial, dark brown, globose to subglobose, solitary to gregarious, immersed to semi-immersed, erumpent through plant host tissue. *Conidiomatal wall* 25–35 μm wide, composed of light brown cells of *textura angularis*. *Paraphyses* up to 30 μm long, 3–4 μm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–10 × 5–6 μm ($\bar{x} = 7 \times 5.3$ μm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-walled. *Conidia* 24–30 × 16–18 μm ($\bar{x} = 26 \times 17$ μm, n = 30), hyaline, subglobose to subcylindrical, with granular content, both ends rounded, wall <2 μm thick.

        Culture characteristics – Colonies on PDA reaching 55 mm diameter after 1 week at 25 °C, colonies from above: light grey, circular, margin entire, slightly dense, cottony to fluffy appearance with abundant aerial mycelia; reverse: cream.

        Material examined – Thailand, Chiang Rai Province, dead twigs attached to the *Magnolia lilifera* (Magnoliaceae), 11 February 2019, N. I. de Silva, NI326 (MFLU 21-0230), living culture, MFLUCC 21-0190.

        Known hosts and distribution – From *Eucalyptus urophylla* in Venezuela and *Santalum album* in Australia (Burgess et al. 2006), *Acacia mellifera* in Nambia, *Vitis vinifera* in South Africa, *Adansonia* sp. in Senegal, *Manihot* esculenta, *Jatropha curcas* in Brazil, *Adansonia* sp. in Zimbabwe, *Adansonia digitata* in Botswana (Zhang et al. 2021), dead twigs attached to *Magnolia lilifera* in Thailand (this study).

        GenBank numbers – ITS: OM614889, *tef1*: OM681513, *tub2*: OM929182.

        Notes – We collected a fungal species from dead twigs of *Magnolia lilifera* and identified it as *Lasiodiplodia crassispora* based on the phylogeny of combined ITS, *tef1* and *tub2* sequence data (Fig. 40). Conidia of *L. crassispora* (28.8 × 16 μm) (Burgess et al 2006) are longer than the new isolate (26 × 17 μm). Conidiogenous cells of the type of *L. crassispora* (11.8 × 5 μm) (Burgess et al 2006) are larger than the new isolate (7 × 5.3 μm). Comparisons of sequence data between the new isolate and the ex-type *L. crassispora* WAC12533 revealed one base pair (0.2%) difference in ITS and one base pair (1.96%) differences in *tef1* gene regions. Sequence data of *tub2* gene region of

both the new isolate and the ex-type *L. crassispora* WAC12533 are similar. *Lasiodiplodia crassispora* was introduced by Burgess et al (2006) from canker of *Santalum album* in Australia. This is the first record of *L. crassispora* from dead twigs attached to the host plant of *Magnolia lilifera* in Thailand.
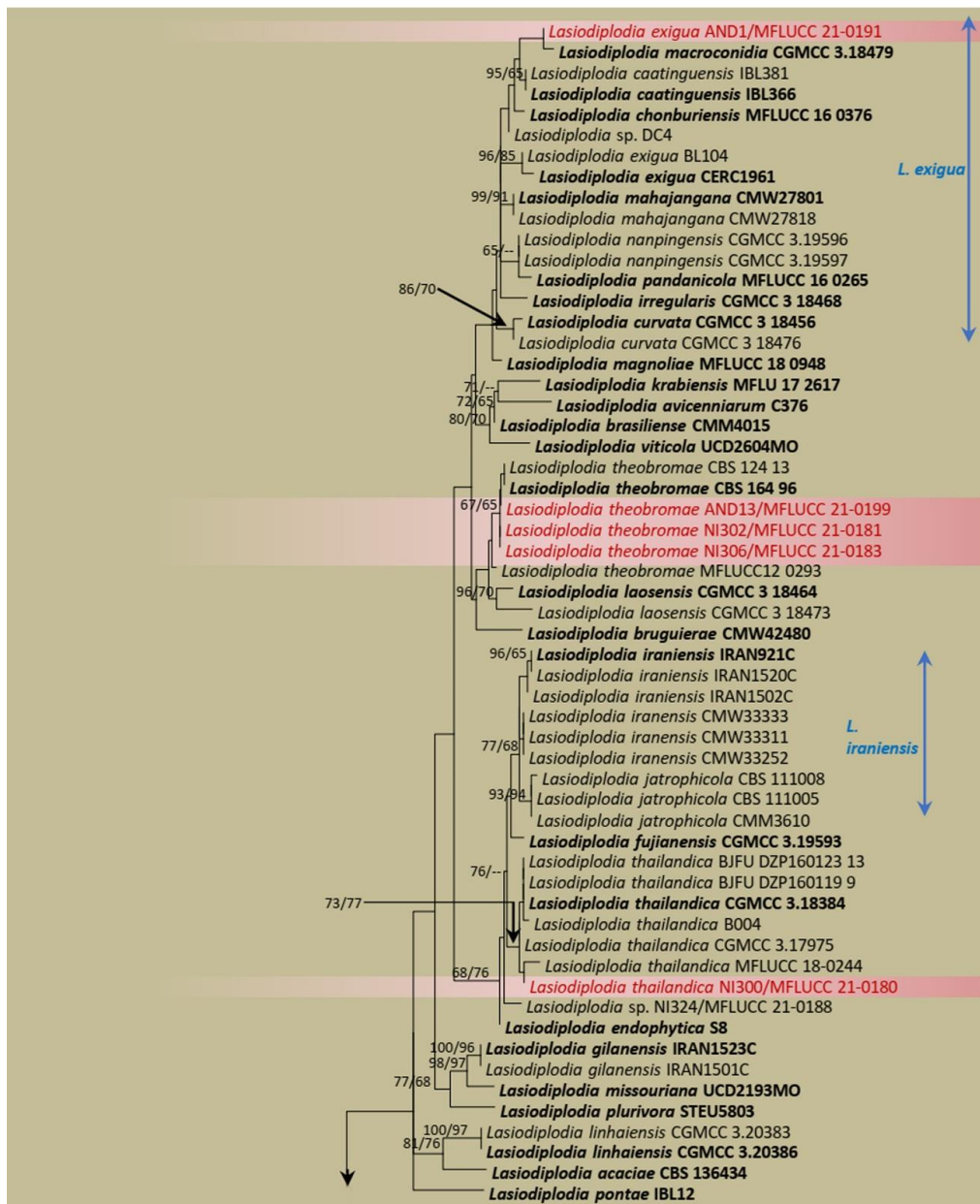

Figure 40 – Phylogram generated from maximum likelihood analysis of combined ITS, *tef1* and *tub2* sequence data. One hundred fifteen strains are included in the combined gene analyses comprising 1180 characters after alignment 500 characters for ITS, 280 characters for *tef1* and 400 characters for *tub2*). *Diplodia mutila* (CMW 7060) and *D. seriata* (CBS 1125551) are used as outgroup taxa. The best RAxML tree with a final likelihood value of - 6062.246467 is presented. The matrix had 464 distinct alignment patterns, with 16.88% undetermined characters or gaps. Bootstrap values for maximum likelihood and maximum parsimony equal to or greater than 50% are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Lasiodiplodia exigua Linald., Deidda & A.J.L. Phillips, Fungal Divers. 71: 207 (2014)

Fig. 42

Index Fungorum number: IF 831469, Faces of Fungi number: FoF 10664

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 150–180 µm high × 150–230 µm diam. ($\bar{x}$ = 160 × 180 µm, n = 10), pycnidial, dark brown, globose to subglobose, solitary, scattered, immersed to semi-immersed, uni-locular, with a central ostiole. *Conidiomatal wall* 20–30 µm wide, composed of brown cells of *textura angularis*. *Paraphyses* up to 40 µm long, 1–2 µm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–12 × 4–6 µm ($\bar{x}$ = 10 × 5 µm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-walled. *Conidia* 20–30 × 12–15 µm ($\bar{x}$ = 26 × 13 µm, n = 30), initially hyaline, subglobose to subcylindrical, with granular content, rounded at both ends, wall <2 µm thick, becoming pigmented, ellipsoid to ovoid, 1-septate with longitudinal striations.
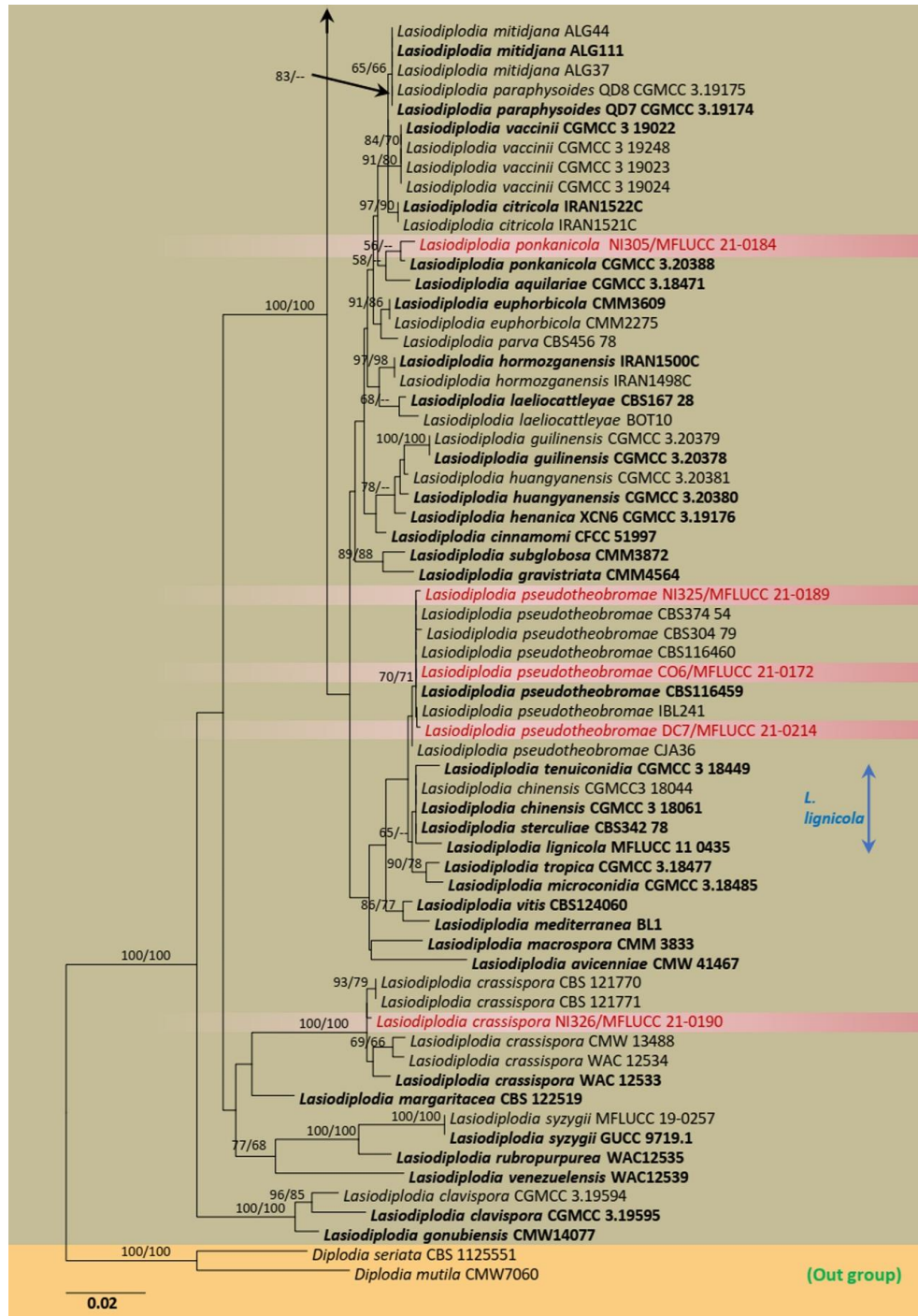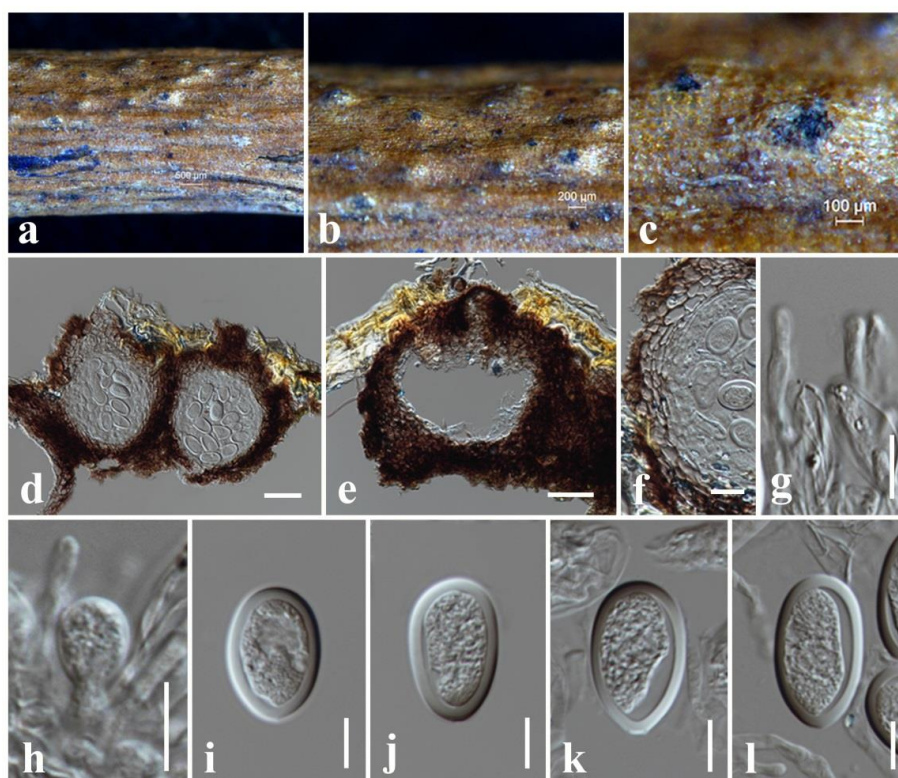

Figure 40 – Continued.

Figure 41 – *Lasiodiplodia crassispora* (MFLU 21-0230). a The specimen. b, c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Paraphyses. h Conidiogenous cells. i–l Conidia. Scale bars: b = 200 µm, c = 100 µm, d, e = 50 µm, f = 20 µm, g–l = 10 µm.

Culture characteristics – Colonies on PDA reaching 80 mm diameter after 1 week at 25 °C, colonies from above: olivaceous-grey, circular, margin entire, fluffy appearance with abundant aerial mycelia; reverse: light brown.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND1 (MFLU 21-0226), living culture, MFLUCC 21-0191.

Known hosts and distribution – From a branch canker of *Retama raetam* in Tunisia, from *Pistacia vera* in USA (Linaldeddu et al. 2015), dead twigs attached to *Anomianthus dulcis* in Thailand (this study).

GenBank numbers – ITS: OM614882, *tub2*: OM864022.

Notes – *Lasiodiplodia exigua* was introduced by Linaldeddu et al (2015) from a branch canker of *Retama raetam* in Tunisia. The phylogeny indicates that our strain clusters with the type *L. exigua* (Fig. 40). Conidia of the new collection (26 × 13 µm) are slightly larger than the type (21.8 × 12.3 µm) (Linaldeddu et al 2015). This is the first record of *L. exigua* from dead twigs of *Anomianthus dulcis*.

Lasiodiplodia ponkanicola X.E. Xiao, Crous & H.Y. Li, Persoonia 47: 128 (2021)   Fig. 43

Index Fungorum number: IF 840685, Faces of Fungi number: FoF 10663

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 250–260 µm high × 270–295 µm diam. ($\bar{x}$ = 255 × 284 µm, n = 10), pycnidial, brown, globose to subglobose, solitary, immersed to semi-immersed, erumpent through plant host tissue. *Conidiomatal wall* 30–40 µm wide, composed of brown cells of *textura angularis*. *Paraphyses* up to 55 µm long, 2–3 µm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–13 × 3–5 µm ($\bar{x}$ = 11 × 4 µm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-

walled. *Conidia* 20–27 × 10–13 μm ($\bar{x}$ = 25 × 12 μm, n = 30), hyaline, subglobose to subcylindrical, with granular content, rounded at both ends, wall <2 μm thick.
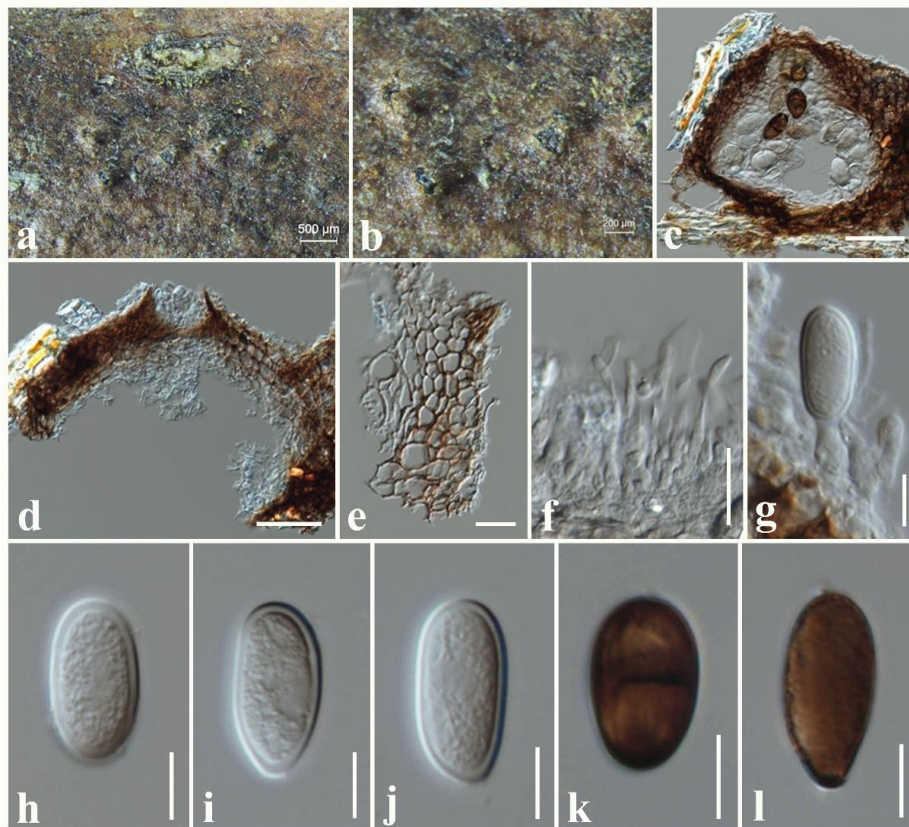

Figure 42 – *Lasiodiplodia exigua* (MFLU 21-0226). a, b Appearance of conidiomata on the substrate. c, d Vertical sections through conidioma. e Conidiomatal wall. f Paraphyses. g Conidiogenous cells. h–l Conidia. Scale bars: a = 500 μm, b = 200 μm, c, d = 50 μm, e, f = 20 μm, g–l = 10 μm.

Culture characteristics – Colonies on PDA reaching 50 mm diameter after 1 week at 25 °C, colonies from above: white, circular, margin entire, dense, cottony to fluffy appearance with abundant aerial mycelia; reverse: cream.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia champaca* (Magnoliaceae), 9 January 2019, N. I. de Silva, NI305 (MFLU 21-0224), living culture, MFLUCC 21-0184.

Known hosts and distribution – From branches of *Citrus unshiu* in China (Xiao et al. 2021), dead twigs attached to *Magnolia champaca* in Thailand (this study).

GenBank numbers – ITS: OM614886, *tef1*: OM681514, *tub2*: OM929181.

Notes – Phylogeny based on a combined ITS, *tef1* and *tub2* sequence data revealed the new isolate closely related to *L. aquilariae* and *L. ponkanicola* (Fig. 40). *Lasiodiplodia aquilariae* was described in Laos from *Aquilaria crassna* (Wang et al. 2019). *Lasiodiplodia ponkanicola* was identified in China from branch of *Citrus unshiu* (Xiao et al. 2021). Morphologically, the new collection (MFLU 21-0224), *L. aquilariae* and *L. ponkanicola* have an overlapping size range of conidia. Conidia of the new isolate are (20–27 × 10–13) μm while *L. aquilariae* are (25–28 (–29) × 12–16) μm (Wang et al. 2019). Conidia of *L. ponkanicola* are (16–)23.5–27.5(–28.5) × (11–)13–14.5(–15.5) (Xiao et al. 2021). A pairwise comparison of *tef1* sequence data between the new isolate MFLUCC 21-0184 and *L. aquilariae* shows four base pair (1.34%) differences. ITS gene region of both the new isolate and *L. aquilariae* are similar. A comparison of *tub2* sequence data was not done as it is not available for *L. aquilariae* in GenBank. A pairwise comparison of *tef1*

sequence data between the new isolate MFLUCC 21-0184 and *L. ponkanicola* CGMCC 3.20388 shows one base insertion in the *L. ponkanicola* CGMCC 3.20388. ITS region of both the new isolate and *L. aquilariae* are similar. A comparison of *tub2* sequence data shows one base pair difference.

Considering phylogeny, base pair comparison and morphology, we identify our isolate as *L. ponkanicola*. This is the first report of *L. ponkanicola* from dead twigs of *Magnolia champaca* in Thailand.
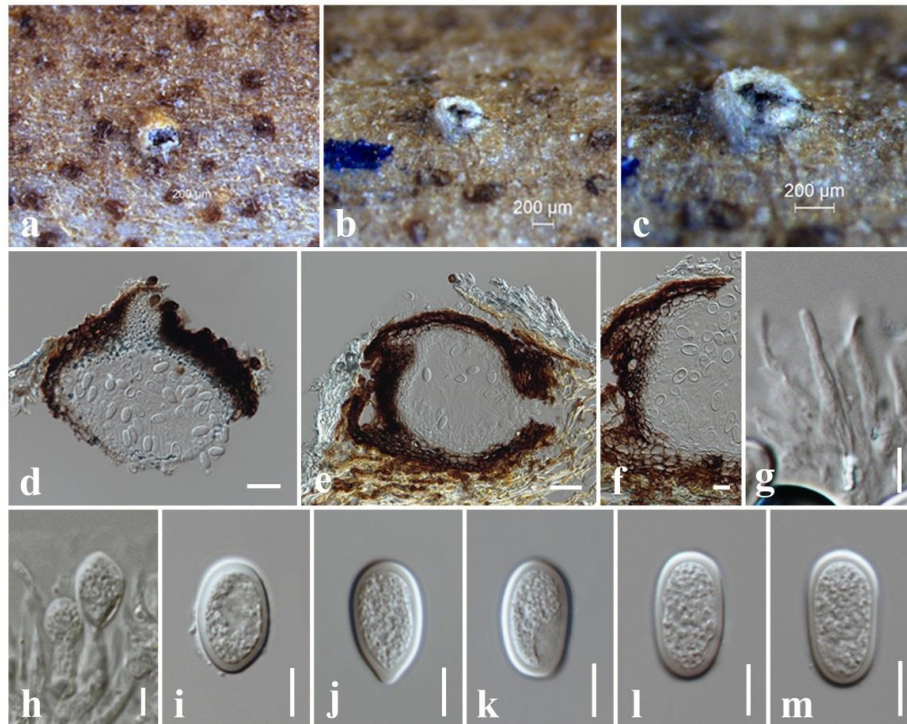

Figure 43 – *Lasiodiplodia ponkanicola* (MFLU 21-0224). a–c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Paraphyses. h Conidiogenous cells. i–m Conidia. Scale bars: b, c = 200 μm, d, e = 50 μm, f = 20 μm, g–m = 10 μm.

Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous, Fungal Divers. 28: 8 (2008)

Fig. 44

Index Fungorum number: IF 510941, Faces of Fungi number: FoF 04567

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: see Tennakoon et al. (2016). Asexual morph: Coelomycetous. *Conidiomata* 240–260 μm high × 230–250 μm diam. ($\bar{x}$ = 250 × 240 μm, n = 10), pycnidial, black, globose to subglobose, solitary, scattered, immersed to semi-immersed, erumpent through plant host tissue. *Conidiomatal wall* 40–70 μm wide, composed of light brown cells of *textura angularis*. *Paraphyses* up to 25 μm long, 2–4 μm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–10 × 4–6 μm ($\bar{x}$ = 9 × 5 μm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-walled. *Conidia* 15–25 × 9–11 μm ($\bar{x}$ = 20 × 10 μm, n = 30), hyaline, subglobose to subcylindrical, with granular content, rounded at both ends.

Culture characteristics – Colonies on PDA reaching 60 mm diameter after 1 week at 25 °C, colonies from above: white, circular, margin entire, slightly dense, cottony to fluffy appearance with abundant aerial mycelia; reverse: cream.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia champaca* (Magnoliaceae), 11 February 2019, N. I. de Silva, NI325 (MFLU 21-0227), living culture, MFLUCC 21-0189; *ibid*., dead twigs attached to *Cananga odorata* (Annonaceae), 2

January 2019, N. I. de Silva, CO6 (MFLU 21-0228), living culture, MFLUCC 21-0172; *ibid.*, dead twigs attached to *Desmos chinensis* (Annonaceae), 8 March 2019, N. I. de Silva, DC7 (MFLU 21-0229), living culture, MFLUCC 21-0214.

Known hosts and distribution – *Lasiodiplodia pseudotheobromae* occurs on numerous host plants and distributed worldwide including *Annona squamosa* in Brazil *Camellia sinensis* in China, *Citrus limon* in Australia, *Eucalyptus grandis* in South Africa, *Terminalia catappa* Madagascar, *Zea mays* India (Far and Rossman 2022), dead twigs attached to *Magnolia champaca*, *Cananga odorata*, *Desmos chinensis* in Thailand (this study).

GenBank numbers – (CO6): ITS: OM614883, *tef1*: OM650185, *tub2*: OM837725, (DC7): ITS: OM614884, *tef1*: OM650186, *tub2*: OM837726, (NI325): ITS: OM614888, *tef1*: OM650187, *tub2*: OM837727.

Notes – The type of *Lasiodiplodia pseudotheobromae* was isolated from *Gmelina arborea* in Costa Rica (Alves et al. 2008). Phylogeny shows that three new strains from *Cananga odorata*, *Desmos chinensis* and *Magnolia champaca* cluster with the type of *L. pseudotheobromae* with 70% ML, 71% MP statistical support (Fig. 40). Conidia of the new collection (MFLU 21-0227) (20 × 10 µm) are smaller than the type of *L. pseudotheobromae* (28 × 16 µm) (Alves et al. 2008).

