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ARTICLE

Taxonomy and phylogeny of ascomycetes associated with selected economically important monocotyledons in China and Thailand

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Abstract

Monocotyledons are one of the important groups of flowering plants that include approximately 60,000 species with economically important crops including coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), and rice (*Oryza sativa*). Studies on these hosts are mainly focused on pathogenic fungi; only a few saprobic species have been reported. This study investigated the saprobic ascomycetes associated with coconut, pineapple, and rice in southern China and northern Thailand. Approximately 200 specimens were collected, and 100 fungal strains were isolated and identified to 77 species based on phylogenetic approaches and morphological characteristics. Among the 77 species, 29, 38, and 12 were found on coconut, pineapple, and rice, respectively, distributed in *Dothideomycetes* (41), *Eurotiomycetes* (one), and *Sordariomycetes* (35). *Pseudomycoleptodiscus*, *Pseudosaprodesmium Pseudosetoseptoria*, *Pseudostriatosphaeria* and *Pseudoteichospora* are introduced as new genera and *Anthostomella cocois*, *Apiospora ananas*, *Chromolaenicola ananasi*, *Epicoccum yunnanensis*, *Exserohilum ananas*, *Hypoxylon cocois*,

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Lasiodiplodia ananasi, *Muyocopron chiangraiense*, *Myrmecridium yunnanense*, *Occultitheca ananasi*, *Periconia chiangraiensis*, *Placidiopsis ananasi*, *Pseudomycoleptodiscus ananas*, *Pseudosaprodesmium cocois*, *Pseudosetoseptoria oryzae*, *Pseudostriatosphaeria chiangraiensis*, *Pseudoteichospora thailandensis*, *Savoryella chiangraiensis*, *Savoryella cocois*, and *Tetraploa oryzae* are introduced as novel species. In addition, 51 species are reported as new hosts or geographical records, and six species are reported as new collections. *Pseudopithomyces pandanicola* and *P. palmicola* are synonymized under *P. chartarum*, *P. diversisporus* synonymized under *P. atro-olivaceus* based on phylogenetic analyses and morphological characteristics. Moreover, comprehensive checklists of fungi associated with coconut, pineapple, and rice are also provided.

Keywords – 25 new taxa – Ascomycota – *Dothideomycetes* – *Pseudomycoleptodiscus* – *Pseudosaprodesmium* – *Pseudosetoseptoria* – *Pseudostriatosphaeria* – *Pseudoteichospora* – *Sordariomycetes* – Taxonomy

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The numbers of taxa in this study are organized following the outline of Ascomycota (Wijayawardene et al. 2022) and updated using recent publications.

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Subclass *Chaetothyriomycetidae* Doweld
Verrucariales Mattick ex D. Hawksw. & O.E. Erikss.
Verrucariaceae Zenker
1. *Placidiopsis ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Class *Dothideomycetes* O.E. Erikss. & Winka
Subclass *Dothideomycetidae* P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker

Muyocopronales Mapook, Boonmee & K.D. Hyde
Muyocopronaceae K.D. Hyde
2. *Muyocopron chiangraiense* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
3. *Pseudomycoleptodiscus* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.
4. *Pseudomycoleptodiscus ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Subclass *Pleosporomycetidae* C.L. Schoch et al.
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Hysteriaceae Chevall.
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Dictyosporiaceae Boonmee & K.D. Hyde
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Didymellaceae Gruyter
7. *Epicoccum italicum* Qian Chen, Crous & L. Cai, Stud. Mycol. 87: 144 (2017), new host and geographical record.
8. *Epicoccum yunnanensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

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12. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, Fungal Divers. 75: 66 (2015), new collection.
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Hermatomycetaceae Locq.
14. *Hermatomyces sphaericus* (Sacc.) S. Hughes, Mycol. Pap. 50: 100 (1953), new host record.

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde
15. *Pseudosetoseptoria* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.
16. *Pseudosetoseptoria oryzae* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

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Paradictyoarthriniaceae Doilom, Ariyaw., Bhat & K.D. Hyde
18. *Paradictyoarthrinium diffractum* Matsush., Matsush. Mycol. Mem. 9: 18 (1996), new host and geographical record.

Periconiaceae Nann.
19. *Periconia chiangraiensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
20. *Periconia delonicis* Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 95 (2019), new host record.
21. *Periconia digitata* (Cooke) Sacc., Syll. Fung., 4: 274 (1886), new host and geographical record.

Phaeosphaeriaceae M.E. Barr
22. *Ophiosphaerella agrostidis* Dern., M.P.S. Câmara, N.R. O'Neill, Berkum & M.E. Palm. Mycologia 92(2): 320 (2000), new host record.
23. *Phaeosphaeria musae* Sawada, Special Publication College of Agriculture, National Taiwan University 8: 66 (1959), new host record.

Pleosporaceae Nitschke
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26. *Curvularia elliptiformis* M. Raza, K.D. Hyde & L. Cai, Fungal Divers. 99: 51 (2019), new host and geographical record.
27. *Curvularia verruculosa* Tandon & Bilgrami ex M.B. Ellis, Mycological Papers 106: 20 (1966), new host record.
28. *Exserohilum ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

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34. ***Tetraploa oryzae*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
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Botryosphaeriales C.L. Schoch et al.
Botryosphaeriaceae Theiss. & P. Syd.
37. ***Lasiodiplodia ananasi*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
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39. ***Lasiodiplodia mahajangana*** Begoude, Jol. Roux & Slippers, Mycol. Prog. 9(1): 110 (2010), new host record.
40. ***Lasiodiplodia pseudotheobromae*** A.J.L. Phillips, A. Alves & Crous, Fungal Divers. 28: 8 (2008), new host record.
41. ***Lasiodiplodia theobromae*** (Pat.) Griffon & Maubl., Bull. trimest. Soc. Mycol. Fr. 25: 57 (1909), new host and geographical record.
42. ***Neoscytalidium dimidiatum*** (Penz.) Crous & Slippers, Stud. Mycol. 55: 244 (2006), new host record.
43. ***Neodeightonia rattanica*** S. Konta & K.D. Hyde, in Konta et al., Mycosphere 7(7): 953 (2016), new host record.
44. ***Neodeightonia phoenicum*** A.J.L. Phillips & Crous, Persoonia 21: 43 (2008), new host and geographical record.

Phyllostictaceae Fr.
45. ***Phyllosticta capitalensis*** Henn., Hedwigia 48: 13. (1908), new host record.

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51. ***Ochronectria thailandica*** Q.J. Shang & K.D. Hyde, Fungal Divers. 78, 1–237 (2016), new host record.
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54. ***Volutella delonicis*** R.H. Perera, E.B.G. Jones & K.D. Hyde, Mycosphere 11 (1): 2164 (2020), new host record.

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56. ***Brevistachys subsimplex*** (Cooke) L. Lombard & Crous, Persoonia 36: 185 (2016), new host record.
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Subclass ***Savoryellomycetidae*** Hongsanan, K.D. Hyde & Maharachch.
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Pleurotheciaceae Réblová & Seifert
58. ***Dematipyriforma aquilariae*** L.Y. Sun, H.Y. Li, X. Sun & L.D. Guo, Cryptog. Mycol. 38(3): 345 (2017), new host and geographical record.

59. ***Pseudosaprodesmium*** X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.
60. ***Pseudosaprodesmium cocois*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
61. ***Rhexoacrodictys erecta*** (Ellis & Everh.) W.A. Baker & Morgan-Jones, Mycotaxon 82: 99 (2002), new host and geographical record.

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones
Savoryellaceae Jaklitsch & Réblová
62. ***Savoryella cocois*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
63. ***Savoryella chiangraiensis*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Subclass ***Sordariomycetidae*** O.E. Erikss & Winka
Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández
Chaetosphaeriaceae Réblová, M.E. Barr & Samuels
64. ***Codinaea lithocarpi*** (R.H. Perera, E.B.G. Jones & K.D. Hyde) W.P. Wu & Y.Z. Diao, Fungal Divers. 116: 1-546 (2022), new host record.
65. ***Dinemasporium ambiguum*** A. Hashim. & Kaz. Tanaka, Mycoscience 56: 88 (2014) [2015], new host and geographical record.
66. ***Dinemasporium pseudostrigosum*** Crous, Persoonia 28: 134 (2012), new host record.

67. ***Pseudostriatosphaeria*** X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.
68. ***Pseudostriatosphaeria chiangraiensis*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Subclass ***Xylariomycetidae*** O.E. Erikss & Winka
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69. ***Apiospora ananasi*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.
70. ***Apiospora rasikravindrae*** (Shiv M. Singh, L.S. Yadav, P.N. Singh, Rahul Sharma & S.K. Singh) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021), new host record.
71. ***Nigrospora oryzae*** (Berk. & Broome) Petch, J. Indian bot. Soc. 4: 24 (1924), new geographical record.

Beltraniaceae Nann.
72. ***Beltrania rhombica*** Penz., Michelia 2(no. 8): 474 (1882), new host and geographical record.

Sporocadaceae Corda
73. ***Neopestalotiopsis chiangmaiensis*** Tibpromma & K.D. Hyde, Fungal Divers. 93: 1–160, (2018), new host record.
74. ***Neopestalotiopsis formicidarum*** Maharachch., K.D. Hyde & Crous [as '*formicarum*'], Stud. Mycol. 79: 140 (2014), new host and geographical record.
75. ***Neopestalotiopsis guajavicola*** I.U Haq, S. Ijaz & N. A. Khan, Pakist. J. Agric. Sci. 58: 1307 (2021), new host and geographical record.
76. ***Neopestalotiopsis terricola*** W.L. Li & J.K. Liu, J. Fungi 8(11, no. 1175): 14 (2022), new host and geographical record.
77. ***Neopestalotiopsis saprophytica*** (Maharachch. & K.D. Hyde) Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 148 (2014), new host and geographical record.
78. ***Pestalotiopsis adusta*** (Ellis & Everh.) Steyaert, Trans. Br. Mycol. Soc. 36: 82 (1953), new collection.

Xylariales Nannf.
Hypoxylaceae DC.
79. ***Daldinia eschscholtzii*** (Ehrenb.) Rehm, Annls Mycol. 2(2): 175 (1904), new host record.
80. ***Hypoxylon cocois*** X.G, Tian, K.D. Hyde & Tibpromma, sp. nov.

Xylariaceae Tul. & C. Tul.
81. ***Anthostomella cocois*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Xylariales genera incertae sedis
82. ***Occultitheca ananasi*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

INTRODUCTION

Monocotyledons, commonly referred to as monocots, are plants that have single seed-bearing leaves; the seeds typically contain only one embryonic leaf, or cotyledon (Arber 1925, Dahlgren et al. 1984). There are approximately 60,000 species of monocots, including the most economically important of all plant families (Poaceae) and the largest of all plant families (Orchidaceae) (Hutchinson 1959, Dahlgren et al. 1984, Tzvelev 1989, Chase et al. 2015). Out of 400,000 plants on earth, approximately 200 plants are used as food crops (Warren 2015). Cereals are mostly monocots and the most dominant group among the world's major crops (Tyczewska et al. 2018). Cereal plants cover over 20% of the global land area and 61% of the total cultivated land (Koçar & Civaş 2013).

Rice (*Oryza sativa*), an edible starchy cereal grain belongs to the family Poaceae. Rice is the world's most important staple food, and it is the third-highest agricultural commodity produced worldwide after sugarcane and corn (Shaheen et al. 2022). The world's rice production is 750

million tonnes annually, led by China and India, with 49% of this total combined. Roughly half of the world's population, including virtually all of East, and Southeast Asia, are wholly dependent upon rice as a staple food; and 95% of the world's rice is eaten by humans. In 2020, the world's production of rice was 756 million tonnes, and China was the largest producer whose output was 211.8 million tonnes. Thailand is the sixth-largest rice-producing country in the world, and the total rice production was 30.2 million tonnes in 2020 (Shaheen et al. 2022).

Coconut (*Cocos nucifera*), the edible fruit of the coconut palm, belongs to the palm family (Arecaceae), and it is the only species in *Cocos* (Menon & Pandalai 1958). Coconut is one of the most important tropical crops (Thampan 1981). The coconut palm is grown throughout the tropics and subtropics for decoration and its many culinary and nonculinary uses (Perera et al. 2009). About 75% of the world's supply of coconuts is produced by Indonesia, the Philippines, and India. Coconut provides food, fuel, folk medicine, and building materials (Ohler 1984). It has a high medicinal value; thus, it helps to control blood sugar levels in the human body (Weickert & Pfeiffer 2018, Malaeb & Spoke 2020, Nikooei et al. 2021). Coconut meat and water contain numerous antioxidants that fight against factors causing cell damage (Fernando et al. 2015). In addition, coconut can prevent and treat Alzheimer's disease (DebMandal & Mandal 2011).

Pineapple (*Ananas comosus*), a tropical plant originating from South America with edible fruit, is the most economically significant plant in Bromeliaceae (Sanewski et al. 2018, Maldonado-Michel et al. 2021). Pineapples are the 11th most cultivated fruit and the third most important tropical fruit in the world, and it is grown all over the world, especially in Latin America, West Africa, and Southeast Asia (Hossain 2016, Scott & Emery 2016, Mohd Ali et al. 2020). The flesh and juice of the pineapple are used in cuisines around the world (Collins 1960, Bartholomew & Malézieux 1994, Leon & Kellon 2012). In addition, pineapple has high nutritional and medicinal value. It contains various vitamins, carbohydrates, crude fiber, and different minerals that are good for health (SabahelKhier et al. 2010, Hossain 2016). Fresh pineapple is rich in bromelain, which is used as an anti-inflammatory agent to reduce swelling and inflammation in acute sinusitis and sore throat (Hossain 2016). In 2020, the world's production of pineapple was 28 million tonnes, and Thailand and China were the two largest producers, whose outputs were 1.7 and 2.2 million tonnes respectively (FAOSTAT 2023).

Fungi are ubiquitous and occur in all terrestrial, freshwater, and marine environments. They are major decomposers in terrestrial and aquatic ecosystems and play important roles in the nutrient cycling and decomposition of dead plant material (Wainwright et al. 2003, Bucher et al. 2004, Barea et al. 2005, Lindahl et al. 2007). The estimated number of fungal diversity in the world ranges between 250,000 to 19 million, and between 92–95% of fungi have yet to be scientifically described (Niskanen et al. 2023). Fungi associated with specific groups of plants in China and Thailand have been studied in recent years, and numerous new fungal species have been reported. Mapook et al. (2020a) described 47 new fungi species on the invasive weed *Chromolaena odorata* (Siam weed); and Phukhamsakda et al. (2020) reported 12 new fungal genera and 50 new fungal species on *Clematis* (Ranunculaceae). However, fungi associated with coconut, pineapple, and rice have poorly been studied in both China and Thailand.

Several studies have been carried out on fungi associated with coconut and pineapple, and several fungal pathogens have been reported from coconut (Butler 1925, Ram 1989, Hyde & Fröhlich 1995, Fröhlich et al. 1997, Karthikeyan & Bhaskaran 1997, Ramos et al. 1998, Koshy 2000, Harrison & Jones 2003, Vinod 2003, Thomas et al. 2010, Niu et al. 2014, Rosado et al. 2015, Rosado et al. 2016, Eris et al. 2017, Vinjusha & Arun Kumar 2021, Coelho et al. 2022, Sunpapao et al. 2022). Harrison & Jones (2003) reviewed the distribution, importance, and control of coconut diseases together with characteristics and production of the fruit, and 44 fungal pathogens were listed. Dollet et al. (2012) listed eight fungal pathogens that cause bud rot and leaf blight in coconut. The endophytes and saprobes associated with coconut, however, are poorly studied.

A few studies have reported fungi associated with pineapple, but these studies mainly focused on pathogens and endophytes (Green & Nelson 2015, Gu et al. 2015, Barral et al. 2019, 2020, Vignassa et al. 2021). Barral et al. (2020) reported three pathogens in pineapple that cause fruitlet

core rot of pineapple. Vignassa et al. (2021) investigated the fungal mycota of healthy and naturally infected pineapple fruitlets and reported 44 fungal species.

Fungi associated with rice have received more attention than coconut and pineapple, and numerous pathogenic species and endophytes of the genera *Alternaria*, *Aspergillus*, *Chaetomium*, *Curvularia*, *Fusarium* and *Penicillium* have been reported (Tian et al. 2004, Zakaria et al. 2010, Wijesooriya & Deshappriya 2016, Afandhi et al. 2017, Kandar et al. 2018, Sun et al. 2019, Tang et al. 2019, Mardina 2021). *Fusarium* spp., *Pythium* spp. and other water molds have been reported to cause rice seed rot during rice germination while, *Curvularia* spp., *Fusarium* spp., and *Rhizoctonia solani* were also reported to cause blights in rice seedlings (Verma et al. 2018).

Most previous studies of fungi associated with coconut, pineapple, and rice focused on pathogenic and endophytic fungi, while saprobic fungi have poorly been studied. Most taxa were identified based on morphological characteristics, and little taxonomic work on fungi associated with pineapple, coconut, and rice with molecular data has been carried out. To address these research gaps, coconut, pineapple, and rice samples were collected in China and Thailand. The known and new fungal species are illustrated and described with complete morphological characteristics and phylogenetic analyses. In addition, comprehensive worldwide checklists of fungi associated with coconut, pineapple, and rice are provided.

MATERIALS AND METHODS

Sample collection, isolation, and morphological examination

Dead and decaying leaves and stems of *Ananas comosus*, *Cocos nucifera* and *Oryza sativa* with fungal fruiting bodies or fungal masses were collected from sampling sites in China and Thailand during 2020–2021. Specimens were brought in plastic bags for observation. Senanayake et al. (2020) was followed for morphological study and single spore isolation. The morphological characteristics were examined by using a stereomicroscope (Motic SMZ-171, Wetzlar, Germany). The micro-morphological characteristics of fungi were observed and photographed using a Nikon camera series DS-Ri2 connected to a Nikon ECLIPSE Ni-U microscope (New York, USA). All microscopic structures were measured using the Image Framework program v.0.9.0.7 and images were processed in Adobe Photoshop CS6 (Adobe Systems, San Jose, CA, USA) (Senanayake et al. 2020, Tian et al. 2021a).

Specimens are deposited in the Herbarium of Mae Fah Luang University (MFLU), Chiang Rai, Thailand and the Herbarium of Guizhou Academy of Agriculture Sciences (GZAAS), Guiyang, China. The descriptions and plates for the northern Thailand specimens are deposited in the Greater Mekong Subregion database (Chaiwan et al. 2021). Living cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC), the Culture Collection of Kunming Institute of Botany (KUNCC), and the Guizhou Culture Collection (GZCC), Guizhou, China. Faces of fungi (FoF) numbers were registered as in Jayasiri et al. (2015), while Index Fungorum (IF) numbers were obtained as in Index Fungorum (2023). The new taxa were established based on guidelines outlined by Chethana et al. (2021), Pem et al. (2021), and Maharachchikumbura et al. (2021).

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted directly from the spore mass, fruiting bodies or four-week-old pure cultures using a Biospin Fungal Genomic DNA Extraction Kit (BioFlux, P.R. China) and E.Z.N.A.® Forensic DAT (D3591–01, Omega Bio-Tek) DNA extraction kit following the manufacturer's instructions. The DNA was subjected to polymerase chain reaction (PCR) to amplify partial gene regions using corresponding primers (Table 1). The PCR amplifications were carried out using the method described by Tibpromma et al. (2018) and Tian et al. (2021a). The genes and primers used in this study are summarized in Table 1. PCR products were checked in 1% agarose gels and sent to TsingKe Biological Technology (Kunming) Co., China for sequencing.

Table 1 Primers used in this study.

Gene/loci	PCR primers (forward/reverse)	References
act	ACT-512F/ ACT-783R	Carbone & Kohn (1999)
gapdh	Gpd1/ Gpd2	Templeton et al. (1992)
his3	CYLH3F/ CYLH3R	Crous et al. (2004)
ITS	ITS4/ ITS5	White et al. (1990)
LSU	LR0R/ LR5	Vilgalys & Hester (1990)
rpb1	Fa/ G2R	O'Donnell et al. (2010)
rpb2	fRPB2-5f/ fRPB2-7CR	Liu et al. (1999)
SSU	NS1/ NS4	White et al. (1990)
tef1-α	EF-1/ EF-2	O'Donnell et al. (2010)
	983F/ 2218R	Rehner & Buckley (2005)
	EF1-728F/ EF-2	Carbone & Kohn (1999)
tub2	T1/ T22	O'Donnell et al. (2010)
	Bt2A/ Bt2b	Glass & Donaldson (1995)

Phylogenetic analyses

The raw sequences were combined using SeqMan and subjected to BLAST in GenBank (https://www.ncbi.nlm.nih.gov, 20 January 2023). Sequences were retrieved from GenBank according to recent publications. Single gene sequence alignment was generated with MAFFT v.7 online program (http://mafft.cbrc.jp/alignment/server/, 22 February 2023) (Katoh & Standley 2013) and trimmed using trimAl v 1.2 with the 'gappyout' option (Capella-Gutiérrez et al. 2009). Multiple genes were concatenated by Sequence Matrix. The FASTA alignment formats were changed to PHYLIP and NEXUS formats by Aliview 2.11. Multigene phylogenetic analyses were constructed from maximum likelihood (ML) and Bayesian inference (BI) analysis.

Maximum likelihood analysis was done by the online RAxML-HPC v.8 on XSEDE Teragrid on CIPRES Science Gateway V. 3.3 (https://www.phylo.org, 22 February 2023) using the GTRGAMMA substitution model with 1,000 bootstrap replicates (Stamatakis et al. 2008, Miller et al. 2010, Dissanayake et al. 2020). The final tree was selected from suboptimal trees from each run by comparing likelihood scores.

Bayesian inference analysis was performed using MrBayes v. 3.2 on the XSEDE tool on the CIPRES portal (Miller et al. 2010). The best fit model for BI analysis was estimated using MrModeltest v. 2.2 (Nylander 2004). Posterior probabilities (PP) (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002) were defined by the Bayesian Markov chain Monte Carlo (BMCMC) sampling method in MrBayes v.3.0b4 (Huelsenbeck & Ronquist 2001). Two parallel runs were conducted using the default settings, six simultaneous Markov chains were run for 1 million to 10 million generations (depending on individual settings for the fungal group), and trees were sampled every 100^{th} to 1000^{th} generation. Tracer v1.6 (Rambaut et al. 2014) was used to examine the log-likelihood scores to decide extra runs and determine the stationary phase. The first 20% of trees were discarded as the burn-in phase. The remaining trees were used for calculating PP in the majority rule consensus tree. The run was stopped when the standard deviation of split frequencies was reached below 0.01 (Mapook et al. 2020a, Tian et al. 2022c). Phylogenetic trees were visualized with FigTree v1.4.4 (Rambaut 2009), and layouts were carried out with Adobe Illustrator CS5 v. 16.0.0 (Adobe Systems, San Jose, CA, USA).

Genealogical concordance phylogenetic species recognition (GCPSR) analysis

The genealogical concordance phylogenetic species recognition analysis is a model test used to check significant recombinant events (Quaedvlieg et al. 2014). The data were analyzed using SplitsTree V4 with the pairwise homoplasy index (PHI) test to determine the recombination level with closely related species (Bruen et al. 2006, Huson & Bryant 2006, Tian et al. 2021b). A multi-locus concatenated dataset with closely related species were used for the analysis. The relationships between closely related taxa were visualized by constructing split graphs from the concatenated

datasets using the LogDet transformation and splits decomposition options. PHI results below a 0.05 threshold ($\Phi w < 0.05$) indicate significant recombination in the dataset.

Taxonomy

Phylum *Ascomycota* Caval.-Sm.
Class *Eurotiomycetes* Tehler ex O.E. Eriksson & K. Winka
Subclass *Chaetothyriomycetidae* Doweld
Verrucariales Mattick ex D. Hawksw. & O.E. Erikss.

Verrucariales, comprises most lichenized ascomycetes and they form typical thallus morphologies, including crustose, squamulose, foliose and rarely subfruticose thalli (Muggia et al. 2010). The latest outline of this order was provided by Wijayawardene et al. (2022) and three families *viz. Adelococcaceae*, *Sarcopyreniaceae* and *Verrucariaceae* are accepted in *Verrucariales*.

Verrucariaceae Zenker

Verrucariaceae, is the largest family in *Verrucariales*, and members of this family are mostly crustose, lichenized ascomycetes with a wide distribution in various habitats e.g. marine and freshwater to arid environments (Gueidan et al. 2007). Species in this family have been reported from diverse substrates, such as rock, soils, wood or bark, mosses, and other lichens (Zehetleiter 1978, Dobbeler & Triebel 1985, Orange 1989, Breuss 1993, Breuss 1994, Breuss 1996, Gueidan et al. 2007). Fifty-two genera are accepted in *Verrucariaceae* (Wijayawardene et al. 2022).

Placidiopsis Beltr., Lich. Bassan. (Bassano): 212

Placidiopsis comprises squamulose lichens and it is phylogenetically close to *Catapyrenium*, but it can be distinguished from *Catapyrenium* in having septate ascospores and lacking pycnidia (Prieto et al. 2010). *Placidiopsis* is characterized by squamulose thalli attached to the substrate by a rhizohyphal web, a central bundle of rhizohyphae, or rhizines. The upper cortex is either absent or cinereum-type, the photobiont is a chlorococcoid alga, the medulla is proso- or subparaplechtenchymatous, and the lower cortex is paraplect enchymatous when present. Perithecia are immersed, with or without an apical involucrellum, asci are clavate with an ocular chamber, and pycnidia have never been observed (Prieto et al. 2010). There are 39 records for *Placidiopsis* listed in Index Fungorum (2023). However, only nine species have sequence data in GenBank. In this study, we describe a new species as a saprobe on dead leaves of *Ananas comosus*.

1. *Placidiopsis ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 1

Index Fungorum number: IF900965; Facesoffungi number: FoF14278

Etymology – Referring to the host plant *Ananas comosus*, on which the fungus was collected.

Holotype – MFLU 23-0160

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: *Ascomata* 50–80(–90) × 45–70(–74) µm ($\overline{x}$ = 67.3 × 55.8 µm, n = 10), erumpent, superficial on the substrate, globose to subglobose, unilocular. *Peridium* 10–20 µm wide, comprising brown to dark brown cells of *textura angularis*. *Hamathecium* comprising unbranched, hyaline pseudoparaphyses. *Asci* 35–50 × 10–15 µm ($\overline{x}$ = 42 × 13.6 µm, n = 20), 8-spored, bitunicate, hyaline, clavate to broadly fusoid-ellipsoid, with a wide, slightly squared apex, lacking a pedicel. *Ascospores* 11–15 × 3–4 µm ($\overline{x}$ = 12.6 × 3.3 µm, n = 30), multiseriate, clavate, with round ends, straight, uniseptate, deeply constricted at septum, hyaline, with broad and short upper cells 4.5–6.5 × 4–5 µm ($\overline{x}$ = 5.5 × 4.4 µm, n = 30), narrower and longer lower cells 6.5 × 3–4 µm ($\overline{x}$ = 7.2 × 3.5 µm, n = 30), the lower cells are tapering towards the end, three large guttules and with one guttule in upper cell and two guttules in lower cells, smooth-walled, without mucilaginous sheath or appendages. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on malt extract agar (MEA) within 24 h and many germ tubes produced from many cells. Colonies growing on potato dextrose agar (PDA),

reaching 15 mm diam. in 7 days at room temperature, flat, sparsely hairy, radially striate, with fimbriate edge, dark brown.

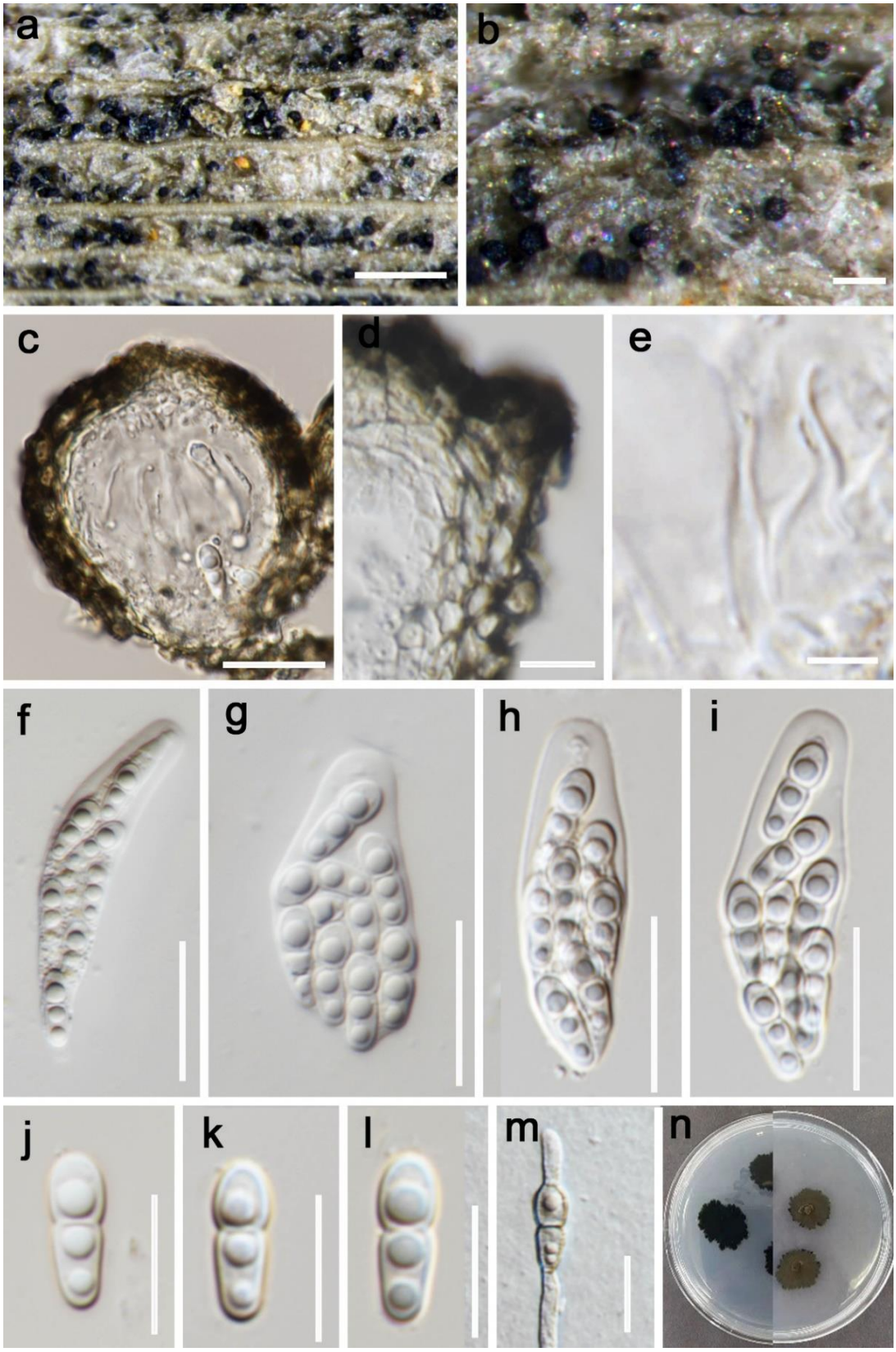

Figure 1 – *Placidiopsis ananasi* (MFLU 23-0160, holotype). a, b Appearance of ascomata on substrate. c Vertical section through stroma. d Peridium. e Hamathecium. f–i Asci. j–l Ascospores. m Germinated conidium. n Colonies on PDA from surface and reverse. Scale bars: a = 500 µm, b = 100 µm, c, f–i = 20 µm, d, k–m = 10 µm, e = 5 µm.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 2 September 2020, X.G. Tian, p9-16 (MFLU 23-0160, holotype), ex-type living culture (MFLUCC 23-0123); *ibid*, 21 May 2020, X.G. Tian, p1-1 (MFLU 23-0159, paratype).

GenBank numbers – MFLUCC 23-0123: ITS: OR438327, LSU: OR438798. MFLU 23-0159: ITS: OR438328, LSU: OR438799.

Notes – In our phylogenetic analyses, *Placidiopsis ananasi* (MFLUCC 23-0123 and MFLU 23-0159) clustered sister to *P. poronioides* (CBS 101262) with 100% ML and 1.00 PP statistical support (Fig. 2). *Placidiopsis ananasi* resembles *P. poronioides* in having globose, unilocular ascomata, clavate asci and 1-septate, ellipsoid, hyaline ascospores. However, *P. ananasi* differs from *P. poronioides* in having erumpent and much larger ascomata (50–80(–90) × 45–70(–74) µm vs. 30–40 × 8–10 µm) and the ascospores have three large guttules and are smooth-walled, while these characters were not observed in *P. poronioides* (Aptroot & Seaward 1999). The PHI test revealed no significant recombination event between *P. ananasi* and the closely related taxa (Φw = 0.35) (Fig. 3). The significant recombination between two strains of *Placidiopsis ananasi* (MFLUCC 23-0123 and MFLU 23-0159) indicates that they are conspecific (Fig. 3) and the nucleotides comparisons revealed 60 bp/512 bp differences in ITS gene region. In addition, *P. poronioides* is a lichenized ascomycete, while our new species (*P. ananasi*) is a saprobe isolated on dead leaves of *Ananas comosus*.

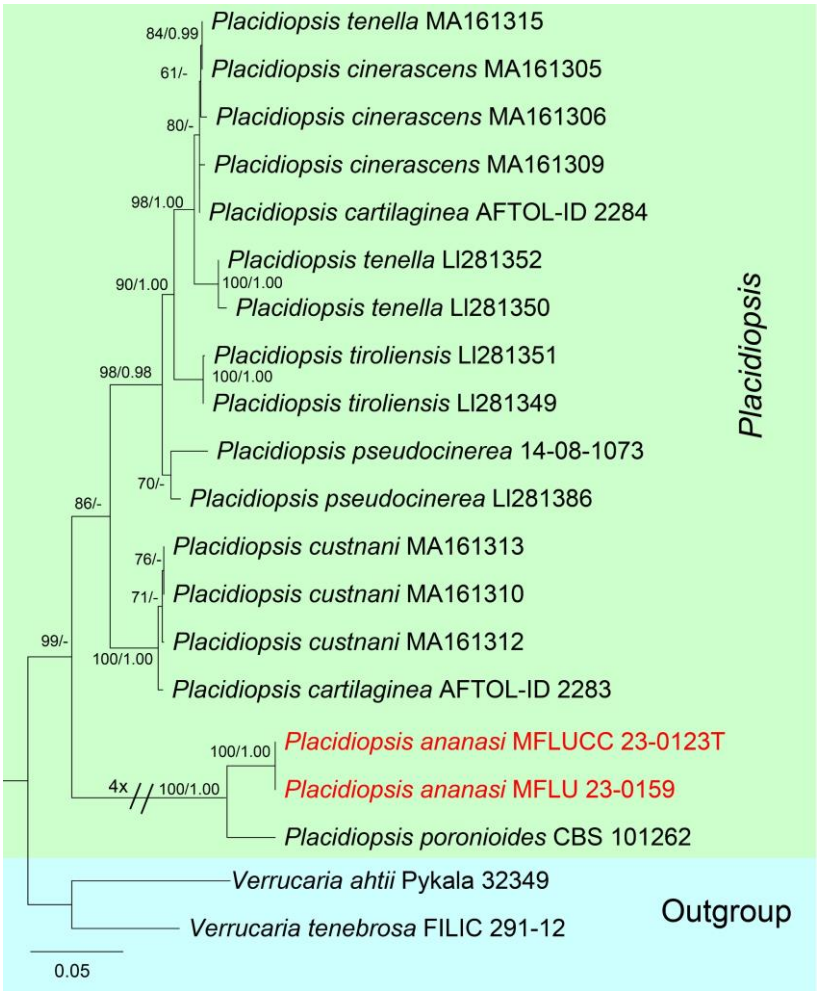

Figure 2 – Phylogram generated from maximum likelihood analysis based on combined ITS, and LSU sequence data. Twenty-two strains are included in the combined sequence analysis, which comprises 1419 characters with gaps. *Verrucaria ahtii* (Pykala 32349) and *V. tenebrosa* (FILIC 291-12) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -4471.775411 is presented. The matrix

had 628 distinct alignment patterns, with 26.32% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.235148, C = 0.248640, G = 0.288052, T = 0.228159; substitution rates AC = 1.344123, AG = 1.686062, AT = 0.880104, CG = 0.930870, CT = 5.873462, GT = 1.000000; gamma distribution shape parameter α = 0.253122. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

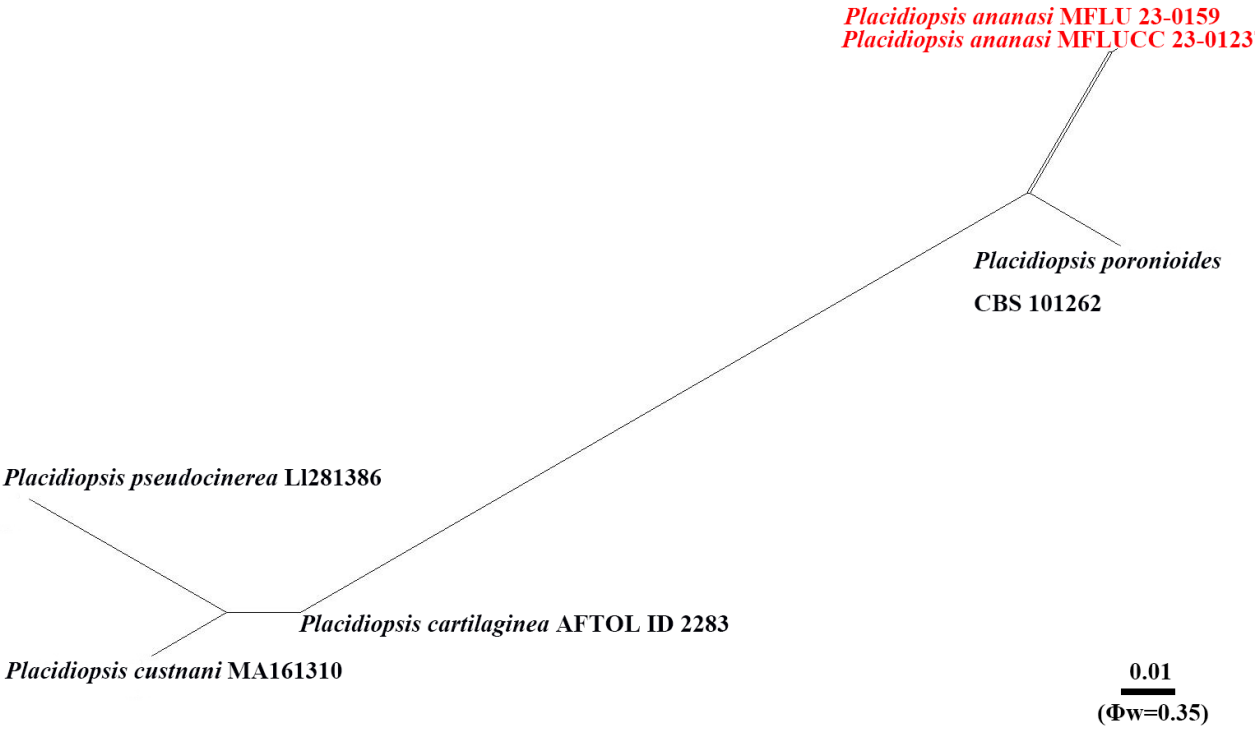

Figure 3 – Results of the PHI test of *Placidiopsis ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test did not find statistically significant evidence for recombination (Φw = 0.35). PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type, and T indicates holotype or ex-type strains.

Class *Dothideomycetes* sensu O.E. Erikss. & Winka
Subclass *Dothideomycetidae* P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker

Muyocopronales Mapook, Boonmee & K.D. Hyde

Muyocopronales was introduced by Mapook et al. (2016) to accommodate the single family *Muyocopronaceae*. *Muyocopronales* formed a distinct clade within *Dothideomycetes* and was related to *Acrospermales* and *Dyfrolomycetales* (Hongsanan et al. 2020b).

Muyocopronaceae K.D. Hyde

Muyocopronaceae was introduced by Luttrell (1951) without a Latin diagnosis and was synonymized under *Microthyriaceae* (Wu et al. 2010, 2011). Hyde et al. (2013) reintroduced the family with a single genus *Muyocopron*, provided an English diagnosis and placed the family in *Dothideomycetes* family, *incertae sedis* (Luttrell 1951, Hyde et al. 2013). To date, *Muyocopronaceae* comprises ten genera (Wijayawardene et al. 2022). In this study, a new species (*Muyocopron chiangraiense*) and a new genus *Pseudomycoleptodiscus*, typified by *Pseudomycoleptodiscus ananasi* are introduced.

Muyocopron Speg., Anal. Soc. Cient. Argent. 12(3): 113 (1881)

Muyocopron was introduced by Spegazzini (1881), with the type species *M. corrientinum*. *Muyocopron* species are characterized by superficial, black spots, without mycelium, sub-carbonaceous ascomata, bitunicate, 8-spored asci, and ellipsoidal, hyaline ascospores (Spegazzini 1881, Luttrell 1951, Hyde et al. 2013, Mapook et al. 2016). This genus occurs worldwide and is associated with various plants (Mapook et al. 2016, Tibpromma et al. 2016, Senwanna et al. 2019). Seventy-two *Muyocopron* records are listed in Species Fungorum (2023), and we introduce a new species, *Muyocopron chiangraiense* which was collected from *Ananas comosus*.

2. *Muyocopron chiangraiense* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 4

Index Fungorum number: IF900967; Facesoffungi number: FoF14279

Etymology – Referring to the Chiang Rai Province where the fungus was collected.

Holotype – MFLU 23-0161

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: *Ascomata* 140–190 × 50–60 μm ($\bar{x}$ = 165 × 54 μm, n = 5), superficial, solitary or scattered, coriaceous, appear as circular, flattened, brown to dark brown spots, covering the host, irregular at margin, with a central ostiole. *Peridium* 30–60 μm wide, thick-walled, widest at sides, consisting two types of cell layers; outer layer thick-walled, composed of black, brittle carbonaceous cells, inner layer comprising light brown pseudoparenchymatous cells of *textura prismatica*. *Hamathecium* comprised of 1.5–3 μm wide, cylindrical to filiform, numerous, septate, branched, broadly cellular pseudoparaphyses. *Asci* 40–75 × 10–20 μm ($\bar{x}$ = 61 × 15 μm, n = 15), 8-spored, bitunicate, broadly cylindrical to obclavate, subsessile to short pedicellate, apically rounded, with well-developed ocular chamber. *Ascospores* 10–15 × 5–10 μm ($\bar{x}$ = 13 × 8 μm, n = 25), irregularly arranged, sometimes overlapping, ellipsoid to obovoid, hyaline, with obtuse ends, aseptate, with granular appearance, rough-walled. Asexual morph: Not observed.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 14 April 2020, X.G. Tian, P1-2 (MFLU 23-0161, holotype, GZAAS 23-0582, isotype).

GenBank numbers – MFLU 23-0161: LSU = OR438802, ITS = OR438331, SSU = OR458328. GZAAS 23-0582: LSU = OR438803, ITS = OR438332, SSU = OR458329.

Notes – In the phylogenetic analyses, our strains (MFLU 23-0161 and GZAAS 23-0582) clustered within *Muyocopron*, sister to *M. atromaculans* (MUCL 34983) and *M. ficinum* (MFLUCC 18-2515) with 100% ML and 1.00 PP statistical support (Fig. 5). Our collection shares similar morphology with *M. ficinum* (MFLUCC 18-2515, ex-type) in having small, superficial, black spots, central ostiolate ascomata, bitunicate, 8-spored asci, and overlapping, oval to obovoid, hyaline ascospores. However, our collection differs from *M. ficinum* (MFLUCC 18-2515) in having different sized ascomata (140–189 × 50–58 μm vs. 200–250 × 60–100 μm); peridia (34–59 μm vs. 10–15 μm wide), asci (13–17 μm vs. 20–25 μm wide) and ascospores (11–15 μm vs. 14–18 μm long). The nucleotide comparisons show that our isolate (MFLU 23-0161) is significantly different from the strains of *M. ficinum* (MFLUCC 18-2515) in 33/ 350 bp (9.43%) of the ITS, 20/795 (2.51%) of the LSU, and 29/990 (2.93%) of the SSU and based on guidelines of Chethana et al. (2021). In addition, the PHI test revealed no significant recombination event between *Muyocopron chiangraiense* and the closely related taxa (Φw = 0.99) (Fig. 6). We introduce our strains (MFLU 23-0161 and GZAAS 23-0582) as a new species.

3. *Pseudomycoleptodiscus* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.

Index Fungorum number: IF900897; Facesoffungi number: FoF14329

Etymology – In reference to the similarity to *Mycoleptodiscus*.

Saprobic on dead leaves or wood in terrestrial habitats. Sexual morph: Not observed. Asexual morph: *Conidiomata* sporodochial, in groups, superficial, dark brown to black, with hyaline conidial mass, setose. *Conidiomatal setae* abundant, dark brown to black, subcylindrical to cylindrical, straight or slightly curved, wide at the base, acute at apex, unbranched, smooth, thick-

walled, arising from basal stroma. *Conidiophores* micronematous, reduced to conidiogenous cells, pale brown to brown, cylindrical to subcylindrical, arranged in a palisade layer, aseptate, smooth-walled, arising from basal stroma. *Conidiogenous cells* ampulliform, monophialidic, without a collarette, determinate, terminal, hyaline, subcylindrical, smooth-walled. *Conidia* solitary, acrogenous, hyaline, 1-septate, slightly constricted at septa, smooth-walled, oval to cylindrical, obtuse rounded at apex and base, straight, guttulate, with a single, unbranched, flexuous, tubular appendage at both ends.

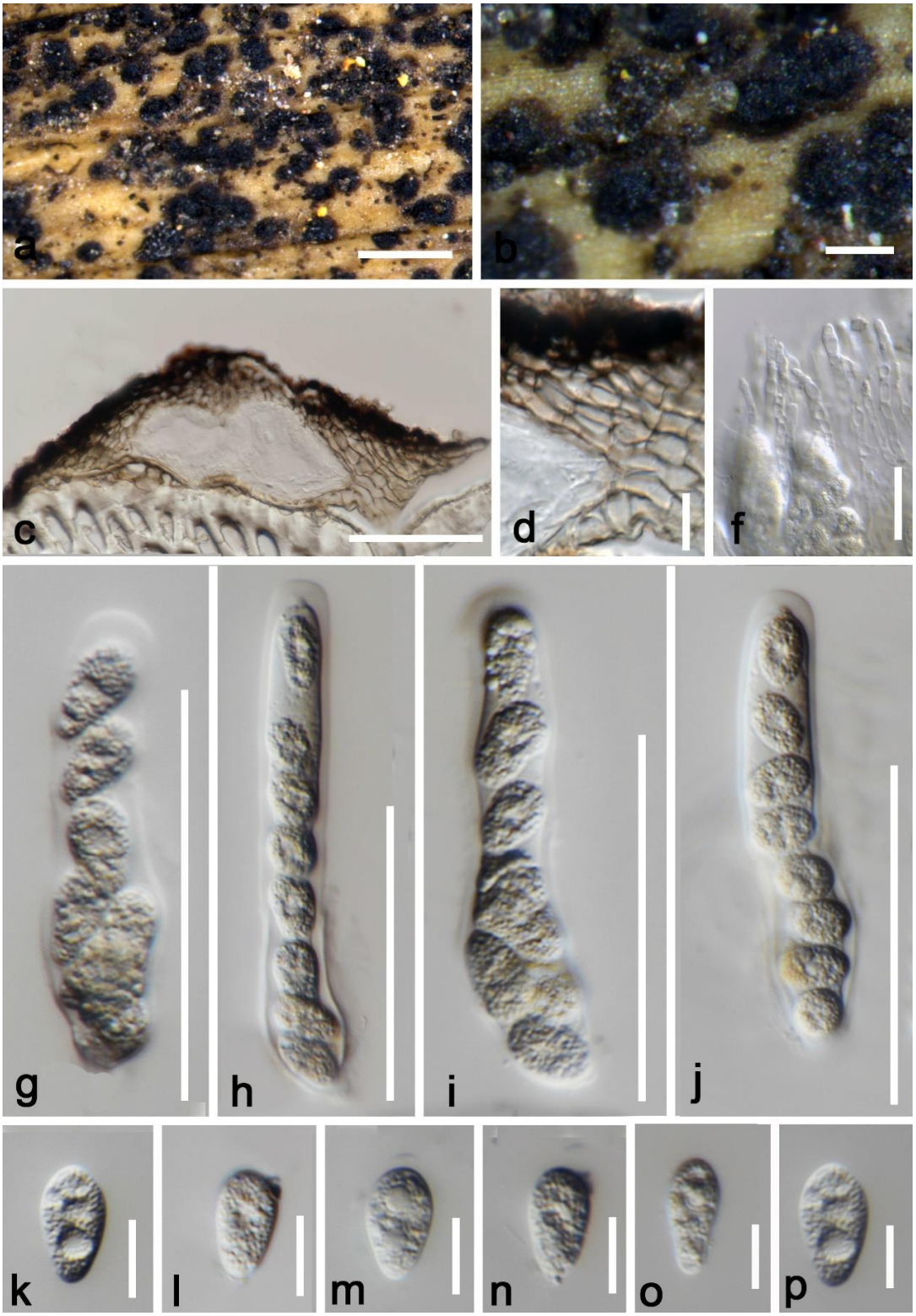

Figure 4 – *Muyocopron chiangraiense* (MFLU 23-0161, holotype) a, b Appearance of ascomata on

the host surface. c Section of ascoma. d Peridium. f Pseudoparaphyses. g–j Asci. k–p Ascospores. Scale bars: a = 500 µm, b = 200 µm, c = 50 µm, g–j = 40 µm, d, f, k–p = 10 µm.

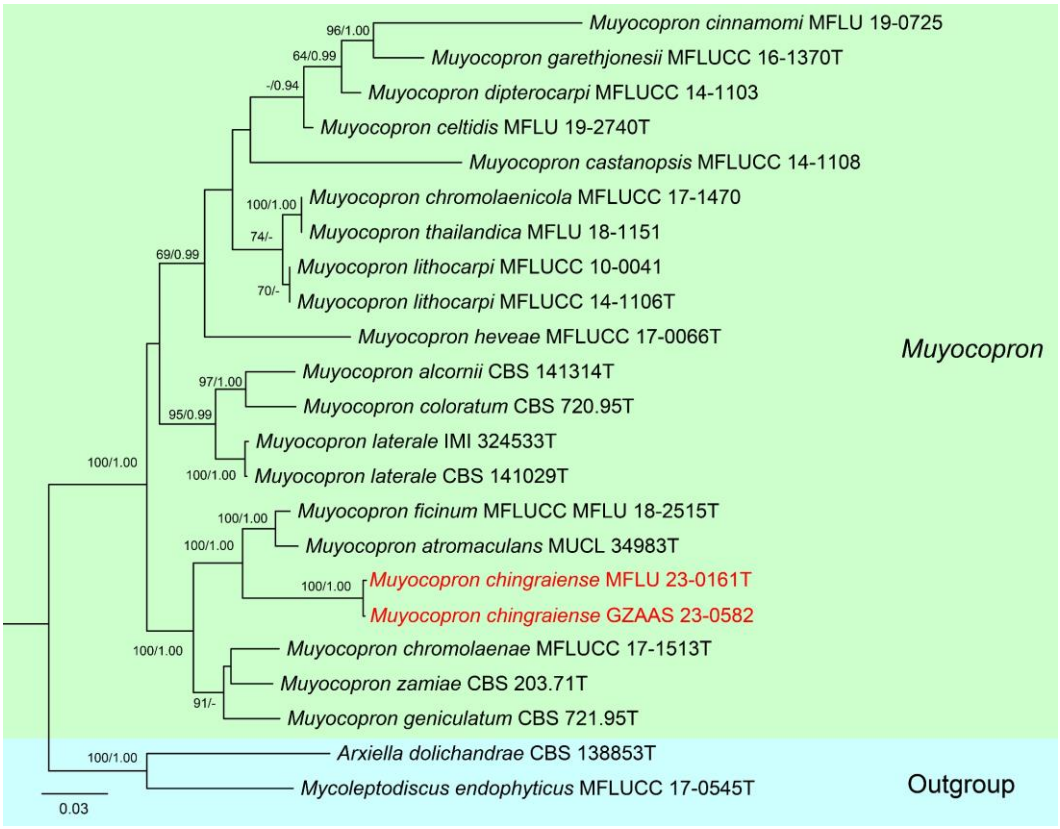

Figure 5 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data. Related sequences were obtained from Tennakoon et al. (2021b). Twenty-two strains are included in the combined sequence analysis, which comprises 2418 characters with gaps. *Mycoleptodiscus endophyticus* (MFLUCC 17-0545) and *Arxiella dolichandrae* (CBS 138853) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -9734.811197 is presented. The matrix had 628 distinct alignment patterns, with 26.32% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.236405, C = 0.251116, G = 0.298054, T = 0.214425; substitution rates AC = 2.349928, AG = 3.747575, AT = 2.097344, CG = 1.947616, CT = 7.210830, GT = 1.000000; gamma distribution shape parameter α = 0.195516. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Type species – *Pseudomycoleptodiscus ananasi* X.G. Tian, K.D. Hyde & Tibpromma

Notes – In our phylogenetic analyses, *Pseudomycoleptodiscus* clusters as an independent branch between *Neocochlearomyces* and *Neomycoleptodiscus* (Fig. 7). Therefore, *Pseudomycoleptodiscus* is introduced as a monophyletic genus with *P. ananasi*. Phylogenetically, the *Pseudomycoleptodiscus* is close to *Neocochlearomyces*. However, *Pseudomycoleptodiscus* is different from *Neocochlearomyces* in having conidiomatal setae, micronematous, aseptate conidiophores that are reduced to conidiogenous cells, ampulliform to doliiform, determinate, terminal conidiogenous cells and oval to cylindrical, obtuse rounded at apex and base, and 1-septate conidia. *Neocochlearomyces* has macronematous, mononematous, septate conidiophores with a stalk forming an apical fanlike conidiogenous region consisting of radiating brown, warty, septate, tightly aggregated cylindrical arms, with acute terminal cells, conidiogenous cells are terminal and intercalary on the one side of the swollen fan-like structure and falcate, aseptate conidia and lacks conidiomatal setae (Crous et al. 2018a).

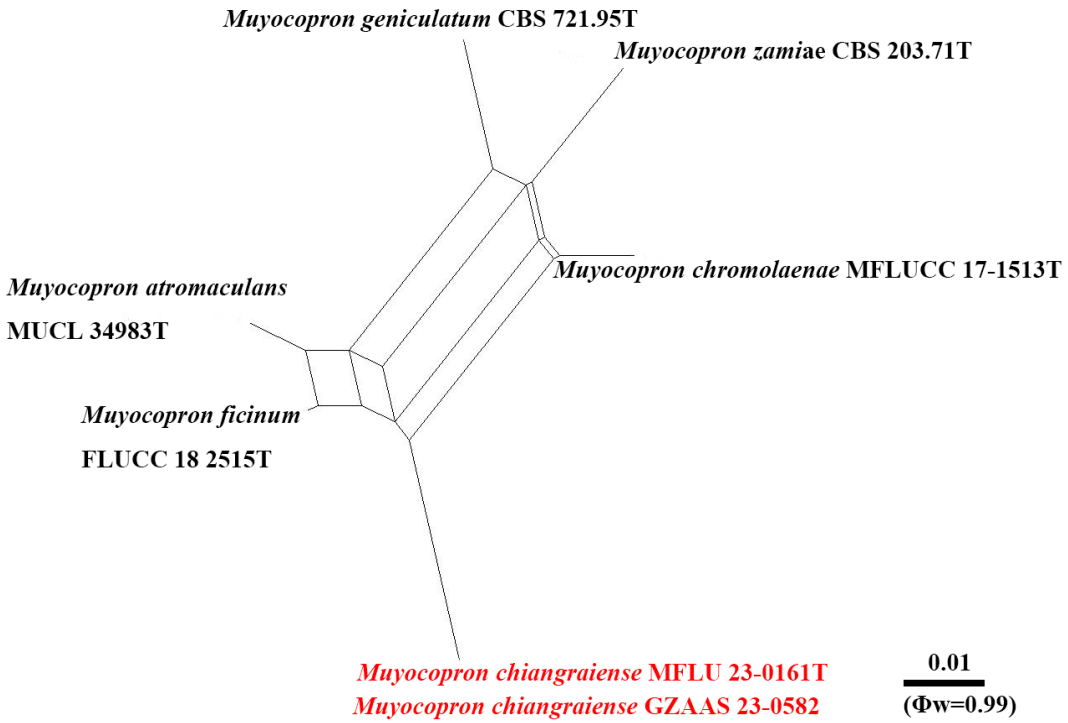

Figure 6 – Results of the PHI test of *Muyocopron chiangraiense* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

Pseudomycoleptodiscus shares similar characters with *Neomycoleptodiscus* in having ampulliform to doliiform conidiogenous cells and cylindrical, 1-septate conidia. In *Pseudomycoleptodiscus*, conidiogenous cells are mono- or polyblastic, discrete, determinate, terminal and conidia are oval to cylindrical, obtuse rounded at apex and base, straight. While, in *Neomycoleptodiscus*, conidiogenous cells are dark brown with cells of *textura globulosa* in face view and with a circular aperture situated in the upper side and conidia are curved at the apex, and truncate at the base. In addition, *Pseudomycoleptodiscus* has conidiomatal setae while, this character was not found in *Neomycoleptodiscus* (Hernández-Restrepo et al. 2019). Therefore, we introduce *Pseudomycoleptodiscus* as a new genus with the type species, *P. ananasi*.

4. *Pseudomycoleptodiscus ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 7

Index Fungorum number: IF900898; Facesoffungi number: FoF14300

Etymology – Referring to the host plant *Ananas comosus*, from which the fungus was collected.

Holotype – MFLU 23-0208

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* sporodochial, in groups, superficial, dark brown to black, with hyaline conidial mass, setose. *Conidiomatal setae* 60–95 µm long, abundant, dark brown to black, subcylindrical to cylindrical, straight or slightly curved, wide at base, acute at apex, unbranched, smooth, septate, thick-walled, arising from basal stroma. *Conidiophores* 10–15 µm long × 5–10 µm wide ($\overline{x}$ = 12.5 × 8 µm, n = 15), macronematous or semi-macronematous, mononematous, arranged in a compact palisade layer, pale brown to brown, cylindrical to subcylindrical, unbranched, aseptate, in groups, smooth-walled, arising from basal stroma. *Conidiogenous cells* monophialidic, without a collarette, determinate, hyaline, subcylindrical, smooth-walled. *Conidia* 15–17 × 6–7 µm ($\overline{x}$ = 15.5 × 6.5 µm, n = 35), solitary, acrogenous, hyaline, 1-septate, rarely slightly constricted at septa, smooth-walled,

oval to cylindrical, obtuse and rounded at apex and base, guttulate, with a single, unbranched, flexuous, tubular appendage at both ends, 30–36 µm long.

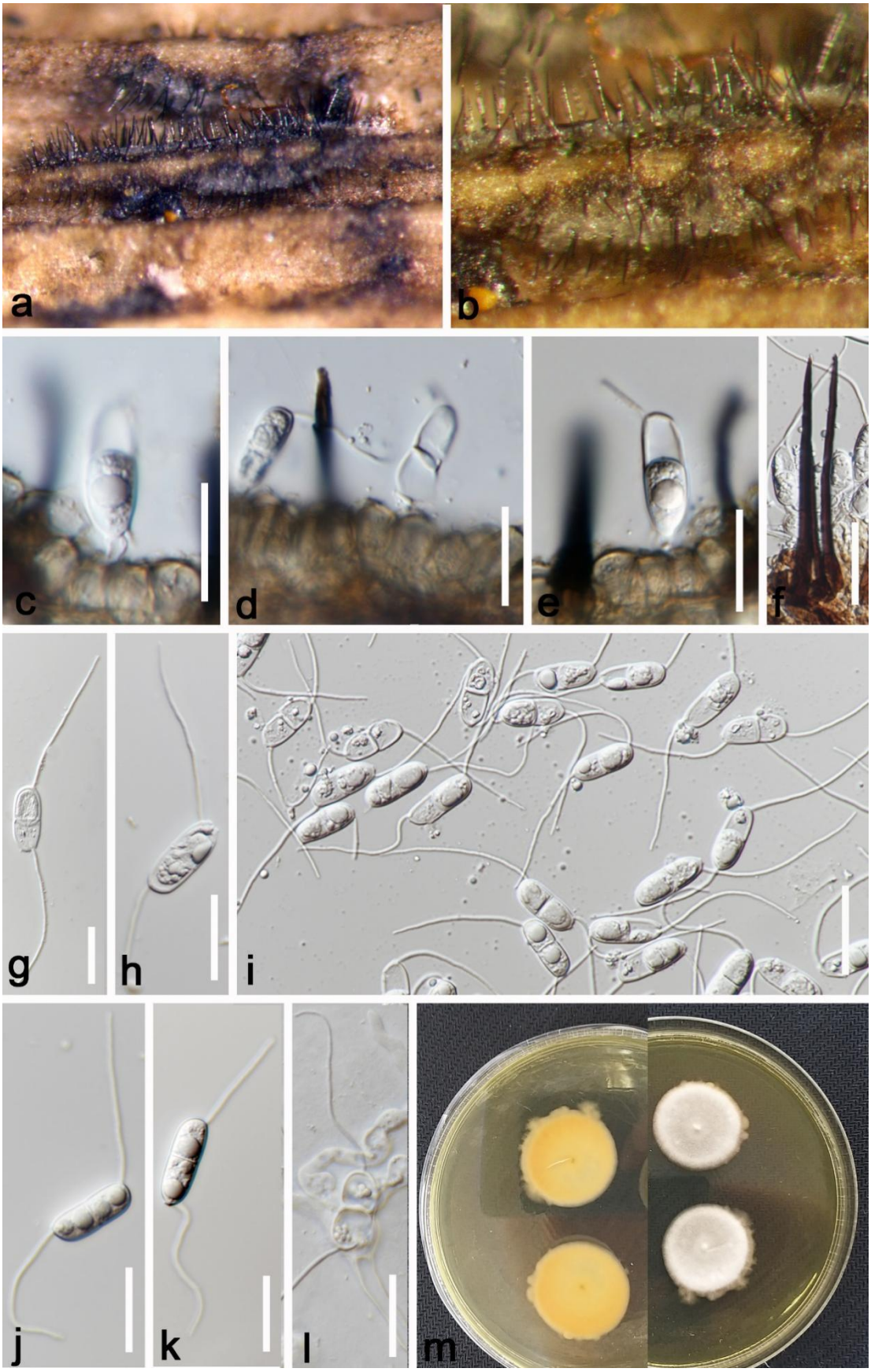

Figure 7 – *Pseudomycoleptodiscus ananasi*)MFLU 23-0208, holotype(. a–b Appearance of

conidiomata on host substrate. c–e Conidiogenous cells, developing conidia and setae. f Setae. g–k Conidia. l Germinated conidium. m Colonies on PDA from surface and reverse. Scale bars: c–l = 20 μm.

Culture characteristics – Conidia germinating on PDA within 12h at room temperature, 15 mm diam. after 1 week. Colonies on PDA circular, slightly raised, filamentous, mycelium creamy-white to pale brown in reverse.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 16 June 2020, X.G. Tian, p2-13)MFLU 23-0208, holotype(, ex-type living culture MFLUCC 23-0165.

GenBank numbers – MFLU 23-0208: LSU = OR438804, ITS = OR438333, SSU = OR458359. MFLUCC 23-0165: LSU = OR438805, ITS = OR438334, SSU = OR458360.

Notes – In our phylogenetic analyses, *Pseudomycoleptodiscus ananasi* clustered sister to *Neocochlearomyces chromolaenae* (Fig. 8). *Pseudomycoleptodiscus ananasi* shares similar characteristics with *Neocochlearomyces chromolaenae* in having macronematous, mononematous conidiophores and aseptate, hyaline, guttulate conidia with a setula at each end. However, they are entirely different in these aspects. *Neocochlearomyces chromolaenae* has 6–8 thickened transverse septa conidiophores and the stalk forming an apical fan-like conidiogenous region, terminal and intercalary on the one side of the swollen fan-like structure, phialidic conidiogenous cells and falcate conidia. In contrast, *Pseudomycoleptodiscus ananasi* has conidiomatal setae, cylindrical to subcylindrical, unbranched, aseptate conidiophores, holoblastic, monoblastic, discrete, determinate conidiogenous cells and 1-septate, oval to cylindrical conidia. *Pseudomycoleptodiscus ananasi* has larger conidia (15–17 × 6–7 μm vs. 1.5–2.5 × 8.5–12.5 μm) and longer appendages (29–36 μm vs. 3.8–5 μm long) as *Neocochlearomyces chromolaenae* (Crous et al. 2018a). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.15) (Fig. 9). The nucleotide comparisons showed that *P. ananasi* (MFLUCC 23-0165) is significantly different from *Neocochlearomyces chromolaenae* (BCC 68250) in ITS (56/527, 10.6%), LSU (35/729, 4.8%), and SSU (7/1009, 0.7%).

Subclass *Pleosporomycetidae* C.L. Schoch et al.

Hysteriales Lindau

Hysteriales was introduced by Engler & Prantl (1899). This is a monotypic family characterized by hysteriform apothecia. We follow the latest treatment and updated accounts of *Hysteriales* in Wijayawardene et al. (2022).

Hysteriaceae Chevall.

Hysteriaceae was introduced by Chevallier (1826) as "*Hysterineae*". The family includes the hysteriaceous fungi, which contain 13 genera (Engler & Prantl 1899, Wijayawardene et al. 2022, Du et al. 2023). Hysteriaceous fungi are characterized by hysterithecioid or apothecioid, semi-immersed to superficial, carbonaceous, thick-walled, and distinctly navicular with a pronounced, longitudinal slit ascomata, hyaline to pigmented, muriform ascospores and one to multi-septate in bitunicate asci (Tibpromma et al. 2017, Ren et al. 2022a, Du et al. 2023).

Rhytidhysteron Speg.

Rhytidhysteron was introduced by Spegazzini (1881) to accommodate *R. brasiliense* and *R. viride* and is typified by *R. brasiliense*. Thirty-six records are listed in Index Fungorum (2023). *Rhytidhysteron* is characterized by closed and navicular ascomata, later opening by a longitudinal slit to become irregularly apothecioid at maturity and heavily pigmented, and with thick-walled ascospores (Manawasinghe et al. 2022, Ren et al. 2022a, Du et al. 2023). *Rhytidhysteron* can be found as saprobes, endophytes, and weak pathogens on woody plants (Spegazzini 1881, Tibpromma et al. 2017, Ren et al. 2022a, Du et al. 2023, Senwanna et al. 2023).

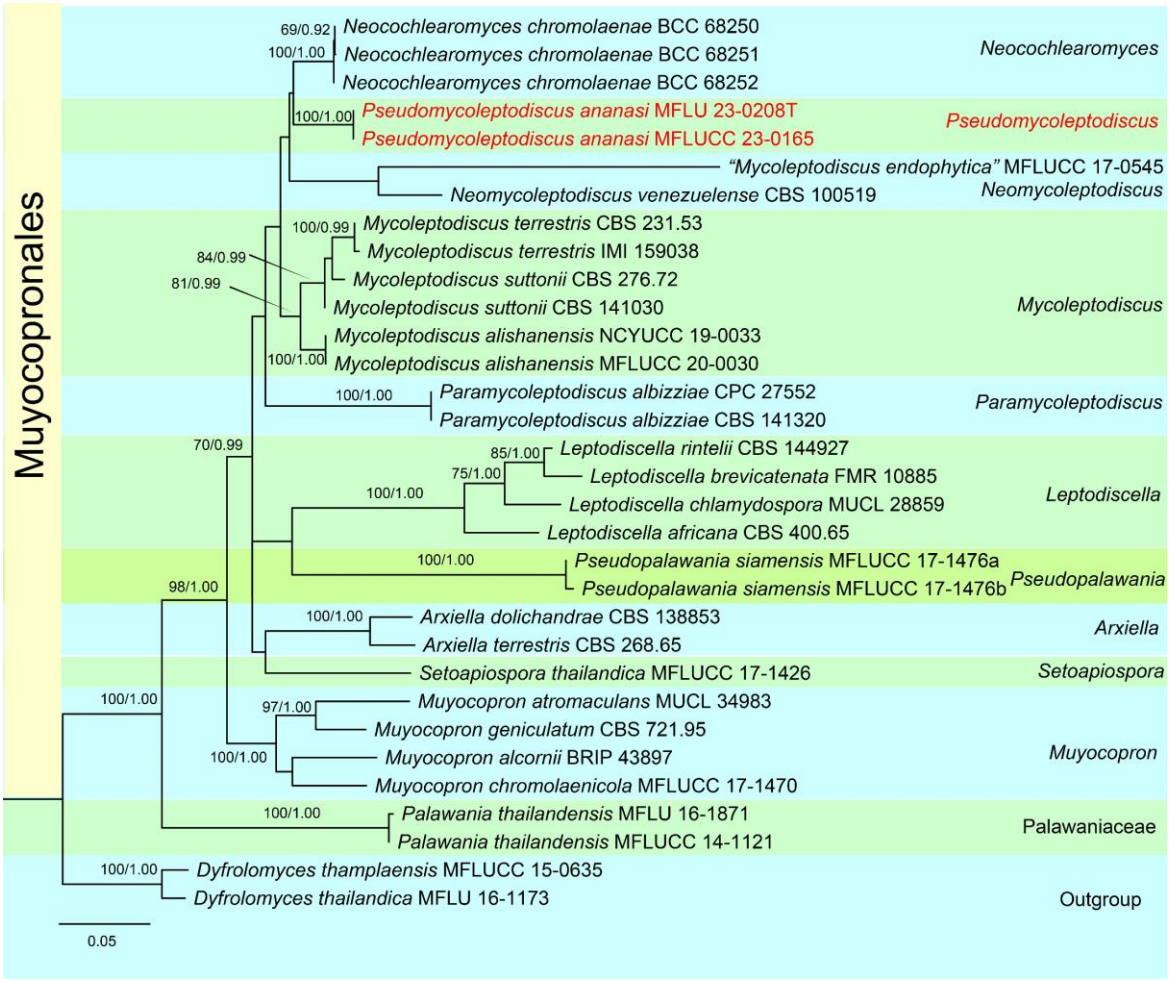

Figure 8 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and SSU sequence data. Thirty-two strains are included in the combined sequence analysis, which comprises 2395 characters with gaps. *Dyfrolomyces thailandica* (MFLU 16-1173) and *D. thamplaensis* (MFLUCC 15-0635) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -12426.202693 is presented. The matrix had 700 distinct alignment patterns, with 35.89% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237641, C = 0.243613, G = 0.295670, T = 0.223076; substitution rates AC = 1.815896, AG = 2.931624, AT = 1.421494, CG = 1.594390, CT = 6.095597, GT = 1.000000; gamma distribution shape parameter α = 0.289945. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

5. *Rhytidhysteron neorufulum* Thambug. & K.D. Hyde, in Thambugala et al., Cryptog. Mycol. 37(1): 110 (2016) Fig. 10

Index Fungorum number: IF551865; Facesoffungi number: FoF01840

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Ascomata* 1330–2180 µm long × 580–950 µm wide × 430–680 µm high ($\bar{x}$ = 1750 × 765 × 558 µm, n = 10), superficial, hysterothecial solitary to aggregated, elliptic or irregular in shape, coriaceous, black, when dry folded at the margin, forming an elongate slit. *Exciple* 70–150 µm wide, composed of dark brown, thick-walled cells of *textura angularis*, outer layer brown to dark brown, inner layer pale brown to hyaline. *Hamathecium* comprised of 1.5–2.5 µm wide, dense, hyaline, septate, branched, cellular pseudoparaphyses. *Asci* 150–200 µm × 10–13.5 µm ($\bar{x}$ = 178 × 13 µm, n = 10), bitunicate, 8-spored, clavate to cylindrical, with a long pedicel, rounded at the apex, without a distinct ocular chamber. *Ascospores* 25–30 µm × 9.5–15 µm ($\bar{x}$ = 28 × 10 µm, n = 30), uniseriate, slightly

overlapping, hyaline to yellowish when immature and reddish brown to brown when mature, ellipsoidal to fusiform, straight or curved, rounded to slightly pointed at both ends, guttulate, (1–)3-septate when mature, constricted at central septum, slightly rough-walled, without a mucilaginous sheath. Asexual morph: Not observed.

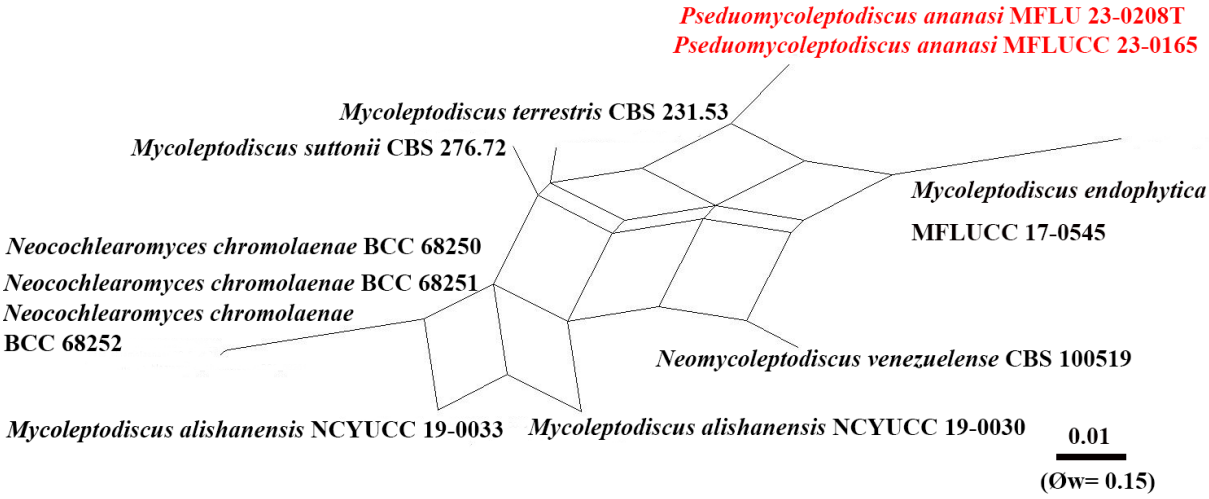

Figure 9 – Results of the PHI test of *Pseudomycoleptodiscus ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

Material examined – China, Yunnan Province, Xishuangbanna City, Jinghong District, on decaying leaves of *Cocos nucifera*, 15 September 2021, X.G. Tian, C10-2 (GZAAS 23-0583).

Known host and distribution – on dead stem in Thailand (Thambugala et al. 2016); on dead twigs/stem *Hevea brasiliensis* in Thailand (Huanraluek et al. 2020, Senwanna et al. 2021); on dead wood of *Tectona grandis* (*Lamiaceae*) in Thailand (Ren et al. 2022a); on decaying wood of *Elaeagnus sarmentosa* (*Elaeagnaceae*) in China (Du et al. 2023); on decaying leaves of *Cocos nucifera* in China (this study).

GenBank numbers – LSU = OR438806, ITS = OR438335, SSU = OR458330, *tef1-α* = OR500303.

Notes – In the multi-loci phylogenetic analyses, our strain (GZAAS 23-0583) is grouped together with *Rhytidhysteron neorufulum* strains (Fig. 11). Our collection is similar to *R. neorufulum* (MFLU 14-0609, holotype) in having superficial, hysterothecial solitary to aggregated, elliptic or irregular, coriaceous ascomata, 8-spored, cylindrical asci, and uniseriate, ellipsoidal to fusiform, reddish brown to brown ascospores when mature (Thambugala et al. 2016). Our collection also shares a similar size range of ascospores (25–30 µm × 9.5–15 µm vs. 27–34 × 7–10.6 µm) and asci (150–200 µm vs. 185–220 µm) to *R. neorufulum* (MFLU 14-0609). Thus, we named our strain as *R. neorufulum*. Our strain *Rhytidhysteron neorufulum* (GZAAS 23-0583) is reported as a new host record on *Cocos nucifera*.

Pleosporales Luttrell ex M.E. Barr

Pleosporales was established by Luttrell (1955) to accommodate members of *Dothideomycetes* having perithecioid ascomata with pseudoparaphyses amongst the asci (Luttrell 1955, Zhang et al. 2009). Among the orders of *Dothideomycetes*, *Pleosporales* is the largest and most diverse order containing more than 90 families (Wijayawardene et al. 2022).

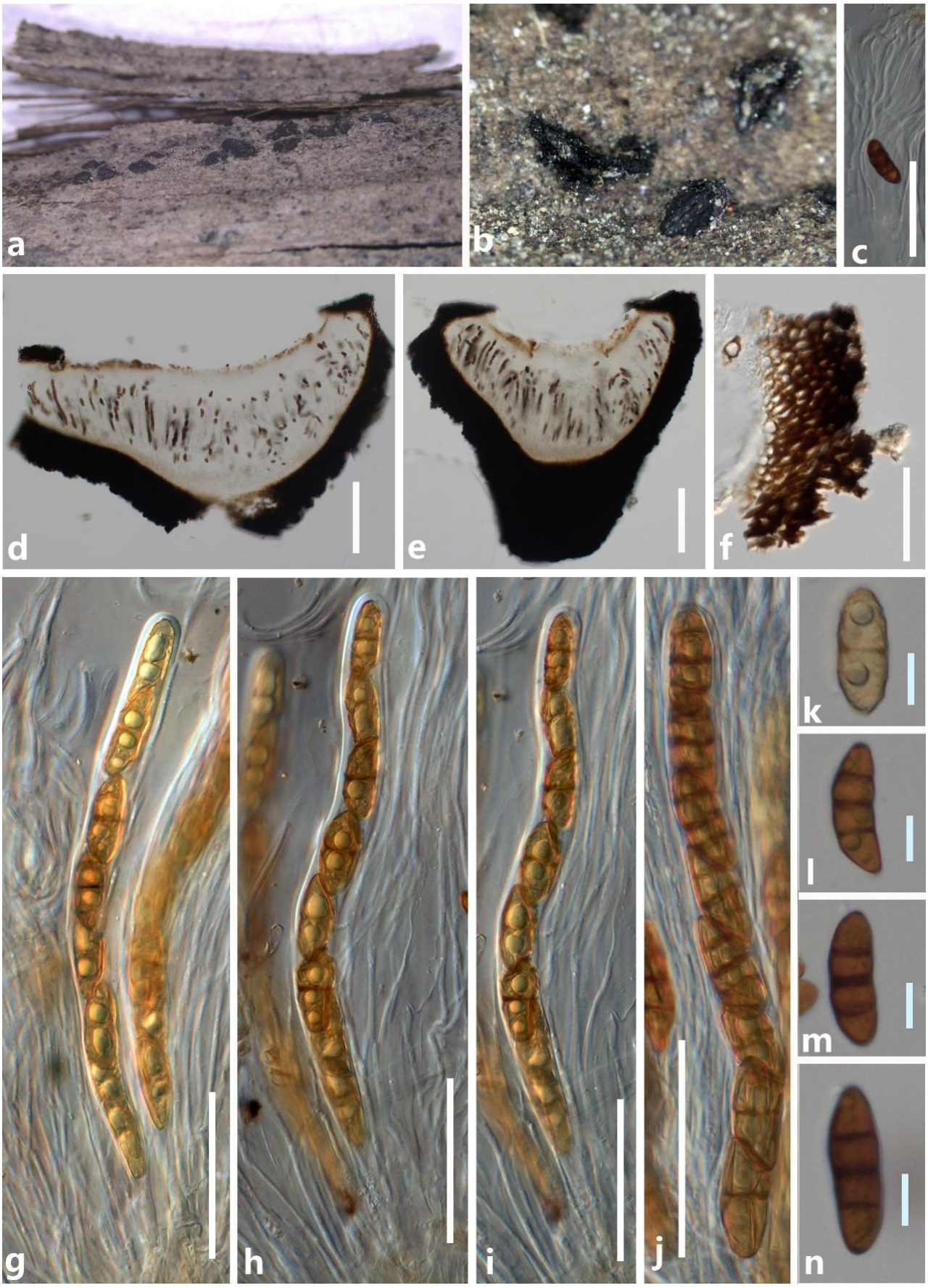

Figure 10 – *Rhytidhysteron neorufulum* (GZAAS 23-0583, new host record). a, b Appearance of ascomata on the host surface. d, e Sections of ascoma. c Pseudoparaphyses f Peridium. g–j Asci, k–n Ascospores. Scale bars: d, e = 200 μm, c, f, g–j = 50 μm, k–n = 10 μm.

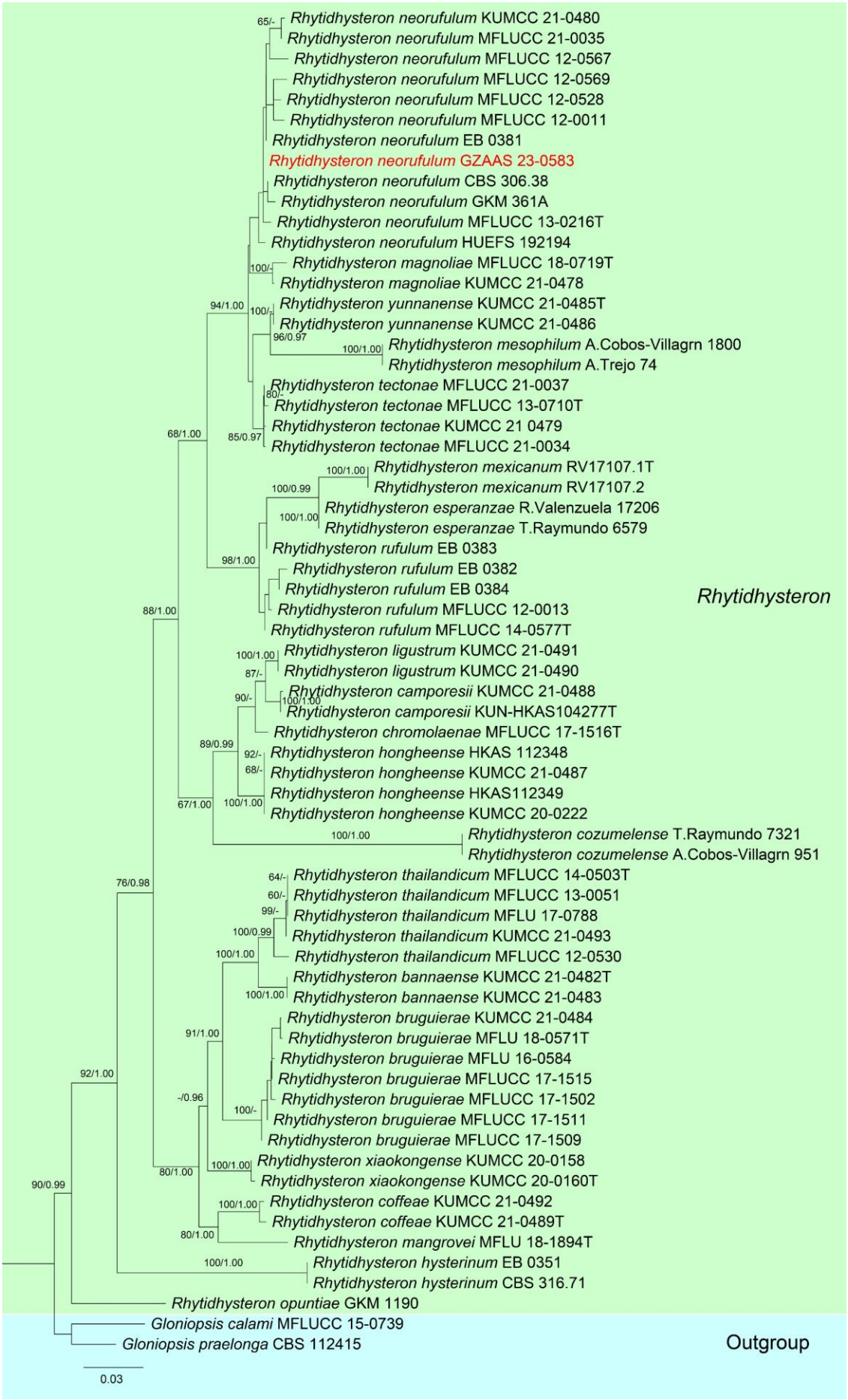

Figure 11 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

SSU, and *tef1-α* sequence data. Related sequences were obtained from Du et al. (2023). Sixty-six strains are included in the combined sequence analysis, which comprise 3603 characters with gaps. *Gloniopsis calami* (MFLUCC 15-0739) and *G. praelonga* (CBS 112415) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -13823.305195 is presented. The matrix had 1020 distinct alignment patterns, with 30.24% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240496, C = 0.248284, G = 0.276517, T = 0.234703; substitution rates AC = 1.296332, AG = 2.756373, AT = 1.619981, CG = 0.911211, CT = 4.806161, GT = 1.000000; gamma distribution shape parameter 0.129289. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Dictyosporiaceae Boonmee & K.D. Hyde

Boonmee et al. (2016) introduced *Dictyosporiaceae* to accommodate mostly aquatic lignicolous species with cheiroid, digitate, palmate and/or dictyosporous conidia and their sexual morphs that form a monophyletic clade in the class. The family comprises 17 genera and the type genus is *Dictyosporium*, which has been reported from plant litter and decaying wood in terrestrial and aquatic habitats, and is worldwide in distribution (Tsui et al. 2000, Cai et al. 2003, Yang et al. 2018, Hongsanan et al. 2020a, Wijayawardene et al. 2022).