Trakunyingcharoen et al. (2015b) identified *L. pseudotheobromae* from many host plants in Thailand including *Bouea burmanica*, *Cananga odorata*, *Coffea arabica*, *Dimocarpus longan*, *Ficus racemosa*, *Hevea brasiliensis*, *Mangifera indica* and *Osmanthus fragrans*. *Lasiodiplodia pseudotheobromae* has not been identified from *Magnolia champaca* and *Desmos chinensis* (Far & Rossman 2022). Therefore, we herein report the new host record of *L. pseudotheobromae* from dead twigs of *Magnolia champaca* and *Desmos chinensis* in Thailand.
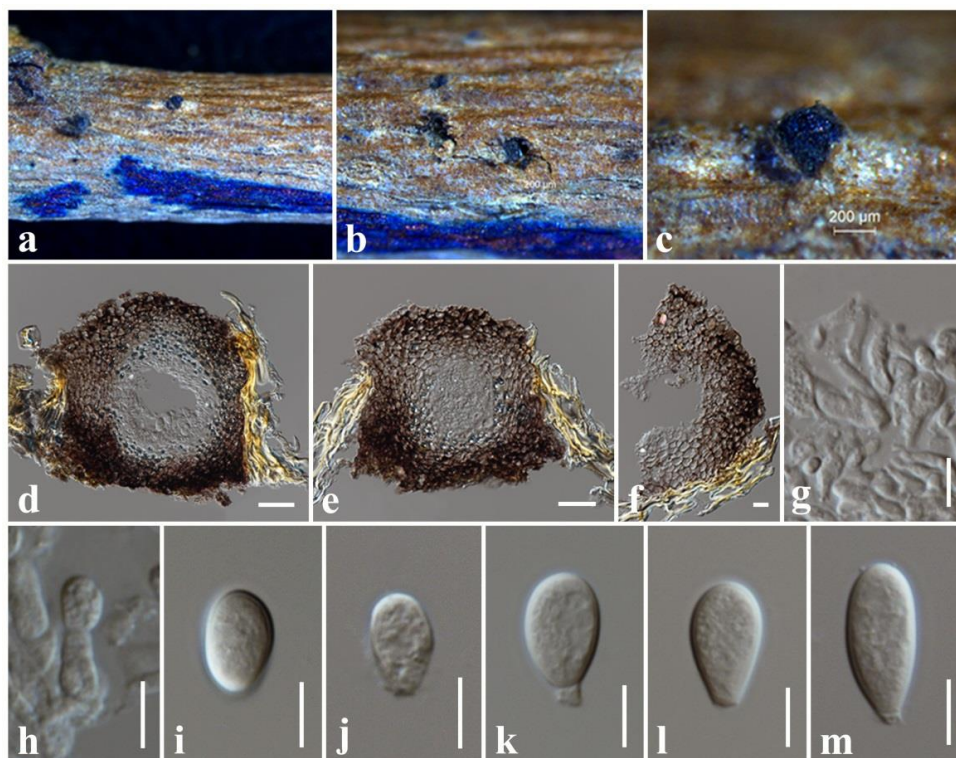

Figure 44 – *Lasiodiplodia pseudotheobromae* (MFLU 21-0227). a–c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Paraphyses. h Conidiogenous cells. i–m Conidia. Scale bars: a–c = 200 µm, d, e = 50 µm, f = 20 µm, g–m = 10 µm.

Lasiodiplodia thailandica Trakun., L. Lombard & Crous, Persoonia 34: 95 (2014)   Fig. 45
Index Fungorum number: IF 810169, Faces of Fungi number: FoF 09333

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 120–150 μm high × 140–180 μm diam. ($\bar{x} = 140 \times 160$ μm, n = 10), pycnidial, black, globose to subglobose, solitary to gregarious, scattered, immersed to semi-immersed, uni-locular. *Conidiomatal wall* 20–25 μm wide, composed of brown cells of *textura angularis*. *Paraphyses* up to 40 μm long, 1–2 μm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 10–12 × 3–4 μm ($\bar{x} = 11 \times 3.5$ μm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-walled. *Conidia* 15–22 × 11–13 μm ($\bar{x} = 19 \times 12$ μm, n = 30), hyaline, subglobose to subcylindrical, with granular content, rounded at both ends, wall <2 μm thick.

Culture characteristics – Colonies on PDA reaching 70 mm diameter after 1 week at 25 °C, colonies from above: light grey, circular, margin entire, slightly dense, cottony to fluffy appearance with abundant aerial mycelia; reverse: grey.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia champaca* (Magnoliaceae), 9 January 2019, N. I. de Silva, NI300 (MFLU 21-0231), living culture, MFLUCC 21-0180.

Known hosts and distribution – From symptomless twigs of *Mangifera indica*, *Phyllanthus acidus* in Thailand (Trakunyingcharoen et al. 2015b), decaying fruit pericarp of *Swietenia mahagoni* in Thailand (Jayasiri et al. 2019), *Acacia confuse* in China (Zhang et al. 2021), dead twigs attached to *Magnolia champaca* in Thailand (this study).

GenBank numbers – ITS: OM614885, *tef1*: OM681511, *tub2*: OM837728.

Notes – Phylogenetically, a new strain (MFLUCC 21-0180) clusters with the ex-type of *Lasiodiplodia thailandica* (CGMCC 3.18384) and some other strains of *L. thailandica* (Fig. 40). *Lasiodiplodia thailandica* was introduced from symptomless twigs of *Mangifera indica* in Thailand by Trakunyingcharoen et al. (2015b). We report a new host record of *L. thailandica* from dead twigs of *Magnolia champaca* in Thailand. However, the new isolate has slightly smaller conidia (15–22 × 11–13 μm) and slightly larger conidiogenous cells (10–12 × 3–4 μm) than the ex-type of *L. thailandica* (Trakunyingcharoen et al. 2015b). The ex-type of *Lasiodiplodia thailandica* has (20–26 × 12–16 μm) conidia and (8–9 × 2–4 μm) conidiogenous cells (Trakunyingcharoen et al. 2015b).

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

Fig. 46

Index Fungorum number: IF 188476, Faces of Fungi number: FoF 00167

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed Asexual morph: Coelomycetous. *Conidiomata* 180–200 μm high × 200–250 μm diam. ($\bar{x} = 190 \times 230$ μm, n = 10), pycnidial, brown, globose to subglobose, mostly immersed, solitary to gregarious, occasionally semi-immersed, erumpent through plant host tissue. *Conidiomatal wall* 30–40 μm wide, composed of light brown cells of *textura angularis*. *Paraphyses* up to 45 μm long, 1–2 μm wide, hyaline, cylindrical, septate, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–12 × 3–5 μm ($\bar{x} = 10 \times 4$ μm, n = 10), hyaline, holoblastic, discrete, cylindrical to subcylindrical, smooth-walled. *Conidia* 22–27 × 9–13 μm ($\bar{x} = 25 \times 11$ μm, n = 30), hyaline, subglobose to subcylindrical, with granular content, rounded at both ends, wall <2 μm thick.

Culture characteristics – Colonies on PDA reaching 50 mm diameter after 1 week at 25 °C, colonies from above: light grey, circular, margin entire, cottony to fairly fluffy appearance with abundant aerial mycelia; reverse: dark grey.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND13 (MFLU 21-0232), living culture, MFLUCC 21-0199, *ibid*., dead twigs attached to *Magnolia champaca* (Magnoliaceae), 9 January 2019, NI302 (MFLU 21-0234), living culture, MFLUCC 21-0181, NI306 (MFLU 21-0233), living culture, MFLUCC 21-0183.

Known hosts and distribution – *Lasiodiplodia theobromae* occurring on numerous host plants and distributed in worldwide including *Acacia cincinnata* in Brazil, *Vitis vinifera* in Australia,

China, Italy, *Magnolia* sp. in Myanmar (Far & Rossman 2022), dead twigs attached to *Anomianthus dulcis* and *Magnolia champaca* in Thailand (this study).

GenBank numbers – (AND13): ITS: OM614890, *tub2*: OM864019, (NI306): ITS: OM614891, *tef1*: OM718700, *tub2*: OM864020, (NI302): ITS: OM614892, *tef1*: OM718701, *tub2*: OM864021.
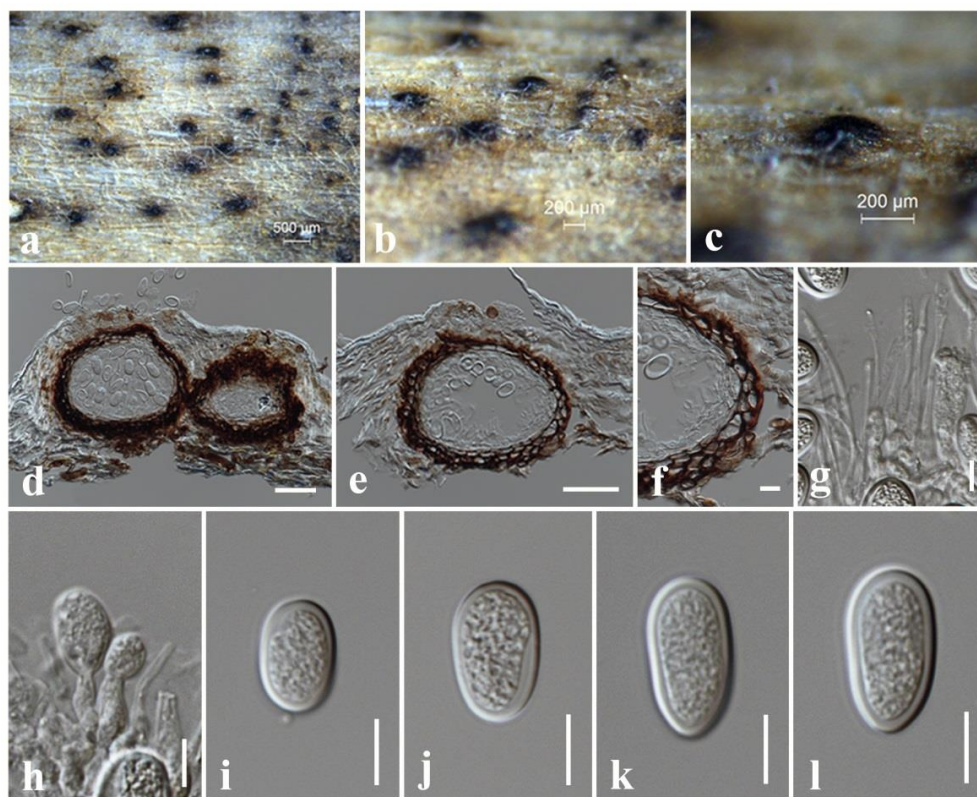

Figure 45 – *Lasiodiplodia thailandica* (MFLU 21-0231). a–c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Paraphyses. h Conidiogenous cells. i–l Conidia. Scale bars: a = 500 μm, b, c = 200 μm, d, e = 50 μm, f–l = 10 μm.

Notes – Phylogenetic analysis of the combined ITS, *tef1* and *tub2* sequence data shows that three new strains (MFLUCC 21-0199, 21-0181, 21-0183) cluster with the ex-neotype strain of *Lasiodiplodia theobromae* (CBS 164.96) and other strains of *L. theobromae*. *Lasiodiplodia theobromae* has been recorded on different host plants in Thailand such as *Hevea brasiliensis*, *Licuala longicalycata*, *Pandanus* sp. and *Tectona grandis* (Pinruan et al. 2007, Seephueak et al. 2011, Doilom et al. 2015, Tibpromma et al. 2018a, Farr & Rossman 2022). However, *L. theobromae* has not been recorded from *Anomianthus dulcis* and *Magnolia champaca* in Thailand (Farr & Rossman 2022). Therefore, we report new host records of *L. theobromae* from *Anomianthus dulcis* and *Magnolia champaca*.

Dothideomycetes incertae sedis
Botryosphaeriales C.L. Schoch et al.
Phyllostictaceae Fr.

Members of Phyllostictaceae are foliicolous, plant pathogenic, endophytic or saprobic (Phillips et al. 2019). The sexual morph is characterized by pseudothecial, uniloculate ascostromata containing hyaline, aseptate, ellipsoid-fusoid to limoniform ascospores and asexual morph by pycnidial, globose conidiomata containing hyaline, ellipsoid-fusoid to obovoid or ovoid conidia with mucilaginous sheath (Wikee et al. 2013, Phillips et al. 2019). Fries (1849) proposed

Phyllostictaceae (as Phyllostictei) and Hawksworth & David (1989) accepted to use of the family name Phyllostictaceae. Seaver (1922) used Phyllostictales and Phyllostictaceae to accommodate *Phyllosticta* species. Wikee et al. (2013) reinstated Phyllostictaceae as a distinct family in Botryosphaeriales to accommodate *Phyllosticta* species (= *Guignardia*) based on morphology and phylogeny. The phylogenies of ITS and LSU sequence data and evolutionary divergence times reported in Phillips et al. (2019) include *Pseudofusicoccum* as an additional genus within Phyllostictaceae.
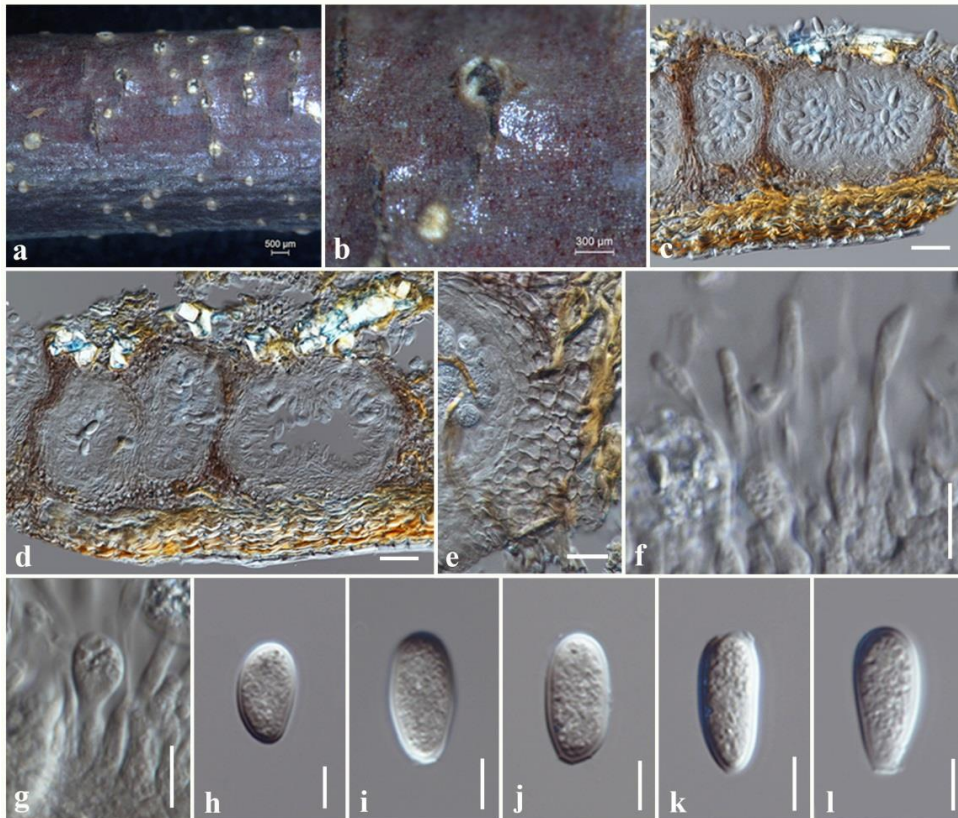

Figure 46 – *Lasiodiplodia theobromae* (MFLU 21-0232). a, b Appearance of conidiomata on the substrate. c, d Vertical sections through conidiomata. e Conidiomatal wall. f Paraphyses. g Conidiogenous cells. h–l Conidia. Scale bars: a = 500 μm, b = 300 μm, c, d = 50 μm, e = 20 μm, f–l = 10 μm.

Pseudofusicoccum Mohali et al.

Crous et al. (2006) introduced *Pseudofusicoccum* with the type *P. stromaticum*. Species of *Pseudofusicoccum* are morphologically similar to *Fusicoccum* and *Neofusicoccum* but phylogenetically distinct from both of these genera (Crous et al. 2006, Phillips et al. 2013). They exhibit as endophytes, saprobes or plant pathogens associated with diseases on stems, twigs, branches and leaves in various hosts and have a worldwide distribution (Mohali et al. 2006, Doilom et al. 2015, Jami et al. 2018, Senwanna et al. 2020). The asexual morph is characterized by immersed to superficial pycnidial conidiomata, and hyaline, aseptate, cylindrical to ellipsoid conidia (Pavlic et al. 2008, Yang et al. 2017, Phillips et al. 2019). The sexual morph is characterized as globose to subglobose spots of ascomata on the host surface consisting hyaline, clavate ascospores surrounded by a mucilaginous sheath (Senwanna et al. 2020).

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

Fig. 49

Index Fungorum number: IF 512048, Faces of Fungi number: FoF 00168

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 150–170 μm high × 120–150 μm diam. ($\bar{x}$ = 160 × 130 μm, n = 10), pycnidial, dark brown, globose to subglobose, solitary to scattered, immersed to semi-immersed, uni-locular, with a central ostiole. *Conidiomatal wall* 20–30 μm wide, inner layers comprising of thin-walled, hyaline cells of *textura angularis*, outer layers comprising of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 1.5–3 μm ($\bar{x}$ = 6 × 2 μm, n = 10), hyaline, phialidic, cylindrical to subcylindrical, smooth-walled. *Conidia* 15–17 × 4–6 μm ($\bar{x}$ = 16 × 5 μm, n = 30), hyaline, ellipsoid, straight or slightly bent, smooth-walled, with fine granular content.

Culture characteristics – Colonies on PDA reaching 50 mm diameter after 1 week at 25 °C, colonies from above: white, circular, margin entire, fluffy appearance; reverse: cream.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND32 (MFLU 21-0244), living culture, MFLUCC 21-0205; *ibid*., dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS15 (MFLU 21-0246), living culture, MFLUCC 21-0208; *ibid*., dead twigs attached to *Magnolia lilifera* (Magnoliaceae), 10 February 2019, N. I. de Silva, NI320 (MFLU 21-0245), living culture, MFLUCC 21-0185.

Known hosts and distribution – *Acacia synchronica*, *Adansonia gibbosa*, *Eucalyptus* sp., *Ficus opposita* in Western Australia (Pavlic et al. 2008), *Cassia fistula*, *Dimocarpus longan*, *Senna siamea* in Thailand (Trakunyingcharoen et al. 2015b), *Jatropha podagrica* in India, *Mangifera indica* in Australia (Sharma et al. 2013), *Pandanus* sp. in Thailand (Tibpromma et al. 2018b), *Tectona grandis* in Thailand (Doilom et al. 2015), from leaves and petioles of *Hevea brasiliensis* in Thailand (Trakunyingcharoen et al. 2015a), associated with canker disease on branches of *Hevea brasiliensis* in Thailand (Senwanna et al. 2020), dead twigs attached to *Anomianthus dulcis*, *Alstonia scholaris*, *Magnolia lilifera* in Thailand (this study).

GenBank numbers – AND32; ITS: OM462369, LSU: OM967170, *tef1*: OK127673, *tub2*: OK236257, AS15; ITS: OM462368, *tub2*: OK236256, NI320; ITS: OM462370, *tef1*: OK127674, *tub2*: OK236258.

Notes – Multigene phylogenetic analyses (Fig. 48) showed that three new strains AND32 (MFLUCC 21-0205), AS15 (MFLUCC 21-0208) and NI320 (MFLUCC 21-0185) clustered with the ex-type of *Pseudofusicoccum adansoniae* CBS 122055. The new collection AND32 (MFLU 21-0244) is similar to the type *P. adansoniae* in having hyaline and ellipsoid conidia. However, AND32 (MFLU 21-0244) has smaller conidiogenous cells (6 × 2 μm) and conidia (16 × 5 μm) than the type *P. adansoniae* (Pavlic et al. 2008). The type *P. adansoniae* has 12.7 × 2.4 μm conidiogenous cells and 22.5 × 5.2 μm conidia (Pavlic et al. 2008). The type of *P. adansoniae* was introduced by Pavlic et al. (2008) from *Adansonia gibbosa* in Western Australia. In this study, we report *P. adansoniae* from three new host plant species *Anomianthus dulcis*, *Alstonia scholaris* and *Magnolia lilifera* in Thailand.

Dothideomycetes *incertae sedis*
Dyfrolomycetales Pang, Hyde & E.B.G. Jones
Pleurotremataceae Watson

Pleurotremataceae was introduced by Watson (1929). The family is typified by *Pleurotrema* with *Pleurotrema polysemum* as the type species and characterized by lacking fissitunicate dehiscence asci in Sordariomycetes (Watson 1929, Barr 1994). Maharachchikumbura et al. (2016) re-examined *P. polysemum* and identified *P. polysemum* as similar to the species of *Saccardoella* and *Dyfrolomyces* in Dyfrolomycetaceae (Dothideomycetes). Pleurotremataceae is considered as the initial name for Dyfrolomycetaceae (Dothideomycetes) (Maharachchikumbura et al. 2016). Pleurotremataceae comprises three genera namely: *Dyfrolomyces*, *Melomastia* and *Pleurotrema* (Hongsanan et al. 2020b). Species of this family are saprobes on wood in terrestrial and aquatic habitats (Hongsanan et al. 2020b).
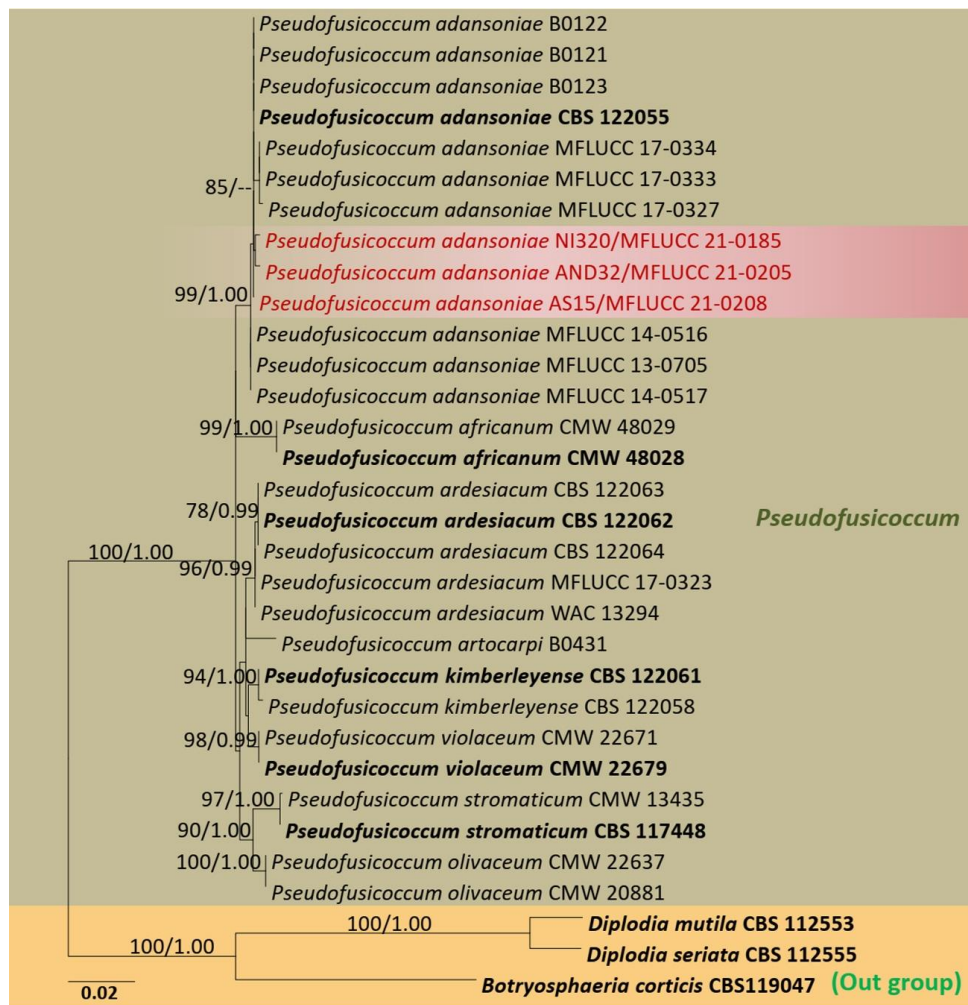
Figure 48 – Phylogram generated from maximum likelihood analysis of combined ITS, LSU, *tef1* and *tub2* sequence data. Related sequences of *Pseudofusicoccum* were obtained from Senwanna et al. (2020). Thirty-two strains are included in the combined gene analyses comprising 2200 characters after alignment (500 characters for ITS, 850 characters for LSU, 400 characters for *tef1* and 450 characters for *tub2*). *Botryosphaeria cortices* (CBS119047), *Diplodia mutila* (CBS 112553) and *D. seriata* (CBS 112555) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -5769.428669 is presented. The matrix had 400 distinct alignment patterns, with 38.74% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Melomastia Nitschke ex Sacc.

Melomastia is characterized by immersed, globose ascomata, 8-spored, cylindrical, J-, subapical ring asci, hyaline and 2-septate ascospores (Norphanphoun et al. 2017). Saccardo (1875) introduced *Melomastia* with the type *M. friesii*. *Melomastia friesii* was synonymized as *M. mastoidea* by Schröter (1894). Based on combined LSU, SSU and *tef1* sequence data (Fig. 50), we report *Cananga odorata* as a new host record for *M. clematidis* and *Anomianthus dulcis* as a new host record for *M. thamplaensis* in Thailand.

Melomastia clematidis Phukhams. & K.D. Hyde, Fungal Divers. 102: 139 (2020)   Fig. 51
Index Fungorum number: IF 557210, Faces of Fungi number: FoF 07334

Saprobic on dead twigs attached to *Cananga odorata*. Sexual morph: *Ascomata* 300–450 μm high × 220–400 μm diam. ($\bar{x} = 370 \times 300$ µm, n = 10), only ostioles visible at the surface of host,

solitary, gregarious, semi-immersed to immersed, globose to compressed globose, carbonaceous, dark brown to black, rough-walled, ostiolate. *Ostiole* central. *Peridium* 12–16 µm wide, outer layer carbonaceous, composed of 5–7 layers of brown cells of *textura angularis*, inner layer comprising thin hyaline layers. *Hamathecium* comprising 1–2 µm wide, filiform, unbranched, septate, numerous, dense, cellular pseudoparaphyses. *Asci* 80–93 × 5–7 µm ($\bar{x}$ = 87 × 6 µm, n = 20), 8-spored, cylindrical, short pedicellate, straight or slightly curved, apically rounded, with an apical ring. *Ascospores* 10–13 × 3–5 µm ($\bar{x}$ = 12 × 4 µm, n = 30), uniseriate, partially overlapping, hyaline, fusiform, tapering towards both ends, 3-septate, straight or slightly curved with smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 35 mm diameter after 1 week at 25 °C, colonies from above: orangish yellow, margin undulate, flat, slightly raised, fluffy appearance; reverse: orangish brown from the centre of the colony, cream at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to the *Cananga odorata* (Annonaceae), 2 January 2019, N. I. de Silva, CO12 (MFLU 21-0235), living culture, MFLUCC 21-0174.

Known hosts and distribution – On dead branches of *Clematis sikkimensis* in Thailand (Phukhamsakda et al. 2020), dead twigs attached to *Cananga odorata* in Thailand (this study).

GenBank numbers – LSU: OL457710, SSU: OL700223.

Notes – *Melomastia clematidis* was described from *Clematis sikkimensis* in Thailand (Phukhamsakda et al. 2020). Our collection (MFLU 21-0235) is similar to the type species of *M. clematidis* (MFLU 17–1500) in having hyaline, fusiform 3-septate ascospores with acute ends, smooth-walled (Phukhamsakda et al. 2020). A pairwise comparisons of DNA sequences of LSU and SSU do not show significant differences. Therefore, we report our collection as a new host record of *M. clematidis* from *Cananga odorata* in Thailand.
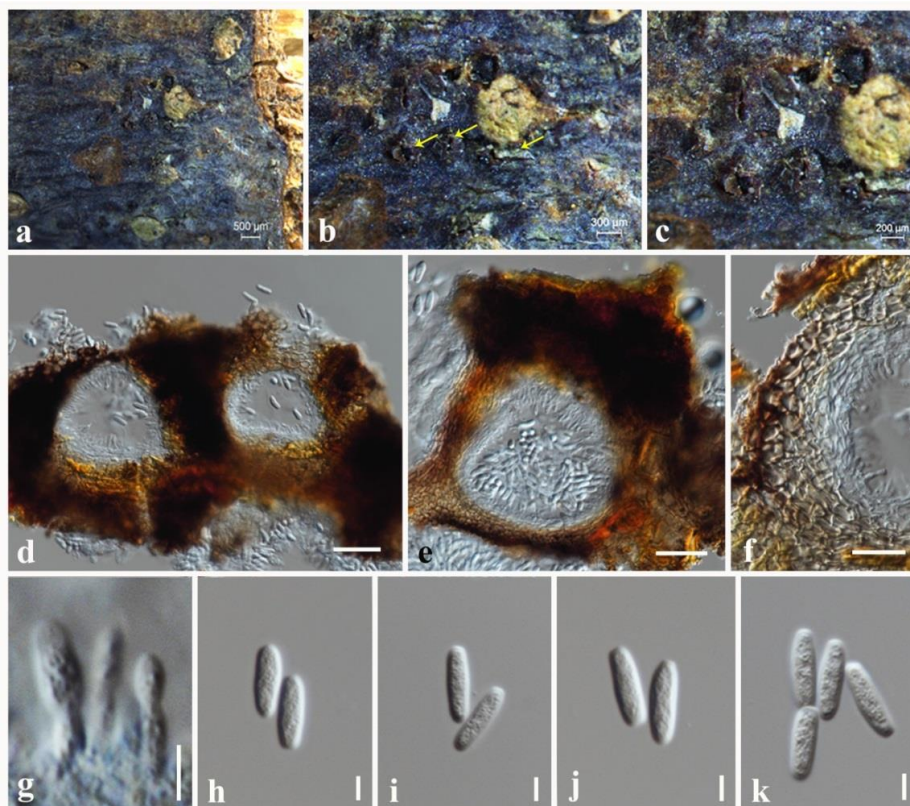

Figure 49 – *Pseudofusicoccum adansoniae* (MFLU 21-0244). a–c Appearance of conidiomata on substrate. d, e Vertical sections through of conidiomata. f Conidiomatal wall. g Conidiogenous cells. h–k Conidia. Scale bars: a = 500 µm, b = 300 µm, c = 200 µm, d, e = 50 µm, f = 20 µm, g–k = 5 µm.
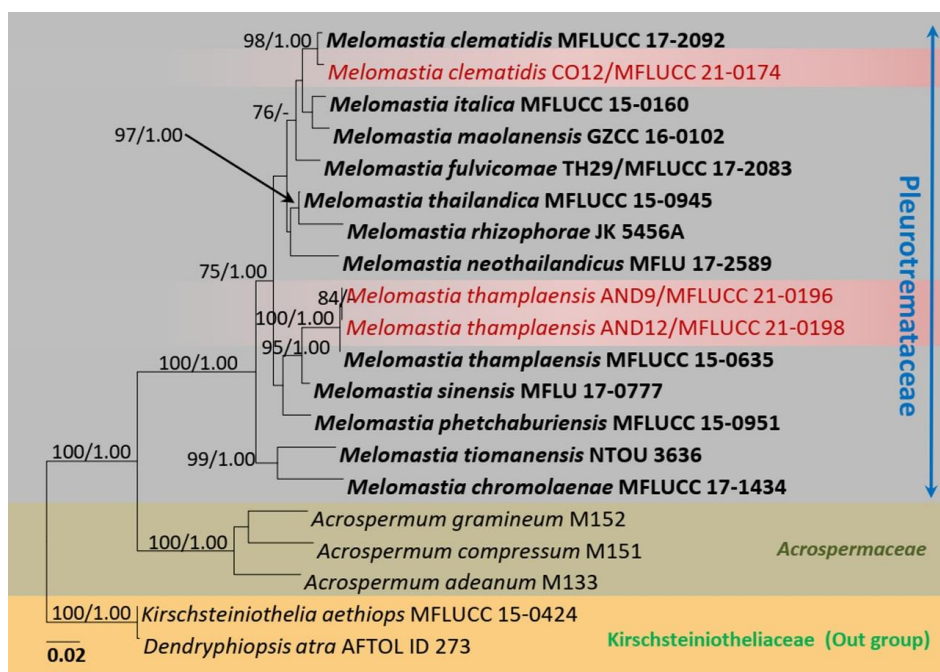
Figure 50 – Phylogram generated from maximum likelihood analysis of combined LSU, SSU and *tef1* sequence data. Related sequences of *Pleurotremataceae* were obtained from Phukhamsakda et al. (2020). Twenty-two strains are included in the combined gene analyses comprising 2850 characters after alignment (930 characters for LSU, 1000 characters for SSU and 920 characters for *tef1*). *Dendryphiopsis atra* (AFTOL-ID 273) and *Kirschsteiniothelia aethiops* (MFLUCC 15-0424) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -9147.539648 is presented. The matrix had 697 distinct alignment patterns, with 34.64% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red. Type and ex-type strains are in **black bold**.

Melomastia thamplaensis (Jin F. Zhang, Jian K. Liu, K.D. Hyde & Zi Y. Liu) W.L. Li, Maharachch. & Jian K. Liu, J. Fungi 8(1, no. 76): 16 (2022)   Fig. 52

　　　Index Fungorum number: IF 842095, Faces of Fungi number: FoF 02612

　　　Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Ascomata* 300–380 µm high × 250–300 µm diam. ($\bar{x} = 350 \times 270$ µm, n = 10), immersed to erumpent through host tissue, solitary or scattered, coriaceous to carbonaceous. *Ostiole* central. *Peridium* 15–25 µm wide, comprising several layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, cylindrical to broadly filiform, septate, branching pseudoparaphyses. *Asci* 120–135 × 6–8 µm ($\bar{x} = 127 \times 7$ µm, n = 20), 8-spored, cylindrical, short pedicellate, straight or slightly curved, apically rounded, with an apical ring. *Ascospores* 17–26 × 4–6 µm ($\bar{x} = 23 \times 5$ µm, n = 30), uniseriate, hyaline, fusiform, tapering towards both ends, 3-septate, straight or slightly curved with smooth-walled. Asexual morph: Not observed.

　　　Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: white, margin undulate, flat, slightly raised; reverse: brown from the centre of the colony, white at margin.

　　　Material examined – Thailand, Chiang Rai Province, dead twigs of *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND12 (MFLU 21-0217), living culture, MFLUCC 21-0198, AND9 (MFLU 21-0216), living culture, MFLUCC 21-0196.

　　　Known hosts and distribution – On dead branch of unknown host in Thailand (Zhang et al. 2017), dead twigs attached to *Anomianthus dulcis* in Thailand (this study).

　　　GenBank numbers – (AND9): LSU: OL457708, SSU: OL700221, (AND12): LSU: OL457709, SSU: OL700222.

Notes – Phylogenetic analysis of combined LSU, SSU and *tef1* sequence data shows that two strains (MFLUCC 21-0198 and MFLUCC 21-0196) clustered with the ex-type *Melomastia thamplaensis* (MFLUCC 15-0635) with 100% ML and 1.00 BYPP statistical support (Fig. 50). We therefore, identify our two strains as *M. thamplaensis* based on phylogeny with morphological comparison and the isolates are introduced here as a new host record from *Anomianthus dulcis* in Thailand.
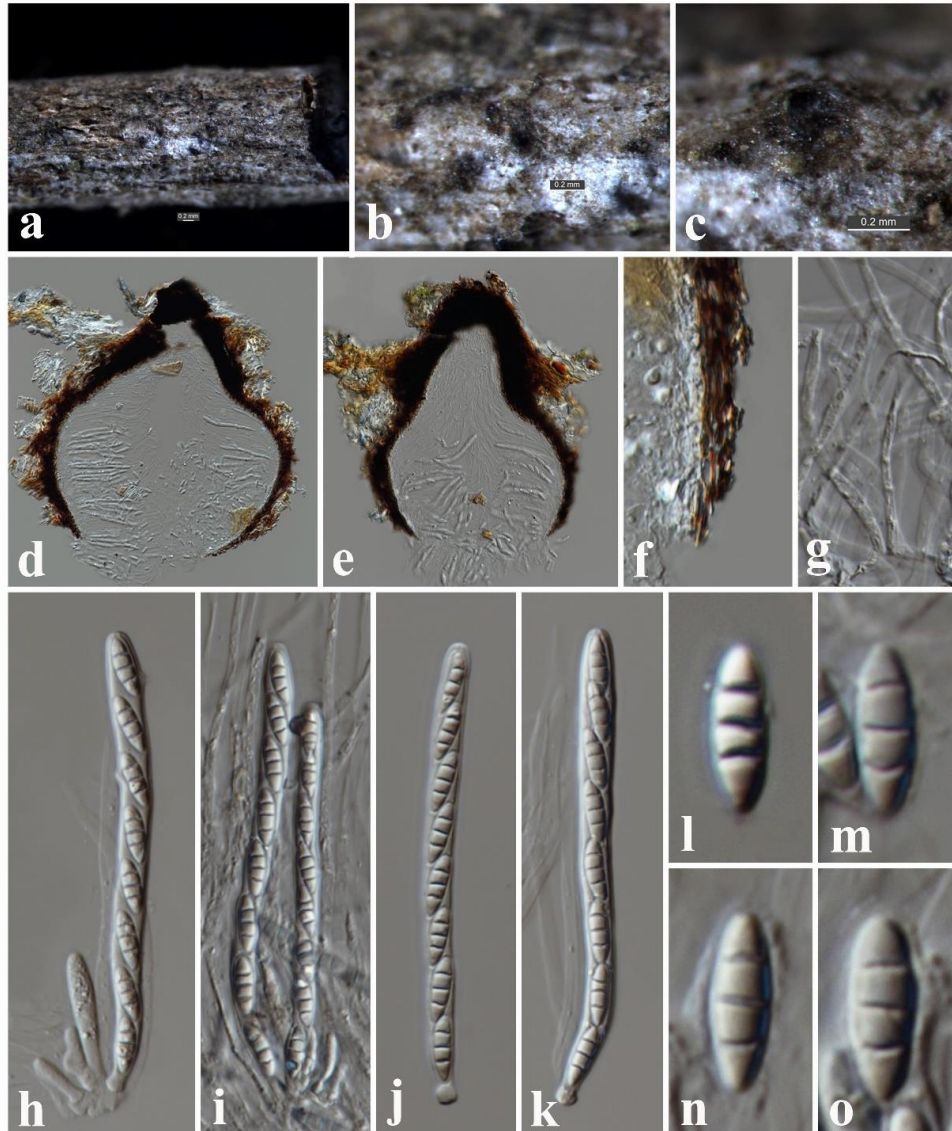

Figure 51 – *Melomastia clematidis* (MFLU 21-0235). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascoma. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: c = 200 μm, d, e = 50 μm, f, g, l–o = 5 μm, h–k = 10 μm.

Dothideomycetes orders *incertae sedis*
Muyocopronales Mapook, Boonmee & K.D. Hyde
Muyocopronaceae K.D. Hyde

Muyocopronaceae was illegitimate since it was introduced without a Latin diagnosis by Luttrell (1951). Hyde et al. (2013) accepted Muyocopronaceae with a single genus *Muyocopron* based on morphology and phylogeny. These species are saprobic on surfaces of dried twigs, stems and less common on leaves, as small black spots on plants (Hyde et al. 2013). Ascomata of the Muyocopronaceae are not considered as true thyriothecia as the upper wall is relatively wide and comprises two layers (Hyde et al. 2013).
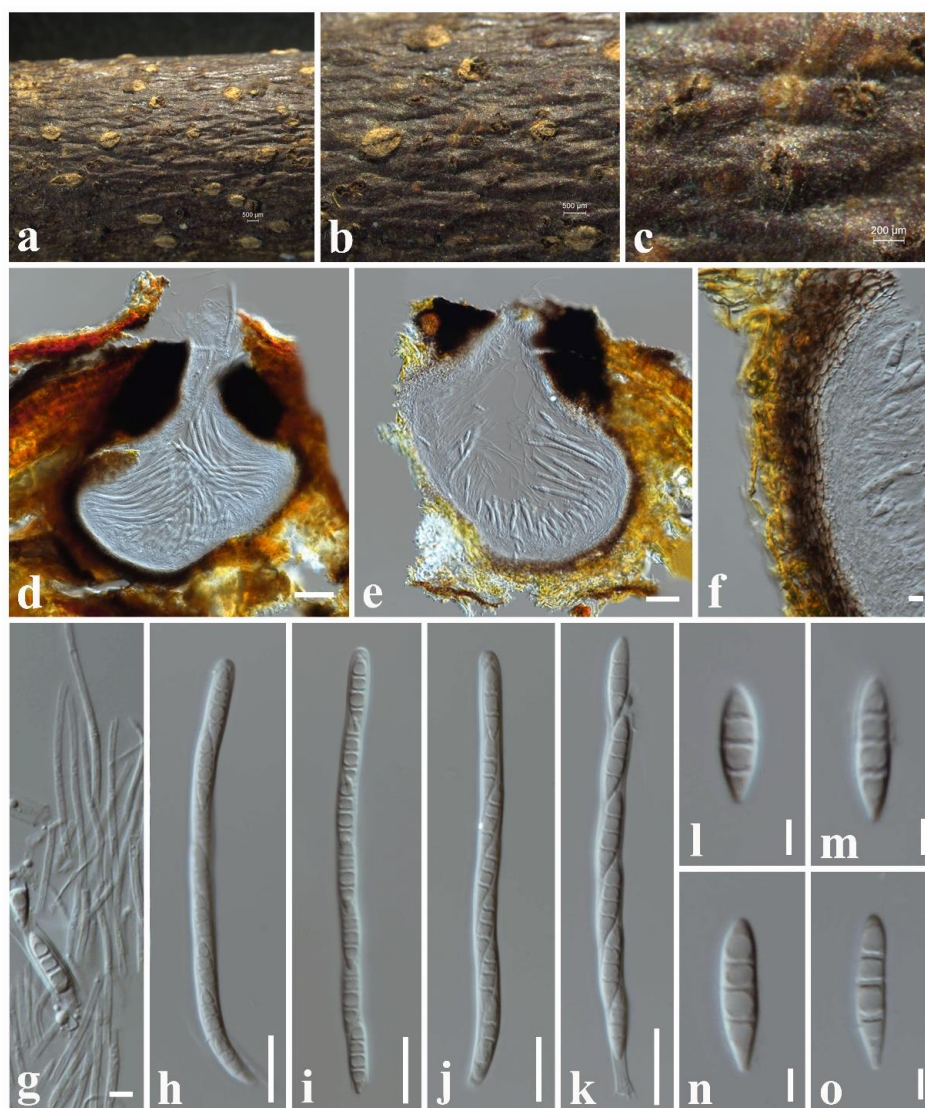
Figure 52 – *Melomastia thamplaensis* (MFLU 21-0217). a The specimen. b, c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. Scale bars: a, b = 500 μm, c = 200 μm, d, e = 50 μm, f, g, l–o = 5 μm, h–k = 20 μm.

Setoapiospora Mapook & K.D. Hyde

Hyde et al. (2020) introduced *Setoapiospora* based on morphology and molecular data. The type species is *Setoapiospora thailandica* that was isolated from dead branches in Thailand (Hyde et al. 2020a). The sexual morph is characterized by in having superficial to semi-immersed, carbonaceous ascomata appearing as dark brown to black spots, bitunicate, cylindrical asci, ellipsoid to broadly fusiform, hyaline, 1-septate ascospores with a small lower cell and a large upper cell (Hyde et al. 2020a). In this study, we provide a new host record for *S. thailandica* from dead twigs of *Anomianthus dulcis* in Thailand.

Setoapiospora thailandica Mapook & K.D. Hyde, in Hyde et al., Fungal Divers. 100: 135 (2020)

Fig. 54

Index Fungorum number: IF 556906, Faces of Fungi number: FoF 06794

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Ascomata* 180–200 μm high × 300–450 μm diam. ($\overline{x}$ = 190 × 370 μm, n = 10), dark brown to black, superficial to semi-immersed, solitary or scattered, carbonaceous, appearing as black spots, with a poorly developed basal layer and an irregular margin. *Ostiole* 50–60 μm diam., central, with external dark

brown setae. *Peridium* 45–60 μm wide, dark brown, comprising of cells of *textura prismatica*. *Hamathecium* comprising 1–2 μm wide, cylindrical to filiform, septate, pseudoparaphyses. *Asci* 100–140 × 15–20 μm ($\bar{x}$ = 130 × 17 μm, n = 20), 8-spored, bitunicate, cylindrical with short, straight or slightly curved pedicellate, apically rounded. *Ascospores* 22–27 × 7–12 μm ($\bar{x}$ = 25 × 8 μm, n = 30), uniseriate, hyaline, ellipsoid to broadly fusiform, 1-septate, constricted at the septum, with a small lower cell and a large upper cell, widest at the centre and tapering towards ends, granular. Asexual morph: Not observed.
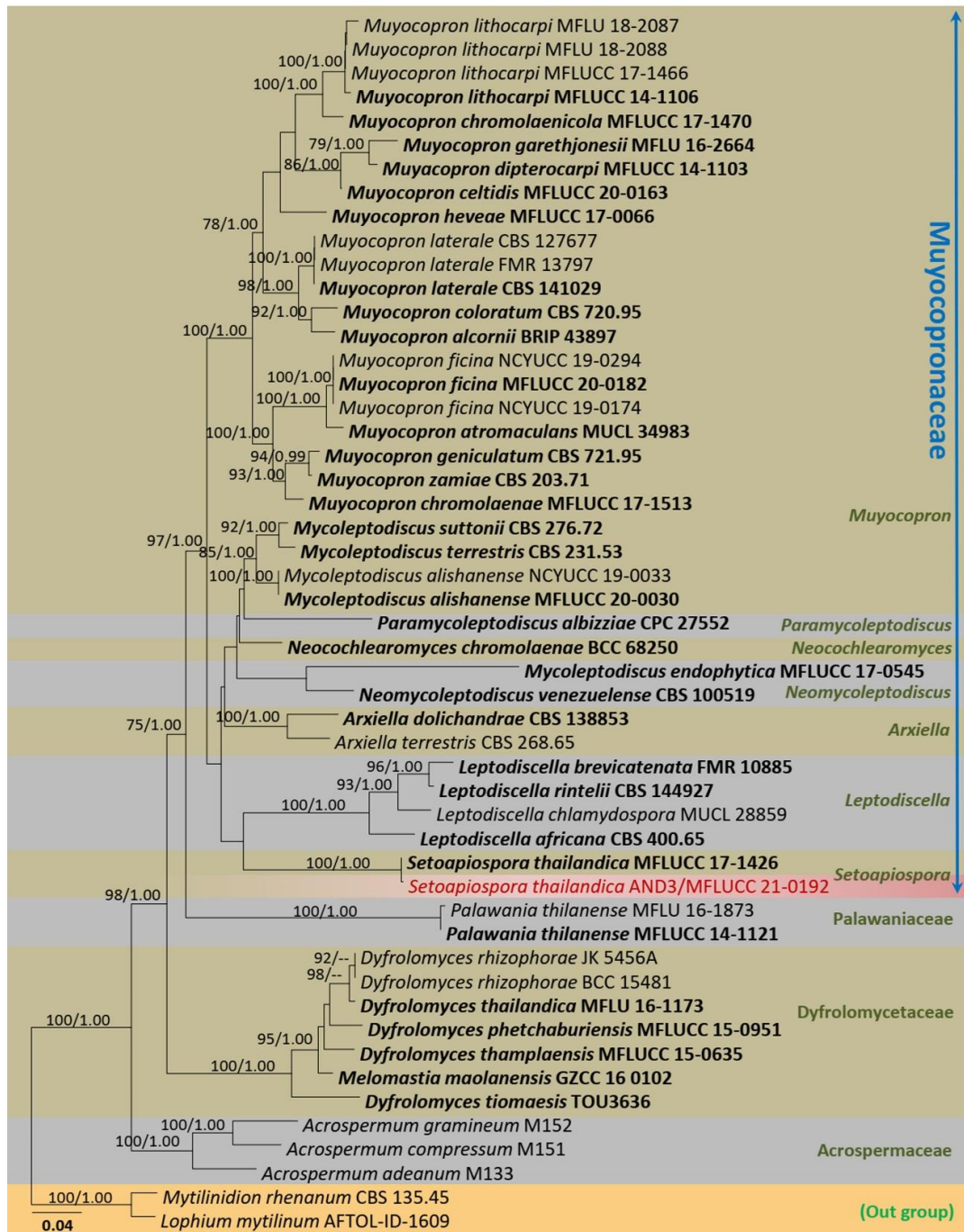

Figure 53 – Phylogram generated from maximum likelihood analysis of combined LSU SSU, ITS and *tef1* sequence data. Related sequences of family Muyocopronaceae were obtained from Hyde et al. (2020). Fifty-one strains are included in the combined gene analyses comprising 3450 characters after alignment (850 characters for LSU, 1000 characters for SSU, 600 characters for ITS and 1000 characters for *tef1*). *Lophium mytilinum* (AFTOL-ID-1609) and *Mytilinidion rhenanum* (CBS 135.45) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -

23560.292072 is presented. The matrix had 1571 distinct alignment patterns, with 47.09% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Culture characteristics – Colonies on PDA reaching 45 mm diameter after 1 week at 25 °C, colonies from above: white, margin undulate, slightly flattened, filamentous; reverse: pale brown from the centre of the colony, white at margin.

Material examined – Thailand, Chiang Rai Province, dead twigs of *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND3 (MFLU 21-0249), living culture, MFLUCC 21-0192.

Known hosts and distribution – On dead branches of wood in Thailand (Hyde et al. 2020a), dead twigs of *Anomianthus dulcis* in Thailand (this study).

GenBank numbers – LSU: OL457707, SSU: OL700220, ITS: OL703584, *tef1*: OL998895.

Notes – *Setoapiospora thailandica* was introduced by Hyde et al (2020) for a collection isolated from dead branches in Thailand. A new fungal isolate MFLUCC 21-0192 was identified as *S. thailandica* that clustered with the ex-type strain of *S. thailandica* (MFLUCC 17-1426) in the combined LSU SSU, ITS and *tef1* phylogenetic analysis with 100% ML and 1.00 BYPP statistical support (Fig. 53). The new collection and the type of *S. thailandica* shares morphology in having superficial to semi-immersed, solitary or scattered, carbonaceous ascomata, similar ranges of asci (100–140 × 15–20 μm *vs* 85–160 × 13–24 μm) and hyaline, ellipsoid to broadly fusiform, 1-septate ascospores (22–27 × 7–12 μm *vs* 20–27 × 10–13 μm). Therefore, we report the new collection (MFLU 21-0249) as a new host record of *S. thailandica* from *Anomianthus dulcis* in Thailand.

Class Sordariomycetes O.E. Erikss. & Winka
Subclass Diaporthomycetidae Senan. et al.
Diaporthales Nannf.
Diaporthaceae Höhn. ex Wehm.

Diaporthaceae was introduced by von Höhnel (1917) with the type *Diaporthe*. Castlebury et al. (2002) confirmed the placement of Diaporthaceae in Diaporthales based on the phylogeny of LSU sequence data of diaporthoid taxa. The family comprises endophytes, pathogens and saprobes on terrestrial and rarely submerged plants (Hyde et al. 2020c). Hyde et al. (2020c) accepted the following 15 genera: *Apioporthella*, *Apiosphaeria*, *Chaetoconis*, *Chiangraiomyces*, *Diaporthe*, *Hyaliappendispora*, *Leucodiaporthe*, *Massariothea*, *Mazzantia*, *Ophiodiaporthe*, *Paradiaporthe*, *Phaeocytostroma*, *Phaeodiaporthe*, *Pustulomyces* and *Stenocarpella*.

Diaporthe Nitschke

Diaporthe was established by Nitschke (1867) and typified with *D. eres*. Species of this genus are found worldwide as endophytes, pathogens and saprobes on a diverse range of host plants (Gomes et al. 2013). *Diaporthe* species were distinguished mainly by their phylogenetic traits (Udayanga et al. 2011, Gomes et al. 2013, Gao et al. 2017). *Phomopsis* was previously considered as the asexual morph and it was linked with *Diaporthe* to resolve nomenclatural complications by Rossman et al. (2015). Following the nomenclature rules, *Diaporthe* was nominated to take priority over *Phomopsis* based on the principle of significance as *Diaporthe* was introduced first and represented the majority of species (Rossman et al. 2014, 2015). The genus contains 1164 species epithets in Index Fungorum (2022).

Diaporthe chiangmaiensis N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Figs 55, 56
Index Fungorum number: IF 559527, Faces of Fungi number: FoF 10724
Etymology – Name reflects the location "Chiang Mai Province" where the type specimen was collected.