Dictyocheirospora M.' souza, Boonmee & K.D. Hyde, Fungal Divers. 80: 465 (2016)

Boonmee et al. (2016) introduced *Dictyocheirospora* which is typified by *D. rotunda* that producing aeroaquatic dark sporodochial colonies with cheiroid dictyospores. No sexual morph has been described from this genus (Boonmee et al. 2016, Dong et al. 2020). *Dictyocheirospora* is saprobic on decaying wood in freshwater and terrestrial habitats (Yang et al. 2018, Jayasiri et al. 2019, Dong et al. 2020, Phukhamsakda et al. 2020). There are 24 records listed in Index Fungorum (2023). In this study, we collected *Dictyocheirospora nabanheensis* from *Cocos nucifera* for the first time.

6. *Dictyocheirospora nabanheensis* Tibpromma & K.D. Hyde, in Tibpromma et al., Fungal Divers. 92: 10 (2018) Fig. 12

Index Fungorum number: IF554474; Facesoffungi number: FoF04483

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Conidiomata* sporodochial, superficial, scattered, dark brown to black on natural substrate. *Mycelium* immersed, composed of pale brown, smooth hyphae. *Conidiophores* micronematous, short, reduced to conidiogenous cells. *Conidiogenous cells* 4.5−15 × 4−5 μm ($\overline{x}$ = 7.5 × 4.5 μm), holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* 35−40 × 15−20 μm ($\overline{x}$ = 37 × 16 μm), solitary, oval to ellipsoid, acrogenous, cheiroid, pale brown to brown, consisting of 5–6 rows of cells, with rows cylindrical, palmately divergent, inwardly curved at the tip, arising from a basal cell, with rounded to cylindrical appendage, each row composed of 8–10 cells, euseptate, slightly constricted at septa, guttulate in each cell, smooth-walled.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, C3-3)MFLU 23-0164(, living culture MFLUCC 23-0171.

Known host and distribution – On *Pandanus* sp. from China (Tibpromma et al. 2018); on *Leucaena* sp. from Thailand (Jayasiri et al. 2019); on *Borassus flabellifer* from India (Rajeshkumar et al. 2021); on *Cocos nucifera* from Thailand (this study).

GenBank numbers – LSU = OR438807, ITS = OR438336, *tef1-α* = OR500304.

Notes – In our phylogenetic analyses, our strain (MFLUCC 23-0171) grouped with two strains of *Dictyocheirospora nabanheensis* (MFLUCC 17-0562 and MFLUCC 22-0094) with 100 ML and 1.00 PP statistical support (Fig. 13). Our new isolate is similar to the holotype of *D. nabanheensis* (HKAS 101807) except for the smaller conidiogenous cells ($\overline{x}$ = 7.5 × 4.5 μm vs.

$\bar{x}$ = 12 × 5.5 µm) (Tibpromma et al. 2018). Based on nucleotide comparisons, our strain (MFLU 23-0164) is not significantly different from the ex-type isolate (MFLUCC 17-0562) in ITS, LSU, SSU and *tef1-α*. Therefore, we identified our isolate as *D. nabanheensis*, which is a new host record from *Cocos nucifera*.

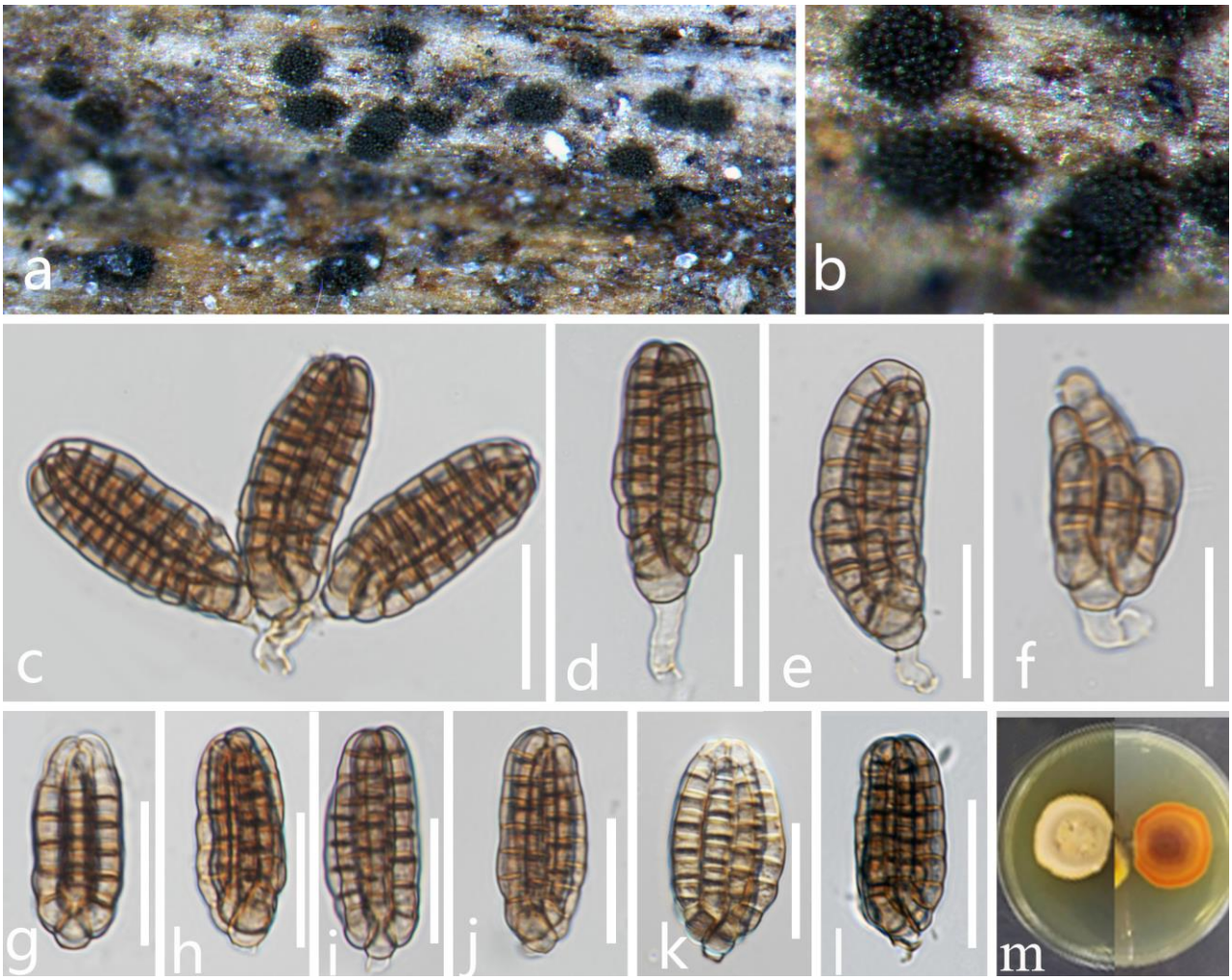

Figure 12 – *Dictyocheirospora nabanheensis*)MFLU 23-0164, new host record(. a, b Appearance of the colonies on dead leaves of *Cocos nucifera*. c–f Conidiophore with conidia. g–l Conidia. m Colonies on PDA from surface and reverse. Scale bars: c–l = 20 µm.

Didymellaceae Gruyter

Didymellaceae was introduced by de Gruyter et al. (2009) with the type *Didymella*. *Didymellaceae* is the largest family in the *Pleosporales*. Species belonging to *Didymellaceae* are cosmopolitan and often plant pathogens on a wide range of hosts, mainly causing leaf and stem lesions (de Gruyter et al. 2009, Chen et al. 2017b). They are also endophytic, saprobic, fungicolous and lichenicolous (Aveskamp et al. 2010). The family comprises 44 genera (Wijayawardene et al. 2022). The sexual morph of this family is characterized mainly by immersed pseudothecia, globose to flattened, ostioles, with pseudoparenchymatal cells, 8-spored bitunicate asci, cylindrical to clavate or saccate, 1-septate ascospores (didymospores) or multi-septate dictyospores. The asexual morphs are coelomycetous with pycnidial conidiomata, sometimes becoming erumpent, uni-locular with cells of *textura angularis*, mostly conidiophores are absent, and then either filiform, septate, and branched, and ramified respectively, enteroblastic conidiogenous cells, phialidic, doliiform to lageniform, smooth-walled and conidia of various shapes (ellipsoid, cylindrical, fusiform, pyriform or globose), hyaline or pigmented, septate or aseptate, guttulate (Hongsanan et al. 2020a).

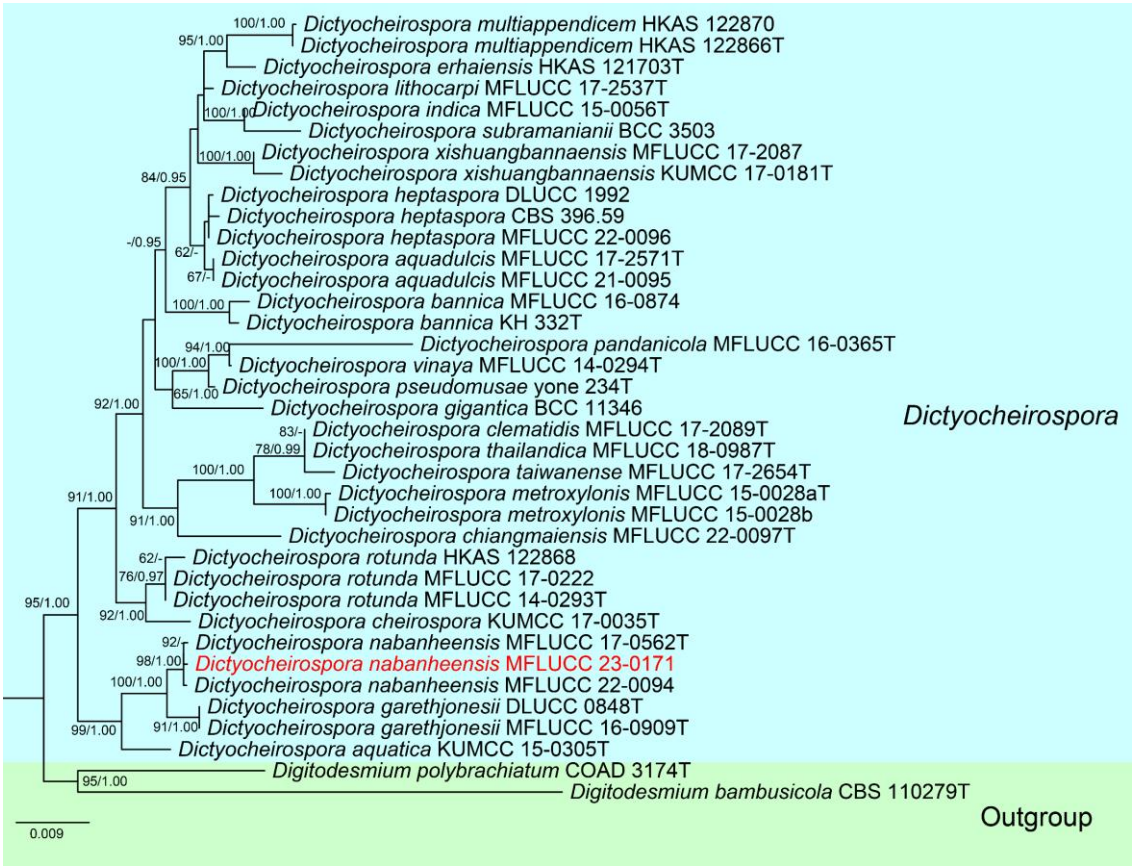

Figure 13 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1-α* sequence data. Related sequences were obtained from Jayasiri et al. (2019). Thirty-seven strains are included in the combined sequence analysis, which comprises 3764 characters with gaps. *Digitodesmium bambusicola* (CBS 110279) and *D. polybrachiatum* (COAD 3174) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -9131.398926 is presented. The matrix had 573 distinct alignment patterns, with 36.80% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241709, C = 0.248410, G = 0.267650, T = 0.242231; substitution rates AC = 2.030907, AG = 3.333139, AT = 2.243761, CG = 0.988458, CT = 10.225470, GT = 1.000000; gamma distribution shape parameter α = 0.020000. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Epicoccum Link

Epicoccum was introduced by Link (1815) with *Epicoccum nigrum* as the type species and emended by Chen et al. (2015). Species are saprobes (Jayasiri et al. 2017), pathogens (Raza et al. 2019), and endophytes (Fávaro et al. 2012, Dzoyem et al. 2017) on various plant parts in aquatic and terrestrial habitats (Voronin et al. 2021, Barreto et al. 2022). *Epicoccum* has hyphomycetous and coelomycetous synanamorphs (Chen et al. 2015, Thambugala et al. 2017). The hyphomycetous anamorph is characterized by having dark sporodochia with branched conidiophores and mono- to polyblastic, colourless conidiogenous cells that produce coloured, sometimes verruculose, dictyoconidia (Link 1815, Chen et al. 2015, de Silva et al. 2021). The coelomycetous anamorph is characterized by the formation of conidia in pycnidial conidiomata (Chen et al. 2015). There are 161 records available in Index Fungorum (2023). However, for most of the species described before the year 2000, sequence data are unavailable and only 48 species are known with sequence data (de Silva et al. 2021, Keirnan et al. 2021). In this study, we introduce a new record (*Epicoccum italicum*) and a new species *E. yunnanensis* to accommodate three strains of *E. endophyticum* and a new collection.

7. *Epicoccum italicum* Qian Chen, Crous & L. Cai, in Chen et al., Stud. Mycol. 87: 144(2017)
Fig. 14

Index Fungorum number: IF818965; Facesoffungi number: FoF14283

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Colonies* effuse on the natural substrate, scattered, dark brown to dark. *Conidiomata* sporodochial, globose, mainly solitary, superficial. *Conidiophores* reduced to holoblastic conidiogenous cells. *Conidia* 10−25 ($\bar{x}$ = 16 µm) diam., multicellular-phragmosporous, verrucose, globose to subglobose-pyriform, truncate at base, brown to dark brown.

Culture characteristics – Colonies on PDA, 15–20 mm diam. after 7 d, margin irregular, yellow with a white margin; reverse salmon to saffron.

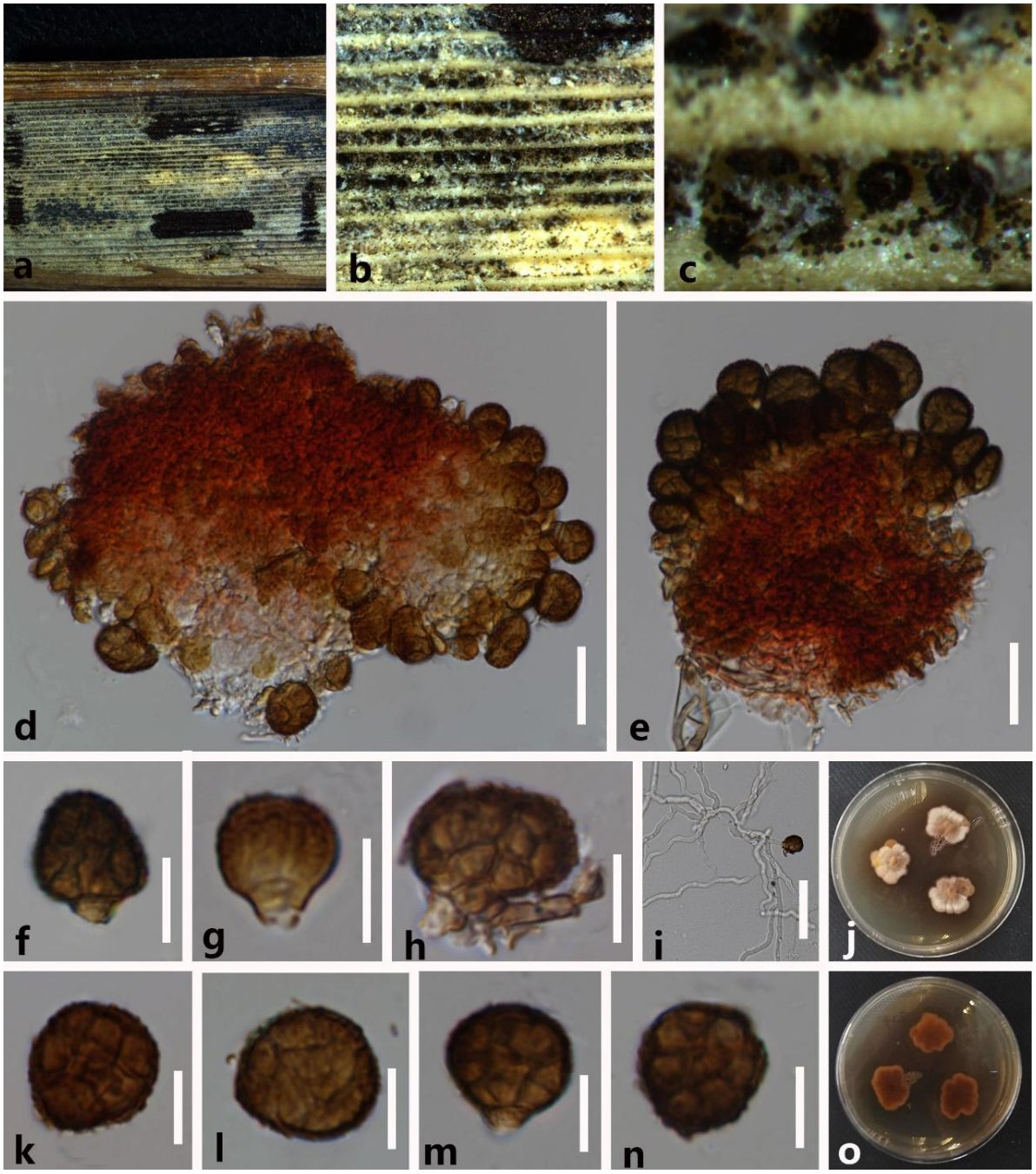

Figure 14 – *Epicoccum italicum* (MFLU 23-0166, new host and geographical record). a–c Colonies on dead leaves of *Ananas comosus*. d, e Sporodochium. f–h, k–n Conidia. i Germinated conidium. j, o Colonies on PDA from surface and reverse. Scale bars: d, e = 20 µm, i = 60 µm, f–h, k–n = 10 µm.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 18 July 2020, X.G. Tian, P4-5 (MFLU 23-0166), living culture MFLUCC 23-0105.

Known hosts and distribution – On seedlings of *Acca sellowiana* in Italy (Chen et al. 2017a); on sediment of Lakes in Antarctic Peninsula (Ogaki et al. 2020); on *Quercus robur* in Poland (Rivera-Vega et al. 2022); on *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438808, ITS = OR438337, *rpb2* = OR634955.

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0105) clusters with the ex-type strain of *Epicoccum italicum* (CGMCC 3.18361) with 100% ML and 1.00 PP statistical support (Fig. 15). Morphologically, our strain is similar to the holotype of *E. italicum* in having sporodochial, superficial conidiomata and multicellular-phragmosporous, verrucose, subglobose-pyriform, brown conidia and the conidial size of our collection is also similar to *E. italicum* (10−25 μm vs. 12.5–28 μm). The nucleotide comparisons showed that our strain (MFLUCC 23-0105) is not significantly different from the type strain of *E. italicum* (CGMCC 3.18361) in ITS and *rpb2*. Thus, based on the recommendations of Chethana et al. (2021), we identified our strain as *E. italicum*. Our strain *E. italicum* (MFLUCC 23-0105) is reported as a new host and geographical record on *Ananas comosus* in Thailand.

8. *Epicoccum yunnanensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 16

Index Fungorum number: IF900970; Facesoffungi number: FoF14282

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: *Colonies* effuse on the natural substrate, scattered, dark brown to dark. *Conidiomata* sporodochial, globose, mostly solitary, superficial. *Conidiophores* micronematous, reduced to holoblastic conidiogenous cells. *Conidia* 10−15 × 6−9 μm ($\overline{x}$ = 14 × 7 μm, n = 40), brown to dark brown, mostly ellipsoid, rarely globose to subglobose, verruculose, truncate at base, sometimes with a basal cell.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Oryza sativa*, 18 September 2020, X.G. Tian, r1-5 (MFLU 23-0165, holotype).

Known hosts and distribution – On *Magnolia candolli* in China (de Silva et al. 2021); on *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438809, ITS = OR438338.

Notes – *Epicoccum endophyticum* (JZB380043 and JZB380044) was introduced by Manawasinghe et al. (2020). Later, de Silva et al. (2021) introduced another new species also named as *E. endophyticum* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097). However, *Epicoccum endophyticum* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097) has different characteristics as compared to *E. endophyticum* (JZB 380043 and JZB 380044) (Manawasinghe et al. 2020, de Silva et al. 2021) and our multi-loci phylogenetic analyses showed that *E. endophyticum* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097) did not cluster with *E. endophyticum* (JZB 380043 and JZB 380044) (Fig. 15). Later, *E. endophyticum* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097) is Nom. illegit., Art. 53.1. Therefore, we identified them as different species and introduced *Epicoccum yunnanensis* as a new name to accommodate the three strains of *E. endophyticum* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097).

In our phylogenetic analyses, our new collection (MFLU 23-0165) grouped with *Epicoccum yunnanensis* (HMCE12, MFLUCC 19-0047 and MFLUCC 19-0097, ex-type) (Fig. 15). Our new collection is similar to *E. yunnanensis* in having sporodochial, globose, mainly solitary conidiomata, with micronematous conidiophores which are reduced to conidiogenous cells and brown to dark brown, mostly ellipsoid, verrucose conidia (de Silva et al. 2021). The conidial size (10−15 × 6−9 μm vs. 10–15 × 8–10 μm) of our new collection is also similar to the holotype of *E. yunnanensis* (MFLUCC 19-0097), and the nucleotide comparisons show that our strain (MFLU 23-0165) is not significantly different from the other *E. yunnanensis* strains (MFLUCC 19-0047 and MFLUCC 19-0097) in ITS. Therefore, we identified our collection as a new species, *E. yunnanensis*. Our new collection was first found as a saprobe on dead leaves of *Oryza sativa* and

a geographic record from Thailand, while de Silva et al. (2021) reported this species as an endophyte in *Magnolia candolli* from China, which shows that this species can have more than one life mode.

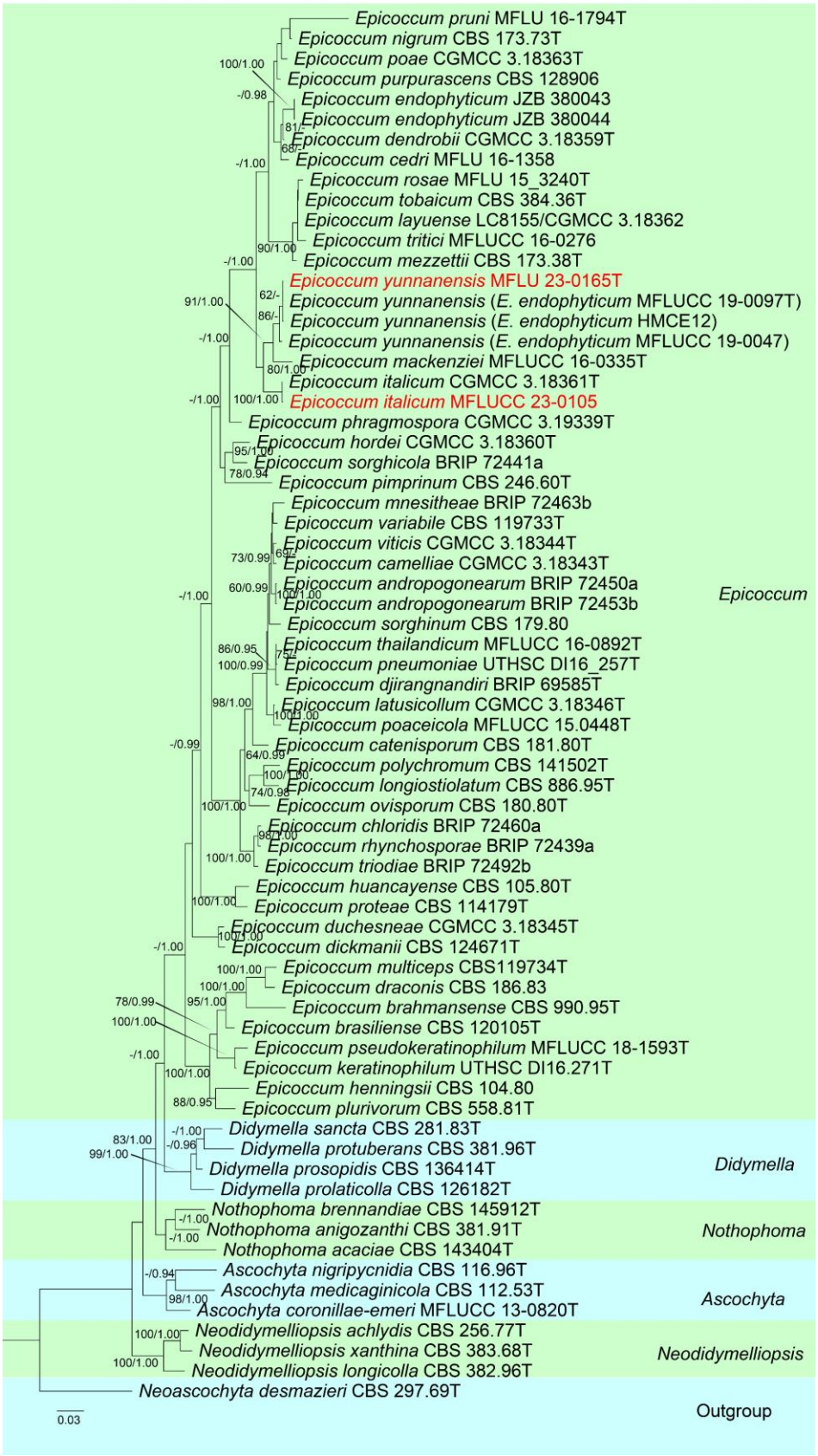

Figure 15 – Phylogram generated from maximum likelihood analysis based on combined LSU,

SSU, *tub2* and *rpb2* sequence data. Related sequences were obtained from Keirnan et al. (2021) and de Silva et al. (2021). Sixty-nine strains are included in the combined sequence analysis, which comprise 2737 characters with gaps. *Neoascochyta desmazieri* (CBS 297.69) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -16285.503408 is presented. The matrix had 815 distinct alignment patterns, with 20.76% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241115, C = 0.245717, G = 0.272236, T = 0.240932; substitution rates AC = 1.558687, AG = 1.558687, AT = 1.850179, CG = 0.904162, CT = 11.412768, GT = 1.000000; gamma distribution shape parameter α = 0.144200. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

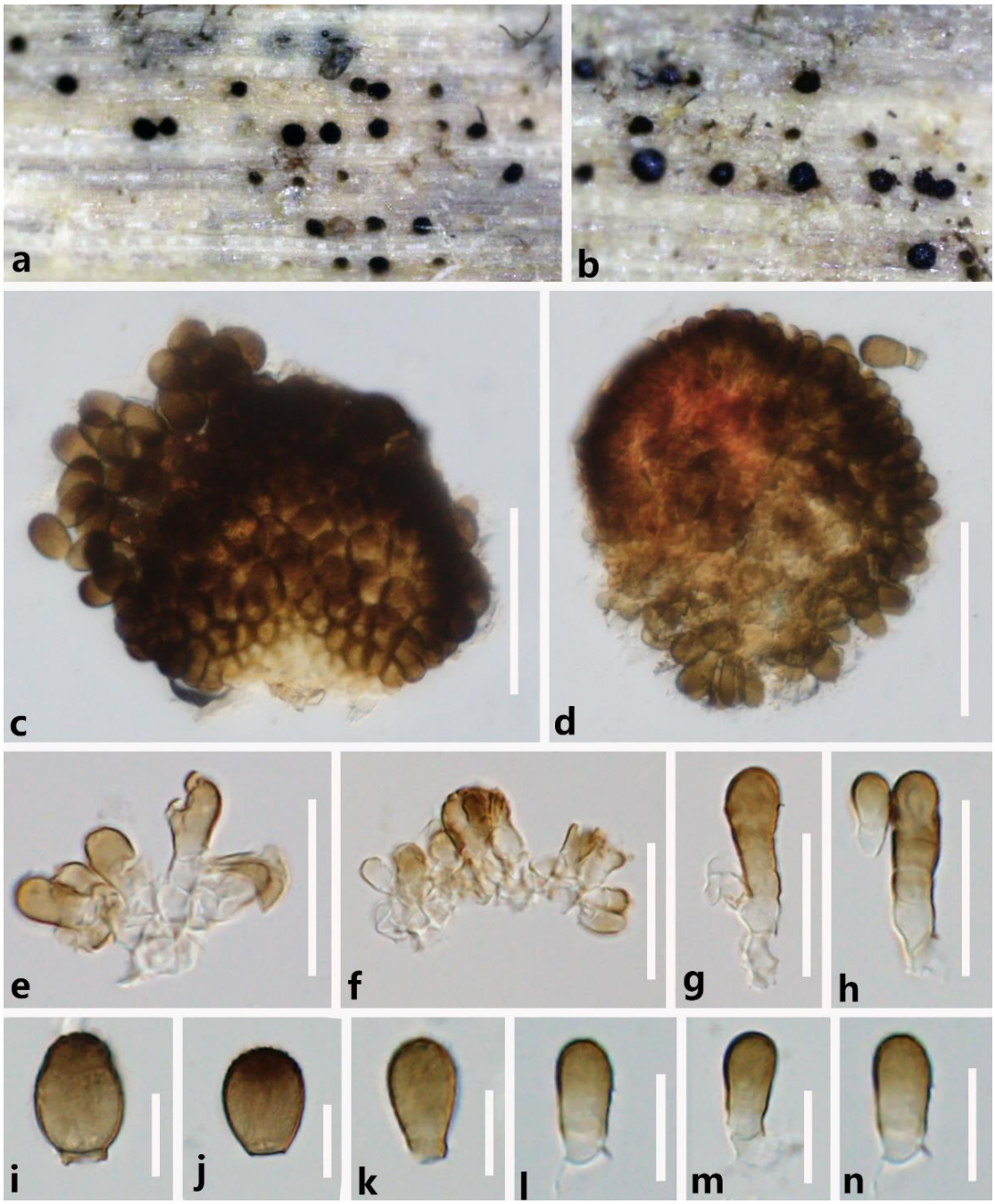

Figure 16 – *Epicoccum yunnanensis* (MFLU 23-0165, holotype). a, b Colonies on dead leaves of *Oryza sativa*. c, d Sporodochium. e–h Conidiogenous cells with attached conidium, i–n Conidia. Scale bars: c, d = 50 μm, e–h = 20 μm, i–n = 10 μm.

Didymosphaeriaceae Munk

Didymosphaeriaceae was introduced by Munk (1953) with *Didymosphaeria epidermidis* as the type species. To date, there are 33 genera with 255 species belonging to *Didymosphaeriaceae* (Wijayawardene et al. 2022). The sexual morphs of *Didymosphaeriaceae* are characterized by globose to subglobose, centrally ostiolate ascomata, trabeculate pseudoparaphyses (Liew et al. 2000), which anastomosed mostly above the asci, cylindric or oblong, pedicellate asci and brown, thick-walled, septate ascospores (Aptroot 1995, Ariyawansa et al. 2014). The asexual morphs of *Didymosphaeriaceae* are fusicladium-like and phoma-like (Hyde et al. 2013). Species in *Didymosphaeriaceae* are mainly found in terrestrial habitats and aquatic environments as saprobes, endophytes, pathogens and hemibiotrophs on woody branches and herbaceous stems and leaves, and are also parasitic on other fungi (Ariyawansa et al. 2014, Thambugala et al. 2017, Phookamsak et al. 2019).

Chromolaenicola Mapook

Chromolaenicola was introduced by Mapook et al. (2020a) with the type species *C. nanensis*. There are six species belonging to this genus, which are saprobes (Mapook et al. 2020a, Phukhamsakda et al. 2020). The sexual morph of *Chromolaenicola* is characterized by immersed to semi-immersed and coriaceous ascomata, cylindrical asci, and uniseriate, ellipsoid, muriform ascospores (Mapook et al. 2020a). The asexual morph is pycnidial, with enteroblastic, phialidic conidiogenous cells, and oblong or oval to ellipsoid, globose to subglobose conidia (Jayasiri et al. 2019, Mapook et al. 2020a). We introduce a new species *C. ananasi* based on morphological comparison and phylogenetic analyses.

9. *Chromolaenicola ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 17

Index Fungorum number: IF900971; Facesoffungi number: FoF14284

Etymology – Referring to the host *Ananas comosus*, on which the specimen was collected.

Holotype – MFLU 23-0167

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Colonies* superficial, scattered, gregarious, punctiform to effuse, dark brown to black. *Conidiophores* filamentous, septate, branched, often reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, monoblastic, terminal, determinate, hyaline to brown, branched, smooth, elongated, flat at apex. *Conidia* 7–8 × 4–5 µm ($\bar{x}$ = 8 × 5 µm, n = 35), solitary, oval to ellipsoid, aseptate, pale brown to brown, guttulate when mature, verruculose, thick-walled.

Culture characteristics – Conidia germinating on PDA within 12 h at room temperature. Colonies circular, mycelium slightly flattened, filamentous, cultures creamy white on surface, white to yellow brown in reverse from edge to the centre of the colony.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 17 August 2020, X.G. Tian, p7-7 (MFLU 23-0167, holotype), ex-type living culture MFLUCC 23-0111.

GenBank numbers – MFLU 23-0167: LSU = OR438810, ITS = OR438339, SSU = OR458331, *tef1-α* = OR500305. MFLUCC 23-0111: LSU = OR438811, ITS = OR438340, SSU = OR458332, *tef1-α* = OR500306.

Notes – In the phylogenetic analyses of combined ITS, LSU, SSU, and *tef1-α* sequence data, our strain (MFLU 23-0167 and MFLUCC 23-0111) formed a separate branch and clusters with *Chromolaenicola sapindi* with 99% ML and 1.00 PP bootstrap support (Fig. 18). *Chromolaenicola sapindi* was introduced by Ren et al. (2022b) based solely on sexual morphs characters. *Chromolaenicola ananasi* shares similar asexual morphology to *C. chiangraiensis*, *C. lampangensis*, and *C. siamensis* in having conidiophores reduced to conidiogenous cells, hyaline and unbranched, smooth, elongated conidiogenous cells and ellipsoid, brown, thick-walled and verruculose conidia. However, *C. ananasi* differs in having pale brown to brown conidia which are aseptate and guttulate when mature, while *C. chiangraiensis*, *C. lampangensis*, and *C. siamensis* have reddish brown conidia which are 1-septate when mature, and not constricted at the septum. In

addition, *C. ananasi* has smaller conidia (7−8 × 4−5 µm in *C. ananasi* vs. 9–14 × 6–9 µm in *C. chiangraiensis* vs. 12–15 × 4–6.5 µm in *C. lampangensis*). The PHI test revealed no significant recombination event between *Chromolaenicola ananasi* and closely related taxa (Φw = 0.3) (Fig. 19). In addition, nucleotide comparisons of ITS and *tef1-α* gene regions revealed 6 bp and 10 bp differences between *C. ananasi* and *C. sapinda* respectively. Thus, we introduce *C. ananasi* as a new species based on phylogenetic analyses and morphological characters.

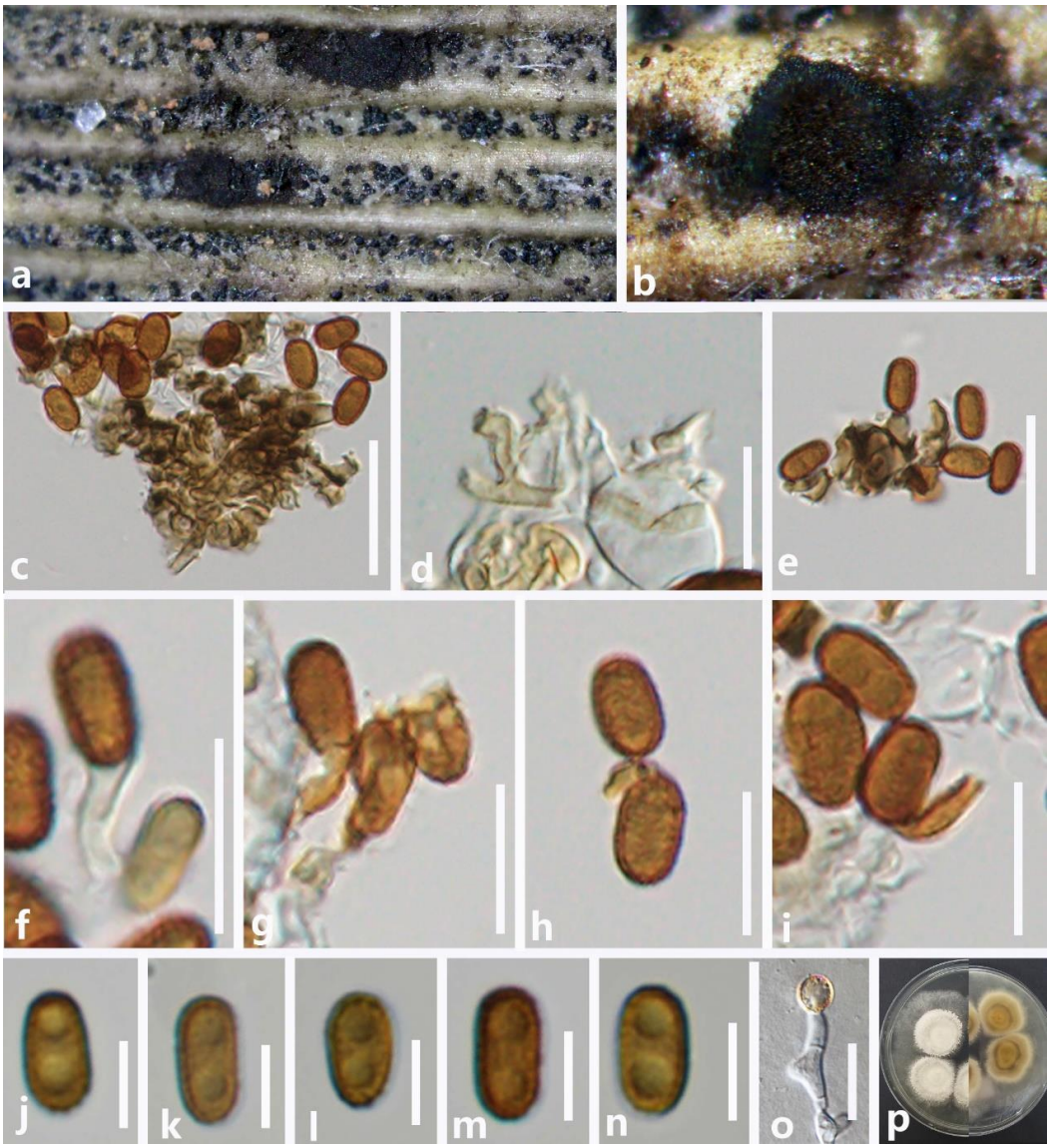

Figure 17 – *Chromolaenicola ananasi* (MFLU 23-0167, holotype). a, b Colonies on dead leaves of *Ananas comosus*. c–h Conidiogenous cells with conidia. i–n Conidia. o Germinated conidium. p Colonies on PDA from surface and reverse. Scale bars: c–e, o = 20 µm, d, f–i = 10 µm, j–n = 5 µm.

Montagnula Berlese

Montagnula was introduced by Berlese (1896) to accommodate *M. infernalis* and the genus was placed in *Didymosphaeriaceae* by Ariyawansa et al. (2014). *Montagnula* comprises saprobes growing on dead plants and *Montagnula* species are characterized by globose, immersed ascomata with a clypeus, claviform asci, fusoid or ellipsoid ascospores with transverse septa and one or more longitudinal septa (Ariyawansa et al. 2014, Mapook et al. 2020a). Recently, Sun et al. (2023) introduced two new species in the genus and synonymized *M. chromolaenicola*, *M. puerensis*, *M. saikhuensis*, and *M. thailandica* under *M. donacina*. Forty-nine records of this genus are listed

in Index Fungorum (2023). In this study, a new host record *M. donacina* is described based on morphology and molecular data.

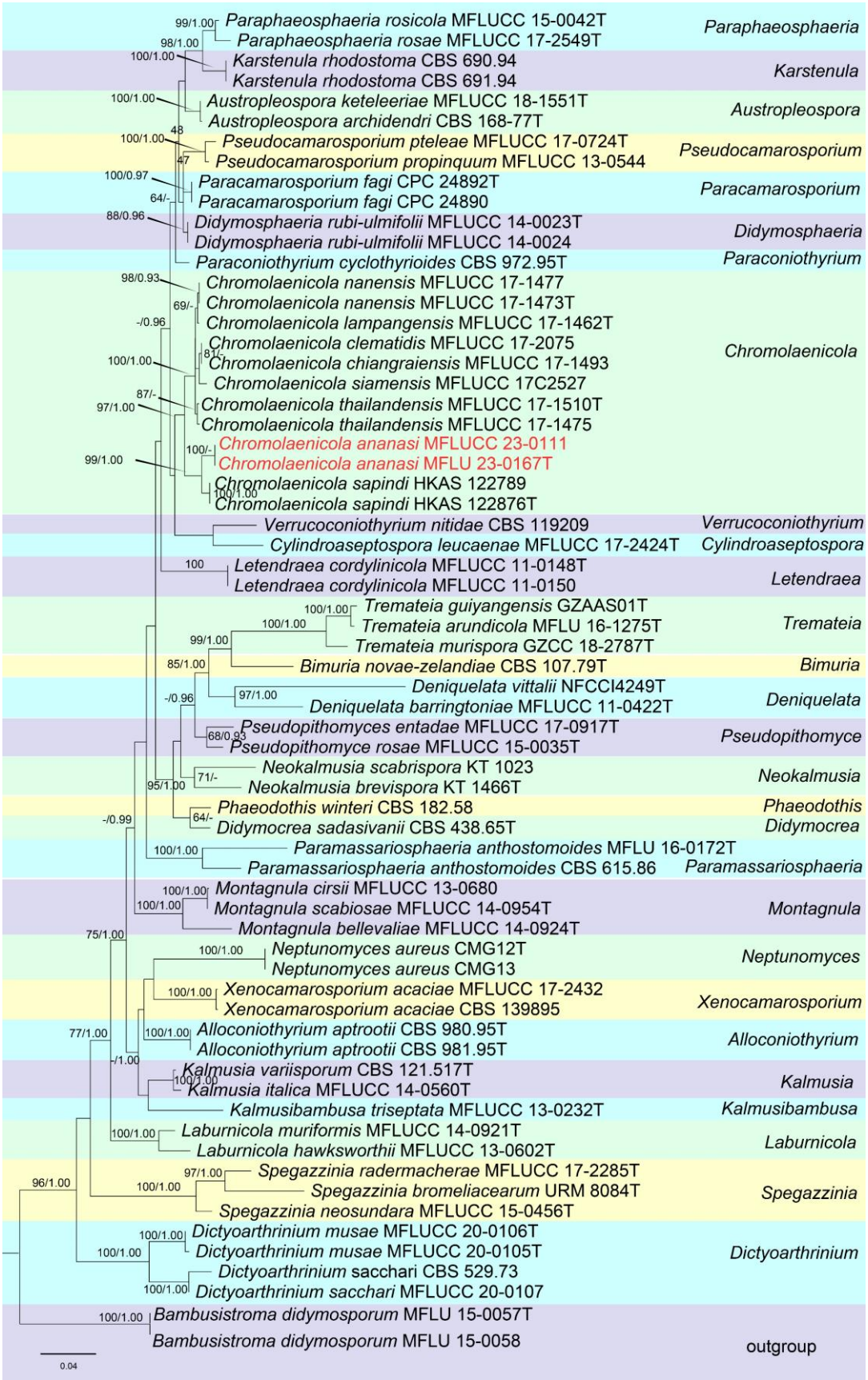

Figure 18 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

SSU, and *tef1-α* sequence data. Related sequences were obtained from Mapook et al. (2020a) and Samarakoon et al. (2020b). Sixty-six strains are included in the combined sequence analysis, which comprise 3416 characters with gaps. *Bambusistroma didymosporum* (MFLU 15-0057T and MFLU 15-0058) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -15435.880186 is presented. The matrix had 858 distinct alignment patterns, with 23.84% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238114, C = 0.250965, G = 0.270076, T = 0.240844; substitution rates AC = 1.378497, AG = 2.210004, AT = 1.406920, CG = 1.029879, CT = 7.001042, GT = 1.000000; gamma distribution shape parameter α = 0.174968. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

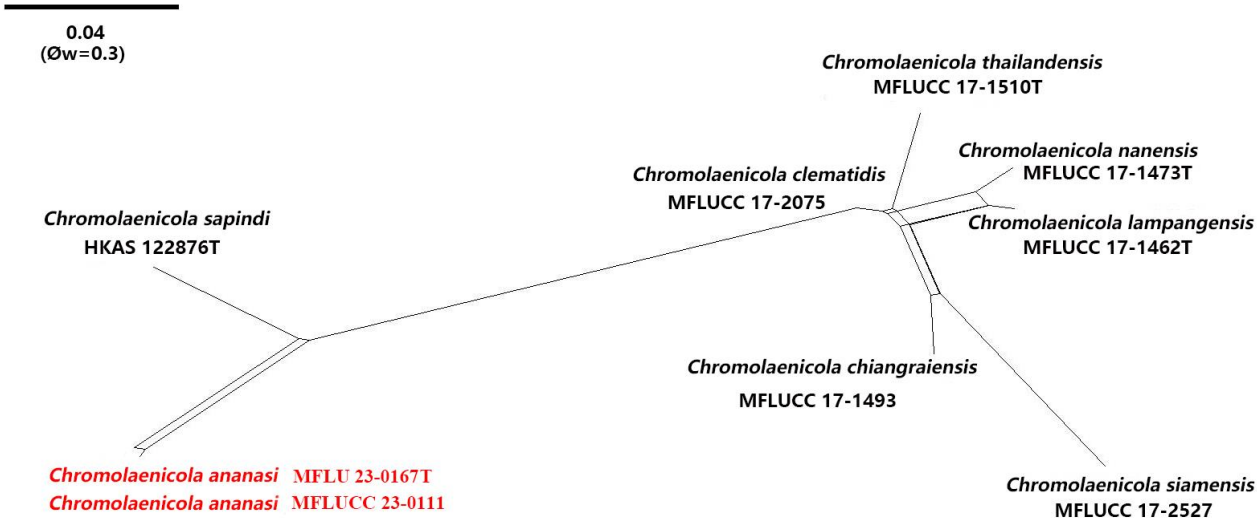

Figure 19 – Results of PHI test of *Chromolaenicola ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

10. ***Montagnula donacina*** (Niessl) Wanas., E.B.G. Jones & K.D. Hyde, in Wanasinghe et al., Fungal Biology 120(11): 1365 (2016) Fig. 20

Index Fungorum number: IF626421; Facesoffungi number: FoF04638

Saprobic on leaves of *Ananas comosus*. Sexual morph: *Ascomata* 320–425 µm high × 295–365 µm diam. ($\bar{x}$ = 382 × 332 µm, n = 7), immersed to erumpent, solitary, uni-loculate, globose to obpyriform, coriaceous, brown to dark brown with ostiole. *Ostiole* papillate, protruding from substratum. *Peridium* 15–25 µm wide, comprising several layers of thin-walled, pale brown to brown cells of *textura primatica*. *Hamathecium* comprising 2–3 µm wide, cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 95–120 × 10–15 µm ($\bar{x}$ = 108 × 13 µm, n = 30), 8-spored, bitunicate, fissitunicate, elongate-clavate, curved, long pedicel. *Ascospores* 10–15 × 4–6 µm ($\bar{x}$ = 15 × 5 µm, n = 25), overlapping, 1–2-seriate, hyaline to pale brown when immature and becoming brown to dark brown when mature, fusiform to ellipsoid, 1-septate, constricted at the septum, slightly wider upper cell and tapering towards ends, straight, with 1–4-guttulate, smooth-walled, without terminal appendages. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 12 h at 25 °C and germ tubes produced from both cells. Colonies on PDA circular, mycelium velvety with fluffy,

flamentous at margin, colony white on PDA from above, colony dark to white from the centre to edge of the colony from below.

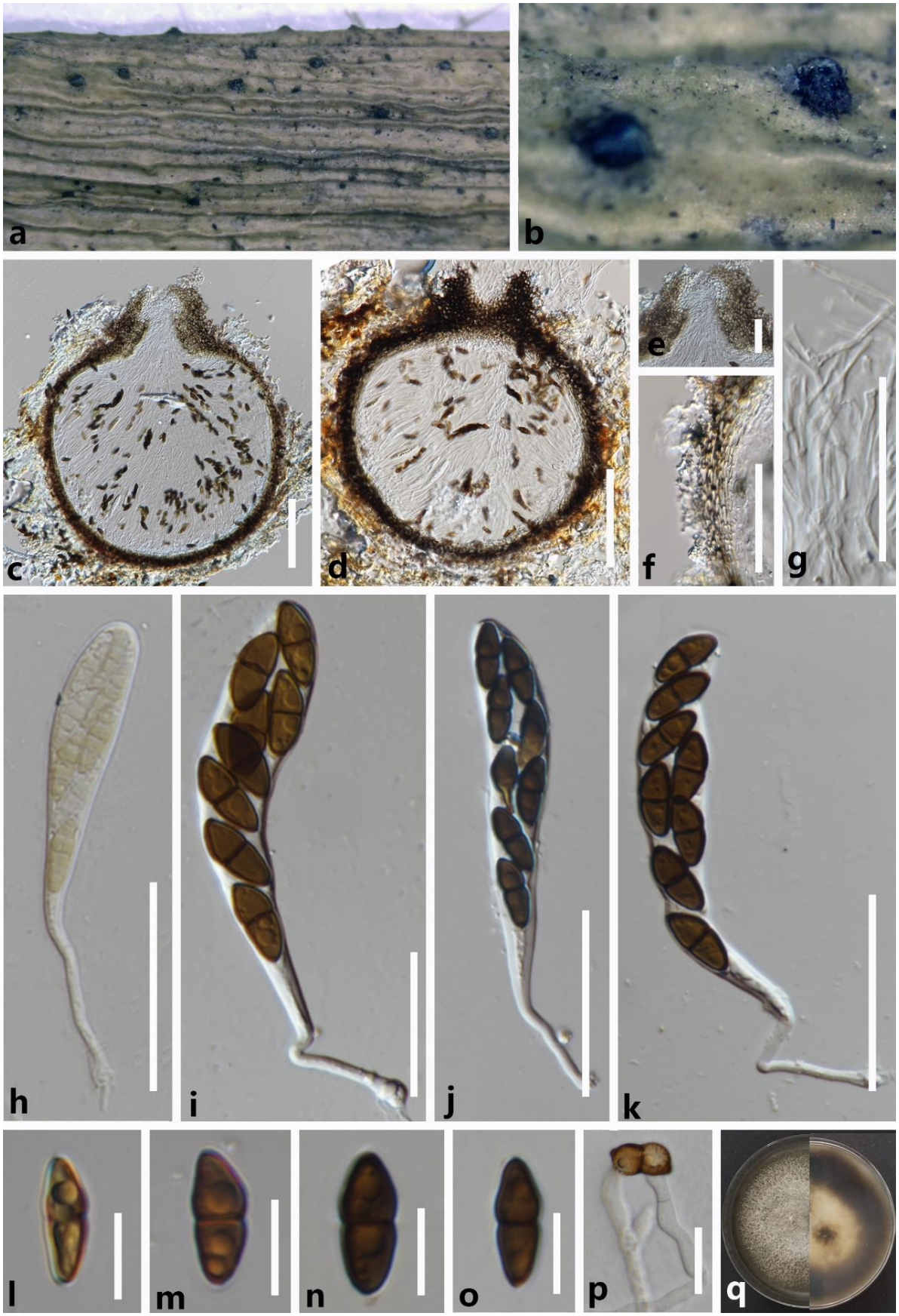

Figure 20 – *Montagnula donacina* (MFLU 23-0168, new host record). a, b Colonies on dead leaves

of *Ananas comosus*. c, d Vertical section through stroma. e Ostiole. f Peridium. g Pseudoparaphyses. h–k Immature and mature asci. l–o Ascospores. p Germinated ascospore. q Colony on PDA from surface and reverse. Scale bars: c–k = 40 μm, p = 20 μm, l–o = 10 μm.

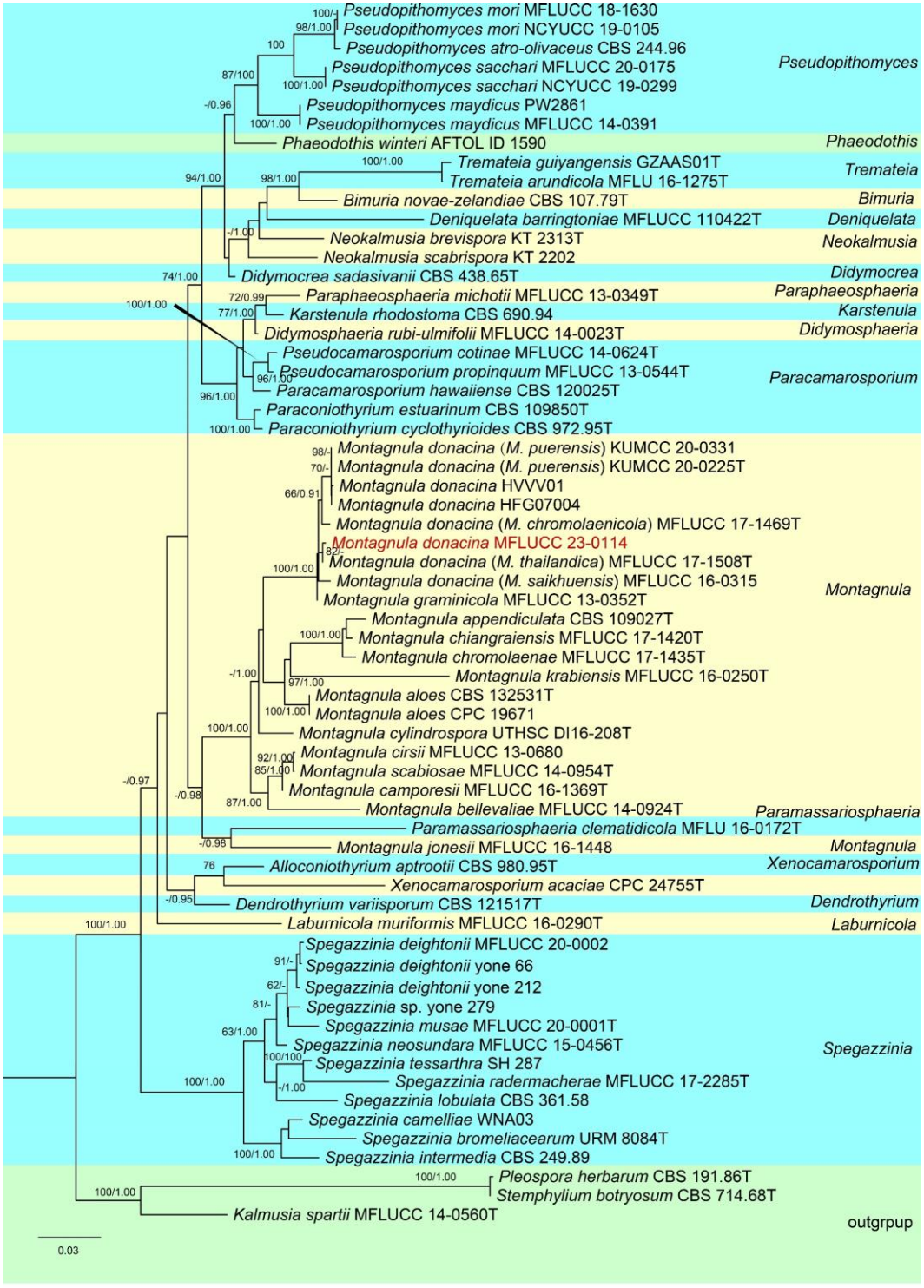

Figure 21 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, and *tef1-α* sequence data. Related sequences were obtained from Samarakoon et al. (2020a). Sixty-five strains are included in the combined sequence analysis, which comprise 2564 characters with gaps. *Kalmusia spartii* (MFLUCC 14-0560), *Pleospora herbarum* (CBS 191.86), and *Stemphylium botryosum* (CBS 714.68T) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best-scoring RAxML tree with a final likelihood value of -18289.739941 is presented. The matrix had 1166 distinct alignment patterns, with 29.63% of

undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240873, C = 0.249236, G = 0.274078, T = 0.235813; substitution rates AC = 1.522676, AG = 2.285230, AT = 1.387842, CG = 1.079948, CT = 6.513998, GT = 1.000000; gamma distribution shape parameter α = 0.192349. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 2 September 2020, X.G. Tian, P9-3 (MFLU 23-0168), living culture MFLUCC 23-0114.

Known hosts and distribution – On dead culms of *Donax arundinaceus* in Portugal (de Thuemen 1881); from soybean in Malaysia (Nik & Kwee 1980); from grapevines and Desert Ash in Australia (Pitt et al. 2014); On dead stems of *Chromolaena odorata* in Thailand (Mapook et al. 2020a); on dead wood in China (Sun et al. 2023); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438812, ITS = OR438341, SSU = OR458333, *tef1*-α = OR500307.

Notes – In the multi-loci phylogenetic analysis, our strain (MFLUCC 23-0114) clustered within *Montagnula donacina* strains with 83% ML bootstrap support (Fig. 21). Morphologically, our strain shares similar morphology with the holotype of *M. donacina* (MFLU 20–0325) in having immersed to erumpent, solitary, uni-loculate, globose to obpyriform, coriaceous, brown to dark brown ascomata, 8-spored, bitunicate, fissitunicate, elongate-clavate, curved, long pedicel asci and fusiform to ellipsoid, 1-septate, constricted at the septum, slightly wider upper cell and tapering towards ends, straight ascospores (Mapook et al. 2020a). Our strain also has similar of asci (95–120 × 10–15 μm vs. 80–100 × 9–15 μm) and ascospores (10–15 × 4–6 μm vs. 14–17 × 4.5–7.5 μm) to *M. donacina* (MFLU 20–0325). Based on recommendations by Chethana et al. (2021), the nucleotide comparisons showed that our strain (MFLU 23-0168) is not significantly different from *M. donacina* (MFLU 20-0325) in ITS, LSU, SSU, and *tef1-α*. Thus, we identified our strain as *M. donacina* based on phylogenetic analyses and morphological characters. Our strain *M. donacina* (MFLUCC 23-0114) is reported as a new host record on *Ananas comosus*.

Pseudopithomyces Ariyaw. & K.D. Hyde

Pseudopithomyces was described by Ariyawansa et al. (2015) with the type species of *P. chartarum*. *Pseudopithomyces* species have been reported as saprobic or parasitic on dead leaves, stems of plants and humans. *Pseudopithomyces* is characterized by flexuous and aseptate conidiophores, monoblastic or blastic, terminal and determinate conidiogenous cells, fusiform, verruculose dark conidia and producing brown to black colonies on the host (Ariyawansa et al. 2015, Hyde et al. 2017, Jayasiri et al. 2019, Tennakoon et al. 2021b). There are 13 *Pseudopithomyces* records listed in Index Fungorum (2023). In this study, two new records and a new collection are introduced, *P. pandanicola* and *P. palmicola* are synonymized under *P. chartarum* while, *P. diversisporu*s is synonymized under *P. atro-olivaceus* based on phylogeny and morphology.

11. *Pseudopithomyces atro-olivaceus* (Cooke & Harkn.) G. Guevara, K.C. Cunha & Gené, Persoonia 37: 261 (2016) Fig. 22

Basionym. *Helminthosporium atro-olivaceum* Cooke & Harkn., Grevillea 12, 64:95. 1884.

≡ *Pithomyces atro-olivaceus* (Cooke & Harkn.) M.B. Ellis, Mycol. Pap. 76: 8. 1960

≡ *Pseudopithomyces diversisporu*s G. Guevara, A.M. Cunha & Gené, Persoonia 37: 261. 2016

Index Fungorum number: IF819007

Saprobic on dead stems of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effused, dark olivaceous brown to black. *Mycelium* partly immersed but mostly superficial, composed of a mat of rather loosely interwoven and anastomosing, subhyaline

to yellowish, thick hyphae. *Conidiophores* macro- to micronematous, sometimes sporodochial, formed laterally, sometimes irregularly on hyphae, peg-like, subhyaline to light brown, septate. *Conidiogenous cells* monoblastic, hyaline, terminal, smooth. *Conidia* 15–25 × 11.5–15 µm ($\bar{x}$ = 19.5 × 13 µm, n = 30), formed, rounded at apex, oblong, elliptical, pyriform or clavate, with 2–3 transverse septa and 1–2 longitudinal septum, sometimes constricted at the septa, brown or dark brown, slightly verruculose to echinulate, often carrying part of conidiogenous cells at the base.

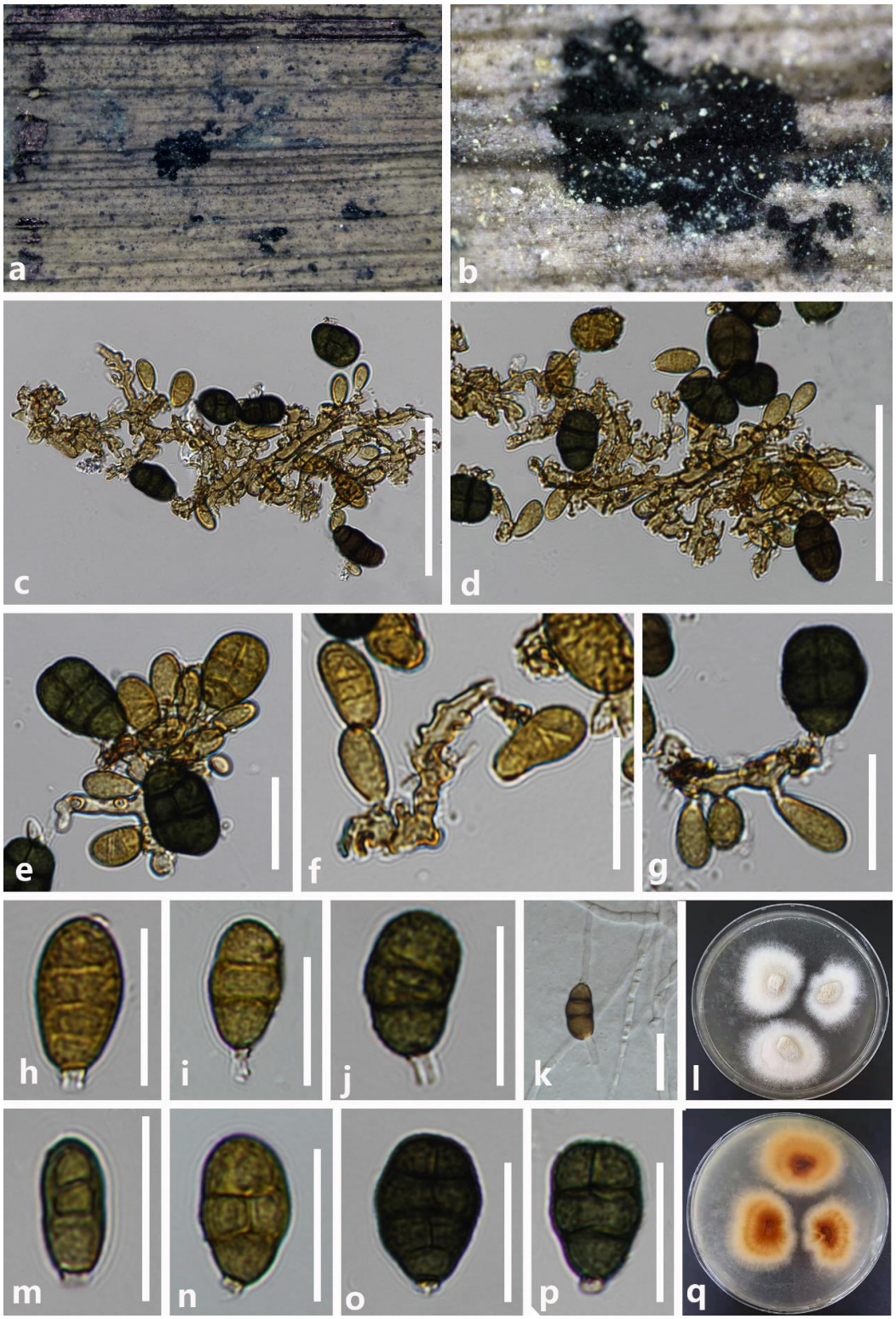

Figure 22 – *Pseudopithomyces atro-olivaceus* (MFLU 23-0169, new host and geographical record). a, b Colonies on dead stems of *Ananas comosus*. c–g Conidiophore with conidia.

h–j Conidia with conidiogenous cells. k Germinated conidium. m–p Conidia. l, q Colonies on PDA from obverse and reverse. Scale bars: c–g = 20 μm, h–p = 10 μm.

Culture characteristics – Colonies on PDA reaching 25 mm in 7 days at 28 °C, flat, hairy or cottony, circular, filamentous, mycelium superficial, effuse, radially striate, with regular edge from forward, reverse white at the margin, reddish brown at the centre.

Material examined – Thailand, Chiang Rai Province, Doi Mae Salong, Mae Fah Luang District, on dead stems of *Ananas comosus*, 3 January 2021, X.G. Tian, P15-3 (MFLU 23-0169), living culture MFLUCC 23-0149.

Known hosts and distribution – On the bark of *Acacia* from California (Ellis 1960); on human toenail, foot, and skin scrapings from Malawi, USA, Zimbabwe (Crous et al. 2016); on dead stems of *Ananas comosus* from Thailand (this study).

GenBank numbers – LSU = OR438814, ITS = OR438343, SSU = OR458335, *tef1-α* = OR500309.

Notes – Our phylogenetic analyses showed that *P. diversisporus* and *P. atro-olivaceus* strains mixed (Fig. 23). Morphologically, *P. diversisporus* is not significantly different from *P. atro-olivaceus*, except the conidia of *P. diversisporus* are verruculose to tuberculate, concolorous, while those of *P. atro-olivaceus* are verruculose to echinulate. There are no significant differences between *P. diversisporus* and *P. atro-olivaceus* in ITS, LSU, *gapdh* and *rpb2* sequence data. Thus, we synonymized *P. diversisporus* under *P. atro-olivaceus*.

In our phylogenetic analyses, our strain (MFLUCC 23-0149) grouped with the strains of *P. atro-olivaceus* and shares similar morphological characteristics with *P. atro-olivaceus* in having brown and septate conidia (Ellis 1960). The nucleotide comparisons showed that our strain (MFLUCC 23-0149) is not significantly different from *P. atro-olivaceus* in ITS, LSU, and SSU gene regions. Thus, we identified our new collection MFLUCC 23-0149 as *P. atro-olivaceus* and reported it as a new host and new geographical record for Thailand.

12. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) J.F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Divers. 75: 66 (2015) Fig. 24

≡ *Pseudopithomyces palmicola* J.F. Li, Ariyaw. & K.D. Hyde, Fungal Divers. 10.1007/s13225-015-0346-5, [41] (2015)

≡ *Pseudopithomyces pandanicola* Tibpromma & K.D. Hyde, Fungal Divers. 10.1007/s13225-018-0408-6, [25] (2018)

Index Fungorum number: IF551393; Facesoffungi number: FoF00938

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* black, separate, later becoming confluent. *Conidiophores* formed laterally and irregularly on the hyphae, micronematous, mononematous, hyaline to yellowish, smooth or occasionally verruculose, septate and branched. *Conidiogenous cells* integrated, hyaline, holoblastic, monoblastic, 5–11 × 2.5–4 μm ($\overline{x}$ = 8 × 3.5 μm, n = 10). *Conidia* 14–18.5 × 7–10.5 μm ($\overline{x}$ = 16 × 9 μm, n = 20), acropleurogenous, mainly pleurogenous, broadly ellipsoid, muriform, 2–3 transverse septate, 1–2 longitudinal septate, sometimes constricted at the septa, light brown to dark brown, verruculose to echinulate, often carrying part of conidiogenous cell at base.

Culture characteristics – Colonies on PDA reaching 30mm in 7 days at 25 °C, colonies from above: flat, circular, grey, surface flocculent, entire edge; reverse: yellowish at the margin, brown to black in the centre.

Material examined – Thailand, Chiang Rai Province, Doi Mae Salong, Mae Fah Luang District, on dead leaves of *Oryza sativa*, 19 October 2020, X.G. Tian, R3-4 (MFLU 23-0170), living culture, MFLUCC 23-0125.

Known hosts and distribution – On dead leaves and stems of *Acoelorrhaphe wrightii*, *Arachis hypogaea*, *Bridelia ferruginea*, *Cajanus indica*, *Calopogomium mhcamoides*, *Centrosema pubescens*, *Foeniculum vulgare*, *Holcus lanatus*, *Ipomoea* sp., *Jatropha podagrica*, *Jatropha* sp., *Musa sapientum*, *Nebouldia laevis*, *Nicotiana tabacum*, *Oryza sativa*, *Pandanus amaryllifolius*,

Pueraria phaseoloides, *Sorghum* sp., *Trifolium repens*, *Triticnm vulgare* and *Zea mays* from Ghana, Jamaica, Malaya, Mauritius, New Zealand, Northern Rhodesia, Nyasaland, Philippines, Sierra Leone, Southern Rhodesia, the Sudan Republic, Thailand, USA (Berkeley 1874, Ellis 1960, Ariyawansa et al. 2015, Tibpromma et al. 2018, this study).

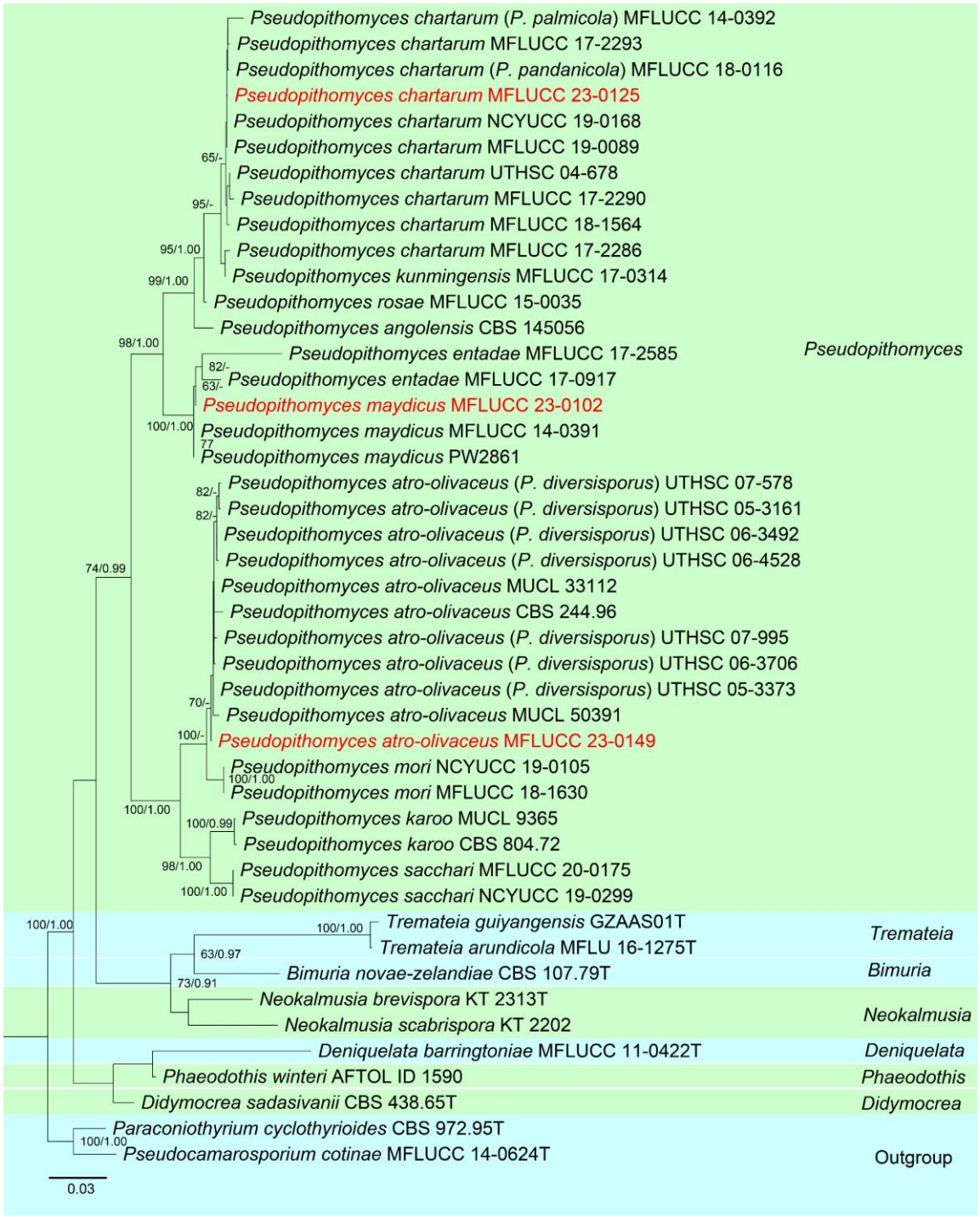

Figure 23 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *rpb2*, SSU, and *tef1-α* sequence data. Forty-five strains are included in the combined sequence analysis, which comprise 4445 characters with gaps. *Pseudocamarosporium cotinae* (MFLUCC 14-0624) and *P. cyclothyrioides* (CBS 972.95) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -14997.450324 is presented. The matrix had 1086 distinct alignment patterns, with 41.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239674, C =

0.253348, G = 0.270675, T = 0.236303; substitution rates AC = 1.523257, AG = 3.234966, AT = 1.469664, CG = 1.108223, CT = 7.982641, GT = 1.000000; gamma distribution shape parameter α = 0.138761. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

GenBank numbers – LSU = OR438815, ITS = OR438344, SSU = OR458336, *tef1*-α = OR500310.

Notes – Based on ITS, LSU, SSU and *tef1-α* blast results, our isolate (MFLUCC 23-0125) is 100% similar to *Pseudopithomyces chartarum* (MT420612, OK655822, MK360082 respectively). In our phylogenetic analyses, our strain grouped with strains of *P. chartarum* and shares similar morphological characteristics with *P. chartarum* in having brown, broadly ellipsoid and septate conidia (Ram 1989, Ariyawansa et al. 2015). *Pseudopithomyces chartarum* was from *Oryza sativa* by Ellis (1960), and we have reisolated this species from *Oryza sativa*.

In addition, our phylogenetic analyses showed that *P. pandanicola* (MFLUCC 14-0392) and *P. palmicola* (MFLUCC 18-0116) clustered within *P. chartarum* clade (Fig. 23). Morphologically *P. pandanicola* and *P. palmicola* are not significantly different from *P. chartarum* (Ariyawansa et al. 2015, Tibpromma et al. 2018). There are no significant differences between *P. pandanicola*, *P. palmicola* and *P. chartarum* in ITS, LSU, SSU and *tef1-α* sequence data. Thus, we synonymized *P. pandanicola* and *P. palmicola* under *P. chartarum*.

13. *Pseudopithomyces maydicus* (Sacc.) J.F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Divers. 75: 69 (2015) Fig. 25

Index Fungorum number: IF551395; Facesoffungi number: FoF00940

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, dark brown to black. *Mycelium* superficial in the substrate, composed of septate, branched, smooth, white hypha. *Conidiophores* semi-micronematous, mononemous, closely packed, hyaline to light brown, thin-walled, septate, smooth, branched, flexuous. *Conidiogenous cells* 5–7.5× 3–4 μm ($\overline{x}$ = 6×3.5 μm, n = 10), monoblastic, integrated, terminal, determinate, hyaline. *Conidia* formed singly as blown-out ends at the apex of each conidiophore, 15.5–21.5 × 8.5–12.5 μm ($\overline{x}$ = 18.5 ×10.5 μm, n = 25), broadly oval, or fusiform, with 2–3 transverse septa, the middle cell sometimes divided by one longitudinal septum, often constricted at the septa, verruculose or finely echinulate, brown to dark brown.

Culture characteristics – Colonies on PDA reaching 20 mm in 7 days at 28 °C, flat, hairy or cottony, white to dark brown, circular, effuse, radially striate, with regular edge. Reverse brown in the center and margin, white in the middle, with some brown spots.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 23 June 2020, X.G. Tian, p3-27 (MFLU 23-0171), living culture, MFLUCC 23-0102.

Known host and distribution – On leaves and occasionally other parts of various plants, including *Acoelorrhaphe wrightii*, *Andropogon gabonensis*, *Bridelia ferruginea*, *Calopogonium mucunoides*, *Centrosema pubescens*, *Chasmopodium caudatum*, *Cinnamomum zeylanicum*, *Coix lachrymal-jobi*, *Oryza sativa*, *Pueraria phaseoloides*, *Saccharum officinarum*, *Sorghum gambicum*, *So. margaritiferum*, *Fragaria ananassa* and *Zea mays* from British Guiana, China, Ghana, Malaya, Philippines, Sierra Leone, Thailand (Ellis 1960, Ariyawansa et al. 2015, Samaradiwakara et al. 2022); on dead leaves of *Ananas comosus* from Thailand (this study).

GenBank numbers – LSU = OR438816, ITS = OR438345, SSU = OR458337.

Notes – Phylogenetic analyses showed that our new isolate (MFLUCC 23-0102) grouped with *Pseudopithomyce maydicus* (Fig. 23). Morphological characteristics of our new strain fits well with *P. maydicus* in having similar shape and size of conidiophores and conidia (Boedijn 1933, Ariyawansa et al. 2015). In addition, the nucleotide comparisons showed that our strain (MFLUCC 23-0102) is not significantly different from *P. maydicus* (PW2861 and MFLUCC 14-0391) in ITS,

and LSU. Therefore, we introduce *P. maydicus* as a new host record from *Ananas comosus* based on morphology and phylogeny.

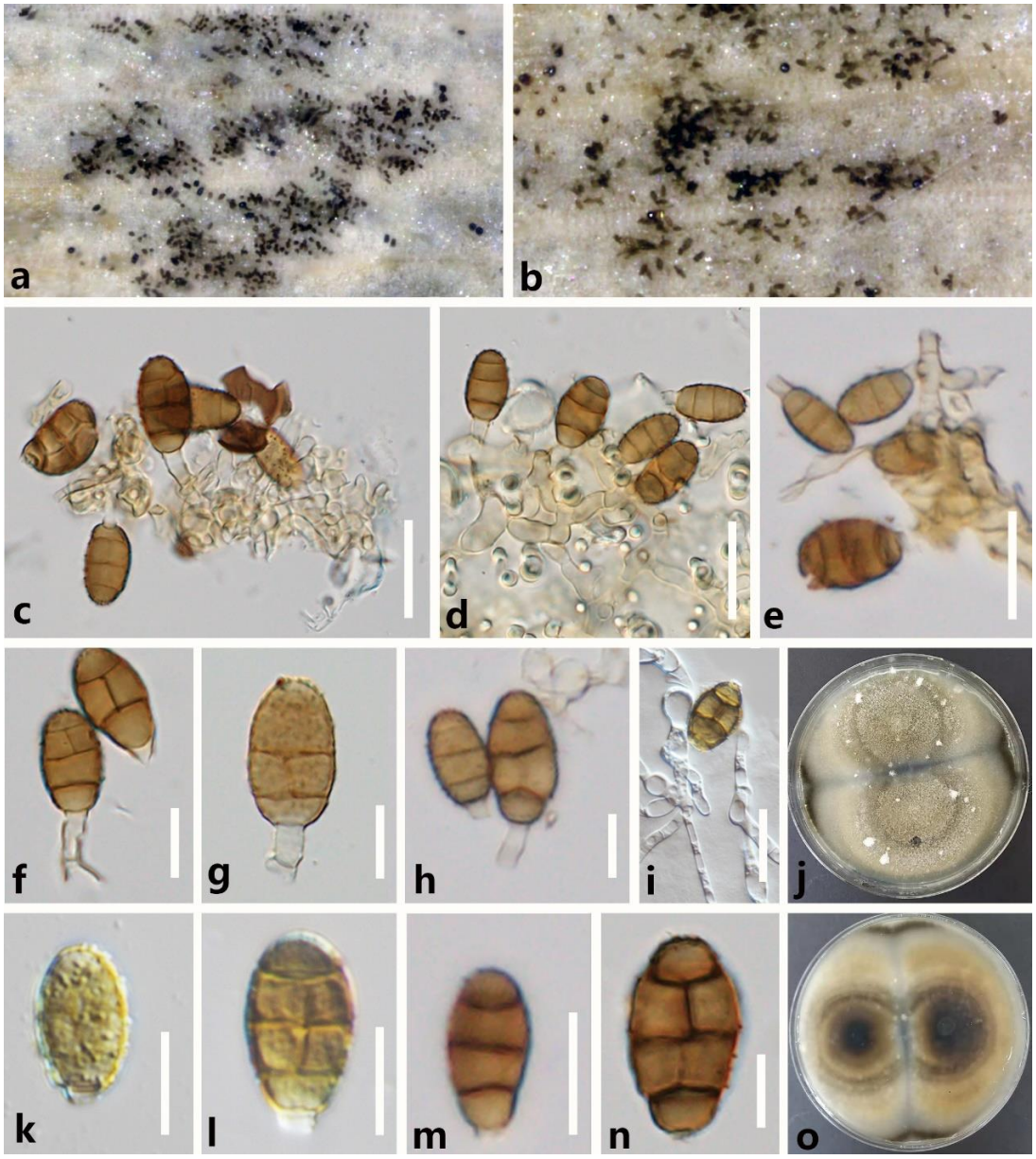

Figure 24 – *Pseudopithomyces chartarum* (MFLU 23-0170, new collection). a, b Colonies on dead leaves of *Oryza sativa*. c–e Conidiophore with conidia. f–h Conidia with conidiogenous cells. i Germinated conidium. k–n Conidia. j, o Colonies on PDA from surface and reverse. Scale bars: c–e = 20 µm, f–i, k–n = 10 µm.

Hermatomycetaceae Locq.

Hermatomycetaceae was introduced by Locquin (1984) based on their distinctive characteristics, with *Hermatomyces* as the generic type. Recently, the placement of this family has been formalized with a robust phylogenetic information (Doilom et al. 2017). To date, only *Hermatomyces* is accepted in *Hermatomycetaceae* (Wijayawardene et al. 2022).

Hermatomyces Speg.

Hermatomyces was introduced by Argentinenses (1910) with *H. tucumanensis* as the type species. *Hermatomyces* is characterized by lenticular to cylindrical, muriform conidia, often with subhyaline to pale brown peripheral cells, and dark brown central cells (Doilom et al. 2017,

Hongsanan et al. 2020b). Sexual morph of *Hermatomyces* have been reported for the first time in de Silva et al. (2022). In this study, a new host for *H. sphaericus* is introduced with a detailed description and illustration.

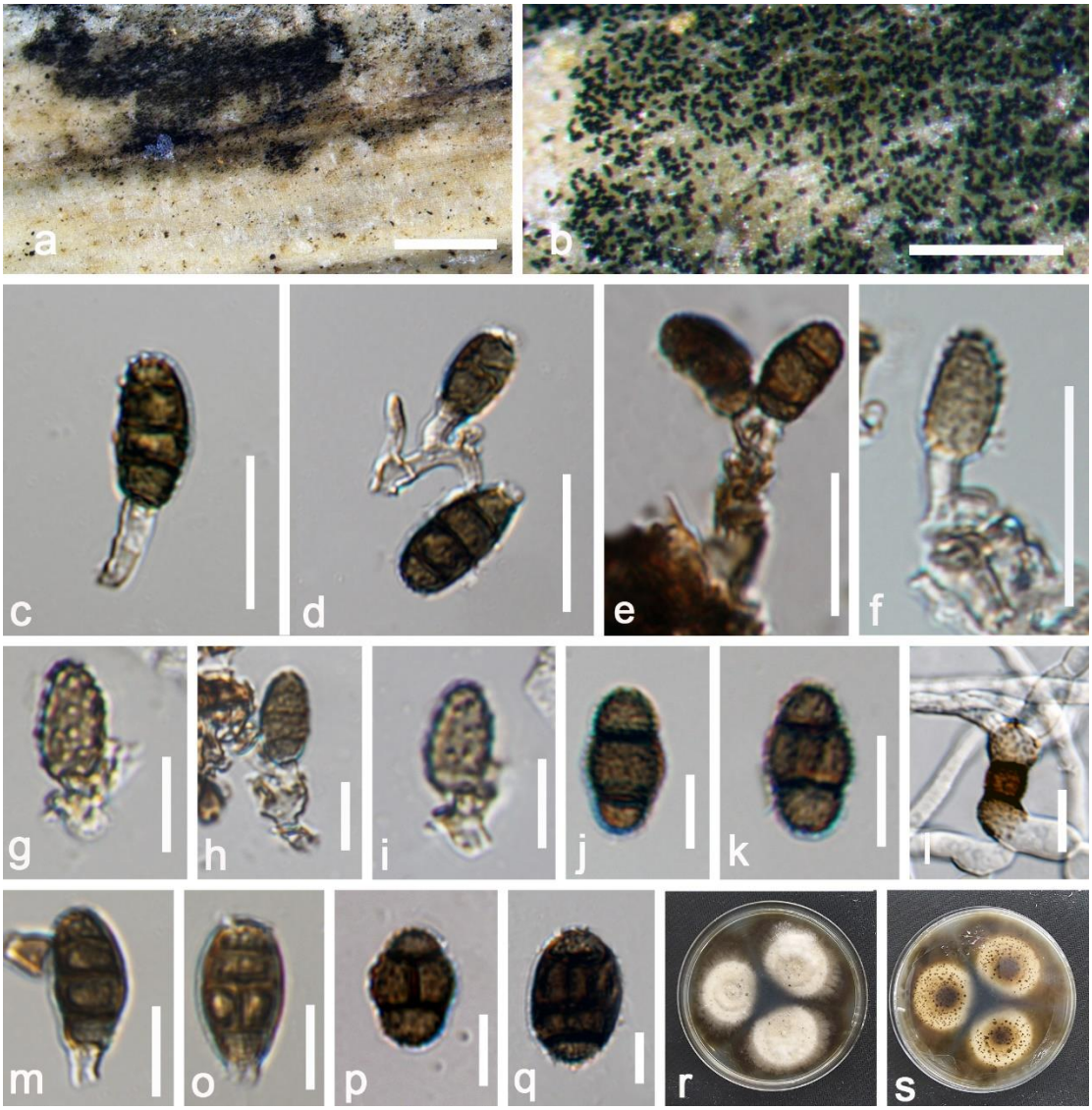

Figure 25 – *Pseudopithomyces maydicus* (MFLU 23-0171, new host record). a, b Colonies on dead leaves of *Ananas comosus*. c–f Conidiophore with conidia. g–k, m–q Conidia. l Germinated conidium. r, s Colonies on PDA from surface and reverse. Scale bars: c–q = 10 μm.

14. *Hermatomyces sphaericus* (Sacc.) S. Hughes, Mycol. Pap. 50: 100 (1953) Fig. 26

Index Fungorum number: IF298410; Facesoffungi number: FoF05259

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Colonies* on natural substrate forming sporodochia, superficial, oval or irregular, scattered, consisting of a velvety, dense, annular, brown, sterile mycelial outer zone and a black, glistening, abundantly sporulating granulose center. *Mycelium* superficial, consisting of branched, septate, smooth or finely verruculose, hyaline or pale brown hyphae. *Conidiophores* 35–90 × 2.5–3 μm ($\overline{x}$ = 62 × 3 μm, n = 5) micronematous, mononematous, cylindrica, branched, smooth or finely verruculose, hyaline to brown. *Conidiogenous cells* 5–15 × 2.5–4 μm ($\overline{x}$ = 8 × 3.5 μm, n = 10), monoblastic, integrated, terminal, cylindrical, hyaline to pale brown, smooth or finely verruculose. *Conidia* of one type, 25–35 μm ($\overline{x}$ = 28 μm, n = 30) diam., solitary, lenticular, globose or disc-shaped in front view, muriform, smooth, central cells brown, dark brown, outer ring of peripheral cells narrow, pale brown to brown; broadly ellipsoidal or oblong in side view where two distinct

adpressed halves can be recognized, each half seen laterally as a row of 4–7 cells with a narrow, sometimes deep constriction between them.

Culture characteristics – Colonies on PDA, reaching 30 mm diam., after 3 weeks at 25 °C, with circular, umbonate, fluffy, velvety edge, a circular raised band, gray white, in reverse gray white to dark gray, black toward the center.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, P6-11 (MFLU 23-0175).

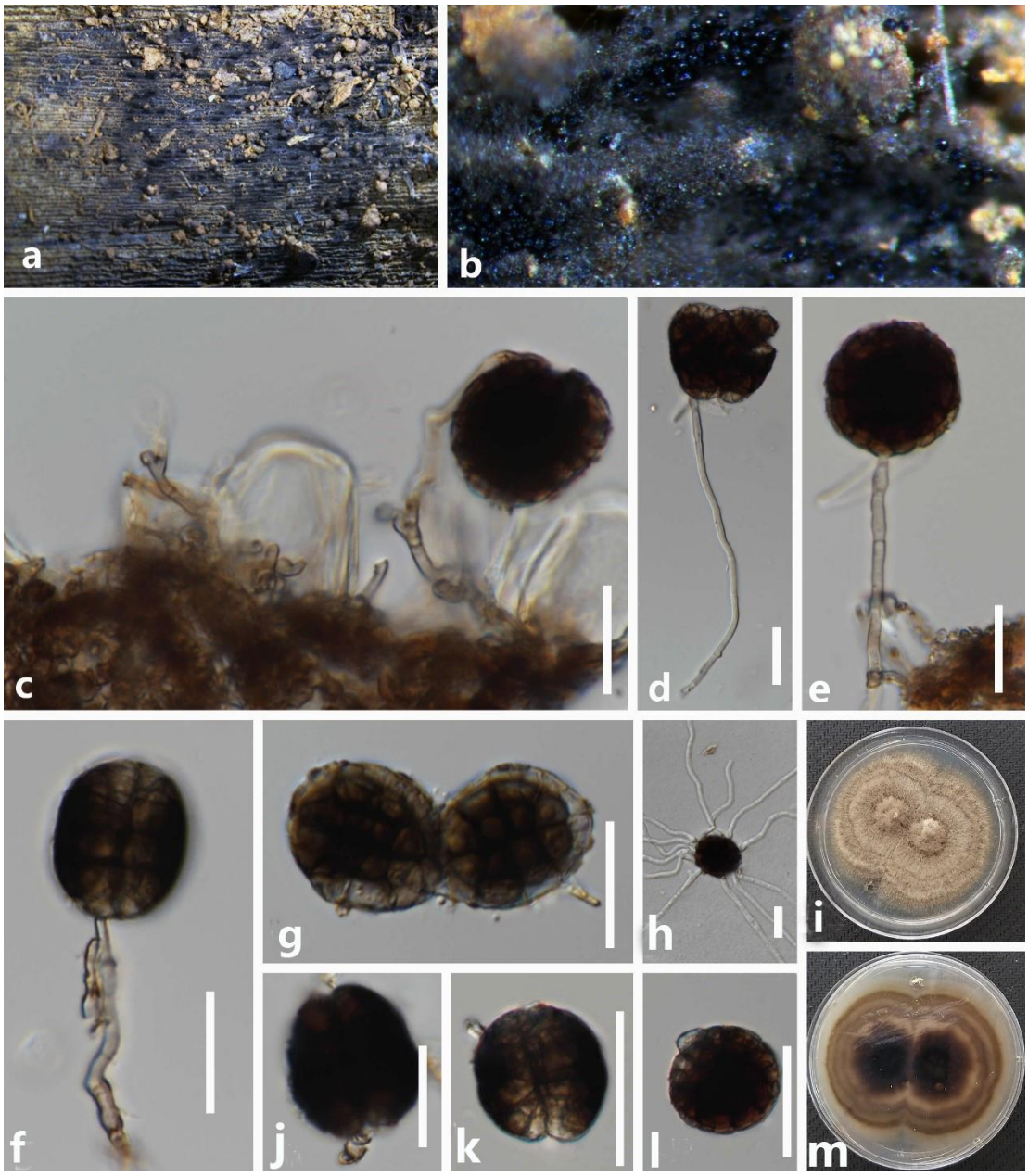

Figure 26 – *Hermatomyces sphaericus* (MFLU 23-0175, new host record). a, b Colonies on dead leaves of *Ananas comosus*. c–f Conidiophores with conidia. g, j, k Conidiogenous cells with conidia. l Conidia. h Germinated conidium. i, m Colonies on PDA from surface and reverse. Scale bars: c–d = 80 μm, e–f, h = 40 μm, g, j–l = 10 μm.

Known hosts and distribution – On dead decorticated twig of *Barleria cristata* in Philippines (Saccardo 1917); on *Coffea robusta*, *Alchornea cordifolia*, *Cassia siamea*, *Bauhinia tomentosa*, *Cathormion dinklagei*, *Bougainvillea spectabilis*, *Acacia farnesiana*, *Rauvolfia vomitoria*, *Albizia gummifera*, *Theobroma cacao* and *Elaeis guineensis* from Sierra Leone; on *Ziziphus jujuba* in India;

on leaves of *Elaeis guineensis* from Malaysia; on dry twig of unknown tree from the USA; on dry twig of unknown tree from Australia (Koukol & Delgado 2019); on woody litter of *Dipterocarpus* sp. in Thailand (Ren et al. 2021); on woody litter of *Ehretia acuminata* in Thailand (Ren et al. 2021); on dead stem of *Chromolaena odorata* in Thailand (Tibpromma et al. 2017); on dead leaves of *Pandanus odorifer* in Thailand (Tibpromma et al. 2016); on dead moist twigs of *Tectona grandis* in Thailand (Doilom et al. 2017); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438821, ITS = OR438350, *tef1-α* = OR500314.

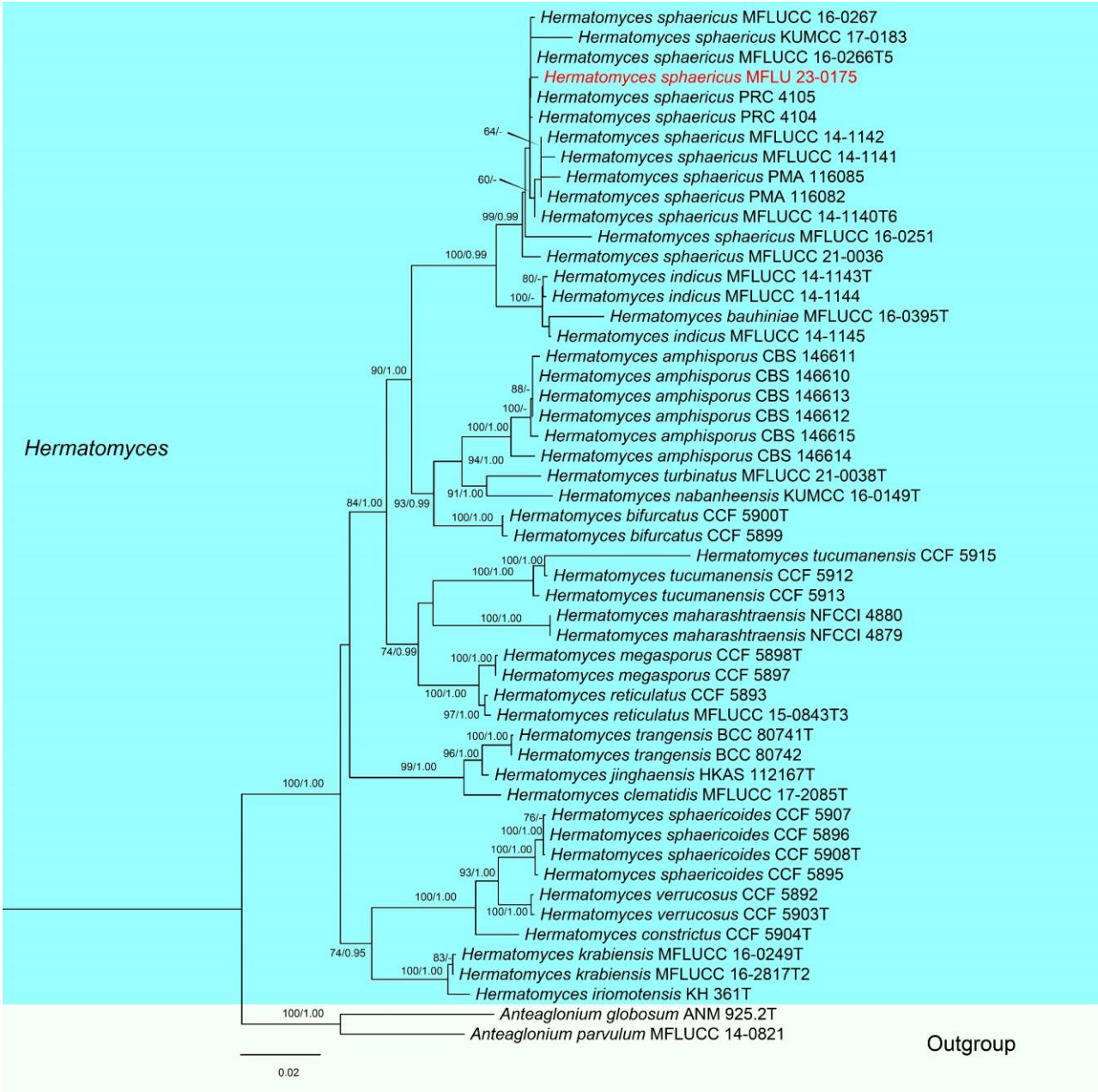

Figure 27 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, *tub2* and *tef1-α* sequence data. Related sequences were obtained from Ren et al. (2021). Fifty-two strains are included in the combined sequence analysis, which comprise 4543 characters with gaps. *Anteaglonium globosum* (ANM 925.2), and *A. parvulum* (MFLUCC 14-0821) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -18289.739941 is presented. The matrix had 1214 distinct alignment patterns, with 36.16% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244189, C = 0.263610, G = 0.258393, T = 0.233808; substitution rates AC = 1.311214, AG = 4.126539, AT = 1.325799, CG = 0.900562, CT = 9.878691,

GT = 1.000000; gamma distribution shape parameter α = 0.183595. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Notes – In our phylogenetic analyses, our strain (MFLU 23-0175) clustered within *Hermatomyces sphaericus* clade (Fig. 27). Morphologically, our strain resembles *H. sphaericus* (MFLUCC 16-0266, HKAS 11-2725 and PMA 116080) in having superficial, oval or irregular, scattered, sporodochia, with monoblastic, integrated, terminal conidiogenous cells and one type, solitary, lenticular, muriform, smooth, conidia. Our strain has similar size of conidia (25–35 μm diam.vs. 7–29 × 26–28 μm) and conidiogenous cells (5–15 × 2.5–4 μm vs. 5–8 × 3–5 μm), but longer conidiophores (35–90 × 2.5–3 μm vs. 10–13 μm) to *H. sphaericus* (HKAS 11-2725) (Ren et al. 2021). The nucleotide comparisons showed that our strain (MFLU 23-0175) is not significantly different from the strains of (HKAS 11-2725 and PMA 116080) in ITS, LSU, and *tef1-α*. Therefore, we identified our strain as *H. sphaericus* based on phylogenetic analyses and morphological characters. Our strain *H. sphaericus* (MFLU 23-0175) is reported as a new host record on *Ananas comosus*.

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

Lentitheciaceae was introduced to accommodate massarina-like species, including *Katumotoa*, *Keissleriella* and the type genus, *Lentithecium* (Zhang et al. 2008, 2012b). Species of *Lentitheciaceae* have been reported as saprobic on stems and twigs of herbaceous and woody plants in terrestrial, marine, or freshwater habitats and endophytic *Darksidea* species have been isolated from semiarid habitats (Wanasinghe et al. 2014, Tanaka et al. 2015, Hongsanan et al. 2020a, Liu et al. 2021c). Fifteen genera have been accepted in the family (Wijayawardene et al. 2022). *Lentitheciaceae* is a well-supported monophyletic family in *Pleosporales* (Wanasinghe et al. 2014, Tanaka et al. 2015). Most genera have sexual morphs except for *Phragmocamarosporium* and *Towyspora*, which only comprise coelomycetous asexual morphs (Liu et al. 2021c). In this study, a new genus *Pseudosetoseptoria* is introduced based on phylogenetic analysis and morphological characters.

15. *Pseudosetoseptoria* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov

Index Fungorum number: IF900974; Facesoffungi number: FoF14287

Etymology – Referring to its similarity with *Setoseptoria*.

Saprobic on dead leaves or wood in terrestrial habitats. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, immersed, solitary, scattered, visible as black spots on host surface, globose to subglobose, brown to dark brown. *Conidiomata wall* thin, composed of 2–4 layers of brown cells of *textura angularis*. *Hamathecium* not observed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity in basal layer, holoblastic, hyaline, subcylindrical to ampulliform, smooth, forming conidia at their tips. *Conidia* hyaline, smooth, 1-septate, ellipsoid to ovoid with both ends rounded, guttulate, thick-walled.

Type species – *Pseudosetoseptoria oryzae* X.G. Tian, K.D. Hyde & Tibpromma

Notes – In the multi-loci phylogenetic analyses, our strains (MFLUCC 23-0151 and MFLUCC 23-0131) clustered together within *Lentitheciaceae*, sister to *Setoseptoria* species with 60 ML and 0.98 PP statistical support (Fig. 29). Morphologically, *Setoseptoria* is different from *Pseudosetoseptoria* in having conidiomata with verruculose to warty setae, collarette inconspicuous, or prominent conidiogenous cells and subcylindrical, multi-euseptate conidia which are tapering in apical part to obtuse or subobtuse apex, base truncate. In contrast, the conidiomata of *Pseudosetoseptoria* lacking setae, conidiogenous cells are subcylindrical to ampulliform and conidia are 1-septate, ellipsoid to ovoid with round ends. In addition, the apical region of conidiogenous cells in *Setoseptoria* is several inconspicuous percurrent proliferations, or with periclinal thickening, which were not observed in *Pseudosetoseptoria* (Quaedvlieg et al. 2013).

16. *Pseudosetoseptoria oryzae* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 28

Index Fungorum number: IF900975; Facesoffungi number: FoF14288

Etymology – Referring to the host plant *Oryza sativa*, on which the fungus was collected.

Holotype – MFLU 23-0177

Saprobic on leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, 45–145 × 50–150 µm ($\overline{x}$ = 97 × 100 µm, n = 10), immersed, solitary, scattered, visible as black spots on host surface, globose to subglobose, brown to dark brown. *Conidiomata wall* 8–20 µm ($\overline{x}$ = 12 µm, n = 15), thin, composed of 2–4 layers of brown textura angularis. *Paraphyses* not observed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity in basal layer, annallidic, hyaline, subcylindrical to ampulliform, smooth, forming conidia at their tips. *Conidia* 10–20 × 7.5–9 µm. hyaline, smooth, 1-septate, ellipsoid to ovoid, rounded at both ends, guttulate, thick-walled.

Culture characteristics – Colonies on PDA reaching 20 mm diameter after two weeks at 25 °C. Colonies on PDA filamentous margins, flat, superficial, circular, smooth or folded surface, superficial and reverse dark brown.

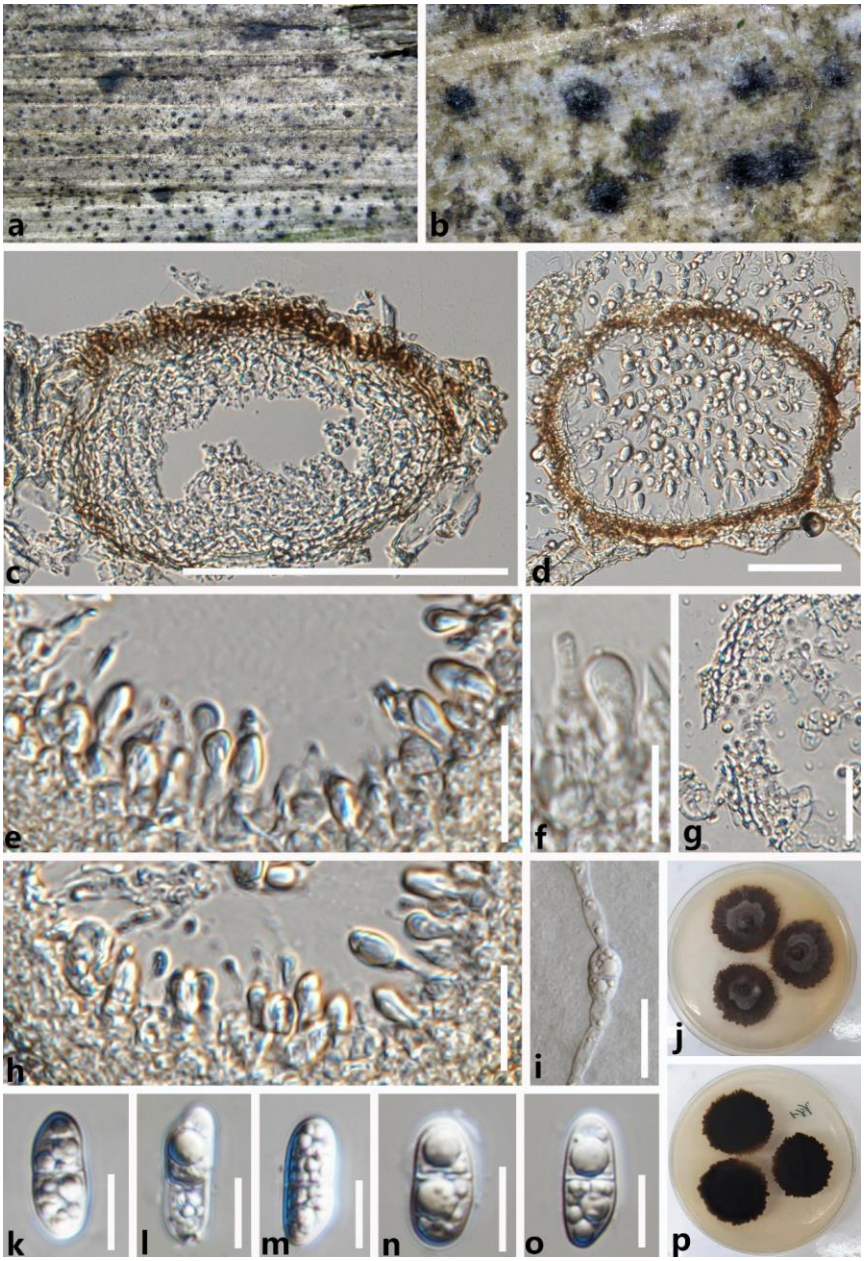

Figure 28 – *Pseudosetoseptoria oryzae* (MFLU 23-0177, holotype). a, b Appearance of

conidiomata on the host. c, d Section through conidioma. e, f, h Conidiogenous cells and developing conidia. g Section of peridium. k–o Conidia. i Germinated conidium. j, p Colonies on PDA from surface and reverse. Scale bars: c, d = 50 μm, e, g–i = 20 μm, f, k–o = 10 μm.

Material examined – Thailand, Chiang Rai Province, Mueang District, Subdistrict, on dead leaves of *Oryza sativa*, 3 January 2021, X.G. Tian, r8-1 (MFLU 23-0177, holotype), ex-type culture MFLUCC 23-0151; *ibid*, 10 November 2020, X.G. Tian, r6-5 (MFLU 23-0176, paratype), ex-paratype living culture MFLUCC 23-0131.

GenBank numbers – MFLUCC 23-0151: LSU = OR438823, ITS = OR438352, SSU = OR458343. MFLUCC 23-0131: LSU = OR438822, ITS = OR438351, SSU = OR458342, *tef1-α* = OR500315.

Notes – In the multi-loci phylogenetic analyses, our strains (MFLUCC 23-0151 and MFLUCC 23-0131) clustered within *Lentitheciaceae*, sister to *Setoseptoria* (Fig. 29). In a BLASTn search of NCBI GenBank, the closest match in *Lentitheciaceae* with the ITS sequences of *Pseudosetoseptoria oryzae* (MFLUCC 23-0131) with 99.31% similarity to *Setoseptoria* sp. (GZCC 19–0487). The closest match with the LSU sequences with 98.11% similarity to *S. magniarundinacea* (HHUF 28293). The closest match of the SSU sequence with 100% similarity to *Phragmocamarosporium hederae* strain KUMCC 18-0166, *Keissleriella caraganae* strain KUMCC 18-0164, *Murilentithecium clematidis* strain MFLUCC 14-0562, and *S. phragmitis* strain GZCC 19-0485. The closest match with the *tef1-α* sequences with 96.47% similarity to *S. arundinacea* strain HHUF 27543. The PHI test revealed no significant recombination event between *Pseudosetoseptoria oryzae* and the closely related taxa (Φw = 0.99) (Fig. 30). The significant recombination between two strains of *Pseudosetoseptoria oryzae* (MFLUCC 23-0151 and MFLUCC 23-0131) indicates that they are conspecific.

Parabambusicolaceae Kaz. Tanaka & K. Hiray

Parabambusicolaceae was introduced by Tanaka et al. (2015) to accommodate *Aquastrom*, *Multiseptospora* and the type genus *Parabambusicola*. Another six genera *viz. Lonicericola*, *Multilocularia*, *Neoaquastroma*, *Paratrimmatostroma*, *Pseudomonodictys*, and *Paramonodictys* were subsequently introduced in *Parabambusicolaceae* based on both morphology and phylogeny (Ariyawansa et al. 2015, Wanasinghe et al. 2017, Phookamsak et al. 2019, Hyde et al. 2020b). Nine genera are accepted in the family (Wijayawardene et al. 2022).

Paramonodictys N.G. Liu, K.D. Hyde & J.K. Liu

Paramonodictys was introduced by Hyde et al. (2020b) with *P. solitarius* as the type species. This genus is morphologically characterized as having superficial black colonies, monoblastic conidiogenous cells, pyriform or clavate, brown to olivaceous brown dictyosporous, subglobose to globose conidia, but no sexual morph has been reported. There are four records available in Species Fungorum (2023). We introduce a new record *P. solitarius* based on morphological comparison and phylogenetic analyses.

17. *Paramonodictys solitarius* N.G. Liu, K.D. Hyde & J.K. Liu, in Hyde et al., Fungal Divers. 100: 91 (2020) Fig. 31

Index Fungorum number: IF662353; Facesofungi number: FoF06710

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, effuse, scattered, solitary, dark brown to black. *Mycelium* mostly immersed, composed of brown, branched, septate hyphae. Stroma present, erect, subcylindrical, brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, monoblastic. *Conidia* 35−55 × 35−50 μm ($\bar{x}$ = 46×41 μm, n = 15), solitary, acrogenous, muriform, globose or subglobose, brown to dark brown, sometimes subtruncate at base, smooth, thin-walled.

Culture characteristics – Colonies circular, reaching 15 mm on PDA in 14 days at 25 °C, grey

from above, brown from below, with dense mycelium, superficial, dry, raised, edge entire.

Material examined – Thailand, Chiang Rai Province, on dead leaves of *Cocos nucifera*, 1 August 2020, X.G. Tian, C6-25 (MFLU 23-0178), living culture MFLUCC 23-0161.

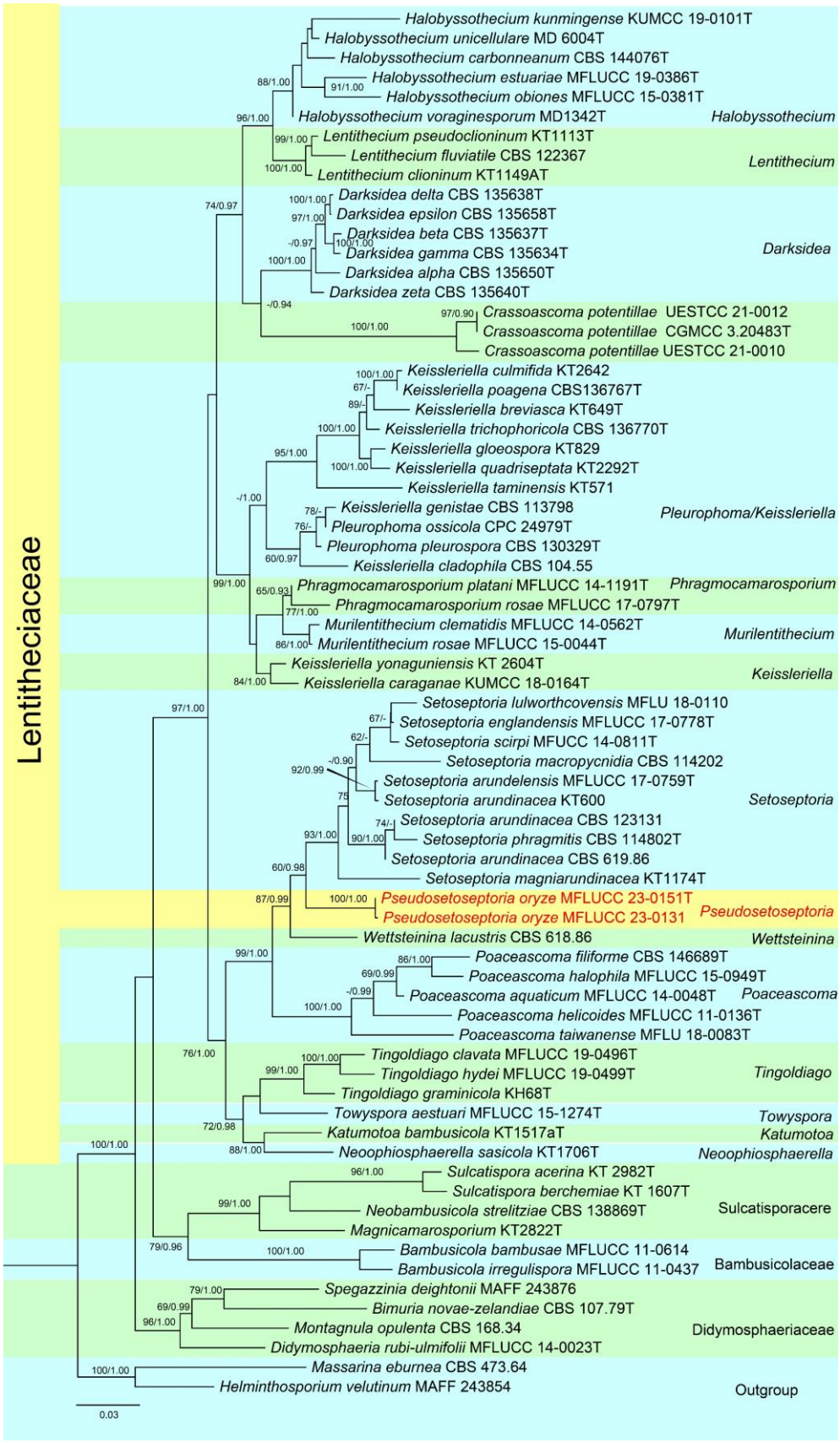

Figure 29 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

SSU, and *tef1-α* sequence data. Related sequences were obtained from Liu et al. (2021c). Sixty-nine strains are included in the combined sequence analysis, which comprise 4143 characters with gaps. *Helminthosporium velutinum* (MAFF 243854) and *Massarina eburnean* (CBS 473.64) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of 23713.546172 is presented. The matrix had 1310 distinct alignment patterns, with 32.08% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239761, C = 0.247852, G = 0.272034, T = 0.240353; substitution rates AC = 1.298345, AG = 2.459949, AT = 1.275662, CG = 1.232515, CT = 6.803258, GT = 1.000000; gamma distribution shape parameter α = 0.171406. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

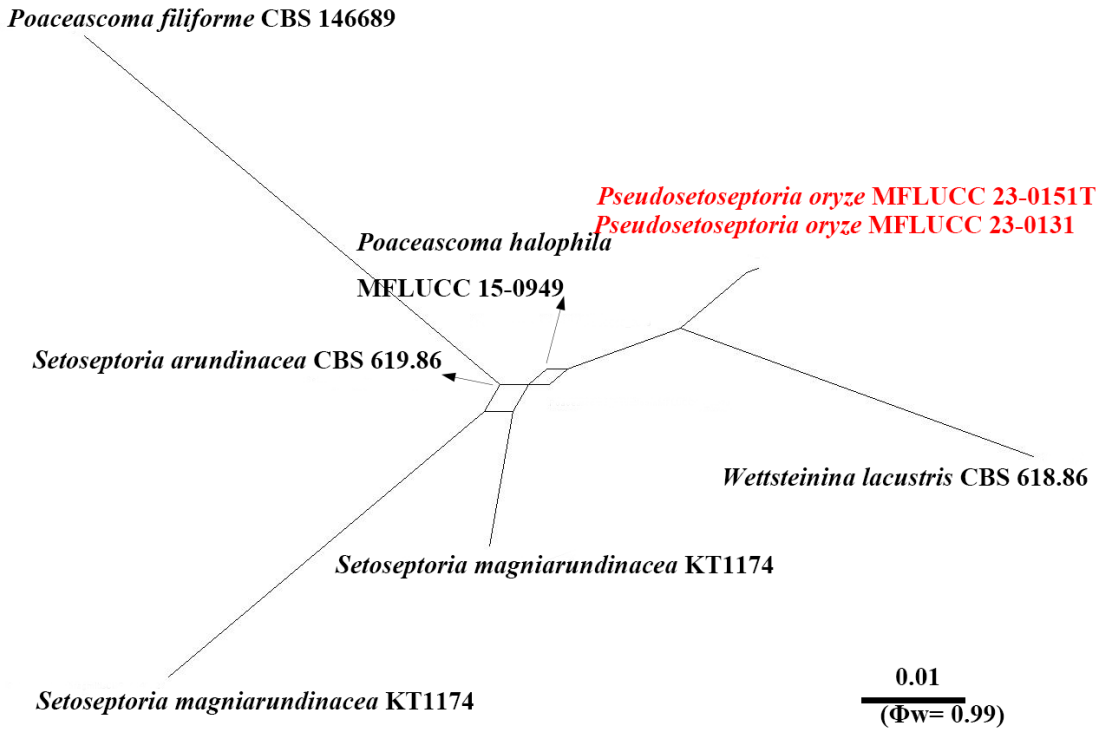

Figure 30 – Results of the PHI test of *Pseudosetoseptoria oryzae* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

Known hosts and distribution – On decaying wood in China (Dong et al. 2020); on submerged wood in a stream in Thailand (Dong et al. 2020); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438824, ITS = OR438353, SSU = OR458344, *tef1-α* = OR500316.

Notes – In the multi-loci phylogenetic analyses, our strain *Paramonodictys solitarius* (MFLUCC 23-0161) clustered within *P. solitarius* strains (Fig. 32). Morphologically, our strain shares similar morphology with *Paramonodictys solitarius* (GZCC 20–0007, ex-type and MFLUCC 17-2353) in having holoblastic, monoblastic conidiogenous cells, with conidiophores reduced to conidiogenous cells and muriform, globose or subglobose, brown to dark brown, smooth conidia, and the conidial size (35−55 × 35−50 µm vs. 30–55 × 25–50 µm) of our strain is also similar to *Paramonodictys solitarius* (MFLUCC 17-2353) (Dong et al. 2020). The nucleotide

comparisons showed that our strain (MFLUCC 23-0161) is not significantly different from *Paramonodictys solitarius* (GZCC 20-0007) in ITS, LSU, and SSU, but different in 10/868 bp (1.15%) of *tef1-α*. Thus, we identified our strain as *P. solitarius* based on phylogenetic analyses and morphological characters. Our strain *Paramonodictys solitarius* (MFLUCC 23-0161) is introduced as a new host record on *Cocos nucifera*.

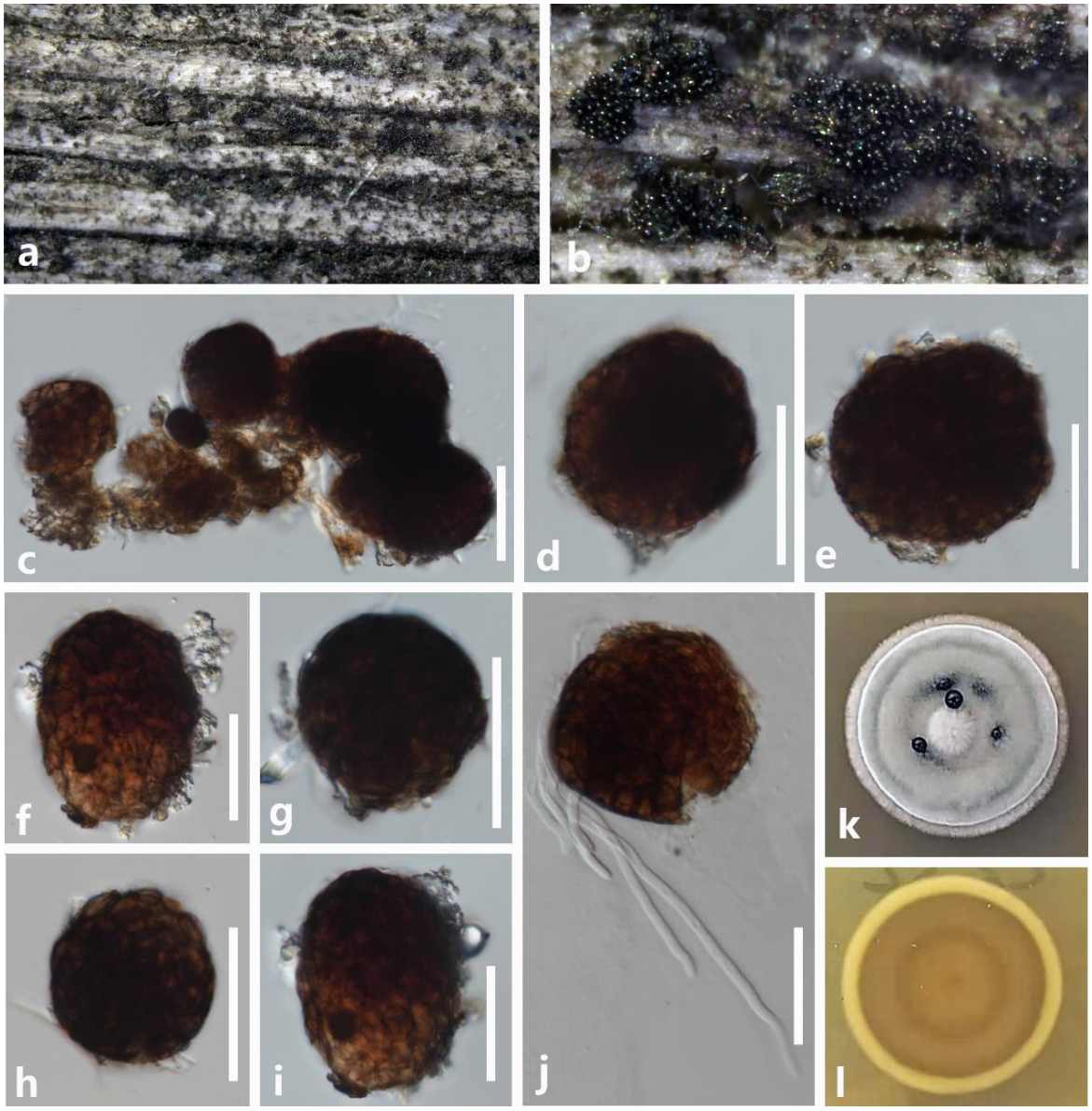

Figure 31 – *Paramonodictys solitarius* (MFLU 23-0178, new host record). a, b Colonies on natural substrate. c Conidia on stromata. d–i Conidia. j Germinated conidium. k, l Colony on PDA from surface and reverse. Scale bars: c–j = 30 μm.

Paradictyoarthriniaceae Doilom, J.K. Liu & K.D. Hyde, Fungal Divers. 72: 133 (2015).

Paradictyoarthriniaceae was introduced by Liu et al. (2015) to accommodate a hyphomycetous genus *Paradictyoarthrinium* based on phylogenetic and morphological characters (Liu et al. 2015). Wanasinghe et al. (2018) introduced the second genus *Xenomassariosphaeria* in the family. Only the two genera are accepted in the family (Hongsanan et al. 2020b).

Paradictyoarthrinium Matsush., Matsush. Mycol. Mem. 9: 18 (1996)

The monotypic genus *Paradictyoarthrinium* was introduced by Matsushima (1996) with *Paradictyoarthrinium diffractum* as the type. Liu et al. (2015) introduced the second species

P. tectonicola and placed *Paradictyoarthrinium* in a newly introduced family *Paradictyoarthriniaceae* based on phylogenetic analyses and morphological characters. Two additional species *P. aquatica* and *P. tectonicola* were subsequently added to the genus. Four species are included in the genus. *Paradictyoarthrinium* is only known by its asexual morph, and it is characterized by superficial, gregarious, black, powdery fruiting bodies and macronematous conidiophores with muriform, subglobose to ellipsoidal dark brown conidia (Liu et al. 2015, Hongsanan et al. 2020b). Species in this genus have been reported as saprobes from both terrestrial and freshwater habitats (Matsushima 1996, Liu et al. 2015, 2018). In this study, we report *P. diffractum* as a new host record on *Cocos nucifera*.

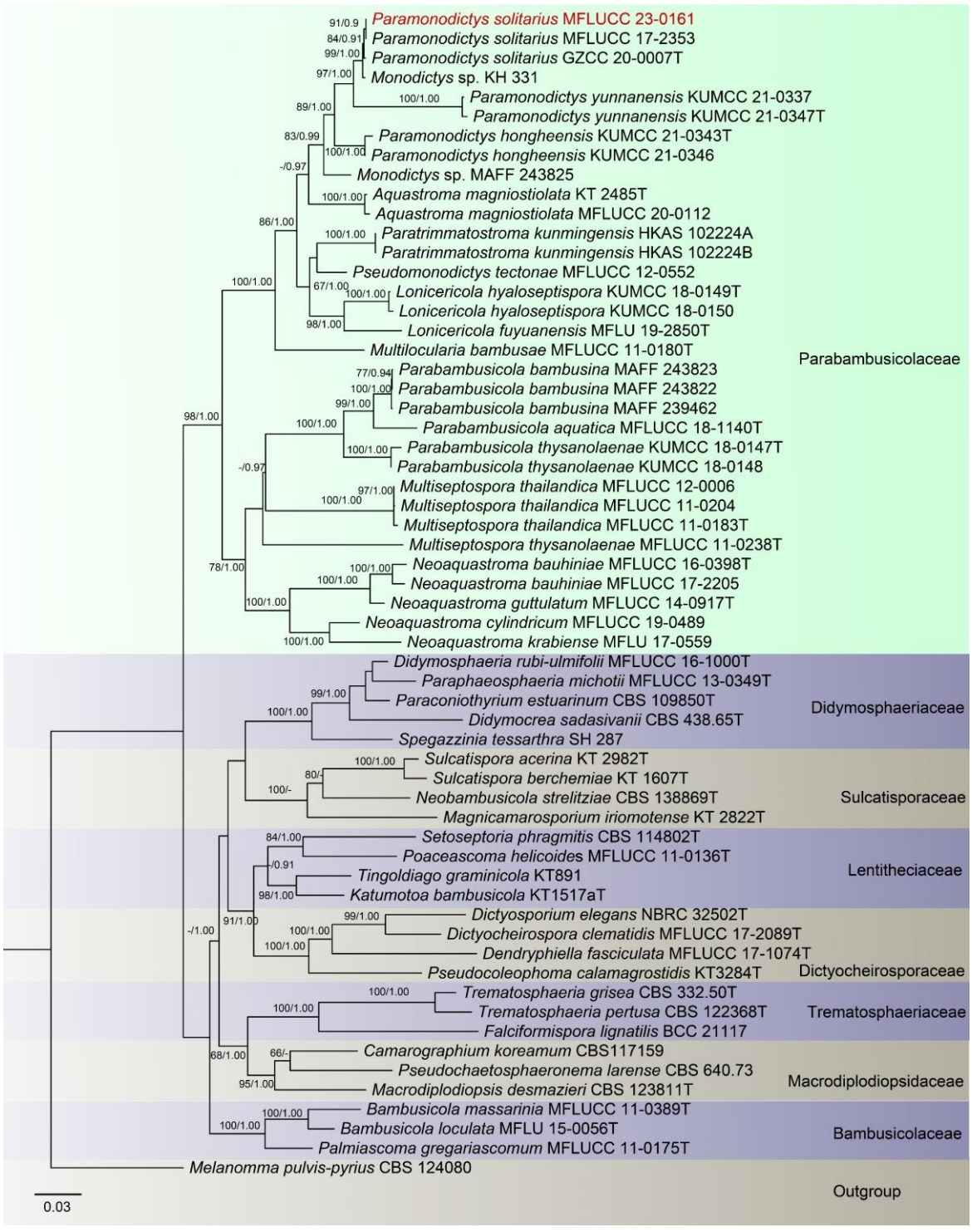

Figure 32 – Phylogenetic tree generated from a Maximum likelihood analysis based on a

concatenated alignment of ITS, LSU, SSU, and *tef1-α* sequences data. Related sequences were obtained from Yang et al. (2022). The tree is rooted with *Melanomma pulvis-pyrius* (CBS 124080). Sixty strains are included in the combined sequence analysis, which comprise 3443 characters with gaps. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -26377.253736 is presented. The matrix had 1370 distinct alignment patterns, with 20.88% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.235338, C = 0.254098, G = 0.272815, T = 0.237749; substitution rates AC = 1.087063, AG = 2.300640, AT = 1.278860, CG = 1.083973, CT = 5.100500, GT = 1.000000; gamma distribution shape parameter α = 0.202194. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

18. ***Paradictyoarthrinium diffractum*** Matsush., Matsush. Mycol. Mem. 9: 18 (1996) Fig. 33

Index Fungorum number: IF415849; Facesofungi number: FoF01854

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on substrate superficial, scattered, gregarious, powdery, black. *Conidiophores* micronematous, arising from hyphae, short, erect to slightly curved, uneven, black, slightly constrict at the septa. *Conidiogenous cells* monoblastic, holoblastic, integrated, terminal. *Conidia* 10–20 × 9–15 μm ($\overline{x}$ = 12.9 × 10.3 μm, n = 30), unevenly dictyoseptate, solitary or forming in basipetally branched chains, muriform, deeply constricted at septa, subglobose to ellipsoidal, dark brown to black, verrucose, hardly separating, variable in size and shape, circular to irregular with a protruding basal cell; rounded to truncate at the base.

Material examined – Thailand, Chiang Rai Province, Doi Mae Salong, Mae Fa Luang District, on dead leaves of *Cocos nucifera*, 1 August 2020, X.G. Tian, C6-24 (MFLU 23-0179).

Known host and distribution – On dead twig in South Africa (Matsushima 1996); from palm litter (Arecaceae) in India (Prabhugaonkar & Bhat 2011); on decaying wood in Thailand (Boonmee et al. 2021); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438825, ITS = OR438354.

Notes – In our phylogenetic analyses, our new isolate (MFLU 23-0179) clustered with two strains of *P. diffractum* with 93% ML and 0.9 PP support (Fig. 34). The nucleotide comparisons of ITS gene region revealed one bp difference between our new isolate and MFLUCC 13-0466 and MFLUCC 12-0557. Morphologically, our new isolate is similar to *P. diffractum* in having micronematous, short, uneven conidiophores, blastic, terminal conidiogenous cells and unevenly dictyoseptate, circular to irregular, dark brown to black on maturity conidia. Thus, based on both phylogeny and morphology, we identified our new isolate as *P. diffractum*. *Paradictyoarthrinium diffractum* was introduced by Matsushima (1996) and has been isolated from Arecaceae in India (Boonmee et al. 2021). Our strain was also isolated from Arecaceae but on *Cocos nucifera* in Thailand.

Periconiaceae Nann.

Periconiaceae has long been placed as members of *Massarinaceae* until Tanaka et al. (2015) revised *Massarineae* and placed it as a distinct family based on phylogenetic analyses (Hyde et al. 2017). We follow the latest treatments and updated accounts of *Periconiaceae* in Wijayawardene et al. (2022).

Periconia Tode

Periconia was introduced with *P. lichenoides* as the type species (Tode 1791). *Periconia* species are mainly hyphomycetous, while a few have been reported as sexual morphs (Tanaka et al. 2015, Phookamsak et al. 2019). The asexual morph of *Periconia* is characterized by macronematous, mononematous, branched, or unbranched conidiophores with spherical apices, holoblastic, monoblastic, or polyblastic conidiogenous cells, which form at the intercalary parts or terminal ends of the conidiophores, and conidia that are usually catenate or solitary, brown, smooth

or verruculose, spherical to sub-spherical and aseptate (Liu et al. 2017, Phookamsak et al. 2019, Hongsanan et al. 2020a). The sexual morph of *Periconia* is characterized by ascomata with necks, hyaline, fusiform ascospores with a nearly median septum, and a gelatinous sheath (Tanaka et al. 2015).

Periconia has 212 records in Index Fungorum (2023), of which 30 species have been transferred to other genera (Saccardo 1886, Benjamin & Hesseltine 1959, Révay & Gönczöl 1990, Aptroot 1998, Okada et al. 2000, Schubert et al. 2007, Chlebicki 2008, Videira et al. 2017, Yin et al. 2020). *Periconia* species are mostly saprobes, endophytes, and plant pathogens of herbaceous plants (Leukel 1948, Rao & Rao 1964, Ellis 1971, Markovskaja & Kačergius 2014, Voronin et al. 2021). In this study, a new species (*P. chiangraiensis*) and two new records (*P. delonicis* and *P. digitata*) are described with detailed descriptions and illustrations.

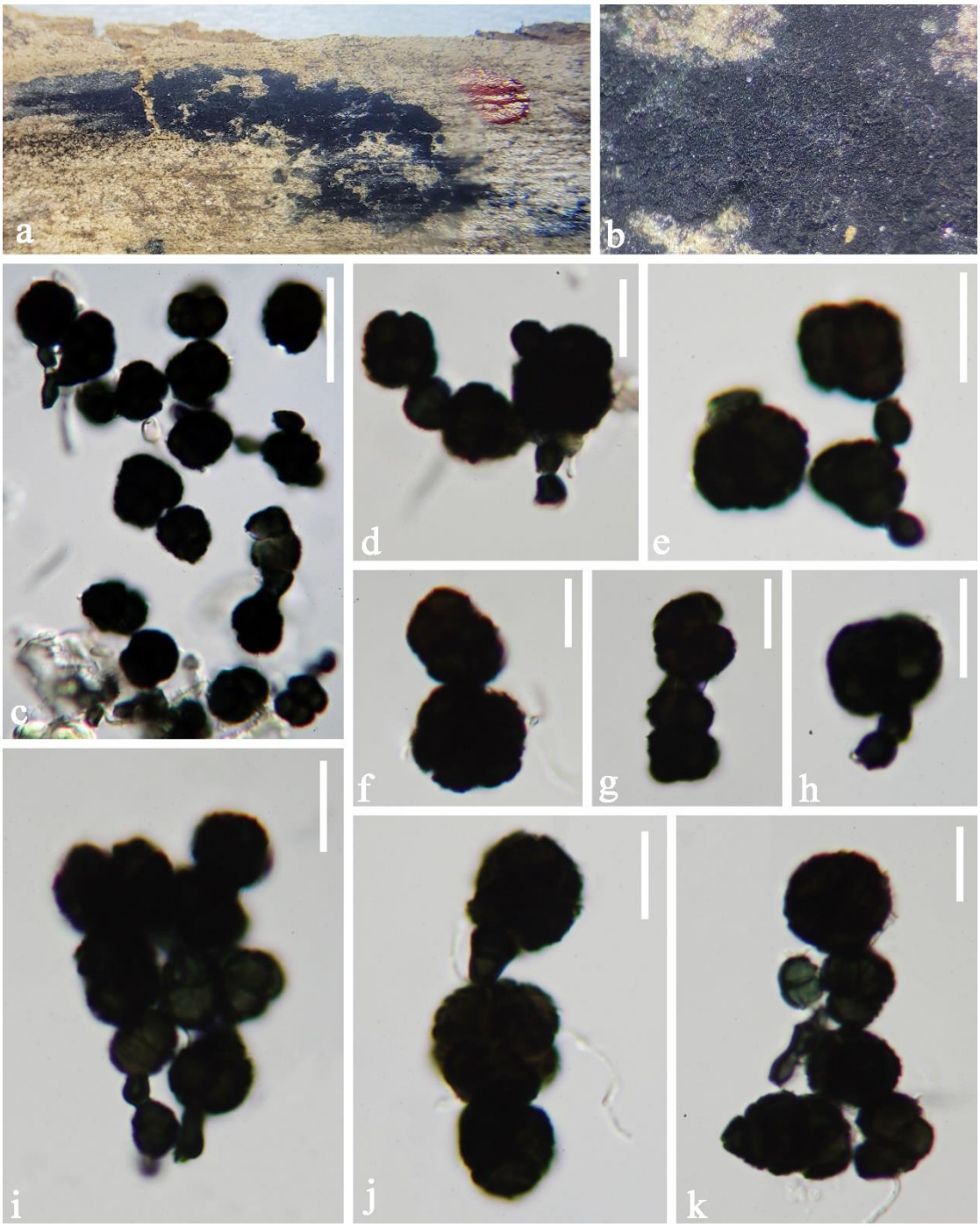

Figure 33 – *Paradictyoarthrinium diffractum* (MFLU 23-0179, new host and geographical record).

a, b Colonies on dead leaves of *Cocos nucifera*. c–k Conidia in chains. Scale bars: c = 20 μm, d–k = 20 μm.

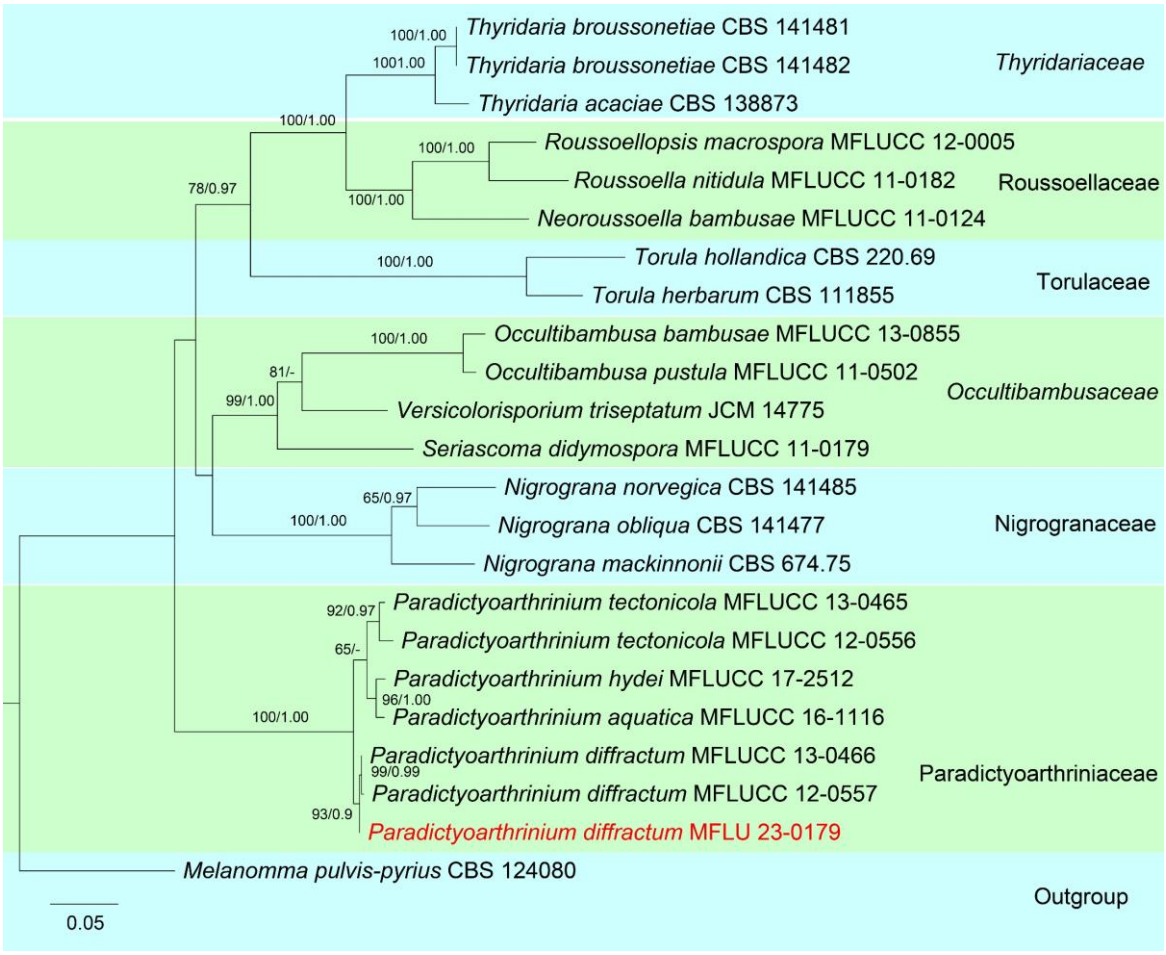

Figure 34 – Phylogenetic tree generated from a maximum likelihood analysis based on a concatenated alignment of ITS, LSU, and *rpb2* sequences data. Related sequences were obtained from Liu et al. (2018). The tree is rooted with *Melanomma pulvis-pyrius* (CBS 124080). Twenty-three strains are included in the combined sequence analysis, which comprises 2584 characters with gaps. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -15077.672723 is presented. The matrix had 1063 distinct alignment patterns, with 19.75% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250708, C = 0.245067, G = 0.278573, T = 0.225652; substitution rates AC = 1.481867, AG = 4.081532, AT = 1.472398, CG = 1.061993, CT = 8.742433, GT = 1.000000; gamma distribution shape parameter α = 0.213084. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

19. *Periconia chiangraiensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 35

Index Fungorum number: IF559513; Facesoffungi number: FoF10574

Etymology – Referring to Chiang Rai Province, Thailand, where the fungus was collected.

Holotype – MFLU 21–0280

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse on the natural substrate, scattered, hairy, powdery, dark brown to dark. *Mycelium* is partly superficial, and composed of septate, brown hyphae. *Conidiophores* (86.5–)100–150(–197) × 5–7 μm ($\bar{x}$ = 125 × 6.5 μm, n = 35), macronematous, mononematous, caespitose, erect, straight or slightly flexuous, unbranched, solitary or in a small group, septate,

cylindrical, brown to dark brown, smooth-walled. *Conidiogenous cells* 10–30 × 6–15 µm ($\bar{x}$ = 16 × 7 µm, n = 20), monoblastic, determinate, discrete on stipe, intercalary, integrated, verruculose, globose to ellipsoid, brown. *Conidia* 6–8 µm diam. ($\bar{x}$ = 7 µm, n = 45), globose, aseptate, pale brown to brown, arising at one point on the curved surface of the conidiogenous cell, catenate, in branched chains, smooth-walled to verruculose or with short spines.

Culture characteristics – Conidia germinated on PDA within 12 hr., reaching 30 mm diam. in 2 weeks at 25 °C. Colonies on PDA with sparse, white mycelia on the surface, cottony, circular, and flattened. The reverse of the colony is yellow. Conidiophores and conidia are not observed in mature colonies.

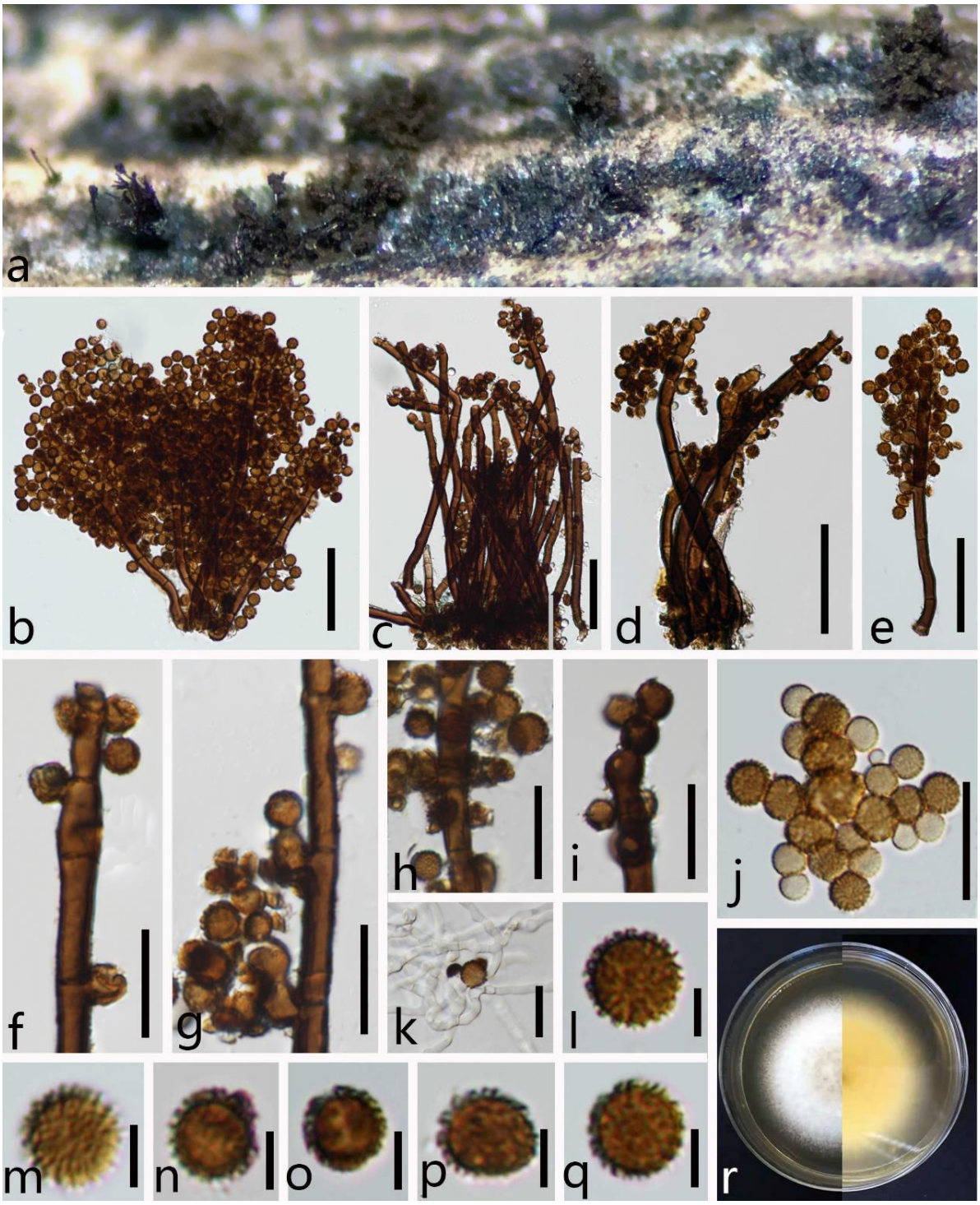

Figure 35 – *Periconia chiangraiensis* (MFLU 21-0280, holotype). a Colonies on natural substrate. b–e Conidiophores with conidia. f–i Conidiogenous cells and conidia. j, l–q Conidia. k Germinated

conidium. r Colony on PDA from surface and reverse. Scale bars: b–e, j = 50 μm, f–k = 20 μm, l–q = 5 μm.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 20 December 2020, X.G. Tian, P9-9 (MFLU 21-0280 holotype), ex-type living culture MFLUCC 21-0164, KUMCC 21-0471.

GenBank numbers – MFLUCC 21-0164: LSU = OL606154, ITS = OL753686, SSU = OL606143, *tef1-α* = OL912947. KUMCC 21–0471: LSU = OL985956, ITS = OM102540, SSU = OL979227, *tef1-α* = OL007978.

Notes – Phylogenetic analyses showed that *Periconia chiangraiensis* (MFLUCC 21-0164 and KUMCC 21-0471) formed an independent lineage within *Periconia* (Fig. 36). *Periconia chiangraiensis* is phylogenetically closer to *P. minutissima* (MFLUCC 15-0245). However, *P. chiangraiensis* is distinguished from *P. minutissima* by unbranched, caespitose conidiophores, conidiogenous cells with intercalary, discrete on the stipe, and larger conidial size (6−8 μm vs. 4–6 μm). While, conidiophores of *P. minutissima* are branched, singly, conidiogenous cells are terminal with discrete stipe and branches). Based on pairwise nucleotide comparisons, our strains (MFLUCC 21-0164 and KUMCC 21-0471) are different from *P. minutissima* (MFLUCC 15-0245) in 15/504 bp (3%) of the ITS, and 9/810 (1.11%) of the LSU, while SSU and *tef1-α* of *P. minutissima* (MFLUCC 15-0245) are not available. In addition, the PHI test revealed no significant recombination event between *P. chiangraiensis* and the closely related taxa. The significant recombination between two strains of *P. chiangraiensis* (MFLUCC 21-0164 and KUMCC 21-0471) indicates that they are conspecific (Φw = 0.77) (Fig. 37). Therefore, we introduced our two strains as a new species, namely *Periconia chiangraiensis* based on phylogenetic analyses and morphological characteristics.

20. *Periconia delonicis* Jayasiri, E.B.G. Jones & K.D. Hyde, in Jayasiri et al. Mycosphere 10(1): 95 (2019) Fig. 38

Index Fungorum number: IF555562; Facesoffungi number: FoF05268

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on substrate numerous, effuse, dark brown to black. *Conidiophores* 200−410 μm high × 6−20 μm diam. ($\overline{x}$ = 285 × 10 μm, n = 15), macronematous, mononematous, branched in the heads, erect, straight or flexuous, single, pale brown to dark brown, septate, smooth, thick-walled. *Conidiogenous cells* monoblastic or polyblastic, brown, terminal, subglobose to globose, thick-walled. *Conidia* 5.5−8 μm diam. ($\overline{x}$ = 6.5 μm, n = 50), catenate, in chains, pale brown to brown, subglobose to globose, smooth to verruculose, aseptate.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, C6-12 (MFLU 23-0180).

Known hosts and distribution – On pods of *Delonix regia* from Thailand (Jayasiri et al. 2019); on dead leaf of *Musa* sp. from Thailand (Samarakoon et al. 2021); on dead leaf of *Cocos nucifera* from Thailand (this study).

GenBank numbers – LSU = OR438826, ITS = OR438355, SSU = OR458345, *tef1-α* = OR500317.

Notes – In the multi-loci phylogenetic analyses, our strain *Periconia delonicis* (MFLU 23-0180) clusters with the ex-type strain of *P. delonicis* (MFLUCC 17-2584) with 100% ML and 1.00 PP support (Fig. 36). Morphologically, our strain shares similar morphology with the type of *Periconia delonicis* in having macronematous and overlap sized conidiophores (200−410 × 6−18 μm vs. 360−420 × 8−12 μm), with monoblastic, terminal conidiogenous cells and brown, globose to subglobose, aseptate, verruculose similar sized conidia (5.5−8 μm diam. vs. 5.5−7 μm diam) (Jayasiri et al. 2019). Based on recommendations by Chethana et al. (2021), the nucleotide comparisons showed that our strain (MFLU 23-0180) is not significantly different from the type strain of *P. delonicis* (MFLUCC 17-2584) in LSU, SSU and *tef1-α*, which indicated that they are the same species.

Thus, we identified our strain as *P. delonicis* based on phylogenetic analyses and morphological characters. Our strain *P. delonicis* (MFLU 23-0180) is reported as a new host record from *Cocos nucifera*. In addition, this species seems to be endemic to Thailand.

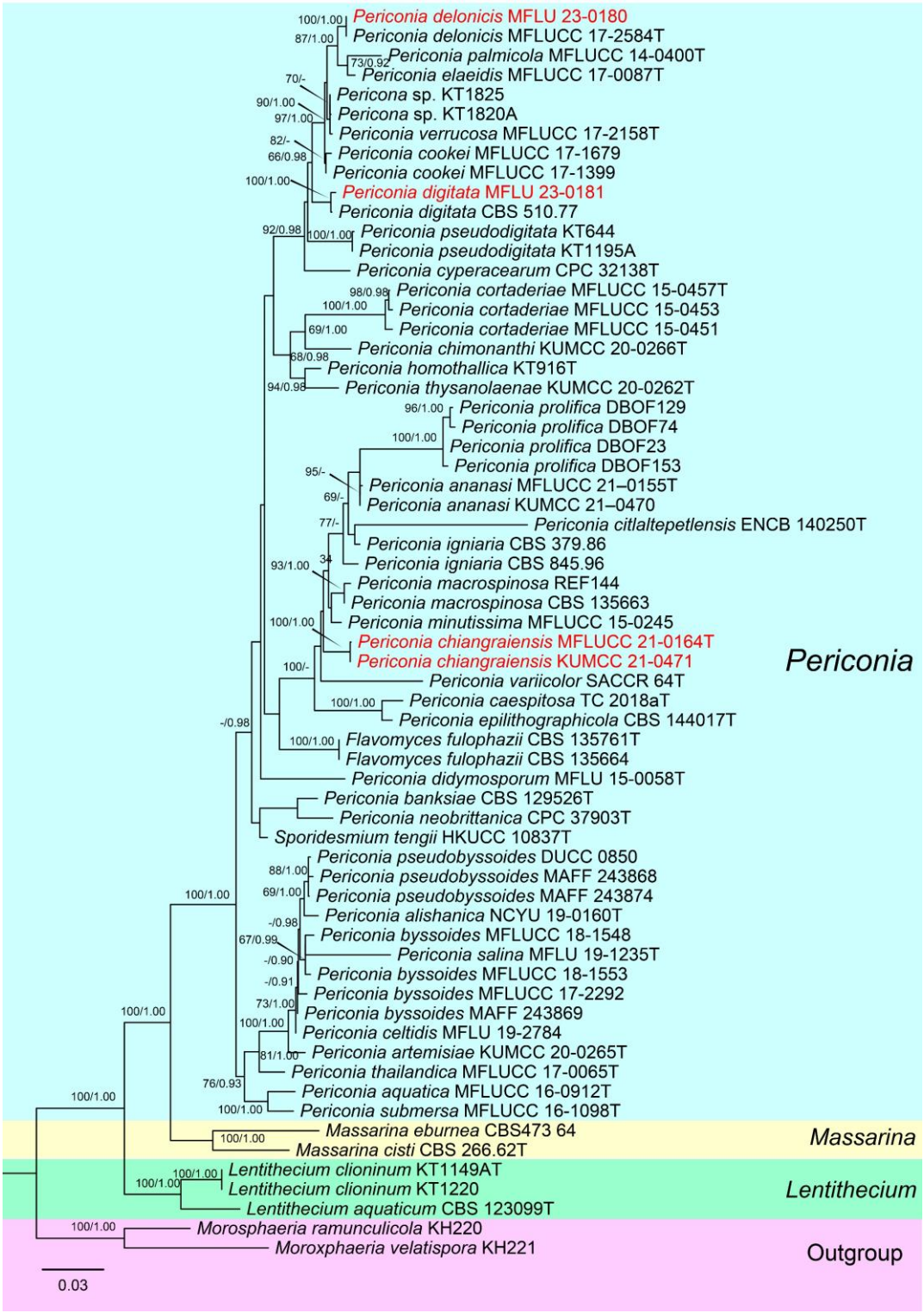

Figure 36 – Phylogenetic tree generated from a maximum likelihood analysis based on a concatenated alignment of ITS, LSU, SSU, and *tef1-α* sequences data in *Periconiaceae*. Related sequences were obtained from TIAN et al. (2022a). The tree is rooted with *Morosphaeria ramunculicola* (KH220) and *M. velatispora* (KH221). Sixty-four strains are included in the combined sequence analysis, which comprise 3412 characters with gaps. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -

16784.357159 is presented. The matrix had 1079 distinct alignment patterns, with 29.19% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237477, C = 0.255670, G = 0.267028, T = 0.239825; substitution rates AC = 1.669931, AG = 2.682018, AT = 1.892402, CG = 1.296178, CT = 9.604842, GT = 1.000000; gamma distribution shape parameter α = 0.206901. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

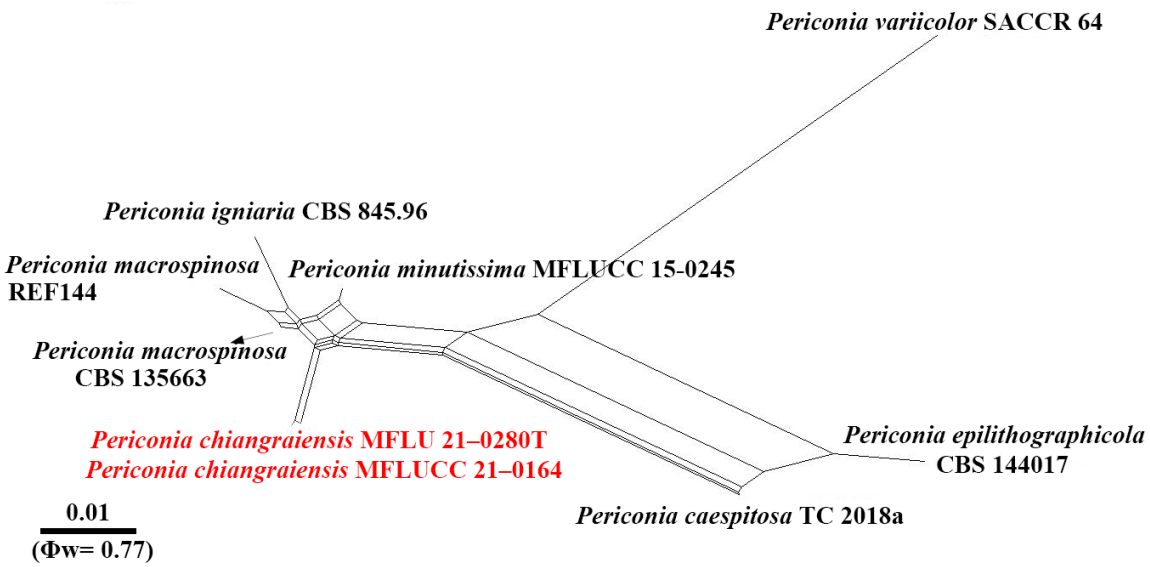

Figure 37 – Results of the PHI test of *Periconia chiangraiensis* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

21. *Periconia digitata* (Cooke) Sacc., Syll. Fung., 4: 274 (1886) Fig. 39

Index Fungorum number: IF240254; Facesoffungi number: FoF14288

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on substrate numerous, effuse, dark brown to black. *Conidiophores* 240−335 µm high × 8−15 µm diam. ($\overline{x}$ = 289 × 11 µm, n = 15), macronematous, mononematous, branched in the head, erect, straight or flexuous, single, pale brown to dark brown, septate, smooth, thick-walled. *Conidiogenous cells* monoblastic or polyblastic, brown, terminal, subglobose to globose, thick-walled. *Conidia* 5−8 µm diam. ($\overline{x}$ = 6 µm, n = 35), catenate, in chains, pale brown to brown, globose, smooth to verruculose, aseptate.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Oryza sativa*, 10 November 2020, X.G. Tian, R6-3 (MFLU 23-0181).

Known hosts and distribution – On dead leaves and culms of *Andropogon*, *Borassus*, *Carex*, *Chloris*, *Cladium*, *Eriopjorum*, *Juncus*, *Musa*, *Panicum*, *Phragmites*, *Sorghum*, and *Zea* from Europe, India, Israel, Indonesia, Kenya, Malawi, Pakistan, Sabah, Sierra Leone and the USA (Ellis 1971, Luo et al. 2004, Prasher & Verma 2012); on dead leaves of *Oryza sativa* from Thailand (this study).

GenBank numbers – LSU = OR438827, ITS = OR438356, *tef1-α* = OR500318.

Notes – In our phylogenetic analyses, our strain *Periconia digitata* (MFLU 23-0181) clusters with*P. digitata* (CBS 510.77) with 100% ML and 1.00 PP statistical support (Fig. 36). Our strain is similar to *P. digitata* in having macronematous, branched in the head conidiophores, with brown, globose, aseptate, verruculose conidia (Ellis 1971) and the conidial size of our isolate is also similar to *P. digitata* (CBS 510.77) (5−8 µm diam. vs. 5−10.5 µm diam.) (Prasher & Verma 2012). In

addition, the nucleotide comparisons showed that our strain (MFLU 23-0181) is not significantly different from the *P. digitata* (CBS 510.77) in ITS, LSU, and *tef1-α*, which indicated that they are the same species. Thus, we identified our strain as *P. digitata* and it is a new host and geographical record on *Oryza sativa* in Thailand.

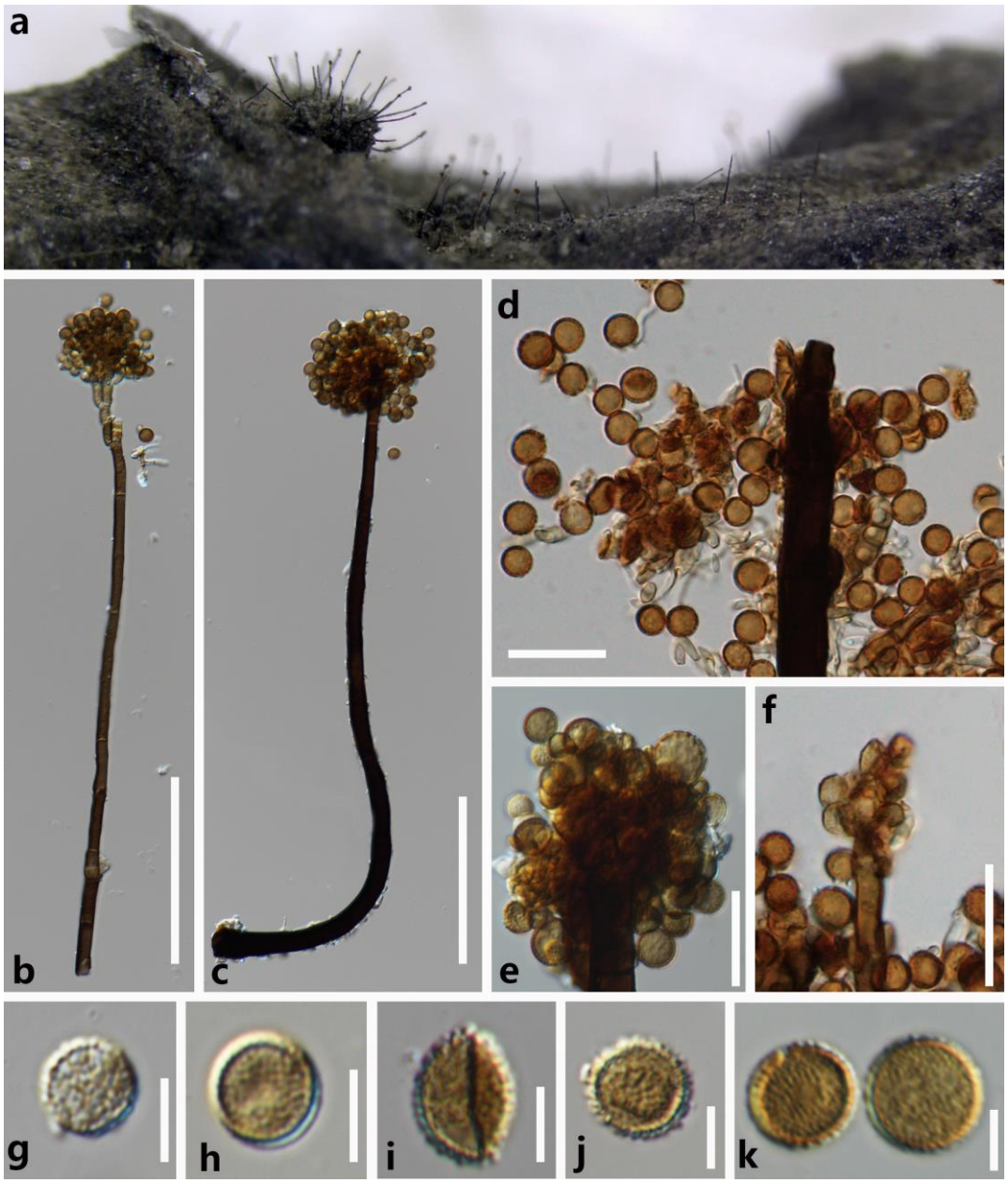

Figure 38 – *Periconia delonicis* (MFLU 23-0180, new host record). a Colonies on natural substrate. b, c Conidiophores with conidia. d–f Conidiogenous cells and conidia. g–k Conidia. Scale bars: b–c = 100 μm, d–f = 20 μm, g–k = 5 μm.