Holotype: MFLU 18-1305

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: *Ascomata* 230–270 μm high × 200–220 μm diam. ($\bar{x}$ = 240 × 210 μm, n = 10), brown, subglobose, semi-immersed, mostly immersed, solitary, scattered, coriaceous. *Peridium* 20–40 μm wide, composed of several layers of hyaline, brown, cells of *textura angularis*. *Hamathecium* aparaphysate or sometimes with a few cellular paraphyses. *Asci* 52–58 × 8–11 ($\bar{x}$ = 55 × 9 μm, n = 20), 8-spored, unitunicate, cylindrical, apex rounded with short pedicellate. *Ascospores* 8–10 × 2–4 ($\bar{x}$ = 9 × 3 μm, n = 30), biseriate, hyaline, fusiform to ellipsoid, 1-septate, mostly 4 guttules. Asexual morph: Coelomycetous. *Conidiomata* 180–200 μm high × 160–180 μm diam. ($\bar{x}$ = 194 × 172 μm, n = 10), pycnidial, dark brown, ovoid, subglobose, immersed to semi-immersed, erumpent at maturity. *Conidiomatal wall* 35–50 μm wide, composed of 6–8 layers of pale brown cells of *textura angularis*. *Hamathecium* aparaphysate. *Conidiophores* 8–12 × 1–2 μm ($\bar{x}$ = 10 × 1.4 μm, n = 10), hyaline, light brown, cylindrical, straight, smooth, densely aggregated. *Conidiogenous cells* 3–5 × 2–3 μm ($\bar{x}$ = 4 × 2.5 μm, n = 10), phialidic, terminal, hyaline, cylindrical, slightly tapering towards the apex. *Alpha conidia* 7–9 × 1.5–3 ($\bar{x}$ = 8 × 2 μm, n = 30), hyaline, fusiform, aseptate, smooth, tapering towards both ends, straight to slightly curved.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin crenate, dense, fluffy appearance, white; reverse: pale brown at the margin, dark brown in the centre.
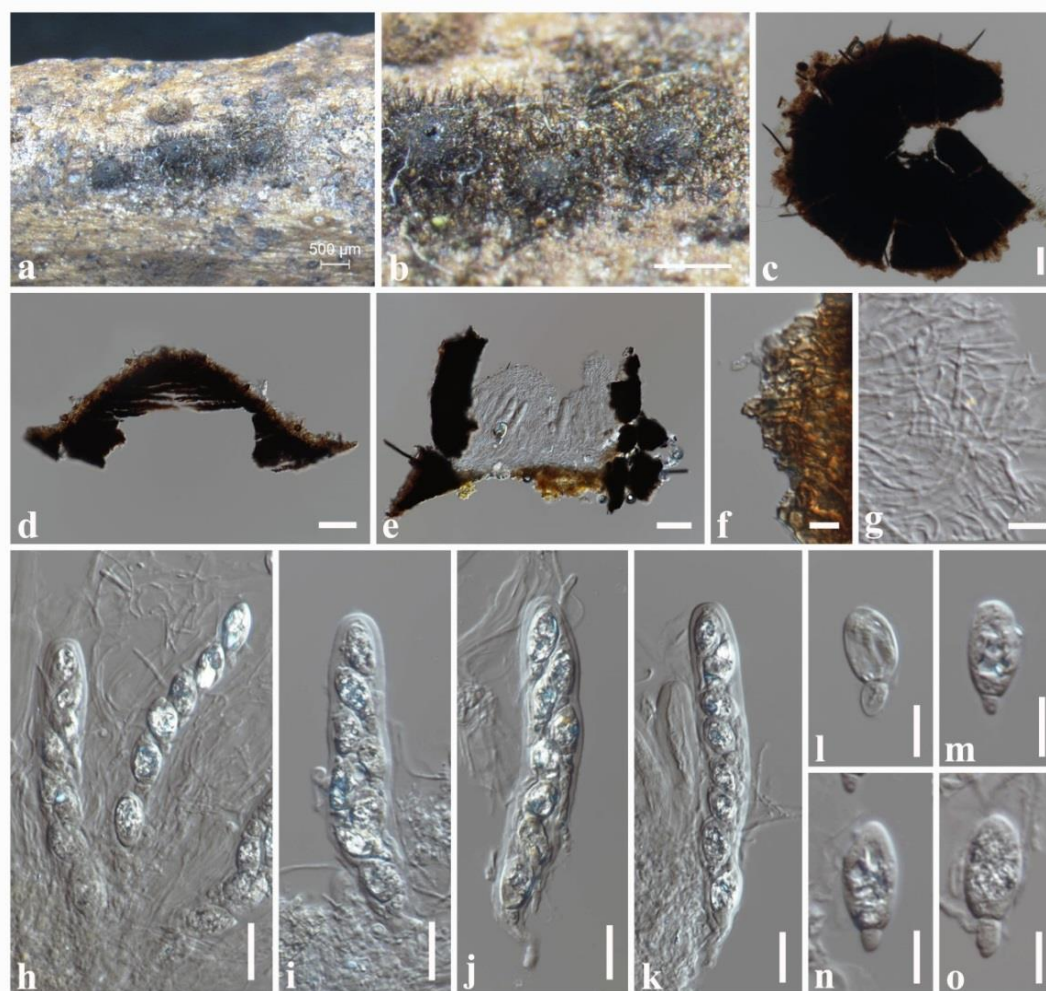

Figure 54 – *Setoapiospora thailandica* (MFLU 21-0249). a, b Appearance of ascomata on substrate. c Squash mount showing ascoma with setae. d, e Vertical sections through ascomata. f Peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. Scale bars: a, b = 500 μm, c–e = 50 μm, f, g = 10 μm, h–k = 20 μm, l–o = 10 μm.
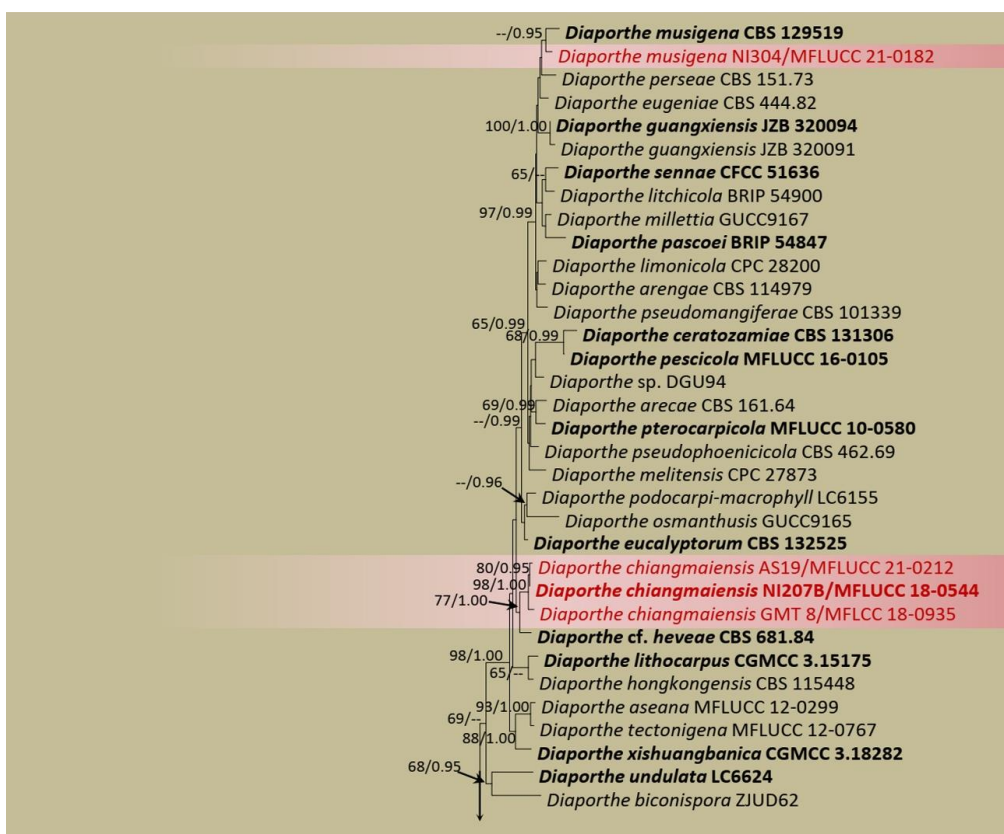
Figure 54 – Phylogram generated from maximum likelihood analysis of combined ITS, *tub2*, *tef1* and CAL sequence data (with additional strains closely related to newly generated sequences and removed some distantly related sequences). Related sequences of *Diaporthe* were obtained from Manawasinghe et al. (2019). Eighty-five strains are included in the combined gene analyses comprising 1660 characters after alignment (500 characters for ITS, 400 characters for *tub2* 320 characters for *tef1* and 440 characters for CAL). *Diaporthella corylina* (CBS 121124) is used as outgroup taxon. The best RAxML tree with a final likelihood value of -20953.278650 is presented. The matrix had 1107 distinct alignment patterns, with 29.27% undetermined characters or gaps. Bootstrap values for maximum likelihood and maximum parsimony equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Material examined –Thailand, Chiang Mai Province, dead twigs attached to *Magnolia lilifera* (Magnoliaceae), 11 February 2019, N. I. de Silva, NI207 (MFLU 18-1305, holotype), ex-type living culture, MFLUCC 18-0544; *ibid*., healthy leaves of *Magnolia lilifera* (Magnoliaceae), 11 February 2019, N. I. de Silva, GMT8 (MFLU 20-0606), living culture, MFLUCC 18-0935, Thailand, Chiang Rai Province, dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS19 (MFLU 21-0211), living culture, MFLUCC 21-0212.

GenBank numbers – (AS19): ITS: OK393702, *tub2*: OK490918, *tef1*: OL439482; (NI207): ITS: OK393703, *tef1*: OL439483; (GMT8): ITS: OK393704, *tef1*: OL439484.

Notes – Phylogenetically, two saprobic strains MFLUCC 18-0544, MFLUCC 21-0212 and an endophytic strain MFLUCC 18-0935 are monophyletic with 98% ML and 1.00 BYPP statistical support (Fig. 54). We introduce these three new strains as *Diaporthe chiangmaiensis*.

Diaporthe chiangmaiensis has a sister relationship to *Diaporthe* cf. *heveae* 2 (CBS 681.84) with 77% ML and 1.00 BYPP statistical support (Fig. 54). *Diaporthe* cf. *heveae* 2 (CBS 681.84) was isolated from leaves on *Hevea brasiliensis* in India (Gomes et al. 2013). *Diaporthe* cf. *heveae* 2 (CBS 681.84) was a sterile strain, thus its morphology was not described. It is revealed that six base pair differences in ITS (500 bp) and 12 base pair differences in *tef1* (300 bp) between the ex-type

Diaporthe cf. *heveae* 2 (CBS 681.84) and ex-type *Diaporthe chiangmaiensis* (MFLUCC 18-0544). We established the sexual-asexual connection of *D. chiangmaiensis* in the current investigation of saprobic fungi recovered from dead twigs of *Magnolia lilifera* (Magnoliaceae) (MFLU 18-1305) as the sexual morph and *Alstonia scholaris* (Apocynaceae) (MFLU 21-0211) as the asexual morph. Further, we were able to identify endophytic lifestyle from healthy leaves (MFLU 20-0606) and saprobic lifestyle from dead twigs (MFLU 18-1305) from *Magnolia lilifera* in this study.
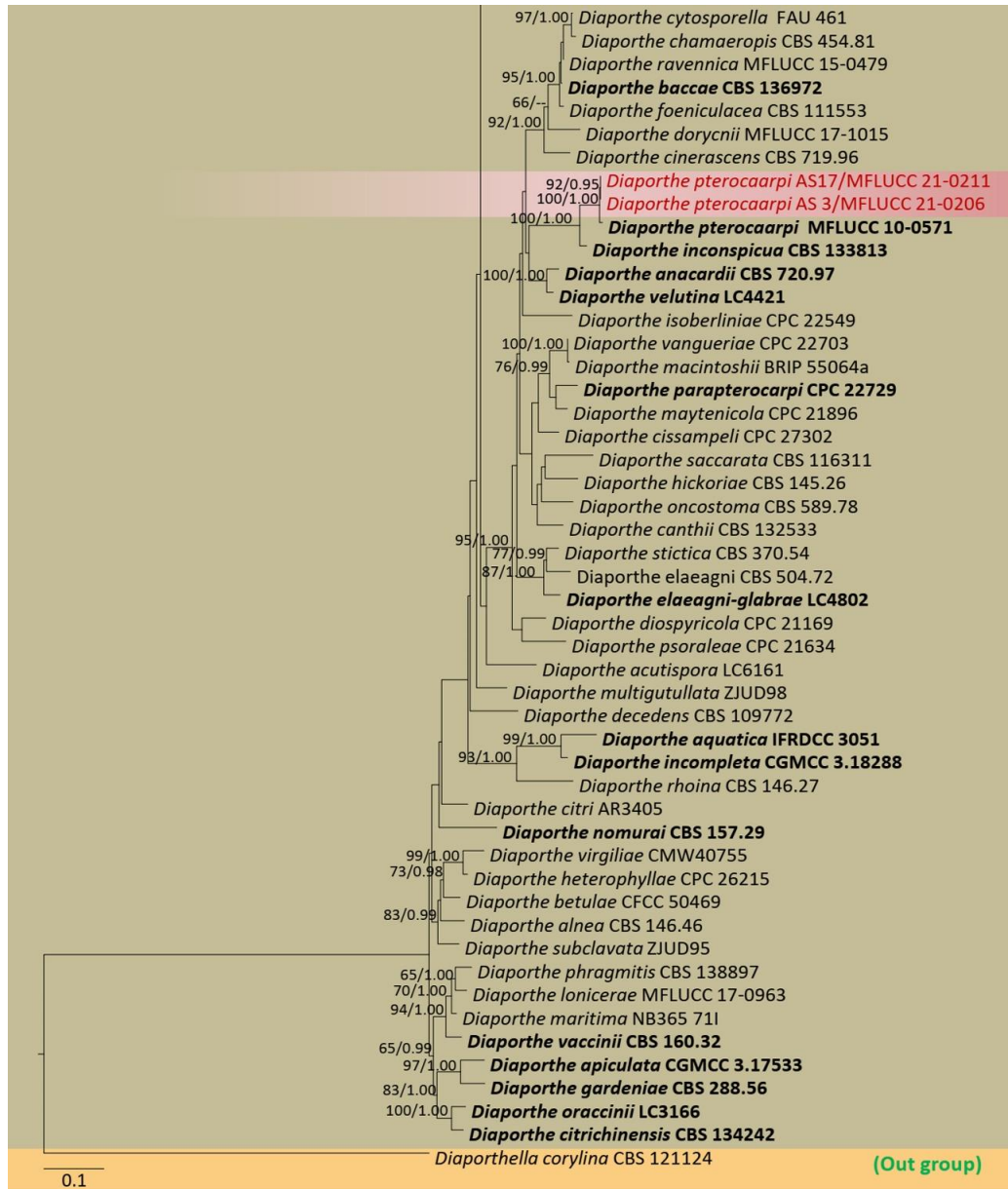

Figure 54 – Continued.

Diaporthe musigena Crous & R.G. Shivas, Persoonia 26: 119 (2011)   Fig. 57

Index Fungorum number: IF 560160, Faces of Fungi number: FoF 10666

Saprobic on dead twigs attached to *Magnolia champaca*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 70–90 μm high × 120–140 μm diam. ($\bar{x} = 84 \times 130$ μm, n = 10), pycnidial, dark brown, pyriform, immersed to semi-immersed, erumpent at maturity. *Conidiomatal wall* 10–20 μm wide, composed of 4–7 layers of pale brown cells of *textura angularis*. *Hamathecium* aparaphysate. *Conidiophores* 10–20 × 1–2 μm, hyaline, cylindrical, unbranched, straight, smooth, densely aggregated. *Conidiogenous cells* 3–4 × 1–2 μm, phialidic, terminal, hyaline, cylindrical, slightly tapering towards the apex. *Alpha conidia* 6–8 × 2–3 ($\bar{x} = 7 \times$

2.4 μm, n = 30), hyaline, fusiform, aseptate, smooth, tapering towards both ends, straight to slightly curved.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, slightly dense, surface smooth, pale brown at the margin, cream in the centre; reverse: pale brown at the margin, dark brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia champaca* (Magnoliaceae), 9 January 2019, N. I. de Silva, NI304 (MFLU 21-0212), living culture, MFLUCC 21-0182.

Known hosts and distribution – On necrotic leaf tissue of *Musa* sp. in Australia (Crous et al. 2011), dead twigs attached to *Magnolia champaca* in Thailand (this study).

GenBank numbers – ITS: OK393699, *tub2*: OK490916, *tef1*: OL439479.

Notes – A new saprobic collection (MFLU 21-0212) isolated from dead twigs of *Magnolia champaca* shares similar characteristics with the type of pathogenic *Diaporthe musigena* (CBS 129519) associated with necrotic leaf tissue of *Musa* sp. in Australia, in having hyaline, fusiform, aseptate alpha conidia with smooth tapering ends. The new strain (6–8 × 2–3 μm) and the type *D. musigena* ((7–)8–10(–12) × (2–)2.5(–3) μm) have a similar size range of alpha conidia (Crous et al. 2011). As morphological characters examined largely overlap with type *D. musigena*, we, report our collection as a new host record of *D. musigena* from *Magnolia champaca* in Thailand.

Diaporthe pterocarpi (S. Hughes) Udayanga, Xing Z. Liu & K.D. Hyde, Cryptog. Mycol. 33(3): 305 (2012)   Fig. 58

Index Fungorum number: IF 801055, Faces of Fungi number: FoF 10667

Saprobic on dead twigs attached to *Alstonia scholaris*. Sexual morph: See Udayanga et al. (2012). Asexual morph: Coelomycetous. *Conidiomata* 130–150 μm high × 200–240 μm diam. ($\bar{x}$ = 142 × 220 μm, n = 10), pycnidial, dark brown, subglobose, immersed to semi-immersed, erumpent at maturity. *Conidiomatal wall* 25–40 μm wide, composed of 5–8 layers of pale brown cells of *textura angularis*. *Hamathecium* aparaphysate. *Conidiophores* 25–30 × 1–2 μm, hyaline, cylindrical, unbranched, straight, smooth, densely aggregated. *Conidiogenous cells* 3–4 × 1–2 μm, phialidic, terminal, hyaline, cylindrical, slightly tapering towards the apex. *Alpha conidia* 6–9 × 2–4 μm ($\bar{x}$ = 7.5 × 2.6 μm, n = 30), hyaline, fusiform, aseptate, smooth, tapering towards both ends, straight to slightly curved, 1 or 2 guttules.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin filamentous, flat, slightly dense, velvety appearance, white; reverse: pale brown at the margin, dark brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS17 (MFLU 21-0214), living culture, MFLUCC 21-0211, KUMCC 20-0094; AS3 (MFLU 21-0213), living culture, MFLUCC 21-0206, KUMCC 20-0085.

Known hosts and distribution – On leaves of *Pterocarpus erinaceus* in Togoland, leaves of *Pterocarpus indicus* in Thailand (Udayanga et al. 2012), on rotting fruits of *Cucumis melo* in Costa Rica (Broge et al. 2020), dead twigs attached to *Alstonia scholaris* in Thailand (this study).

GenBank numbers – (AS17) ITS: OK393700, *tub2*: OK490917, *tef1*: OL439480, (AS3) ITS: OK393701, *tef1*: OL439481.

Notes – Phylogenetic analyses based on concatenated ITS, *tub2*, *tef1* and CAL sequence data depicted two new strains of *Diaporthe* sp. (MFLUCC 21-0211 and MFLUCC 21-0206) cluster with the ex-type *D. pterocarpi* (MFLUCC 10-0571) with 100% ML, 1.00 BYPP statistical support (Fig. 54). The new collections morphologically resemble the type *D. pterocarpi* in having hyaline, fusiform, aseptate, smooth, guttulate alpha conidia. The type *D. pterocarpi* has (5–)6–7(–9) × (2–)2.5(–3) μm, biguttulate, rarely three guttulate alpha conidia (Udayanga et al. 2012) and the new collection (MFLU 21-0213) has (6–9 × 2–4) μm, one or two guttulate alpha conidia. Hence, we include our new collection as a new host record of *D. pterocarpi* from dead twigs of *Alstonia scholaris* in Thailand.
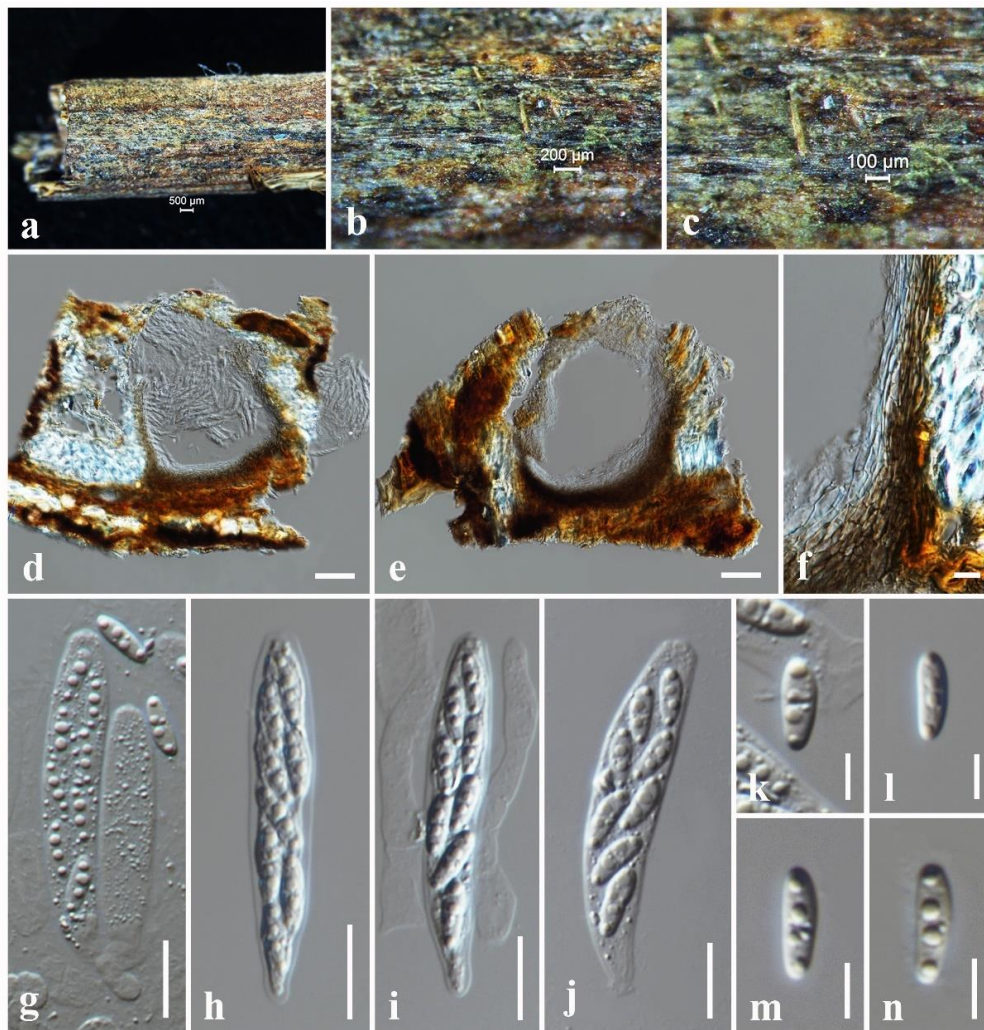
Figure 55 – *Diaporthe chiangmaiensis* (MFLU 18-1305, holotype). a The specimen. b, c Appearance of ascomata on the substrate. d, e Vertical sections through ascomata. f Peridium. g–j Asci. k–n Ascospores. Scale bars: a = 500 μm, b = 200 μm, c = 100 μm, d, e = 50 μm, f = 10 μm, g–j = 20 μm, k–n = 5 μm.

Subclass Hypocreomycetidae O.E. Erikss. & Winka
Hypocreales Lindau
Nectriaceae Tul. & C. Tul.

The family was established by Tulasne & Tulasne (1865) and typified by *Nectria*. Members of this family are nectria-related fungi possessing brightly pigmented ascomata with fusiform to allantoid ascospores and globose to fusiform phialidic conidia (Rossman 2000, Lombard et al. 2015, Yang et al. 2019b). These fungi can be endophytic, foliicolous or saprobic on the bark of recently dead woody substrates. Some are entomogenous in terrestrial and aquatic habitats and a few species are human pathogens (Rossman et al. 1999, Lombard et al. 2015). They have worldwide distribution and have higher diversity in warm temperate and tropical regions (Rossman et al. 1999, Rossman 2000, Yang et al. 2019b). In a recent treatment of Sordariomycetes Hyde et al. (2020) accepted 69 genera in Nectriaceae.

Nectria (Fr.) Fr.

The genus consists of species referred to as the nectrioid or nectria-like fungi (Hirooka et al. 2012). Fries (1849) initially established *Nectria* that was typified by *N. cinnabarina*. They are weak parasites of woody plants and shrubs throughout the temperate zone of the northern hemisphere (Hirooka et al. 2011, Yang et al. 2018, 2019b). The genus is characterized by well-developed

stromata, red to dark red, subglobose to globose, fleshy, soft-textured, uniloculate perithecia with coelomycetous asexual morphs containing hyaline, narrowly ellipsoidal to cylindrical and non-septate conidia (Rossman et al. 1999, Hirooka et al. 2009, 2012, Yang et al. 2019b).

Nectria pseudotrichia Berk. & M.A. Curtis, J. Acad. nat. Sci. Philad., N.S. 2(6): 289 (1854) [1853]

Fig. 60

Index Fungorum number: IF 206961, Faces of Fungi number: FoF 01990

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Mycelium* not visible around ascomata or on host. Stromata erumpent through epidermis, pseudoparenchymatous, intergrading with ascomatal wall. *Ascomata* 230–260 µm high × 240–280 µm diam. ($\overline{x}$ = 250 × 270 µm, n = 10), orangish brown, subglobose to globose, superficial on stroma, solitary or caespitose, sometimes cupulate upon drying, papillate, apical region darker, smooth to rough. *Ascomatal wall* 45–65 µm wide, composed of two regions: outer region 35–55 µm wide, 3–5 layers of hyaline, cells of *textura prismatica*; inner region 10–15 µm wide, several layers of yellow, cells of *textura angularis*. *Asci* 45–70 × 10–16 ($\overline{x}$ = 60 × 13 µm, n = 20), 8-spored, unitunicate, clavate, with inconspicuous ring at apex. *Ascospores* 23–32 × 7–11 ($\overline{x}$ = 25 × 8.5 µm, n = 30), hyaline, obovoid, ellipsoidal to fusiform, muriform with 5–7 transverse septa and 1-2 longitudinal septa, straight, sometimes slightly curved, rounded at both ends. Asexual morph: see Hirooka et al. (2012).

Culture characteristics – Colonies on PDA reaching 40 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, flat, surface cottony with aerial mycelium, white; reverse: cream.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND25 (MFLU 21-0237), living culture, MFLUCC 21-0203.
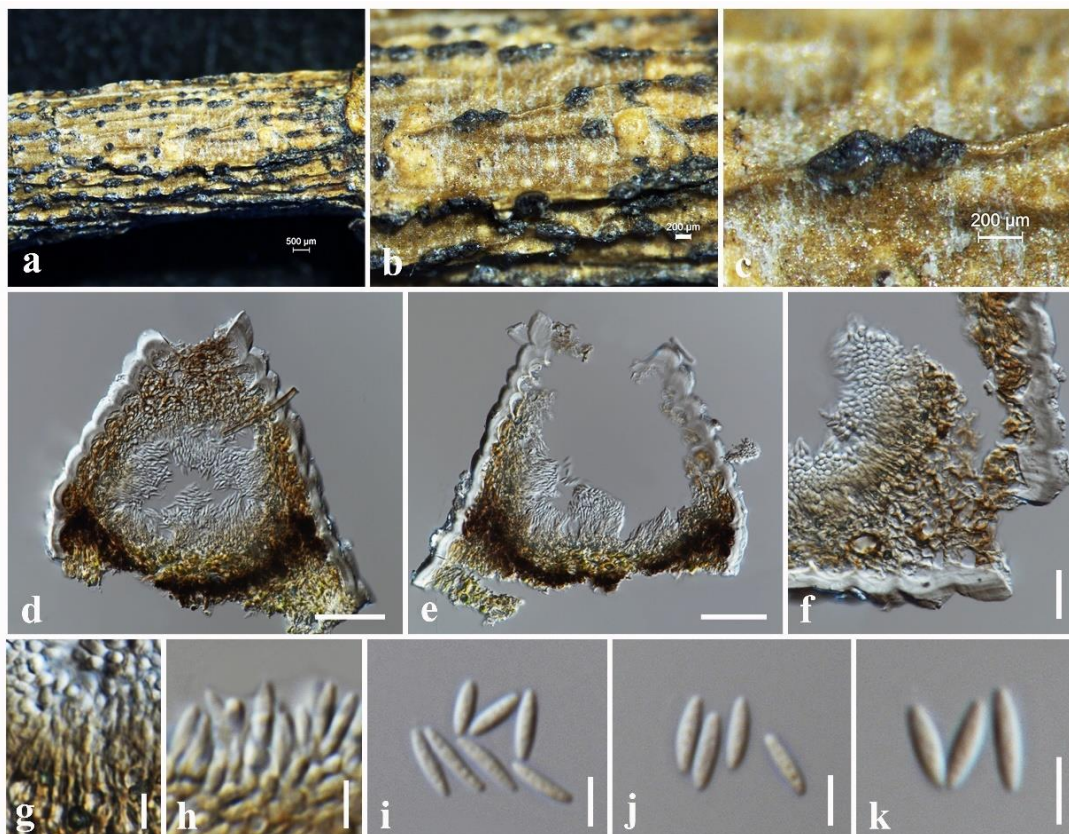

Figure 56 – *Diaporthe chiangmaiensis* (MFLU 21-0211). a The specimen. b, c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Conidiogenous cells. h–j Alpha conidia. Scale bars: a = 500 µm, b, c = 200 µm, d, e = 50 µm, f = 20 µm, g–k = 5 µm.
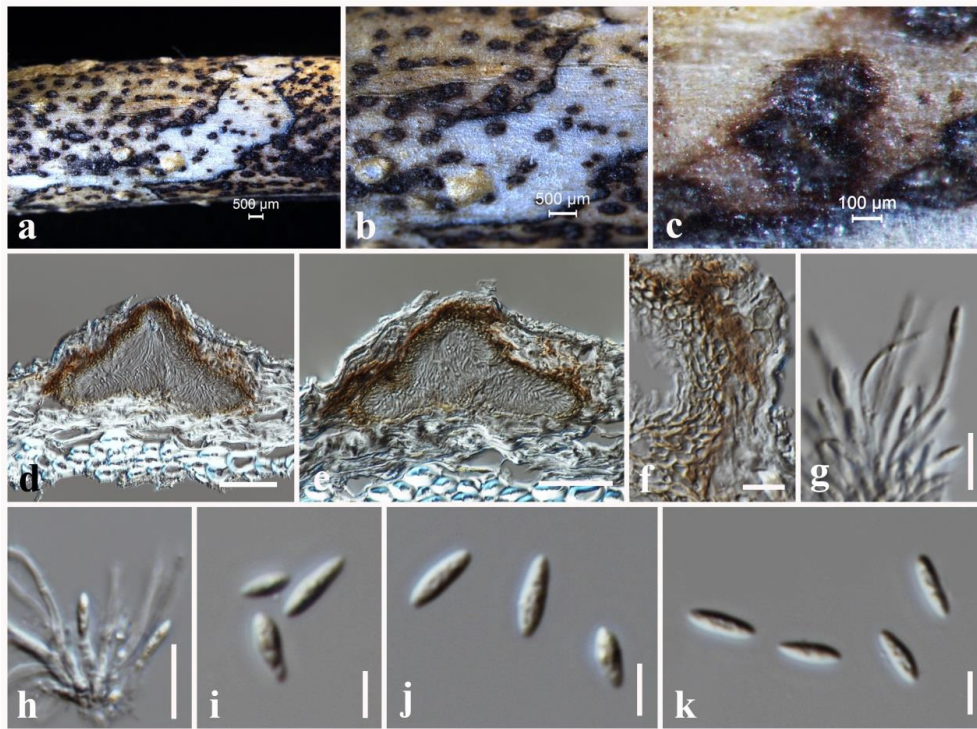
Figure 57 – *Diaporthe musigena* (MFLU 21-0212). a The specimen. b, c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g, h Conidiogenous cells. i–k Alpha conidia. Scale bars: a, b = 500 μm, c = 100 μm, d, e = 50 μm, f–h = 10 μm, i–k = 5 μm.
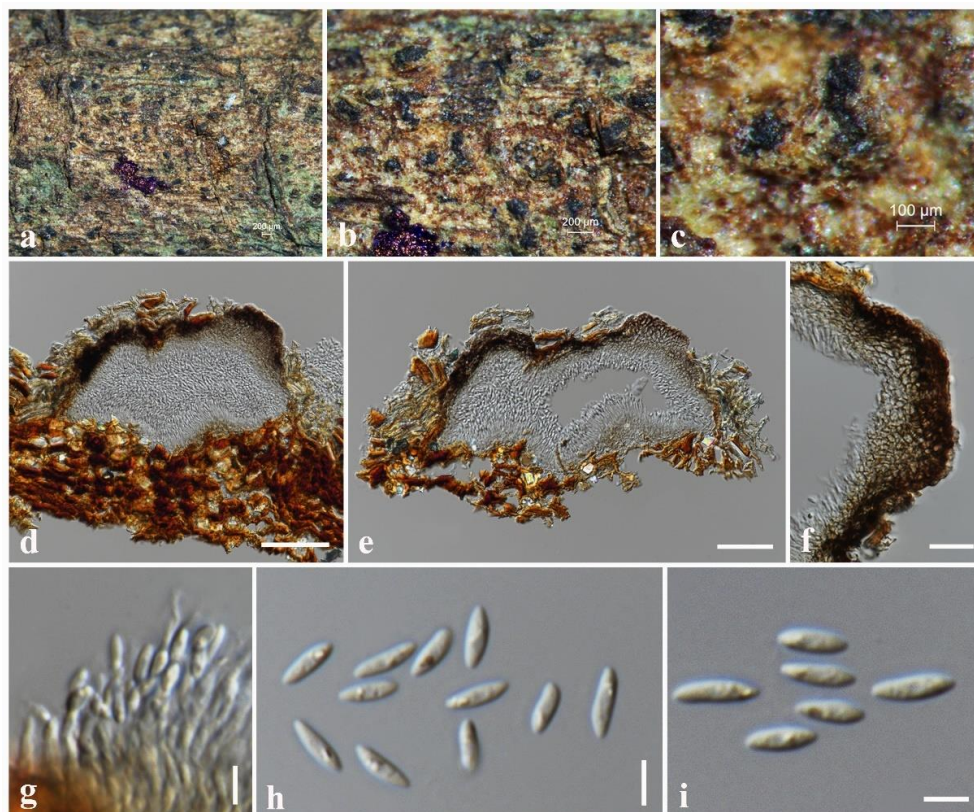

Figure 58 – *Diaporthe pterocarpi* (MFLU 21-0214). a–c Appearance of conidiomata on the substrate. d, e Vertical sections through conidiomata. f Conidiomatal wall. g Conidiogenous cells. h, i Alpha conidia. Scale bars: b = 200 μm, c = 100 μm, d, e = 50 μm, f = 20 μm, g–i = 5 μm.
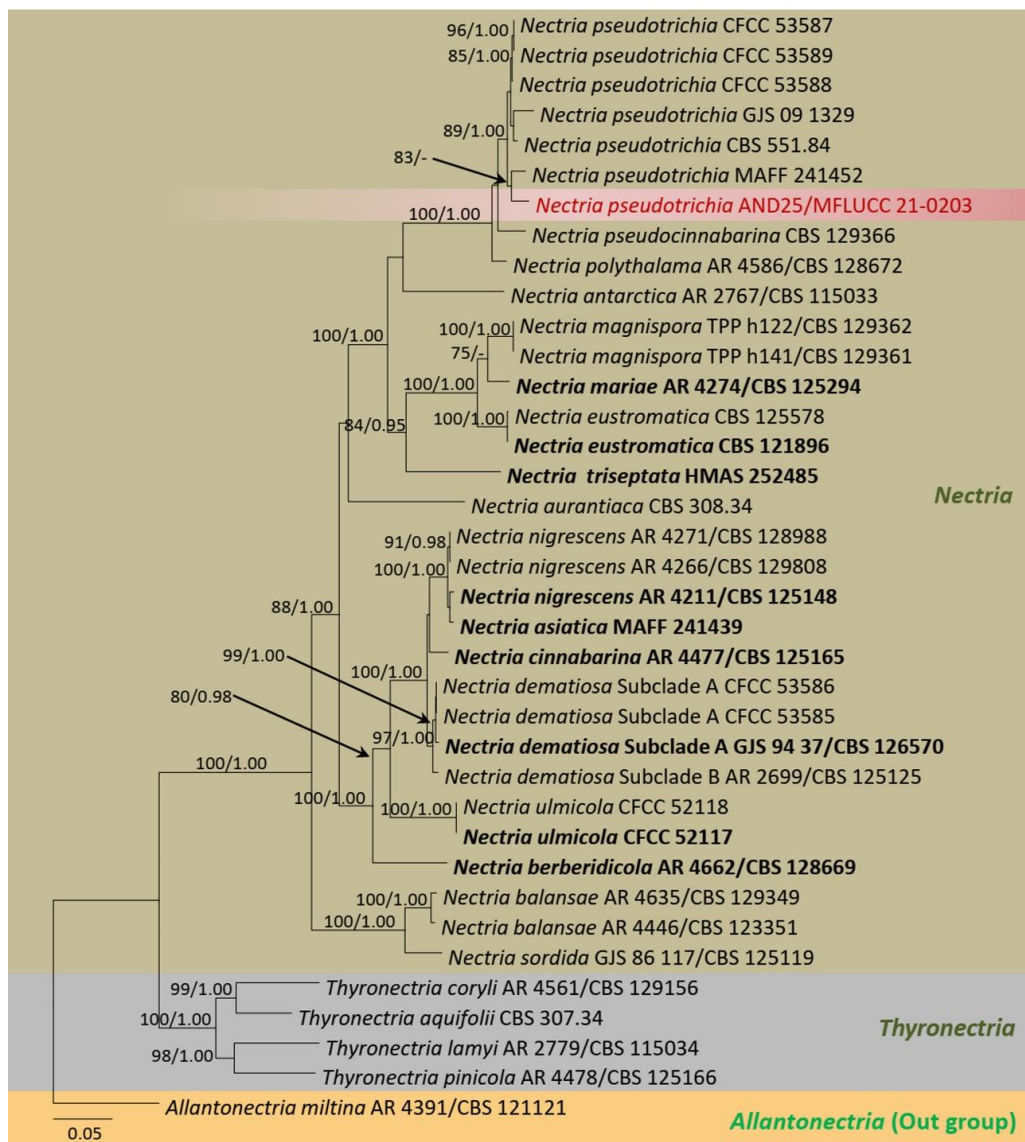
Figure 59 – Phylogram generated from maximum likelihood analysis of combined ITS, LSU, *tef1* and *tub2* sequence data. Related sequences of *Nectria* species were obtained from Yang et al. (2018). Thirty-seven strains are included in the combined gene analyses comprising 2520 characters after alignment (460 characters for ITS, 800 characters for LSU, 760 characters for *tef1* and 500 characters for *tub2*). *Allantonectria miltina* (AR 4391/CBS 121121) is used as outgroup taxon. The best RAxML tree with a final likelihood value of -15997.041280 is presented. The matrix had 934 distinct alignment patterns, with 20.38% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Known hosts and distribution – *Nectria pseudotrichia* occurs on numerous host plants and is distributed worldwide including *Schinus myrtifolia* in Argentina, *Litchi chinensis* in Australia, *Persea americana* in Bolivia, *Hydrangea* sp., *Mallotus* sp. in China, *Erythrina indica* in India, *Stilbella cinnabarina* in Indonesia, the bark of deadwood in Japan, the woody substrate in Malaysia, *Theobroma cacao* in Papua New Guinea, newly killed wood in Taiwan Province of China, *Albizia julibrissin*, *Ficus* sp., *Jussiaea peruviana* in the USA (Hirooka et al. 2012), dead twigs attached to *Anomianthus dulcis* in Thailand (this study).

GenBank numbers – ITS: OK284455, LSU: OK179727, *tef1*: OK274276, *tub2*: OK430881.

Notes – *Nectria pseudotrichia* can be distinguished from other species in the genus in having a combination of muriform ascospores and a synnematous anamorph (Hirooka et al. 2012). Morphology of the new isolate differs from the type *N. pseudotrichia*. Ascomata of the new isolate are smaller (230–260 μm high × 240–280 μm diam.) than the type (333–548 μm high × 296–534 μm diam.) (Hirooka et al. 2012). Asci of the new isolate are slightly smaller (45–70 × 10–16 μm) than the type (65–125 × 13–32 μm) (Hirooka et al. 2012). However, ascospores of the new isolate (23–32 × 7–11 μm) and the type (14.8–41.3 × 4.6–15 μm) have an overlapping size range.

Nectria pseudotrichia is commonly found as a saprobe in tropical and warm temperate regions (Hirooka et al. 2012). This fungus can also be a facultative parasite because Becker (2003) confirmed its pathogenicity on *Pyrus pirifolia* in Brazil. *Nectria pseudotrichia* has been recorded from Thailand on various hosts such as on the bark of recently dead trees, dead twigs of unknown plants and *Acacia* sp. in Saraburi Province, on decorticated wood of unknown plants in Phetchaburi Province and on the bark of the recently dead tree of unknown plants in Prachinburi Province (Hirooka et al. 2012). However, *N. pseudotrichia* has not been recorded from *Anomianthus dulcis* (Annonaceae) in Thailand (Farr & Rossman 2022). Developmental morphology of *Nectria pseudotrichia* has been studied by Subramanian & Bhat (1985). We report the first record of *N. pseudotrichia* from *Anomianthus dulcis* in Thailand in the present study.

Stachybotryaceae L. Lombard & Crous

Stachybotryaceae was introduced by Crous et al. (2014) to accommodate three genera, *viz.* *Myrothecium*, *Peethambara* and *Stachybotrys*. Subsequently, Lombard et al. (2016) monographed Stachybotryaceae and accepted 33 genera, based on both morphology and phylogeny. Thiry-six genera are accepted in the family Stachybotryaceae (Hyde et al. 2020c).

Memnoniella Höhn.

Memnoniella is one of the diverse genera in Stachybotryaceae and, 24 epithets listed in Index Fungorum (2022). *Memnoniella* members are characterized by having macronematous, mononematous, unbranched conidiophores, phialidic conidiogenous cells with conspicuous collarettes, and unicellular, aseptate, smooth to verrucose conidia arranged in dry chains or slimy masses (Lombard et al. 2016, Zheng et al. 2019). This study followed Tennakoon et al. (2021) as the latest treatment for this genus.

Memnoniella ellipsoidea L. Lombard & Crous, Persoonia 36: 197 (2016)   Fig. 62
Index Fungorum number: IF 816005, Faces of Fungi number: FoF 10668

Saprobic on dead twigs attached to *Cananga odorata*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Conidiophores* 50–130 × 3–6 μm ($\bar{x}$ = 100 × 4.5 μm, n = 20), macronematous, mononematous, erect, simple, straight or flexuous, unbranched, smooth, thick-walled, septate, bearing at its apex a crown of phialides, light brown at the base, olive-grey to light brown at the apex, wider at the base, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* 11–13 × 4–5 μm μm ($\bar{x}$ = 12 × 4.5 μm, n = 20), monophialidic, discrete, determinate, terminal, clustered at the apex of conidiophores, clavate to subcylindrical, smooth, subhyaline to light brown. *Conidia* 9–11 × 4–7 μm ($\bar{x}$ = 10 × 5.5 μm, n = 30), acrogenous, aseptate, ellipsoidal, olivaceous brown to dark brown, verrucose, with 1-2 large guttules, thick-walled, rounded at both ends.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after 1 week at 25 °C, colonies from above: circular, margin entire, flat, surface smooth, white at the margin, cream in the centre; reverse: cream at the margin, pale brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Cananga odorata* (Annonaceae), 2 January 2019, N. I. de Silva, CO2 (MFLU 21-0236), living culture, MFLUCC 21-0170.

Known hosts and distribution – On a dead twig of *Bromelia* sp. in Brazil (Lombard et al. 2016), on dead twigs attached to *Cananga odorata* in Thailand (this study).

GenBank numbers – LSU: OK179728, ITS: OK284456.

Notes – Our collection (MFLU 21-0236) shares similar morphology with *Memnoniella ellipsoidea* in having macronematous, mononematous, erect, simple and septate conidiophores, monophialidic, discrete, determinate, terminal, clavate to subcylindrical conidiogenous cells and aseptate, ellipsoidal, olivaceous brown to dark brown conidia (Lombard et al. 2016). Multi-gene phylogeny (LSU, ITS, *tub2* and *rpb2*) also indicates that our collection clustered with *M. ellipsoidea* isolates (CBS 136199, CBS 136200, CBS 135201 and CBS 136202) with 75% ML, 100 BYPP support (Fig. 63). Therefore, based on both morphology and phylogeny evidence, we introduce our collection as a new host record of *M. ellipsoidea* from *Cananga odorata* in Thailand.
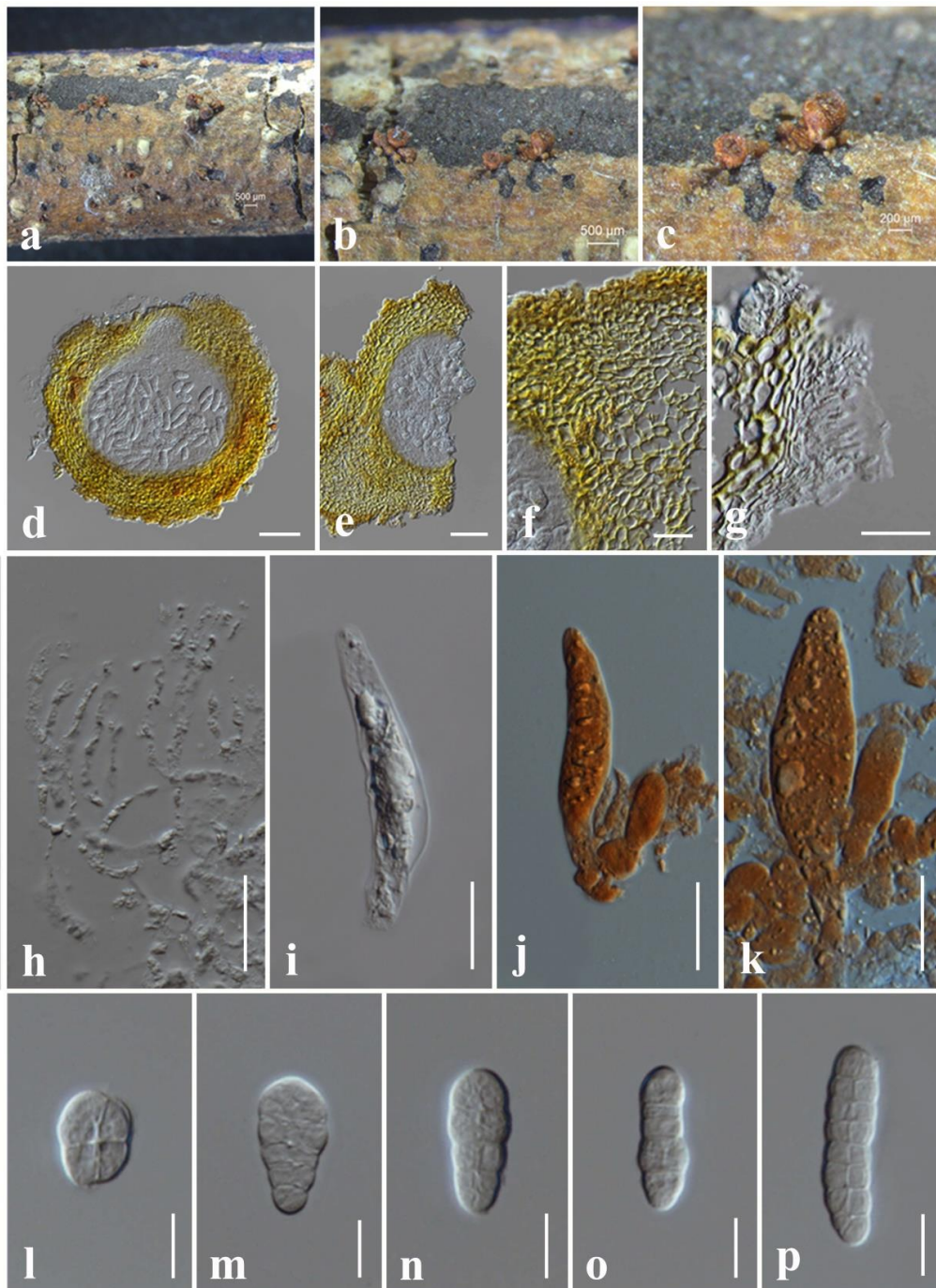

Figure 60 – *Nectria pseudotrichia* (MFLU 21-0237). a The specimen. b, c Appearance of perithecia on substrate. d, e Vertical sections through perithecia. f, g Peridium. h Paraphyses. i–k Asci (j, k stained with Congo red). l–p Ascospores. Scale bars: b = 500 μm, c = 200 μm, d, e = 50 μm, f–k = 20 μm, l–p = 10 μm.
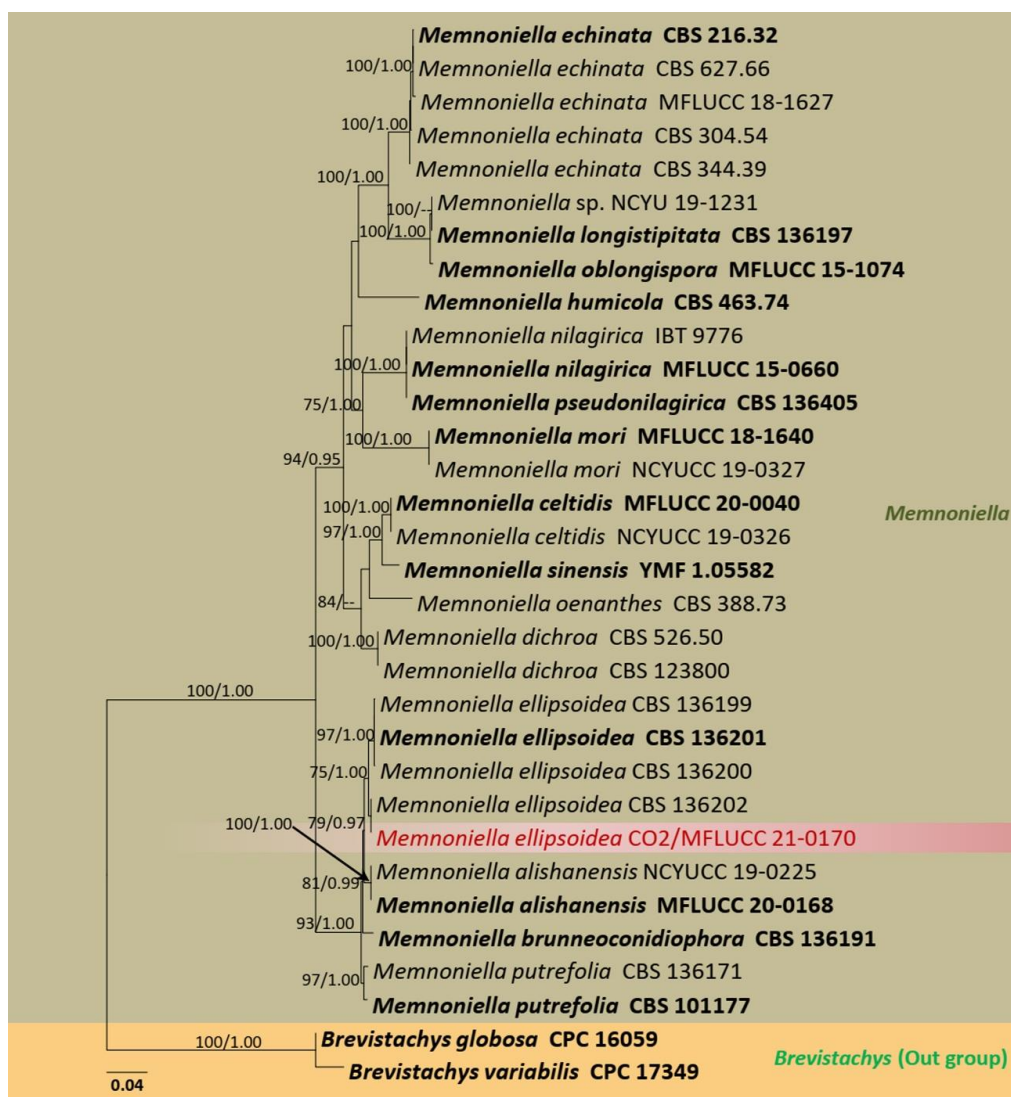
Figure 61 – Phylogram generated from maximum likelihood analysis of combined LSU, ITS, *tub2* and *rpb2* sequence data. Related sequences of *Memnoniella* were obtained from Tennakoon et al. (2021). Thirty-two strains are included in the combined gene analyses comprising 2480 characters after alignment (800 characters for LSU, 580 characters for ITS, 400 characters for *tub2* and 700 characters for *rpb2*). *Brevistachys globosa* (CPC 16059) and *B. variabilis* (CPC 17349) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -9212.463671 is presented. The matrix had 632 distinct alignment patterns, with 25.75% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Subclass Xylariomycetidae O.E. Erikss. & Winka
Amphisphaeriales D. Hawksw. & O.E. Erikss.
Amphisphaeriaceae G. Winter

Winter (1885) introduced the family with *Amphisphaeria* as the type genus. Amphisphaeriaceous taxa are mainly saprobes on dead plant material in terrestrial, aquatic and marine habitats (Senanayake et al. 2015, Samarakoon et al. 2019, Hyde et al. 2020c). Sexual morph is characterized by pseudostromata on host plant consisting 8-spored, unitunicate asci with J+ or J-, apical ring, brown, ellipsoidal to fusiform, 1-septate ascospores (Hyde et al. 2020c). Asexual morph is coelomycetous with dichotomously branched conidiophores bearing hyaline, 1-celled conidia

(Hyde et al. 2020c). Samarakoon et al. (2020) synonymized *Lepteutypa* under *Amphisphaeria* based on holomorphic morphology and multigene phylogeny and thereby *Amphisphaeria* is the only genus in Amphisphaeriaceae.
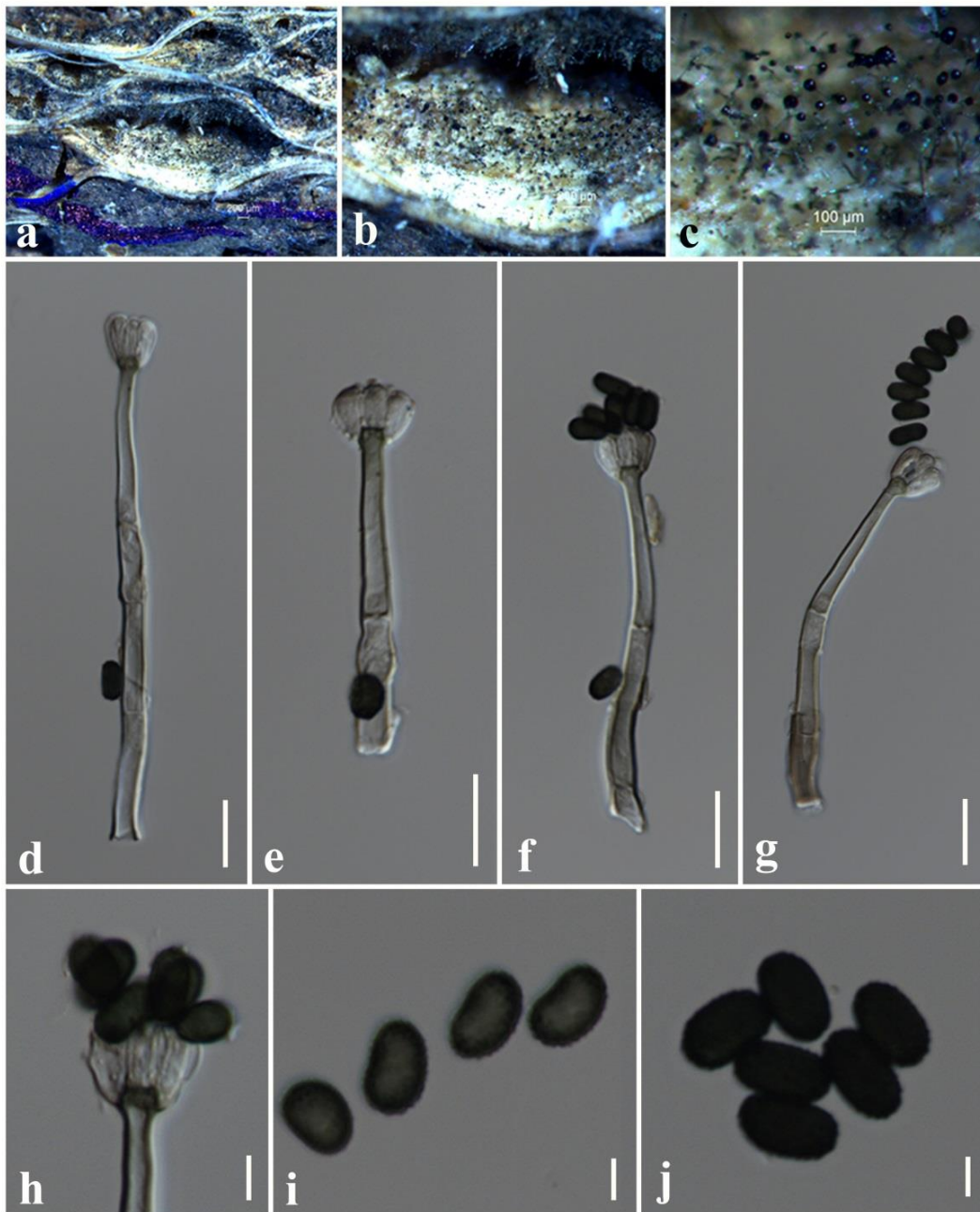
Figure 62 – *Memnoniella ellipsoidea* (MFLU 21-0236). a–c Conidiophores on the substrate surface. d, e Conidiophores. f, g Conidiophores with attached conidia. h Conidiophore with conidiogenous cells and attached conidia. i, j Conidia. Scale bars: c = 100 μm, d–g = 20 μm, h–j = 5 μm.

Amphisphaeria Ces. & De Not.

Cesati & De Notaris (1863) introduced *Amphisphaeria*. The type species is *A. umbrina* with a coelomycetous asexual morph (Samuels et al. 1987, Barr 1990). These species are characterized by immersed, clypeate, globose, periphysate ostiolate ascomata, 8-spored, unitunicate, asci with J+ or J- subapical ring and two-celled, light brown to dark brown ascospores (Cesati & De Notaris 1863, Wang et al. 2004). *Amphisphaeria* species are recorded as saprobes on woody branches and some monocotyledons including grasses (Samarakoon et al. 2019).