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae was introduced by Barr (1979) with 15 genera and *Phaeosphaeria* was designated as the type. Species in this family are highly diverse and have been reported as plant pathogens, saprobes and endophytes on a wide variety of plant hosts (Hyde et al. 2013, Hongsanan et al. 2020b, Wijayawardene et al. 2022). The recent treatment of *Phaeosphaeriaceae* was provided by Wijayawardene et al. (2022) with 84 valid genera. In this study, we follow the treatment of Wijayawardene et al. (2022). Two new host records are introduced based on phylogeny and morphology herein.

Ophiosphaerella Speg.

Ophiosphaerella was introduced by Spegazzini (1909) and is typified by *O. graminicola*. Species of this genus are characterized by papillate ascomata bearing fissitunicate, cylindrical asci frequently narrower near the base, with a short furcate pedicel and filamentous, pale brown, multi-septate ascospores without swollen cells or separating into part spores (Spegazzini 1909, Thambugala et al. 2017, Tennakoon et al. 2020). Most species of this genus are found as pathogens or saprobes worldwide on Poaceae and Cyperaceae (Phookamsak et al. 2014). Twelve *Ophiosphaerella* species are listed in Index Fungorum (2023), eight species with molecular data. In this study, we introduce a new record, *Ophiosphaerella agrostidis* on *Oryza sativa*.

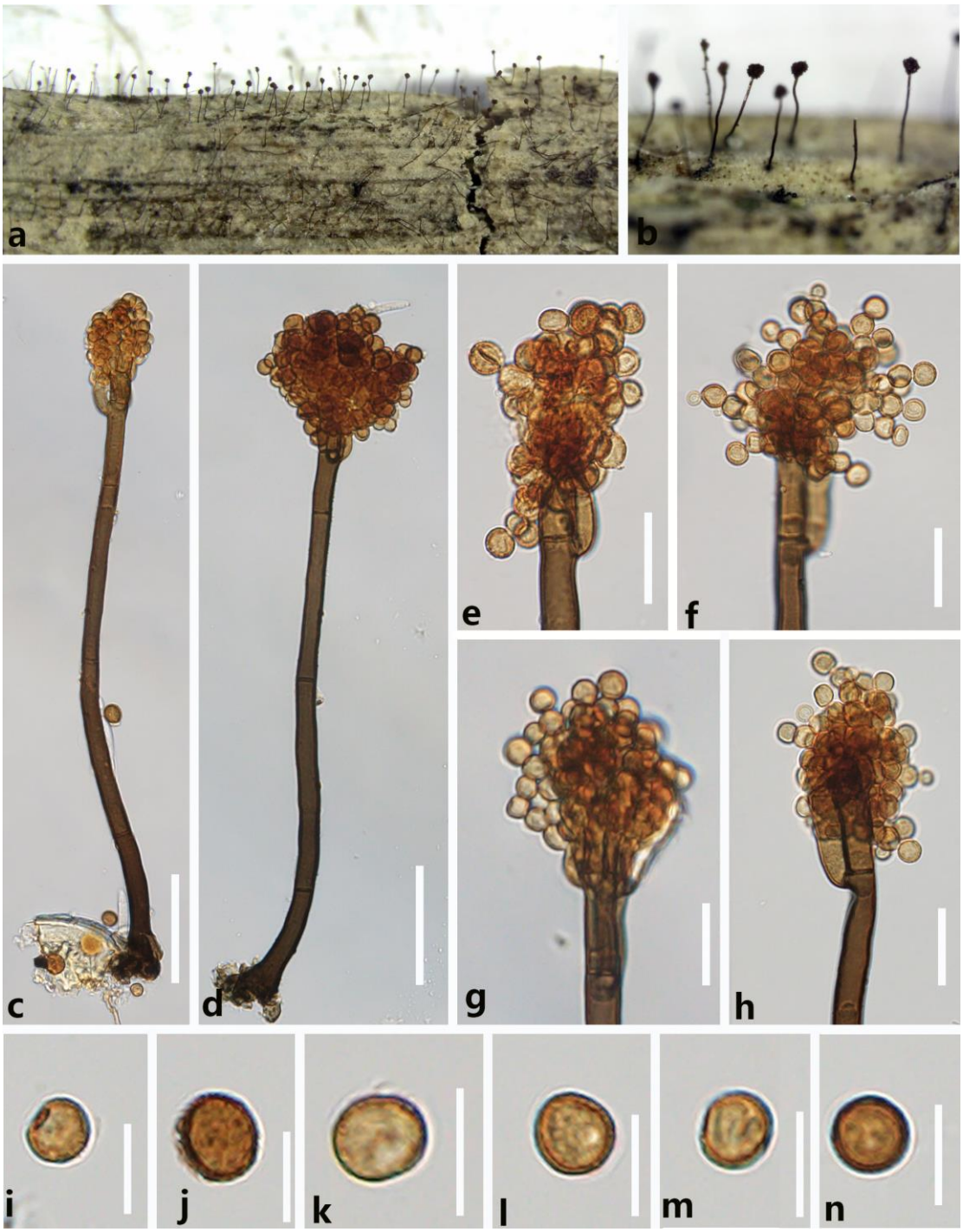

Figure 39 – *Periconia digitata* (MFLU 23-0181, new host and geographical record). a, b Colonies on natural substrate. c, d Conidiophores with conidia. e–h Conidiogenous cells and conidia. i–n Conidia. Scale bars: c, d = 50 µm, e–h = 20 µm, i–n = 5 µm.

22. *Ophiosphaerella agrostidis* Dern., M.P.S. Câmara, N.R. O'Neill, Berkum & M.E. Palm, in Câmara et al., Mycologia 92(2): 320 (2000) Fig. 40

Index Fungorum: IF464614; Faces of fungi number: FoF00258

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: *Ascomata* 220–330 μm high, 190–285 μm diam., scattered, solitary, semi-immersed, visible as small black dots on host surface, unilocular, globose to subglobose, glabrous, brown to black, ostiole central, papilla. *Peridium* 15–25μm wide, thin-walled, of equal thickness, composed of 3−7 layers of brown to dark brown, pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* composed of numerous, 2–3 μm wide, filamentous, pseudoparaphyses, with distinctsepta, anastomosing at the apex and embedded in mucilaginous matrix. *Asci* 115–145 × 9–15 μm ($\overline{x}$ = 131 × 10 μm, n = 30), 8-spored, bitunicate, apically rounded, fissitunicate, short pedicellate, cylindric-clavate. *Ascospores* 110–140 × 2–3 μm ($\overline{x}$ = 126 × 3 μm, n = 30), fasciculate, spiral, scolecosporous, narrowing towards ends, filiform, septate, not constricted at the septa, brown, smooth-walled, guttulate. Asexual morph: See Thambugala et al. (2017).

Culture characteristics – Ascospores germinating on PDA within 12 h at room temperature. Colonies on PDA circular, mycelium cottony, flat, spreading, filiform. Colony white from above, reverse yellow to brown with a white margin.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Oryza sativa*, 5 November 2020, X.G. Tian, r5-9 (MFLU 23-0182), living culture MFLUCC 23-0130.

Known hosts and distribution – On *Agrostis palustris* in the USA (Câmara et al. 2000); on dead culms of grass in Thailand (Phookamsak et al. 2014); on stems of grass (Poaceae) in Thailand (Thambugala et al. 2017); on dead leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438828, ITS = OR438357, SSU = OR458346, *tef1-α* = OR500319.

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0130) grouped within *Ophiosphaerella* and clusters with two strains of *O. agrostidis* (MFLUCC 11-0152 and MFLUCC 16-0895) (Fig. 41). Morphologically, our strain is similar to *O. agrostidis* (MFLUCC 11-0152) in having immersed, solitary, scattered, slightly raised, visible as black spots on host surface ascomata, with 8-spored, bitunicate, cylindrical-clavate, short-pedicellate, apically rounded asci. and fasciculate, spiral, scolecosporous, filiform or filamentous, not constricted at the septum, multi-septate, ascospores. The size of asci (115–145 × 9–15 μm vs. 100–135 × 7–9 μm) and ascospores (110–140 × 4−6 μm vs. 98–120 × 2–2.5 μm) is also similar to *O. agrostidis* (MFLUCC 11-0152) (Phookamsak et al. 2014). The nucleotide comparisons showed that our strain (MFLUCC 23-0130) is not significantly different from the strain of *O. agrostidis* (MFLUCC 11-0152) in ITS, LSU, SSU, and *tef1-α*. Thus, we identified our strain as *O. agrostidis* based on phylogenetic analyses and morphological characters. Our strain *O. agrostidis* (MFLUCC 23-0130) is a new host record on *Oryza sativa*.

Phaeosphaeria Miyake

Phaeosphaeria was introduced by Miyake (1909) and is typified by *P. oryzae*. Recent phylogenetic analyses have shown that *Phaeosphaeria* is polyphyletic and many *Phaeosphaeria sensu lato* were treated in different genera in *Phaeosphaeriaceae* (Hongsanan et al. 2020a). So far, this genus has 169 records listed in Index Fungorum (2023). In this study, we introduce a new record, *Phaeosphaeria musae* on *Oryza sativa*.

23. *Phaeosphaeria musae* Sawada, Special Publication College of Agriculture, National Taiwan University 8: 66 (1959) Fig. 42

Index Fungorum number: IF336200; Facesoffungi number: FoF00262

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: *Ascomata* 95–120 μm high, 110–120 μm diam. ($\overline{x}$ = 110 × 113 μm, n = 5), immersed, solitary, scattered, slightly raised, visible as black spots on host surface. *Ostiole* central, brown to black, aperiphysate layers with minute papilla. *Peridium* 7–11 μm wide, thin-walled, comprising several layers brown to dark brown-walled cells

of textura angularis. *Hamathecium* composed of 1.5–2.5 µm wide, cellular, hyaline, septate, rarely branching, pseudoparaphyses, anastomosing mostly above the asci and embedded in a mucilaginous matrix. *Asci* 35–45 × 9–15 µm ($\bar{x}$ = 41 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apically rounded, with indistinct ocular chamber. *Ascospores* 15–20 × 4–5 µm ($\bar{x}$ = 18 × 4 µm, n = 20), overlapping 2–3-seriate, fusiform, hyaline when young, turning yellowish-brown to brown, 3-septate, slightly constricted at the septa, slightly curved, guttulate, rough-walled, lacking a mucilaginous sheath. Asexual morph: Not observed.

Figure 40 – *Ophiosphaerella agrostidis* (MFLU 23-0182, new host record). a, b Appearance of

ascomata on the host surface. c Pseudoparaphyses. d Ascus tip. e, f Section of ascoma. g Peridium. h–j Asci. k–n Ascospores o Germinated ascospore. p, q Colonies on PDA from surface and reverse. Scale bars: c, e–o = 50µm, d = 20 µm.

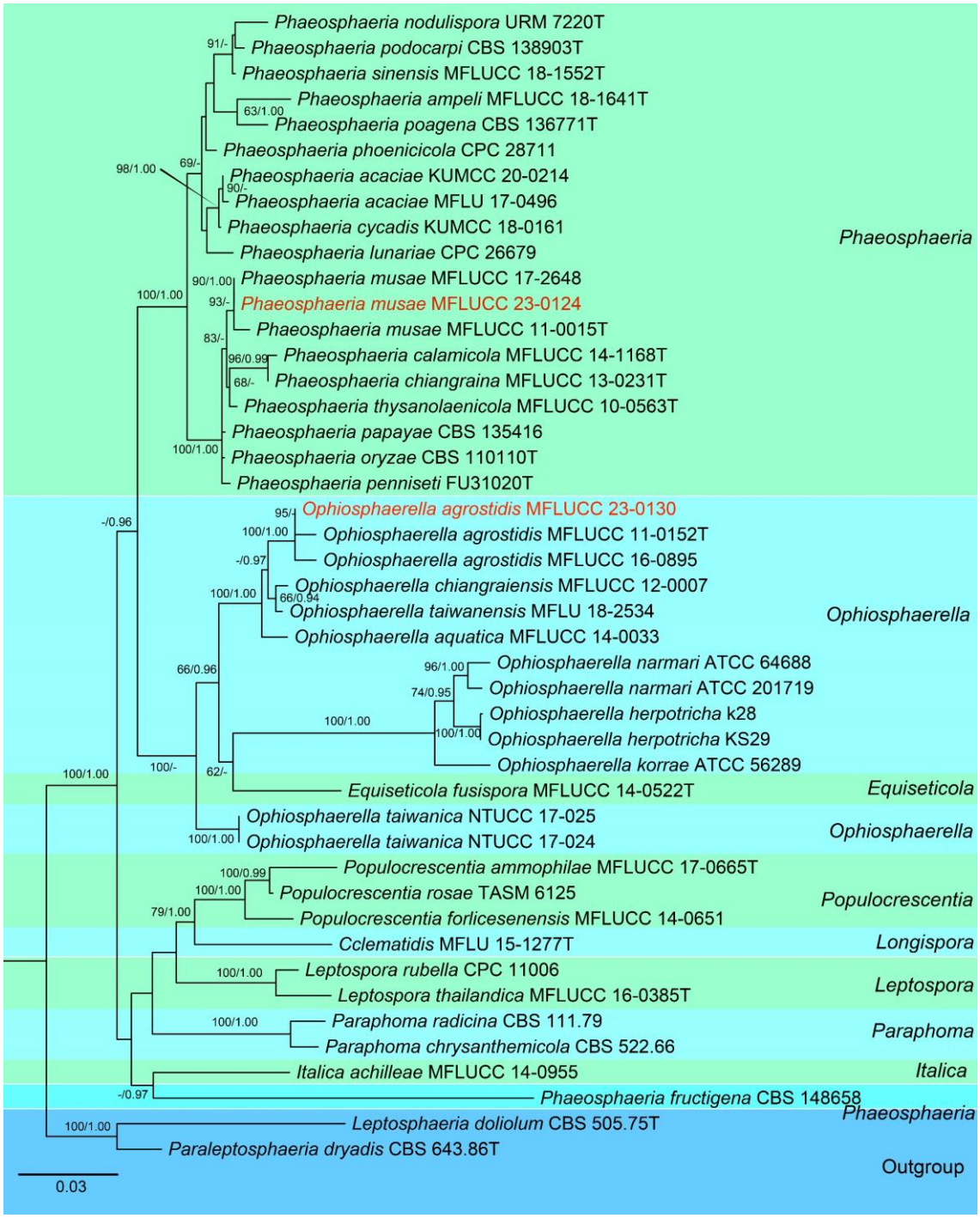

Figure 41 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, and *tef1-α* sequence data. Related sequences were obtained from Liao et al. (2021). Fourth-four strains are included in the combined sequence analysis, which comprises 2564 characters with gaps. *Leptosphaeria doliolum* (CBS 505.75) and *Paraleptosphaeria dryadis* (CBS 643.86) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -13231.613290 is presented. The matrix had 838 distinct alignment patterns, with 29% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245657, C = 0.237090, G = 0.261248, T = 0.256005; substitution rates AC = 1.198534, AG = 2.759752, AT = 2.849260, CG = 0.664917, CT = 7.218917,

GT = 1.000000; gamma distribution shape parameter α = 0.135911. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Culture characteristics: Colonies on PDA reaching 15 mm diameter after two weeks at 25 °C, colonies circular, convex, surface slightly rough on PDA, mycelium dense, effuse, velvety. Colony white from above, white at the margin, light brown to yellowish at the centre from reverse.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Oryza sativa*, 16 September 2020, X.G. Tian, r1-11 (MFLU 23-0183), living culture MFLUCC 23-0124.

Known hosts and distribution – On *Musa cavendishii* in Taiwan Province, China; on dead leaf of *Roystonea regia* in Taiwan Province, China (Tennakoon et al. 2019); on leaves of *Musa* sp. in Mauritius (Arzanlou & Crous 2006, Thambugala et al. 2014); on dead leaf of palms in Thailand (Liu et al. 2015); on living leaves of *Calathea* sp. in Thailand (Phookamsak et al. 2014); on living leaves of *Cordyline* sp. in Thailand (Phookamsak et al. 2014); on dead leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438829, ITS = OR438358, SSU = OR458347, *tef1-α* = OR500320.

Notes – In the phylogenetic analyses, our strain (MFLUCC 23-0124) clusters with two strains of *P. musae* (MFLUCC 11-0015 and MFLUCC 17-2648) (Fig. 41). Our strain shares similar morphology to *Phaeosphaeria musae* (MFLUCC 17-2648) in having immersed, solitary, scattered, slightly raised, visible as black spots on host surface ascomata, with 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apically rounded asci and fusiform, yellowish-brown to brown, 3-septate, slightly constricted at the septa, slightly curved, rough-walled ascospores. The size of asci (35–45 × 9–15 μm vs. 30–40×10–12 μm) and ascospores (15–20 × 4–5 μm vs. 15–21× 3–5.5 μm) overlap between our strain and *P. musae* (MFLUCC 17-2648) (Tennakoon et al. 2019). The nucleotide comparisons showed that our strain (MFLUCC 23-0124) is not significantly different from *P. musae* (MFLUCC 11-0015 and MFLUCC 17-2648) in ITS, LSU, and SSU. Thus, we identified our strain as *P. musae*, and it is a new host record on *Oryza sativa.*

Pleosporaceae Nitschke

Pleosporaceae was earlier placed in *Pseudosphaeriaceae* by Theissen & Sydow (1917). Lumbsch & Huhndorf (2010) confirmed the familial placement of *Pleosporaceae* with respect to other families in *Pleosporales* according to multi-gene phylogenetic studies (Lumbsch & Huhndorf 2010). Hongsanan et al. (2020b) and Wijayawardene et al. (2022) accept 23 genera in *Pleosporaceae*.

Bipolaris Shoemaker

Bipolaris has traditionally been treated as part of the helminthosporioid complex because the conidia and conidiophores morphologically resemble species of *Helminthosporium*. *Bipolaris* was initially established to accommodate species that formed fusoid conidia with two septa (Shoemaker 1959). The classification of *Bipolaris* species was based entirely on morphological characteristics until the late 1990s (Sivanesan 1987). In recent years, the helminthosporioid complex fungi (*Curvularia*, *Drechslera*, *Exserohilum*, *Johnalcornia* and *Porocercospora*) have been more clearly defined with the help of molecular sequence data. Subsequent multi-gene phylogenetic studies have established the synonymy between *Bipolaris* (typified by *B. maydis*) and its sexual morph, *Cochliobolus* (typified by *C. heterostrophus*). Species of *Bipolaris* are saprobes or commonly pathogens associated with leaf spots, leaf blights and root rots with worldwide distribution (Sivanesan 1987, Iftikhar et al. 2009, Manamgoda et al. 2011, Manamgoda et al. 2014). In this study, *Bipolaris oryzae* was recollected from rice in Thailand.

24. *Bipolaris oryzae* (Breda de Haan) Shoemaker, Can. J. Bot. 37(5): 883 (1959) Fig. 43

Index Fungorum number: IF482518; Facesoffungi number: FoF14290

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: *Conidiophores* mononematous, erect, straight to flexuous, branched, brown to dark brown, smooth, septate, 95–170 × 6–8.5 µm ($\overline{x}$ = 134 × 8 µm, n = 20); basal cell swollen. *Conidiogenous cells* 9–30 × 5.5–9 µm ($\overline{x}$ = 18 × 7 µm, n = 15), integrated, terminal or intercalary, with sympodial proliferation, brown, smooth, mono- or polytretic with thickened circular scars. *Conidiogenous loci* distinct and swollen. *Conidia* fusiform, ellipsoidal, straight to slightly curved, 40–70 × 15–25 µm ($\overline{x}$ = 53 × 18 µm, n = 20), brown to dark brown, broadest in the middle, 2–8-distoseptate. Hilum darkened.

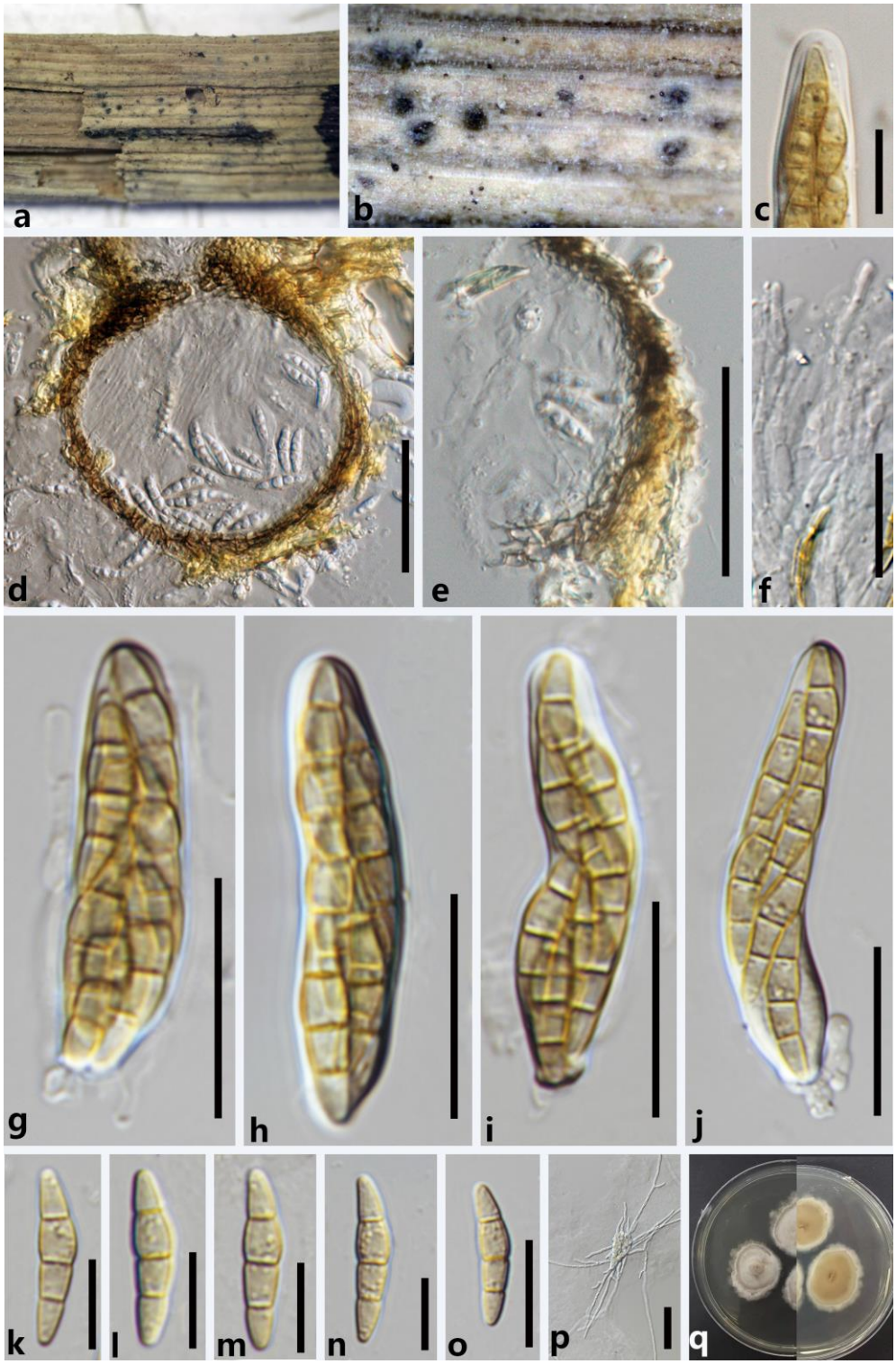

Figure 42 – *Phaeosphaeria musae* (MFLU 23-0183, new host record) a, b Appearance of ascomata

on the host surface. c Ascus apex. d Section of ascoma. e Peridium. f Pseudoparaphyses. g–j Asci. k–o Ascospores. p Germinated ascospore. q Colonies on PDA from surface and reverse. Scale bars: f–j, q = 20μm, d, e = 50 μm, c, k–q = 10 μm.

Culture characteristics – Colonies cover on PDA, 40 mm diam. after two weeks. Colonies surface grey, velutinous with abundant aerial mycelium.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Oryza sativa*, 3 January 2021, X.G. Tian, R8-2 (MFLU 23-0187), living culture MFLUCC 23-0152.

Known hosts and distribution – On *Oryza australiensis* in Australia (Khemmuk et al. 2016); on *Oryza sativa* and *Panicum virgatum* in Thailand and the USA, respectively (Manamgoda et al. 2014); on rice (*Oryzae sativa*) in India (Kumar et al. 2011); on rice in Philippines (Burgos et al. 2013); on Switchgrass in the United States (Waxman & Bergstrom 2011); on *Alopecurus aequalis*, *Chikusichloa aquatic*, *Cordia trichotoma*, *Eleusine indica*, *Leersia hexandra*, *Oxalis latifolia*, *Panicum colonum*, *P. maximum*, *P. virgatum*, *Setaria italica*, *Triticum aestivum*, *Zizania latifolia*, and *Z. palustris* in Bangladesh, Bhutan, Bolivia, Brazil, Brunei Darussalam, China, Colombia, Egypt, Fiji, Gambia, Ghana, Guinea, India, Indonesia, Iran, Jamaica, Japan, Korea, Malawi, Malaysia, Mauritius, Mexico, Myanmar, Nepal, New Zealand, Nicaragua, Nigeria, Pakistan, Panama, Papua New Guinea, South Africa, Thailand, Venezuela, Yugoslavia, Zambia, and Zimbabwe (Farr & Rossman 2020).

GenBank numbers – ITS = OR438361, *gapdh* = OR567319, *tef1-α* = OR887683.

Notes – In the phylogenetic analyses, our strain (MFLUCC 23-0152) clustered within *Bipolaris oryzae* strains (Fig. 44). Morphologically, our strain (MFLUCC 23-0152) shares similar characteristics with *B. oryzae* in having simple, straight to flexuous conidiophores, straight to rarely curved, brown to dark brown conidia (Manamgoda et al. 2014, Tan et al. 2016). The nucleotide comparisons showed that our strain *B. oryzae* (MFLUCC 23-0152) is not significantly different from the strains of *B. oryzae* in ITS, *tef1-α*, and *gapdh*. Thus, we identified our strain as *B. oryzae* based on both phylogeny and morphology.

Curvularia Boedijn

Curvularia was erected by Boedijn (1933) with *C. lunata* as the type species and characterized by polytretic conidiophores, and curved, often versicoloured and multi-septate conidia. Most *Curvularia* species encountered as saprobes or endophytes can be latent, opportunistic or invasive pathogens on the same or different hosts (Hongsanan et al. 2020b, Ferdinandez et al. 2021). More than 230 epithets are listed in Index Fungorum (2023). In this study, for new records *C. dactylocteniicola*, *C. elliptiformis* and *C. verruculosa* are reported with detailed descriptions and illustrations.

25. *Curvularia dactylocteniicola* Y. Marín, Senwanna & Crous [as '*dactyloctenicola*'], in Marin-Felix et al., Mycosphere 8(9): 1567 (2017) Fig. 45

Index Fungorum number: IF827459; Facesoffungi number: FoF14291

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiophores* 105–145 × 3–4.5 μm ($\overline{x}$ = 125.2 × 3.6 μm, n = 15), macronematous, mononematous, septate, unbranched, straight or slightly flexuous, brown to dark brown. *Conidiogenous cells* polyblastic, proliferating sympodially, terminal or intercalary, subcylindrical to swollen, pale brown to brown. *Conidia* 16–19 × 8.5–10 μm ($\overline{x}$ = 18× 9.2 μm, n = 30), acropleurogenous, ellipsoidal to obovoid, with round ends, straight or curved, smooth-walled to slightly verruculose, middle cells are darker and larger than the basal cells, sometimes the third cell larger than other cells, pale brown to brown, (2–)3-distoseptate.

Cultural characteristics – Colonies on PDA reaching 55–65 mm diam. in 14 days, with sparse aerial mycelium, margins slightly lobate; surface grayish white to cream white, reverse dark brown to black.

Material examined – Thailand, Chiang Rai Province, on dead leaves of *Ananas comosus*,

17 August 2020, X.G. Tian, P7-1 (MFLU 23-0188), living culture MFLUCC 23-0142.

Known host and distribution – On *Dactyloctenium aegyptium* in Thailand (Marin-Felix et al. 2017); on sugarcane in southern China (Raza et al. 2019); on ripe mango (*Mangifera indica*) from Sri Lanka (Adikaram et al. 2023); on sorghum from Indonesia (Hidayat & Ramadhani 2019); on *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438362, *tef1-α* = OR500324, *gadph* = OR567318.

Figure 43 – *Bipolaris oryzae* (MFLU 23-0187, new collection). a, b Appearance of colonies on the host surface. c–f Conidiophores with conidia. g–l Conidia. m Germinated conidium. n, o Colonies

from surface and reverse. Scale bars: c–f, m = 20 µm, g–l = 10 µm.

Figure 44 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1-α* and *gapdh* sequence data. Related sequences were obtained from Bhunjun et al. (2020) and (Hernández-Restrepo et al. 2018). Fifty-five strains are included in the combined sequence analysis, which comprises 2215 characters with gaps. *Curvularia nodosa* (CPC 28800) and *Exserohilum macginnisii* (CBS 325.87) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -8463.363647 is presented. The matrix had 598 distinct alignment patterns, with 14.49% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.232598, C = 0.299205, G = 0.239160, T = 0.229037; substitution rates AC = 0.827748, AG = 2.633078, AT = 1.449850, CG = 0.835597, CT = 5.917631, GT = 1.000000; gamma distribution shape parameter α = 0.150801. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90

are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

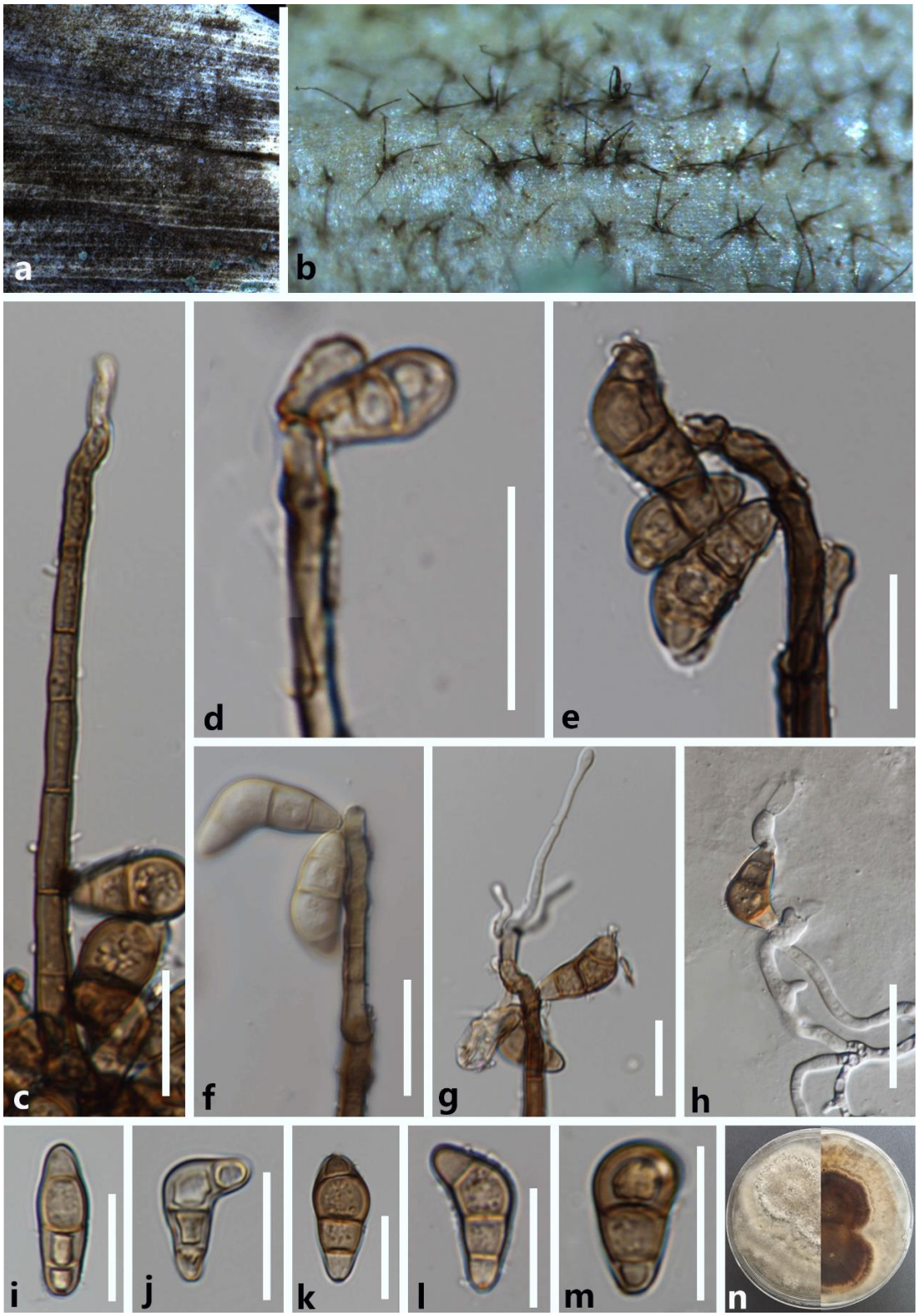

Figure 45 – *Curvularia dactyloctenicola* (MFLU 23-0188, new host record). a, b Colonies on the natural substrate. c Conidiophores. d–f conidiophores with conidia. d–g Conidiogenous cells with conidia. h Germinated conidium. i–m Conidia. n Colonies on PDA from surface and reverse. Scale bars: c–m = 20 μm.

Notes – In our phylogenetic analyses, our new isolate (MFLUCC 23-0142) clustered with the

ex-type strain of *C. dactylocteniicola* (CPC 28810) (Fig. 46). The comparison of nucleotide in ITS, *tef1-α* and *gapdh* genes regions between our new isolate and *C. dactylocteniicola* (CPC 28810) revealed no differences. Morphologically, our new isolate shares similar characteristics with the holotype of *C. dactylocteniicola* in having mononematous, septate, unbranched conidiophores, polyblastic, proliferating sympodially, terminal or intercalary conidiogenous cells and ellipsoidal to obovoid, 3-distoseptate, smooth-walled to slightly verruculose conidia with darker and larger middle cells and paler, smaller basal cells (Marin-Felix et al. 2017). However, the conidiophores in our isolate are macronematous which are semi- to macronematous in the holotype. This difference may be attributed to their distinct lifestyles. Our isolate is a saprobe on dead leaves of *Ananas comosus*, whereas, the holotype of *C. dactylocteniicola* is a pathogen from *Dactyloctenium aegyptium* (Marin-Felix et al. 2017). Hence, based on both phylogeny and morphology, we identified our new isolate as *C. dactylocteniicola* which is a new host record on *Ananas comosus*.

26. *Curvularia elliptiformis* M. Raza, K.D. Hyde & L. Cai, in Raza et al., Fungal Divers. 99: 51 (2019) Fig. 47

Index Fungorum number: IF556658; Facesoffungi number: FoF06148

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiophores* 135–205 × 4–4.5 µm ($\overline{x}$ = 167 × 4.2 µm, n = 10), mononematous, macronematous, septate, with inflated apical cell, slightly geniculate, brown, smooth to asperulate. *Conidiogenous cells* 6.5 × 30 × 3.5–6 µm ($\overline{x}$ = 17.5 × 4.7 µm, n = 10), proliferating sympodially, integrated, smooth-walled to verruculose, terminal becoming intercalary, mono or polyblastic, cylindrical, pale brown to brown. *Conidia* 15.5–25 × 7.5–15.5 µm ($\overline{x}$ = 20.5 × 11.5 µm, n = 15), ellipsoidal and oval, borne singly or in clusters, straight or slightly flexuous, 3-septate, slightly darker at septa, with brown middle cells, with apical and basal cells hyaline to subhyaline, guttulate, smooth-walled; Hilum 1–3.5 µm wide non-protruding, flat, darkened and slightly thickened.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 21 July 2020, X.G Tian. P4-21 (MFLU 23-0189), living culture MFLUCC 23-0103.

Known hosts and distribution – On *Saccharum officinarum* in China; on *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438363, *tef1-α* = OR500325.

Notes – Our strain *Curvularia elliptiformis* (MFLUCC 23-0103) shares similar morphological characteristics with the holotype reported on dead leaves of *Saccharum officinarum* (HMAS 248051) in China (Raza et al. 2019). They both have mononematous, macronematous, septate conidiophores, proliferating sympodially, mono or polyblastic conidiogenous cells and ellipsoidal, 3-septate, darker septa conidia. Phylogenetic analyses using combined ITS, *tef1-α*, and *gadph* sequence data demonstrate that our strain is *Curvularia elliptiformis* (Fig. 46) and compare nucleotides there are same nucleotide in ITS and *tef1-α*. This is the new host and geographical record of *C. elliptiformis* on *Ananas comosus* in Thailand.

27. *Curvularia verruculosa* Tandon & Bilgrami ex M.B. Ellis, Mycological Papers 106: 20 (1966) Fig. 48

Index Fungorum number: IF329454; Facesoffungi number: FoF00571

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Conidiophores* 135–220 × 5.5–8 µm ($\overline{x}$ = 177.5 × 6.5 µm, n = 15), mononematous, macronematous, septate, rarely branched, straight or slightly curved, geniculate near the apex, pale brown, smooth to asperulate. *Conidiogenous cells* 10–20 × 5.5–7 µm ($\overline{x}$ = 13.5 × 6.5 µm, n = 15), proliferating sympodially, terminal or intercalary, integrated, polytretic, pale brown to brown, cylindrical, smooth-walled. *Conidia* 20–30 × 10–15 µm ($\overline{x}$ = 24.5 × 14 µm, n = 20) straight, ellipsoidal or curved, borne singly or in clusters, 3 septate rounded at both ends; with third cell larger than other cells, verruculose, pale brown to brown, occasionally apical or basal cells are paler than middle cells.

Figure 46 – Phylogram generated from maximum likelihood analysis based on combined ITS, *gapdh*, and *tef1-α* sequence data. Related sequences were obtained from Ferdinandez et al. (2021) and (Raza et al. 2019). One hundred and seventy-three strains are included in the combined sequence analysis, which comprise 2162 characters with gaps. *Bipolaris maydis* (CBS 136.29) and *Johnalcornia aberrans* (CBS 510.91) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -

21086.789675 is presented. The matrix had 947 distinct alignment patterns, with 19.59% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.233699, C = 0.298855, G = 0.242894, T = 0.224552; substitution rates AC = 0.901480, AG = 3.283644, AT = 1.129208, CG = 1.085513, CT = 5.902740, GT = 1.000000; gamma distribution shape parameter α = 0.190321. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red and T indicates holotype or ex-type strains.

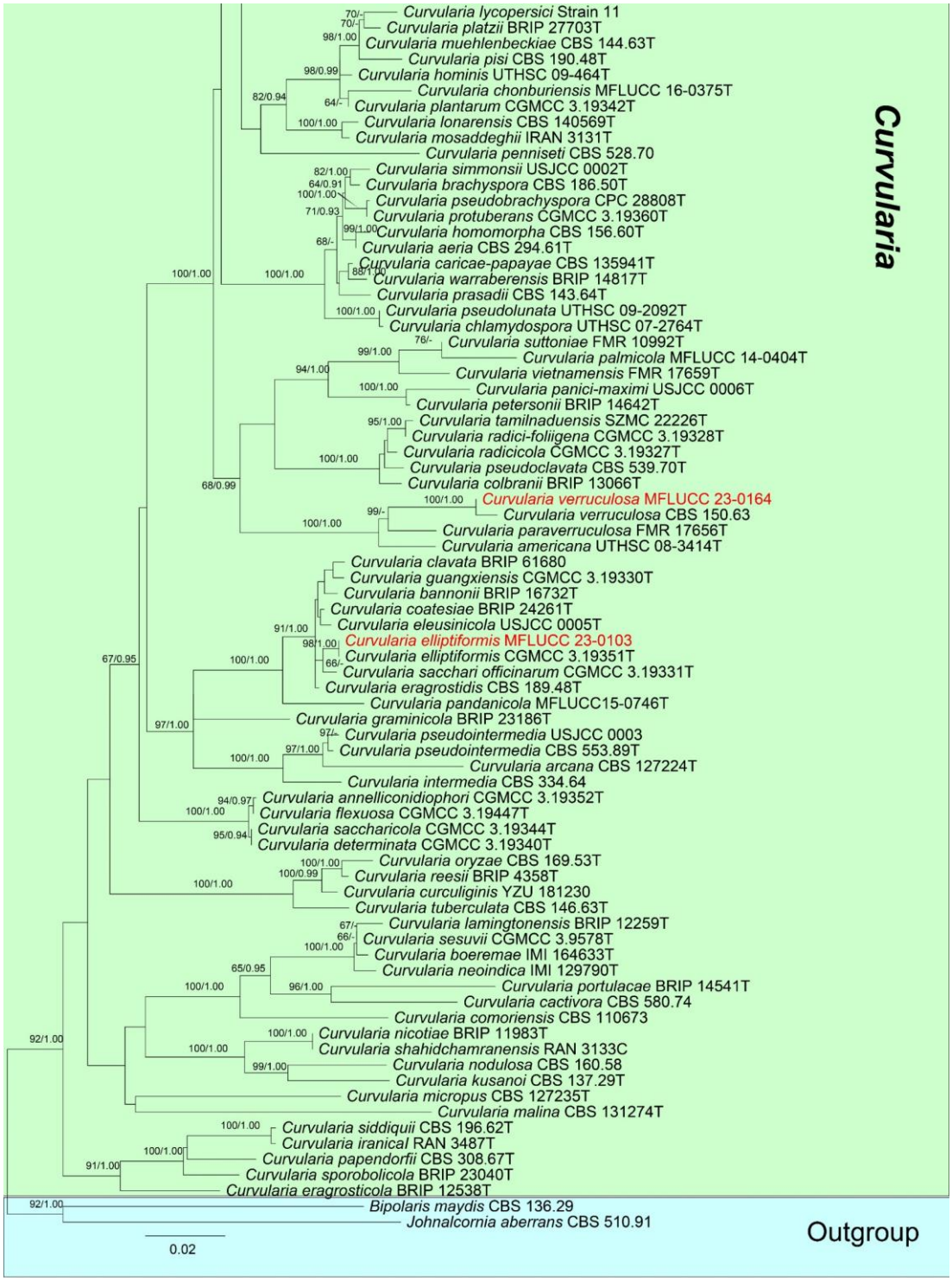

Figure 46 – Continued.

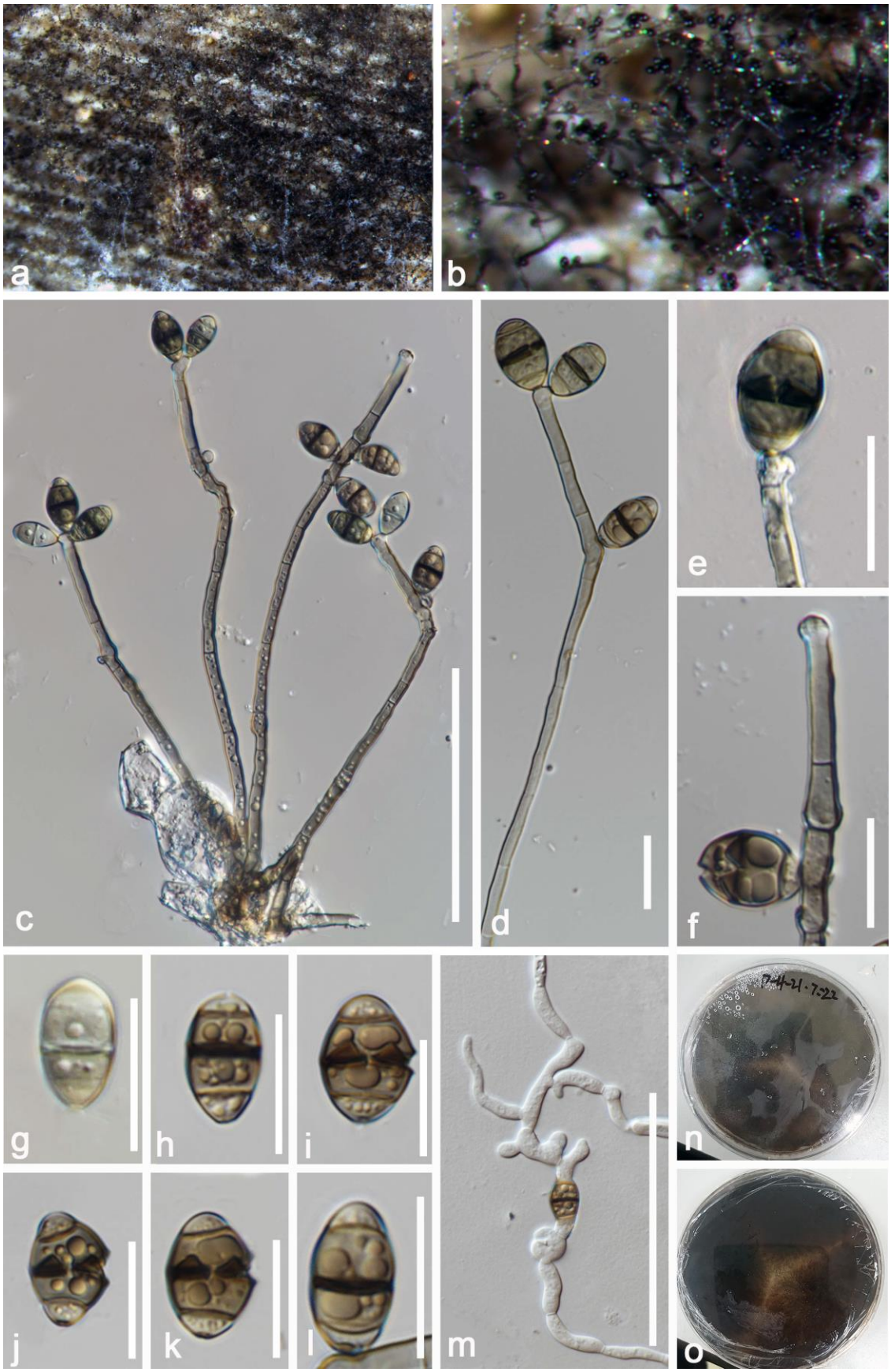

Figure 47 – *Curvularia elliptiformis* (MFLU 23-0189, new host and geographical record). a, b Colonies on natural substrate. c, d Conidiophores with conidia. e, f Conidiogenous cells and conidia. g–l Conidia. m Germinated conidium. n, o Colonies on PDA from surface and reverse. Scale bars: c, m = 100 μm, d–i, j–l = 20 μm.

Figure 48 – *Curvularia verruculosa* (MFLU 23-0190, new host record). a, b Colonies on natural substrate. c–e Conidiophores. f Conidiogenous cells and conidia. g Conidiogenous cells. j–n Conidia. h Germinated conidium. i Colony on PDA from surface and reverse. Scale bars: c–e = 60 μm, f–h, j–n = 10 μm.

Cultural characteristics – Colonies on PDA fast growing, reaching 15 cm diam. in 7 days after incubation at 25 °C, colony rough surface, hairy, flat, smooth, slightly radiating at margin; colony from above, white grey to brown from the center to margin; from below, black and white margin.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 1 August 2020, X.G Tian. c6-32 (MFLU 23-0190), living culture MFLUCC 23-0164.

Known host and distribution – On *Cycas rumphii* and *Punica granatum* in India (Ellis 1966); on *Cynodon* sp. in China (Huang et al. 2005); on submerged wood in China (Su et al. 2015); on Poaceae in Thailand (Marin-Felix et al. 2017); on cotton in India (Shirsath et al. 2018); on leaves of *Catharanthus roseus* from India (Parthasarathy et al. 2020); on *Vitis vinifera* in Afghanistan (Rajput et al. 2020); on sugarcane in southern China (Raza et al. 2019); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – ITS = OR438364, *tef1-α*= OR500326, *gadph* = OR567317.

Notes – Our strain (MFLUCC 23-0164) of *Curvularia verruculosa* shares similar characteristics to the holotype (HKAS 84009) that was reported on decaying wood submerged in a stream in China (Su et al. 2015). They both have mononematous, macronematous, septate, branched conidiophores, proliferating sympodially, polytretic, terminal or intercalary conidiogenous cells and ellipsoidal, 3-septate, verruculose conidia and the larger third cell conidia. Phylogenetic analyses using combined ITS, *tef1-α* and *gadph* sequence data demonstrate that our strain is *C. verruculosa* (Fig. 46) and the nucleotides in ITS, *tef1-α* and *gadph* of our strain are not significantly different from the holotype. Our strain is reported on *Cocos nucifera* for the first time.

Exserohilum K.J. Leonard & Suggs, Mycologia 66(2): 289 (1974).

Exserohilum was established by Leonard & Suggs (1974) to include taxa with a conspicuously protuberant conidial hilum that was previously placed in *Bipolaris. Setosphaeria* was also introduced to place the sexual morphs of *Exserohilum* (Leonard & Suggs 1974). The asexual name *Exserohilum* has priority over *Setosphaeria*. Hence, *Setosphaeria* was synonymized under *Exserohilum*. *Exserohilum* includes several plant pathogenic, saprobic and clinically relevant fungi (Hernández-Restrepo et al. 2018). In this study, we introduce a new species *E. ananasi* based on morphological characters and phylogenetic analysis.

28. *Exserohilum ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 49

Index Fungorum number: IF900977; Facesoffungi number: FoF14292

Etymology – Referring to *Ananas comosus*, on which the fungus was collected.

Holotype – MFLU 23-0191

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiophores* 120–175 × 5–10 µm ($\overline{x}$ = 146 × 6 µm, n = 25), macronematous, mononematous, erect, straight or less flexuous, septate, unbranched, cylindrical, olivaceous brown to brown, becoming paler at apex, smooth-walled. *Conidiogenous cells* 15–35 × 4.5–6 µm ($\overline{x}$ = 25 × 5.5 µm, n = 15) integrated, terminal and intercalary, subcylindrical, mono- to polytretic, sympodial, cicatrized. *Conidia* mostly 65–90 × 10–20 µm ($\overline{x}$ = 79 × 14 µm, n = 15), subcylindrical to obclavate rostrate, straight to moderately curved, pale olivaceous brown, 3–12-distoseptate, hilum strongly protruding, smooth-walled.

Culture characteristics – Colonies cover on PDA, reaching 40 mm diam. after two weeks at 25 °C. Colonies surface flat with hairy aerial mycelium, whitish at the periphery, becoming cottony and pale olivaceous grey on PDA.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 15 July 2020, X.G. Tian, p5-7 (MFLU 23-0191, holotype), ex-type living culture MFLUCC 23-0135.

GenBank numbers – MFLU 23-0191: LSU = OR438834, ITS = OR438365. MFLUCC 23-0135: LSU = OR438835, ITS = OR438366.

Notes – In the phylogenetic analyses, our strain (MFLUCC 23-0135) clusters as sister to *Exserohilum holmii* (CBS 505.90 and CBS 318.64) with 84% ML support (Fig. 50).

Morphologically, our strain resembles *E. holmii* in having macronematous, mononematous, straight, conidiophores; integrated, terminal and intercalary, mono- to polytretic, sympodial, cicatrized conidiogenous cells. However, our strain has subcylindrical to obclavate, rostrate, and 3–12-distoseptate conidia. While *E. holmii* has obovoid to clavate, obclavate rostrate, with a small paler area at each pole, 3–9-distoseptate conidia. In addition, our strain has shorter conidiophores (120–175 μm vs. 57–857.5 μm) and wider conidia (10–20 μm vs. 16.5–32 μm) than those of *E. holmii*. Based on nucleotide comparisons, our strain (MFLUCC 23-0135) is not significantly different from the ex-type isolate (CBS 318.64) in LSU, but different in 13/547 bp (2.38%) of the ITS. The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.85) (Fig. 51). Thus, both phylogenetic analyses and morphological characteristics supported our species *E. ananasi* as a distinct new species.

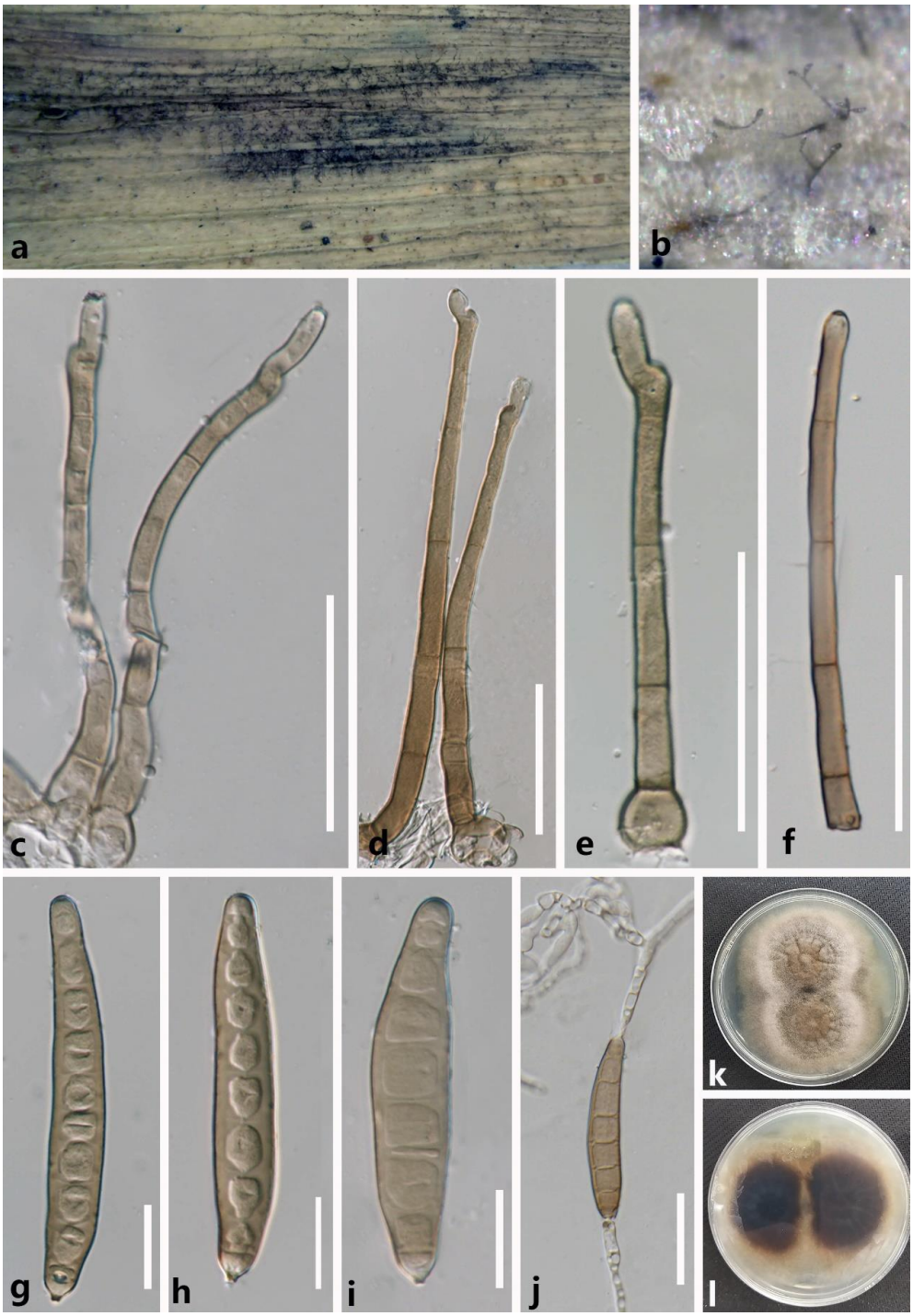

Figure 49 – *Exserohilum ananasi* (MFLU 23-0191, holotype) a, b Appearance of colonies on the

host surface. c–f Conidiophores with conidia. g–i Conidia. j Germinated conidium. k, l Colonies from surface and reverse. Scale bars: c–f, m = 50 µm, g–l = 20 µm.

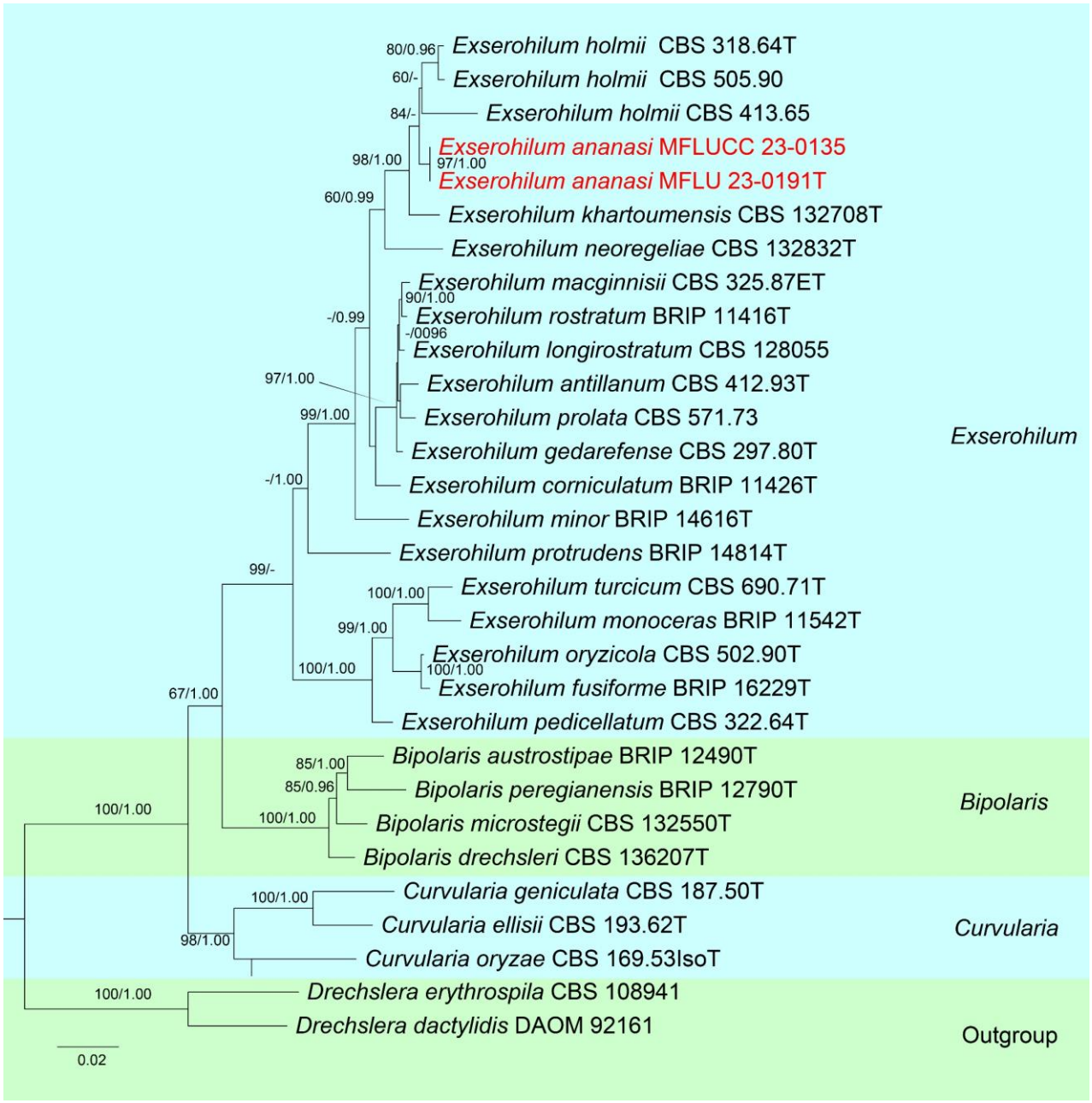

Figure 50 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1-α*, and *gapdh* sequence data. Related sequences were obtained from Ferdinandez et al. (2020) and Hernández-Restrepo et al. (2018). Thirty-one strains are included in the combined sequence analysis, which comprises 3126 characters with gaps. *Drechslera dactylidis* (DAOM 92161) and *D. erythrospila* (CBS 108941) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -11478.448503 is presented. The matrix had 738 distinct alignment patterns, with 12.99% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239921, C = 0.271487, G = 0.263690, T = 0.224901; substitution rates AC = 0.807785, AG = 1.890718, AT = 1.046563, CG = 1.113870, CT = 4.537831, GT = 1.000000; gamma distribution shape parameter α = 0.102035. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

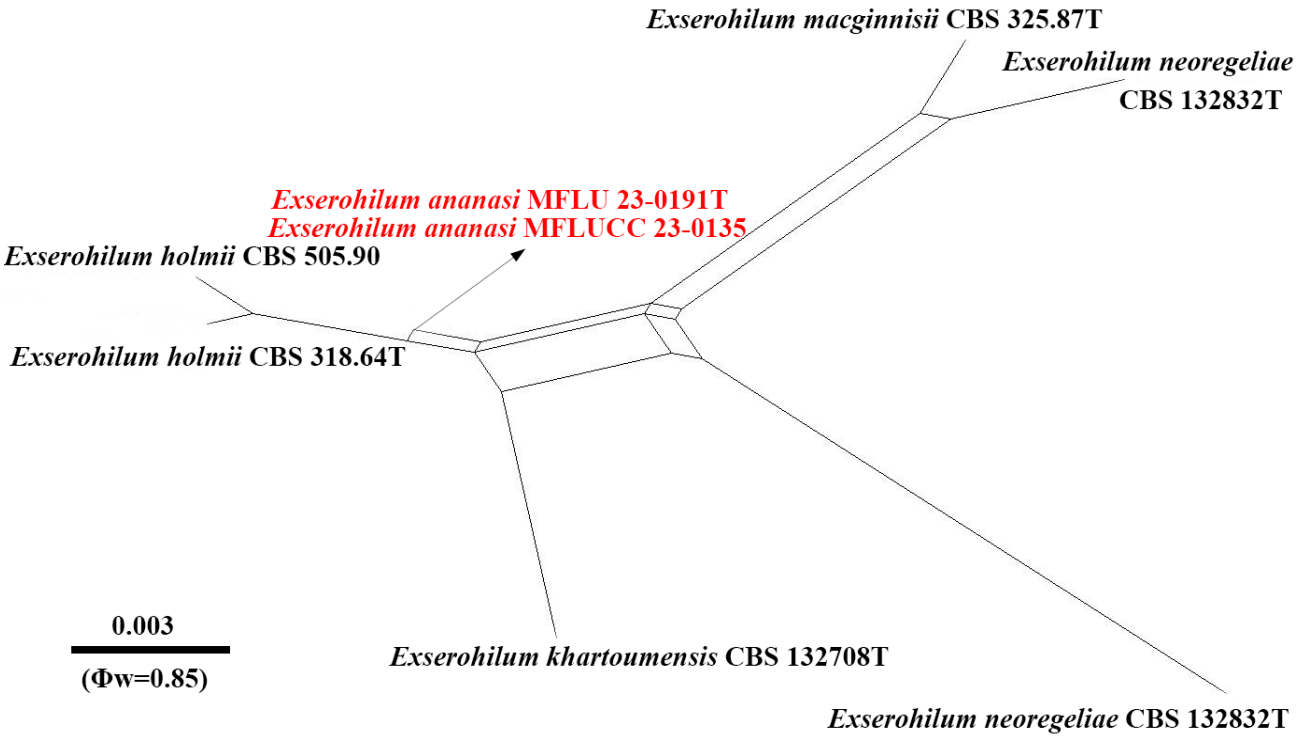

Figure 51 – Results of the PHI test of *Exserohilum ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

Pseudoberkleasmiaceae Phukhams & K.D. Hyde

Pseudoberkleasmiaceae was introduced by Hyde et al. (2019) to accommodate berkleasmium-like taxa that formed a clade related to *Hermatomytaceae* within *Pleosporales* (Hyde et al. 2019, Jayasiri et al. 2019, Hongsanan et al. 2020b). Only asexual morph is known for *Pseudoberkleasmiaceae* and characterized by reduced conidiophores, holoblastic, monoblastic, integrated, terminal, determinate conidiogenous cells and acrogenous, solitary, broadly ellipsoidal to obovoid, muriform, guttulate, with or without guttules, usually with conidiogenous cell attached conidia (Hyde et al. 2019).

Pseudoberkleasmium Tibpromma & K.D. Hyde

The monotypic genus *Pseudoberkleasmium* was introduced with *P. pandanicola* as the type species isolated from *Pandanus* sp. in China (Tibpromma et al. 2018). *Pseudoberkleasmium* is phylogenetically placed in *Pseudoberkleasmiaceae*, which was introduced by Hyde et al. (2019) to accommodate berkleasmium-like taxa that formed a clade related to *Pseudoberkleasmiaceae* within *Pleosporales* (Hyde et al. 2019, Hongsanan et al. 2020). *Pseudoberkleasmium* is characterized by holoblastic, monoblastic, integrated, terminal, hyaline, globose to subglobose conidiogenous cells and brown, acrogenous, solitary, muriform, guttulate conidia, usually with attached conidiogenous cells (Tibpromma et al. 2018, Hyde et al. 2019, Jayasiri et al. 2019, Hongsanan et al. 2020b). Three *Pseudoberkleasmium* species are listed in Index Fungorum (2023), and all of them have sequence data in GenBank. Only asexual morphs have been reported from this genus. *Pseudoberkleasmium* species are reported as saprobes from decaying wood and leaves in terrestrial and freshwater habitats and they play a vital role in recycling organic matter (Hyde et al. 2019, Jayasiri et al. 2019, Hongsanan et al. 2020b).

29. *Pseudoberkleasmium chiangraiense* X.G. Tian & Tibpromma, in Tian et al., Phytotaxa 547(3): 239 (2022) Fig. 52

Index Fungorum number: IF558909; Facesoffungi number: FoF10572

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph Not observed. Asexual morph Hyphomycetous. *Colonies* on natural substrate, superficial, in groups, scattered, black, velvety, glistening. *Mycelium* immersed in the substrate, composed of septate, branched, smooth, hyaline to pale brown hyphae. *Conidiophores* micronematous, mononematous, hyaline, smooth. *Conidiogenous cells* 5–12 × 5–12 μm ($\overline{x}$ = 10 × 9 μm, n = 15), holoblastic, monoblastic, determinate, terminal, globose to subglobose or cup-shaped, integrated, smooth, hyaline. *Conidia* 20–25 × 10–15 μm ($\overline{x}$ = 23 × 14 μm, n = 35), acrogenous, solitary, ellipsoidal to obovoid, flattened, muriform, smooth-walled, dark brown to black at apical, pale brown at basal, guttulate.

Culture characteristics – Conidia germinating on PDA within 12 h at 25 °C. Surface with hyphal growth, circular, umbonate, fluffy, gray at the margin, dark brown to black at the centre; reverse white to pale brown at the margin, black at the centre. Mycelium superficial, circular, partially immersed, hyaline to brown, smooth.

Material examined – China, Yunnan Province, Jinghong District, on decaying leaves of *Cocos nucifera*, 15 September 2021, X.G. Tian, C8-2 (GZAAS 23-0584), living culture, GZCC 23-0578.

Known hosts and distribution – On dead leaves of *Cocos nucifera* in Thailand (Tian et al. 2022b); On dead leaves of *Cocos nucifera* in China (this study).

GenBank numbers – LSU = OR438836, ITS = OR438367, *tef1-α* = OR500323

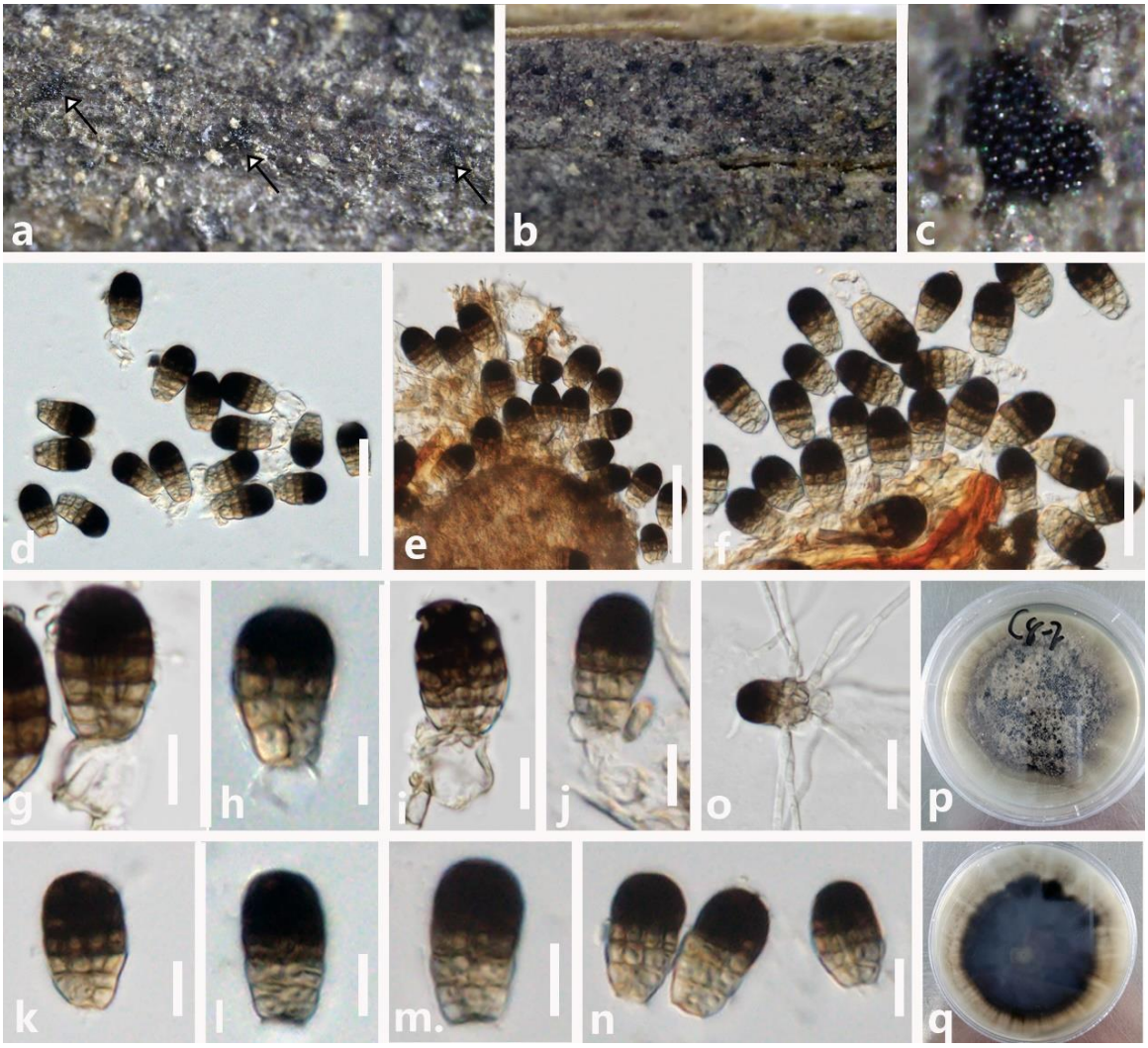

Figure 52 – *Pseudoberkleasmium chiangraiense* (GZAAS 23-0584, new geographical record). a–c Appearance of conidiomata on the host substrate. d–j Conidia with basal cell. k–n Conidia. o Germinated conidium. p, q Colony on PDA from surface and reverse. Scale bars: d, e, f, o = 20 μm, g–n = 10 μm.

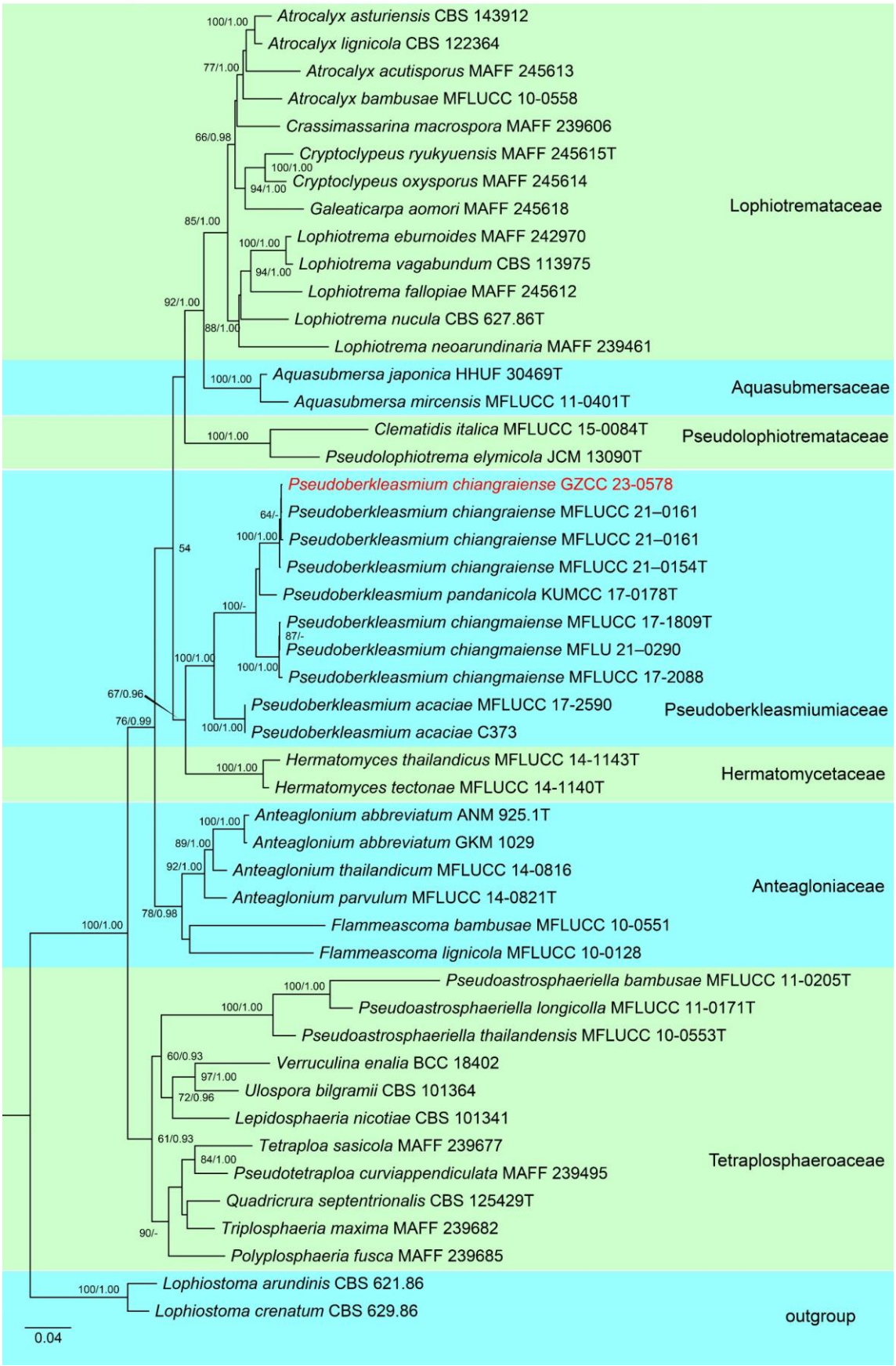

Figure 53 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data. Related sequences were obtained from Tian et al. (2022b). Forty-eight strains are included in the combined sequence analysis, which comprises 4841 characters with gaps. *Lophiostoma arundinis* (CBS 621.86) and *L. crenatum* (CBS 629.86) were

used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -30214.772440 is presented. The matrix had 1761 distinct alignment patterns, with 29.04% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249022, C = 0.249113, G = 0.269676, T = 0.232189; substitution rates AC = 1.479121, AG = 3.635786, AT = 1.312783, CG = 1.040232, CT = 8.411871, GT = 1.000000; gamma distribution shape parameter α = 0.200516. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Notes – In the multi-loci phylogenetic analyses, our strain (GZAAS 23-0584) clustered with *Pseudoberkleasmium chiangraiense* (Fig. 53). Morphologically, our strain is similar to *P. chiangraiense* (MFLU 21-0291, holotype) in having micronematous, mononematous conidiophores, with holoblastic, monoblastic, conidiogenous cells and acrogenous, muriform, guttulate conidia and the conidial size (20–25 × 10–15 μm vs. 26–30 × 14–17.5 μm) of our strain is also similar to the *P. chiangraiense* (MFLU 21-0291). The nucleotide comparisons showed that our strain (GZAAS 23-0584) is not significantly different from with *P. chiangraiense* (MFLU 21-0291, holotype) in ITS, LSU, and *tef1-α*. Thus, we identified our strain as *P. chiangraiense* based on phylogenetic analyses and morphological characters. Our strain *P. chiangraiense* (GZAAS 23-0584) is reported as a new geographical record in China.

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

Roussoellaceae was introduced by Liu et al. (2014) to accommodate *Neoroussoella*, *Roussoella* and *Roussoellopsis* with *R. nitidula* as the type species (Liu et al. 2014). Jaklitsch & Voglmayr (2016) synonymized *Roussoellaceae* under *Thyridariaceae* based on the multigene analysis of limited taxa. Tibpromma et al. (2017) reinstated *Roussoellaceae* and treated *Roussoellaceae* and *Thyridariaceae* as distinct families within *Pleosporales*. Twelve genera are accepted in *Roussoellaceae* (Wijayawardene et al. 2022).

Xenoroussoella Mapook & K.D. Hyde

Xenoroussoella was introduced by Mapook et al. (2020a) to accommodate *X. triseptata* *Xenoroussoella* members are characterized by immersed, solitary ascomata, cylindrical to clavate asci, and brown to dark brown, ellipsoid to obovoid, 3-septate ascospores (Mapook et al. 2020a). This is a monotypic genus in Species Fungorum (2023). This study reports *Xenoroussoella triseptata* as a new host record on *Ananas comosu* based on phylogenetic analysis and morphological characters.

30. ***Xenoroussoella triseptata*** Mapook & K.D. Hyde, in Mapook et al., Fungal Divers. 101: 95 (2020) Fig. 54

Index Fungorum number: IF557368; Facesoffungi number: FoF07823

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: See Mapook et al. (2020). Asexual morph: Coelomycetes. *Conidiomata* pycnidial, solitary to gregarious, unilocular, brown, immersed, becoming erumpent at maturity, ostiole not clear, up to 115 μm high × 70 μm diam. *Conidiomatal wall* composed of thick-walled, brown cells of textura angularis; inner layer thin, hyaline, 10–18 μm wide. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, ampulliform to cylindrical, hyaline, smooth-walled, 2.5–6.5 × 2.5–5 μm ($\overline{x}$ = 5.7 × 5.1 μm, n = 15), with a flared collarette. *Conidia* initially hyaline, becoming brown when mature, oblong to ovoid, straight, broadly rounded, at both ends, aseptate, smooth-walled, 3–4 × 2–3 μm ($\overline{x}$ = 3.6 × 2.6 μm, n = 40).

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 15 July 2020, X.G. Tian, P16-1 (MFLU 23-0192), living culture MFLUCC 23-0166.

Known hosts and distribution – From Soil in Korea (Ryu et al. 2022); on dead stems of *Chromolaena odorata* in Thailand (Mapook et al. 2020a); on dead twigs attached to *Anomianthus*

dulcis (*Annonaceae*) and *Desmos chinensis* (*Annonaceae*) in Thailand (de Silva et al. 2022); on decaying leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438837, ITS = OR438368, *tef1-α* = OR500328

Notes – *Xenoroussoella triseptate* is the type species of *Xenoroussoella*, reported by Mapook et al. (2020). In our phylogenetic analyses, our strain (MFLUCC 23-0166) grouped within the *Xenoroussoella triseptata* strains (Fig. 55). Morphologically, our strain resembles *X. triseptata* (MFLU 21-0252) in having pycnidial, unilocular, immersed conidiomata, phialidic, ampulliform to cylindrical conidiogenous cells, and oblong to ovoid, straight, both ends broadly rounded, aseptate and a similar size range of conidia (3–4 × 2–3 µm vs. 3–5 × 2–3 µm) (de Silva et al. 2022). Thus, we identified our strain as *X. triseptata* based on phylogenetic analyses and morphological characters. Our strain *X. triseptata* (MFLUCC 23-0166) is a new host record on *Ananas comosus*.

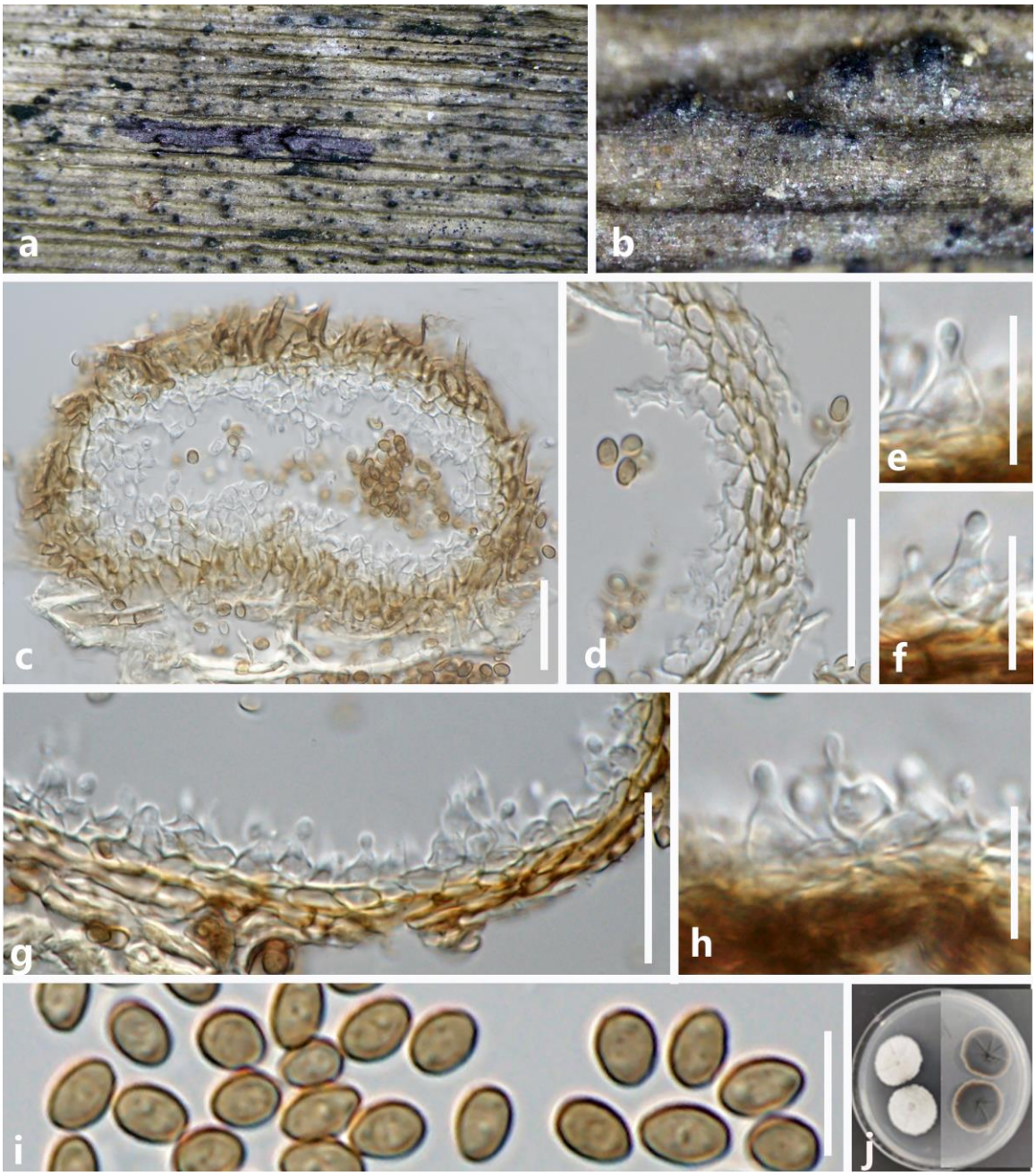

Figure 54 – *Xenoroussoella triseptata* (MFLU 23-0192, new host record). a, b Colonies on the host surface. c Vertical sections through conidiomata. d Conidiomatal wall. e–h Conidiogenous cells. i Conidia. j Colonies on PDA from surface and reverse. Scale bars: c, d, g = 20 µm, e, f, h, i = 10 µm.