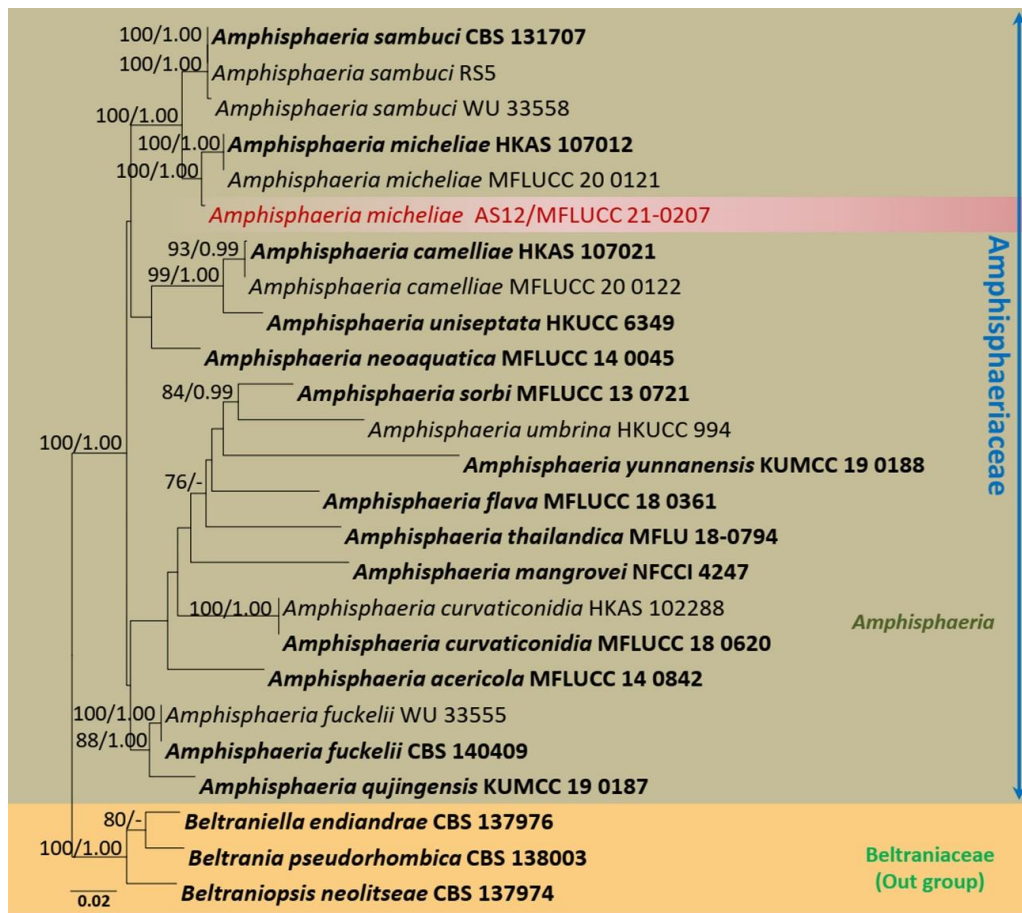**Figure 63** – Phylogram generated from maximum likelihood analysis of combined LSU-ITS sequence data. Related sequences of Amphisphaeriaceae were obtained from Samarakoon et al. (2020). Twenty-five strains are included in the combined gene analyses comprising 1500 characters after alignment (900 characters for LSU and 600 characters for ITS). *Beltrania pseudorhombica* (CBS 138003), *Beltraniella endiandrae* (CBS 137976), *Beltraniopsis neolitseae* (CBS 137974) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -6546.017970 is presented. The matrix had 553 distinct alignment patterns, with 13.23% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Amphisphaeria micheliae Samarak., Jian K. Liu & K.D. Hyde, J. Fungi 6(3): 16 (2020)

Fig. 64

Index Fungorum number: IF 836112, Faces of Fungi number: FoF 08752

Saprobic on dead twigs attached to *Alstonia scholaris*. Sexual morph: *Ascomata* 150–180 high × 270–340 diam. ($\bar{x}$ = 160 × 290 µm, n = 10), visible as brown spots on the host, subglobose, solitary, scattered. *Peridium* two-layered; outer layer 10–13 µm diam. densely arranged, reddish-brown, thick-walled cells of *textura angularis*; inner layer 10–12 µm diam. loosely arranged, hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 3–4 µm diam. hyaline, highly delicate, cellular, constricted septate, guttulate, embedded in a gelatinous matrix. *Asci* 100–138 × 7–10 µm ($\bar{x}$ = 120 × 8 µm, n = 25), 8-spored, unitunicate, cylindrical, thin-walled, short-pedunculate, apically rounded, with a J+, discoid apical ring. *Ascospores* 13–18 × 4.5–7 µm ($\bar{x}$ = 15 × 6 µm, n = 30), uniseriate, oblong or narrowly fusiform, initially hyaline, guttulate, turning yellow to yellow-brown, 1-septate, slightly constricted at septum, straight to slightly curved, smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: circular, margin undulate, dense, surface smooth, orangish brown at the margin, white in the centre; reverse: cream at the margin, yellowish brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Alstonia scholaris* (Apocynaceae), 25 April 2019, N. I. de Silva, AS12 (MFLU 21-0207), living culture, MFLUCC 21-0207, KUMCC 20-0089.

Known hosts and distribution – On a dead branch of *Michelia alba* (Magnoliaceae) in China (Samarakoon et al. 2020), dead twigs attached to *Alstonia scholaris* (Apocynaceae) in Thailand (this study).

GenBank numbers – LSU: OK179729, ITS: OK284457.

Notes – A newly collected fungus (MFLU 21-0207) shares morphology with the type of *Amphisphaeria micheliae* (HKAS 107012). *Amphisphaeria micheliae* was introduced from dead branch of *Michelia alba* in Sichuan Province, China (Samarakoon et al. 2020). The new collection has 100–138 × 7–10 µm, 8-spored, unitunicate, cylindrical asci with a J+, discoid apical ring that are similar to the type *A. micheliae* 92–135 × 7–10.5 µm (Samarakoon et al. 2020). The new collection has 13–18 × 4.5–7 µm, initially hyaline, guttulate, turning yellow to yellow-brown, 1-septate ascospores that are similar in colour and septation with the type *A. micheliae* while slightly smaller to the type *A. micheliae* 15.5–21 × 6–7.5 µm (Samarakoon et al. 2020). A comparison of ITS sequence data shows 100% (552/552 bp) similarity of our new strain to the ex-type of *A. micheliae* (MFLUCC 20-0121). We identify our new strain as *A. micheliae* based on morphology and phylogeny. This is a new host record from *Alstonia scholaris* and a new geographical record from Thailand.

Xylariales Nannf.
Diatrypaceae Nitschke

Diatrypaceae was introduced by Nitschke (1869) with *Diatrype* as the type genus. This family includes 22 genera and more than 1500 species (Mehrabi et al. 2019, Dissanayake et al. 2021). The family is characterized by perithecial ascomata embedded in a stroma, long-stalked asci and allantoid ascospores (Glawe & Rogers 1984, Rappaz 1987). Diatrypaceae species exhibit as common saprophytes or pathogens or endophytes from an extensive range of woody plants in terrestrial and aquatic environments worldwide (Glawe & Rogers 1984, de Errasti et al. 2014, Liu et al. 2015).

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

Dissanayake et al. (2021) introduced *Paraeutypella* to accommodate *P. citricola* and *P. vitis*, two species previously placed in *Eutypella sensu lato* and *P. guizhouensis*. The type species is *P. guizhouensis* (Dissanayake et al. 2021). These species are saprobes on twigs and deadwood materials (Dissanayake et al. 2021).

Paraeutypella citricola (Speg.) L.S. Dissan., Wijayaw., J.C. Kang & K.D. Hyde, Biodiversity Data Journal 9: e63864, 14 (2021)   Fig. 66

Index Fungorum number: IF 558003, Faces of Fungi number: FoF 09150

Saprobic on dead twigs attached to *Magnolia* sp. Sexual morph: *Stromata* immersed in the substrate, erumpent, aggregated, circular to irregular in shape, blackening the periderm, surface black, rugose due to the necks of perithecia, surrounded by a black line in the host tissue, with groups of 6–10 perithecia. *Perithecia* 480–500 high × 300–350 diam. ($\bar{x}$ = 490 × 320 µm, n = 10), dark brown, black, globose to subglobose, compressed, necks of the perithecia arranged in a valsoid configuration. *Ostiolar canals* 170–200 high × 50–70 diam. ($\bar{x}$ = 190 × 60 µm, n = 10), dark brown, opening separately, sulcate or smooth, periphysate. *Peridium* 30–40 µm thick, comprising several layers of cells of *textura angularis*; inner layer cells hyaline, outer layer cells brown to dark brown. *Hamathecium* 1–2 µm wide, composed of filiform, septate, hyaline paraphyses. *Asci* 65–85 × 7–9 µm ($\bar{x}$ = 70 × 8 µm, n = 20), unitunicate, cylindrical, 8-spored, with rounded apex, apical

rings inamyloid, long stalked. *Ascospores* 7–12 × 2–4 µm ($\bar{x}$ = 9 × 2.5 µm, n = 30), uniseriate to irregularly arranged, sometimes agglomerated at the base of ascus, hyaline, becoming pale brown, allantoid, aseptate, smooth. Asexual morph: Not observed.
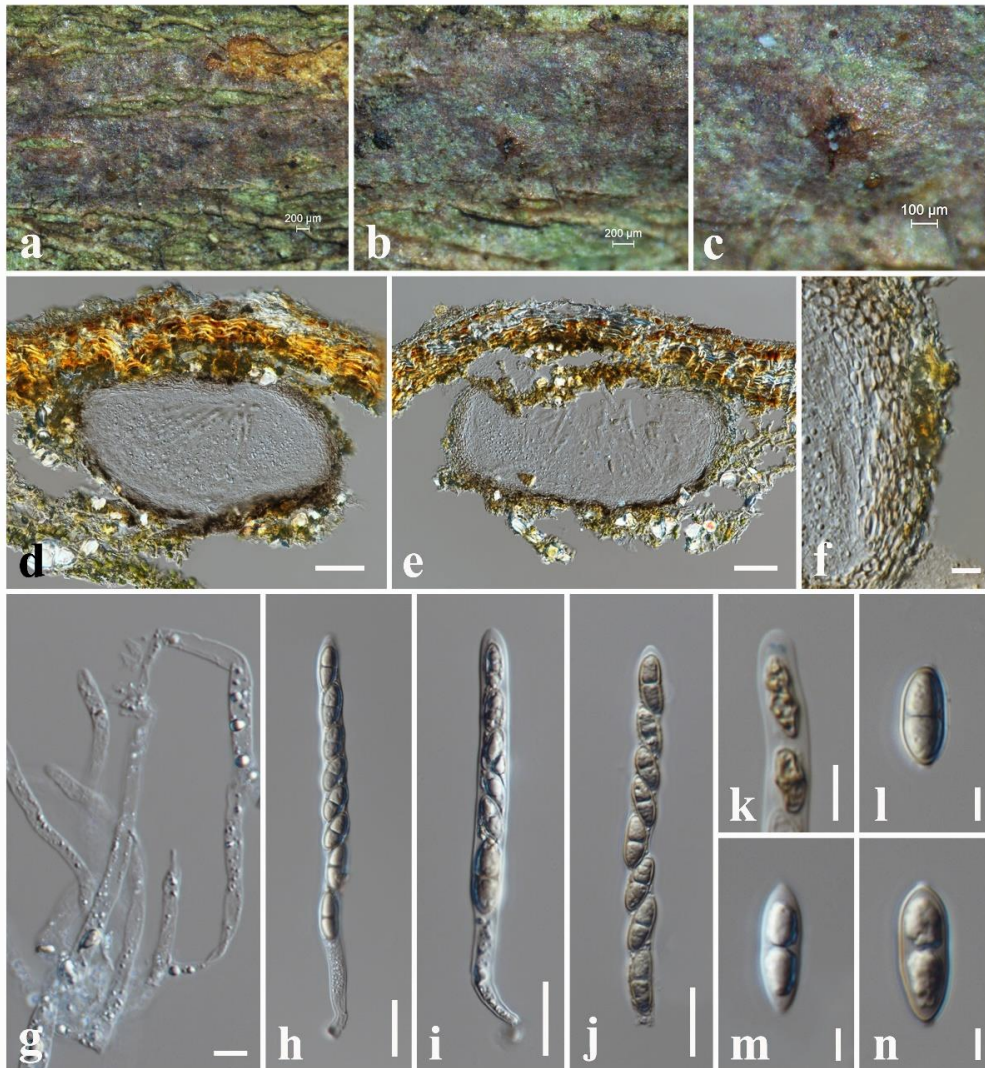

Figure 64 – *Amphisphaeria micheliae* (MFLU 21-0207). a–c Appearance of ascomata on substrate. d, e Vertical sections through ascomata. f Peridium. g Paraphyses. h–j Asci. k apical ring bluing in Melzer's reagent. l–n Ascospores. Scale bars: a, b = 200 µm, c = 100 µm, d, e = 50 µm, f, g = 10 µm, h–j = 20 µm, k = 10 µm, l–n = 5 µm.

Culture characteristics – Colonies on PDA reaching 35 mm diameter after 1 week at 25 °C, colonies from above: circular to slightly irregular, margin entire, slightly raised, cottony, fluffy appearance, white; reverse: cream at the margin, pale brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Magnolia* sp. (Magnoliaceae), 11 February 2019, N. I. de Silva, NI329 (MFLU 21-0240).

Known hosts and distribution – *Paraeutypella citricola* occurs on numerous host plants and is distributed in worldwide including *Citrus aurantifolia* in Ghana, *C. aurantium* in Argentina, *C. grandis* in China, *C. limon* in Australia, *Eriobotrya japonica* in South Africa, *Salix* sp. in Iran, *Vitis vinifera* in Australia (Farr & Rossman 2022), dead twigs attached to *Magnolia* sp. in Thailand (this study).

GenBank numbers – ITS: OK393706, *tub2*: OK430882.

Notes – *Eutypella citricola* was described by Spegazzini (1898) from *Citrus* in Argentina. Dissanayake et al. (2021) placed *Eutypella citricola* in *Paraeutypella* as *P. citricola* based on the

phylogeny of combined ITS, and *tub2* sequence data. In our phylogenetic analysis of combined ITS, and *tub2* sequence data, a new strain (MFLU 21-0240) clustered with two strains of *P. citricola* (IRAN 2349C and CBS 128330) with 99% ML, 1.00 BYPP statistical support (Fig. 67). *Paraeutypella citricola* was recorded from various woody plants including *Citrus limon*, *C. sinensis*, *C. paradisi*, *Salix* spp., *Schinus molle*, *Ulmus procera* and *Vitis vinifera* in warm temperate and tropical regions (Trouillas et al. 2011, Mehrabi et al. 2016, Farr & Rossman 2022). We here report the first record of *Paraeutypella citricola* on dead twigs of *Magnolia lilifera* in Thailand.

Peroneutypa Berl.

Peroneutypa was erected by Berlese (1902) to accommodate *P. bellula P. corniculata* and *P. heteracantha* without designating the type species. Rappaz (1987) proposed *P. bellula* as the type species of *Peroneutypa*. Carmarán et al. (2006) reinstated *Peroneutypa* based on morphology and phylogeny. Phylogenetic analyses of previous studies (Dai et al. 2016, Shang et al. 2017, Mehrabi et al. 2019) agree that *Peroneutypa* is an independent genus within the Diatrypaceae. Members of this genus are characterized by valsoid ascostromata, perithecia with long necks octosporous, clavate, sessile to subsessile asci, allantoid, hyaline or yellowish ascospores (Carmarán et al. 2006, Vasilyeva & Rogers 2010, Mehrabi et al. 2016, Shang et al. 2017).

Peroneutypa anomianthi N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.　　　　　Fig. 67

Index Fungorum number: IF 559525, Faces of Fungi number: FoF 10722

Etymology – Name reflects the host genus *Anomianthus*, from which the new species was isolated.

Holotype – MFLU 21-0242.

Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: *Stromata* with the poorly developed interior, solitary to gregarious, 1–5 locules, immersed, becoming raised to erumpent by a long ostiolar canal, dark brown to black, glabrous, circular to irregular in shape, arranged in longitudinally, with conspicuous, clustered, roundish to prominent cylindrical ostioles in the centre. *Ascomata* (excluding necks) 280–350 μm high, 350–450 μm diam. ($\bar{x} = 320 \times 400$ μm, n = 10), perithecial, immersed in a stroma, dark brown to black, globose to subglobose, glabrous, individual ostioles with long neck. *ostiolar canals* 320–360 μm high, 90–110 μm diam. ($\bar{x} = 340 \times 100$ μm, n = 10), cylindrical, sulcate, at the apex curved, periphysate. *Peridium* 20–30 μm wide, composed of two section layers, outer section comprising 4–5 layers, of relatively small, brown to dark brown, thick-walled cells, arranged in a *textura angularis*, inner part comprising 3–5 layers of flattened, hyaline cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of 2–3 μm wide, dense, cylindrical, septate, slightly swell at the basal cells, constricted at the basal septa, hyaline, paraphyses slightly swollen at the septa. *Asci* 26–36 × 3–5 μm ($\bar{x} = 29 \times 4$ μm, n = 20), unitunicate, cylindrical, 8-spored, urn-shaped, long pedicellate, apically rounded to truncate, with a J-, subapical ring. *Ascospores* 3–5 × 1–2 μm ($\bar{x} = 4.5 \times 1.5$ μm, n = 30), overlapping 1–2-seriate, hyaline to pale yellowish, allantoid, aseptate with smooth-walled. Asexual morph: Not observed.

Culture characteristics– Colonies on PDA reaching 30 mm diameter after 1 week at 25 °C, colonies from above: irregular, margin fimbriate, slightly raised, cottony, fluffy to fairly fluffy, white; reverse: cream at the margin, pale brown in the centre.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND6 (MFLU 21-0242, holotype), living culture, MFLUCC 21-0195.

GenBank numbers – ITS: OK393705.

Notes – A new strain MFLUCC 21-0195 forms an independent lineage that is closely related to *Peroneutypa polysporae* (NFCCI 4392) and *P. mangrovei* (PUFD 526) with 99% ML, 1.00 BYPP statistical support in our phylogeny of combined ITS, and *tub2* sequence data (Fig. 67).
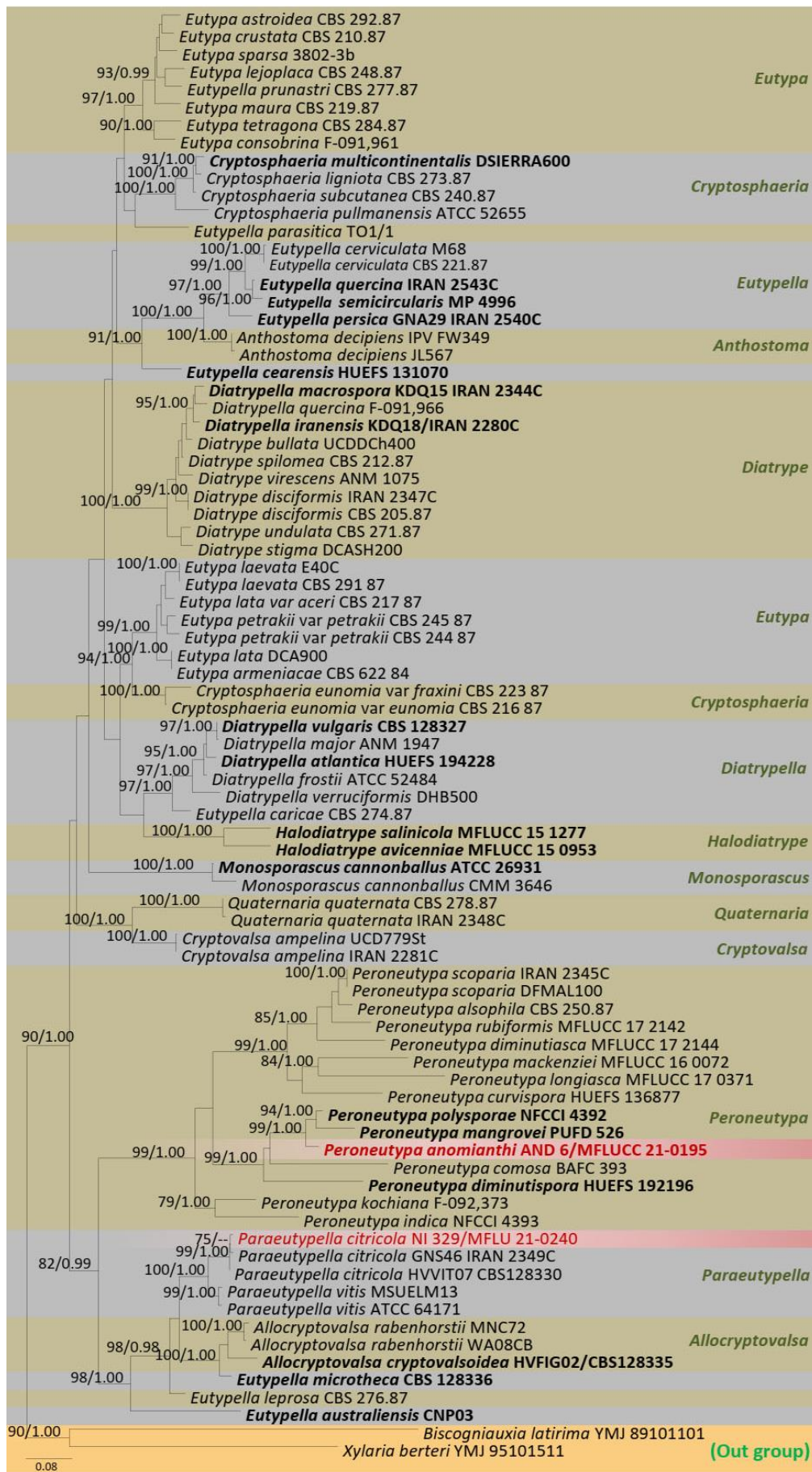
Figure 65 – Phylogram generated from maximum likelihood analysis of combined ITS, and *tub2* sequence data. Related sequences of Diatrypaceae were obtained from Mehrabi et al. (2019).

Eighty-two strains are included in the combined gene analyses comprising 1270 characters after alignment (500 characters for ITS and 770 characters for *tub2*). *Biscogniauxia latirima* (YMJ 89101101) and *Xylaria berteri* (YMJ 95101511) are used as outgroup taxa. The best RAxML tree with a final likelihood value of -19392.622548 is presented. The matrix had 1205 distinct alignment patterns, with 57.40% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.
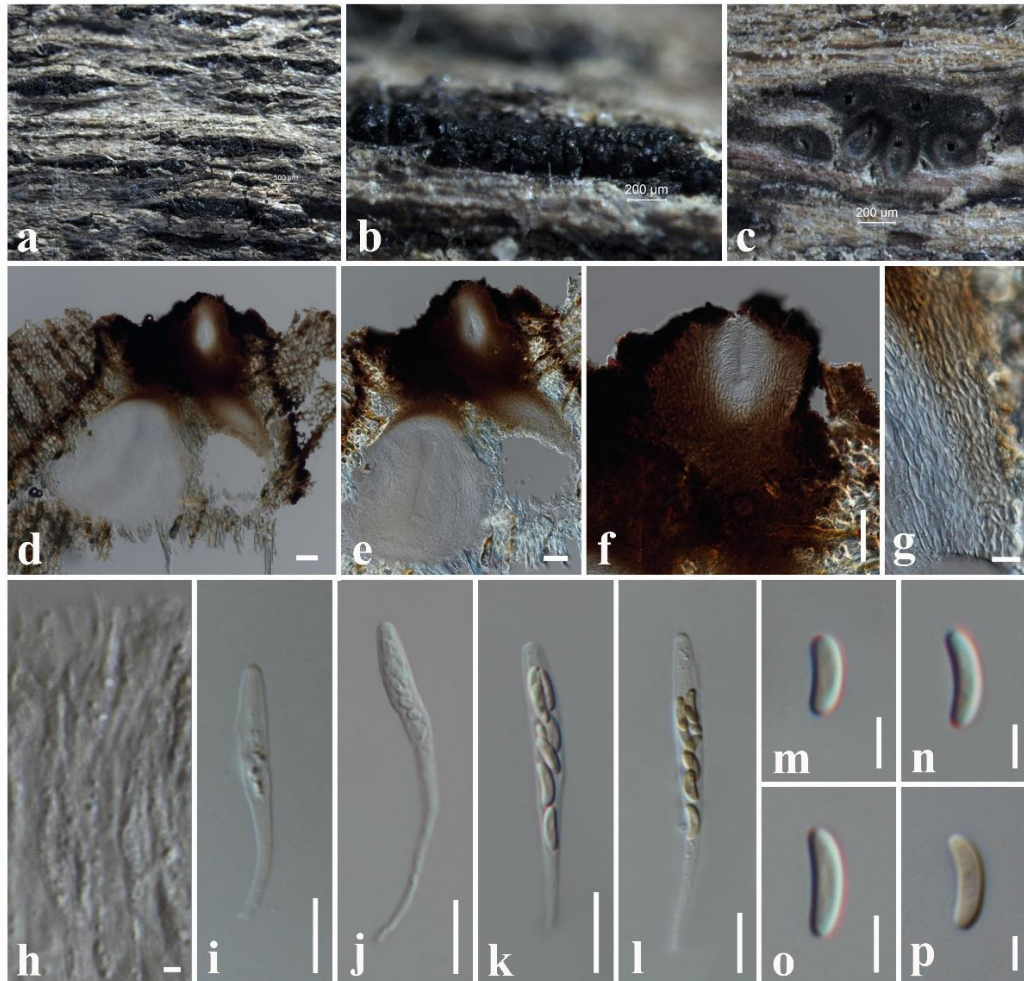

Figure 66 – *Paraeutypella citricola* (MFLU 21-0240). a–c Appearance of stromata on substrate. d, e Vertical sections through stromata. f Ostiolar canal. g Peridium. h Paraphyses. i–l Asci. m–p Ascospores. Scale bars: b, c = 200 µm, d–f = 50 µm, g = 10 µm, h = 2 µm, k = 10 µm, i–l = 20 µm, m–p = 5 µm.

Peroneutypa polysporae differs from the new strain in having (113 × 12 µm), polysporous asci (Dayarathne et al. 2020). *Peroneutypa mangrovei* has small asci (17 × 3.5 µm) with short pedicellate (Phookamsak et al. 2019), while the new strain has large asci (29 × 4 µm) with long pedicellate. *Peroneutypa polysporae* was isolated on decaying wood of *Suaeda monoica* in India (Dayarathne et al. 2020) while *P. mangrovei* was isolated on decaying wood of *Avicennia marina* in India (Phookamsak et al. 2019). *Peroneutypa comosa* was isolated on rotten stems of Celtis tala in Buenos Aires in having (25–30 × 6–9 µm) asci and (5–7 × 2–2.5 µm) ascospores (Spegazzini 1881). The new strain was collected from dead twigs of *Anomianthus dulcis* in Thailand. Therefore, we introduced *Peroneutypa anomianthi* as a novel species based on morphology, phylogeny and host association.

Xylariales Incertae sedis
Gyrothrix (Corda) Corda

    Gyrothrix was introduced by Corda 1842 and typified by *G. podosperma*. These species are hyphomycetous, mostly saprobes (Bhardwaj et al. 2019). The genus is characterized by superficial, effuse, grayish-brown velvety sporodochial or stromatic colonies, repeatedly branched, dark brown or olivaceous brown, erect setae, micronematous flexuous, irregularly branched and anastomosing subhyaline to pale olivaceous brown, smooth conidiophores and polyblastic, discrete, conidiogenous cells. Conidia are initially arranged in a ring just below the apex of the conidiogenous cell and later detached in bundles and become simple, hyaline, acerose, falcate, cylindrical or fusiform (Corda 1842). Becerra-Hernández et al. (2016) indicated that *Gyrothrix* as a polyphyletic genus of Xylariales based on molecular phylogenetic studies of combined ITS, LSU and *tef1* sequence data. Therefore, the phylogenetic placement of the genus *Gyrothrix* at the family level cannot be determined. *Gyrothrix* contains 30 epithets in Index Fungorum (2022).
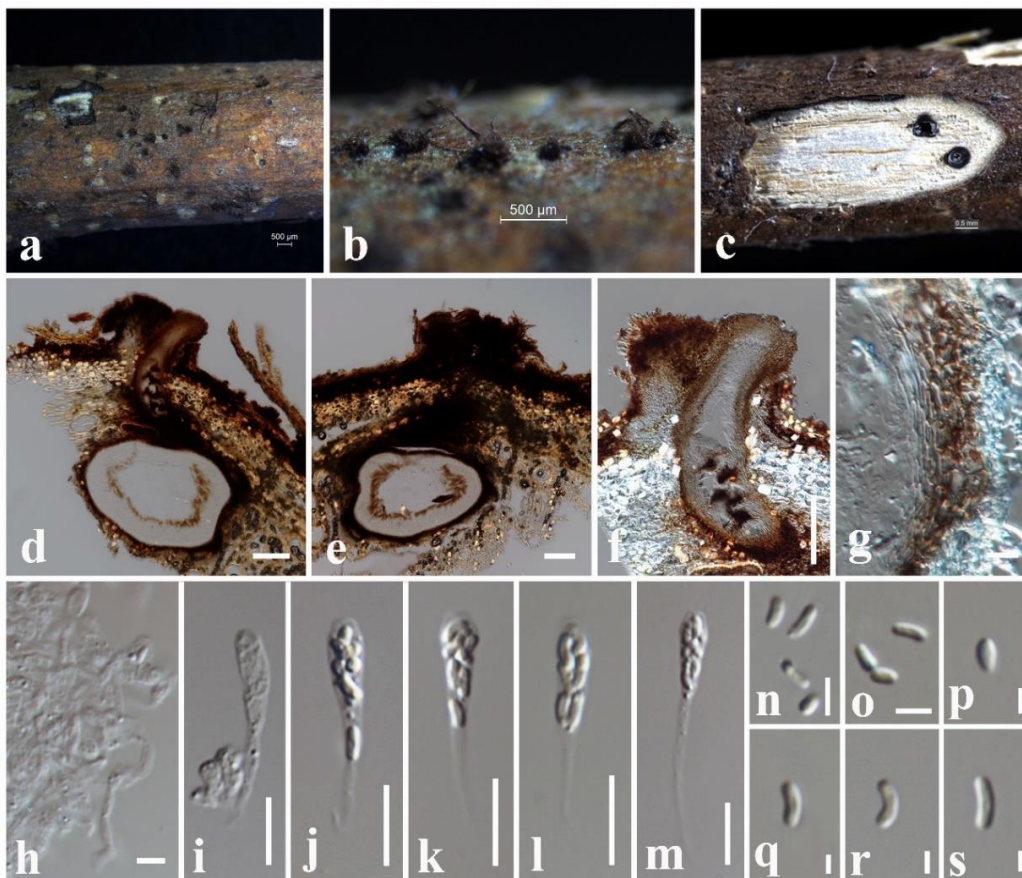

Figure 67 – *Peroneutypa anomianthi* (MFLU 21-0242, holotype). a–c Appearance of stromata on substrate. d, e Vertical sections through stromata. f Ostiolar canal. g Peridium. h Paraphyses. i–m Asci. n–s Ascospores. Scale bars: b, c = 500 µm, d–f = 100 µm, g = 10 µm, h, n–s = 5 µm, k = 10 µm, i–m = 10 µm.

Gyrothrix anomianthi N.I. de Silva, S. Lumyong & K.D. Hyde, sp. nov.   Fig. 69
    Index Fungorum number: IF 559526, Faces of Fungi number: FoF 10723
    Etymology – Name reflects the host genus *Anomianthus*, from which the new species was isolated.
    Holotype – MFLU 21-0219.
    Saprobic on dead twigs attached to *Anomianthus dulcis*. Sexual morph: Not observed. Asexual morph: *Mycelium* 1–2.5 µm diam., hyaline, branched, septate, smooth hyphae. *Setae* 70–130 µm long, 2–3 µm diam., dark brown at bulbous base and primary stalk, moderate brown in

remaining part, subcylindrical, erect, multiseptate, dichotomously branched at right angles to main axis, thick-walled, smooth to verruculose, spirally curved at apex of all lateral branches, bulbous at base. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–3 × 1–2 µm ($\overline{x}$ = 2.5 × 1.4 µm, n = 20), holoblastic, hyaline, ampulliform to lageniform develop like a mat at the base of setae. *Conidia* 10–13 × 1.5–3 µm ($\overline{x}$ = 12 × 2 µm, n = 30), hyaline, fusoid, inequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, aseptate, smooth.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: circular, margin lobate, flat, with moderate aerial mycelium, light grey; reverse: dark grey.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Anomianthus dulcis* (Annonaceae), 4 April 2019, N. I. de Silva, AND20 (MFLU 21-0219, holotype), ex-type living culture, MFLUCC 21-0200.

GenBank numbers – ITS: OK284458, LSU: OK179730.

Notes – During our investigation of microfungi from *Anomianthus dulcis* plants, a hyphomycetous fungus was recovered which is characterized by superficial, effuse, grayish brown, velvety, stromatic colonies with brown, repeatedly branched erect setae. This new isolate (MFLUCC 21-0200) constituted an independent lineage basal to *Gyrothrix encephalarti* (CPC 35966) and *G. eucalypti* (CPC 36066) in phylogenetic analyses of combined LSU, ITS, *tef1* sequence data with 81% ML, 1.00 BYPP statistical support (Fig. 71). Forty-eight base pair differences (9.6%) between the new isolate (MFLUCC 21-0200) and *G. encephalarti* (CPC 35966) and 50 base pair differences (10%) between the new isolate (MFLUCC 21-0200) and *G. encephalarti* (CPC 36066) were detected in ITS (500 bp) nucleotide sequences. The new collection (MFLU 21-0219) (10–13 × 1.5–3 µm) has slightly smaller conidia than *G. encephalarti* and *G. eucalypti*. Conidia of *G. encephalarti* are 7–14 × 3–3.5 µm (Crous et al. 2020), whille *G. eucalypti* are 8–15 × 2–2.5 µm (Crous et al. 2019b). Coupled with morphology and phylogeny, we introduce *G. anomianthi* as a novel species from *Anomianthus dulcis* in Thailand.

Gyrothrix oleae Crous, Persoonia 43: 305 (2019)   Fig. 70

Index Fungorum number: IF 832895, Faces of Fungi number: FoF 10669

Saprobic on dead twigs attached to *Desmos chinensis*. Sexual morph: Not observed. Asexual morph: *Mycelium* 1–2.5 µm diam., hyaline, branched, septate, smooth hyphae. *Setae* 60–100 µm long, 2–3 µm diam., brown, subcylindrical, erect, multiseptate, thick-walled, verruculose to warty, apex spirally recurved at apex of all lateral branches, bulbous at base. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* inconspicuous, develop at base of setae. *Conidia* 4–8 × 1.3–2 µm ($\overline{x}$ = 6.5 × 1.7 µm, n = 30), hyaline, fusoid, inequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, aseptate, smooth.

Culture characteristics – Colonies on PDA reaching 25 mm diameter after 1 week at 25 °C, colonies from above: circular, margin lobate, flat, margin entire, slightly raised with aerial mycelium, cream; reverse: dark brownish grey.

Material examined – Thailand, Chiang Rai Province, dead twigs attached to *Desmos chinensis* (Annonaceae), 8 March 2019, N. I. de Silva, DC 8 (MFLU 21-0220), living culture, MFLUCC 21-0215.

Known hosts and distribution – On leaves of *Olea capensis* and *Diospyros whyteana* in South Africa (Crous et al. 2019b), dead twigs attached to *Desmos chinensis* in Thailand (this study).

GenBank numbers – ITS: OK284459, LSU: OK179731, *tef1*: OK322700.

Notes – *Gyrothrix oleae* was introduced by Crous et al. (2019) on leaves of *Olea capensis* in South Africa. In this study, one of our new isolates, (MFLUCC 21-0215) clustered with *G. oleae* as a monophyletic clade. The new isolate (MFLUCC 21-0215) shares similar morphological characteristics with the type species, in having similar size, hyaline, fusoid conidia (Crous et al. 2019b). Therefore, based on morphology and phylogenetic analyses, we identify our strain as *G. oleae*. This is the first report of *G. oleae* from dead twigs of *Desmos chinensis* in Thailand.
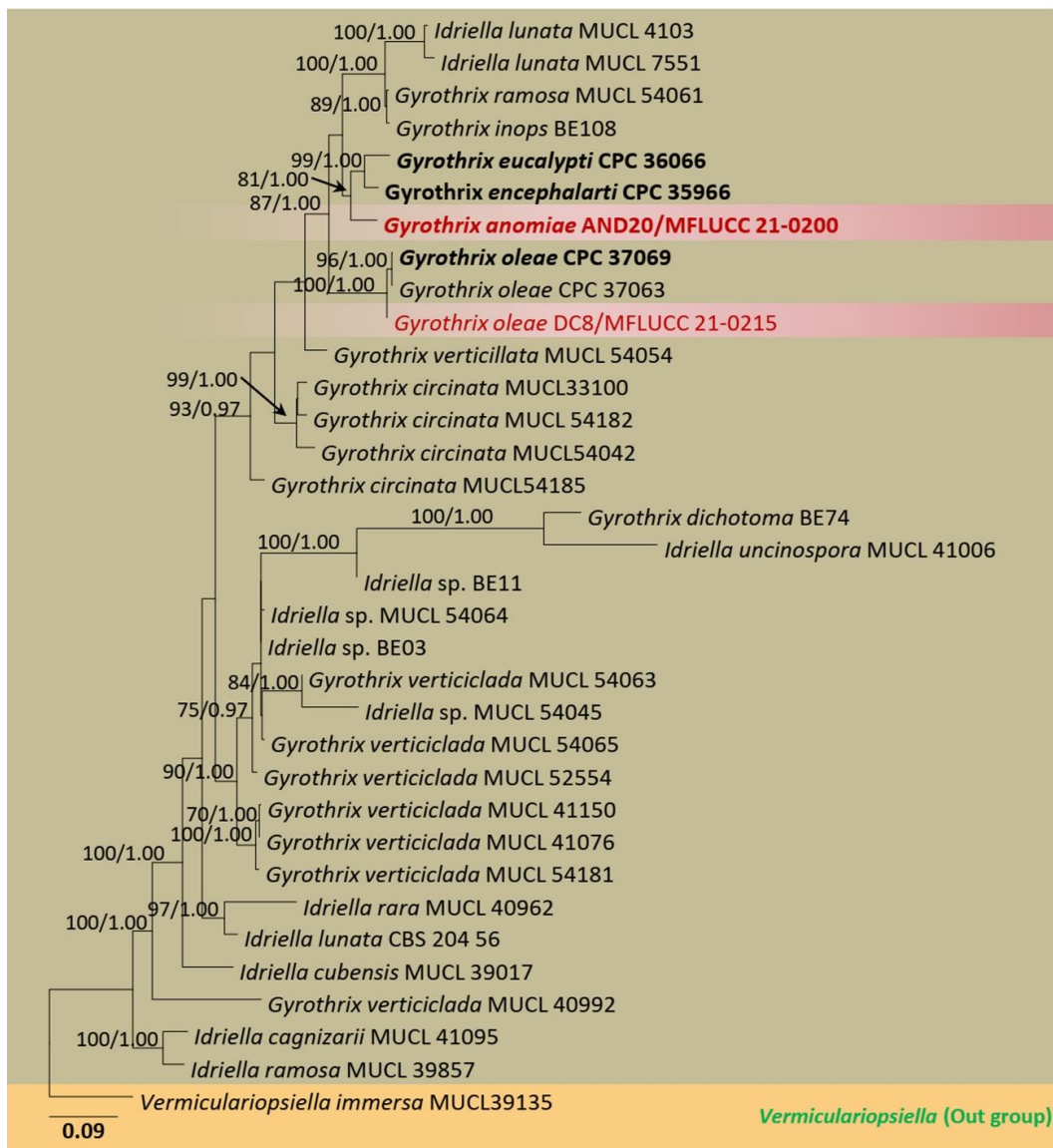
Figure 68 – Phylogram generated from maximum likelihood analysis of combined ITS, LSU and *tef1* sequence data. Related sequences of *Gyrothrix* were obtained from Becerra-Hernández et al. (2016). Thirty-four strains are included in the combined gene analyses comprising 1860 characters after alignment (500 characters for ITS, 820 characters for LSU, 540 characters for *tef1*). *Vemiculariopsiella immersa* (MUCL 39135) is used as outgroup taxon. The best RAxML tree with a final likelihood value of -15511.024364 is presented. The matrix had 922 distinct alignment patterns, with 19.30% undetermined characters or gaps. Bootstrap values for maximum likelihood equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in red and type species are in red bold. Type and ex-type strains are in **black bold**.

Discussion

This explorative study advances our understanding of morphology, phylogeny, host association, and geography of several novel and interesting microfungi associated with plants in the families of Annonaceae, Apocynaceae, and Magnoliaceae in Yunnan Province, China and northern Thailand. The patterns of fungal colonization on different host plants, *viz.*, *Anomianthus dulcis*, *Cananga odorata*, *Desmos chinensis* (Annonaceae), *Magnolia champaca*, *Magnolia garetti*, *Magnolia lilifera* (Magnoliaceae) and *Alstonia scholaris* (Apocynaceae) and their recorded fungal composition are briefly discussed as follows.
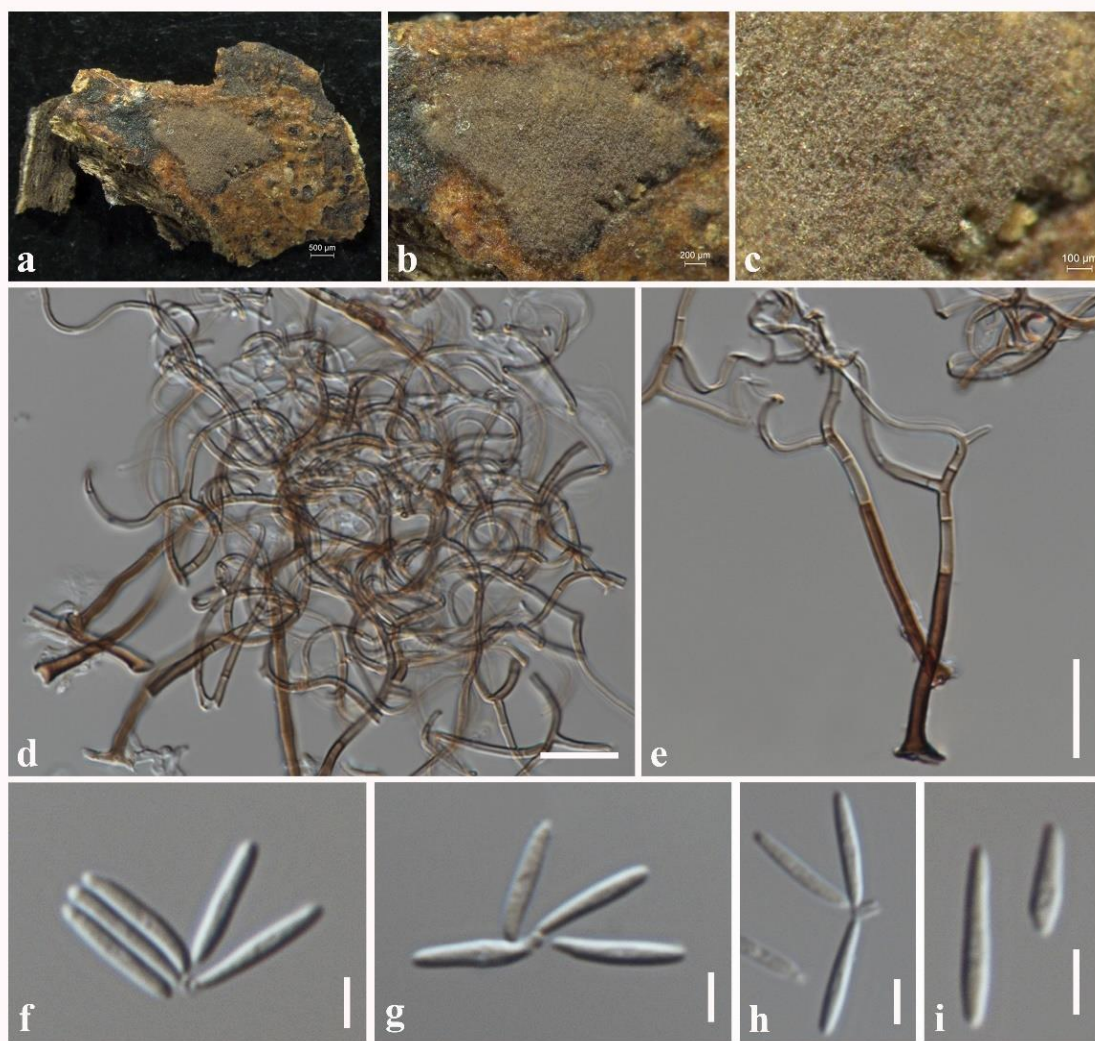
Figure 69 – *Gyrothrix anomianthi* (MFLU 21-0219, holotype). a–c Specimen. d, e Setae. f–i Conidia. Scale bars: a = 500 μm, b = 200 μm, c = 100 μm, d, e = 20 μm, f–i = 5 μm.

Magnolia species

Magnolia plants are distributed in temperate and tropical regions of the South East and East Asia. The wood is used extensively for the interior finish of houses and door panels (e.g., *Magnolia champaca*), while the bark of *Magnolia officinalis* and other species are used in China as a valuable drug (Nooteboom & Chalermglin 2009). Many species of *Magnolia* and their hybrids are cultivated as temple trees and ornamental trees in gardens and the flowers are used for decorations (Nooteboom & Chalermglin 2009).

We isolated saprobic fungi from *Magnolia* species in Yunnan, China and northern Thailand. We introduce a novel genus, *Muriformispora*, collected from China. Further, *Pseudochaetosphaeronema magnoliae* was introduced as a novel species collected from dead twigs attached to *Magnolia* species in Thailand and China. In our previous collections, *Neoroussoella magnolia* (Yuan et al. 2020), *Rhytidhysteron magnoliae* (de Silva et al. 2020) and *Lasiodiplodia magnoliae* (de Silva et al. 2019) were introduced as novel species from dead twigs attached to *Magnolia* species in Yunnan, China. In our previous collections, *Lasiodiplodia pseudotheobromae* was reported as a new host record from *Magnolia* species in China (de Silva et al. 2019). In this study, *Acrocalymma magnoliae*, *Diaporthe chiangmaiensis*, *Fuscostagonospora magnoliae*, and *Neoroussoella thailandica* are introduced as novel species from dead twigs of *Magnolia* species in Thailand. In addition, five and 15 species are reported herein as new host records in China and Thailand, respectively, and details are given in Table 6.
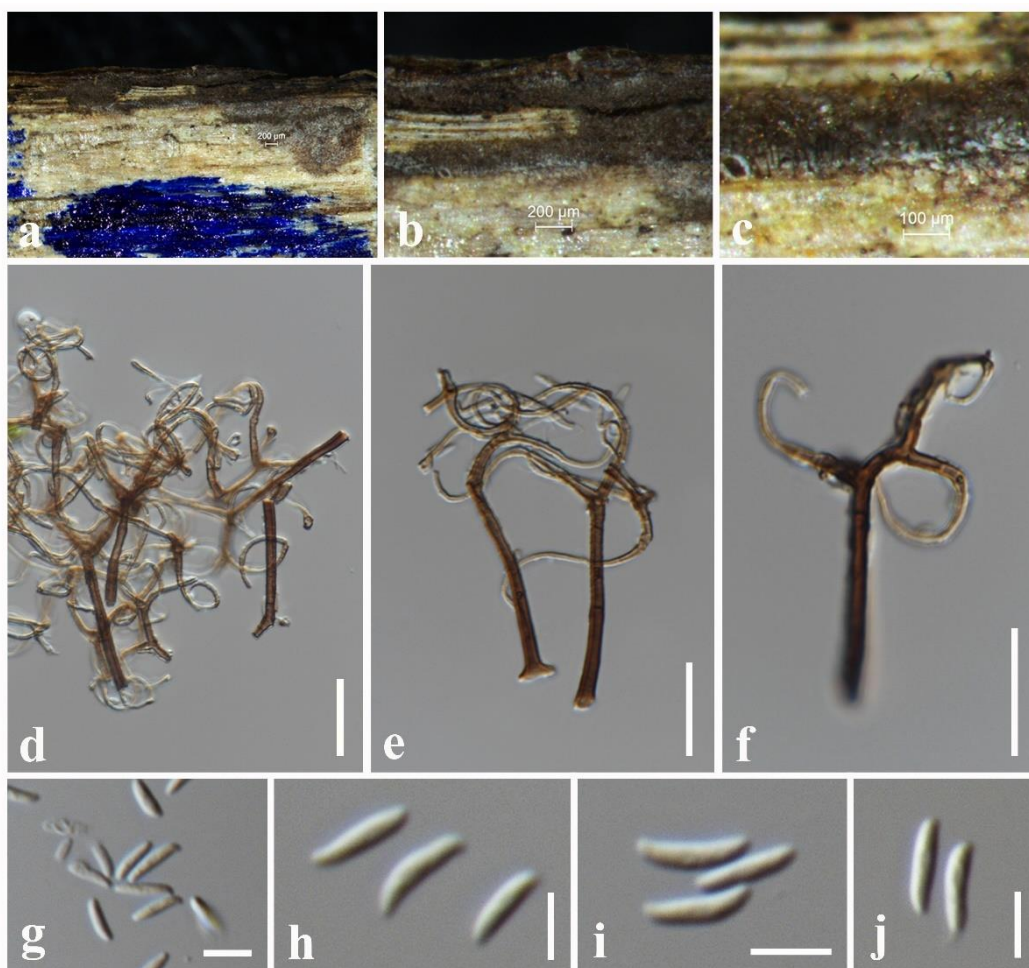
Figure 70 – *Gyrothrix oleae* (MFLU 21-0220) a–c Specimen. d–f Setae. g–j Conidia. Scale bars: b = 200 μm, c = 100 μm, d–f = 20 μm, f = 10 μm, g–j = 5 μm.

The comparison of fungal species associated with twigs of *Magnolia* species revealed that *Lasiodiplodia pseudotheobromae* and *Rhytidhysteron neorufulum* have common occurrence in China and Thailand. *Lasiodiplodia* represents one of the most well-known genera in the Botryosphaeriaceae and the species are commonly encountered as endophytes, pathogens, and saprobes (Abdollahzadeh et al. 2010, Trakunyingcharoen et al. 2015b). They have a cosmopolitan distribution especially in tropical and subtropical regions and are found on a wide range of monocotyledonous, dicotyledonous, and gymnosperm hosts (Abdollahzadeh et al. 2010). *Lasiodiplodia* species are abundant in the current collection. We report *Lasiodiplodia crassispora*, *L. exigua*, *L. ponkanicola*, *L. thailandica*, and *L. theobromae* as new host records from *Magnolia* species in Thailand while *L. pseudotheobromae* is reported from *Magnolia* species in China and Thailand. A previous study by Trakunyingcharoen et al. (2015b) isolated *L. pseudotheobromae* from *Bouea burmanica*, *Cananga odorata*, *Coffea arabica*, *Dimocarpus longan*, *Ficus racemose*, *Hevea brasiliensis*, *Juniperus chinensis*, *Mangifera indica*, *Osmanthus fragrans*, *Persea americana*, *Phyllanthus acidus*, *Psidium* sp., and *Syzygium samarangense* in Thailand. In addition, they collected *L. theobromae* from *Pinus kesiya*, *Manilkara zapota* and *Syzygium samarangense* in Thailand. In this study, we report new host records of *L. theobromae* associated with *Anomianthus dulcis* and *Magnolia champaca* in Thailand. In the present study, we isolated *L. pseudotheobromae* from *Cananga odorata*, similarly to Trakunyingcharoen et al. (2015b). In addition, we report new host records of *L. pseudotheobromae* associated with *Magnolia champaca* and *Desmos chinensis* in Thailand.

The following section discusses the fungi associated with *Anomianthus dulcis, Cananga odorata*, and *Desmos chinensis* from Annonaceae (Magnoliales). We aim to discuss fungi collected

on Annonaceae according to the plant species selection. First, fungi species collected from each plant species *viz. Anomianthus dulcis, Cananga odorata*, and *Desmos chinensis* are mentioned. Then, the exciting findings of diverse fungal species from Annonaceae plants are discussed. Further, overlapping fungi species associated with Annonaceae and Magnoliaceae plants in Thailand (Annonaceae and Magnoliaceae belong to Magnoliales) are discussed. We also provide Table 7 to list different fungi recorded from Annonaceae plants, while Table 8 for fungi associated with Annonaceae and Magnoliaceae plants.

Anomianthus dulcis

Anomianthus dulcis belongs to Annonaceae grows in many parts of Southeast Asia (Sinz et al. 1999). This plant species is widely distributed in Southern and Northeastern parts of Thailand (Ubonopas et al. 2014). Leaves of *Anomianthus dulcis* contain several phenolic compounds (Sinz et al. 1999). *Anomianthus dulcis* is used in traditional Thai medicine to treat fever (Ubonopas et al. 2014). There is no previous record of fungal species from *Anomianthus dulcis* worldwide according to the Farr & Rossman (2022). We introduce *Acrocalymma magnoliae, Gyrothrix anomianthi, Hermatomyces anomianthi, Neomassaria* sp., and *Peroneutypa anomianthi* as novel species associated with *Anomianthus dulci* in Thailand. In addition, *Pseudopithomyces chartarum, Hermatomyces sphaericus, Xenoroussoella triseptata, Lasiodiplodia theobromae, Lasiodiplodia microconidia, Pseudofusicoccum adansoniae, Dyfrolomyces thamplaensis, Setoapiospora thailandica*, and *Nectria pseudotrichia* are reported as new host records associated with *Anomianthus dulcis* in Thailand.

Table 6 Different microfungi species recorded from *Magnolia* species in China and Thailand.

Magnolia sp. (Thailand)	*Magnolia* sp. (China)	Overlapping species/genera
Acrocalymma magnoliae*	**Muriformispora magnoliae***	**Pseudochaetosphaeronema magnoliae***
Diaporthe chiangmaiensis*	**Pseudochaetosphaeronema magnoliae***	*Lasiodiplodia pseudotheobromae*
Fuscostagonospora magnoliae*	*Acrocalymma pterocarpi*	*Rhytidhysteron neorufulum*
Neoroussoella thailandica*	*Lasiodiplodia magnoliae*	
Pseudochaetosphaeronema magnoliae*	*Lasiodiplodia pseudotheobromae*	*Acrocalymma*
Acrocalymma walker	*Neoroussoella magnolia*	*Lasiodiplodia*
Angustimassarina populi	*Nigrograna thymi*	*Neoroussoella*
Aurantiascoma minimum	*Periconia pseudobyssoides*	*Pseudochaetosphaeronema*
Diaporthe musigena	*Phaeosphaeria sinensis*	*Rhytidhysteron*
Eutypella citricola	*Rhytidhysteron neorufulum*	
Lasiodiplodia theobromae	*Rhytidhysteron magnoliae*	
Lasiodiplodia thailandica		
Lasiodiplodia ponkanicola		
Lasiodiplodia crassispora		
Lasiodiplodia pseudotheobromae		
Magnibotryascoma kunmingense		
Neoroussoella entadae		
Pseudofusicoccum adansoniae		
Rhytidhysteron neorufulum		

* = New species introduced in this study

Cananga odorata

Cananga odorata, a medicinally important plant belonging to Annonaceae is native to tropical Asia (Tan et al. 2015, Toghueo et al. 2017). The plant is a valuable source for treating different diseases such as, malaria, stomach ailments, asthma, gout, and rheumatism (Tan et al. 2015). Seeds of this plant are used to treat fever, flowers are used against malaria and leaves are rubbed on the skin to treat itchiness (Toghueo et al. 2017). *Cananga odorata* flowers are well-known for their intensely sweet scent that is similar to jasmine (Tan et al. 2015). The essential oil

extracted from the flowers of this plant is widely used in various cosmetic and household products such as massage oils, moisturizing creams, perfumes, and even scented candles (Tan et al. 2015). There is no previous record of fungal species from *Cananga odorata* worldwide according to the Farr & Rossman (2022). Our study introduces *Torula canangae* as a novel species associated with *C. odorata* in Thailand. *Lasiodiplodia pseudotheobromae*, *Melomastia clematidis*, *Memnoniella ellipsoidea*, and *Periconia byssoides* are reported as a new host or geographical records associated with *Cananga odorata* in Thailand.