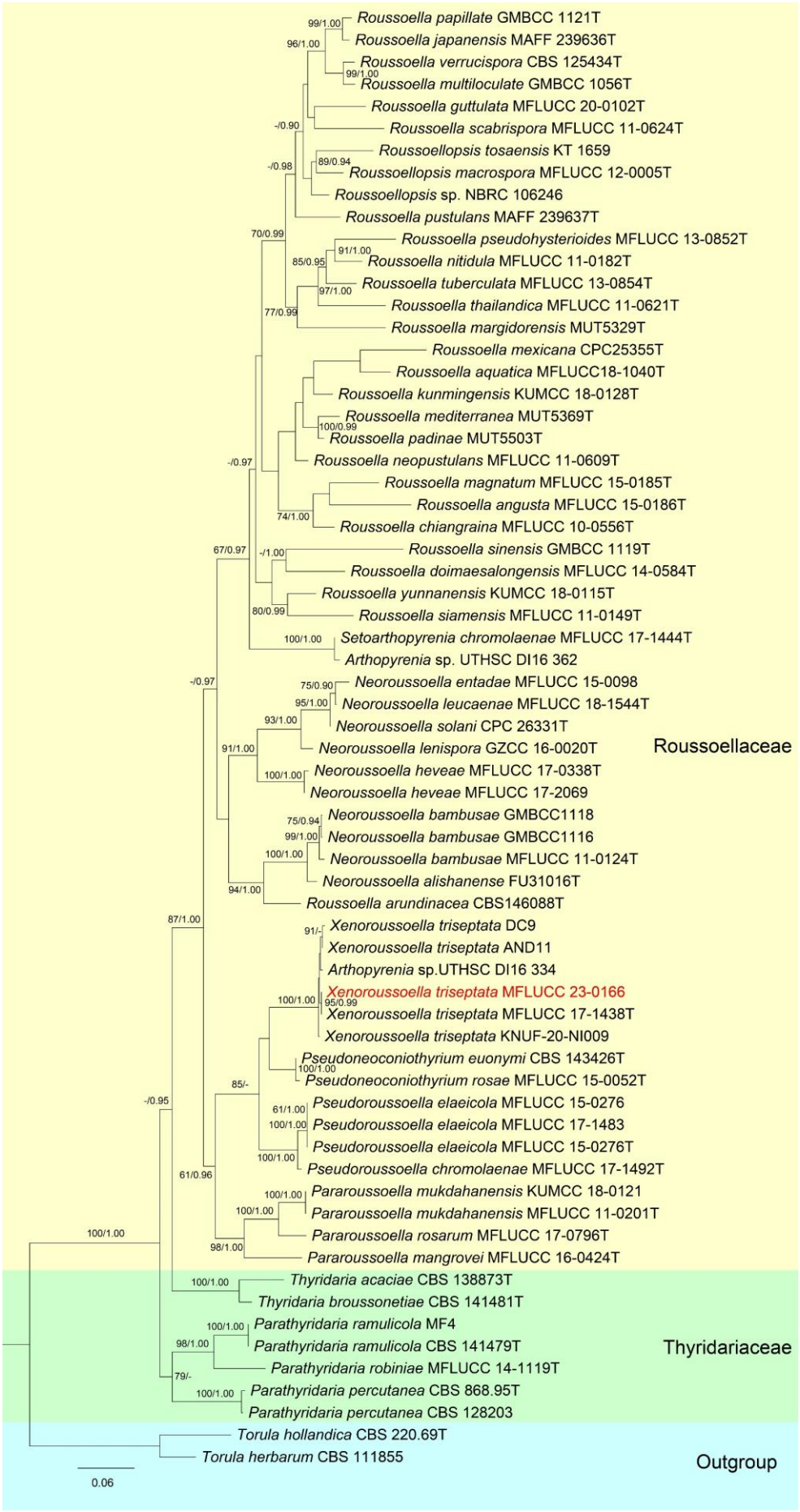

Figure 55 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

rpb2, and *tef1-α* sequence data. Related sequences were obtained from de Silva et al. (2022). Sixty-six strains are included in the combined sequence analysis, which comprises 3406 characters with gaps. *Torula herbarum* (CBS 111855) and *T. hollandica* (CBS 220.69) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -28445.996813 is presented. The matrix had 1441 distinct alignment patterns, with 28.09% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242646, C = 0.264950, G = 0.271235, T = 0.221168; substitution rates AC = 1.715617, AG = 4.828906, AT = 1.876087, CG = 1.273550, CT = 8.696907, GT = 1.000000; gamma distribution shape parameter 0.177254. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. The newly generated sequence is in red, while T indicates holotype or ex-type strains.

Teichosporaceae M.E. Barr

Teichosporaceae was established by Barr (2002) to accommodate eight genera, *Teichospora* (the type genus), *Bertiella*, *Byssothecium*, *Chaetomastia*, *Immotthia*, *Loculohypoxylon*, *Moristroma*, and *Sinodidymella* based on morphological characteristics. According to the recent outline of Wijayawardene et al. (2022), seventeen genera are accepted in *Teichosporaceae*. This study introduces a new genus *Pseudoteichospora* based on phylogenetic analyses and morphological characters.

31. *Pseudoteichospora* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.

Index Fungorum number: IF 900978; Facesoffungi number: FoF 14293

Etymology – Referring to its similarity with *Teichospora*.

Saprobic on dead leaves or wood in terrestrial habitats. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, immersed or semi-immersed, dark brown to black, solitary, unilocular, globose to subglobose. *Ostiole* central, papillate. *Conidiomatal wall* 3–5 layers of brown, composed of *textura prismatica* cells, with a hyaline inner lining bearing conidiogenous cells. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* hyaline, phialidic, indeterminate, cylindrical and smooth-walled. *Conidia* hyaline to pale brown, aseptate, ellipsoidal to oval with obtuse ends, granular to guttulate.

Type species – *Pseudoteichospora thailandensis* X.G. Tian, K.D. Hyde & Tibpromma

Notes – In the multi-loci phylogenetic analyses, our strains (MFLUCC 23-0109 and MFLUCC 23-0121) form a separate branch and groups with the clade comprising *Floricola* species, *Asymmetrispora* species, *Pseudomisturatosphaeria cruciformis*, *Paulkirkia arundinis* and *Teichospora kingiae* with 96% ML and 1.00 PP support value (Fig. 56). Morphologically, coelomycetous, pycnidial, with conidiophores reduced to conidiogenous cells and hyaline to pale brown unicellular indicates our strain belongs to *Teichospora*. Among the known species of the genus, most species are sexual morph. Our strain shares similar asexual morphology to *Teichospora grandicipis*, however, our strain differs from *Teichospora grandicipis* in have 3–5 layers brown conidiomatal wall, and ellipsoidal to oval, granular to guttulate conidia, while *Teichospora grandicipis* have 2–3 layers of light brown conidiomatal wall and fusiform to clavate with obtuse ends, guttulate conidia.

32. *Pseudoteichospora thailandensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 57

Index Fungorum number: IF900979; Facesoffungi number: FoF14294

Etymology – Referring to Thailand where the fungus was collected.

Holotype – MFLU 23-0193

Saprobic on dead leaves of *Ananas comosus*. Sexual morph Not observed. Asexual morph Coelomycetous. *Conidiomata* 90–175(–216) × 95–155(–196) μm ($\bar{x}$ = 134–127 μm, n = 7), pycnidial, immersed or semi-immersed, dark brown to black, solitary, unilocular, globose to subglobose. *Ostiole* central, papillate. *Conidiomatal wall* 10–20 μm wide, with 3–5 layers of brown, cells of *textura prismatica*, with a hyaline inner lining bearing conidiogenous cells. Conidiophores

reduced to conidiogenous cells. *Conidiogenous cells* 5–11 × 2–3 µm ($\bar{x}$ = 9 × 3 µm, n = 15) hyaline, phialidic, indeterminate, cylindrical and smooth-walled. *Conidia* 5–6 × 2.5–3 µm ($\bar{x}$ = 5.5 × 3 µm, n = 40), hyaline to pale brown, aseptate, ellipsoidal to oval with obtuse ends, granular to guttulate.

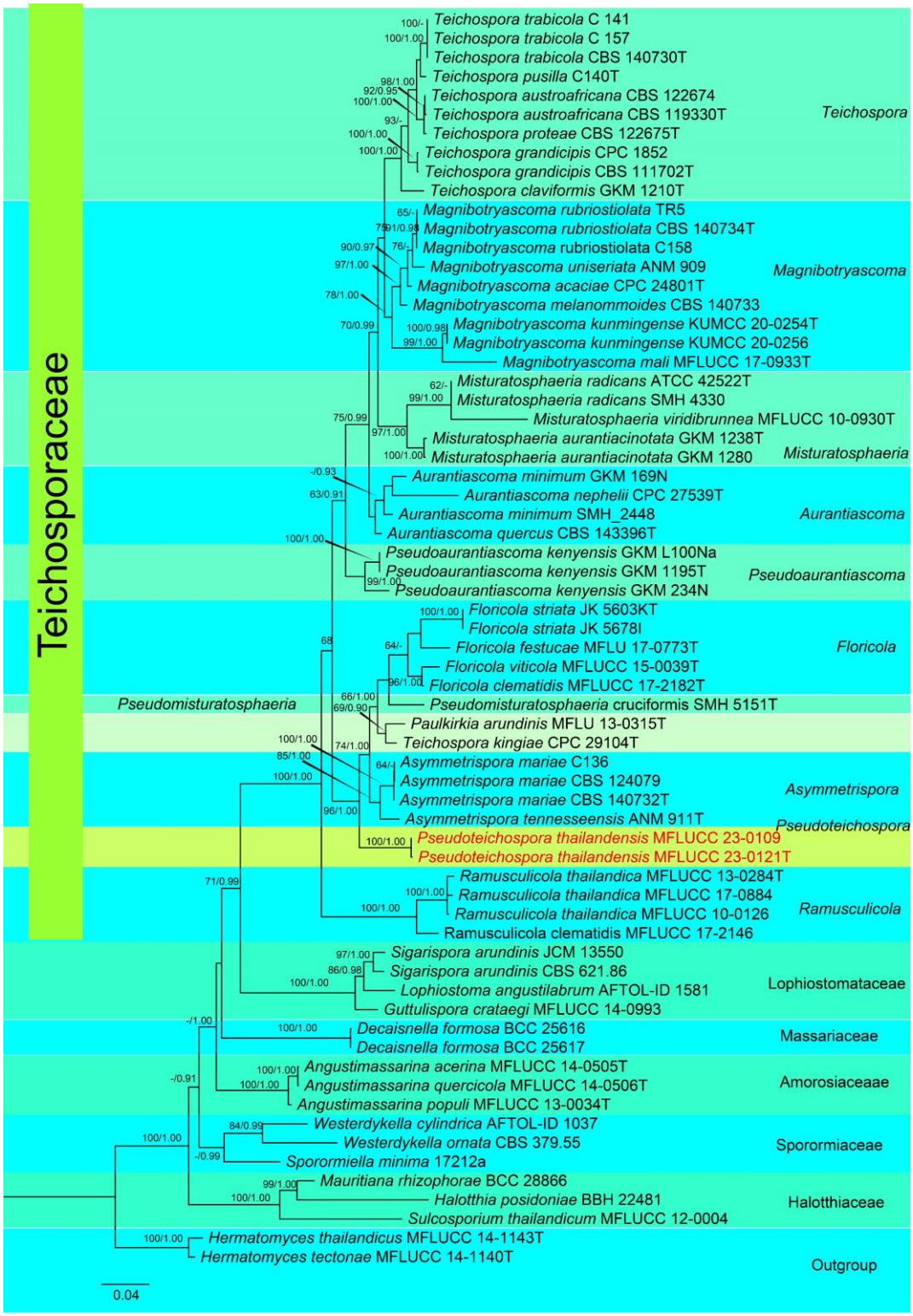

Figure 56 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data. Related sequences were obtained from Tennakoon et al. (2021a). Sixty-six strains are included in the combined sequence analysis, which comprise 5603 characters with gaps. *Hermatomyces tectonae* (MFLUCC 14-1140) and *H. thailandicus* (MFLUCC 14-1143) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best-scoring RAxML tree with a final likelihood value of -27116.477317 is presented. The

matrix had 1765 distinct alignment patterns, with 53.84% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245383, C = 0.249742, G = 0.279009, T = 0.225866; substitution rates AC = 1.228274, AG = 2.850033, AT = 1.534079, CG = 1.039345, CT = 7.758656, GT = 1.000000; gamma distribution shape parameter α = 0.191940. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red.

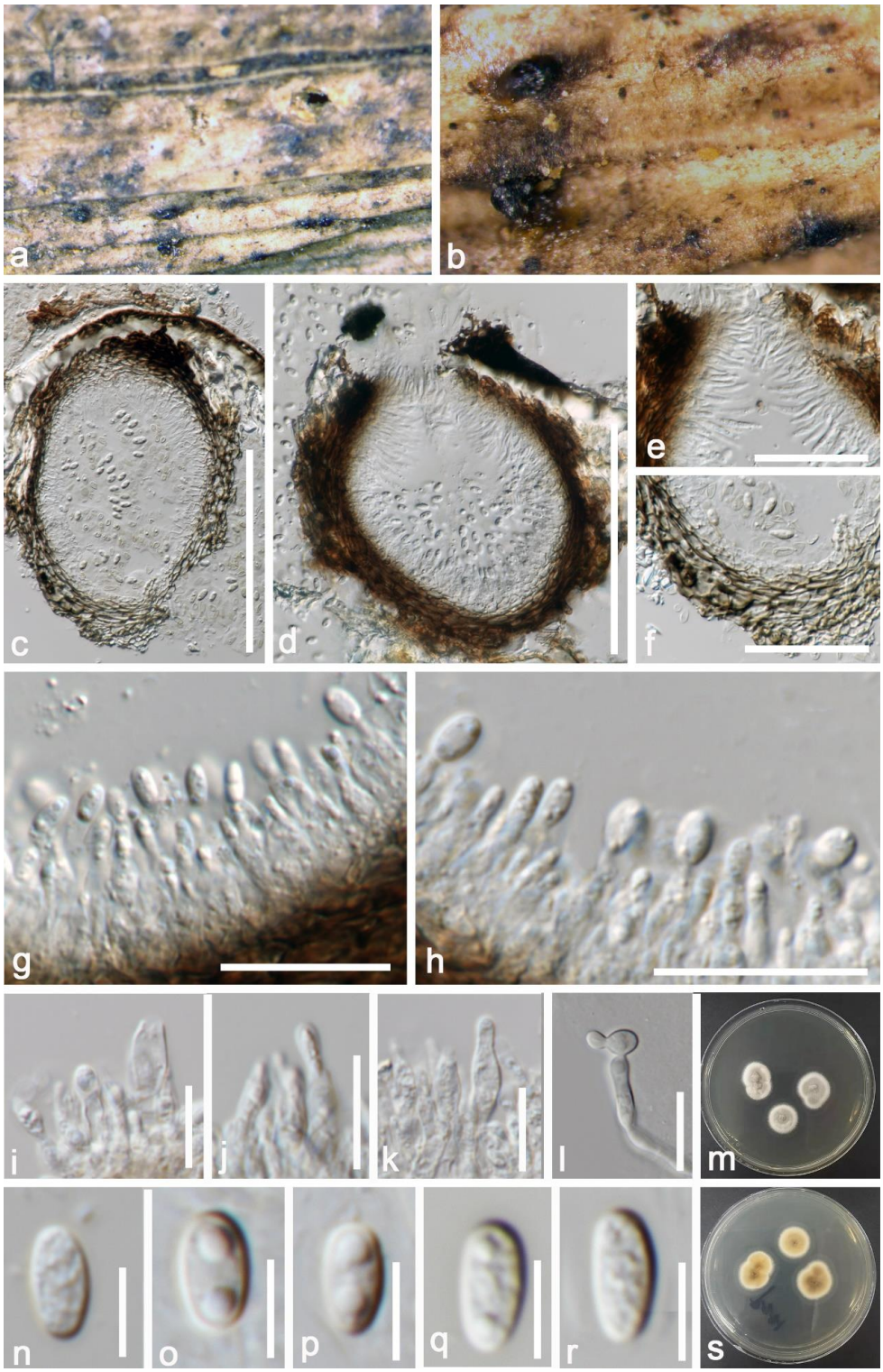

Figure 57 – *Pseudoteichospora thailandensis* (MFLU 23-0193, holotype). a, b Appearance of conidiomata on host. c, d Section through of conidiomata. e Section of ostiole. f Section of peridium. e–h Conidiogenous cells and conidia. n–r Conidia. l Germinated conidium. m, s Colonies

on PDA from surface and reverse. Scale bars: c, d = 50 µm, e–h = 20 µm, i–l = 10 µm, n–r = 5 µm.

Material examined – Thailand, Chiang Rai Province, Nang Lae Subdistrict, on dead leaves of *Ananas comosus*, 15 June 2020, X.G. Tian, P2-21 (MFLU 23-0193, holotype), ex-type living culture MFLUCC 23-0121; Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas* comosus, 1 August 2020, X.G. Tian, P6-6 (MFLU 23-0194 paratype), ex- paratype living culture MFLUCC 23-0109.

GenBank numbers – MFLUCC 23-0121: LSU = OR438839, ITS = OR438370, *rpb2* = OR634956. MFLUCC 23-0109: LSU = OR438838, ITS = OR438369, SSU = OR458350, *tef1-α* = OR500329

Notes – In a BLASTn search of NCBI GenBank, the closest match of the ITS sequence of *Pseudoteichospora thailandensis* (MFLUCC 23-0121, ex-type) with 93.69% similarity was *Teichospora mariae* (C134). The closest match with the LSU sequences with 98.3% similarity was *Floricola festucae* strain MFLU 17-0773. The closest match with the SSU sequences with 93.92% similarity was *Cryptocoryneum condensatum* strain CBS 113959. The closest match with the *rpb2* sequences with 88.51% similarity was *Asymmetrispora mariae* strain C136. The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 1) (Fig. 58).

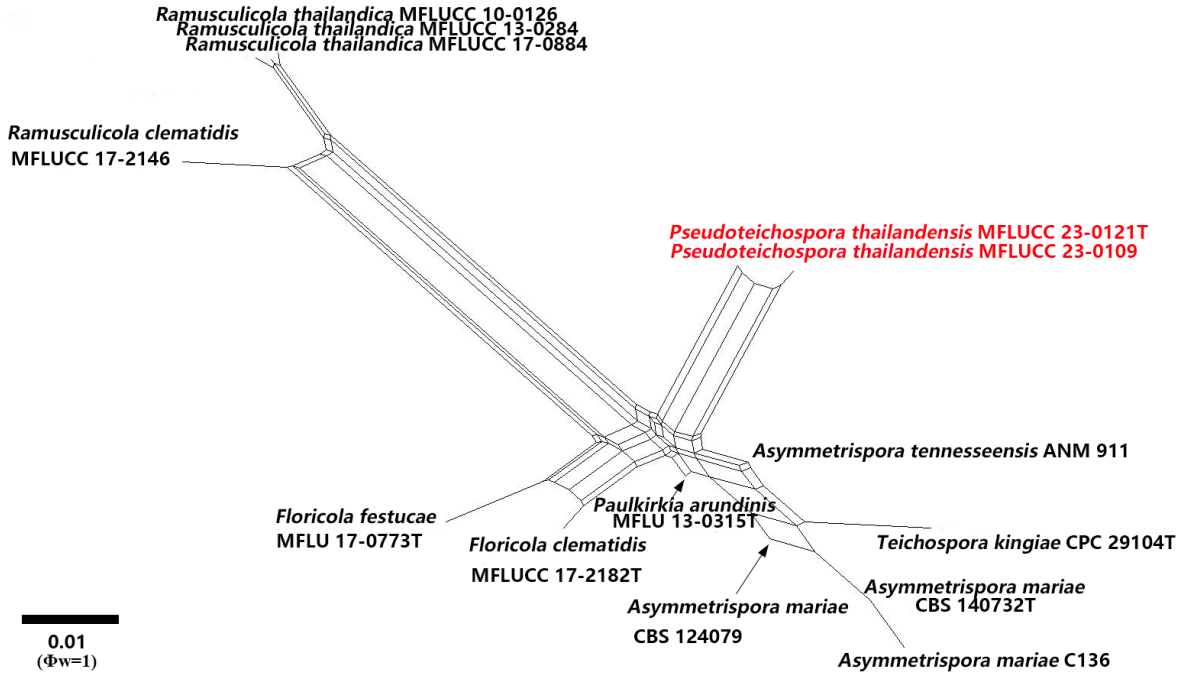

Figure 58 – Results of the PHI test of *Pseudoteichospora thailandensis* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray

Tetraplosphaeriaceae was introduced by Tanaka et al. (2009) with the type *Tetraplosphaeria* to accommodate five new genera, *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria* and *Triplosphaeria*. *Tetraplosphaeria* was treated as a synonym of *Tetraploa* due to nomenclatural priority. *Tetraplosphaeriaceae* species have massarina-like sexual morphs which are characterized by hyaline, 1–3-septate ascospores surrounded by a sheath. While asexual morphs are characterized by conidia with setose appendages in this family (Hyde et al. 2013, Tibpromma et al. 2018, Hongsanan et al. 2020b).

Ernakulamia Subram.

Ernakulamia was introduced by Subramanian (1994) with the type *E. cochinensis* and sequence data was provided by Delgado et al. (2017). *Ernakulamia* is characterized by micronematous or semi-macronematous conidiophores and brown, muriform conidia with appendages. There are four records available in Species Fungorum (2023). In this study, *Ernakulamia cochinensis* was reported as a new geographical record in China.

33. *Ernakulamia cochinensis* (Subram.) Subram., Kavaka 22/23: 67 (1994) Fig. 59

Index Fungorum number: IF374840; Facesofungi number: FoF09277

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, dark brown or black on natural substrate. *Conidiophores* and *conidiogenous cells* are not seen. *Conidia* 50–65 × 40–55 μm ($\overline{x}$ = 57 × 47 μm, n = 20), variable in shape but often obconical or broadly pyriform, blackish brown to black, muriform which is not clear when mature, thin-walled, with numerous (up to 7), cylindrical, septate, straight or flexuous, brown, with smooth appendages, 40–105 × 3–4 μm ($\overline{x}$ = 72 × 3 μm, n = 10).

Culture characteristics – Colony circular, reaching 30 mm on PDA in 14 days at 25 °C, grey from above, brown dark brown from below, with dense mycelium, superficial, dry, raised, edge entire.

Material examined – China, Yunnan Province, Jinghong District, on dead leaves of *Cocos nucifera*., 17 September 2021, X.G. Tian, C8-17 (GZAAS 23-0585), living culture GZCC 23-0579.

Figure 59 – *Ernakulamia cochinensis* (GZAAS 23-0585, new geographical record). a, b Conidia on natural substrate. c–i Conidia. j Germinated conidium. k Colony on PDA from the surface and reverse. Scale bars: c–j = 50 μm.

Known hosts and distribution – On rotten leaves of *Astrocaryum standleyanum* in Panama (Delgado et al. 2017); on dead spathe of *Cocos nucifera* in India (Delgado et al. 2017); on submerged wood in a stream in Thailand (Dong et al. 2020); on Spathe of *Syagrus romanzoffiana* in Argentina (Capdet & Romero 2010); India (Ellis 1976); Japan, Mexico (Capdet & Romero 2010); Cuba (Holubová-Jechová & Mercado Sierra 1986); Malaysia (Capdet & Romero 2010); on dead leaves of *Cocos nucifera* in China (this study).

GenBank numbers – LSU = OR438840, ITS = OR438371, SSU = OR458351

Notes – In our phylogenetic analyses, our strain (GZCC 23-0579) clustered with *Ernakulamia cochinensis* (Fig. 60). Our strain is similar to *E. cochinensis* (MFLUCC 18-1237) in having obconical or broadly pyriform, black, muriform, thin-walled, conidia with appendages. Our strain also shares a similar size range of conidia (50–65 × 40–55 μm vs. 55–85 × 35–55 μm) with *E. cochinensis* (MFLUCC 18-1237). The nucleotide comparisons showed that our strain (GZCC 23-0579) is not significantly different from *E. cochinensis* (MFLUCC 18-1237) in ITS, LSU, and SSU. Thus, we identified our strain as *E. cochinensis* and it is a new geographical record in China.

Tetraploa Berk. & Broome, Ann. Mag. nat. Hist., Ser. 25: 459 (1850).

Tetraploa is introduced by Berkeley & Broome (1850) with *T. aristate* as the type. Tanaka et al. (2009) introduced the sexual morph genus *Tetraplosphaeria* with *Tetraploa sensu stricto* asexual morphs observed from culture. The sexual morph is characterized by fusiform, 1-septate ascospores with mucilaginous appendage-like sheath (Tanaka et al. 2009). Asexual morph is characterized by monoblastic conidiogenous cells, and short-cylindrical conidia with 4 setose appendages (Ellis 1971, Tanaka et al. 2009). In this study, a new species (*T. oryzae*) and a new host record (*T. yunnanensis*) are introduced with detailed morphological descriptions and illustrations.

34. *Tetraploa oryzae* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 61

Index Fungorum number: IF900980; Facesofungi number: FoF14295

Etymology – Referring to the host plant *Oryza sativa*, on which the fungus was collected.

Holotype – MFLU 23-0195

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Mycelia* superficial or immersed, brown euseptate. *Conidiophores* and *conidiogenous cells* are not seen. *Conidia* short cylindrical, conidial body with four vertical columns of cells, sparsely verruculose, 35–45 × 20–30 μm ($\overline{x}$ = 39 × 24 μm, n = 15), pale brown, smooth, with four apical setose appendages at the apical part, 55–100 × 3–4 μm ($\overline{x}$ = 76 × 3 μm, n = 30), partly split conidia, smooth, unbranched, straight, 2–6-septate.

Culture characteristics – Colony circular, reaching 20 mm on PDA in 14 days at 25 °C, grey from above, velutinous, greyish brown with white thin margin from below, with dense mycelium, superficial, dry, raised, edge entire. Soluble pigments and exudates are absent.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Oryza sativa*, 10 November 2020, X.G. Tian, R6-8 (MFLU 23-0195 holotype), ex-type living culture MFLUCC 23-0169.

GenBank numbers – MFLU 23-0195: LSU = OR438841, ITS = OR438372, SSU = OR458352. MFLUCC 23-0169: LSU = OR438842, SSU = OR458353

Notes – In the phylogenetic analyses, our two new strains *Tetraploa oryzae* (MFLU 23-0195 and MFLUCC 23-0169) clustered sister to *T. thrayabahubeeja* (NFCCI 4627) with 100% ML and 1.00 PP statistical support (Fig. 60). Morphologically, *T. oryzae* is similar to *T. thrayabahubeeja* (NFCCI 4627) in having superficial or immersed mycelia and conidiophores reduced to conidiogenous. However, *T. oryzae* differs from *T. thrayabahubeeja* by its conidial body have four columnar, coarsely verruculose, with four apical setose appendages at the apical part, 2–6-septate. While *T. thrayabahubeeja* has conidial body that has 3 columns or rarely one with one apical appendage, 2–4-septate. Conidia (30–45 × 20–30 μm vs. 20–32 × 15–20 μm) of *T. oryzae* are larger than *T. thrayabahubeeja* (NFCCI 4627). In addition, the nucleotide comparisons revealed that our strain (MFLUCC 23-0169) is different from *T. thrayabahubeeja* (NFCCI 4627) in 19/531 bp

(3.58%) of the ITS, and 8/768 (1.04%) of the LSU and the PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.19) (Fig. 62). Thus, we identified our strain as a distinct new species as *T. oryzae*.

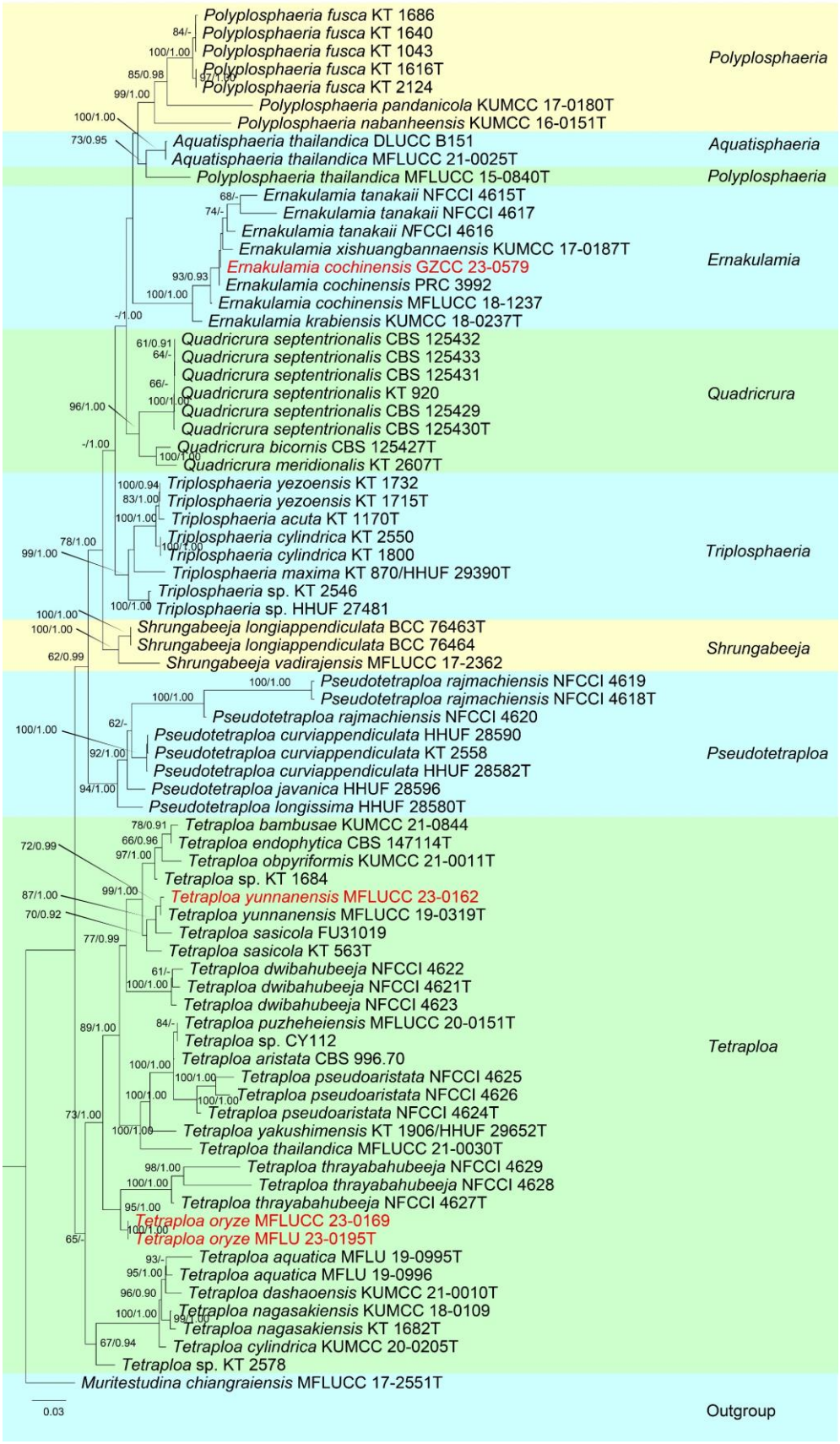

Figure 60 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS,

SSU, *tub2*, and *tef1-α* sequence data. Related sequences were obtained from Bao et al. (2021) and Jayawardena et al. (2022). Seventy-seven strains are included in the combined sequence analysis, which comprises 3788 characters with gaps. *Muritestudina chiangraiensis* (MFLUCC 17-2551) was used as the outgroup taxon. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -24451.861006 is presented. The matrix had 1426 distinct alignment patterns, with 28.39% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245422, C = 0.247694, G = 0.273639, T = 0.233245; substitution rates AC = 1.917730, AG = 3.024516, AT = 1.464198, CG = 1.258162, CT = 5.795532, GT = 1.000000; gamma distribution shape parameter α = 0.213894. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

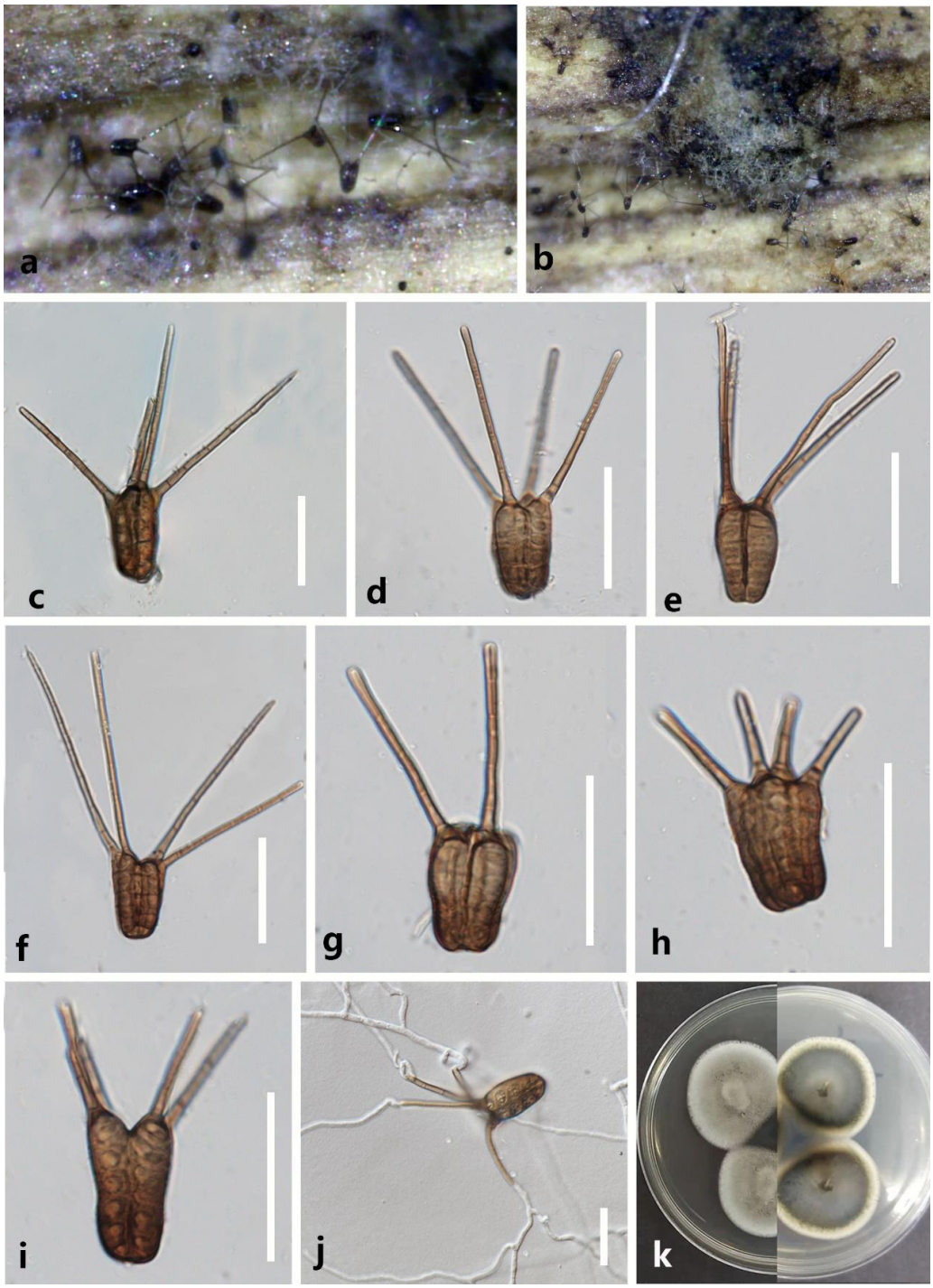

Figure 61 – *Tetraploa oryzae* (MFLU 23-0195, holotype). a, b Conidia on natural substrate.

c–i Conidia. j Germinated conidium. k Colonies on PDA from above and below. Scale bars: j = 100 µm, c–i = 50 µm.

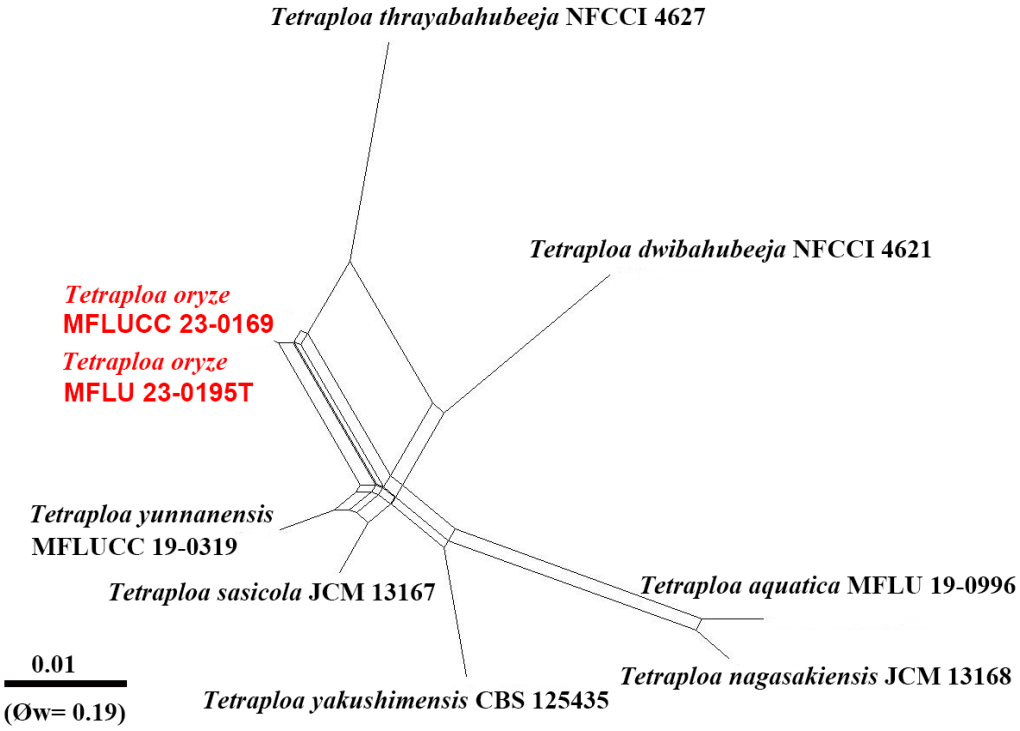

Figure 62 – Results of the PHI test of *Tetraploa oryzae* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

35. *Tetraploa yunnanensis* W. Dong, H. Yang & H. Zhang, in Dong et al., Fungal Divers. 105(1):319–575 (2020) Fig. 63

Index Fungorum number: IF557937; Facesofungi number: FoF09282

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Mycelium* superficial, composed of septate, branched, subhyaline hyphae. *Conidiophores* absent. *Conidiogenous cells* monoblastic, holoblastic, integrated, terminal or intercalary, determinate, cylindrical. *Conidia* solitary, short to long cylindrical, brown to reddish brown, verrucose, setose, septate, with 1–3 apical appendages. *Conidial body* 25–35 × 10–20 µm ($\bar{x}$ = 31.6 × 15.9 µm, n = 30), brown to reddish brown, verrucose, narrowly ovate or ovate, composed of 2–3 columns of cells, with each column 4–6-celled. *Appendages* 40–90 µm long, 4–6.5 µm wide at the base, 2–3.5 µm wide at the apex, 1–8-septate, brown, smooth, unbranched, straight.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 1 August 2020, X.G. Tian, C6-26 (MFLU 23-0196), living culture MFLUCC 23-0162.

Known host and distribution – On submerged wood in China and Thailand (Dong et al. 2020); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438843, ITS = OR438373

Notes – In our phylogenetic analyses, our new isolate *Tetraploa yunnanensis* (MFLUCC 23-0162) clustered with the ex-type of *T. yunnanensis* with 100% ML and 1.00 PP support (Fig. 60). Morphologically, our new isolate is similar to the holotype of *T. yunnanensis* in having monoblastic, holoblastic conidiogenous cells and solitary, short to long cylindrical, septate, conidia, which composed of 2–3 columns of cells, with 1–3 apical appendages. However, the conidia of our new

isolate are reddish brown and the conidial appendages are 1–8-septate, while conidia are brown to dark brown and conidial appendages are 1–5-septate in the holotype (Dong et al. 2020). The ITS of our new isolate is identical to the ex-type of *T. yunnanensis*. Thus, we identified our new isolate as *T. yunnanensis* based on phylogenetic analyses and morphological characters.

Tetraploa yunnanensis was introduced by Dong et al. (2020), and collected from freshwater habitats in China and Thailand. Our strain *Tetraploa yunnanensis* (MFLU 23-0196) is reported as a new host record on *Cocos nucifer*a and this species was collected for the first time from terrestrial habitat.

Figure 63 – *Tetraploa yunnanensis* (MFLU 23-0196, new host record). a–c Colonies on natural substrates. b–i Conidia bearing 1–4 appendages. Scale bars: d–i = 30 µm.

Torulaceae Corda

Torulaceae was introduced by Corda (1829) to accommodate *Torula* and typified by *T. herbarum*. This family is circumscribed only by asexual morph characters. *Torulaceae* includes six genera *viz*. *Cylindrotorula*, *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides*, and *Torula* (Wijayawardene et al. 2022).

Torula Pers.

Torula was introduced by Persoon (1795) with *T. herbarum* as the type species. Members in this genus are hyphomycetous asexual morphs and characterized by superficial dark colonies and branched chains, dark brown conidia (Su et al. 2018, Tibpromma et al. 2018, Li et al. 2020a, Yang et al. 2022). There are 543 *Torula* epithets listed in Index Fungorum (2023), but only 49 species have morphological descriptions, and 17 species have molecular data support (Hongsanan et al.2020a). In this study, based on morphological and phylogenetic analyses, *Torula fici* is reported as a new record from on dead leaves of *Ananas comosus*.

36. *Torula fici* Crous, IMA Fungus 6: 192 (2015) Fig. 64

Index Fungorum number: IF816154; Faces of fungi number: FoF14296

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse on the substrate, scattered, powdery, dark brown to dark. *Mycelium* partly immersed or superficial, composed of hyaline, branched, smooth, septate, hyphae. *Conidiophores* reduced to conidiogenous cells or with a supporting cell. *Conidiogenous cells* up to 20 μm, solitary on mycelium, cylindrical, pale to dark, smooth to verruculose, cupulate on maturity, mono-to polyblastic. *Conidia* (3–)10–20 × 5–10 μm ($\overline{x}$ = 17 × 8 μm, n = 40), phragmosporous, in long branched chains, 1–5-septate, cells subglobose, smooth to distinctly verrucose, subcylindrical, acrogenous, pale brown to brown, constricted at septa, fragmenting into segments.

Culture characteristics – Conidia germinated in PDA within 12 hr. at 25 ℃, rapidly growing, reaching around 20 mm after one week, circular with entire margin, flat, effuse, white or yellow; reverse, white or yellow in PDA.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on dead leaves of *Ananas comosus*, 26 August 2020, X.G. Tian, P8-3 (MFLU 23-0197), living culture MFLUCC 23-0115.

Known hosts and distribution – On *Ficus* sp. in Cuba (Crous et al. 2015a); on dead stems of *Chromolaena odorata* in Thailand (Li et al. 2020a); on dead leaf of *Pandanus* sp. in Thailand (Tibpromma et al. 2018); on decaying cone of *Magnolia grandiflora* in China (Jayasiri et al. 2019); on decaying fruit pericarp of *Garcinia* sp. in Thailand (Jayasiri et al. 2019); on submerged decaying wood in China (Su et al. 2018); on dead branch of *Mangifera indica* in China (Yang et al. 2022); on dead leaves of *Ananas comosus* from Thailand (this study).

GenBank numbers – LSU = OR438844, ITS = OR438374, SSU = OR458354, *tef1-α* = OR500330

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0115) grouped within the strains of *Torula fici* (CBS 595.96, MFLUCC 16-0038, MFLUCC 16-0035 and MFLUCC 16-1348) (Fig. 65). Morphologically, our strain resembles the type strain of *T. fici* (CBS 595.96) in having conidiophores reduced to conidiogenous cells, with hyaline to pale brown, supporting cell, and brown or dark brown, phragmosporous, long branched chains, septate conidia. In addition, the nucleotides in ITS, LSU, SSU, and *tef1-α* of our strain (MFLUCC 23-0115) are not significantly different from *T. fici* (CBS 595.96). Thus, we identified our strain as *T. fici* based on phylogenetic analyses and morphological characters. Our strain *Torula fici* (MFLUCC 23-0115) was collected on *Ananas comosus* for the first time.

Botryosphaeriales C.L. Schoch et al.

Botryosphaeriales was introduced by Schoch et al. (2006) with a single family *Botryosphaeriaceae*. The latest treatment of *Botryosphaeriales* was provided by Hongsanan et al. (2020b) with accepted six families *viz. Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Phyllostictaceae*, *Planistromellaceae* and *Saccharataceae*.

Botryosphaeriaceae Theiss. & H. Syd.

Botryosphaeriaceae was established by Theissen & Sydow (1918) to accommodate three genera, *Botryosphaeria*, *Dibotryona* and *Phaeobotryon*, and *Botryosphaeria* as the type genus.

Wijayawardene et al. (2022) accepted 22 genera in *Botryosphaeriaceae*. *Botryosphaeriaceae* species are widely distributed in all regions of the world except polar regions (Hyde et al. 2013, Tibpromma et al. 2018, Hongsanan et al. 2020b). Members of *Botryosphaeriaceae* are well-known as saprobes, endophytes and opportunistic pathogens, and many species cause losses to ecologically and economically important plants, especially for plant genera such as *Citrus* (Slippers & Wingfield 2007, Mehl et al. 2014, Tibpromma et al. 2018, Xiao et al. 2021).

Lasiodiplodia Ellis & Everh.

Lasiodiplodia was formally established by Clendenin (1896), and the type species is *L. theobromae*. Most members of this genus are plant pathogens that can cause cankers, die-back, fruit or root rot, branch blight or discoloration on a wide range of woody hosts, and are mostly distributed in tropical and subtropical regions (Ismail et al. 2012, Tibpromma et al. 2018, Zhang et al. 2021). There are 87 records of *Lasiodiplodia* listed in Index Fungorum (2023). In this study, we introduce four new records and one new species in this genus from Thailand based on morphology and phylogeny.

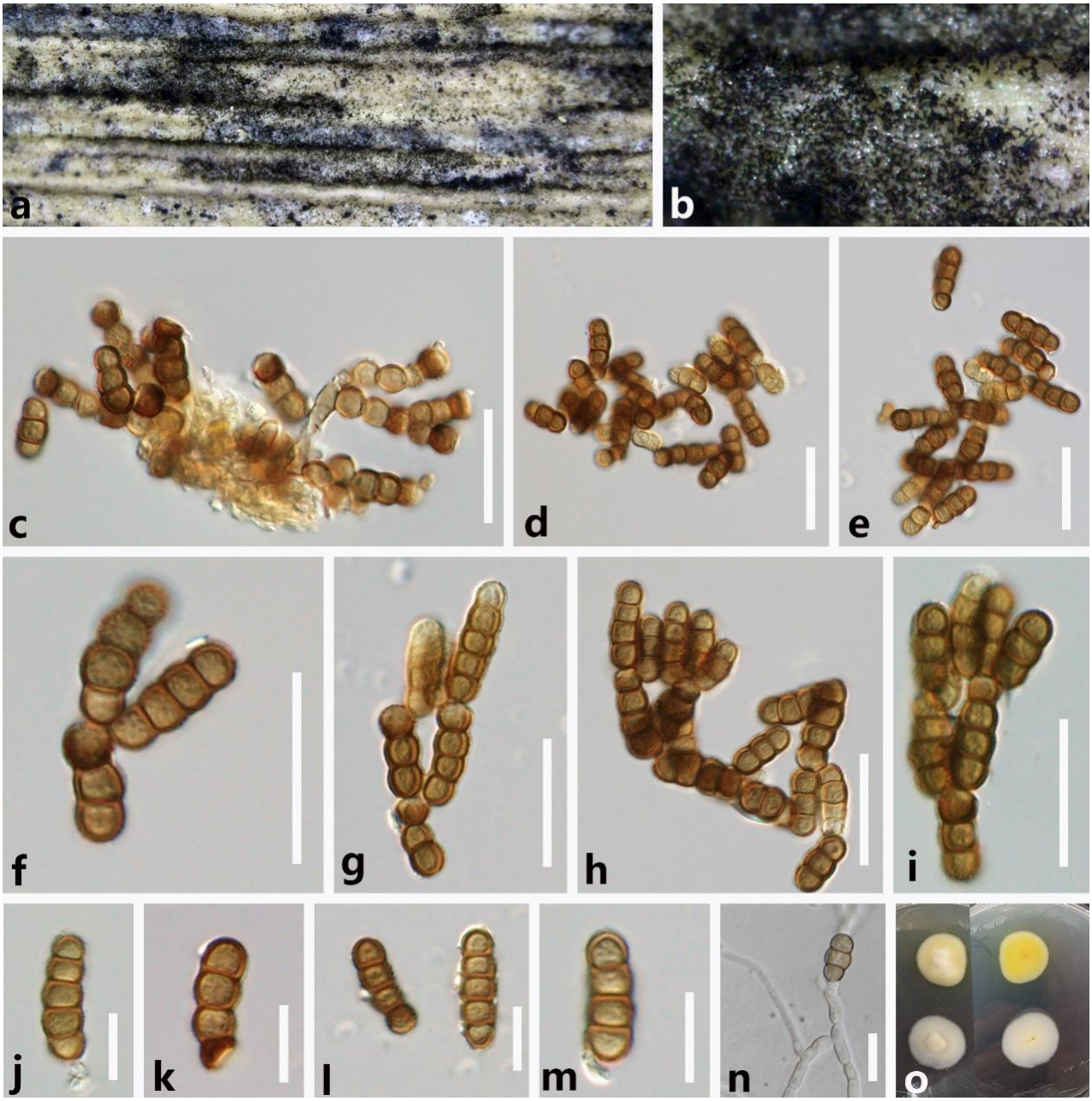

Figure 64 – *Torula fici* (MFLU 23-0197, new host record). a, b Colonies on dead leaf of *Ananas*

comosus. c–e Conidial masses. f–i Conidial masses (in chain). j–m Conidia. n Germinated conidium. o Colonies on PDA from surface and reverse. Scale bars: c–i, n = 20 μm, j–m = 10 μm.

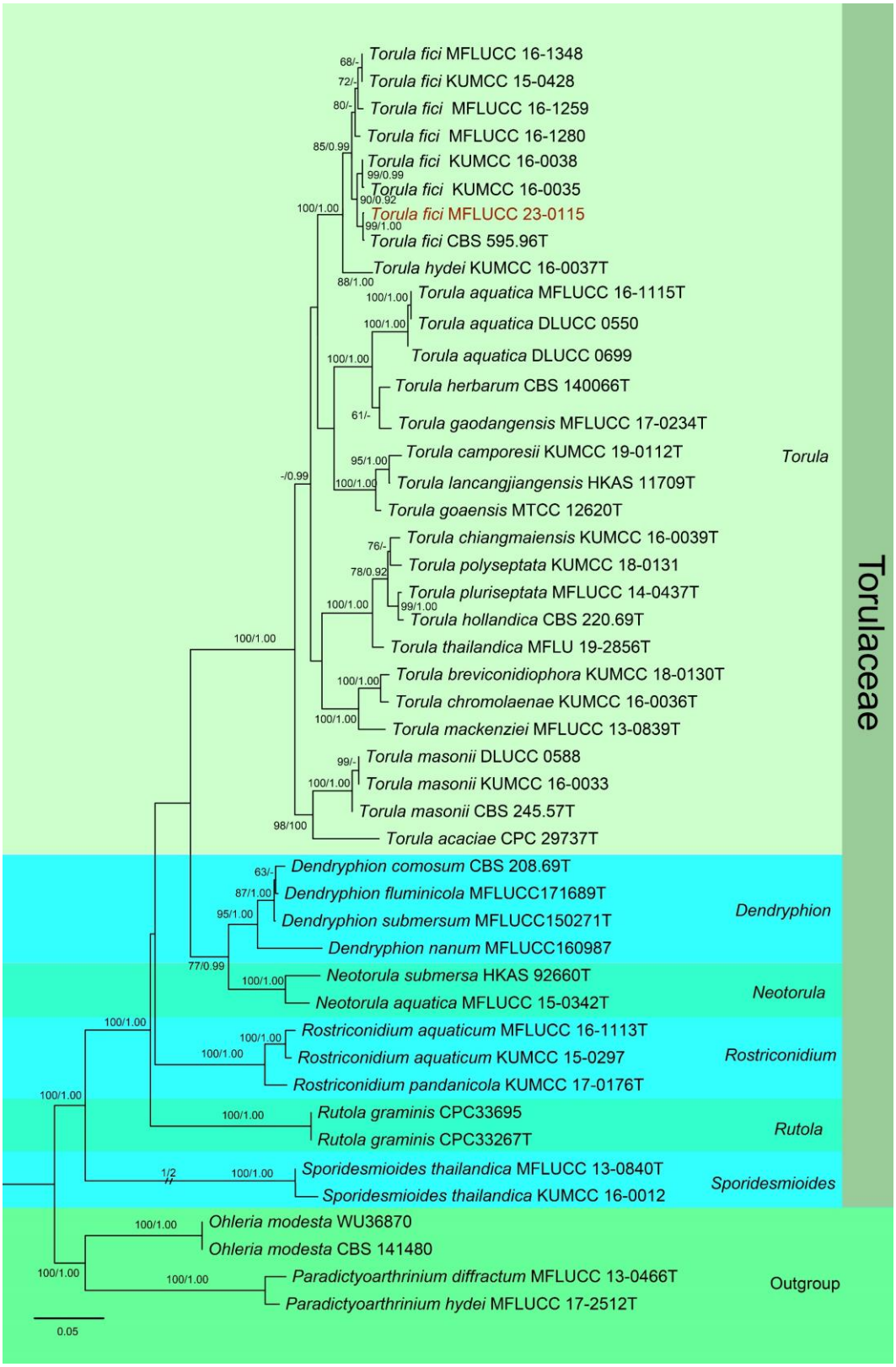

Figure 65 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1-α* and *rpb2* sequence data. Related sequences were obtained from Boonmee et al. (2021). Forty-six strains are included in the combined sequence analysis, which comprise 4258 characters with gaps. *Ohleria modesta* (CBS141480 and WU36870), *Paradictyoarthrinium hydei* (MFLUCC

17-2512) and *P. diffractum* (MFLUCC 13-0466) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -19922.692765 is presented. The matrix had 1266 distinct alignment patterns, with 41.42% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243920, C = 0.260745, G = 0.272896, T = 0.222438; substitution rates AC = 1.627038, AG = 2.972298, AT = 1.432160, CG = 0.872172, CT = 7.470706, GT = 1.000000; gamma distribution shape parameter α = 0.138378. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

37. *Lasiodiplodia ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 66

Index Fungorum number: IF900981; Facesoffungi number: FoF14297

Etymology – Referring to the host plant *Ananas comosus*, on which the fungus was collected.

Holotype – MFLU 23-0199

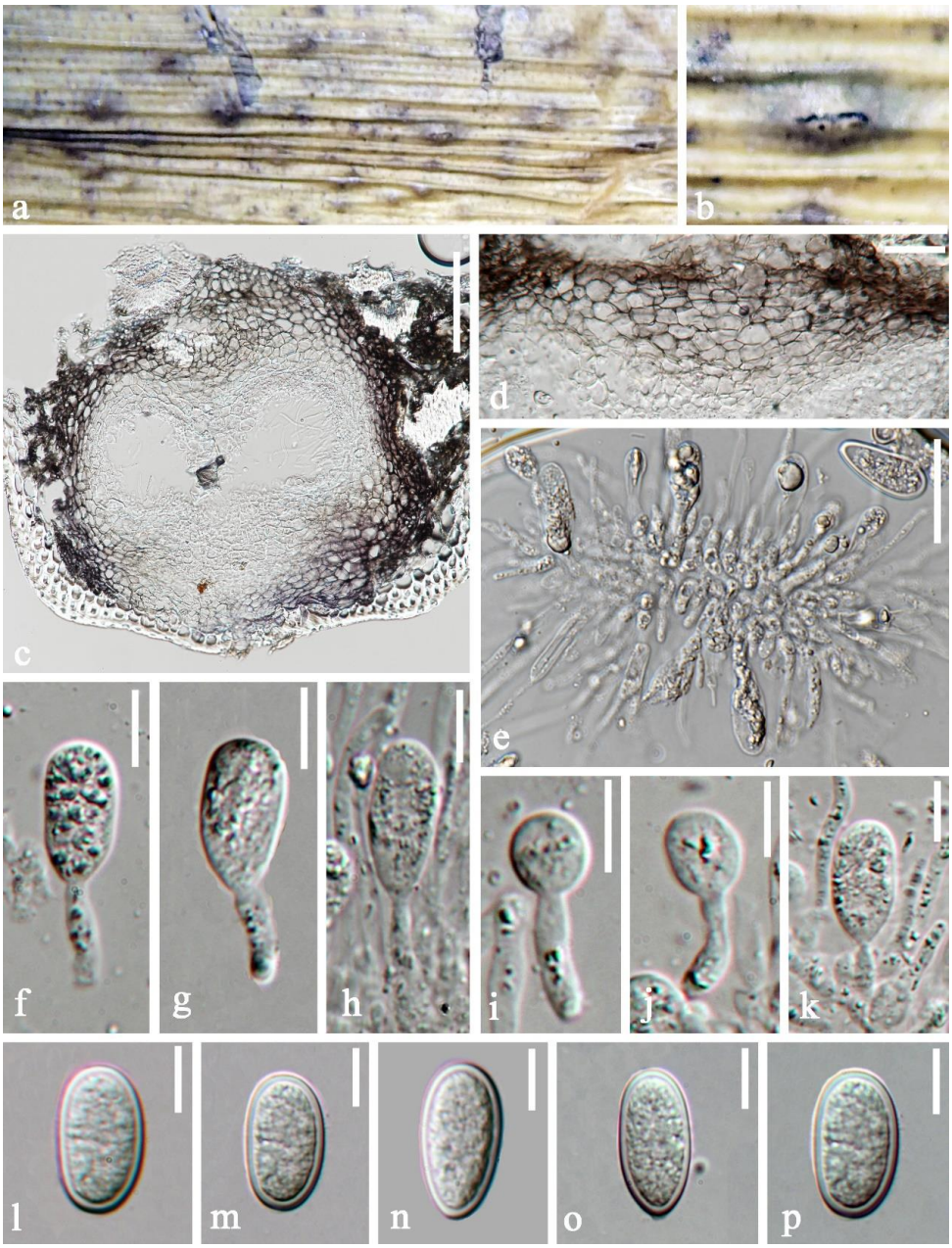

Figure 66 – *Lasiodiplodia ananasi* (MFLU 23-0199, holotype). a, b Appearance of conidiomata. c Vertical sections through conidiomata. d Peridium. e Conidiogenous cells and paraphyses.

f–k Conidiogenous cells with conidia. l–p Conidia. Scale bars: c = 50 μm, d, e = 30 μm, f–p = 10 μm.

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 270–425 μm diam., 290–350 μm high, pycnidial, scattered, solitary, globose to subglobose, dark brown to black, immersed and unilocular without a conspicuous ostiolate. *Conidiomatal* wall 40–60 μm wide, comprises several layers of pale brown to brown cells of *textura angularis* to *textura globulosa*. *Paraphyses* 30–45 × 2–3 μm ($\overline{x}$ = 39.4 × 2.4 μm, n = 30), hyaline, cylindrical, septate and rounded at apex. *Conidiophores* reduced to conidiogenous cells, hyaline, cylindrical, smooth-walled. *Conidiogenous cells* 10–15 × 2–3 μm ($\overline{x}$ = 12.5 × 2.6 μm, n = 15), holoblastic, monoblastic, terminal, discrete, cylindrical to subcylindrical, hyaline, smooth-walled. *Conidia* 20–25 × 10–15 μm ($\overline{x}$ = 23.7 × 13.4 μm, n = 30), ellipsoid to ovoid, rounded at both ends, hyaline, aseptate, with granular content.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 23 June 2020, X.G. Tian, p3-31 (MFLU 23-0199 holotype), ex-type living culture (MFLUCC 23-0140).

GenBank numbers – MFLU 23-0199: LSU = OR438845, ITS = OR438375, *tub2* = OR538078. MFLUCC 23-0140: LSU = OR438846, ITS = OR438376, *tub2* = OR538079

Notes – In our phylogenetic analyses, our new collection (MFLU 23-0199, MFLUCC 23-0140) clustered with *Lasiodiplodia linhaiensis* (MFLUCC 23-0163, BE28, BE51 and MFLUCC 23-0144) (Fig. 67). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.08) (Fig. 68). In morphology, our isolate (MFLUCC 23-0140) differs from *L. linhaiensis* in having immersed, solitary conidiomata and hyaline, aseptate conidia without longitudinal striations, while conidiomata superficial or semi-immersed, solitary or aggregated in *L. linhaiensis* and conidia of *L. linhaiensis* are hyaline and aseptate when young, becoming dark brown to dark olive and 1-septate at maturity with longitudinal striations (Xiao et al. 2021). Our isolate has smaller conidia (20–25 μm long vs. 27–30 μm long), shorter paraphyses (30–45 μm long vs. up to 80 μm long) and smaller conidiomata (270–425 μm diam. vs. up to 950 μm diam.) than those of *L. linhaiensis*. Thus, we identified our new isolate as a new species *Lasiodiplodia ananasi*.

38. *Lasiodiplodia linhaiensis* X.E. Xiao, P.W. Crous & H.Y. Li, in Xiao et al., Persoonia 47: 127 (2021) Fig. 69

Index Fungorum number: IF840684; Facesoffungi number: FoF14298

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 160–240 μm diam., 195–240 μm high, scattered, solitary or aggregated, globose to subglobose, dark brown to black, immersed or semi-immersed, without a conspicuous ostiole. *Conidiomatal* wall 40–65 μm wide, inner layers comprised pale brown to hyaline cells of *textura angularis*, out layers composed dark brown cells. *Paraphyses* 40–60 × 3–4.5 μm ($\overline{x}$ = 39.4 × 2.4 μm, n = 30), hyaline, cylindrical, septate, unbranched, rounded at apex. *Conidiophores* reduced to conidiogenous cells, hyaline, cylindrical, smooth-walled. *Conidiogenous cells* 10–15 × 3.5–5 μm ($\overline{x}$ = 13 × 4.4 μm, n = 25), holoblastic, monoblastic, discrete, terminal, cylindrical to subcylindrical, hyaline, smooth-walled. *Conidia* 25–30 × 10–15 μm ($\overline{x}$ = 27.9 × 13.5 μm, n = 30), ellipsoid to ovoid, rounded at both ends, hyaline and aseptate when young, becoming dark brown to dark olive and 1-septate at maturity, with granular content.

Cultural characteristics – On PDA, colony circular, reaching 40–55 mm in 30 days at 25 °C, dark grey to black from above, black from below, surface rough, dry, raised, with dense mycelium, edge entire.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, c6-28 (MFLU 23-0201), living culture MFLUCC 23-0163; *ibid*, on dead leaves of *Ananas comosus*, 18 October 2020, X.G. Tian, p6-10 (MFLU 23-0200), living culture MFLUCC 23-0144.

Figure 67 – Phylogram generated from maximum likelihood analysis based on combined ITS, *rpb2*, *tef1-α*, and *tub2* sequence data. Related sequences were obtained from Zhang et al. (2021). Ninety-four strains are included in the combined sequence analysis, which comprise 2051 characters with gaps. *Diplodia mutila* (CMW 7060) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -9386.856373 is presented. The matrix had 683 distinct alignment patterns, with 25.48% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.221697, C = 0.288664, G = 0.263631, T = 0.226009; substitution rates AC = 0.890877, AG = 2.935464, AT = 1.069913, CG = 0.775315, CT = 5.406080, GT = 1.000000; gamma distribution shape parameter α = 0.212016 0.138378. Bootstrap support values for ML equal to or greater than 60% and PP equal

to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

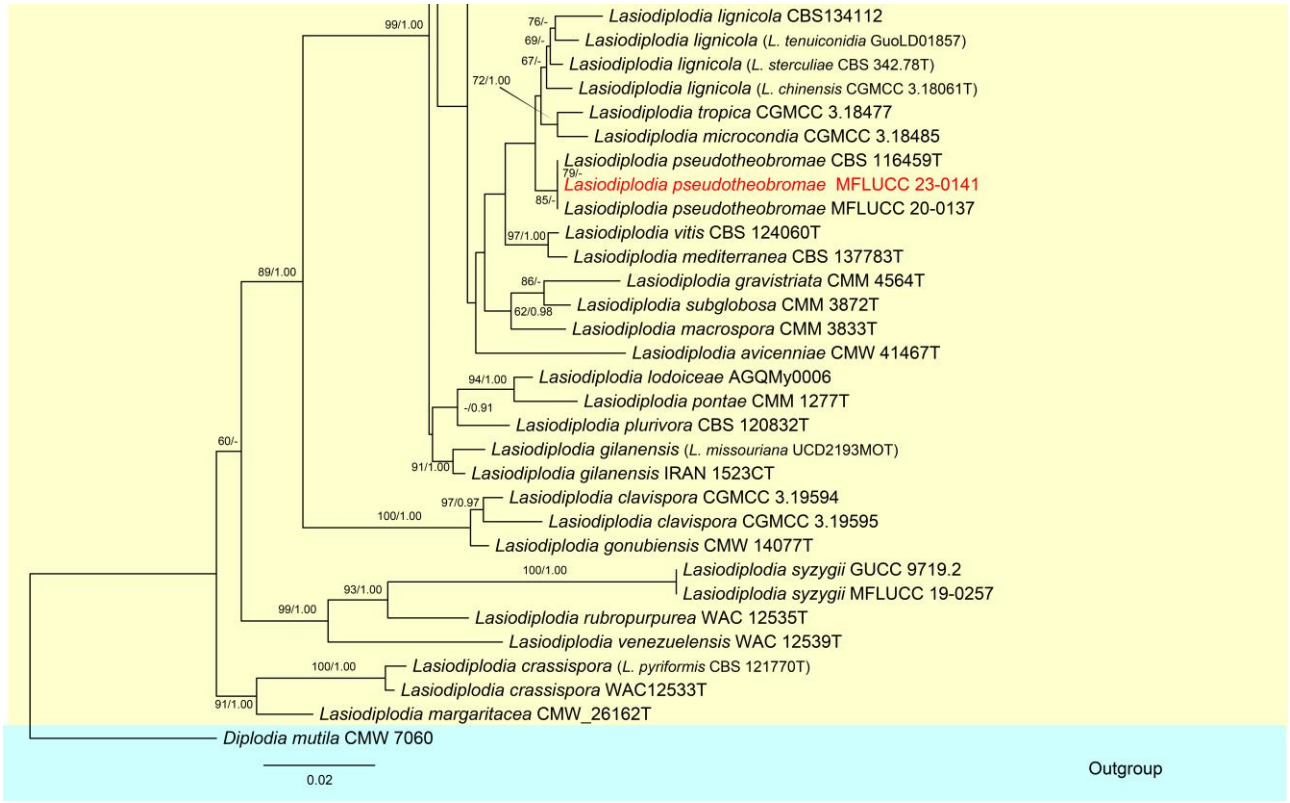

Figure 67 – Continued.

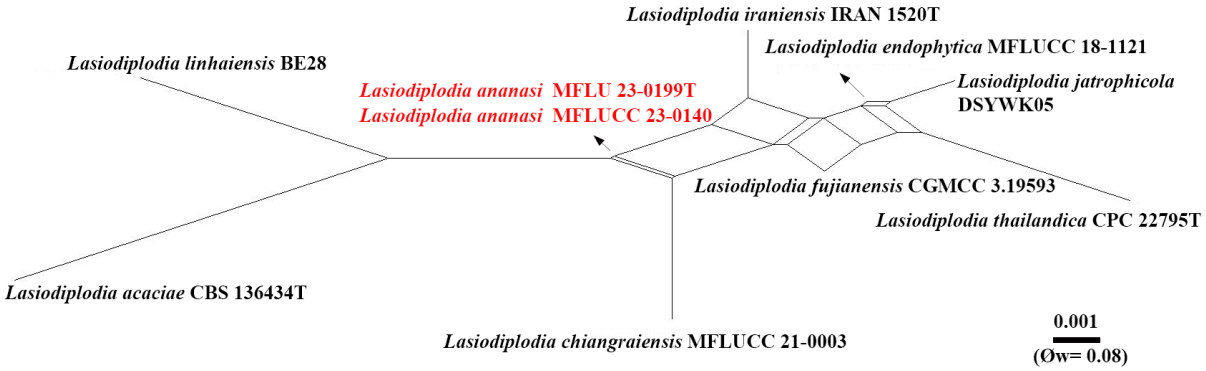

Figure 68 – Results of the PHI test of *Lasiodiplodia ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

Known hosts and distribution – On branch of *Citrus unshiu* in China (Xiao et al. 2021); on dead leaves of *Cocos nucifera* and *Ananas comosus* in Thailand (this study).

GenBank numbers – MFLUCC 23-0163: ITS = OR438378, *tub*2 = OR538080. MFLUCC 23-0144: LSU = OR438847, ITS = OR438377, *tub*2 = OR538081

Notes – *Lasiodiplodia linhaiensis* was introduced by Xiao et al. (2021). Our isolate (MFLUCC 23-0163 and MFLUCC 23-0144) clusters with *L. linhaiensis* (Fig. 67). In morphology, our isolate is almost similar to the holotype of *L. linhaiensis* except for the conidiomata. Our new

isolate has semi-immersed to immersed conidiomata, while conidiomata are superficial or semi-immersed in the holotype (Xiao et al. 2021). The nucleotide comparisons of ITS and *tub2* between our strain (MFLUCC 23-0163 and MFLUCC 23-0144) and *L. linhaiensis* (BE28 and BE51) are not significantly different. Thus, based on both phylogeny and morphology, we identified our new isolate as *Lasiodiplodia linhaiensis* and it is a new host and geographical record on *Ananas comosus* and *Cocos nucifera* in Thailand.

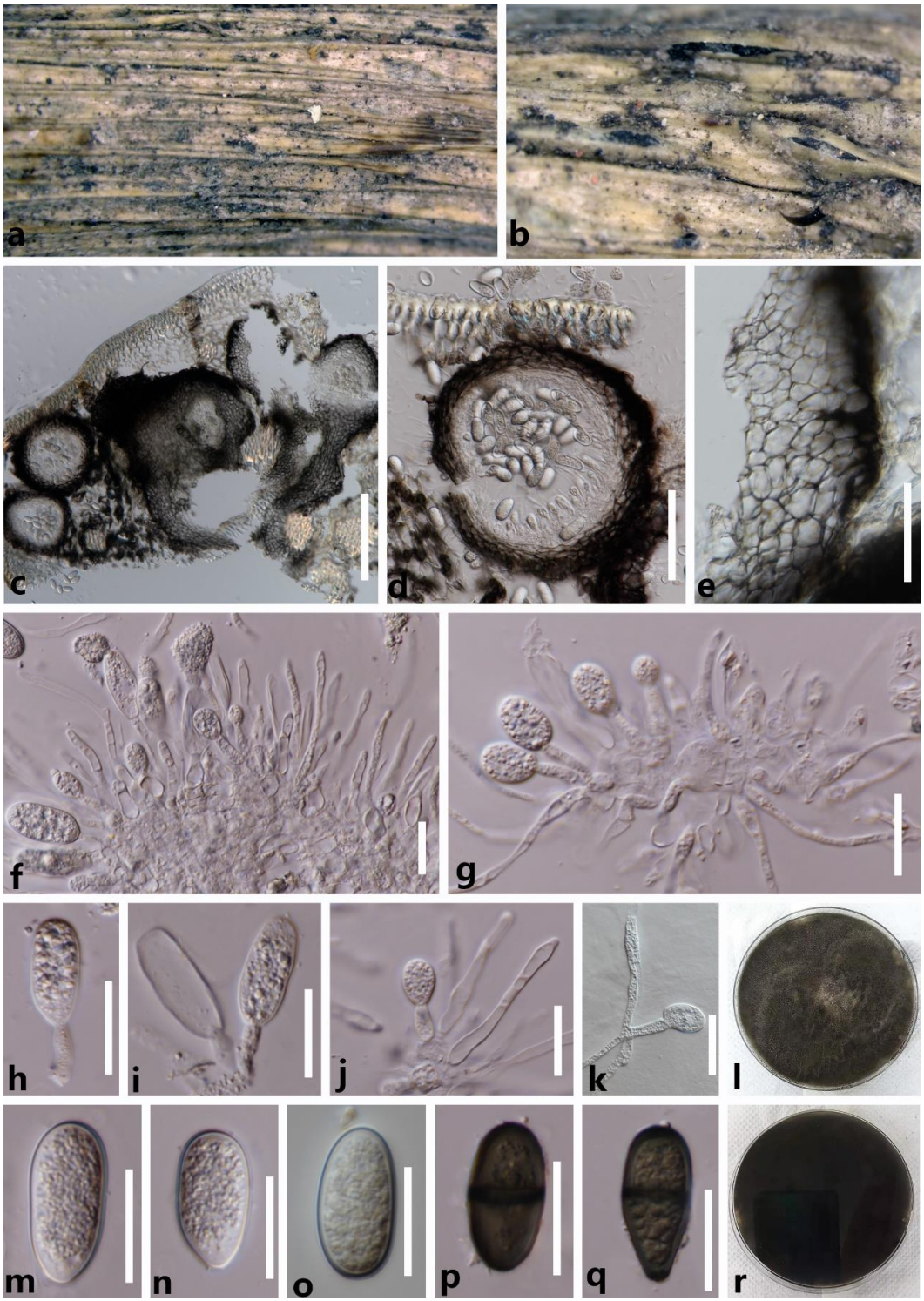

Figure 69 – *Lasiodiplodia mahajangana* (MFLU 23-0200, new host and geographical record). a, b Appearance of conidiomata on the substrate. c, d Vertical sections through conidiomata. e Peridium. f, g Conidiogenous cells and paraphyses. h–j Conidiogenous cells with conidia. k Germinated conidium. m–q Conidia. l, r Colonies on PDA from surface and reverse. Scale bars:

c = 200 µm, d = 100 µm, e, k = 40 µm, f–j, m–q = 20 µm.

39. ***Lasiodiplodia mahajangana*** Begoude, Jol. Roux & Slippers, in Begoude et al., Mycol. Prog. 9(1): 110 (2010) Fig. 70

Index Fungorum number: IF514012; Facesoffungi number: FoF14045

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 190–290 × 230–350 µm ($\overline{x}$ = 243 ×292 µm, n = 7), scattered or gregarious, solitary, black, conspicuous on host surface, immersed, unilocular, globose to subglobose, ostiole without papilla. *Pycnidial wall* 55–100 µm, composed of several layers of thick-walled, hyaline to black cells of *textura angularis*. *Paraphyses* filamentous to cylindrical, hyaline, septate, unbranched, ends rounded, 45–60 × 2–3 µm ($\overline{x}$ = 53 ×2.5 µm, n = 25), formed between conidiogenous cells. *Conidiogenous cells* 5–15 × 3–5 µm ($\overline{x}$ = 10.5 ×4 µm, n = 20), annellidic, cylindrical, thick-walled, hyaline, smooth. *Conidia* 20–30 × 10–15 µm ($\overline{x}$ = 26 × 14 µm, n = 40), aseptate, subglobose to oval, hyaline when young, guttulate, without longitudinal striations and mucilaginous sheath.

Known hosts and distribution – On *Anacardium occidentale*, *Citrus sinensis*, *Spondias purpurea* and *S. mombin* in Brazil (Coutinho et al. 2017); on cashew trunks from Africa (Monteiro et al. 2020); on *Aquilaria crassna* in Laos (Wang et al. 2019b); on Grapevine in Turkey (Akgül et al. 2019); on a branch canker of *Retama raetam* in Tunisia (Linaldeddu et al. 2015); on *Pistacia vera* in the USA (Linaldeddu et al. 2015); on *Aquilaria crassna* in Laos (Wang et al. 2019b); on dead leaves of *Pandanus* in Thailand (Tibpromma et al. 2018); on *Terminalia catappa* in Madagascar (Begoude et al. 2010); on dying *Euphorbia ingens* in South Africa (van der Linde et al. 2011); on *Mangifera indica* in Puerto Rico (Quimbita-Reyes et al. 2023); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438379, *tef1-α* = OR887681, *tub*2 = OR538082

Notes – *Lasiodiplodia mahajangana* was described by Begoude et al. (2010) and it was reported as an endophyte from healthy branches of *Terminalia catappa* in Madagascar. Zhang et al. (2021) synonymized *L. caatinguensis*, *L. curvata*, *L. exigua*, *L. irregularis*, *L. macroconidia*, and *L. pandanicola* under *Lasiodiplodia mahajangana* based on phylogenetic analyses. In the multi-gene phylogeny, our strain clusters with *Lasiodiplodia mahajangana* (Fig. 67). Our new isolate is similar to the holotype of *L. mahajangana* in having unilocular, immersed, globose to subglobose conidiomata, holoblastic, monoblastic, discrete conidiogenous cells and ellipsoid to ovoid conidia that are hyaline and aseptate when young (Zhang et al. 2021). Based on phylogeny and morphology, we identified our new isolate as *L. mahajangana* and introduced it as a new host on *Ananas comosus* from Thailand.

40. ***Lasiodiplodia pseudotheobromae*** A.J.L. Phillips, A. Alves & Crous, Fungal Divers. 28: 8 (2008) Fig. 71

Index Fungorum number: IF510941; Facesoffungi number: FoF04567

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: See Tennakoon et al. (2016). Asexual morph: *Conidiomata* up to 300 × 330 µm, pycnidial, scattered, solitary, dark brown to black, conspicuous on host surface, immersed, unilocular, obpyriform, ostiole with periphysis. *Pycnidial wall* 40–75 µm, composed of several layers of thick-walled, pale brown to dark brown cells of *textura angularis*. *Paraphyses* filamentous to cylindrical, hyaline, mostly septate, branched, ends at ends, 40–70 × 2–3 µm ($\overline{x}$ = 55.5 × 2.5 µm, n = 25), formed between conidiogenous cells. *Conidiogenous cells* 5–15 × 3–5 µm ($\overline{x}$ = 12 × 3.5 µm, n = 25), holoblastic, cylindrical, thick-walled, hyaline, smooth, slightly swollen at the base. *Conidia* 20–30 × 12–15 µm ($\overline{x}$ = 24.5 × 14 µm, n = 30), initially hyaline and aseptate, apex and base rounded, widest at the middle, ellipsoid, thick-walled, with granular content.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies on PDA, raised, velvety, circular, with entire edge, white at first, becoming black with age, black in reverse, with smooth margin.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on

dead leaves of *Ananas comosus*, 18 September 2020, X.G. Tian, p10-2 (MFLU 23-0198), living culture, MFLUCC 23-0118.

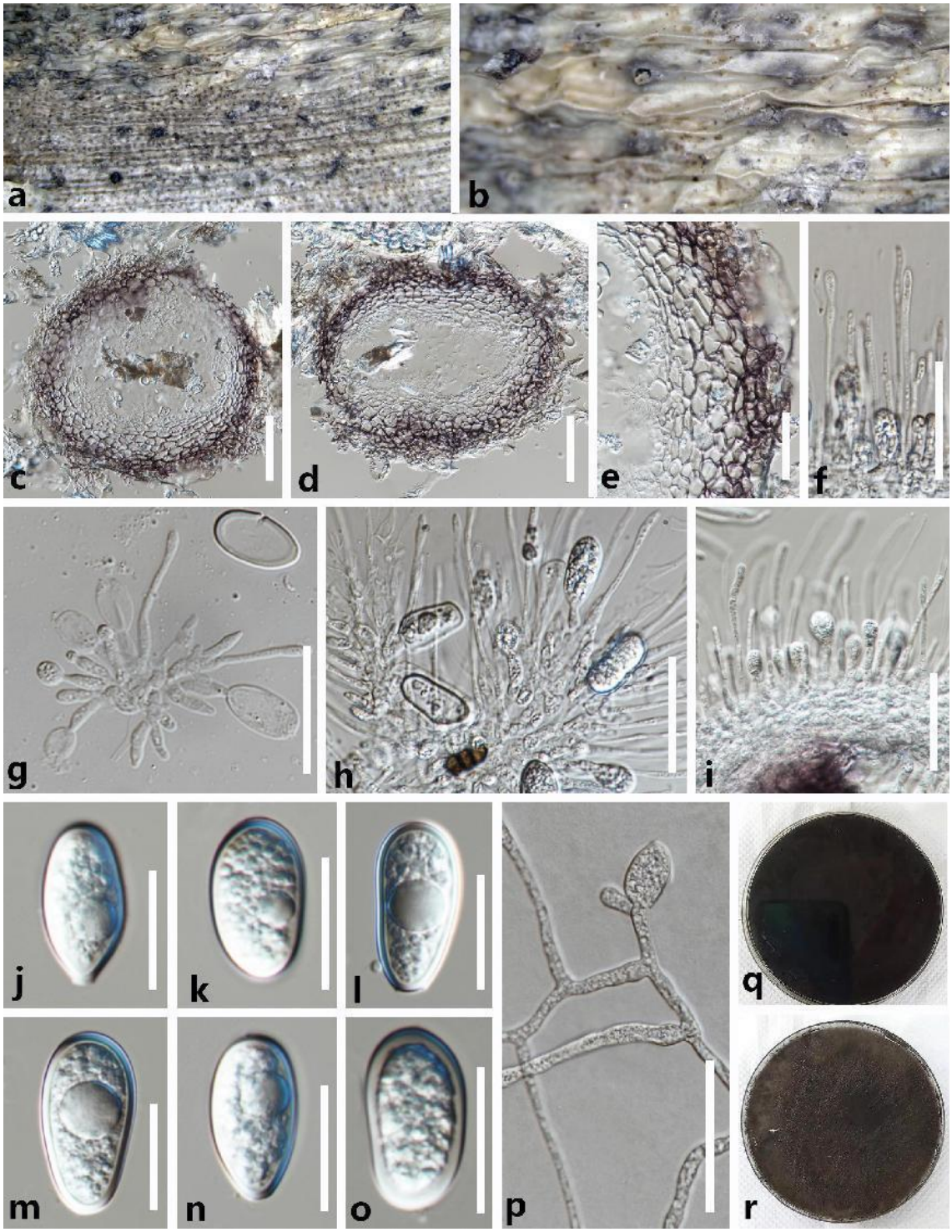

Figure 70 – *Lasiodiplodia mahajangana* (MFLU 23-0198, new host record). a, b Conidiomata on host surface. c, d Section of conidioma. e Conidioma wall. f–i Conidiogenous cells with conidia. j–o Conidia. p Germinated conidium. q, r Colonies on PDA from surface and reverse. Scale bars: c–i, p = 40 µm, j–o = 20 µm.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies on PDA, raised, velvety, circular, with entire edge, white at first, becoming dark brown to black with age, black in reverse, with smooth margin.