Table 7 Different microfungi species recorded in this study from Annonaceae (Order Magnoliales) species in Thailand.

Annonaceae (Magnoliales)			
Anomianthus dulcis	*Cananga odorata*	*Desmos chinensis*	Overlapping species/genera
Acrocalymma magnoliae* *Hermatomyces anomianthi**	*Torula canangae**	*Gyrothrix oleae* *Lasiodiplodia pseudotheobromae*	*Lasiodiplodia*
Neomassaria thailandica*	*Lasiodiplodia pseudotheobromae*	*Xenoroussoella triseptata*	
Peroneutypa anomianthi*	*Melomastia clematidis*		
Gyrothrix anomianthi*	*Memnoniella ellipsoidea*		
Pseudopithomyces chartarum	*Periconia byssoides*		
Hermatomyces sphaericus			
Xenoroussoella triseptata			
Lasiodiplodia theobromae			
Lasiodiplodia microconidia			
Pseudofusicoccum adansoniae			
Dyfrolomyces thamplaensis			
Setoapiospora thailandica			
Nectria pseudotrichia			

* = New species introduced in this study

Desmos chinensis

Desmos chinensis is the only species of *Desmos* (Annonaceae) that is widely distributed in Bangladesh, Bhutan, Cambodia, China, India, Indonesia, Laos, Malaysia, Myanmar, Nepal, Philippines, Singapore, Thailand and Vietnam (Nikmah et al. 2021). In traditional medicine, *D. chinensis* is used to cure diseases such as dysentery, vertigo, fever, and parturition, especially in China, Thailand, and Peninsular Malaysia (Lemmens 2003). Leaf extracts of *D. chinensis* have antimicrobial activity against human pathogens, including bacteria, yeast and dermatophytic fungi (Kummee & Intaraksa 2008). In addition, *D. chinensis* provides habitats for butterflies *viz.* *Drupadia ravindra*, *Graphium Agamemnon* and *G. doson*, beetle (*Amystrops*) and oriental fruit fly *Bactrocera dorsalis* (Nikmah et al. 2021). In the current investigation, *Lasiodiplodia pseudotheobromae* and *Xenoroussoella triseptata* are recorded as new host records from *D. chinensis* while *Gyrothrix oleae* is reported herein as a new host record from *D. chinensis* and the first geographical occurrence in Thailand.

This study reports fungi associated with plant species *Anomianthus dulcis, Cananga odorata* and *Desmos chinensis* belonging to Annonaceae. *Lasiodiplodia* is one of the commonly recorded fungal genera in the current study. *Lasiodiplodia pseudotheobromae* is reported from *C. odorata* and *D. chinensis* while *L. theobromae* is reported from *A. dulcis*. In addition, *Xenoroussoella triseptata* is reported from *A. dulcis* and *D. chinensis*. *Xenoroussoella* in Roussoellaceae was introduced by Mapook et al. (2020). The genus comprises single species, *X. triseptata* and is only known from dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020). In this study, the saprobic fungal collection of *X. triseptata* expand the host range to *A. dulcis* and

D. chinensis in Annonaceae from Thailand. *Gyrothrix* species are another interesting fungal group associated with Annonaceae that was found in this study. These saprobic and hyphomycetous species are considered as a polyphyletic genus in Xylariales (Sordariomycetes) (Becerra-Hernández et al. 2016). In this study, we report two *Gyrothrix* species associated with Annonaceae. *Gyrothrix anomianthi* is introduced as a novel species from *A. dulcis* while *G. oleae* is reported as a new host and a geographical record from *D. chinensis* in Thailand.

There are four overlapping species and three overlapping genera associated with Magnoliaceae and Annonaceae (Order Magnoliales) plant species in Thailand (Table 8). *Acrocalymma*, *Lasiodiplodia* and *Pseudofusicoccum* genera were recorded from Magnoliaceae and Annonaceae plants. *Acrocalymma* species have mainly been isolated from terrestrial habitats, with a few reported from aquatic habitats (Mortimer et al. 2021). These species can be endophytic, pathogenic and saprobic (Mortimer et al. 2021). Among eleven species recorded in Index Fungorum (2022), two were introduced in Thailand. *Acrocalymma aquatica* was isolated from submerged wood and *A. pterocarpi* was isolated from *Pterocarpus indicus* in Thailand (Table 2). This study introduces a novel species, *Acrocalymma magnoliae* from *Magnolia* sp. (Magnoliaceae) and *A. dulcis* (Annonaceae). Further we reported a new host record of *A. walkeri* from *Magnolia* sp. in Thailand. With these new findings, the current investigation expands the host range of *Acrocalymma* species in Thailand to *Magnolia* sp. and *A. dulcis*.

In addition, two genera of Botryosphaeriales reported in this study, namely *Pseudofusicoccum* and *Lasiodiplodia* show common occurrence among Magnoliaceae and Annonaceae plant species. *Lasiodiplodia pseudotheobromae* is recorded from *C. odorata* and *D. chinensis* (Annonaceae) and *Magnolia champaca*. Similarly, *L. theobromae* was recorded from *A. dulcis* and *Magnolia champaca*. *Pseudofusicoccum* is widely distributed and found commonly on various hosts' stems, twigs, branches and leaves. They are endophytes, saprobes or plant pathogens (Doilom et al. 2015, Jami et al. 2018, Senwanna et al. 2020). *Pseudofusicoccum adansoniae* has been recorded from many plant species in Thailand *viz. Cassia fistula*, *Dimocarpus longan*, *Senna siamea*, (Trakunyingcharoen et al. 2015b), *Pandanus* sp. (Tibpromma et al. 2018b), *Tectona grandis* (Doilom et al. 2015), *Hevea brasiliensis* (Trakunyingcharoen et al. 2015a, Senwanna et al. 2020). This study reports *Pseudofusicoccum adansoniae* from *Anomianthus dulcis* and *Magnolia lilifera* for the first time in Thailand.

Finally, we discuss fungal species collected from *Alstonia scholaris* (Apocynaceae, Gentianales). According to the plant species selection, *Alstonia scholaris* belongs to a different order than Magnoliales. The previous section mentioned different fungi collected from Annonaceae and Magnoliaceae plants (Magnoliales). This section discusses fungi collected from *Alstonia scholaris* and overlapping taxa between *Alstonia scholaris* and *Magnolia* species.

Alstonia scholaris

Alstonia scholaris is considered an evergreen tropical tree species native to Southeast Asia (Khyade et al. 2014). *Alstonia scholaris* belongs to Apocynaceae and grows widely in deciduous and evergreen forests in the Asia-Pacific region (Arulmozhi et al. 2007). The timber of the plant is used for light indoor construction purposes and pulp and paper production (Arulmozhi et al. 2007). The wood of this plant has traditionally been utilized for school black-boards, that is why the species epithet '*scholaris*' has been used (Arulmozhi et al. 2007). Leaves of this plant were used in traditional Chinese medicine to treat chronic respiratory diseases (Shang et al. 2010). In our fungal collection, *Diaporthe chiangmaiensis* and *Neomassaria alstoniae* are introduced as novel species in Thailand. In addition, *Diaporthe pterocarpi*, *Hermatomyces sphaericus* and *Pseudofusicoccum adansoniae* are reported as new host records in Thailand while *Amphisphaeria micheliae* is recorded as a new host record of *Alstonia scholaris* and a new geographical record to Thailand.

In this study, two overlapping fungal species belonging to two genera reported between Apocynaceae (Gentianales) and Magnoliaceae (Magnoliales) plants in Thailand are reported (Table 9). *Diaporthe chiangmaiensis* and *Pseudofusicoccum adansoniae* are reported from Apocynaceae and Magnoliaceae. *Diaporthe chiangmaiensis* is introduced as a novel species from *Magnolia*

lilifera in Thailand. Further we establish the sexual-asexual connection of *D. chiangmaiensis* as the sexual morph from *Magnolia lilifera* and the asexual morph from *Alstonia scholaris*. Furthermore, *Pseudofusicoccum adansoniae* is observed from *Anomianthus dulcis*, *Magnolia lilifera* and *Alstonia scholaris* in the current investigation. This study reveals that *Pseudofusicoccum adansoniae* inhabits diverse plant species, including three new host association of *Anomianthus dulcis*, *Magnolia lilifera* and *Alstonia scholaris* for the first time in Thailand. Our study shows that *Pseudofusicoccum adansoniae* is a common taxon associated with Magnoliaceae, Annonaceae and Apocynaceae plants in Thailand. In addition, Table 10 lists different fungi species associated with Annonaceae and Apocynaceae plants in Thailand.

Table 8 Different microfungi species recorded in this study from Magnoliaceae and Annonaceae (Order Magnoliales) species in Thailand.

Magnoliaceae (Magnoliales)	Annonaceae (Magnoliales)			Overlap species/genera
Magnolia sp.	*Anomianthus dulcis*	*Cananga odorata*	*Desmos chinensis*	
Acrocalymma magnoliae*	*Acrocalymma magnoliae**	*Torula canangae**	*Gyrothrix oleae*	*Acrocalymma magnoliae**
Diaporthe chiangmaiensis*	*Hermatomyces anomianthi* *		*Lasiodiplodia pseudotheobromae*	*Lasiodiplodia pseudotheobromae*
Fuscostagonospora magnoliae*	*Neomassaria thailandica**	*Lasiodiplodia pseudotheobromae*	*Xenoroussoella triseptata*	*Pseudofusicoccum adansoniae*
				Lasiodiplodia theobromae
Neoroussoella thailandica*	*Peroneutypa anomianthi**	*Melomastia clematidis*		
	Gyrothrix anomianthi*	*Memnoniella ellipsoidea*		*Acrocalymma*
Acrocalymma walker		*Periconia byssoides*		*Lasiodiplodia*
Angustimassarina populi	*Pseudopithomyces chartarum*			*Pseudofusicoccum*
Aurantiascoma minimum	*Hermatomyces sphaericus*			
Diaporthe musigena	*Xenoroussoella triseptata*			
Eutypella citricola	*Lasiodiplodia theobromae*			
Lasiodiplodia theobromae	*Lasiodiplodia microconidia*			
Lasiodiplodia thailandica	*Pseudofusicoccum adansoniae*			
Lasiodiplodia ponkanicola	*Dyfrolomyces thamplaensis*			
Lasiodiplodia crassispora	*Setoapiospora thailandica*			
Lasiodiplodia pseudotheobromae	*Nectria pseudotrichia*			
Magnibotryascoma kunmingense				
Neoroussoella entadae				
Pseudofusicoccum adansoniae				
Rhytidhysteron neorufulum				

* = New species introduced in this study

Table 9 Different microfungi species recorded in this study from Apocynaceae (Order Gentianales) and Magnoliaceae (Order Magnoliales) species in Thailand.

Apocynaceae (Gentianales)	Magnoliaceae (Magnoliales)	Overlapping taxa
Alstonia scholaris	*Magnolia* sp.	
*Neomassaria alstoniae**	*Acrocalymma magnoliae**	*Diaporthe chiangmaiensis**
*Diaporthe chiangmaiensis**	*Diaporthe chiangmaiensis**	*Pseudofusicoccum adansoniae*
	*Fuscostagonospora magnoliae**	
Hermatomyces sphaericus	*Neoroussoella thailandica**	*Diaporthe*
Diaporthe pterocarpi		*Pseudofusicoccum*
Pseudofusicoccum adansoniae	*Acrocalymma walker*	
Amphisphaeria micheliae	*Angustimassarina populi*	
	Aurantiascoma minimum	
	Diaporthe musigena	
	Eutypella citricola	
	Lasiodiplodia theobromae	
	Lasiodiplodia thailandica	
	Lasiodiplodia ponkanicola	
	Lasiodiplodia crassispora	
	Lasiodiplodia pseudotheobromae	
	Magnibotryascoma kunmingense	
	Neoroussoella entadae	
	Pseudofusicoccum adansoniae	
	Rhytidhysteron neorufulum	

* = New species introduced in this study.

Different fungal colonization patterns in plant hosts in this study show the number of taxa (species/genera) restricted to *Magnolia* species in China or Thailand is more significant than the number of overlapping taxa (species/genera) associated with *Magnolia* species in China and Thailand. The fungal taxa isolated in the current study show that the number of taxa reported only from Magnoliaceae or Annonaceae (Order Magnoliales) is more significant than the number of overlapping taxa reported from Magnoliaceae and Annonaceae. Similarly, the number of taxa reported only from Magnoliaceae (Order Magnoliales) or Apocynaceae (Order Gentianales) is more significant than the number overlapping taxa reported from Magnoliaceae and Apocynaceae. Furthermore, the number of taxa reported only from Annonaceae (Order Magnoliales) or Apocynaceae (Order Gentianales) is more significant than the number of overlapping taxa reported from Annonaceae and Apocynaceae.

Host specificity of saprobes

Some saprobic fungi in the current study inhabit single host plant species or families. However, it was not confirmed that these fungi only occur on that host. The term 'host-specificity' was proposed by plant pathologists to describe the relationship between hosts and fungi (Zhou & Hyde 2001). Host-specificity is maintained by both the parasite genotype and host genotype, influencing the outcome of the relationship (Zhou & Hyde 2001). Some scientists use host-specificity to describe a specific relationship between live host plants and non-pathogenic endophytes (Guo et al. 2000), as well as beneficial mycorrhizal symbionts (Zhou & Hyde 2001). Some endophytes are considered as host-specific, particularly, clavicipitaceous endophytes that reside in grasses (Zhou & Hyde 2001). *Mycosphaerella* spp. *Venturia* spp. are assumed to be host-specific in Fraxinus excelsior (Schlegel et al. 2018). However, host-specificity might not be suitable for saprobes unless they have a symbiotic phase (e.g., endophytes) during other parts of their life cycle (Zhou & Hyde 2001). Therefore, host-exclusivity and host-recurrence are used to describe saprobe-plant interactions instead of host-specificity. Zhou & Hyde (2001) defined host-exclusivity as the exclusive occurrence of a strictly saprobic fungus on a particular host or a restricted range of related host plants. They defined host-recurrence as the frequent or predominant occurrence of a symbiotic, parasitic or saprobic fungus on a particular host or a range of hosts,

however, the fungus also occurs infrequently on other host plants in the same habitat. Similarly, Mukwevho et al. (2020) followed Zhou & Hyde (2001) to explain host-exclusivity and host-recurrence in saprobic fungi. Host-exclusivity is considered as growing on material that originated from a particular host or a restricted range of related hosts, while host-recurrent is defined as growing predominantly on material originating from a particular host, but can also occur on a material that originates from other hosts in the same habitat (Mukwevho et al. 2020).

Table 10 Different microfungi species recorded in this study from Apocynaceae (Order Gentianales) and Annonaceae (Order Magnoliales) plants in Thailand.

Apocynaceae (Gentianales)	Annonaceae (Magnoliales)			Overlap taxa
Alstonia scholaris	*Anomianthus dulcis*	*Cananga odorata*	*Desmos chinensis*	
Neomassaria alstoniae*	*Acrocalymma magnoliae**	*Torula canangae**	*Gyrothrix oleae*	*Pseudofusicoccum adansoniae*
Diaporthe chiangmaiensis*	*Hermatomyces anomianthi* *		*Lasiodiplodia pseudotheobromae*	
	Neomassaria thailandica*		*Xenoroussoella triseptata*	*Hermatomyces*
Hermatomyces sphaericus	*Peroneutypa anomianthi**	*Lasiodiplodia pseudotheobromae*		*Neomassaria*
Diaporthe pterocarpi	*Gyrothrix anomianthi**	*Melomastia clematidis*		*Pseudofusicoccum*
Pseudofusicoccum adansoniae		*Memnoniella ellipsoidea*		
	Pseudopithomyces chartarum	*Periconia byssoides*		
	Hermatomyces sphaericus			
	Xenoroussoella triseptata			
	Lasiodiplodia theobromae			
	Lasiodiplodia microconidia			
	Pseudofusicoccum adansoniae			
	Dyfrolomyces thamplaensis			
	Setoapiospora thailandica			
	Nectria pseudotrichia			

* = New species introduced in this study.

Our current and previous investigations found some novel fungi *viz. Fuscostagonospora magnoliae* and *Neoroussoella thailandica* in Thailand and *Muriformispora magnoliae*, *Neoroussoella magnolia* (Yuan et al. 2020), and *Rhytidhysteron magnoliae* (de Silva et al. 2020) in China, are only from *Magnolia* species. In addition, a few other new fungal species namely, *Anomianthus dulcis,* namely, *Gyrothrix anomianthi*, *Hermatomyces anomianthi* and *Neomassaria thailandica* were described only from *Anomianthus dulcis* in Thailand. Two new species, *Torula canangae* and *Neomassaria alstoniae* were introduced only from *Cananga odorata* and *Alstonia scholaris* respectively in Thailand. In contrast, a novel species, *Acrocalymma magnoliae* was isolated from both *Magnolia* sp. (Magnoliaceae) and *Anomianthus dulcis* (Annonaceae). Interestingly, sexual and asexual morphs of a new species, *Diaporthe chiangmaiensis* was identified from *Magnolia lilifera* (Magnoliaceae) and *Alstonia scholaris* (Apocynaceae)

respectively. Abdollahzadeh et al. (2010) argued that a recently introduced fungal species' narrow host range reflects a lower sampling than the actual representation of host range. It is therefore, suggested to carry out future investigations to identify microfungi from similar host species studied here as well as different host species to understand host-exclusivity or host-recurrence. In a previous study by Mukwevho et al. (2020), host-exclusivity has been observed between saprobic *Knoxdaviesia* and *Sporothrix* species and *Protea* plant species. For example, *Knoxdaviesia proteae* is only known from *Protea repens* while the closely related *K. capensis* is found on numerous *Protea* species including *P. neriifolia*. *Sporothrix phasma* inhabits all *Protea* species that host *K. capensis*, except *P. repens* (Mukwevho et al. 2020). This saprobe-host association is suggested that host chemistry might play a significant role in determining the level of host exclusivity of these fungi (Roets et al. 2012, Mukwevho et al. 2020). It is challenging to describe host-exclusivity and/or host-recurrence for saprobes, however, it often links to differences in substrate nutrient levels and/or physical structure. These differences of substrates might cause variability in the competitive abilities of saprobic fungi when colonizing different host material and ultimately result in the co-existence and diversification of fungi (Kubicek et al. 2014, Mukwevho et al. 2020). Further, the resource availability and differences in competitive abilities during succession of different fungal species on the same substrate, can result in high fungal diversity (Mukwevho et al. 2020).

Saprobic fungal assemblages in forest ecosystems

The degree of specialization of microfungi in particular plant families, genera or species can be determined by a combination of factors such as intrinsic (e.g., tree species properties, stand structure of forest) and environmental factors (e.g., temperature, moisture, pH) that are discussed in the following section.

Plants and decomposer communities are interdependent subsystems that work mutually for their long-term maintenance (Santana et al. 2005). Plants produce carbon and nutrients and decomposers release mineral nutrients through enzymatic degradation by a wide range of extracellular enzymes, which is critical for plant growth (Santana et al. 2005, Pioli et al. 2018). During decomposition, the fungal community exposes to succession, which is controlled by abiotic and biotic factors (Pioli et al. 2018). Abiotic factors of the environment, for example, pH and soil moisture, appear to play a significant role in determining the composition of a saprobic community during decomposition. Generally, fungi show efficient decomposition at lower pH and relatively dry conditions (Rousk et al. 2010, Yuste et al. 2011, van der Wal et al. 2013). Exposure to sunlight causes temperature variations and the water availability in the forests. Fluctuating microclimate, in particular, temperature affect the diversity of fungal species because different fungal species have different sensitivity to sunlight exposure (Bässler et al. 2010). Silviculture management practices such as logging opens the canopy and increases sunlight exposure, as well as other microclimate changes negatively impact the diversity of wood-decaying fungi in forests (Bässler et al. 2010).

The fungal assemblages of forest ecosystems are significantly correlated with the time since last utilization and the compositional heterogeneity of the stand of forest ecosystems. The stand structure of forest ecosystems in managed versus unmanaged forests, especially in temperate and boreal regions, is also responsible for the fungal community (Pioli et al. 2018). Forest stands that develop to high structural and compositional complexity levels provide multiple niches for establishing diverse fungal taxa. Kubart et al. (2016) confirmed that fungal community structure and OTU richness are greatly influenced by stand age. This indicates that the old forest stands support specific fungal communities (Pioli et al. 2018). In addition, forests that have not been subjected to human exploitation represent the highest level of naturalness, with their large volumes of deadwood hosting the richest and most diverse mycoflora. These types of natural forests are also characterized by different degrees of structural heterogeneity as a function of forest type, time since last utilization, climatic conditions, and disturbance regimes (Lombardi et al. 2012, Pioli et al. 2018). On the other hand, managed forests host significantly fewer wood-inhabiting fungi. The

reduced availability of deadwood is the main reason for the loss of fungal biodiversity (Ylisirniö et al. 2012).

Effect of physical and chemical properties of wood for fungal assemblages

Wood from various plant species has different chemical compositions and physical structures, which provide alternative microhabitats for various fungal taxa (Kögel-Knabner 2002, Pioli et al. 2018).

The physical properties of a substrate are essential factors in determining the abundance and diversity of wood decay fungi (Bässler et al. 2010). Wood decay fungal communities on fallen twigs and small branches differ from those on bulky woody debris because these two types of substrates differ in their microclimate. In particular, small twigs desiccate more rapidly than bulky woody debris (Norden et al. 2004, Bässler et al. 2010). Twigs and branches with a small diameter are considered to be important for the occurrence of common species. Bässler et al. (2010) discovered that woody debris with a large diameter had a high abundance and species richness of fungi. Biological explanations for this would be that large logs provide more niches over a longer period of time than small logs and can support a greater mycelial biomass (Norden et al. 2004). Large logs with a long infection history might be crucial for the establishing certain specialized fungal species (Bässler et al. 2010). Bässler et al. (2010) confirmed this by using a species indicator analysis and showed that more species are specialized on large logs than on small logs.

The lignin content of the substrate fluctuates according to the forest tree species and wood decomposition stage (Hoppe et al. 2015, Arnstadt et al. 2016). The high lignin content of the substrate will negatively affect wood decay as lignin is relatively higher than cellulose or hemicelluloses (Kahl et al. 2017). Only a few fungal species, white-rot fungi, degrade recalcitrant polymers by secreting a set of extracellular ligninolytic enzymes (Arnstadt et al. 2016, Pioli et al. 2018). Lignin acts as a barrier to restrict the penetration of enzyme molecules into the lignocellulose complex and thereby slowing down the wood decomposition (Kahl et al. 2017). Fungal communities differ according to the lignin content of the substrate (Pioli et al. 2018). In contrast to that sulfur showed the most potent effect on the decay rate by facilitating fungal growth in wood. Sulfur is essential for two amino acids and various biochemical cofactors for fungal growth and hence accelerates wood decay (Kahl et al. 2017). The concentrations of phenols and organic extractives show a negative correlation with the decay rate because these compounds are able to inhibit fungal growth (Gierlinger et al. 2004). Different fungal taxa especially ascomycetes, have specific decaying abilities, ranging from the breakdown of simple sugars (sugar fungi) to the degradation of the lignocellulose complex (van der Wal et al. 2013, Pioli et al. 2018). In particular, white-rot fungi (Agaricomycotina, Basidiomycota) decompose lignin, cellulose and hemicellulose while Xylariales fungi (Ascomycota) decompose lignin (Osono et al. 2011, Floudas et al. 2012, van der Wal et al. 2013). Another group of fungi known as brown-rot fungi have the ability to modify lignin, thereby producing the primary energy resource for litter- and wood-degrading fungi (van der Wal et al. 2013). In addition, cellulolytic ascomycetes contribute significantly to the decomposition of lignin-rich organic matter, as thin perforation hyphae of these fungi can reach cellulose-rich layers in woody cell walls (Schmidt 2006).

Role of fungal endophytes in decomposition

Apart from the dead plant materials, living plants acting as a reservoir for endophytes and symbionts which also have the potential to become decomposers after tree death (Pioli et al. 2018). Fungi show a variety of lifestyles ranging from biotrophy to necrotrophy and ultimately to saprotrophy (de Silva et al. 2016). Previous studies indicated that endophytes switch their nutritional mode from saprotrophic to parasitic or vice versa (Promputtha et al. 2007, 2010). Promputtha et al. (2010) examined the capability to produce specific degrading enzymes by endophyte and saprobe (same species) isolated from *Magnolia liliifera* in Thailand. These studies concluded that endophytes and saprobes (same species) produced the same degrading enzymes. They further explained that endophytes with capability to produce degrading enzymes are be able

to act as litter decomposers in a later stage, but they do not decompose living host tissue. This implies the degrading enzymes play a crucial role in the transition of endophytes to saprobes (Promputtha et al. 2010).

In this study, we identified two life-styles of *Diaporthe chiangmaiensis*, endophytic lifestyle from healthy leaves and saprobic lifestyle from dead twigs *Magnolia lilifera*. This indicated that endophytic *D. chiangmaiensis* might have the potential to change the life-style to be saprobic when plant tissues senescence occurs. It might be possible to find saprobic life-style of *D. chiangmaiensis* on dead leaves and endophytic life-style on asymptomatic twigs in the same plant. Another possibility is that endophytic *Diaporthe chiangmaiensis* live inside asymptomatic leaves might switch their life-style to saprobe during leaf senescence and then disperse to colonize on dead twigs. Further studies are needed to investigate fungi from different substrates of same host plant to identify different lifestyles of a particular fungus. *Lasiodiplodia pseudotheobromae* also exhibits different life-styles in nature as endophytes, pathogens and saprobes (Doilom et al. 2015, Tennakoon et al. 2016). Interestingly, in one of our previous investigations, we isolated endophytic (from healthy leaves) and saprobic (from dead twigs) life-styles of *L. pseudotheobromae* in Xishuangbanna, Yunnan Province, China (de Silva et al. 2019). This indicated that endophytic *L. pseudotheobromae* might be able to switch their lifestyle during plant tissues senescence. Further, we identified endophytic and saprobic strains of *Neopestalotiopsis saprophyta* from fresh leaves and dead leaves of *Magnolia candolii* respectively, in Yunnan, China (de Silva et al. 2021). This is the first report of endophytic *N. saprophyta* on asymptomatic leaves of *Magnolia candolii* and we identified its saprobic counterparts from dead leaves of same plant host. This also confirms that *N. saprophyta* occupies the same substrate successfully as an endophyte in the healthy plant tissues (leaves) and a saprobe when plant tissues senescence (leaves). These examples imply that some of the fungal species colonizing as endophytes in living plant tissues can switch their trophic strategy and behave as saprotrophs when microhabitat conditions become suitable.

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