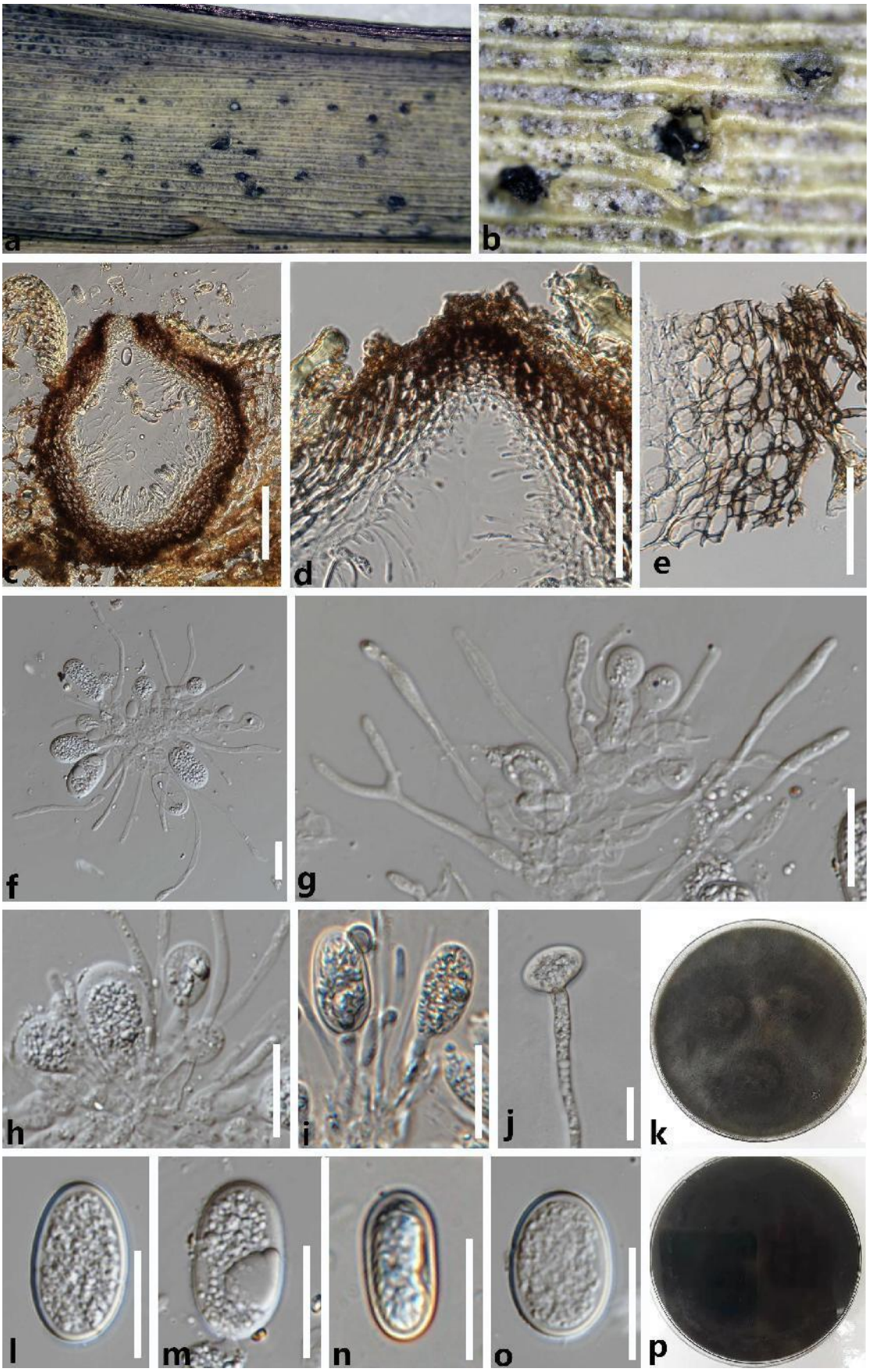

Figure 71 – *Lasiodiplodia pseudotheobromae* (MFLU 23-0202, new host record). a, b Conidiomata on the host surface. c Section of conidioma. d Ostiole. e Conidioma wall. f–i Conidiogenous cells with conidia. j Germinated conidium. k, p Colonies on PDA from surface and reverse. l–o Conidia. Scale bars: c, d = 100 µm, e = 50 µm, f, h–o = 20 µm.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, p6-19 (MFLU 23-0202), living culture, MFLUCC 23-0141.

Known hosts and distribution – On *Gmelina arborea* in Costa Rica (Alves et al. 2008); on grapes, Citrus, Chinese hackberry, English Walnut in China (Dissanayake et al. 2015, Li et al. 2016a, Liang et al. 2020, Chen et al. 2021); on mango in Korea (Kwon et al. 2017); on postharvest fruit in Thailand (Pipattanapuckdee et al. 2019); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438380, *tub2* = OR887682

Notes – *Lasiodiplodia pseudotheobromae* was introduced by Alves et al. (2008). Our isolate clusters with *L. pseudotheobromae* with 91% ML and 0.98 PP support (Fig. 67). Our strain shares similar morphology to *Lasiodiplodia pseudotheobromae* (CBS 116459) in having unilocular, dark brown to black, immersed conidiomata, holoblastic, hyaline, cylindrical, slightly swollen at the base conidiogenous cells, ellipsoid, initially hyaline and aseptate, apex and base rounded, thick-walled conidia. However, our isolate did not show mature conidia after being released from the conidiomata, while, *L. pseudotheobromae* (CBS 116459) have 1-septate, dark brown, with longitudinal striations conidia after release from the conidiomata (Alves et al. 2008). Thus, we identified our strain as *L. pseudotheobromae* based on phylogenetic analyses and morphological characters. Our strain *L. pseudotheobromae* (MFLUCC 23-0141) is introduced as a new host record on *Ananas comosus*.

41. *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl., Bull. Soc. Mycol. Fr. 25: 57 (1909) Fig. 72

Index Fungorum number: IF188476; Facesoffungi number: FoF00167

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: See Phillips et al. (2013). Asexual morph: *Conidiomata* up to 336 × 391 µm, pycnidial, scattered or gregarious, solitary, black, always sporulating on host surface, immersed, unilocular, subglobose, ostiole with papilla. *Pycnidial wall* 45–70 µm, composed of several layers of thick-walled, hyaline to pale brown cells of *textura angularis*. *Paraphyses* filamentous to cylindrical, hyaline, septate, branched, rounded at ends, 45–65 × 2–3 µm ($\overline{x}$ = 57 × 2.5 µm, n = 20), formed between conidiogenous cells. *Conidiogenous cells* 10–15 × 3–5 µm ($\overline{x}$ = 12.5 × 4 µm, n = 7), holoblastic, cylindrical, thick-walled, hyaline, smooth. *Conidia* 20–30 × 15–20 µm ($\overline{x}$ = 25.5 × 16.5 µm, n = 40), initially hyaline, aseptate, ellipsoid to ovoid, thin-walled, becoming brown to dark brown, 1-septate, with dark band at the septum, not constricted at septum, subovoid to ellipsoid-ovoid, with granular content, thick-walled, with longitudinal striations when mature.

Culture characteristics – Conidia germinating on PDA within 10 h. Colonies on PDA, raised, velvety, circular, with entire edge, white at first, becoming black with age, black in reverse, with smooth margin.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on dead leaves of *Ananas comosus*, 3 October 2020, X.G. Tian, p11-6 (MFLU 23-0203), living culture, MFLUCC 23-0119.

Known hosts and distribution – On fruit of *Theobroma* in Ecuador (Patouillard & Lagerheim 1892); on fruit of coral reef coast, *Persea americana*, *Musa sapientum*, sail-cloth, *Cocos nucifera*, phaeohyphomycotic cyst, *Zea mays*, *Vitis vinifera*, *Pinus* sp., *Vitex doniana* in the USA, New Guinea, Tanzania, Australian, Canada, South Africa, Mexico, Uganda, Argentina (Alves et al. 2008); on Mango in India (Khanzada et al. 2005); on Grapevines in Mexico (Úrbez-Torres et al. 2008); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438848, ITS = OR438381, *tef1-α* = OR500332

Notes – *Lasiodiplodia theobromae* was introduced by Griffon & Maublanc (1909). Our isolate clusters within *L. theobromae* in phylogenetic analyses (Fig. 67). Our strain shares similar morphology to *L. pseudotheobromae* (CBS116459) in having black, unilocular, immersed conidiomata, ostiole with papilla, septate and branched paraphyses and 1-septate, subovoid to ellipsoid-ovoid, with longitudinal striations when mature conidia (Phillips et al. 2006, Alves et al.

2008). Thus, we identified our strain as *L. theobromae* based on phylogenetic analyses and morphological characters. *Lasiodiplodia theobromae* (MFLUCC 23-0119) was collected on *Ananas comosu*s in Thailand for the first time.

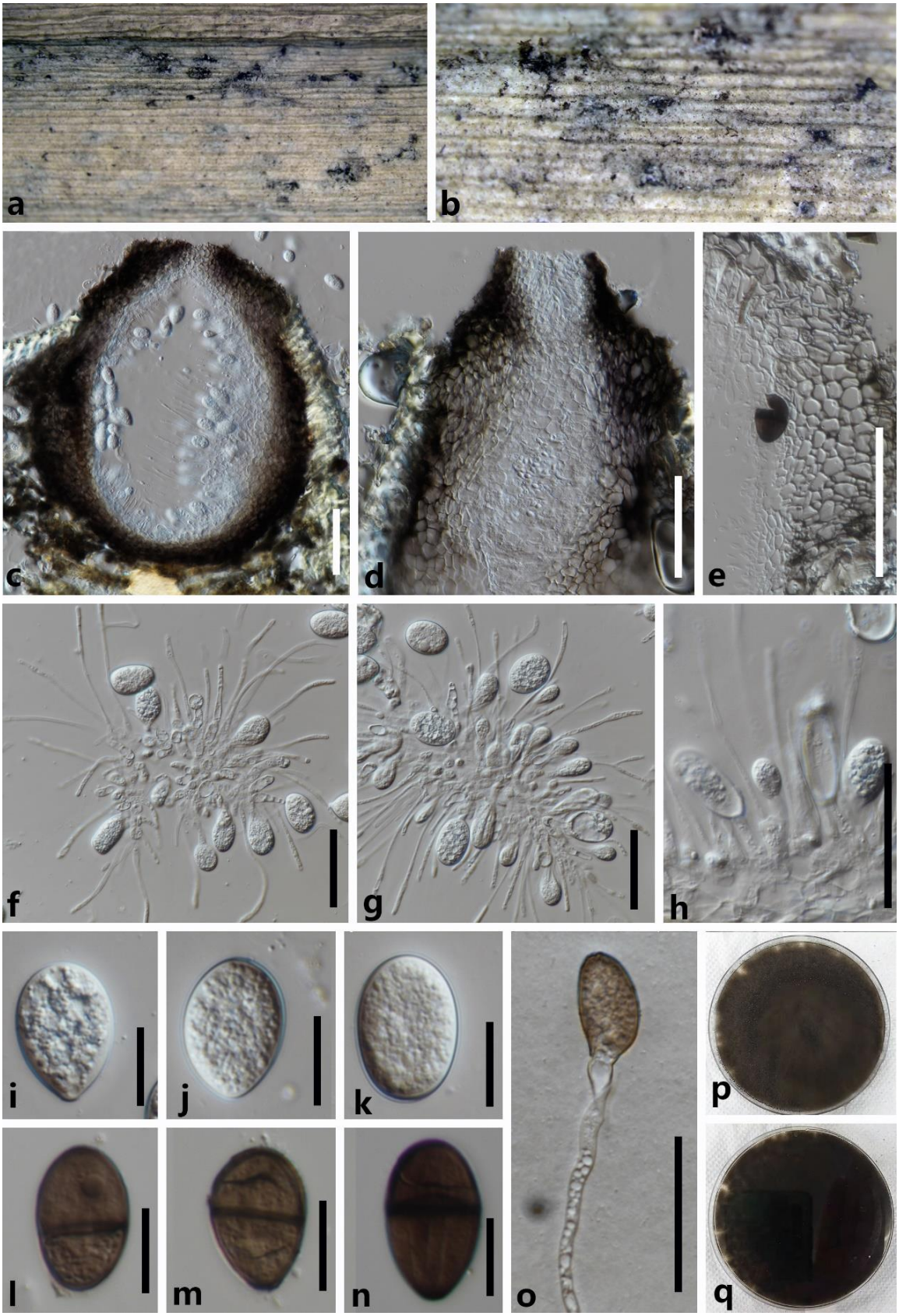

Figure 72 – *Lasiodiplodia theobromae* (MFLU 23-0203, new host and geographical record). a, b Conidiomata on host surface. c Section of conidioma. d Ostiole. e Conidioma wall.

f–h Conidiogenous cells with conidia. i–n Conidia. o Germinated conidium. p, q Colonies on PDA from surface and reverse. Scale bars: c, d = 80 µm, e–h, o = 40 µm, i–n = 10 µm.

Neoscytalidium Crous & Slippers

Neoscytalidium was introduced by Crous et al. (2006), with *N. dimidiatum* as the type species. Phillips et al. (2013) incorrectly stated that *N. hyalinum* is the type species of this genus. The oldest epithet is *N. dimidiatum* based on *Torula dimidiat*e (Dissanayake et al. 2016). Subsequently, Huang et al. (2016) corrected this error and placed *N. dimidiatum* as type species of the genus. This genus was described as conidia occurring in arthric chains in aerial mycelium, powdery to the touch, disarticulating, cylindrical-truncate, oblong-obtuse to doliiform, dark brown, thick-walled, 0–2-septate (Crous et al. 2006). There are eight records of *Neoscytalidium* listed in Index Fungorum (2023). In this study, we introduce a new record, *Neoscytalidium dimidiatum* on dead leaves of *Ananas comosus* based on morphology and phylogeny.

42. *Neoscytalidium dimidiatum* Crous & Slippers, in Crous et al., Stud. Mycol. 55: 244 (2006) Fig. 73

Index Fungorum number: IF500869; Facesoffungi number: FoF11892

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* up to 210 × 190 µm, pycnidial, scattered or gregarious, black, conspicuous on host surface, semi-immersed to superficial, multiloculate, globose to subglobose, ostiole without papilla. *Pycnidial wall* 35–50 µm, composed of several layers of thick-walled, pale brown to brown cells of *textura angularis*. *Conidiogenous cells* 5–10 × 2–3 µm ($\overline{x}$ = 8.5 × 2.5 µm, n = 20), holoblastic, cylindrical, thick-walled, hyaline, smooth. *Conidia* 10–15 × 4.5–5.5 µm ($\overline{x}$ = 12 × 5 µm, n = 30), ellipsoid, with an acutely rounded apex, truncate at base, initially hyaline, becoming dark brown at maturity, 0–2-septate, brown to dark brown at the middle cell, pale brown at both ends cells, not constricted at septum, thick-walled when mature, guttulate.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies on PDA, raised, velvety, circular, with entire edge, white at first, becoming pale brown with age, brown in reverse, with smooth margin.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, p6-4 (MFLU 23-0204), living culture, MFLUCC 23-0108.

Known hosts and distribution – On corticate branches of *Citrus limon* in Italy (Penzig 1882); on *Mangifera indica* and *Ficus carica* in Australia (Ray et al. 2010); on red-fleshed dragon fruit (*Hylocereus polyrhizus*) in Malaysia (Mohd et al. 2013); on almond in California (Nouri et al. 2018); on *Hylocereus undatus* and *H. polyrhizus* in China (Chuang et al. 2012); on *Solanum lycopersicum* in Turkey (Türkölmez et al. 2019); on *Hylocereus undatus* in China (Lan et al. 2012); on Grapevine in the USA (Rolshausen et al. 2013); on *Citrus* in Italy (Polizzi et al. 2009b); on *Hylocereus polyrhizus* in China (Xu et al. 2019); on *Hylocereus undatus* in the USA (Sanahuja et al. 2016); on *Sansevieria trifasciata* in Malaysia (Kee et al. 2017); on pitahaya in China (Yi et al. 2015); on English walnut in the USA (Chen et al. 2015); on *Hylocereus polyrhizus* in Thailand (Dy et al. 2022); in *Assiut governorate* in Egypt (Al-Bedak et al. 2018); on pitaya *China* (Xu et al. 2018); on *Ficus carica* in California (Gusella et al. 2021); on *Ficus carica* in Turkey (Gusella et al. 2021); on sweet potato in Brazil (Mello et al. 2019); on *Citrus* in Italy (Polizzi et al. 2009a); on apple in Turkey (Ören et al. 2022); on apricot in Turkey (Oksal et al. 2020); on walnut in Turkey (Derviş et al. 2019); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438849, ITS = OR438382, SSU = OR458355

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0108) grouped with *Neoscytalidium dimidiatum* strains (Fig. 74). Morphologically, our strain is similar to *Neoscytalidium dimidiatum* in having hyaline conidiogenous cells, ellipsoid, hyaline with an acutely rounded apex, truncate base,0−2-septate conidia with the central cell darker than the end cells (Crous et al. 2006). Our strain also shares a similar size range of conidia (12 × 5 µm vs. 10.99

× 5.02 µm) (Mohd et al. 2013). The nucleotide comparisons showed that our strain (MFLUCC 23-0108) is not significantly different from *N. dimidiatum* (CBS 499.66) in ITS and LSU. Thus, we identified our strain as *N. dimidiatum* and introduced it as a new host record on *Ananas comosus*.

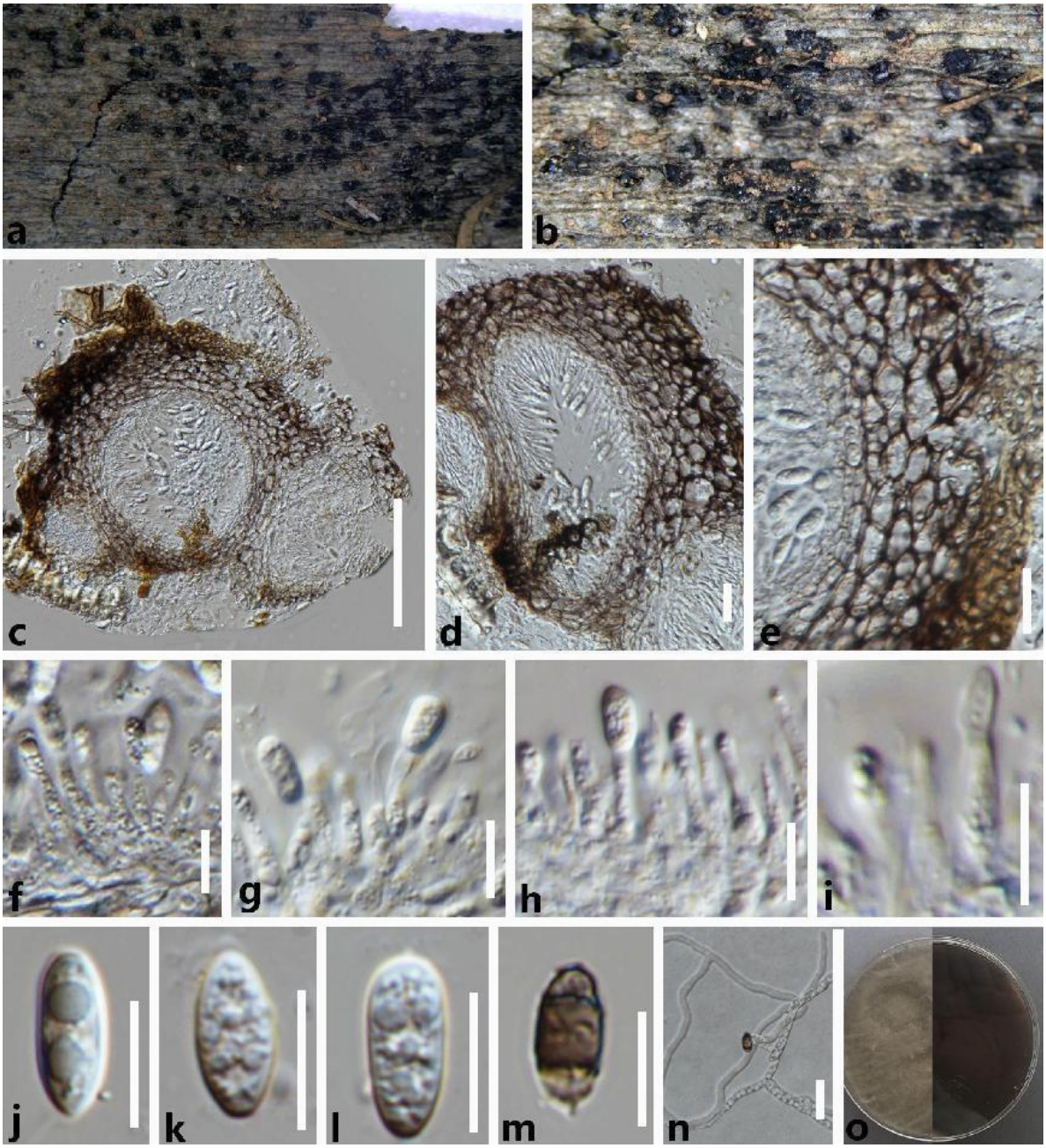

Figure 73 – *Neoscytalidium dimidiatum* (MFLU 23-0204, new host record). a, b Conidiomata on host surface. c, d Section of conidiomata. e Section of pycnidial wall. f–i Conidiogenous cells with conidia. j–m Conidia. n Germinated conidium. o Colonies on PDA from surface and reverse. Scale bars: c = 100 µm, d–i = 20 µm, j–m = 10 µm.

Neodeightonia C. Booth

Neodeightonia was introduced by Punithalingam (1980), with *N. subglobosa* as the type species. However, von Arx & Muller (1950) transferred *N. subglobosa* to *Botryosphaeria*, and synonymized *Neodeightonia* under *Botryosphaeria*. Subsequently, Phillips et al. (2008) distinguished this genus from *Botryosphaeria* based on both morphological and phylogenetic data, and accepted *Neodeightonia* as a separate genus in *Botryosphaeriaceae*. The asexual morph is characterized by conidia initially hyaline, become brown and 1-septate at maturity with smooth to

finely roughened walls or with fine striations, this is unique to the genus *Neodeightonia* (Phillips et al. 2006, Konta et al. 2016, Rathnayaka et al. 2022). There are 13 species of *Neodeightonia* listed in Index Fungorum (2023). In this study, we introduce two new records in this genus from Thailand based on morphology and phylogeny.

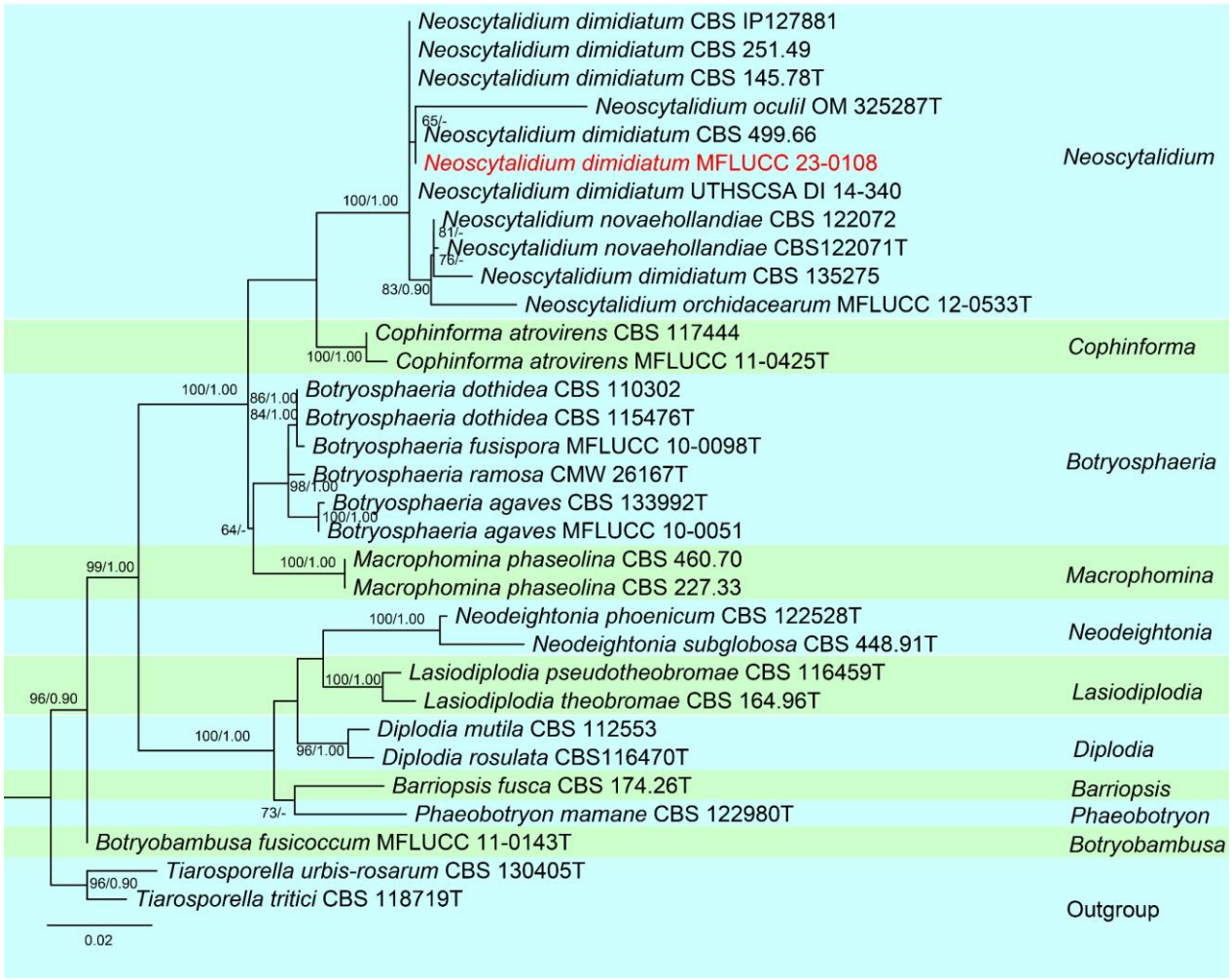

Figure 74 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Huang et al. (2016). Thirty-two strains are included in the combined sequence analysis, which comprise 1472 characters with gaps. *Tiarosporella tritici* (CBS 118719) and *T. urbis-rosarum* (CBS 130405) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -4579.715519 is presented. The matrix had 347 distinct alignment patterns, with 15.22% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238625, C = 0.249818, G = 0.290937, T = 0.220620; substitution rates AC = 1.327677, AG = 3.665062, AT = 1.538350, CG = 1.989314, CT = 6.706680, GT = 1.000000; gamma distribution shape parameter a = 0.081870. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red and T indicates holotype or ex-type strains.

43. ***Neodeightonia rattanica*** S. Konta & K.D. Hyde, in Konta, Hongsanan, Phillips, Jones, Boonmee & Hyde, Mycosphere 7(7): 953 (2016) Fig. 75

Index Fungorum number: IF552168; Facesoffungi number: FoF02237

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 160–325 × 100–160 µm ($\bar{x}$ = 242 × 129 µm, n = 7), pycnidial, solitary or gregarious, subglobose to wide-oval, dark brown to black, conspicuous on host surface,

unilocular, immersed in the host, ostiole without papilla. *Conidiomata wall* 30–105 µm wide, outer layer composed of thick-walled, dark brown cells of *textura angularis*, inner layer composed of thick-walled, hyaline to pale brown cells of *textura angularis*. *Paraphyses* filamentous, hyaline, septate, unbranched, 55–90 × 1.5–2.5 µm ($\overline{x}$ = 73 × 2 µm, n = 40), formed between conidiogenous cells. *Conidiogenous cells* 9.5–15 × 3–5.5 µm ($\overline{x}$ = 12 × 4.5 µm, n = 20), holoblastic, hyaline, cylindrical, discrete, determinate, swollen at base, smooth-walled. *Conidia* 25–30 × 15–17 µm ($\overline{x}$ = 30 × 15.5 µm, n = 30), ellipsoid, initially hyaline and aseptate, becoming dark brown 1-septate when mature, thick-walled, broadly rounded at both ends, granulate, without longitudinal striations and mucilaginous sheath.

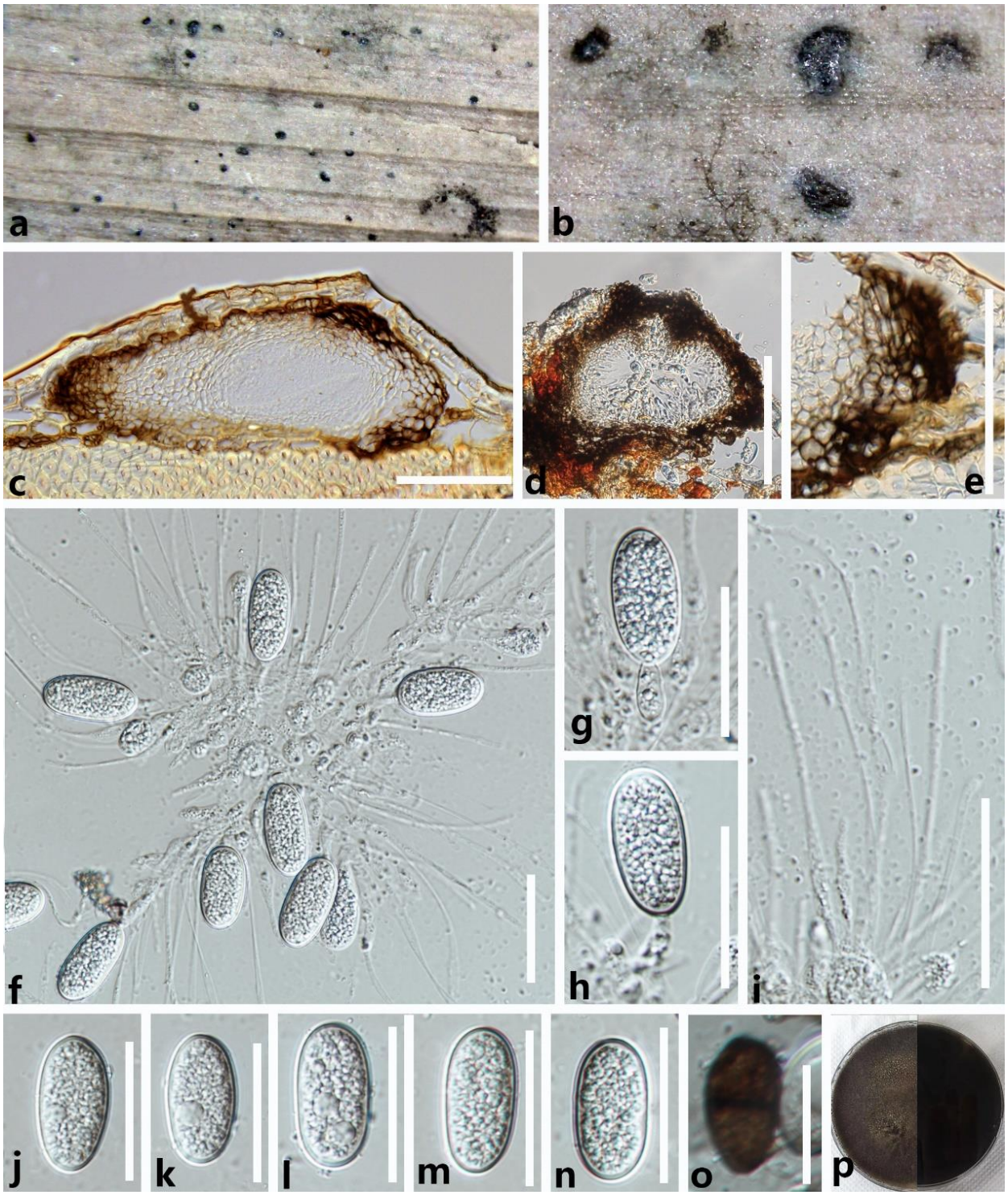

Figure 75 – *Neodeightonia rattanica* (MFLU 23-0205, new host record). a, b Conidiomata on host

surface. c, d Section of conidioma. e Conidioma wall. f–h Conidiogenous cells with conidia. i Paraphyses. j–o Conidia. p Colonies on PDA from surface and reverse. Scale bars: c–e = 100 μm, f–n = 30 μm.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies on PDA, raised, velvety, circular, dark brown to black, with entire edge, black in reverse, with smooth margin.

Material examined – Thailand, Chiang Rai Province, Mueang District, ThaSut Subdistrict, on dead leaves of *Cocos nucifera*, 22 September 2020, X.G. Tian, c1-10 (MFLU 23-0205), living culture, MFLUCC 23-0117.

Known hosts and distribution – on dead rachis of *Calamus* sp. (Arecaceae) in Thailand (Konta et al. 2016); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – MFLU 23-0205: ITS = OR438383, SSU = OR458356, *tef1-α* = OR500333. MFLUCC 23-0117: ITS = OR438384, SSU = OR458357, *tef1-α* = OR500334

Notes – In the multi-loci phylogenetic analyses, our new isolate (MFLUCC 23-0117) clustered with *N. rattanica* (MFLUCC 15-0712 and MFLUCC 15-0313) with 99% ML and 0.98 PP support (Fig. 76). Morphologically, our strain is almost identical to *N. rattanica* in having ellipsoid, aseptate, hyaline conidia that are becoming dark brown when mature. Except for the size of the conidia, our new isolate has larger conidia than those of *N. rattanica* (25–30 × 15–17 μm vs. 19–22 × 7–9 μm) (Konta et al. 2016). The nucleotide comparisons showed that our strain (MFLU 23-0117) is not significantly different from *N. rattanica* (MFLUCC 15-0313.) in *tef1-α* (7/279, 2 gaps, 97.49%). Thus, we identified our new isolate as *N. rattanica*. *Neodeightonia rattanica* was collected on rachis of *Calamus* sp., while our new isolate was also collected on *Cocos nucifera*. We report our new isolate as a new host record.

44. *Neodeightonia phoenicum* A.J.L. Phillips & Crous, in Phillips et al., Persoonia 21: 43 (2008) Fig. 77

Index Fungorum number: IF511708; Facesoffungi number: FoF11670

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 95–135 × 95–145 μm ($\bar{x}$ = 115 × 121 μm, n = 9), pycnidial, solitary or gregarious, subglobose, dark brown to black, multiloculate, immersed in the host, ostiole without papilla. *Conidiomata wall* 20–40 μm wide, outer layer composed of thick-walled, dark brown cells of *textura angularis*, inner layer composed of thin-walled, hyaline to pale brown cells of *textura angularis*. *Conidiogenous cells* 5–10 × 3–4 μm ($\bar{x}$ = 6.5 × 3.5 μm, n = 15), phialidic, hyaline, cylindrical, discrete, determinate, swollen at base, smooth-walled. *Conidia* 10–15 × 5–10 μm ($\bar{x}$ = 14 × 9 μm, n = 30), ovoid to ellipsoid, hyaline, aseptate, thick-walled, broadly rounded at both ends, guttulate, without longitudinal striations and mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies on PDA, raised, velvety, circular, white, with entire edge, white in reverse, with smooth margin.

Material examined – Thailand, Chiang Rai Province, Nang Lae Subdistrict, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, c6-11 (MFLU 23-0206), living culture, MFLUCC 23-0157.

Known hosts and distribution – On *Phoenix* in Spain (Phillips et al. 2008); on *Phoenix* spp. in Greece (Ligoxigakis et al. 2013); on Pygmy Date Palm (*Phoenix roebelenii*) in China (Zhang & Song 2022); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438850, ITS = OR438385, *tef1-α* = OR500335

Notes – In our phylogenetic analyses, our new isolate (MFLUCC 23-0157) clusters with *Neodeightonia phoenicum* with 100% ML and 1.00 PP support (Fig. 76). Our new isolate is similar to *N. phoenicum* in having multiloculate, immersed conidiomata, holoblastic conidiogenous cells and conidia ovoid to ellipsoid, aseptate (Phillips et al. 2008, Rathnayaka et al. 2022). In addition, our strain shares a similar size range of conidia (10–15 × 5–10 μm vs. 11–17 × 6–10 μm) and conidiogenous cells (5–10 × 3–4 μm vs. 5–10 × 2–5 μm) to *N. phoenicum* (Rathnayaka et al. 2022).

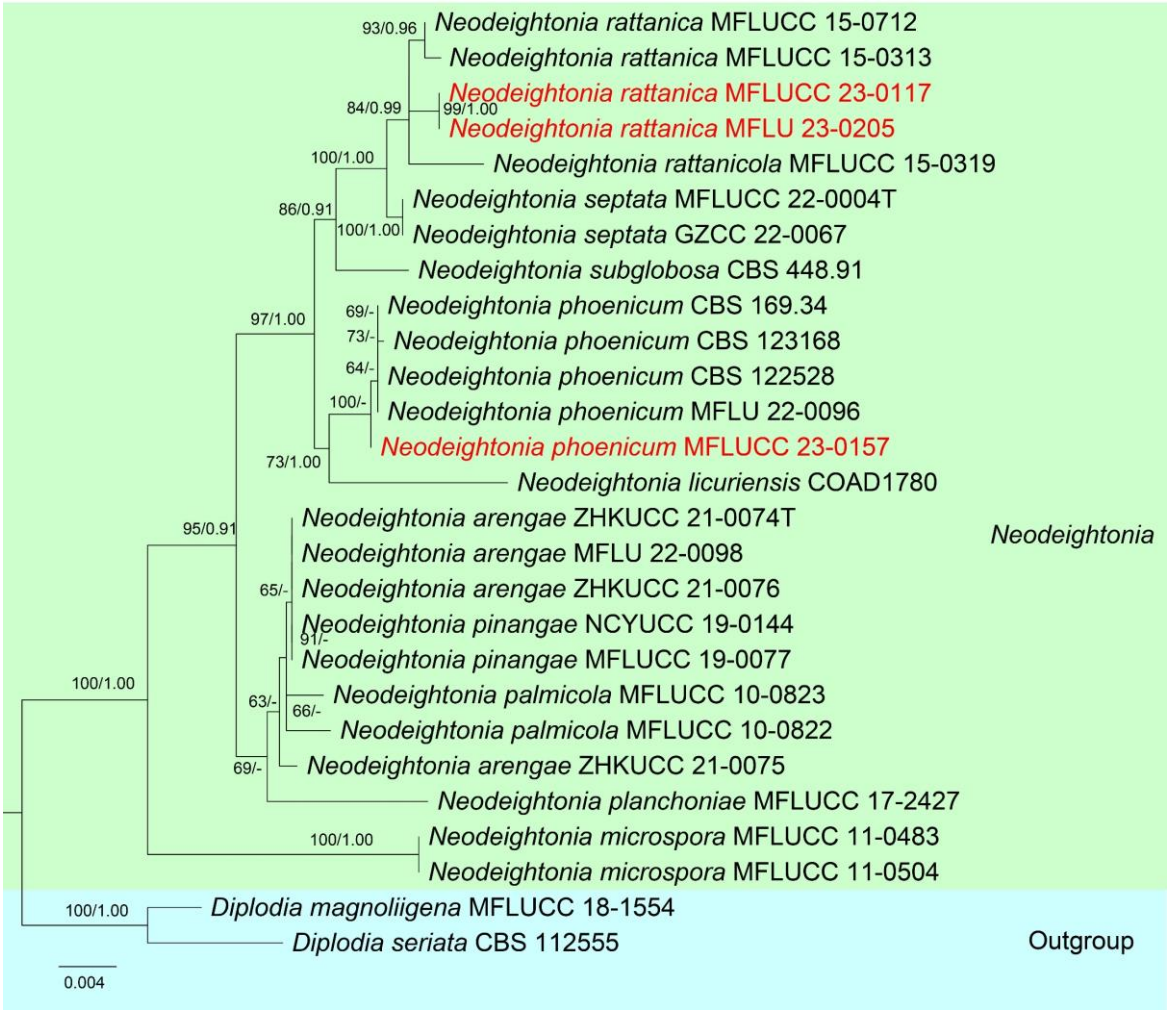

Figure 76 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, and *tef1-α* sequence data. Related sequences were obtained from Xiao et al. (2021). Twenty-seven strains are included in the combined sequence analysis, which comprise 2712 characters with gaps. *Diplodia magnoliigena* (MFLUCC 18-1554) and *D. seriata* (CBS 112555) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -5337.739353 is presented. The matrix had 270 distinct alignment patterns, with 20.68% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237624, C = 0.245371, G = 0.282079, T = 0.234926; substitution rates AC = 2.063247, AG = 2.613623, AT = 0.785640, CG = 1.931190, CT = 5.924823, GT = 1.000000; gamma distribution shape parameter a = 0.020000. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red and T indicates holotype or ex-type strains.

Our new isolate is not significantly different from the holotype of *N. phoenicum* (CBS 122528) in ITS, LSU, SSU and *tef1-α* sequence data. Thus, we identified our new isolate as *N. phoenicum*.

Neodeightonia phoenicum has been reported mostly from Arecaceae species and it was collected on *Phoenix* spp. from China, Spain and Greece (Phillips et al. 2008, Ligoxigakis et al. 2013, Zhang & Song 2022). In this study, *N. phoenicum* was collected on *Cocos nucifera* (Arecaceae) in Thailand, we report it as a new host and geographical record for China.

Phyllostictaceae Fr.

Phyllostictaceae was first proposed by Fries (1849). The status of this family has been revised and changed by different authors (Seaver 1922, Crous et al. 2006, Schoch et al. 2006, Liu et

al. 2012, Slippers et al. 2013, Wikee et al. 2013b, Hongsanan et al. 2020b). *Phyllosticta* was treated in *Botryosphaeriaceae* by Schoch et al. (2006) and Crous et al. (2006). Liu et al. (2012) showed that *Saccharata* clustered with *Phyllosticta* and formed a clade with *Melanops* at the base of *Botryosphaeriales*, which suggested this clade may be a distinct family in *Botryosphaeriales*. Wikee et al. (2013b) suggested *Phyllostictaceae* as a distinct family in *Botryosphaeriales* and the family was subsequently re-instated by Slippers et al. (2013). The recent treatment of *Phyllostictaceae* was provided by Hongsanan et al. (2020), two genera *Phyllosticta* and *Pseudofusicoccum* are accepted in the family.

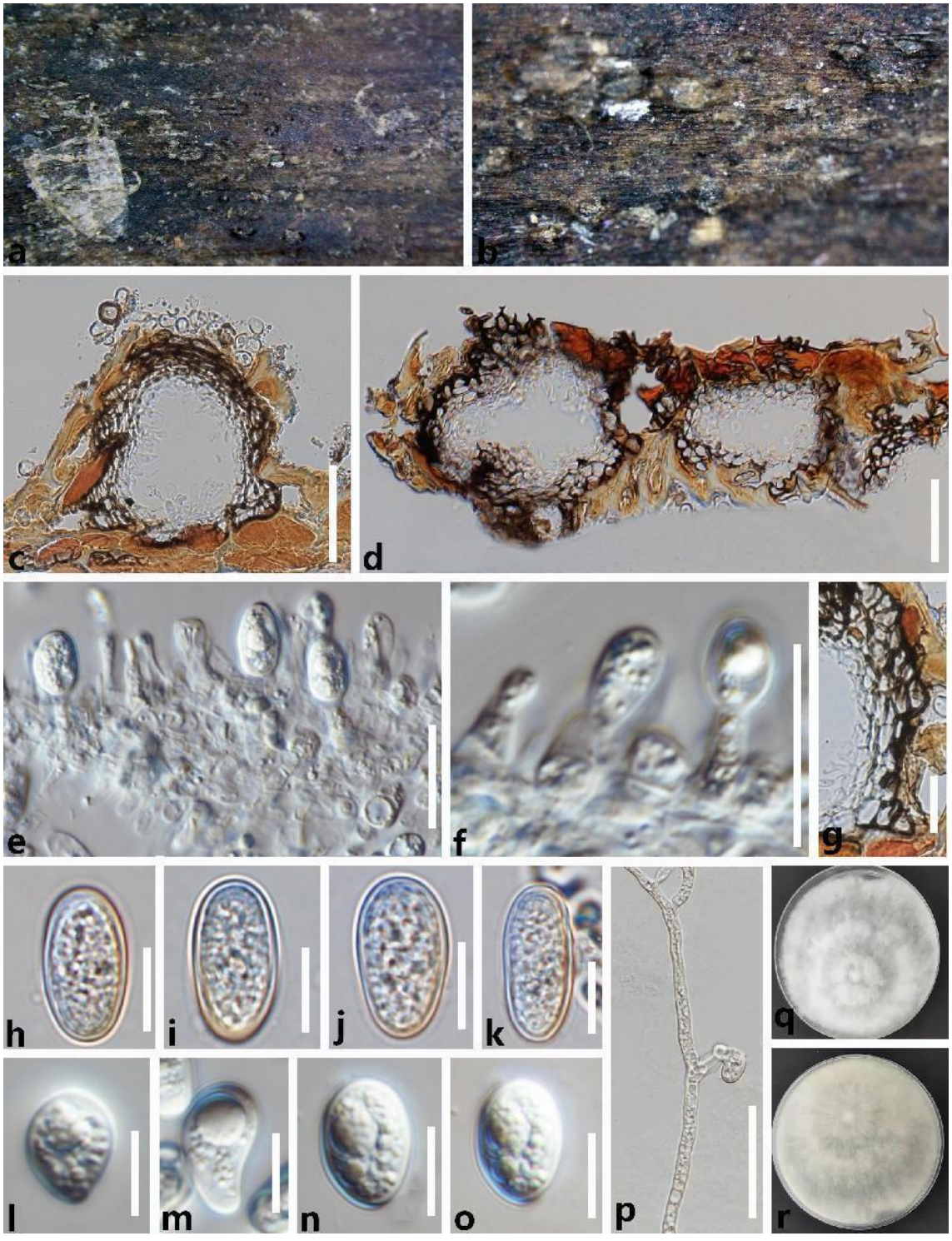

Figure 77 – *Neodeightonia phoenicum* (MFLU 23-0206, new host and geographical record). a, b Conidiomata on host surface. c, d Section of conidiomata. e, f Conidiogenous cells with conidia.

g Conidiomatal wall. h–o Conidia. p Germinated conidium. q, r Colonies on PDA from surface and reverse. Scale bars: c–d, p = 50 µm, e, f = 20 µm, g–o = 10 µm.

Phyllosticta Pers., Traité champ. Comest. (Paris): 55, 147 (1818)

Phyllosticta was introduced by Persoon (1818) with *P. convallariae* as the type. Species in this genus are commonly reported as endophytes, plant pathogens or saprobes (Persoon 1818, Baayen et al. 2002, Okane et al. 2003, Silva et al. 2008, Huang et al. 2009, Zhang et al. 2022c). There are 3,211 records of *Phyllosticta* listed in Index Fungorum (2023). Recently, two new species have been added to the genus by Zhang et al. (2022c). In this study, a new record of *P. capitalensis* is described based on morphological and phylogenetic analyses, the description and illustration are also provided.

45. *Phyllosticta capitalensis* Henn., Hedwigia 48: 13. 1908 Fig. 78

Index Fungorum number: IF168326; Facesoffungi number: FoF06888

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Ascomata* 110–190 × 90–180 µm ($\bar{x}$ = 150 × 135 µm, n = 5), erumpent, globose to pyriform, often irregularly shaped, unilocular, central ostiole forming by dehiscence when mature. *Peridium* 15–30 µm wide, comprising two strata, outer stratum of thick-walled, thin-lumened, comprising brown to dark brown cells of *textura angularis*, inner layer of thin-walled, comprising pale brown to hyaline cells of *textura angularis* to *textura globulosa*. *Asci* 40–65 × 10–15 µm ($\bar{x}$ = 55 × 13 µm, n = 20), 8-spored, bitunicate, hyaline, clavate to broadly fusoid-ellipsoid, with a wide, slightly squared apex, tapering gradually to a small pedicel, bitunicate, with a well-developed ocular chamber. *Ascospores* 10–15 × 5–6 µm ($\bar{x}$ = 14 × 6 µm, n = 30), bi- to multiseriate, limoniform with obtuse ends, sometimes slightly elongated, slightly buldged in the middle, aseptate, hyaline, smooth, granular to guttulate, rarely curved, with mucilaginous polar appendages at both ends. Asexual morph: see Glienke et al. (2011).

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 15 July 2020, X.G. Tian, C8-16 (MFLU 23-0207).

Known hosts and distribution – On wild plant, *Punica granatum*, *Saccharum officinarum*, Arecaceae, *Ophiopogon japonicus*, *Ficus benjamina*, Orchidaceae, Magnoliaceae, *Polyscias* sp., *Hibiscus syriacus*, *Tectona grandis*, *Polyalthia longifolia*, *Euphorbia milii*, *Philodendron* ‘Xanadu’, *Alocasia* sp., *Dieffenbachia* sp., *Anthurium* sp., *Sansevieria Hyacinthoides*, *Tinospora craspa*, *Calophyllum* sp., *Citrus* sp., *Vaccinium* sp., *Myracrodruon urundeuva*, *Aspidosperma polyneuron*, *Bowdichia nitida*, *Musa paradisiaca*, *Paphiopedilum callosum*, *Citrus lalifolia*, *Citrus reticulata*, *Citrus sinensis*, *Mangifera indica*, *Stanhopea graveolens* in Thailand, Brazil, New Zealand, Germany (Wikee et al. 2013a); on *Bifrenaria harrisoniae* in Brazil (Silva et al. 2008); on Tea Plant (*Camellia sinensis*) in China (Cheng et al. 2019); on oil palm in Malaysia (Nasehi et al. 2020); on Japanese privet (*Ligustrum japonicum*) in Iran (Sabahi et al. 2022); on persimmon (*Diospyros kaki*) fruit in China (Duan et al. 2017); on decaying leaves of *Cocos nucifera* in China (this study).

GenBank numbers – LSU = OR438851, ITS = OR438386, SSU = OR458358

Notes – In our phylogenetic analyses, our new strain (MFLU 23-0207) clustered with *Phyllosticta capitalensis* (Fig. 79). Morphologically, the new collection is similar to *P. capitalensis* in having erumpent, globose to pyriform ascomata, 8-spored, clavate to broadly fusoid-ellipsoid asci with a well-developed ocular chamber and limoniform with obtuse ends, sometimes slightly elongated, aseptate, hyaline ascospores with mucilaginous polar appendage at both ends (Glienke et al. 2011). Based on both phylogeny and morphology, we identified our new collection as *P. capitalensis*. *Phyllosticta capitalensis* was introduced by Hennings (1908) and collected on leaves of *Stanhopea graveolens* (Hennings 1908, Glienke et al. 2011). Zhang et al. (2022c) reported the fungus from diseased leaves of *Rhapis excelsa*. While our new collection was collected on *Cocos nucifera* for the first time.

In addition, our phylogenetic analysis showed that *Phyllosticta camelliae* (MUCC 0059), *P. fallopiae* (MUCC 0113), *P. harai* (MUCC 0043), and *P. miurae* (MUCC 0065) clustered within

Phyllosticta capitalensis clade. However, Norphanphoun et al. (2020) mentioned that the placements of *Phyllosticta camelliae*, *P. fallopiae*, *P. harai*, and *P. miurae* are not stable in the phylogenetic trees. Thus, we did not synonymize *Phyllosticta camelliae, P. fallopiae, P. harai*, and *P. miurae* under *Phyllosticta capitalensis*. However, future studies are required to resolve this problem with further phylogenetic and morphological analyses.

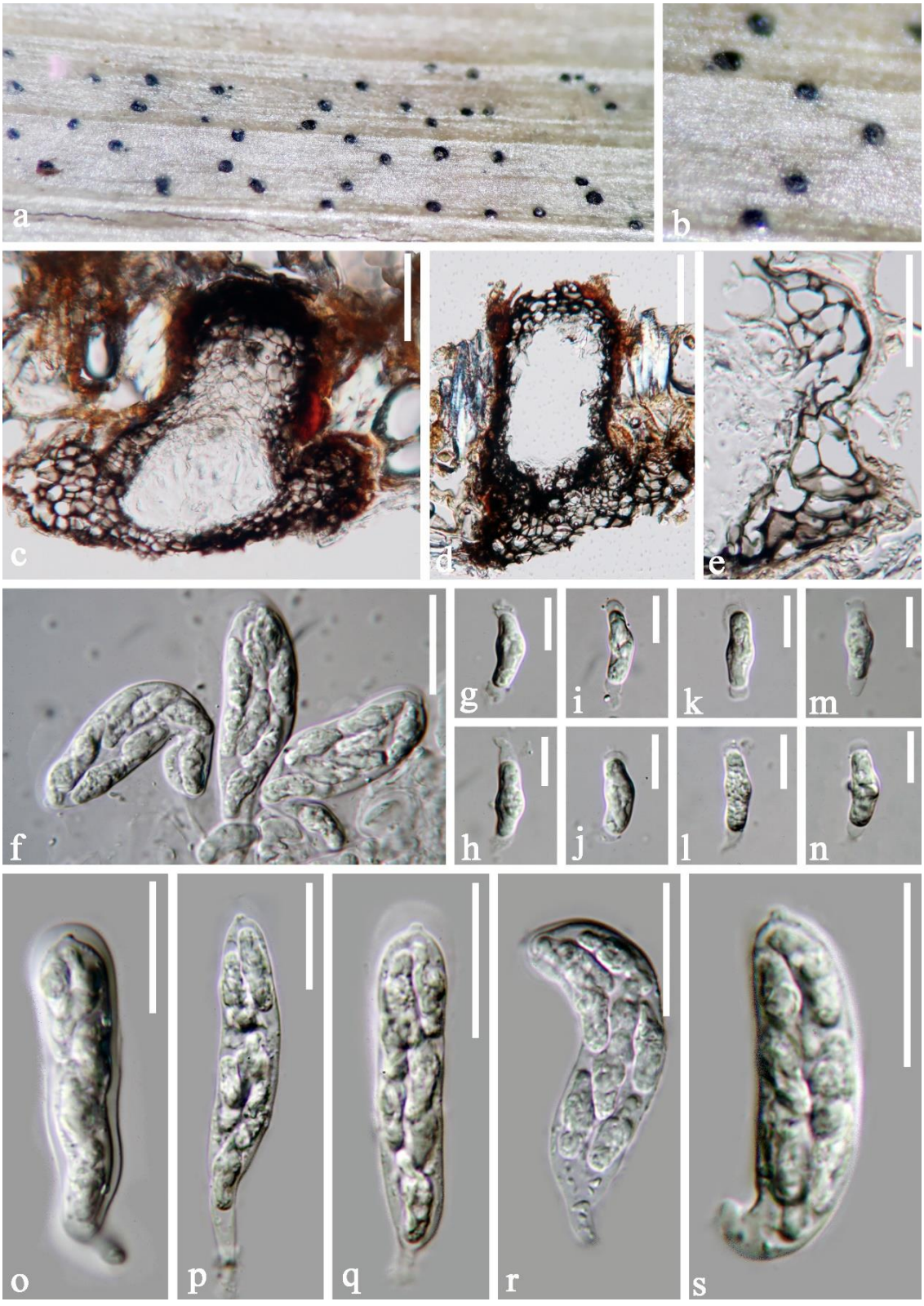

Figure 78 – *Phyllosticta capitalensis* (MFLU 23-0207, new host record). a–b Appearance of ascomata on the host. c, d Section through ascoma. e Section through peridium. f, o–s Asci.

g–n Ascospores. Scale bars: c–d = 50 µm, e = 30 µm, f, o–s = 20 µm, g–n = 10 µm.

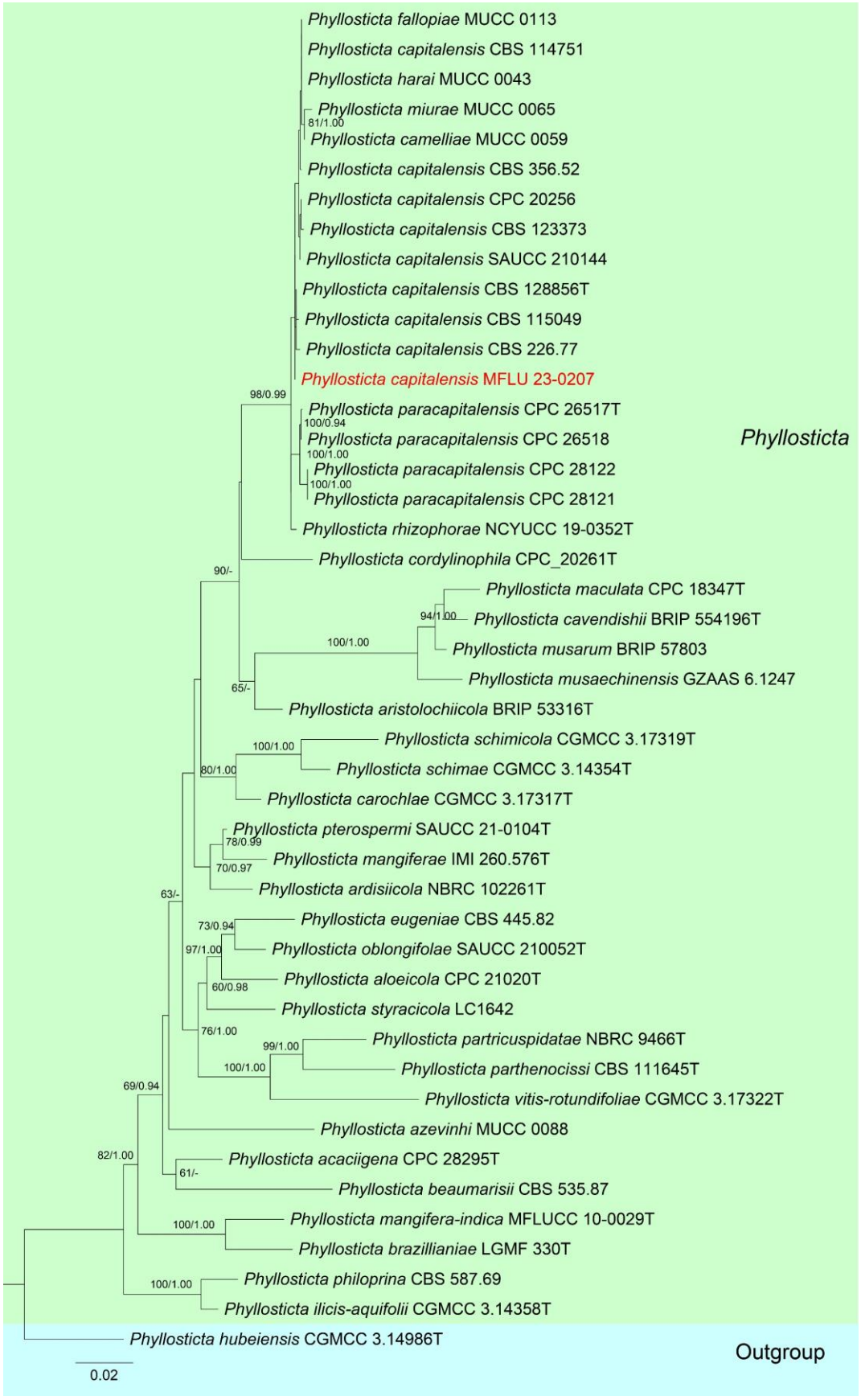

Figure 79 – Phylogram generated from maximum likelihood analysis based on the combined *act*, ITS, LSU, *tef1-α*, and *gapdh* sequence alignment, with *Phyllosticta hubeiensis* (CGMCC 3.14986)

as outgroup taxon. Related sequences were obtained from Zhang et al. (2022c). Forty-five strains are included in the combined sequence analysis, which comprises 3361 characters with gaps. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -12996.449073 is presented. The matrix had 888 distinct alignment patterns, with 38.97% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.216652, C = 0.283500, G = 0.276320, T = 0.223528; substitution rates AC = 0.826079, AG = 2.584823, AT = 1.065382, CG = 0.922092, CT = 6.319952, GT = 1.000000; gamma distribution shape parameter a = 0.238963. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Class ***Sordariomycetes*** O.E. Erikss. & Winka
Subclass ***Diaporthomycetidae*** Senan., Maharachch. & K.D. Hyde
Diaporthales Nannf.

Diaporthales was introduced by Nannfeldt (1932). We follow the latest treatments and updated accounts of *Diaporthales* (Hyde et al. 2020b, Wijayawardene et al. 2022).

Cytosporaceae Fr.

Cytosporaceae was established by Fries (1825) and typified by *Cytospora*. The family is placed in *Diaporthales*, and Maharachchikumbura et al. (2016) accepted 13 genera in the family. Senanayake et al. (2017) excluded seven genera from *Cytosporaceae* and accepted only five genera *viz. Cytospora*, *Pachytrype*, *Paravalsa*, *Waydora*, and *Xenotypa* based on phylogenetic analysis and morphological characters. Later *Cryptascoma* and *Hypophloeda* were added to the family by Senanayake et al. (2018). However, Hyde et al. (2020a) transferred *Hypophloeda* to *Diaporthales* genera *incertae sedis*. Currently, are six genera *viz. Cryptascoma*, *Cytospora*, *Pachytrype*, *Paravalsa*, *Waydora* and *Xenotypa* are accepted in the family (Hyde et al. 2020a, Wijayawardene et al. 2022).

Cytospora Ehrenb.

Cytospora was introduced by Ehrenberg (1818) with *C. chrysosperma* as the type species. Species in the genus are characterized by stromatic, pycnidial, unilocular to multilocular and labyrinthine conidiomata with long necks, cylindrical, branched conidiophores, phialidic conidogenous cells and hyaline, unicellular, allantoid conidia (Sutton 1980, Li et al. 2020b). The sexual morph is characterized by stromatic, perithecial, multilocular, globose to subglobose ascomata with long or short necks, 8-spored, unitunicate, clavate, sessile asci with a J - apical ring and hyaline, allantoid, aseptate ascospores (Adams et al. 2004, Norphanphoun et al. 2018, Shang et al. 2020).

Cytospora species are reported as endophytes, saprobes and plant pathogens with a worldwide distribution (Adams et al. 2004, Adams et al. 2006, Norphanphoun et al. 2017, Lawrence et al. 2018, Norphanphoun et al. 2018, Jayawardena et al. 2019b, Shang et al. 2020, Chen et al. 2022). However, the morphologies of *Cytospora* species are quite similar, and it is difficult to identify them based on morphology and most *Cytospora* species lack sequence data in the GenBank. There are more than 692 records of *Cytospora* listed in Index Fungorum (2023), while more than 150 species are estimated in *Cytospora* (Lawrence et al. 2017, Fan et al. 2018, 2020, Chen et al. 2022). In this study, a new record of *Cytospora eugeniae* is described based on phylogenetic analyses and morphological characters.

46. ***Cytospora eugeniae*** (Nutman & F.M. Roberts) G.C. Adams & Rossman, in Rossman et al., IMA Fungus 6(1): 147 (2015) Fig. 80

Index Fungorum number: IF812489; Facesoffungi number: FoF14301

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Stromata* solitary to gregarious, immersed, becoming raised to erumpent by the ostiolar canal, dark brown to black, glabrous,

circular in shape, arranged with conspicuous, clustered, roundish to cylindrical prominent ostioles. *Ascomata* 110–220 × 120–235 μm ($\overline{x}$ = 168 × 180 μm, n = 10), perithecial, immersed in a stroma, brown to dark brown, globose to subglobose, glabrous, individual ostiole with the neck. *Ostiolar canal* 150–190 × 45–75 μm ($\overline{x}$ = 169 × 61 μm, n = 10), cylindrical, sulcate, periphysate. *Peridium* 11–20 μm wide, composed of two section layers, outer section comprising 3–5 layers, yellow to brown, thick-walled cells, arranged in textura angularis, the inner part comprising 3–4 layers of hyaline cells of *textura angularis*. *Hamathecium* composed of 3–5 μm wide, cylindrical, septate, hyaline paraphyses. *Asci* (16–)20–25(–26) × 4–6 μm ($\overline{x}$ = 21.4 × 4.9 μm, n = 30), 8-spored, unitunicate, sessile, cylindrical to clavate, rounded at both ends, or sometimes tractate at the apex, with a J- apical ring. *Ascospores* 4.5–6.0 × 1.5–2 μm ($\overline{x}$ = 4.8 × 1.8 μm, n = 30), 1–2-seriate, overlapping, sausage-shaped, oblong to elongate–allantoid, hyaline, aseptate, smooth-walled. Asexual morph: Not observed.

Materials examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 22 September 2020, X.G. Tian, c1-3)MFLU 23-0209(.

Known hosts and distribution – On *Eugenia aromatica* in Tanzania (Nutman & Roberts 1953); on clove trees in Brazil (Santos da Silva et al. 2020); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438852, ITS = OR438387

Notes – *Cytospora eugeniae* was previously introduced by Nutman & Roberts (1953) as *Valsa eugeniae*. Rossman et al. (2015) synonymized *Cytospora* instead of *Valsa* based on its priority. *Cytospora eugeniae* is characterized by perithecial stromata, globose to subglobose, glabrous ascomata with a long neck, 8-spored, unitunicate, cylindrical to clavate, rounded at both ends, sessile asci and sausage-shaped, hyaline and aseptate ascospores (Nutman & Roberts 1954). Our species fits well with the original description of *C. eugeniae*. Phylogenetic analyses showed that the new collection clustered with three strains of *C. eugeniae* with 100% ML and 1.00 PP support (Fig. 81). Thus, based on both phylogeny and morphology, we identified our new collection as *C. eugeniae*. Our new collection was collected on *Cocos nucifera* leaves from Thailand. This is the first record of *Cytospora eugeniae* on *Cocos nucifera* in Thailand.

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

Magnaporthaceae, *Ophioceraceae*, and *Pyriculariaceae* are listed in *Magnaporthales* by Maharachchikumbura et al. (2016) based on the literature and phylogenetic analyses. *Magnaporthales* comprises five families and 39 genera.

Magnaporthaceae P.F. Cannon

Magnaporthaceae was established by Cannon (1994). The classification of this family has been studied and revised by different authors since it was established (Lumbsch & Huhndorf 2007). Thongkantha et al. (2009) introduced *Magnaporthales* to accommodate *Magnaporthaceae* based on phylogenetic and morphological analyses and the placement of *Magnaporthaceae* was confirmed by Maharachchikumbura et al. (2016) and they accepted 22 genera in the family. Later, two new genera (*Aquafiliformis* and *Atripes*) were introduced to the family (Maharachchikumbura et al. 2016, Luo et al. 2019, Custódio et al. 2021). There are 24 genera accepted in *Magnaporthaceae* (Wijayawardene et al. 2022).

Nakataea Hara

Nakataea, the type genus of *Magnaporthaceae* was described by Hara (1939) to accommodate *N. oryzae*. Krause & Webster (1972) showed that *Nakataea oryzae* and *Magnaporthe salvinia* are the same species and they therefore synonymized *M. oryzae* under *N. oryzae*, which is the oldest name and has priority. Thus, *Nakataea* became the type genus of *Magnaporthaceae* (Klaubauf et al. 2014). Ma et al. (2014) introduced a new species (*N. setulose*) in the genus and provided the key to species of *Nakataea* with six accepted species (*N. curvularioides*, *N. fusispora*, *N. oryzae*, *N. rarissima*, *N. setulose*, and *N. serpens*). A new species *N. multiseptata* was

subsequently added to the genus (Ma et al. 2018). There are seven species accepted in the genus, of which only *N. oryzae* has sequence data available in the GenBank.

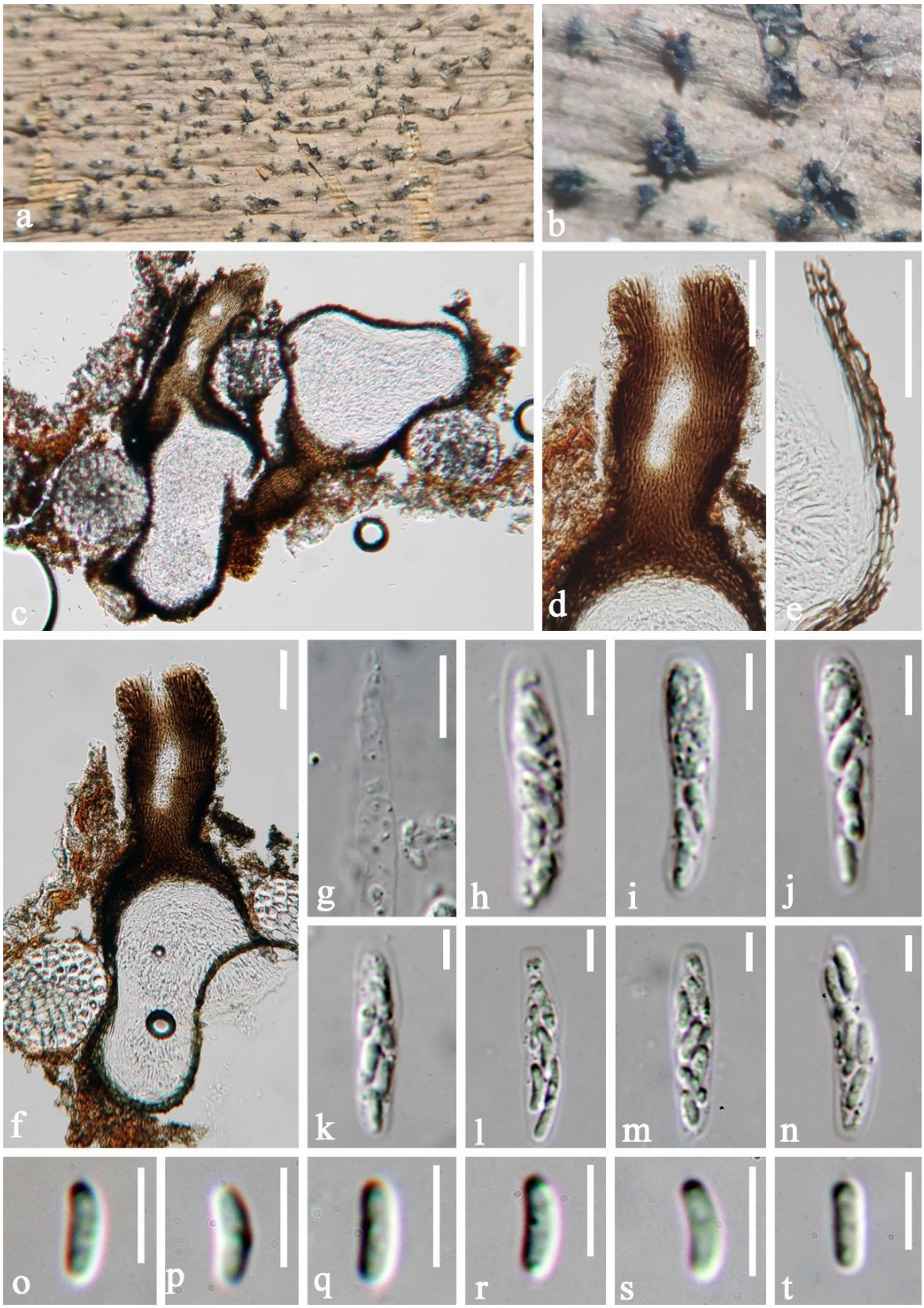

Figure 80 – *Cytospora eugeniae* (MFLU 23-0209, new host and geographical record). a, b Appearance of stromata on substrate. c, f Vertical section through stroma. d Ostiolar canal. e Peridium. g paraphyses. h–n Asci. o–t Ascospores. Scale bars: c = 100 µm, d–f = 50 µm, g, h = 10 µm, i–t = 5 µm.

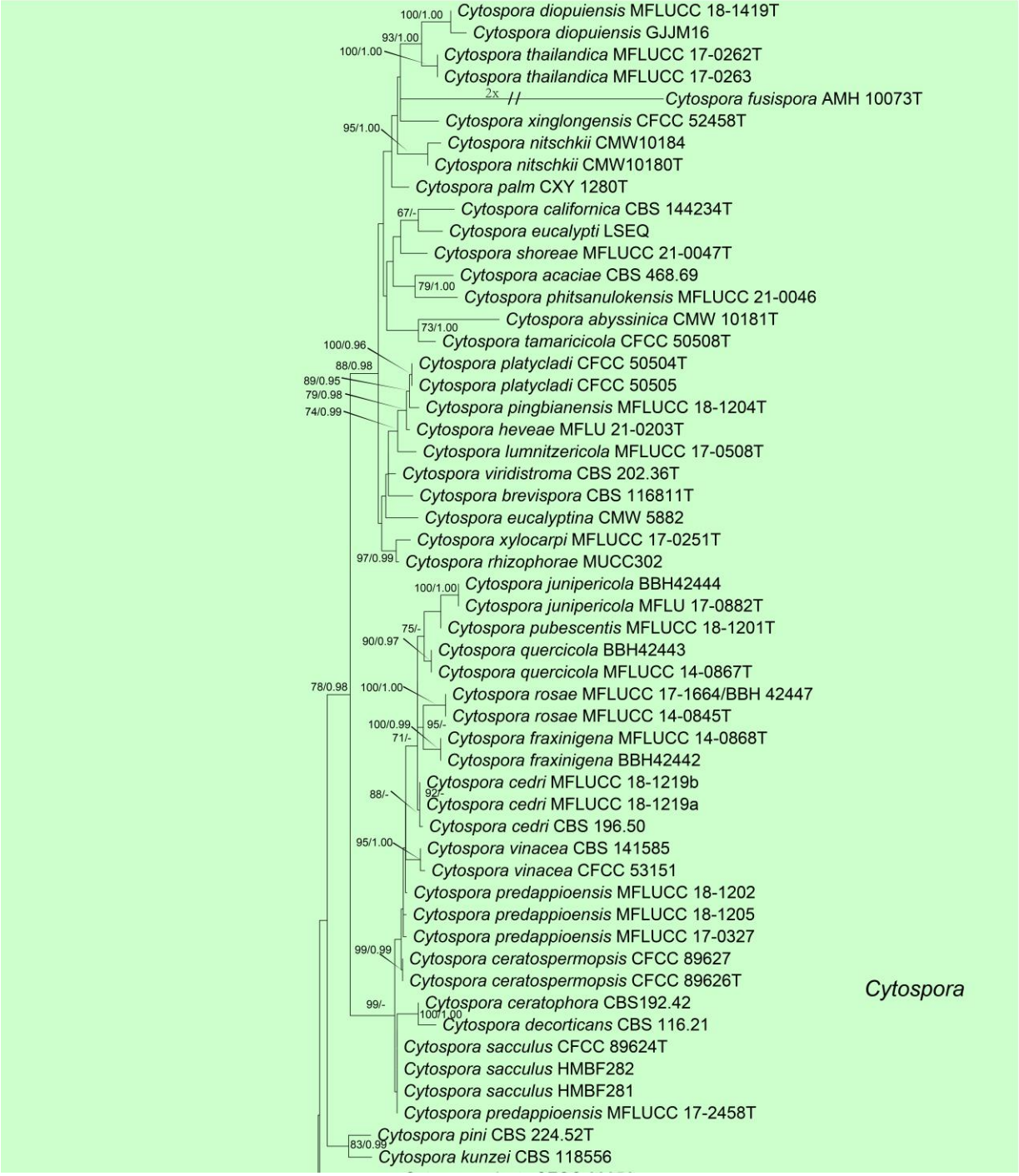

Figure 81 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and *rpb2* sequence data. Related sequences were obtained from Li et al. (2020b). One hundred and ninety strains are included in the combined sequence analysis, which comprises 2140 characters with gaps. *Diaporthe eres* (CBS 145040) was used as the outgroup taxon. The tree topology of the ML analysis was similar to the PP. The best-scoring RAxML tree with a final likelihood value of -22047.853428 is presented. The matrix had 861 distinct alignment patterns, with 37.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249559, C = 0.255131, G = 0.274010, T = 0.221300; substitution rates AC = 1.603244, AG = 5.620105, AT = 1.771775, CG = 1.469760, CT = 12.491374, GT = 1.000000; gamma distribution shape parameter α = 0.189811. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly record sequences are in red, while T indicates holotype or ex-type strains.

Figure 81 – Continued.

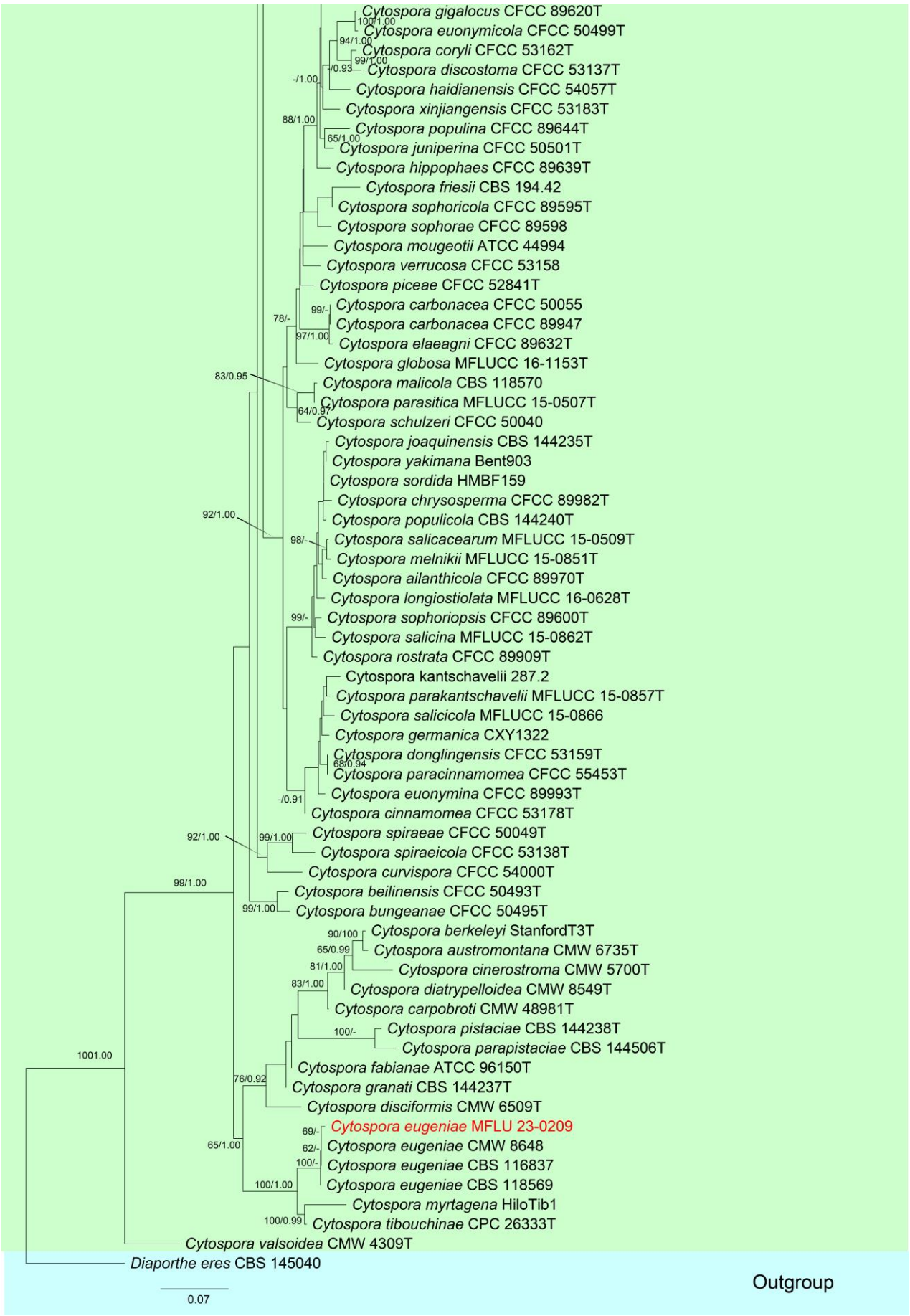

Figure 81 – Continued.

Nakataea is characterized by macronematous, mononematous, unbranched or rarely branched, brown conidiophores, polyblastic, integrated, terminal becoming intercalary, sympodial, conidiogenous cells that are sometimes geniculate, denticulate and acropleurogenous, alcate, often sigmoid, 3-septate conidia with hyaline or very pale brown end cells and pale to mid-pale brown intermediate cells (Hara 1939, Krause & Webster 1972, Ma et al. 2018). In this study, *Nakataea oryzae* was collected on decaying leaves of *Oryza sativa* from Thailand, and it is a new record from Thailand.

47. *Nakataea oryzae* (Catt.) J. Luo & N. Zhang, Mycologia 105(4): 1025 (2013) Fig 82

≡ *Sclerotium oryzae* Catt., Arch. Triennale Lab. Bot. Crittog. 1:10 (1877)

= *Nakataea sigmoidea* (Cavara) Hara, Diseases Rice Plant, 2:185 (1939)

≡ *Helminthosporium sigmoideum* Cavara, Mat. Lomb.:15 (1889)

= *Magnaporthe salvinii* (Catt.) R.A. Krause & R.K. Webster, Mycologia 64: 110 (1972)

≡ *Leptosphaeria salvinii* Catt., Arch. Labor. Bot. Critt. Univ. Pavia 2, 3:115–128 (1879)

Index Fungorum number: IF802971; Facesoffungi number: FoF01103

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: not overserved. Asexual morph: *Colonies* effuse, brown to dark brown, hairy on natural substrate. *Mycelium* partly superficial, partly immersed, composed of pale brown, smooth, septate, branched hyphae. *Conidiophores* 90–160 × 4–6.5 µm ($\overline{x}$ = 125 × 6 µm, n = 10), macronematous, mononematous, solitary, erect, unbranched or sparsely branched, straight or curved, cylindrical, brown, smooth, multiseptate, thick-walled. *Conidiogenous cells* 15–30 × 3.5–5 µm ($\overline{x}$ = 20 × 5 µm, n = 8), polyblastic, sympodial, integrated, terminal or intercalary, pale brown, smooth, with 0–1 hyaline, unthickened denticles. *Conidia* 60–70 × 10–20 µm ($\overline{x}$ = 65 × 15 µm, n = 15), solitary, acropleurogenous, falcate, curved, smooth and thick-walled, 3-septate, acute at the ends, subhyaline to pale brown at ends cells, brown at central cells.

Culture characteristics – Conidia germinating on PDA within 12 h at 25 °C. Colonies on PDA, reaching 50 mm diam. after 14 days, with white aerial mycelium that diffused into the medium and reverse brown.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on decaying leaves of *Oryza sativa*, 23 October 2020, X.G. Tian, R4-9 (MFLU 23-0210), living culture, MFLUCC 23-0128.

Known hosts and distribution – On rice (*Oryza sativa*) in Italy (Cattaneo 1876); on *Oryza sativa* in Japan (Luo & Zhang 2013); from diseased rice in the United States, Japan, and India (Tullis 1933); on rice in California (Krause & Webster 1972); on decaying leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – ITS = OR438388, *tef1-α* = OR500336, *rpb1* = OR553096

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0128) clustered with *Nakataea oryzae* (CBS 288.52 and CBS 252.34) (Fig. 83). Morphologically, our strain resembles *N. oryzae* in having unbranched or sparsely branched, brown, smooth, septate conidiophores, with terminal, pale brown, smooth conidiogenous cells and falcate, curved, unequally colored, 3-septate conidia with similar size. The nucleotide comparisons showed that our strain (MFLUCC 23-0128) is not significantly different from *N. oryzae* (CBS 288.52 and CBS 252.34) in ITS and *rpb1* sequence data. Thus, we identified our strains as *N. oryzae* based on phylogenetic analyses and morphological characters.

Nakataea oryzae seems host specificity with rice as this species only reported from rice (Cattaneo 1876, Tullis 1933, Krause & Webster 1972, Luo & Zhang 2013). In this study, our new isolate was also collected from rice, which we report as a new geographical record in Thailand.

Myrmecridiales Crous

Myrmecridiales is a monotypic order in *Diaporthomycetidae*. The order was introduced by Crous et al. (2015b) with a single family which comprises two genera, *Myrmecridium* and *Neomyrmecridium* (Crous et al. 2018a, Hyde et al. 2020b).

Figure 82 – *Nakataea oryzae* (MFLU 23-0210, new geographical record). a, b Colonies on decaying leaves of *Oryza sativa*. c, e Conidiophores. d Conidiophores with conidia. f–k Conidia. l Germinated conidium. m, n Colonies on PDA from surface and reverse. Scale bars: c–e, l = 50 μm, f–k = 20 μm.

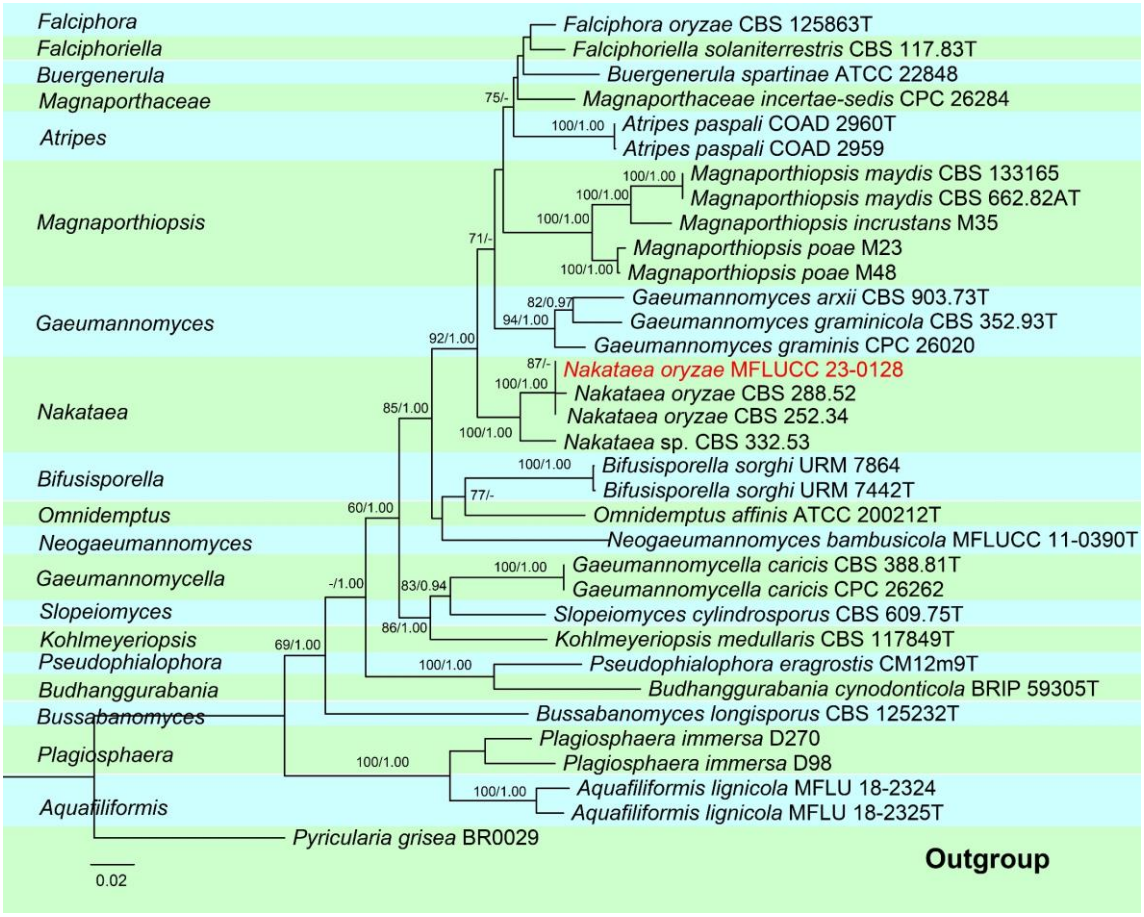

Figure 83 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb1*, and *tef1-α* sequence data. Related sequences were obtained from Custódio et al. (2021). Three-four strains are included in the combined sequence analysis, which comprises 3174 characters with gaps. *Pyricularia grisea* (BR0029) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -17110.659828 is presented. The matrix had 1050 distinct alignment patterns, with 34.86% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241064, C = 0.278976, G = 0.283958, T = 0.196002; substitution rates AC = 1.344009, AG = 2.737883, AT = 1.531523, CG = 1.233490, CT = 5.708993, GT = 1.000000; gamma distribution shape parameter α = 0.181511. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Myrmecridiaceae Crous

Myrmecridiaceae was established by Crous et al. (2015b) with *Myrmecridium* as the type genus. *Neomyrmecridium* was subsequently introduced to the family (Crous et al. 2018a). Species in this family are reported on a wide range of plant substrates from aquatic and terrestrial habitats, a few species have been reported in soil, house dust or associated with humans (Arzanlou et al. 2007, Peintner et al. 2016, Crous et al. 2018a, Hyde et al. 2020b).

Myrmecridium Arzanlou

Myrmecridium, is a well-studied genus, which was described by Arzanlou et al. (2007) with *M. schulzeri* as the type species. *Myrmecridium* was previously placed in *Sordariomycetes* genera *incertae sedis*. Crous et al. (2015b) showed that *Myrmecridium* formed a monophyletic clade within *Sordariomycetes*. Hence, *Myrmecridiales* and *Myrmecridiaceae* were introduced to accommodate *Myrmecridium* species.

Myrmecridium is characterized by the production of obovoid or fusiform conidia, tapering towards a narrowly truncate base, hyaline mycelium with pale to unpigmented, and pimple-like denticles. Species in the genus are widely distributed and commonly isolated from soil and plant tissues (Arzanlou et al. 2007, Peintner et al. 2016, Réblová et al. 2016a, Hyde et al. 2020b). This study introduces a new species *Myrmecridium yunnanense*, with detailed description and illustration with phylogenetic support.

48. ***Myrmecridium yunnanense*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 84

Index Fungorum number: IF900983; Facesoffungi number: FoF14363

Etymology – Referring to the location where the specimen was collected, Yunnan Province, China.

Holotype – GZAAS 23-0586

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Colonies* superficial, effuse, hairy, brown to dark brown, with immersed mycelium. *Conidiophores* 70−105 × 4−5 μm ($\overline{x}$ = 89 × 4.5 μm, n = 15), macronematous, mononematous, erect, unbranched, multi-septate, straight or slightly flexuous, cylindrical, percurrently proliferating, dark brown below, paler brown to subhyaline towards the apex, smooth. *Conidiogenous cells* holoblastic, polyblastic, sympodial, integrated, terminal, subhyaline to pale brown, 30−40 × 3.5−4 μm ($\overline{x}$ = 34 × 3.5 μm, n = 12). *Conidia* 4.5−6.5 × 2.5−3.5 μm ($\overline{x}$ = 5.5 × 3 μm, n = 10), solitary, acrogenous, aseptate, obovoid or fusiform, tapering towards the ends, pointed at the base, obtuse at the apex, subhyaline to pale brown, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h at room temperature. Colonies circular, flat, spreading, with sparse to moderate aerial mycelium, cultures white to yellow edge and dark the centre of the colony in reverse and surface.

Material examined – China, Yunnan Province, Xishuangbanna City, on dead leaves of *Cocos nucifera*, 17 September 2021, X.G. Tian, c8-4 (GZAAS 23-0586 holotype), ex-type living culture GZCC 23-0580.

GenBank numbers – GZAAS 23-0586: LSU = OR438853, ITS = OR438389. GZCC 23-0580: LSU = OR438854, ITS = OR438390

Notes – In the multi-loci phylogenetic analyses, our strains *Myrmecridium yunnanense* (GZAAS 23-0586 and GZCC 23-0580) formed a separate branch within *Myrmecridium*. *Myrmecridium yunnanense* is phylogenetically close to *M. juncicola* and *M. sambuci* (Fig. 85). Morphologically, *M. yunnanense* is similar to *M. juncicola* and *M. sambuci* in having macronematous, mononematous, erect, unbranched, multi-septate conidiophores polyblastic, sympodial, integrated conidiogenous cells and acrogenous, obovoid or fusiform conidia. However, *M. yunnanense* can be easily distinguished from *M. juncicola* and *M. sambuci* in having conidia without a mucoid sheath. Whereas, conidia of *M. juncicola* and *M. sambuci* with a mucoid sheath surrounding the median region. In addition, conidia of *M. yunnanense* are much shorter (4.5−6.5 μm vs. 14–16 μm) and with less septa (0 vs. 0–1) than those of *M. juncicola* (Crous et al. 2021). *Myrmecridium yunnanense* is different from *M. sambuci* in having shorter (4.5−6.5 μm vs. (7–)8–9(–10) μm), fusiform conidia that are tapering towards the ends, pointed at the base and obtuse at the apex. While, conidia of *M. sambuci* are ellipsoid to fusoid with rounded apex (Crous et al. 2021). The comparison of the nucleotide of ITS gene regions between *M. yunnanense* and *M. sambuci* revealed 12bp differences. The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 1) (Fig. 86). Thus, we introduced our strain as a new species based on phylogeny and morphology.

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

Glomerellales Chadef. ex Réblová, W. Gams & Seifert

Chadefaud (1960) introduced *Glomerellales* with *Colletotrichum* as the type and three other genera in a non-ranked group “Eu-Glomérellales”, but it was not validly published. There are five families and 32 genera in this order (Maharachchikumbura et al. 2016, Wijayawardene et al. 2022).

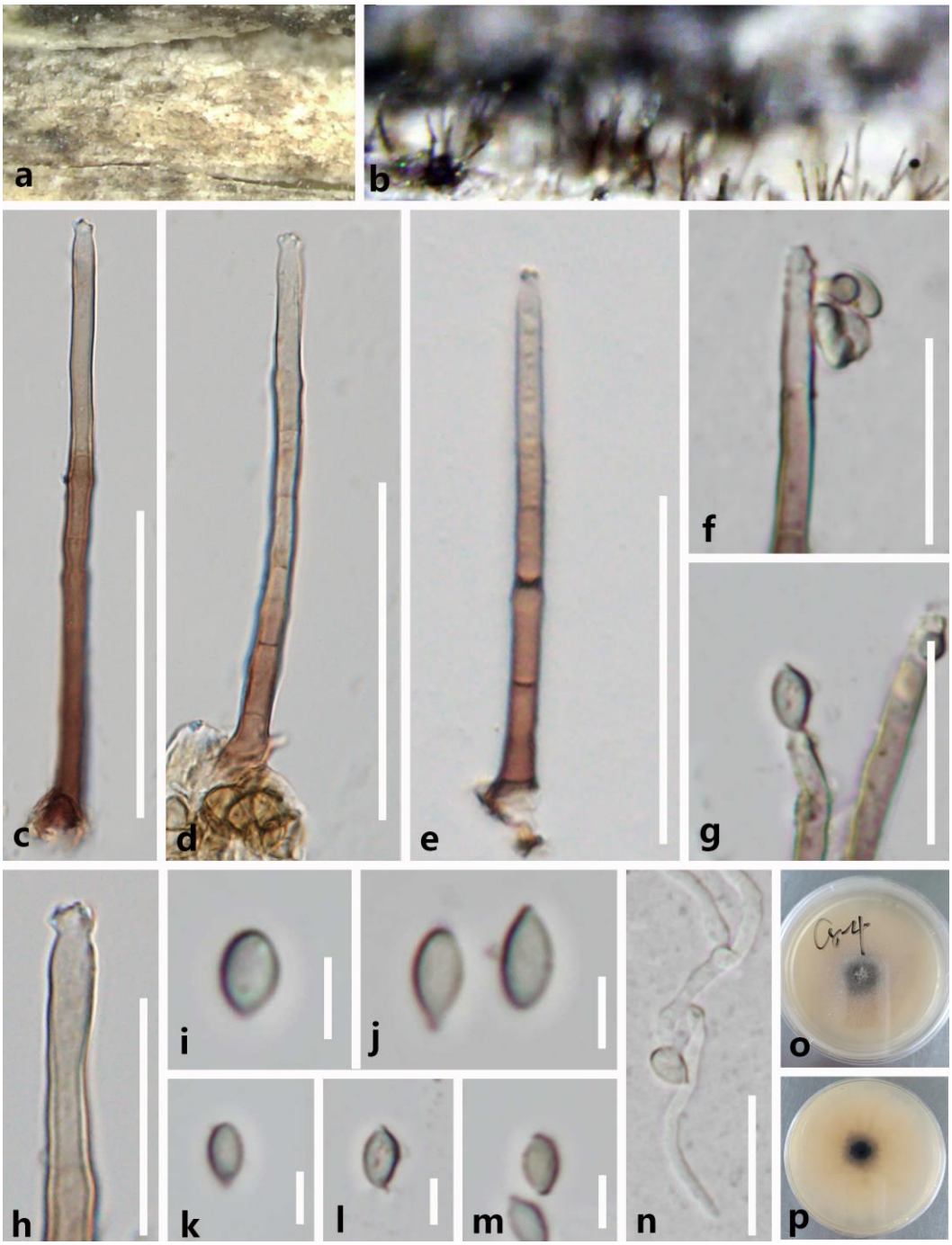

Figure 84 – *Myrmecridium yunnanense* (GZAAS 23-0586, holotype). a, b Colonies on dead leaves of *Cocos nucifera*. c–e Conidiophores. f, g Conidiogenous cells with attached conidium. h Conidiogenous cells. i–m Conidia. n Germinated conidium. o, p Colonies on PDA from surface and reverse. Scale bars: c–d = 50 μm, f–h, n = 20 μm, i–m = 5 μm.

Plectosphaerellaceae W. Gams, Summerbell & Zare

Plectosphaerellaceae was introduced by Zare et al. (2007) based on the plant pathogen *Plectosphaerella cucumerina* as the type species. Twenty-four genera are accepted in the family (Wijayawardene et al. 2022). The sexual morph of *Plectosphaerellaceae* is characterized by perithecial or cleistothecial, brown to dark brown ascomata, with paler and elongate neck, multi-layered, with textura angularis peridium, conspicuous in young stages or absent paraphyses, unitunicate asci and ellipsoidal or ovoid, 1- or 2-celled ascospores (Zare et al. 2007, Maharachchikumbura et al. 2016, Giraldo & Crous 2019). The asexual morph of *Plectosphaerellaceae* is characterized by synnematous, sporodochial or acervular conidiomata,

simple or branched conidiophores, mono- or polyphialidic conidiogenous cells and arranged in slimy heads or chains conidia (Zare et al. 2007, Maharachchikumbura et al. 2016, Giraldo & Crous 2019). Several asexual morph genera in this family have verticillate conidiophores, such as *Acrostalagmus* and *Verticillium* (Hyde et al. 2019).

The habitats of *Plectosphaerellaceae* are very diverse, it has been reported as pathogens on many plants (legumes, banana, cucurbits, potatoes and others) and animals (fish and shrimp) (Duc et al. 2009, Cannon et al. 2012, Hyde et al. 2014), as saprobes on soil-borne and plant debris (Zare et al. 2007), and also can be found on human (human nails and sputum) (Giraldo et al. 2017).

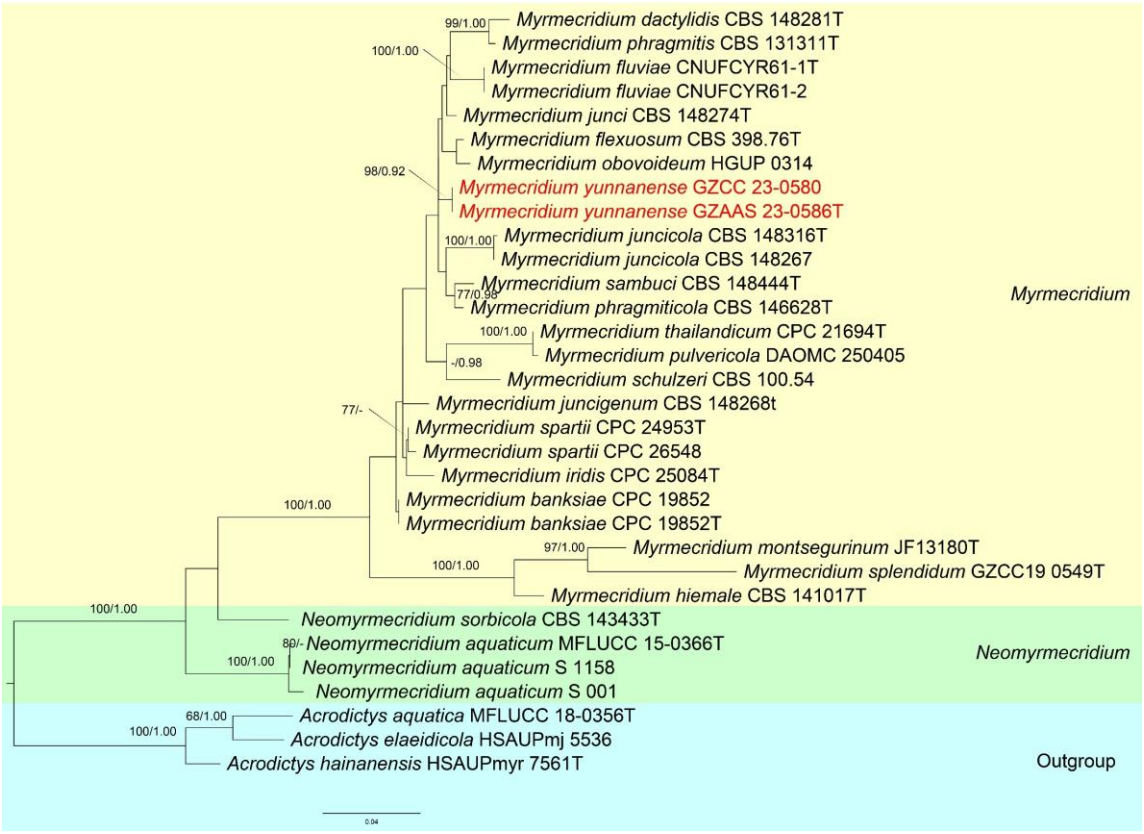

Figure 85 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Luo et al. (2019). Thirty-two strains are included in the combined sequence analysis, which comprises 1438 characters with gaps. *Acrodictys aquatica* (MFLUCC 18-0356), *A. elaeidicola* (HSAUPmj 5536) and *A. hainanensis* (HSAUPmyr 7561) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -5890.484640 is presented. The matrix had 450 distinct alignment patterns, with 24.01% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243458, C = 0.251466, G = 0.288043, T = 0.217034; substitution rates AC = 1.832354, AG = 1.991650, AT = 1.684266, CG = 0.689101, CT = 6.041964, GT = 1.000000; gamma distribution shape parameter α = 0.186243. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Acrostalagmus Corda

Acrostalagmus was described by Corda (1838) with the type species *A. cinnabarinus*. The species of *Acrostalagmus* are characterized by verticillate conidiophores, with hyaline, egg-shaped conidia formed singly (Rasoul et al. 2004). Members of *Acrostalagmus* are found in saffron soil, vermicompost, and branches of cacao and a few species are reported as fungicolous fungi (Rubini et al. 2005, Mohammadi & Amini 2015). They are also known for their ability to produce a variety of secondary metabolites (Nguyen et al. 2019). To date, 58 epithets belonging to this genus are

recorded in Index Fungorum (2023). In this study, we recollected *Acrostalagmus annulatus* from the dead leaves of *Ananas comosus* in Thailand.

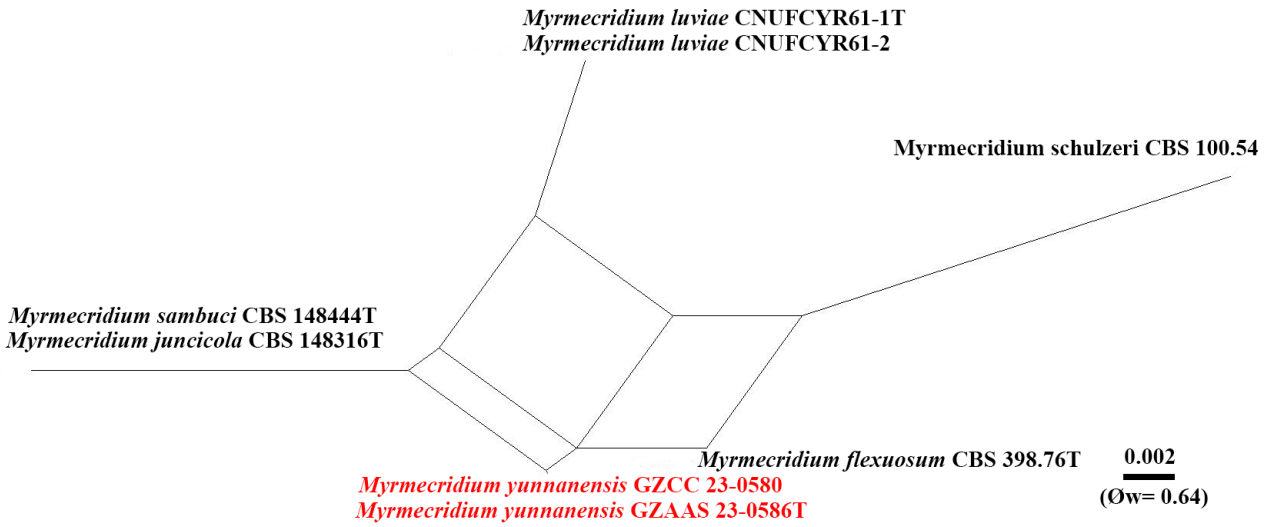

Figure 86 – Results of the PHI test of *Myrmecridium yunnanense* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

49. *Acrostalagmus annulatus* (Berk. & Broome) Seifert, in Réblová et al., Stud. Mycol. 68: 186 (2011) Fig. 87

Index Fungorum number: IF518663; Facesoffungi number: FoF14302

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Synnemata* scattered, gregarious or caespitose, forming rounded pale reddish-brown slimy heads, oval. *Conidiophores* erect, septate, repeatedly branched, hyaline to pale reddish brown. *Conidiogenous cells* phialidic, 10–20 × 2–2.5 µm ($\bar{x}$ = 16 × 2 µm, n = 10), lateral and terminal, light yellow to reddish brown, hemispherical, narrowly flask-shaped in the widest part, arising in whorls at several levels along the main stipe and its branches. *Conidia* 5–6 × 2.5–3 µm ($\bar{x}$ = 5.5 × 3 µm, n = 50), sub-globose to cylindrical, oblong-ellipsoidal, smooth-walled, single-celled, hyaline.

Culture characters – Colonies on PDA reaching 20 mm in 7 days at 28°C, flat with lobate margin, aerial mycelium low, felty, arachnoid near inoculum, with white to pink powder areas on the surface, reverse yellow to light brown.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 3 October 2020, X.G. Tian, p11-1 (MFLU 23-0211).

Known hosts and distribution – Saprophytic on wood, bark, leaves and fruits, herbaceous stems, occasionally on boletes; occasionally isolated from soil; recorded from Apiaceae (*Pastinaca sativa*), Arecaceae (*Cocos* sp, *Elaeis guineensis*), Brassicaceae (*Brassica* sp.), Bromeliaceae (*Ananas comosus*), Gnetaceae (*Gnetum gnemon*), Leguminaceae (*Glycine max*), Malvaceae (*Gossypin* sp., Manihotutilissima), Moraceae (*Ficus elastica*), Musaceae (*Musa* sp.), Sterculiaceae (*Theobroma cacao*), and from North America (Arizona, Louisiana, Ontario), Central America (Costa Rica, Mexico). West Indies (Cuba), South America (Peru, Surinam, Venezuela). Africa (Sierra Leone), SE Asia (Japan, MalayaNew Guinea), Europe (Netherlands, Czechoslovakia), Thailand (Chiang Mai) (Seifert 1985, Réblová et al. 2011, Hyde et al. 2019); on dead leaves of *Ananas comosus* in Thailand (this study).

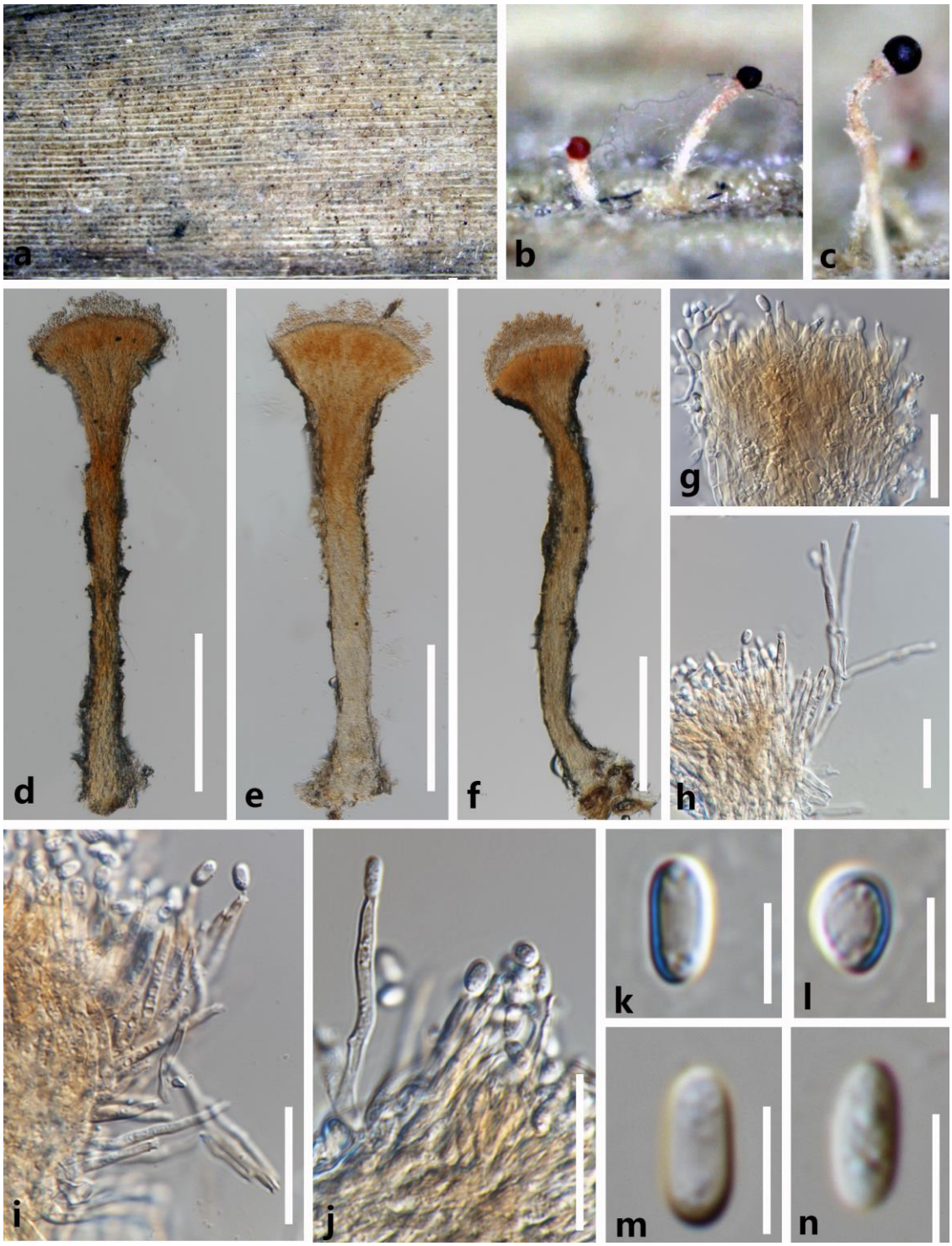

Figure 87 – *Acrostalagmus annulatus* (MFLU 23-0211). a–c Synnemata on natural substrate. d–f Conidiophore with conidia. g–j Conidiogenus cells with conidia. k–n Conidia. Scale bars: g–f = 200 µm, g–j = 20 µm, k–n = 5 µm.

GenBank numbers – LSU = OR438855, ITS = OR438391

Notes – In our phylogenetic analysis, our new isolate clustered with *Acrostalagmus annulatus* strains (Fig. 88). The morphological characteristics of our new isolate fits well with *A. annulatus* by having erect conidiophore, phialidic and hemispherical conidiogenous cells and oblong-ellipsoidal conidia accumulate in slime (Seifert 1985, Hyde et al. 2019). ITS and LSU sequence data blast results also showed that our strain is 100% similar to *A. annulatus* (MT138627, GU180646, respectively). *Acrostalagmus annulatus* have been reported from the host *Ananas comosus* (Seifert

1985) and from Thailand (Hyde et al. 2019). Therefore, based on morphology and phylogenetic analysis, we identified our new collection as *A. annulatus*, which was recollected on *Ananas comosus* from Thailand.

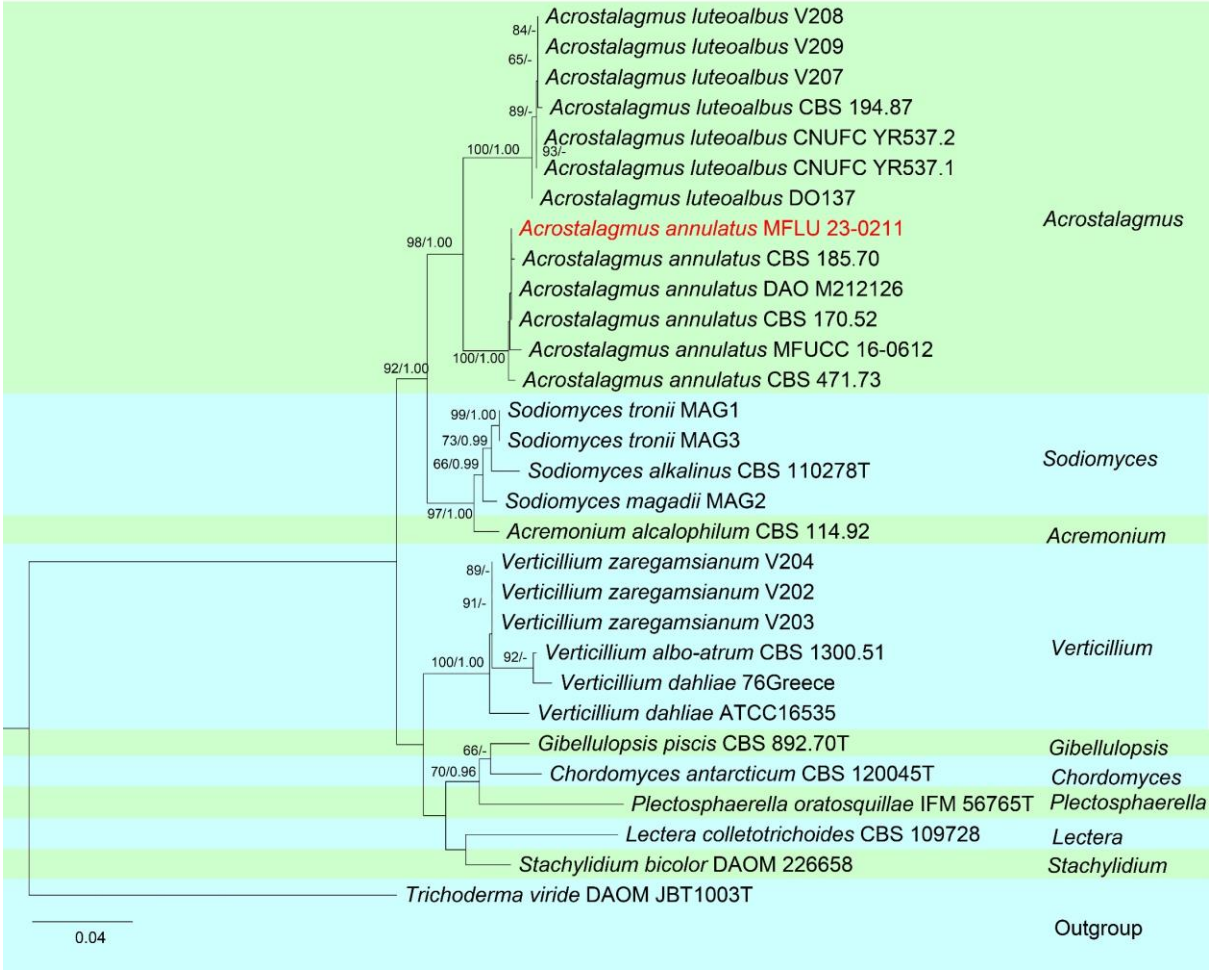

Figure 88 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Hyde et al. (2019). Thirty strains are included in the combined sequence analysis, which comprises 2596 characters with gaps. *Trichoderma viride* (DAOMJBT 1003) was used as the outgroup taxon. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -7700.483345 is presented. The matrix had 488 distinct alignment patterns, with 44.73%% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.231597, C = 0.256100, G = 0.295087, T = 0.217217; substitution rates AC = 0.879178, AG = 2.234799, AT = 2.440336, CG = 0.498165, CT = 5.753401, GT = 1.000000; gamma distribution shape parameter α = 0.178607. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Hypocreales Lindau

Lindau (1897) introduced *Hypocreales* and we follow the updated accounts of *Hypocreales* in Perera et al. (2023). The order comprises 18 families and 320 genera based on morphology and molecular data (Wijayawardene et al. 2022).

Bionectriaceae Samuels & Rossman

Bionectriaceae was introduced by Rossman et al. (1999) with *Clonostachys* as the type and accepted 26 genera, including five cleistothecial genera (Rossman et al. 1999). In subsequent

studies, Maharachchikumbura et al. (2015, 2016) accepted 39 genera and Wijayawardene et al. (2022) accepted 47 genera. The recent treatment of *Bionectriaceae* was provided by Perera et al. (2023) with accepted 41 genera. *Bionectriaceae* species mostly occur in terrestrial or freshwater habitats but less in marine habitats as coprophilous, corticolous, fungicolous, herbicolous or lichenicolous taxa (Hyde et al. 2020b). Wijayawardene et al. (2022) listed 47 genera in the family.

Clonostachys Corda

Clonostachys was introduced by Corda (1839) and typified by *Clonostachys araucaria*. *Clonostachys* is typically characterized by an asexual morph with a distinctive penicillate, frequently sporodochial conidiophores, while the sexual morph is mainly characterized by white, yellow to orange or brown, usually crowded and roughened ascomata (Rossman et al. 1999, 2013, Schroers 2001, Lechat et al. 2020, Torcato et al. 2020). The sexual morph of *Clonostachys* was linked to *Bionectria* which was segregated into six subgenera *viz. Astromata*, *Bionectria*, *Epiphloea*, *Myronectria*, *Uniparietina*, and *Zebrinella* (Schroers 2001). Recently, Zhao et al. (2023) revised *Clonostachys* and their phylogenetic analysis supported the subgenera *Astromata*, *Bionectria*, *Myronectria* and *Zebrinella* within *Clonostachys*. While, the former subgenera *Epiphloea* and *Uniparietina* were transferred to *Sesquicillium* which is a sister genus of *Clonostachys*, as well as 19 new species were added to the genus (Zhao et al. 2023). The species of *Clonostachys* are commonly isolated in soils, as well as in plants as endophytes, epiphytes or saprotrophs, and some have even been reported as mycoparasites of nematodes and insects (Schroers et al. 2001, Moreira et al. 2016, Zhang et al. 2008, Torcato et al. 2020). In this study, a new host record *C. eriocamporesii* is described.

50. *Clonostachys eriocamporesii* R.H. Perera & K.D. Hyde, in Hyde et al., Fungal Divers. 100: 199 (2020) Fig. 89

Index Fungorum number: IF556897; Facesoffungi number: FoF06964

Saprobic on leaves of *Ananas comosus*. Sexual morph: *Ascomata* 87–148 µm diam., solitary to gregarious, superficial, globose, strongly warted, orange to bright orange. *Peridium* 24–49 µm thick, of two regions; outer region 5–25 µm thick, composed of subglobose to ellipsoidal cells 1–8 × 0.5–2 µm, with pale yellow walls 1–2.5 µm thick, containing numerous pale orange oily droplets; inner region 3–8 µm thick composed of subglobose to elongate cells 1–8 × 0.5–3.5 µm with hyaline wall 1.5–2 µm thick. *Paraphyses* 4–11 µm wide ($\overline{x}$ = 7.20 µm, n = 20), moniliform, interspersed between the asci. *Asci* evanescent, unitunicate, cylindrical to clavate, short-stipitate 40–50 × 7–9 µm ($\overline{x}$ = 42.5 × 8 µm, n = 25), with 8 ascospores biseriate or irregularly disposed in upper part and uniseriate in lower part, with J- apical ring. *Ascospores* 9–12 × 3.5–4 µm ($\overline{x}$ = 10.5 × 4 µm, n = 50), fusiform, acute at ends, equally 1–2-septate, hyaline, smooth to faintly verrucose. Asexual morph: Not observed.

Culture Characters – Ascospores germinating on PDA within 24 hours. Colonies growing on PDA, reaching up to 55 mm in 30 days at 25 °C, flat, initially white, aerial mycelium forming concentric rings with cottony texture, margin undulate, white, reverse white to light yellow.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 23 June 2021, X.G. Tian, P3-30 (MFLU 23-0212), living culture MFLUCC 23-0134.

Known hosts and distribution – On *Pennisetum polystachion* in Thailand (Hyde et al. 2020b); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438392, *tub*2 = OR538083

Notes – In the phylogenetic analyses, our new collection is phylogenetically closely related to *Clonostachys eriocamporesii* with 82% ML bootstrap support value (Fig. 90). Morphologically, our strain shares similar morphology with *C. eriocamporesii* (MFLUCC 19-0486) in having perithecial, superficial, solitary to gregarious, globose to subglobose ascomata, unitunicate, cylindrical to narrowly clavate, short pedicellate, apical ring J asci, and 1–2-seriate, hyaline, ellipsoidal ascospores. The nucleotide comparisons showed that our strain (MFLUCC 23-0134) is not significantly different from *C. eriocamporesii* (MFLUCC 19-0486) in ITS. Our strain *Clonostachys*

eriocamporesii (MFLUCC 23-0134) is herein introduced as a new host record on *Ananas comosus* in Thailand.

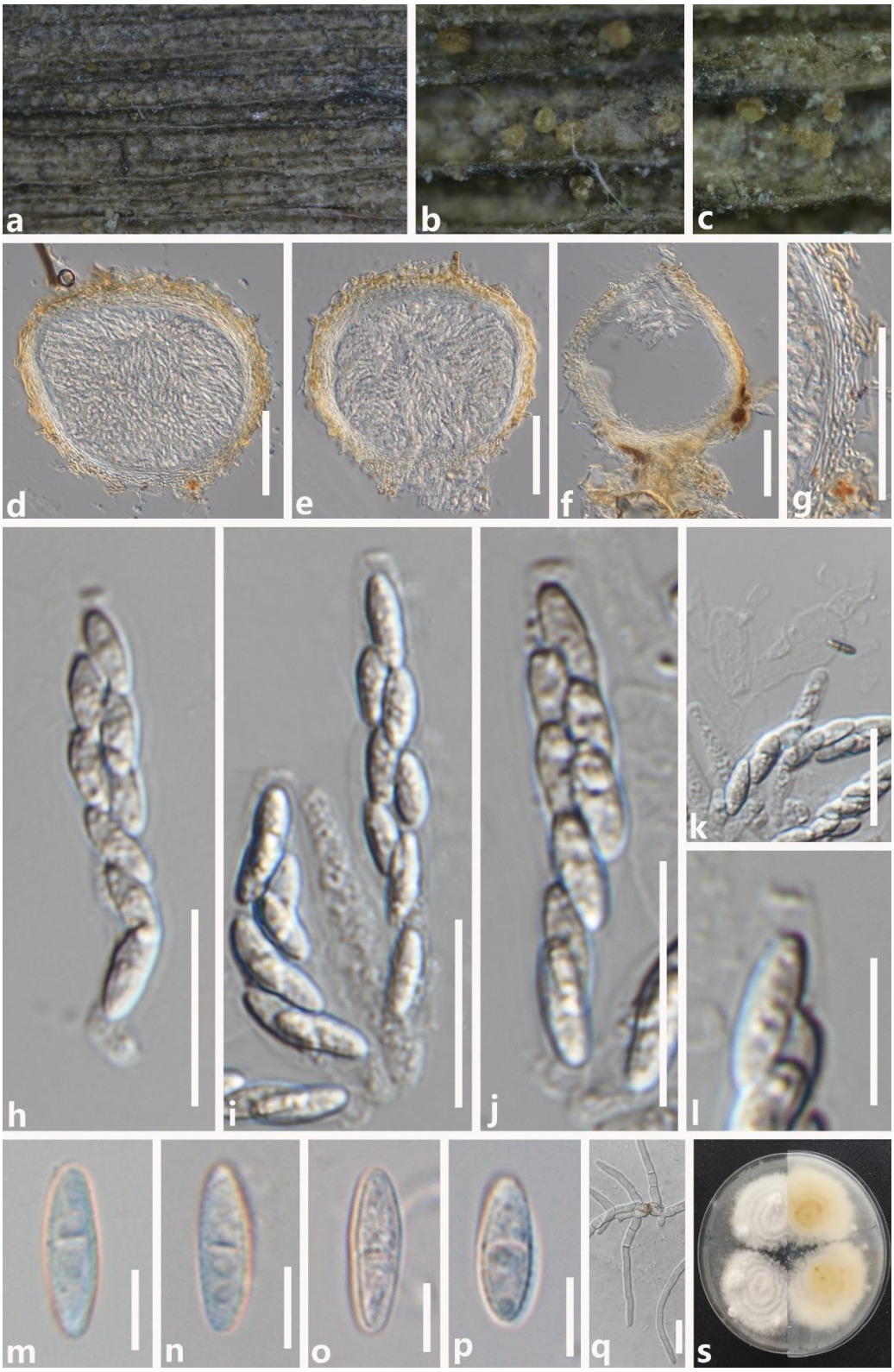

Figure 89 – *Clonostachys eriocamporesii* (MFLU 23-0212, new host record). a–c Ascomata on dead leaves of *Ananas comosus*. d–f Vertical section through an ascoma and basal stroma. g Ascomatal wall in vertical section. h–j Asci and ascospores. k Paraphyses and asci. l Ring at the ascus apex. m–p Ascospores. q Germinated ascospore. s Colonies on PDA from surface and reverse. Scale bars: d–g = 50 µm, h–k, q = 20 µm, l = 10 µm, m–p = 5 µm.

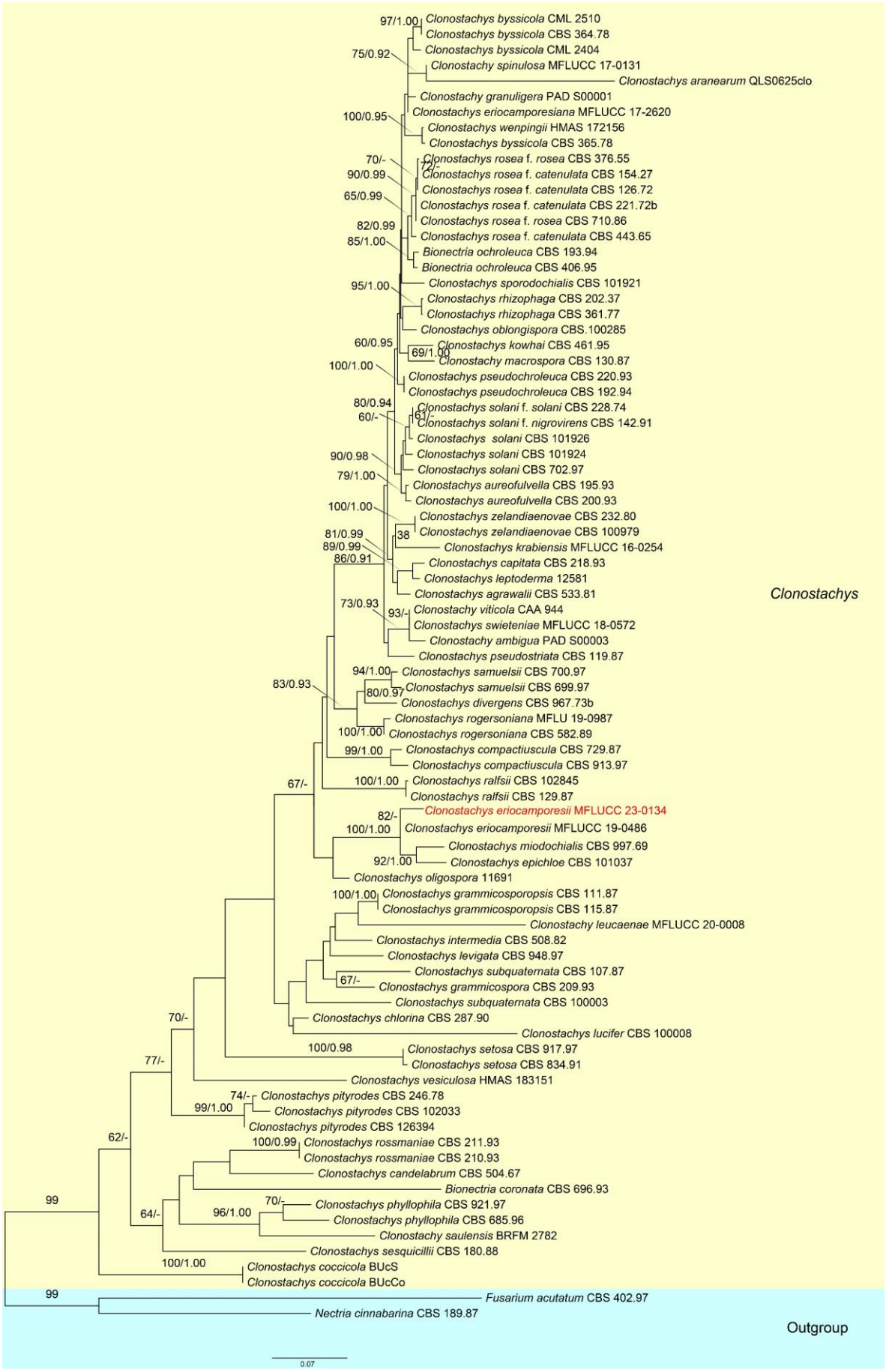

Figure 90 – Phylogram generated from maximum likelihood analysis based on combined ITS and *tub2* sequence data. Related sequences were obtained from Perera et al. (2020). Eighty-five strains

are included in the combined sequence analysis, which comprises 1179 characters with gaps. *Fusarium acutatum* (CBS 402.97) and *Nectria cinnabarina* (CBS 189.87) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best-scoring RAxML tree with a final likelihood value of -13270.758460 is presented. The matrix had 668 distinct alignment patterns, with 28.71% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.215864, C = 0.279726, G = 0.249843, T = 0.254567; substitution rates AC = 1.092316, AG = 3.072508, AT = 1.166932, CG = 0.690706, CT = 3.751630, GT = 1.000000; gamma distribution shape parameter α = 0.275747. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Ochronectria Rossman & Samuels

Ochronectria was introduced by Rossman et al. (1999) based on *Ochronectria calami*. This genus is characterized by subglobose to globose ascomata, that are cupulate when dry, three-layered peridium, clavate asci and fusiform ascospores with guttules (Rossman et al. 1999, Lechat 2010). Lechat (2010) introduced the second species *O. courtecuissei* based on morphological characters. Subsequently, a new species *O. thailandica* was added to the genus (Li et al. 2016b). Three species are accepted in the genus, of which only *O. calami* and *O. thailandica* have sequence data available in GenBank. In this study, we introduce a new record *O. thailandica* for this genus.

51. *Ochronectria thailandica* Q.J. Shang & K.D. Hyde, Fungal Divers. 78, 1–237 (2016)

Fig. 91

Index Fungorum number: IF551918; Facesoffungi number: FoF01815

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Ascomata* 140–190 × 90–150 μm ($\overline{x}$ = 165 × 119 μm, n = 10), solitary to gregarious, superficial, black, globose to subglobose or collapsing laterally when dry, unilocular, thick-walled, glabrous. *Ostioles* brown to dark brown, with paraphyses. *Peridium* 20–40 μm wide, composed of three layers, inner 1–3 layers, comprising of hyaline, thin-walled, elongated cells, central 3–4 layers of yellow to brown cells arranged in a textura angularis, outer 5–6 layers, comprising dark brown to black, thick-walled cells of textura angularis to globose, having yellow oily droplets between the cells. *Hamathecium* not observed. *Asci* 25–35 × 6–7 μm ($\overline{x}$ = 30 × 7 μm, n = 10), 8-spored, unitunicate, clavate, with short pedicel, slightly rounded at the apex. *Ascospores* 10–15 × 3–4 μm ($\overline{x}$ = 13 × 3.5 μm, n = 30), fusiform, overlapping 2-seriate, 1-septate, slightly constricted at the septa, hyaline, straight to curved, guttulate, smooth and thick-walled. Asexual morph: Not observed.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, c6-9 (MFLU 23-0213), living culture MFLUCC 23-0156.

Known hosts and distribution – On unidentified wood in the water in Thailand (Li et al. 2016b); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438856, ITS = OR438393, SSU = OR458361

Notes – *Ochronectria thailandica* was introduced by Li et al. (2016), their phylogenetic analysis showed that *O. thailandica* is phylogenetically closely related to *O. calami*, which may be because of *O. thailandica* lacks protein coding genes, only LSU and ITS sequence data available for *O. thailandica*. While *O. calami* has LSU, *rpb1*, *rpb2* and *tef1-α* sequence data in GenBank. Therefore, they could not be distinguished from each other based on sequence data properly, and our phylogenetic analysis showed a similar result to Li et al. (2016). However, morphologically *O. thailandica* can be easily distinguished from *O. calami* by the size and colour of ascomata, peridium colour and number of ascospores septa (Li et al. 2016).

In the phylogenetic analyses, our new collection formed a sister lineage with *O. calami* and *O. thailandica* with 99% ML support (Fig. 92). Our isolate has black ascomata, a peridium composed of black brown outer layers, yellow middle layers, and hyaline inner layers, clavate asci and fusiform ascospores with guttulate, which are similar to the holotype *O. thailandica* (MFLU 16-0030). However, our isolate has smaller asci (25–35 μm vs. 34–56 μm long) which may be due to

their different habitats, our isolate was collected from terrestrial habitat, while the holotype *O. thailandica* (MFLU 16-0030) from freshwater habitats (Li et al. 2016b). The nucleotide comparisons showed that our strain (MFLU 23-0213) has two bp different in ITS and the same in LSU from the strains of *O. thailandica*. Therefore, we identified our new isolate as *O. thailandica*.

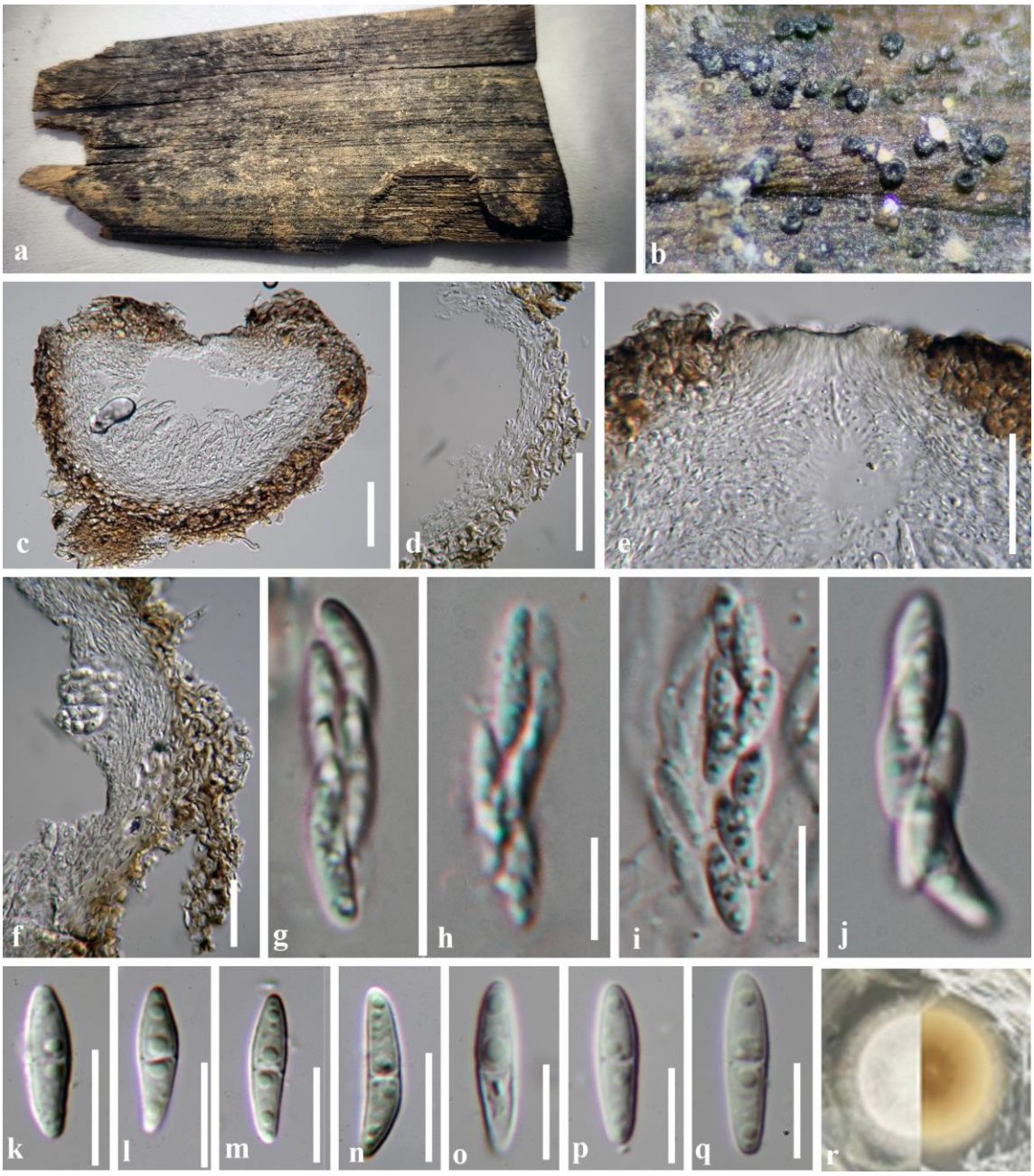

Figure 91 – *Ochronectria thailandica* (MFLU 23-0213, new host record). a Herbarium specimen. b Appearance of black ascomata on the host. c Vertical sections of ascomata. d, f Section of peridium. e Ostiole. g–j Asci. k–q Ascospores. r Colonies on PDA from surface and reverse. Scale bars: c–f = 30 μm, g–q = 10 μm.

Stephanonectria Schroers & Samuels.

Stephanonectria was introduced by Schroers et al. (1999) with the type species *S. keithii*. *Stephanonectria* is characterized by superficial, gregarious to crowded, brown, smooth to rough, minutely papillate perithecia, surrounded by a crown-like structure ostiolum, consisting of two regions perithecial wall, and 1-septate, covered with short striae ascospores (Schroers et al. 1999). *Stephanonectria* is a monotypic genus. Recently, a new species *S. chromolaenae* was introduced by

Perera et al. (2023). In this study, we introduce *Stephanonectria keithii* as a new host and geographical record from *Ananas comosus* from Thailand based on morphological and phylogenetic analyses.

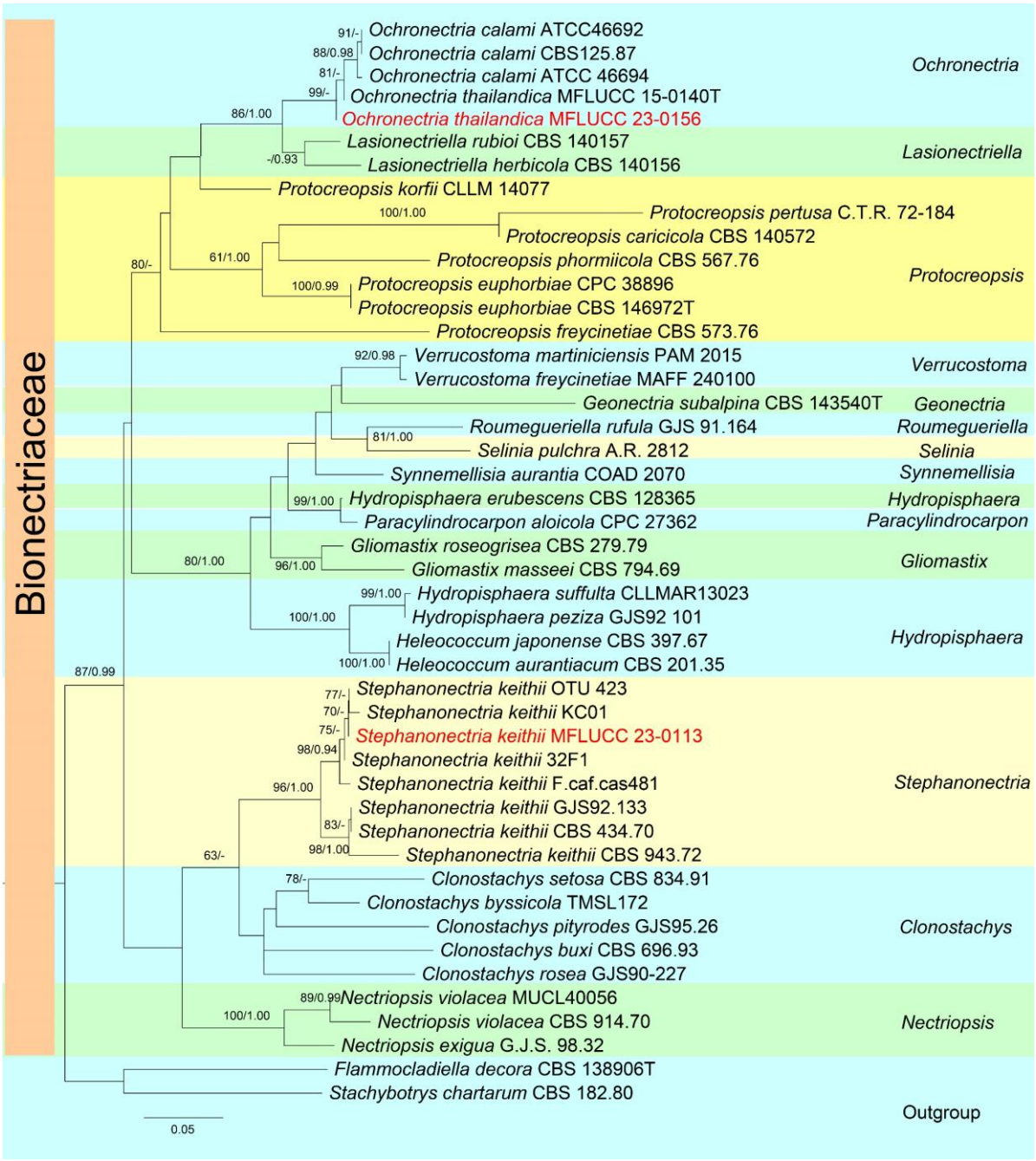

Figure 92 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb1*, *tef1-α*, and *rpb2* sequence data. Related sequences were obtained from Voglmayr & Jaklitsch (2019). Forty-six strains are included in the combined sequence analysis, which comprises 4055 characters with gaps. *Stachybotrys chartarum* (CBS 182.80) and *Flammocladiella decora* (CBS 138906) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -22799.075584 is presented. The matrix had 1449 distinct alignment patterns, with 63.14% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238620, C = 0.256785, G = 0.284627, T = 0.219968; substitution rates AC = 1.327748, AG = 2.084784, AT = 1.356917, CG = 1.026664, CT = 6.092936, GT = 1.000000; gamma distribution shape parameter α = 0.396596. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the

nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

52. *Stephanonectria keithii* (Berk. & Broome) Schroers & Samuels, Sydowia 51(1): 116 (1999) Fig. 93

≡ *Nectriella keithii* (Berk. & Br.) Sacc, Michelia 1: 279. 1879

≡ *Nectria keithii* Berk. & Br., Ann. Mag. Nat. Hist., Ser. 4, 27: 144. 1876 (basionym)

Index Fungorum number: IF460028; Facesoffungi number: FoF10906

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: *Ascomata* 160−200 μm diam. ($\overline{x}$ = 180 μm), superficial on the stroma, solitary to densely crowded in groups, subglobose to globose, golden-brown or brown, smooth, flat at apex due to a crown surrounding the ostiolum. *Ostiolar* crown paler than the rest of the perithecial wall, light brown to pale orange. *Peridium* 15–20 μm wide, thin-walled, comprising 3–5 layers brown-walled cells of *textura angularis*. *Hamathecium* composed of 6–11 μm wide, cellular, hyaline, septate, rarely branching, paraphyses, anastomosing mostly above the asci and embedded in a mucilaginous matrix. *Asci* 35−45 × 6−8 μm ($\overline{x}$ = 41 × 7 μm, n = 15) 8-spored, straight, unitunicate, cylindrical-clavate, sessile, apex broadly flat, rarely rounded, with a barely visible refractive ring. *Ascospores* ellipsoidal, septate, slightly constricted at the septa, 8−9 × 3−3.5 μm ($\overline{x}$ = 8.5 × 3 μm, n = 30), hyaline, biseriate or uniseriate, smooth-walled. Asexual morph: not observed.

Culture characteristics – Colonies on PDA reaching 15 mm diameter after two weeks at 25 °C, colonies white, circular, convex, surface smooth on PDA.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 2 September 2020, X.G. Tian, p9-11 (MFLU 23-0214), living culture MFLUCC 23-0113.

Known hosts and distribution – On stalks of *Brassica* in Great Britain (Berkeley & Broome 1876); on bark of *Eleagnus* in France (Castlebury et al. 2004); on *Dracaena* sp. in China (Cui et al. 2011); on decorticated stems of cabbage in UK (Perera et al. 2023); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438857, ITS = OR438394, *tef1-α* = OR500337, *rpb*1 = OR553097

Notes – In our phylogenetic analyses, our strain (MFLUCC 23-0113) clustered within the strains of *Stephanonectria keithii* (Fig. 92). Morphologically, our strain is similar to *S. keithii* (BPI 802669 and IMI 77877) in having superficial, golden-brown ascomata with flat apex, 8-spored asci with flat or rounded apex and refractive ring and ellipsoidal, septate, hyaline, ascospores (Schroers et al. 1999). Thus, we identified our strain as *S. keithii* based on phylogenetic analyses and morphological characters and it is a new host and geographical record on *Ananas comosus* from Thailand.

Nectriaceae Tul. & C. Tul.

Nectriaceae was introduced in 1865 with *Nectria* as the type genus, and includes numerous important plant and human pathogens, as well as several species used extensively in industrial and commercial applications as bio-degraders and bio-control agents (Hirooka et al. 2012, Lombard et al. 2015, Zeng & Zhuang 2019). Seventy genera are accepted in this family (Wijayawardene et al. 2022). *Nectriaceae* species are characterized by uniloculate ascomata that are white, yellow, orange-red or purple, and usually change colour in potassium hydroxide (KOH) and lactic acid (LA), and are not immersed in a well-developed stroma (Rossman et al. 1999, 2000, Lombard et al. 2015). Species in *Nectriaceae* are reported as soil-borne saprobes or weak to virulent, facultative or obligate plant pathogens, pathogens of humans, but some can produce mycotoxins of medical concern (Rossman et al. 1999, 2000, Chang et al. 2006, Chaverri et al. 2011, Hyde et al. 2020, Perera et al. 2023)

Volutella Fr.

Volutella was described with the type species of *V. ciliate* (Fries 1832). *Volutella* is a widespread genus of *Nectriaceae* (Han et al. 2021) with 150 epithets recorded in Index Fungorum

(2023). Members of *Volutella* grow in diverse habitats, including soil as facultative plant pathogens and plant debris as saprophytes and decomposers (Babu et al. 2015). *Volutella* is characterized by discoid sporodochia with marginal setae, simple to verticillate conidiophores, compact and phialidic conidiogenous cells, and 1-celled, ovoid to oblong conidia, synasexual morph present in some species and with two or more whorls of conidiogenous cells (Gräfenhan et al. 2011, Luo & Zhuang 2012, Lombard et al. 2015, Zhang et al. 2017). In this study, two new host records *V. consors* and *V. delonicis* are described based on phylogenetic analyses and morphological characters.

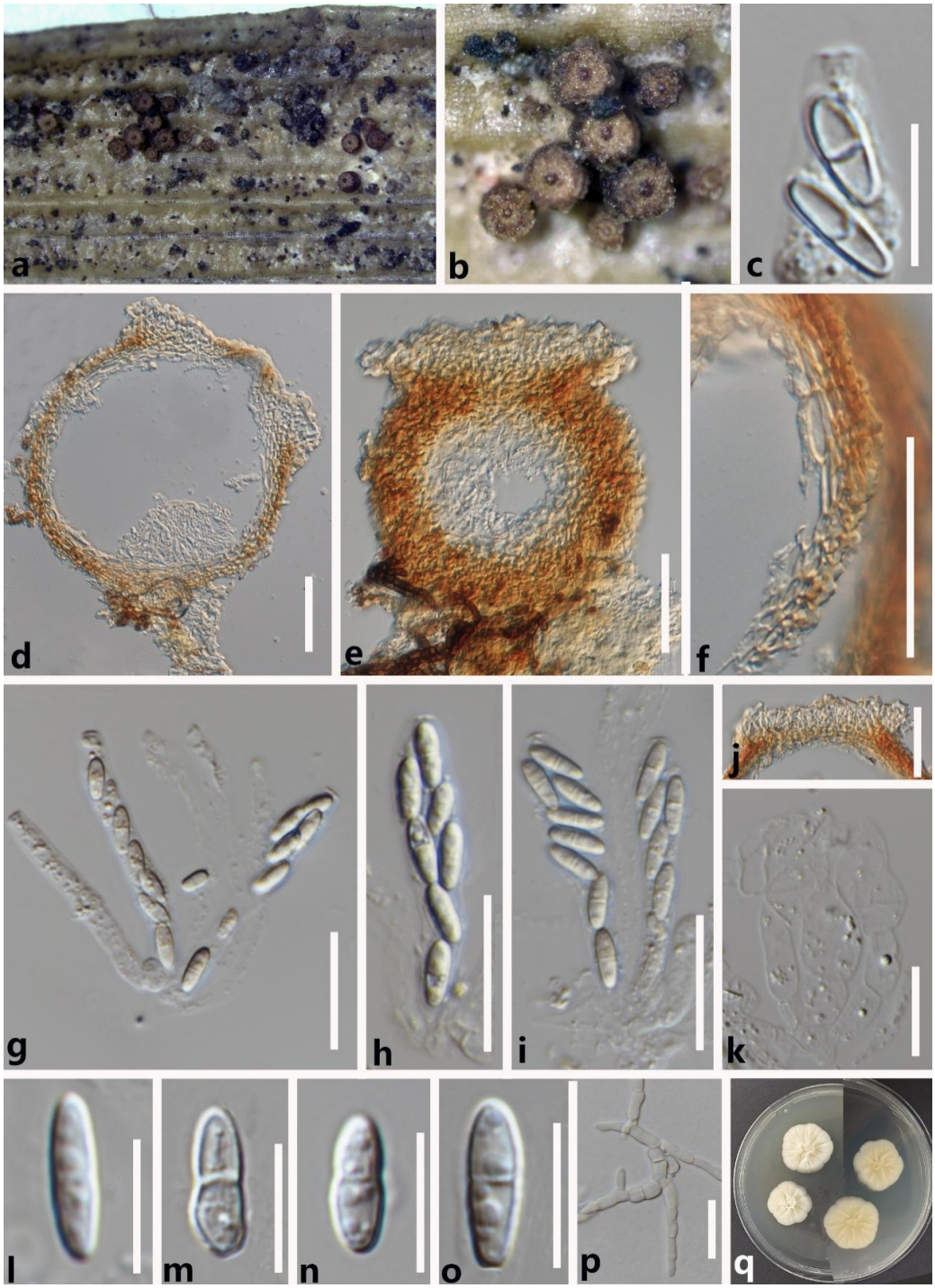

Figure 93 – *Stephanonectria keithii* (MFLU 23-0214, new host and geographical record). a, b Appearance of ascomata on the host surface. c Apical ring. d, e Section of ascoma. f Peridium. g–i Asci. k Pseudoparaphyses. l–o Ascospores. p Germinated ascospore. q Colonies on PDA from surface and reverse. Scale bars: d–f, j = 50 µm, g–i, k, p = 20 µm, l–o = 5 µm.

53. *Volutella consors* (Ellis & Everh.) Seifert, Gräfenhan & Schroers, in Gräfenhan et al., Stud. Mycol. 68: 79–113. 2011 Fig. 94

≡ *Dialonectria consors* Ellis & Everh., J. Mycol. 4: 122. 1888

≡ *Nectriella consors* (Ellis & Everh.) Saccardo, Syll. Fung. 9: 941. 1891

≡ *Nectria consors* (Ellis & Everh.) Seaver, Mycologia 1: 61. 1909

≡ *Cosmospora consors* (Ellis & Everh.) Rossman & Samuels, Stud. Mycol. 42: 119. 1999

Index Fungorum number: IF519455 Facesoffungi number: FoF11028

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous, sporodochial. *Sporodochia* solitary or gregarious on substrate, sessile, white to yellow, setiferous. *Setae* 110–220(–337) × 3–4 µm ($\overline{x}$ = 164 × 3.5 µm, n = 35), arising from sporodochial base and surrounding the conidiophores, wide at base, tapering to a round apex, hyaline to light brown, septate, stiff, cylindrical. *Conidiophores* hyaline, septate, unbranched, closely aggregated. *Conidiogenous cells* 5–10 × 1.5–2.5 µm ($\overline{x}$ = 7 × 2 µm, n = 20), hyaline, cylindrical, phialidic. *Conidia* 5–6.5 × 2–2.5 µm ($\overline{x}$ = 6 × 2 µm, n = 50), aseptate, hyaline, gelatinous, oblong, smooth-walled, 1-celled.

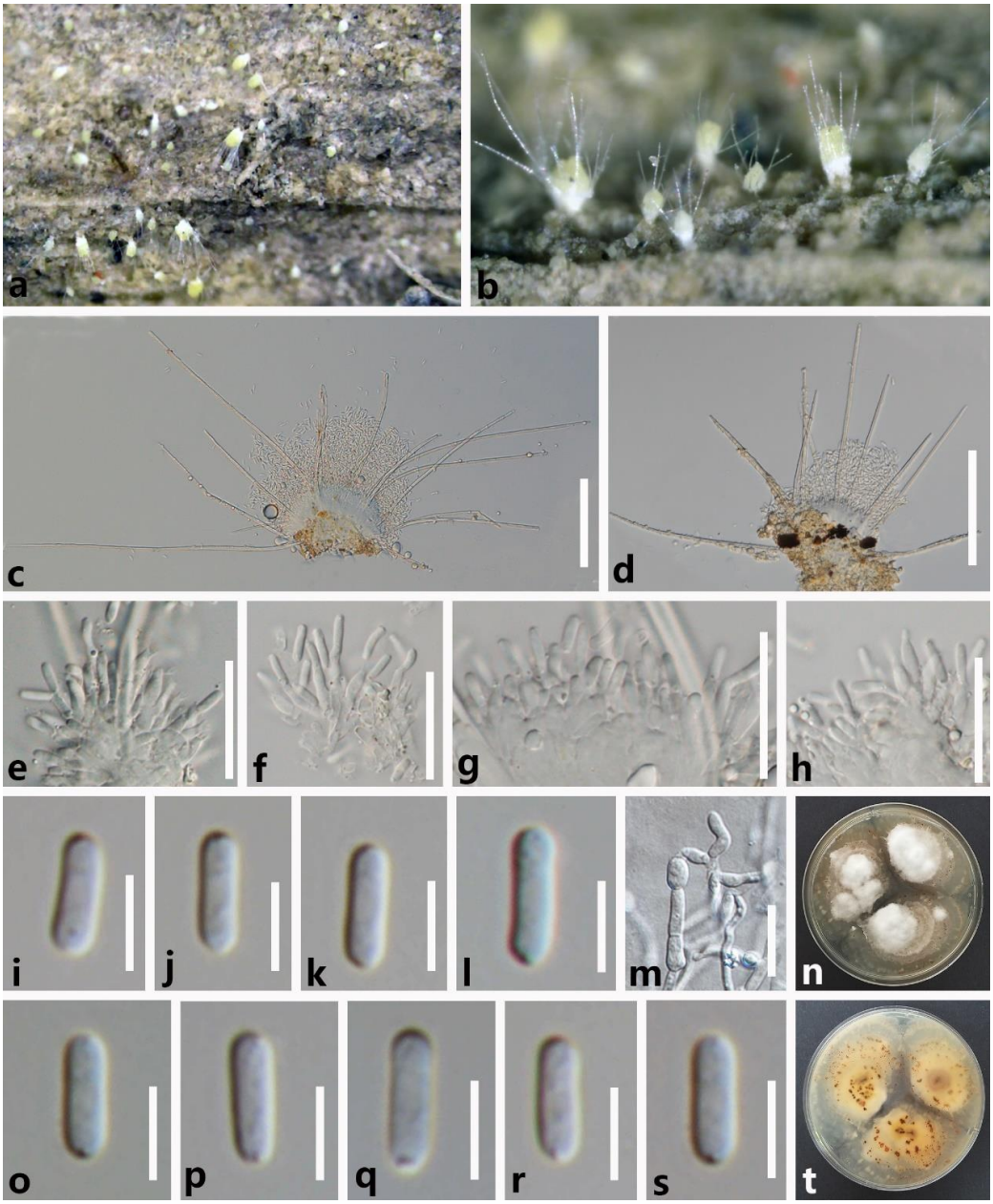

Figure 94 – *Volutella consors* (MFLU 23-0219, new host and geographical record).

a, b Sporodochia on natural substrates. c, d Sporodochium mounted in water. e–h Conidiophore with conidiogenous and conidia. i–l, o–s Conidia. m Germinated conidium. n, t Colonies on PDA from the surface and reverse. Scale bars: c–d = 100 µm, e–h, m = 20 µm, i–l, o–s = 5 µm.

Culture Characters – Colonies on PDA reaching 30 mm in 7 days at 28 °C, surface velvety, slightly raised, entire margin, aerial mycelium white, reverse light yellow, with some brown spots.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 15 July 2020, X.G. Tian, p5-2 (MFLU 23-0219), living cultures, MFLUCC 23-0106.

Known hosts and distribution – On *Magnolia fraseri* and old in floresce in the USA, on decaying orchid bulb in Netherlands, on fallen petioles on *Robinia* in the USA (Gräfenhan et al. 2011); on dead leaves of *Phormium* sp. in the New Zealand (Perera et al. 2023); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438858, ITS = OR438395, *rpb2* = OR634957

Notes – Our strain clusters with other strains of *Volutella consors* with 85% ML and 0.97 PP statistical support (Fig. 95). Our strain and *V. consors* are morphologically similar in having the same sporodochia characters and gelatinous 1-celled and hyaline conidia (Samuels 1977). Both morphological and phylogeny analyses support our new isolate as *V. consors*. We report *V. consors* as a new host and a new geographical record on dead leaves of *Ananas comosus* in Thailand.

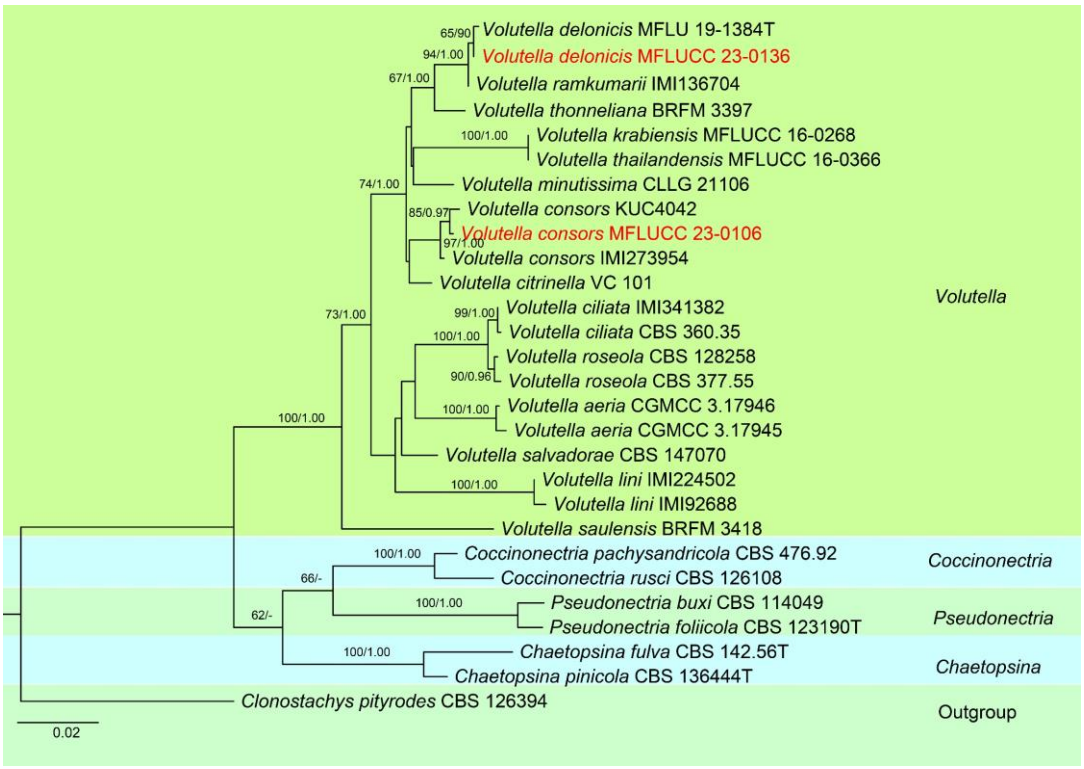

Figure 95 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Perera et al. (2020) and Lechat et al. (2022). Twenty-eight strains are included in the combined sequence analysis, which comprise 1402 characters with gaps. *Clonostachys pityrodes* (CBS 126394) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -5078.503660 is presented. The matrix had 355 distinct alignment patterns, with 14.92% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244189, C = 0.243785, G = 0.279920, T = 0.232106; substitution rates AC = 1.367368, AG = 2.306402, AT = 2.257569, CG = 0.825357, CT = 5.679072, GT = 1.000000; gamma distribution shape parameter α = 0.124585. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red,

while T indicates holotype or ex-type strains.

54. ***Volutella delonicis*** R.H. Perera, E.B.G. Jones & K.D. Hyde, in Perera et al., Mycosphere 11 (1): 2164 (2020) Fig. 96

Index Fungorum number: IF556863; Facesoffungi number: FoF07767

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: see Perera et al. (2020). Asexual morph: Hyphomycetous, sporodochial, stroma inconspicuous. *Sporodochia* sessile, yellow. *Setae* 140–290 × 2.5–4 µm ($\overline{x}$ = 211 × 3.5 µm, n = 50), forming around the margin of conidiomata, hyaline, septate, stiff, cylindrical. *Conidiophores* hyaline, septate. *Conidiogenous cells* monophialidic, with subulate, venter and elongated neck, 5–10 × 2–2.5 µm ($\overline{x}$ = 8.5 × 2.5 µm, n = 30), hyaline, with periclinal thickening, collarette prominent. *Conidia* 5.5–6.5 × 2–2.5 µm ($\overline{x}$ = 6 × 2 µm, n = 40), aseptate, hyaline, oblong to cylindrical, smooth-walled, without mucilaginous sheath, forming slimy yellow masses.

Culture characters – Colonies on PDA reaching 30 mm in 7 days at 28 °C, circular, entire margin, with dense and white aerial mycelium on surface, the center of the reverse side is red, and the edge is light pinkish cinnamon to white.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 2 September 2020, X.G. Tian, p9-17 (MFLU 23-0220), living cultures, MFLUCC 23-0136.

Known host and distribution – On decaying seed pods of *Delonix regia* (Fabaceae) in Thailand (Perera et al. 2020); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438859, ITS = OR438396

Notes – In the phylogenetic analyses, our new isolate clustered with *Volutella delonicis* (MFLUCC 23-0136) (Fig. 95). The morphology of our new isolate (MFLUCC 23-0136) is similar to *V. delonicis* in having sessile and yellow sporodochia, oblong and aseptate conidia (Perera et al. 2020). Therefore, our strain (MFLUCC 23-0136) is identified as *V. delonicis*, and it is a new host record for pineapple in Thailand.

Stachybotryaceae L. Lombard & Crous

Stachybotryaceae was established by Crous et al. (2014), it is characterized by mononematous to sporodochial to synnematous conidiomata, usually with phialidic conidiogenous cells that produce 0–1-septate conidia in dark green to black slimy or dry masses (Crous et al. 2014, Wang et al. 2015b, Lombard et al. 2016). The recent treatment of *Stachybotryaceae* was updated by Bao et al. (2023) with 39 genera accepted. In this study, following the treatment of Bao et al. (2023), we introduce three new records (*Achroiostachys aurantispora*, *Brevistachys subsimplex* and *Sirastachys phaeospora*) and a new species (*Alfaria oryzae*), in this family.

Achroiostachys L. Lombard & Crous

Achroiostachys was introduced by Lombard et al. (2016) with the type species *A. humicola*. *Achroiostachys* is characterized by hyaline, smooth, thin-walled conidiophores and hyaline, smooth, ellipsoidal to limoniform conidia. Seven species are listed in the Index Fungorum (2023) and we introduce *A. aurantispora* as a new collection on *Oryza sativa* based on morphological and phylogenetic analyses.

55. ***Achroiostachys aurantispora*** L. Lombard & Crous, in Lombard et al., Persoonia 36: 172 (2016) Fig. 97

Index Fungorum number: IF815917; Facesoffungi number: FoF14305

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Hyphomycetes. *Conidiophores* 70−130 × 3−4.5 µm ($\overline{x}$ = 101 × 3.5 µm, n = 5) macronematous, mononematous, single or in groups, unbranched, erect, straight or flexuous, septate, smooth, hyaline, thin-walled, with an apical cluster of 3–6 conidiogenous cells. *Conidiogenous cells* 10−15 × 3−5 µm ($\overline{x}$ = 11.5 × 4 µm, n = 10), terminal, determinate, discrete, phialidic, elongate

ampulliform to ventricose, hyaline, smooth, thin walled. *Conidial mass* slimy, pale orange, globose. *Conidia* 10−11.5× 4.5−5.5 µm ($\bar{x}$ = 11 × 5 µm, n = 50), aseptate, ellipsoidal or fusiform, smooth, hyaline, guttulate, with an inconspicuous basal hilum and a rounded apex.

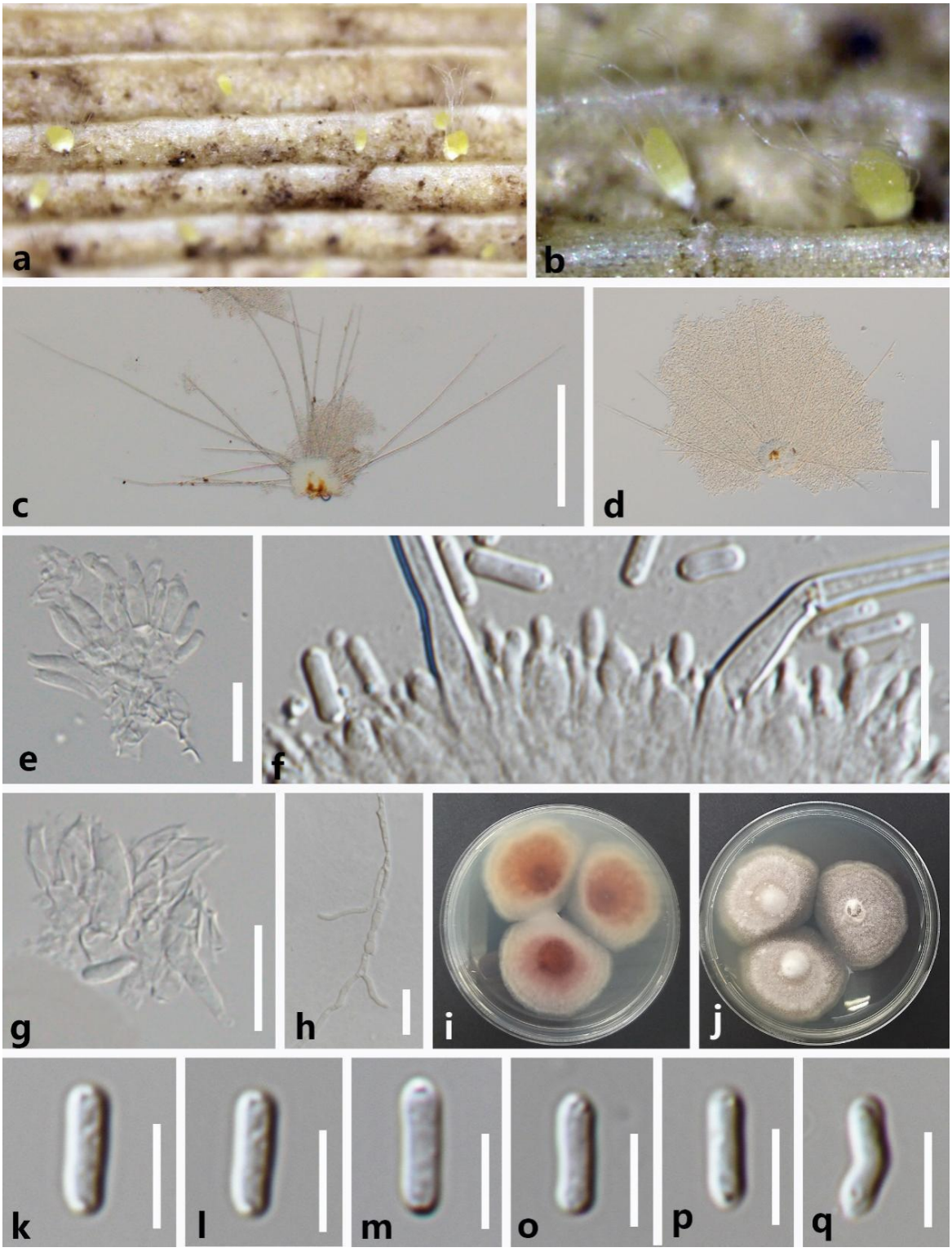

Figure 96 – *Volutella delonicis* (MFLU 23-0220, new host record). a, b Sporodochia on substrate. c, d Sporodochium mounted in water. e, g Conidiophore. f Conidiogenous with conidia. h Germinated conidium. i, j Colonies on PDA from surface and reverse. k–q Conidia. Scale bars: c, d = 200 µm, e–f, g = 10 µm, h = 20 µm, k–q = 5 µm.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Oryza*

sativa, 18 September 2020, X.G. Tian, R1-12 (MFLU 23-0221).

Known host and distribution – On unknown substrate in Italy and straw in a cushion seized in Thailand (Lombard et al. 2016); on dead leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438860, ITS = OR438397, *rpb2* = OR634958

Notes – In the multi-loci phylogenetic analyses, our strain (MFLU 23-0221) clustered together with the strains of *Achroiostachys aurantispora* (CBS 187.73 and DAOM 225565) (Fig. 98). Our strain has similar characteristics with *A. aurantispora* which was collected from Thailand (Lombard et al. 2016). They both have macronematous, mononematous conidiophores with an apical cluster of phialidic conidiogenous cells, elongate ampulliform to ventricose conidiogenous cells and slimy, pale orange, globose conidial mass and aseptate, guttulate, ellipsoidal conidia. The nucleotide comparisons showed that our strain (MFLU 23-0221) is not significantly different from the strains of *Achroiostachys aurantispora* (CBS 187.73 and DAOM 225565, holotype) in ITS, LSU and *rpb2* sequence data. Thus, we identified our strain as *Achroiostachys aurantispora* based on phylogenetic analyses and morphological characters.

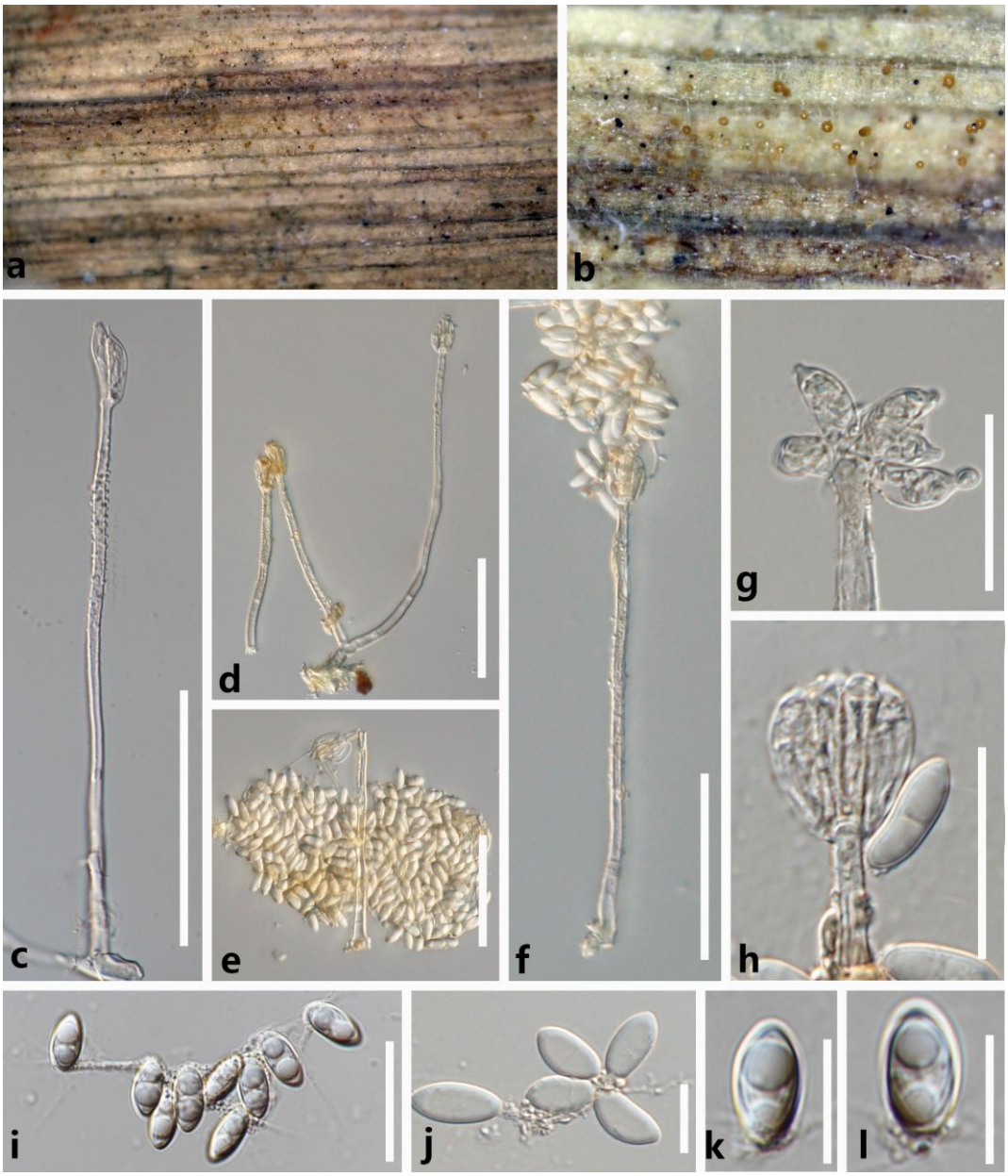

Figure 97 – *Achroiostachys aurantispora* (MFLU 23-0221, new collection). a, b Appearance of the fungus on dead leaves of *Oryza sativa*. c–h Conidiophores with conidia. i–l Conidia. Scale bars: c–f, j = 50 μm, g–i = 20 μm, k, l = 10 μm.

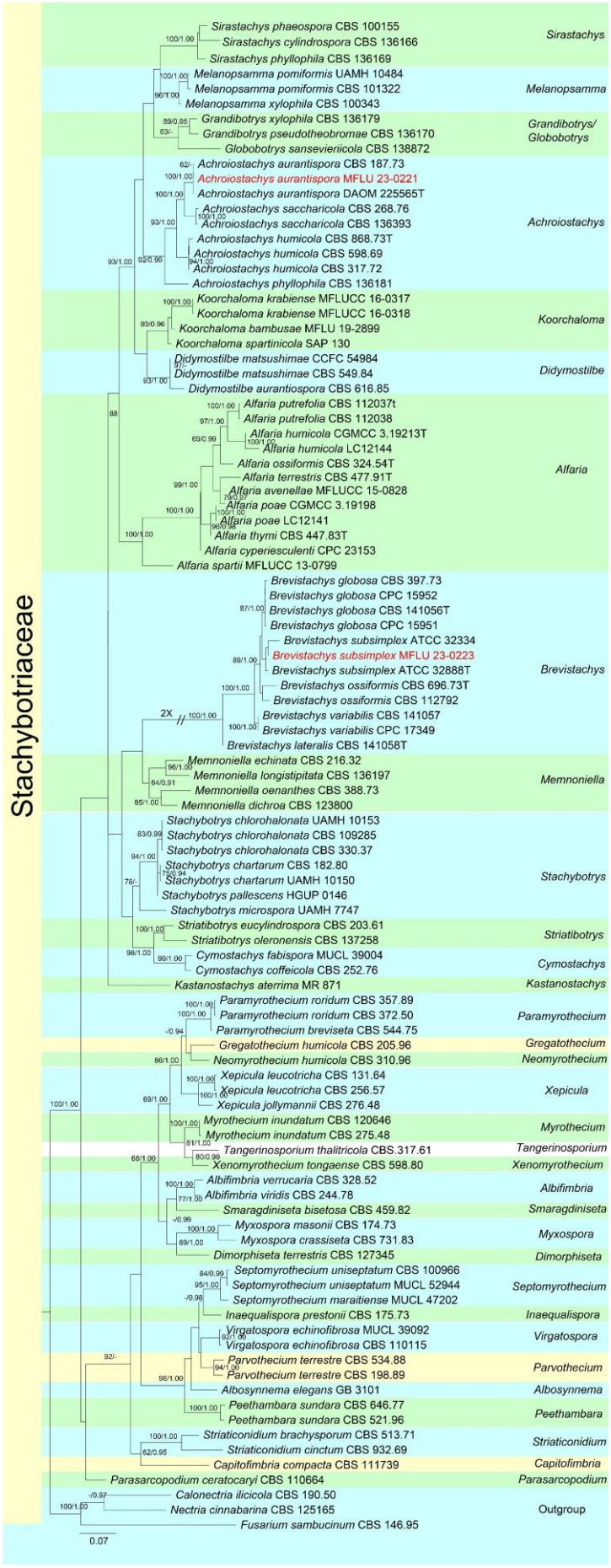

Figure 98 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

and *rpb2* sequence data. Related sequences were obtained from Li et al. (2020b). One hundred and one strains are included in the combined sequence analysis, which comprises 2093 characters with gaps. *Capitofimbria compacta* (CBS 111739), *Striaticonidium cinctum* (CBS 932.69), and *Striaticonidium brachysporum* (CBS 513.71) were used as the outgroup taxa. The tree topology of the ML analysis was similar to the PP. The best-scoring RAxML tree with a final likelihood value of -25205.704728 is presented. The matrix had 907 distinct alignment patterns, with 17.47% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249440, C = 0.254169, G = 0.283255, T = 0.213135; substitution rates AC = 1.400957, AG = 3.872807, AT = 1.237579, CG = 0.882589, CT = 7.111863, GT = 1.000000; gamma distribution shape parameter α = 0.199419. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Brevistachys L. Lombard & Crous

Brevistachys was introduced by Lombard et al. (2016) to accommodate several stachybotrys-like species. The genus is characterized by distinctly short conidiophores and conidiogenous cells borne on conidiophores or directly from vegetative hyphae. There are five species accepted in the genus (Lombard et al. 2016, Wijayawardena et al. 2022).

56. *Brevistachys subsimplex* (Cooke) L. Lombard & Crous, in Lombard et al. Persoonia 36: 185 (2016) Fig. 99

Index Fungorum number: IF815938; Facesoffungi number: FoF14307

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Colonies* on the substrate, superficial, effuse, dark brown to black. *Conidiophores* 40–65 × 2.5–3 μm ($\overline{x}$ = 50.7 × 2.9 μm, n = 15), simple, macronematous, mononematous, single or in groups, unbranched, erect, straight to slightly flexuous, olivaceous to brown, septate, smooth or verrucose, sometimes with a slightly bulbous apice, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* 5–10 × 3–4 μm ($\overline{x}$ = 6.1 × 3.3 μm, n = 30), phialidic, terminal or born laterally on vegetative hyphae and stipe of the conidiophores, subcylindrical, pyriform or ellipsoid, subhyaline to pale olivaceous, smooth. *Conidia* 4–4.5 × 3–4 μm ($\overline{x}$ = 4.3 × 3.8 μm, n = 30), acrogenous, borne in chains, aggregating in slimy masses, aseptate, globose to ellipsoidal, subhyaline when young, brown to dark brown at maturity, initially smooth and becoming verrucose at maturity.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 9 March 2021, X.G. Tian, c7-2 (MFLU 23-0223).

Known host and distribution – On *Musa* sp., *Costus afer*, *Hibiscus esculentus*, *Arachis hypogaea* in worldwide (Deighton 1960); on leaves of *Musa* in Georgia (Cooke 1883); from water hyacinth in water hyacinth in the USA (Castlebury et al. 2004); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438861, ITS = OR438398

Notes – In our phylogenetic analyses, our new collection (MFLU 23-0223) and two strains of *Brevistachys subsimplex* grouped with a highly supported (Fig. 98). Morphologically, our new collection shares similar characters with *B. subsimplex* (KM 165386, holotype) in having unbranched, septate, olivaceous to brown conidiophores, phialidic, pyriform or ellipsoid, subhyaline to pale olivaceous conidiogenous cells and aseptate, globose to ellipsoidal, subhyaline to brown conidia. While our collection has shorter conidiophores (40–65 μm vs. 100–140 μm) and smaller conidia (4–4.5 × 3–4 μm vs. 4–7 × 7–8 μm) than the holotype (Deighton 1960). *Brevistachys subsimplex* has been reported from various hosts (*Musa* sp., *Costus afer*, *Hibiscus esculentus*, and *Arachis hypogaea*) worldwide (Deighton 1960). Our strain is a new record collected on *Cocos nucifera*.

Sirastachys L. Lombard & Crous

Sirastachys was introduced by Lombard et al. (2016) to accommodate seven stachybotrys-like species. *Sirastachys* is characterized by mononematous, unbranched or branched conidiophores arising laterally from synnemata, phialidic conidiogenous cells and ellipsoidal to obovoid to cylindrical, aseptate, hyaline to pale olivaceous, brown to dark brown conidia (Lombard et al. 2016, Crous et al. 2018b, Tibpromma et al. 2018). There are nine epithets listed in Index Fungorum (2023).

Figure 99 – *Brevistachys subsimplex* (MFLU 23-0223, new host record). a, b Colonies on substrate. c–e Conidiophores and conidia. f–i Conidiogenous cells with attached conidia. j−o Conidia. Scale bars: c–e = 20 µm, f, g = 10 µm, h–o = 5 µm.

57. *Sirastachys phaeospora* L. Lombard & Crous, in Lombard et al., Persoonia 36: 218 (2016) Fig. 100

Index Fungorum number: IF816026; Facesoffungi number: FoF14308

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Mycelium* composed of septate, branched, smooth, hyaline to subhyaline hyphae. *Conidiophores* 70−85 × 3−4 µm ($\bar{x}$ = 78 × 3.5 µm, n = 10), macronematous, mononematous, wider at the base, single or in groups, unbranched or branched once, erect, straight, septate, hyaline, smooth to verrucose, thin-walled, bearing a whorl of 4–8 conidiogenous cells. *Conidiogenous cells* 7.5−10 × 3−4 µm ($\bar{x}$ = 8.5 × 3.5 µm, n = 25), terminal, elongate doliiform to clavate, hyaline, smooth to slightly verrucose. *Conidia* 4.5−5.5 × 2−3 µm ($\bar{x}$ = 5 × 3 µm, n = 40), acrogenous, aseptate, obovoid to ellipsoidal, verrucose, brown, guttulate, rounded at both ends.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, P7-13 (MFLU 23-0224), living culture, MFLUCC 23-0122.

Known host and distribution – On decaying leaves in Cuba (Lombard et al. 2016); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438862, ITS = OR438399, *tub*2 = OR538084

Notes − In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0122) grouped within *Sirastachys phaeospora* strains (Fig. 101). Morphologically, our strain shares similar morphology with the type strain of *S. phaeospora* (CBS H-22460) in having macronematous, unbranched or branched once, septate conidiophores, elongate doliiform to clavate, smooth to verrucose conidiogenous cells and acrogenous, aseptate, obovoid to ellipsoidal conidia (Lombard et al. 2016). Furthermore, shares a similar size range of conidia (4.5−5.5 × 2−3 µm vs. 4–5 × 2–3 µm) and conidiogenous cells (7.5−10 × 3−4 µm vs. 7–9 × 2–4 µm), but longer conidiophores (70−85 µm vs. 40–65 µm) to *Sirastachys phaeospora* (CBS H-22460). Thus, we identified our strain as *Sirastachys phaeospora* based on phylogenetic analyses and morphological characters. Our strain *Sirastachys phaeospora* (MFLUCC 23-0122) is introduced as a new host and geographical record on *Ananas comosus* in Thailand.

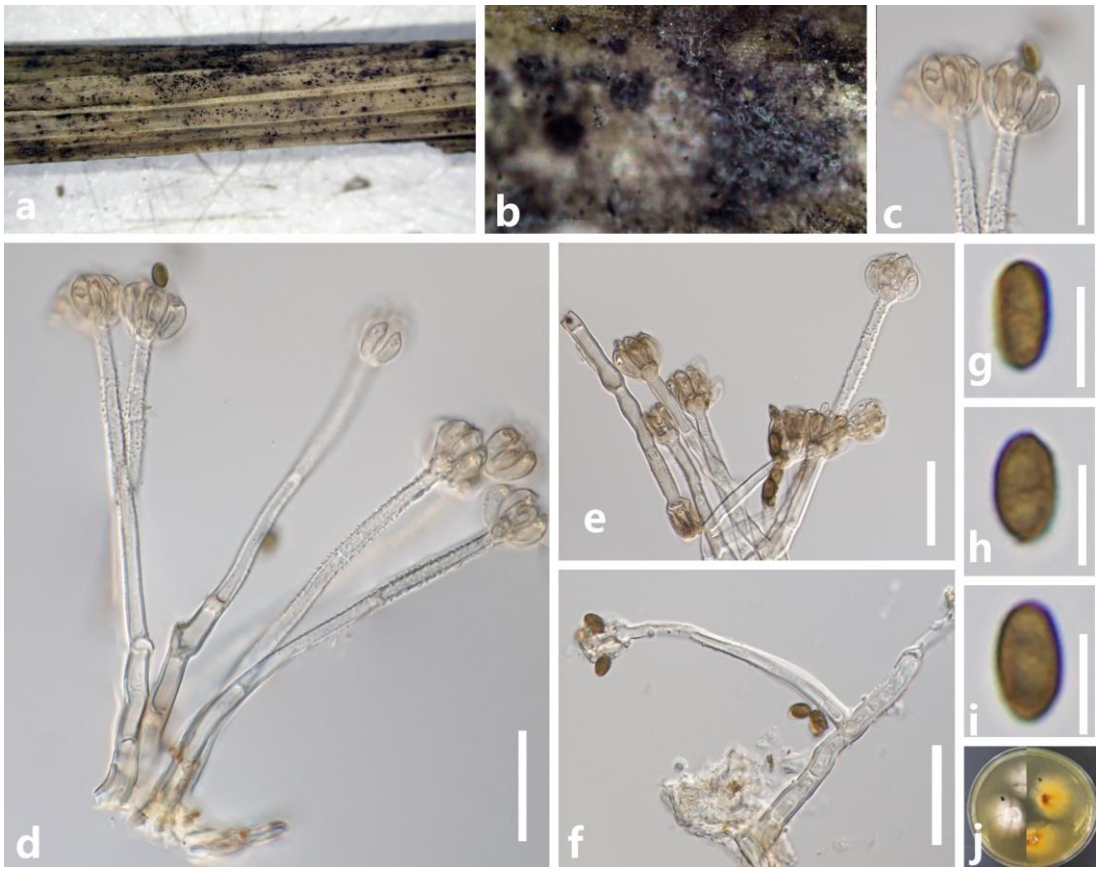

Figure 100 – *Sirastachys phaeospora* (MFLU 23-0224, new host and geographical record). a, b Colonies on dead leaves of *Ananas comosus*. c Conidiogenous cells with conidia.

d–f Conidiophores and conidia. g–i Conidia. j Colony on PDA from surface and reverse. Scale bars: c–f = 20 µm, g–i = 5 µm.

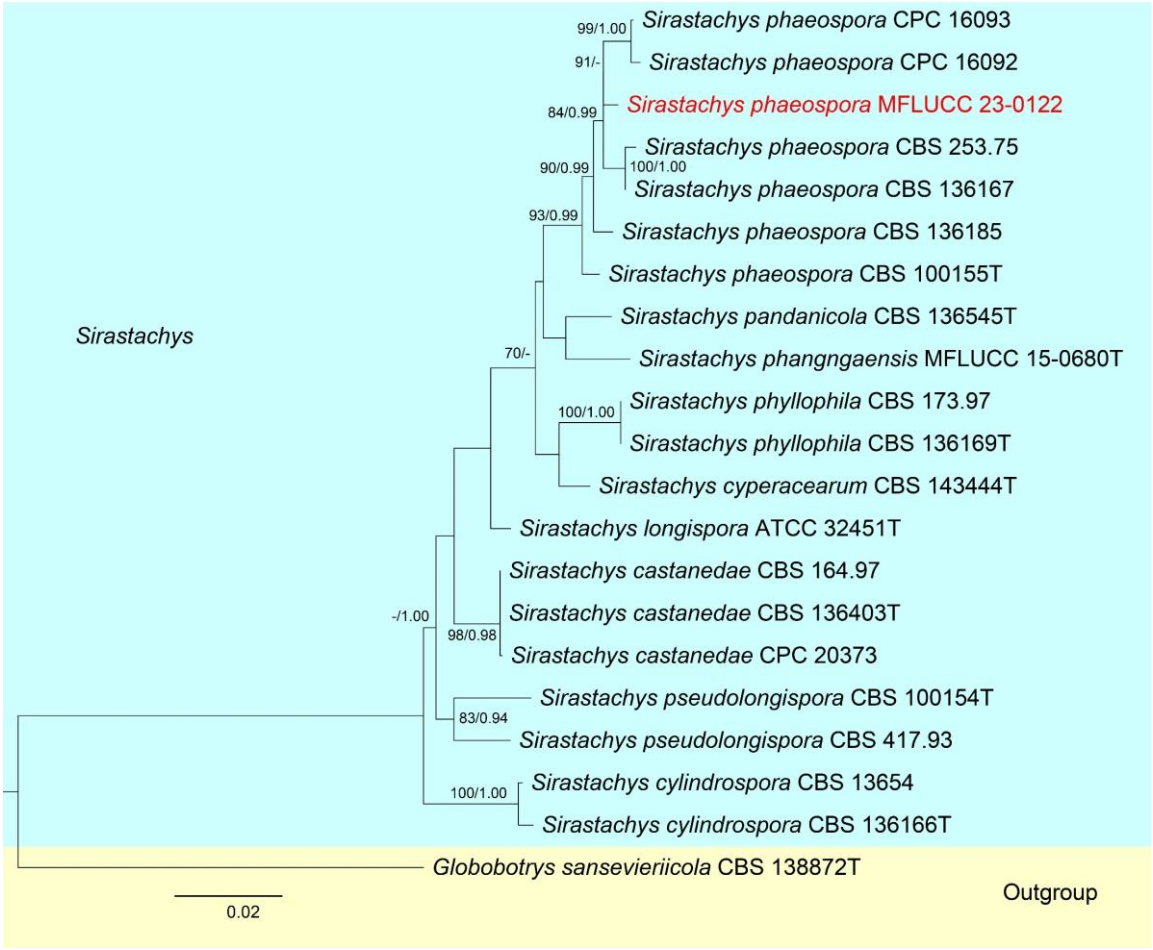

Figure 101 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1-α*, and *rpb2* sequence data. Related sequences were obtained from Crous et al. (2018b). Twenty-one strains are included in the combined sequence analysis, which comprises 2493 characters with gaps. *Globobotrys sansevieriicola* (CBS 138872) was used as the outgroup taxon. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -5988.333596 is presented. The matrix had 307 distinct alignment patterns, with 14.02% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241592, C = 0.262908, G = 0.281113, T = 0.214388; substitution rates AC = 1.510412, AG = 3.919016, AT = 1.317274, CG = 0.732537, CT = 8.727583, GT = 1.000000; gamma distribution shape parameter 0.020000. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Subclass *Savoryellomycetidae* Hongsanan, K.D. Hyde & Maharachch.
Pleurotheciales Réblová & Seifert

Pleurotheciales was introduced by Réblová et al. (2016b) based on morphological characters and phylogenetic analyses to accommodate the family *Pleurotheciaceae*. The order was initially placed in *Hypocreomycetidae* by Réblová et al. (2016b). Hongsanan et al. (2017) transferred *Pleurotheciales* to *Savoryellomycetidae* based on multi-gene phylogenetic analyses and the placement has been accepted by Dong et al. (2021) and Boonmee et al. (2021). There is one family and fourteen genera in *Pleurotheciales* (Hongsanan et al. 2017, Boonmee et al. 2021, Dong et al. 2021).

Pleurotheciaceae Réblová & Seifert

Pleurotheciaceae was introduced by Réblová et al.)2016b(with *Pleurothecium* as the type genus. Fourteen genera *viz. Adelosphaeria*, *Anapleurothecium*, *Coleodictyospora*, Dematipyriforma, *Helicoascotaiwania*, *Melanotrigonum*, *Monotosporella*, *Neomonodictys*, *Phaeoisaria*, *Phragmocephala*, *Pleurotheciella*, *Pleurothecium*, *Saprodesmium*, and *Sterigmatobotrys* are accepted in the family (Boonmee et al. 2021, Dong et al. 2021). Species in *Pleurotheciaceae* are cosmopolitan, with a wide range of hosts and substrates from terrestrial and freshwater habitats (Boonmee et al. 2021, Dong et al. 2021). The sexual morphs of *Pleurotheciaceae* share perithecial, immersed to superficial, papillate ascomata, leathery to fragile, carbonaceous peridial walls, unitunicate, cylindrical, 8-spored, asci with a distinct non-amyloid apical annulus, abundant paraphyses and ellipsoidal to fusiform, septate, hyaline or versicolorous ascospores)Réblová et al. 2016b, Luo et al. 2018(. The asexual morphs of *Pleurotheciaceae* have been reported as hyphomycetes forming indeterminate synnemata or loose fascicles. Conidiophores are macronematous or semi-macronematous. Conidiogenous cells produce holoblastic conidia, with rhexolytic conidial secession on short denticles or extending polyblastically on a sympodial rachis. Conidia are hyaline to brown, varied in shape, septate or aseptate (Baker et al. 2002, Réblová et al. 2016b, Bao et al. 2022).

Dematipyriforma Sun

Dematipyriforma was introduced by Sun et al. (2017) with a single species *D. aquilariae* which is an endophyte isolated from *Aquilaria crassna*. *Dematipyriforma* was initially placed in Savoryellales and Dong et al. (2022) transferred the genus to Pleurotheciaceae, Pleurotheciales based on phylogenetic analyses. Recently, Bao et al. (2022) introduced a new species *D. muriformis* and transferred *Rhexoacrodictys nigrospora* to *Dematipyriforma*. Three species are accepted in the genus (Sun et al. 2017, Bao et al. 2022).

58. ***Dematipyriforma aquilariae*** L. Y. Sun, Hai-Yan Li, Xiang Sun & L.D. Guo, Cryptog. Mycol. 38(3): 345 (2017) Fig. 102

Index Fungorum number: IF842402; Facesoffungi number: FoF12831

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Colonies* on natural substrate superficial, dark brown to black. *Mycelium* mostly immersed, hyphae hyaline to pale brown, smooth, thin-walled. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, integrated, terminal intercalary, brown, determinate, cylindrical, smooth, thin-walled. *Conidia* 30–40 × 20–30 μm)$\bar{x}$ = 35 × 26.5 μm, n = 30(, solitary, smooth, thin-walled, pyriform or ellipsoidal, rounded at the apex, olivaceous brown to dark brown, muriform, with 8 cells, with 4 transverse septa and 1 longitudinal septum, slightly constricted at the septa.

Culture characteristics – Colonies on PDA, 30 mm diam. after two weeks at 25 °C, brown to blackish at the front sides, mycelium sparse; reverse blackish.

Material examined – China, Yunnan Province, Xishuangbanna District, on dead leaves of *Cocos nucifera*, 17 September 2021, X.G. Tian, C8-15)GZAAS 23-0587(, living culture, GZCC 23-0581.

Known host and distribution – On wood of *Aquilaria crassna* from Laos (Sun et al. 2017); on dead leaves of *Cocos nucifera* in China (this study).

GenBank numbers – LSU = OR438863, ITS = OR438400, SSU = OR458362

Notes – Phylogenetic analyses combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data demonstrated that our strain (GZCC 23-0581) clustered with the ex-type of *Dematipyriforma aquilariae* (CGMCC 3.17268) (Fig. 103). Our strain *D. aquilariae* (GZCC 23-0581) is similar to the holotype of *D. aquilariae* in having monoblastic, integrated, brown, determinate conidiogenous cells and solitary, pyriform, smooth, thin-walled conidia with transverse and longitudinal septate. Based on both phylogeny and morphology, our strain)GZCC 23-0581(is identified as *Dematipyriforma aquilariae*, a new host and geographical record from *Cocos nucifera* in China.

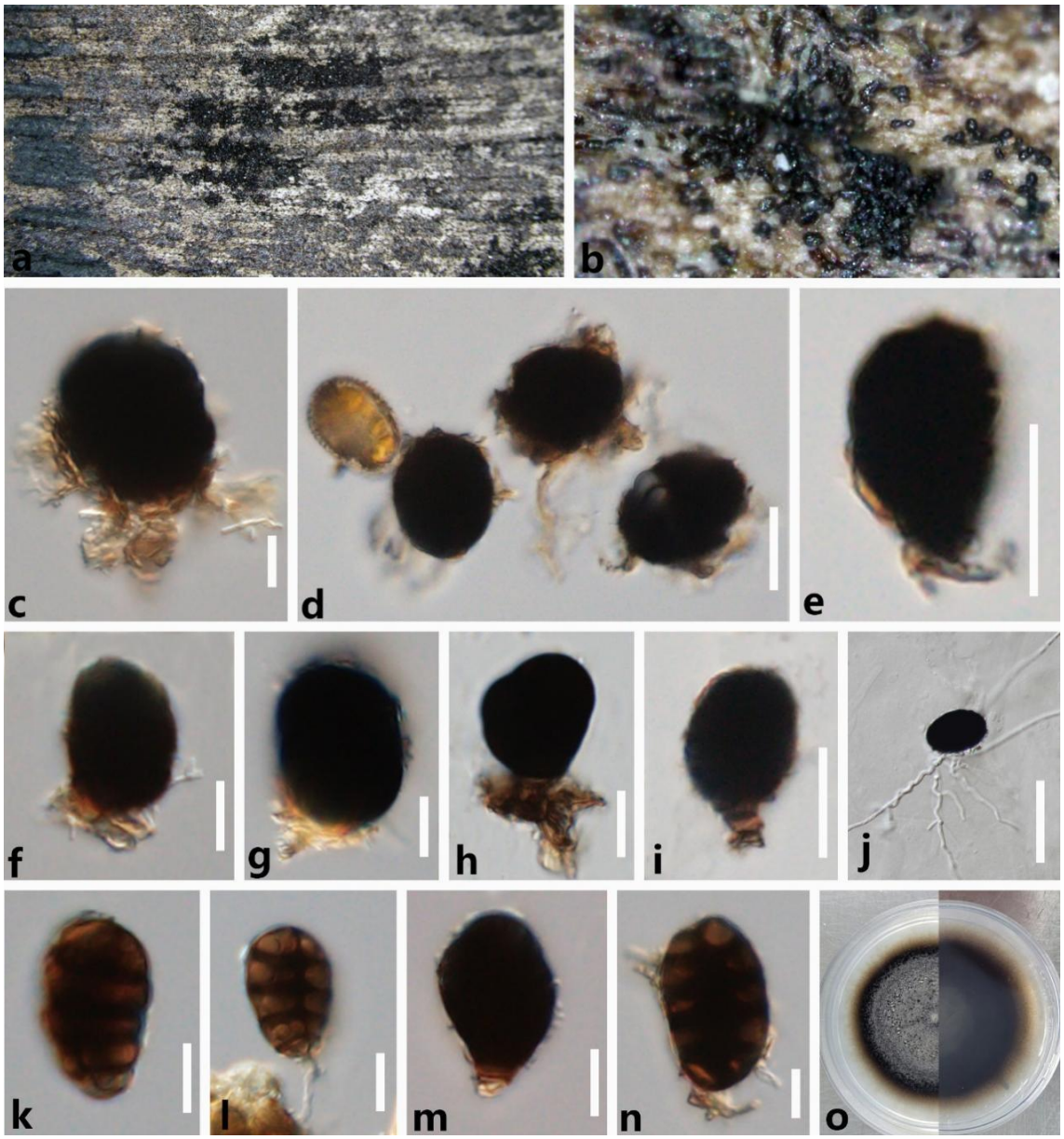

Figure 102 – *Dematipyriforma aquilariae* (GZAAS 23-0587, new host and geographical record). a, b Sporodochia with a mass of conidia and scattered conidia on natural substrate. c–i, k–n Conidia. j Germinated conidium. o Colony on PDA from surface and reverse. Scale bars: j = 50 μm, d, e, i = 20 μm, c, f–h, k–n = 10 μm.

59. *Pseudosaprodesmium* X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.

Index Fungorum number IF 900984; Facesoffungi number: FoF 14309

Etymology – The genus epithet reflects its morphological similarity to *Saprodesmium*

Saprobic decaying leaves and wood in terrestrial habitats. Sexual morph: Not observed. Asexual morph: hyphomycetous. *Colonies* on natural substrate, superficial, effuse, gregarious, punctiform, raised, dark brown to black. *Mycelium* mostly immersed, composed of hyaline, smooth, thin-walled hyphae. *Conidiophores*, micronematous, mononematous, fasciculate, cylindrical, branched, hyaline to pale brown, cylindrical, smooth. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindrical, terminal, determinate, hyaline, smooth, thin-walled. *Conidia* acrogenous, solitary, smooth, subglobose, ellipsoidal to obovoid, or irregular, thick-walled, irregularly muriform, hyaline when young, becoming dark brown when maturity, sometimes slightly constricted at septa.

Type species – *Pseudosaprodesmium cocois* X.G. Tian, K.D. Hyde & Tibpromma

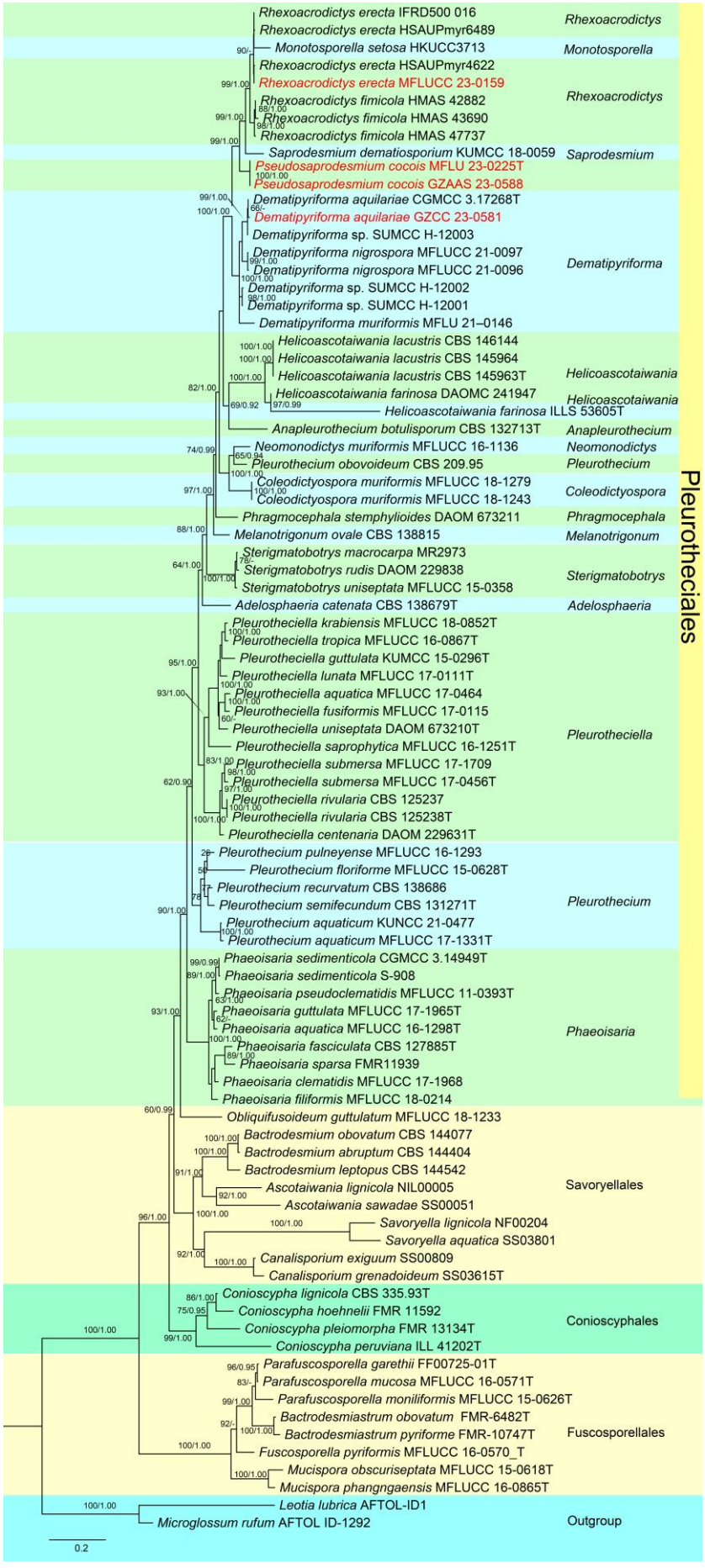

Figure 103 – Phylogram generated from maximum likelihood analysis based on combined ITS,

LSU, SSU, *rpb2*, and *tef1-α* sequence data. Related sequences were obtained from Bao et al. (2022). Eight-six strains are included in the combined sequence analysis, which comprise 4742 characters with gaps. *Microglossum rufum* (AFTOL ID-1292) and *Leotia lubrica* (AFTOL-ID1) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -49961.696810 is presented. The matrix had 2783 distinct alignment patterns, with 46.74% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.236865, C = 0.257530, G = 0.288413, T = 0.217191; substitution rates AC = 1.358103, AG = 2.791664, AT = 1.505543, CG = 1.098815, CT = 6.471874, GT = 1.000000; gamma distribution shape parameter α = 0.318614. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

Notes – In a BLASTn search of NCBI GenBank, the closest match of the ITS sequence of our strains with 89% similarity was *Pleurotheciella guttulata* (strain MFLU 17-0914) and 88% similarity was *Rhexoacrodictys erecta* (strain HSAUP myr6489 and HSAUP myr4622), while the closest match with the LSU sequences with 97.72% similarity was *Rhexoacrodictys erecta* (strain IFRD500-016) and the closest match with the SSU sequences with 100% similarity was *Rhexoacrodictys* sp. (strain TBRC-BCC 94390 and TBRC-BCC 94389) and *Dematipyriforma* sp. (strain SUMCC H-12001).

In the multi-loci phylogenetic analyses of ITS, LSU, SSU, *tef1-α*, and *rpb2* sequence data, our strains (MFLU 23-0225 and GZAAS 23-0588) clusters between *Dematipyriforma* and *Saprodesmium* clade and form independent branch with 99% ML and 1.00 PP bootstrap support (Fig. 103). Morphologically, our strains are similar to *Saprodesmium* and *Rhexoacrodictys* in having muriform conidia. However, our strains are different from *Saprodesmium* and *Rhexoacrodictys* in having mirconematous, fasciculate, cylindrical, branched conidiophores and subglobose, ellipsoidal to obovoid, or irregular conidia that are hyaline when young, becoming dark brown when mature. Whereas, the conidiophores of *Saprodesmium* are vesiculate and consist of 1–4 subglobose, subglobose conidiogenous cells and conidia are obovoid to ellipsoidal, and olivaceous when young, becoming blackish with age and obscuring the septa, with several subhyaline basal cells (Dong et al. 2021). *Rhexoacrodictys* has macronematous conidiophores and, broadly oval to subglobose, truncated at the base, dark-blackish brown to black conidia with transverse septa typically spanning the whole conidial width and longitudinal septa incomplete (Baker et al. 2002).

Pseudosaprodesmium shares similar morphological characteristics with *Dematipyriforma* in having micronematous conidiophores, holoblastic conidiogenous cells and septate conidia. However, they are entirely different in the conidia. Conidia of *Dematipyriforma* are elongate pyriformare elongate pyriform, 4–5 transverse septate, sometimes 1–2 longitudinal septate, pale grey olivaceous to pale brown (Sun et al. 2017). In contrast, the conidia of *Pseudosaprodesmium* are subglobose, ellipsoidal to obovoid, or irregular, hyaline when young, becoming dark brown when mature with irregularly muriform in all cells. Hence, a new genus, *Pseudosaprodesmium* is established to accommodate *Pseudosaprodesmium cocois*.

60. *Pseudosaprodesmium cocois* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 104

Index Fungorum number: IF900985; Facesoffungi number: FoF14310

Etymology – Referring to the host plant *Cocos nucifera*, on which the fungus was collected.

Holotype – MFLU 23-0225

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: hyphomycetous. *Colonies* on natural substrate, superficial, effuse, gregarious, punctiform, raised, dark brown to black. *Mycelium* mostly immersed, composed of hyaline, smooth, thin-walled hyphae. *Conidiophores* 15–30 × 3–7 μm ($\overline{x}$ = 21.5 × 5 μm, n = 20), micronematous, mononematous, fasciculate, cylindrical, branched, hyaline to pale brown, cylindrical, smooth. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindrical, terminal, determinate, hyaline to pale brown,

smooth, thin-walled. *Conidia* 25–35 × 20–25 μm ($\bar{x}$ = 30.5 × 22.5 μm, n = 30), acrogenous, solitary, smooth, subglobose, ellipsoidal to obovoid, or irregular, thick-walled, irregularly muriform, hyaline when young, becoming dark brown when maturity, sometimes slightly constricted at septa.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 9 March 2021, X.G. Tian, C7-3)MFLU 23-022, holotype; GZAAS 23-0588, isotype(.

GenBank numbers – MFLU 23-0225: LSU = OR438864, ITS = OR438401, SSU = OR458363. GZAAS 23-0588: LSU = OR438865, ITS = OR438402, SSU = OR458364

Notes – *Pseudosaprodesmium cocois* (MFLU 23-0225) is phylogenetically closer and morphologically similar to *Saprodesmium dematiosporum* (Fig. 103). *Pseudosaprodesmium cocois* is similar to *Saprodesmium dematiosporum* in having micronematous conidiophores, holoblastic conidiogenous cells and muriform conidia. However, they are entirely different in the following aspects. The conidiophores of *P. cocois* are fasciculate, cylindrical, branched, while they are vesiculate in *Saprodesmium*. The conidia of *P. cocois* are subglobose, ellipsoidal to obovoid, or irregular, hyaline when young, becoming dark brown when mature. In contrast, the conidia of *S. dematiosporum* are obovoid to ellipsoidal, and olivaceous when young, becoming blackish with age and obscuring the septa, with several subhyaline basal cells (Dong et al. 2021). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.64) (Fig. 105).

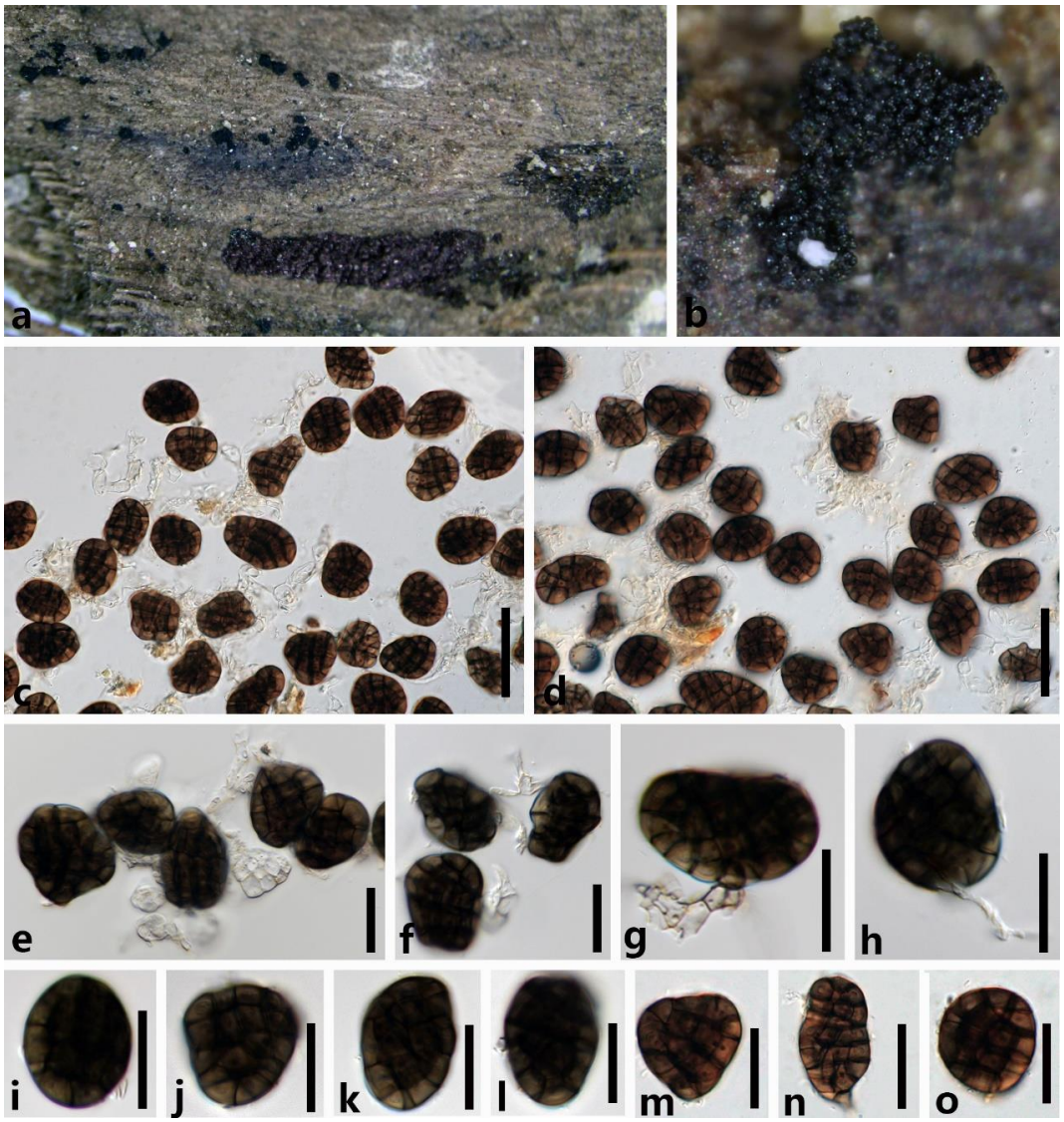

Figure 104 – *Pseudosaprodesmium cocois* (MFLU 23-0225, holotype). a, b Sporodochia with a

mass of conidia and scattered conidia on natural substrate. c–h Conidia and conidiophores. i–o Conidia. Scale bars: c, d = 40 μm, e–o = 20 μm.

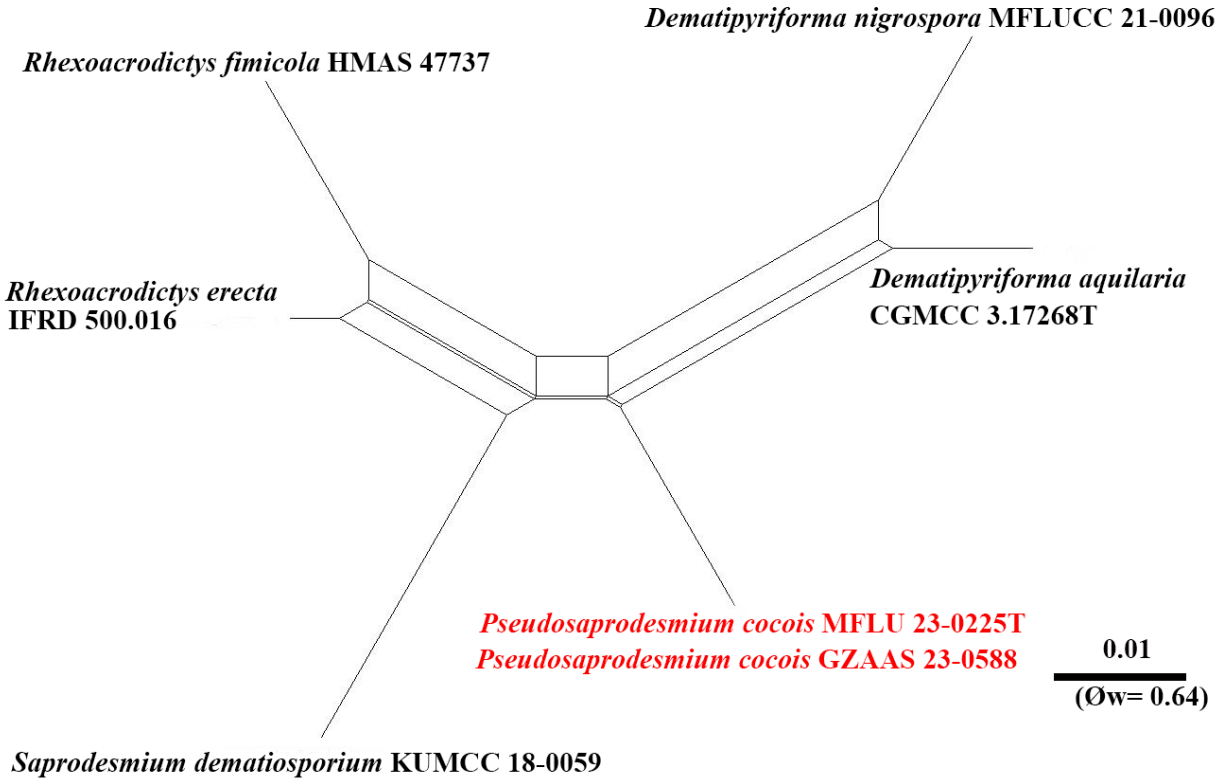

Figure 105 – Results of the PHI test of *Pseudosaprodesmium cocois* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

Rhexoacrodictys W.A. Baker & Morgan-Jones

Rhexoacrodictys was introduced by Baker et al. (2002) to accommodate four *Acrodictys* species *viz. A. erecta*, *A. fimicola*, *A. fuliginosa* and *A. queenslandica* as their conidial disarticulation is rhexolyitc and it is in contrast with the schizolytic process typical of *Acrodictys*. Delgado (2009) and Xiao et al. (2018) introduced another two species *R. martini* and *R. broussonetiae* in the genus (Delgado 2009, Xiao et al. 2018). Xia et al. (2017) transferred *R. martini* and *R. queenslandica* to *Distoseptispora* and *Junewangia* respectively, based on phylogenetic analyses (Xia et al. 2017). Recently, *R. nigrospora* was introduced to the genus by Boonmee et al. (2021). There are five species accepted in the genus.

The placement of *Rhexoacrodictys* was questionable since it was established. Xia et al. (2017) showed that *Rhexoacrodictys* grouped within *Savoryellaceae*. However, Luo et al. (2019) and Dong et al. (2021) showed that *Rhexoacrodictys* clustered within Pleurotheciaceae. While Boonmee et al. (2021) and Wijayawardene et al. (2022) placed the genus in *Savoryellaceae*. The recent treatment of *Rhexoacrodictys* was provided by Bao et al. (2022), who placed the genus in *Pleurotheciaceae* based on phylogenetic analyses and morphological characteristics. The genus is characterized by macronematous, mononematous, septate, smooth and thick-walled, brown conidiophores and holoblastic, monoblastic, terminal conidiogenous cells and acrogenous, broad oval to obovate, subspherical, muriform, brown to dark brown conidia which are often with a paler basal cell (Baker et al. 2002).

61. *Rhexoacrodictys erecta* (Ellis & Everh.) W.A. Baker & Morgan-Jones, in Baker et al., Mycotaxon 82: 99 (2002) Fig. 106

Index Fungorum number: IF381123; Facesoffungi number: FoF14311

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Colonies* on the surface of substrate, hairy, effuse, blackish, shining. *Mycelium* mostly immersed, cylindrical, brown hyphae. *Conidiophores*, macronematous, mononematous, erect, single, straight or somewhat flexuous, cylindrical, smooth-walled, brown to dark brown, septate, 30–65 × 4–5 μm)$\overline{x}$ = 46 × 4.5 μm, n = 15(. *Conidiogenous cells* 2.5–4 × 3.5–5 μm)$\overline{x}$ = 3 × 4 μm, n = 15(, monoblastic, integrated, terminal, pale brown to brown. *Conidia* holoblastic, solitary, dry, oval to subglobose, top-shaped, muriform, acrogenous, transversely and longitudinally septate, dark brown to black when mature, truncate at base, smooth-walled, 20–25 × 15–20 μm)$\overline{x}$ = 23 × 17.5 μm, n = 15(.

Culture characteristics – Colonies on PDA, 20 mm diam. after two weeks at 25 °C, brown to blackish at the front sides, mycelium sparse; reverse blackish.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, C6–14)MFLU 23-0226(, living culture, MFLUCC 23-0159.

Known host and distribution – On decaying stalks of *Zea mays* in the USA (Ellis 1961); on *Arundo donax* in Venezuela and dead twig in South Africa (Baker et al. 2002); dead bark of palm tree, decaying stalk of Sorghum bicolor, rotten stalk of *Zea mays* and rotten stems of bamboo in China (Zhao et al. 2011); on dead branches of an unidentified broadleaf tree in China (Xia et al. 2017); on submerged wood in China (Shi et al. 2021); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438866, ITS = OR438403, SSU = OR458365

Notes – *Rhexoacrodictys erecta* was introduced by Baker et al. (2002), it was originally introduced as *Acrodictys erecta* by Ellis (1961). Baker et al. (2002) considered that four *Acrodictys* species, *A. erecta*, *A. fimicola*, *A. fuliginosa*, and *A. queenslandica* differ from *Acrodictys* by rhexolyitc conidial disarticulation which is in contrast with the schizolytic process typical of *Acrodictys*. Hence, they transferred *A. erecta* and the other three species to a newly introduced genus *Rhexoacrodictys* based on morphological differences. *Acrodictys erecta* was synonymized under *Rhexoacrodictys erecta*. In our phylogenetic analyses, our new isolate)MFLUCC 23-0159(clustered with three strains of *Rhexoacrodictys erecta* and *Monotosporella setosa* in a monophyletic clade and sister to *R. fimicola* (Fig. 103). Morphologically, our new collection is similar to *R. erecta* in having macronematous, mononematous, brown, septate conidiophores, integrated, terminal, monoblastic, percurrent conidiogenous cells and acrogenous, brown to dark brown conidia with transversely and longitudinally septate. Thus, we identified our new isolate as *R. erecta* and it is a new host and geographical record on *Cocos nucifera* in Thailand.

Our phylogenetic analyses showed that *Monotosporella setosa* grouped between strains of *Rhexoacrodictys erecta* with high bootstrap support (99% ML and 1.00 PP, Fig. 103), which is consistent with Bao et al. (2022). Morphologically, *R. erecta* is different from *M. setosa* by the conidial septate. *Rhexoacrodictys erecta* has transverse and longitudinal septate, while, conidia of *M. setosa* only have transverse septate (Hughes 1958, Baker et al. 2002). In addition, the strain of *M. setosa* (HKUCC 3713) was not the ex-type strain and lacks a morphological description; only LSU sequence data is available for *M. setosa*. Our strain (MFLUCC 23-0159) is different from *M. seteosa* (HKUCC 3712) in 13/520 bp (2.5%) of the LSU (data contains 6 gaps). Thus, we identified our new isolate as *R. erecta*. However, *M. setosa* needs further study and recommendations to clarify the placement of this genus which should target a more variable region and need more collection.

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones

Savoryellales was introduced to accommodate *Ascotaiwania*, *Ascothailandia*, and *Savoryella*

species in the *Sordariomycetes* (Boonyuen et al. 2011). There is one family and six genera (*Ascotaiwania*, *Canalisporium*, *Kaseifertia*, *Obliquifusoideum*, *Rhexoacrodictys* and *Savoryella*) in *Savoryellales* (Wijayawardene et al. 2022).

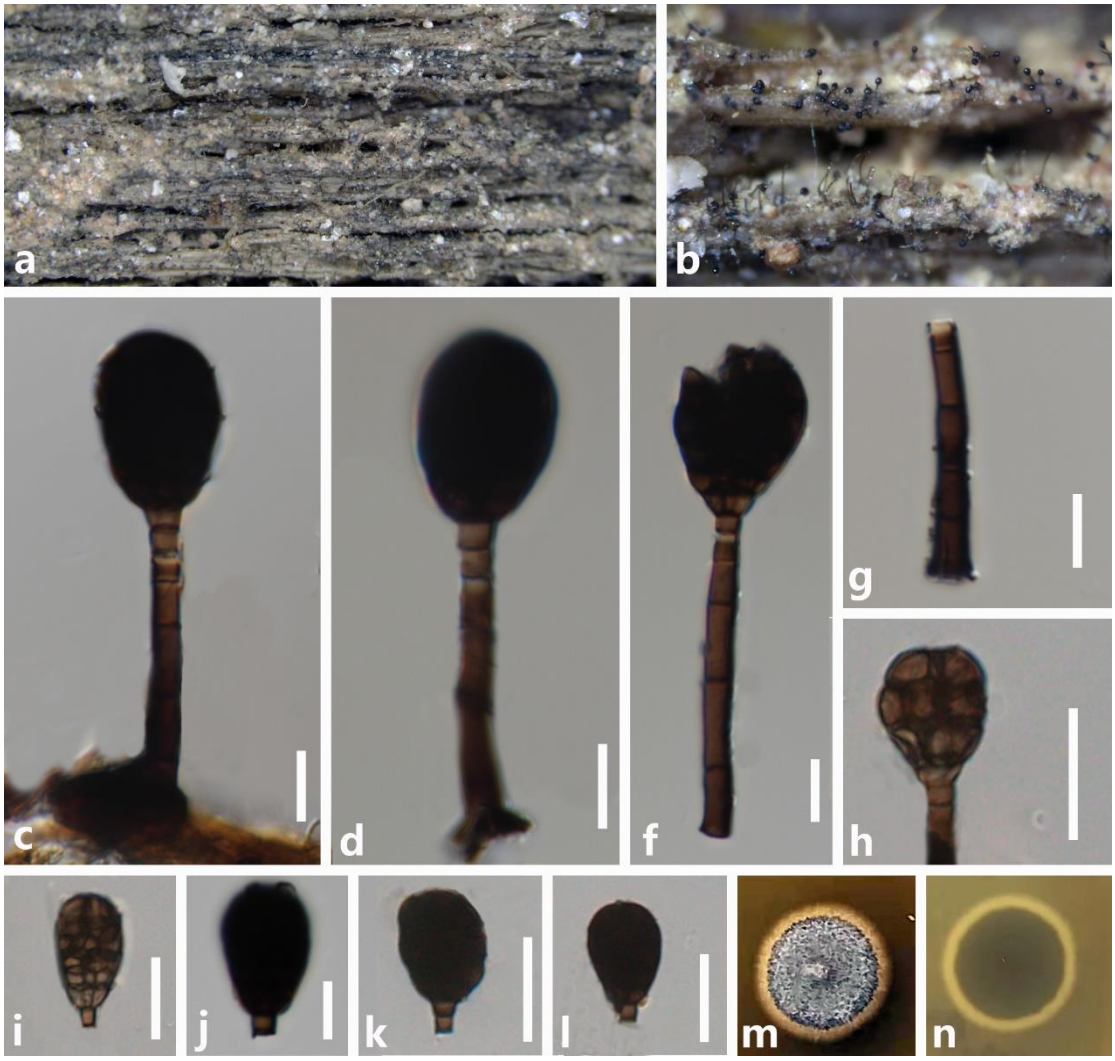

Figure 106 – *Rhexoacrodictys erecta*)MFLU 23-0226, new host and geographical record(. a, b Appearance of the fungus on dead leaves of *Cocos nucifera*. c–f Conidiophore with conidia. g Conidiophore. h Conidiogenous cells with conidia. i–l Conidia. m, n Colony on PDA from surface and reverse. Scale bars: c–l = 10 μm.

Savoryellaceae Jaklitsch & Réblová

Savoryellaceae, a single family of *Savoryellales*, which was introduced by Jaklitsch & Réblová (2015) with *Savoryella* as the type genus. Phylogenetic analyses of Boonyuen et al. (2011) showed that *Savoryella* clustered with *Ascotaiwania*, *Ascothailandia*, and *Canalisporium* within *Sordariomycetes*. Hence, a new order *Savoryellales* was established to accommodate these genera (Jaklitsch 2015, Dayarathne et al. 2019). Dayarathne et al. (2019) revised *Savoryellaceae* and accepted three genera *Ascotaiwania*, *Ascothailandia* and *Canalisporium*, while, *Neoascotaiwania* was synonymized under *Ascotaiwania*. Luo et al. (2019) introduced a new genus *Dematiosporium* to this family. Réblová et al. (2020) showed that *Neoascotaiwania* species formed a monophyletic clade and were distinct from *Ascotaiwania*. Therefore, they segregated *Neoascotaiwania* from *Ascotaiwania* and placed *Neoascotaiwania* in Savoryellaceae. In addition, *Bactrodesmium* is also assigned in the family based on phylogenetic analyses. Six genera *viz. Ascotaiwania*, *Ascothailandia*, *Bactrodesmium*, *Canalisporium*, *Dematiosporium*, and *Neoascotaiwania* are included in this family (Luo et al. 2019, Réblová et al. 2020a).

The sexual morph of *Savoryellaceae* is characterized by immersed, semi-immersed to superficial, non-stromatic, heavily pigmented, coriaceous ascomata, paraphyses, unitunicate asci comprise non-amyloid apical annulus, and fusiform to ellipsoidal, transversely septate ascospores with hyaline end cells and brown median cell. The asexual morph of *Savoryellaceae* is diverse in morphology, with different types of asexual morphs, such as monotosporella-like, monodictys-like, trichocladium-like and bactrodesmium-like (Ranghoo & Hyde 1998, Sivichai et al. 1998, Hernandez-Restrepo et al. 2017). Species in the family are commonly found on submerged wood in aquatic habitats and some species have been reported from terrestrial woody plants (Linder 1929).

Savoryella E.B.G. Jones & R.A. Eaton

Savoryella was introduced by Jones & Eaton (1969) with *Savoryella lignicola* as the type species. The taxonomic placement of *Savoryella* has been changed several times based on morphological characters (Jones & Eaton 1969, Jones & Hyde 1992) and phylogenetic analyses (Vijaykrishna & Hyde 2006, Boonyuen et al. 2011). Boonyuen et al. (2011) showed that *Savoryella* clustered with the genera *Ascotaiwania*, *Ascothailandia*, and *Canalisporium* (the asexual morph of *Ascothailandia*) in a monophyletic cade. Hence, *Savoryellales* was established to accommodate these genera, and *Savoryellaceae* was subsequently introduced by Jaklitsch (2015).

Both asexual and sexual morphs of *Savoryella* are known. Members of this genus are characterized by immersed to superficial, papillate, periphysate ascomata, clavate to cylindrical, unitunicate asci with a nonamyloid apical thickening containing a pore, and ellipsoidal, 3-septate ascospores with brown central cells and hyaline polar end cells (sexual morph); inconspicuous or micronematous, mononematous, hyaline to pale brown conidiophores, holoblastic, determinate, integrated conidiogenous cells and solitary or aggregated, pyriform to obovoid, septate conidia with brown middle cells and subhyaline or pale brown basal cell (asexual morph) (Boonyuen et al. 2011, Zhang et al. 2019). There are 14 species listed in Index Fungorum (2023), of which only 10 have sequence data. This paper introduces two new species *Savoryella cocois* and *S. chiangraiense* based on phylogenetic analyses and morphological characters.

62. *Savoryella cocois* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 107

Index Fungorum number: IF900986; Facesoffungi number: FoF14312

Etymology – Referring to the host plant *Cocos nucifera*, on which the fungus was collected.

Holotype – MFLU 23-0227

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, black, glistening, punctiform. *Mycelium* subhyaline to pale brown. *Conidiophores* micronematous, mononematous, hyaline to pale brown, smooth, thin-walled. *Conidiogenous cells* holoblastic, determinate, integrated, termnal, cylindrical. *Conidia* 25–35 × 15−25 ($\overline{x}$ = 29 × 20 μm, n = 20), solitary or aggregated, rhexolytic, pyriform to obovoid, thick-walled, with rough surface, uniseptate, dividing the conidium into two unequal cells, the upper cell largest and dark brown to black, basal cell pale brown to brown.

Material examined – Thailand, Chiang Rai Province, Muang District, on decaying leaves of *Cocos nucifera* (Arecaceae), 3 January 2021, X.G. Tian, C5-10 (MFLU 23-0227, holotype), GZAAS 23-0589, isotype.

GenBank numbers – MFLU 23-0227: LSU = OR438867, ITS = OR581911 SSU = OR458366. GZAAS 23-0589: LSU = OR438868, ITS = OR581912, SSU = OR458367

Notes – In the multi-loci phylogenetic analyses, our strain (MFLU 23-0227) clustered with *Savoryella sarushimana* (NBRC 105262), *S. nypae* (MFLUCC 18-1570) and an unverified strain of *Savoryella* sp. (L347) (Fig. 108). Morphologically, our strain resembles *Savoryella sarushimana* (NBRC105262) and *Savoryella nypae* (MFLUCC 18-1570) in having micronematous, mononematous conidiophores, with holoblastic, monoblastic, conidiogenous cells and acrogenous, pyriform to obovoid conidia. However, *Savoryella cocois* differs from *S. sarushimana* and *Savoryella nypae* in having uniseptate conidia with larger and dark brown to black upper cell and pale brown to dark brown basal cell. Conidia of *S. sarushimana* have 3–5-septate and proliferating

to give new smaller conidia and septate dark-colored filaments and this character was not observed in *Savoryella cocois*. In addition, the conidia of *Savoryella cocois* are much shorter than those of *S. sarushimana* (25–35 × 15−25 µm vs. 42–63 × 32–50 µm). *Savoryella nypae* has 2(−3)-septate conidia with three unequal cells which is distinct from *Savoryella cocois*. Furthermore, comparison of nucleotide between *Savoryella cocois* (MFLU 23-0227) and *Savoryella nypae* (MFLUCC 18-1570) in ITS gene region revealed 34 bp differences. The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.99) (Fig. 109). Thus, based on both phylogeny and morphology, we introduce our new isolate as a new species.

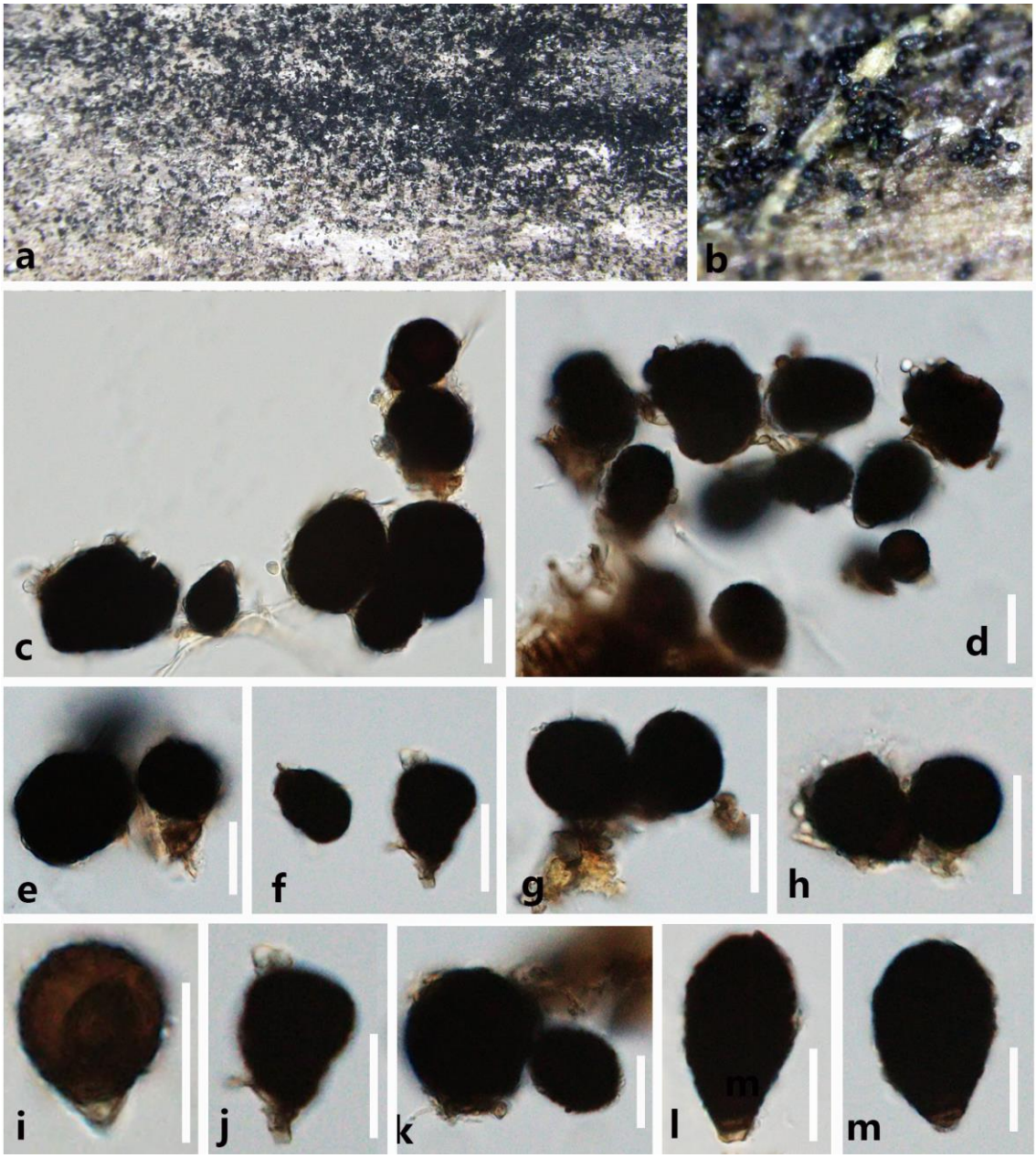

Figure 107 – *Savoryella cocois* (MFLU 23-0227, holotype). a, b The appearance of conidiomata on the host substrate. c–m Conidia. Scale bars: c–m = 10 µm.

63. *Savoryella chiangraiensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 110

Index Fungorum number: IF900987; Facesoffungi number: FoF14313

Etymology – Referring to the location where the specimen was collected, Chiang Rai Province, Thailand.

Holotype – MFLU 23-0228

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, black, glistening, punctiform. *Mycelium* subhyaline to pale brown. *Conidiophores* micronematous, mononematous, hyaline to pale brown, smooth, thin-walled. *Conidiogenous cells* holoblastic, determinate, integrated, terminal, cylindrical. *Conidia* 20–25 × 15−20 ($\bar{x}$ = 22.5 × 18 μm, n = 35), solitary or aggregated, rhexolytic, pyriform to obovoid, broadly rounded at the apex, straight or slightly curved, thick-walled, with rough surface, hyaline when young, becoming dark brown to black when mature, 1−2-septate, septa thick and band like, dividing the conidium into unequal cells, the upper cell being largest and dark brown to black, the middle cell dark brown to black, the basal cell pale brown to brown.

Material examined – Thailand, Chiang Rai Province, Muang District, on decaying leaves of *Cocos nucifera* (Arecaceae), 3 January 2021, X.G. Tian, C7-4 (MFLU 23-0228, holotype); China, Yunnan Province, Xishuangbanna, *Cocos nucifera*, 13 September 2021, X.G. Tian, C8-10 (GZAAS 23-0590, paratype).

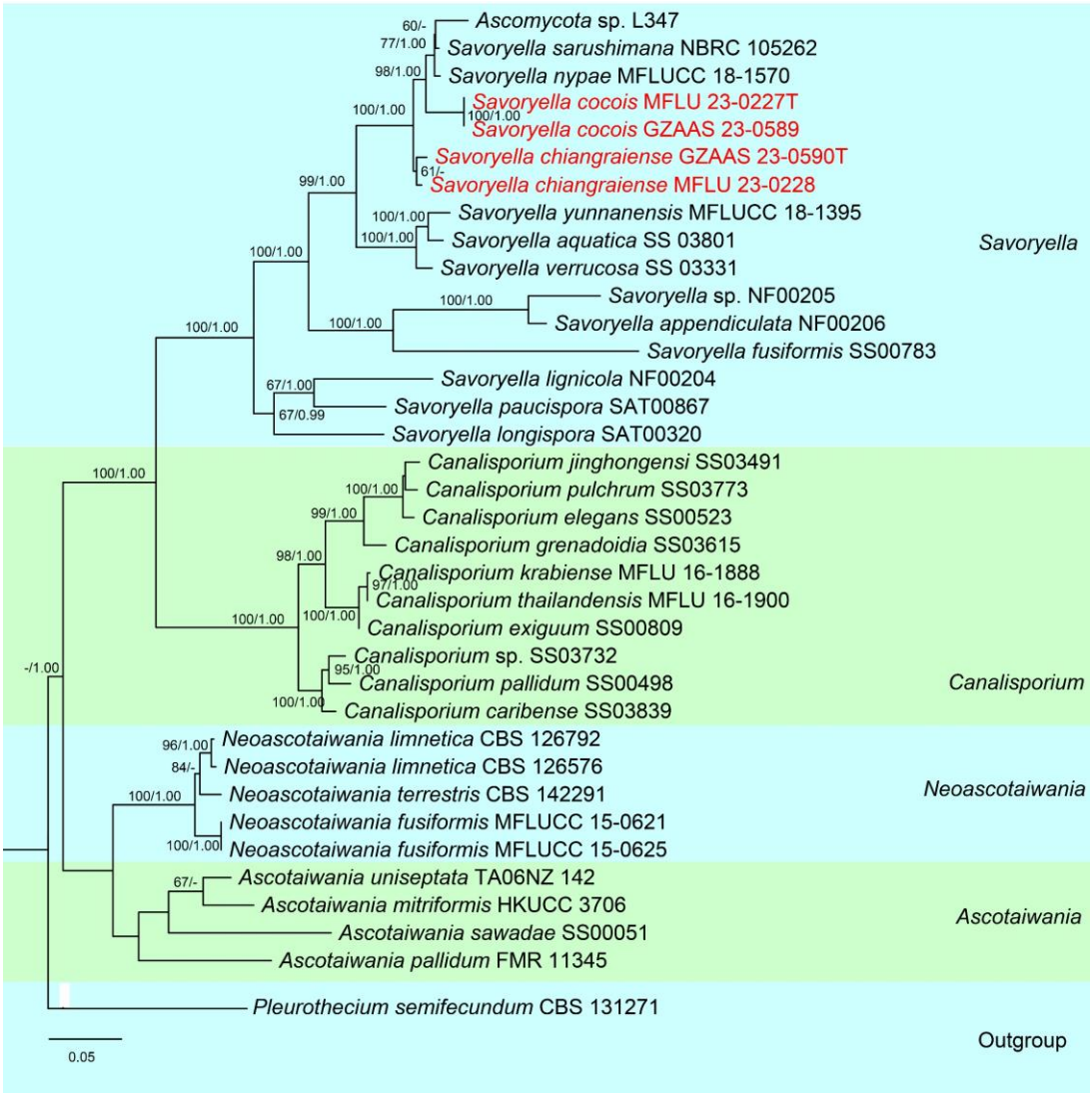

Figure 108 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *rpb2*, and *tef1-α* sequence data. Related sequences were obtained from Yang et al. (2022) and Zhang et al. (2019). Thirty-six strains are included in the combined sequence analysis, which comprises 5082 characters with gaps. *Pleurothecium semifecundum* (CBS131271) was used as the outgroup taxon. The tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -30195.213793 is presented. The matrix had 2120 distinct alignment patterns, with 40.88% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.229475, C = 0.272218, G = 0.296516, T = 0.201792;

substitution rates AC = 1.287163, AG = 2.474590, AT = 1.416277, CG = 1.118198, CT = 5.536441, GT = 1.000000; gamma distribution shape parameter α = 0.283805. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

GenBank numbers – MFLU 23-0228: LSU = OR438869, ITS = OR581913, SSU = OR458368; GZAAS 23-0590: LSU = OR438870, ITS = OR581914, SSU = OR458369

Notes – In our phylogenetic analyses, *Savoryella chiangraiensis* formed a distinct lineage basal to *S. sarushimana* (NBRC 105262), *S. nypae* (MFLUCC 18-1570), *S. cocois* (MFLU 23-0227) and an unverified strain of *Savoryella* sp. (L347) (Fig. 108). *Savoryella chiangraiensis* shares similar characteristics with *S. sarushimana*, *S. nypae*, and *S. cocois* in having micronematous, mononematous, hyaline to pale brown conidiophores, holoblastic, determinate, integrated, terminal conidiogenous cells and rhexolytic, pyriform to obovoid conidia. However, *Savoryella chiangraiensis* differs from *S. sarushimana*, *S. nypae*, and *S. cocois* in having 1-2-septate conidia with dark brown to black upper and middle cells and brown basal cell. *Savoryella sarushimana* has 3–5-septate conidia that are proliferating to give new smaller conidia and septate dark-colored filaments. Conidia of *S. nypae* are 2(−3)-septate with dark brown upper cell, brown or paler middle cell and subhyaline or pale brown basal cell. Conidia of *Savoryella cocois* are 1-septate, with black upper and paler basal cells. Phylogenetically, *Savoryella chiangraiensis* is closer to *S. cocois* (Fig. 108), we compared the base pairs of ITS gene region between these two species and there are 44 bp differences (including 4 gaps). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.99) (Fig. 109). Therefore, we introduce our new isolate as a new species.

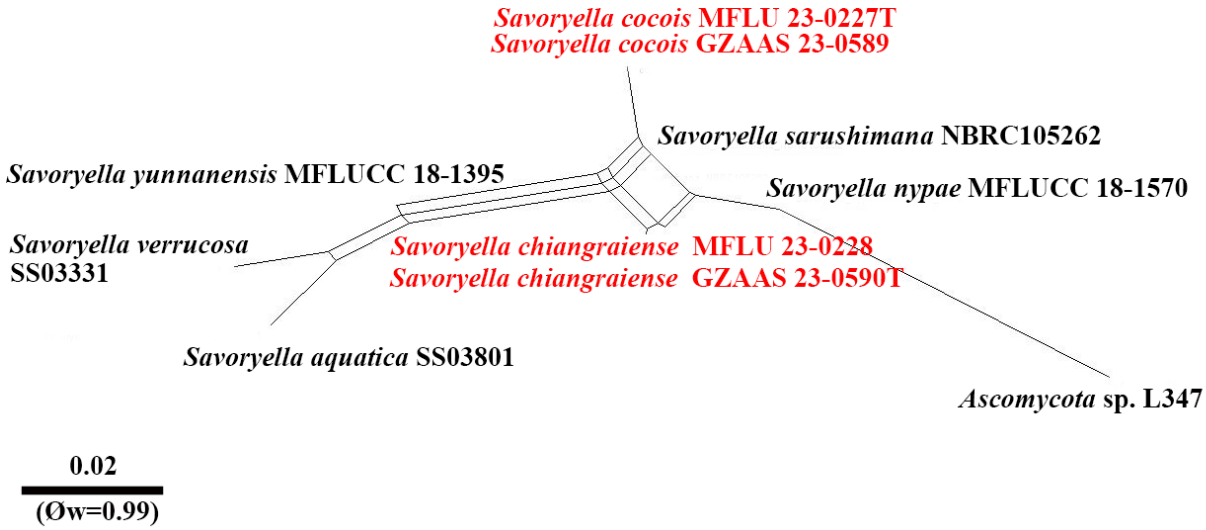

Figure 109 – Results of the PHI test of *Savoryella cocois*, *S. chiangraiense* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

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

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

Chaetosphaeriales was introduced to a accommodate *Chaetosphaeriaceae* by Huhndorf et al. (2004). Three additional families *viz. Helminthosphaeriaceae*, *Linocarpaceae*, and *Leptosporellaceae* were subsequently added to the order (Samuels et al. 1997, Huhndorf et al. 2004, Konta et al. 2017). The recent treatment of *Chaetosphaeriales* was provided by Hyde et al. (2020a), where they accepted four families (*Chaetosphaeriaceae*, *Helminthosphaeriaceae*, *Linocarpaceae*,

and *Leptosporellaceae*) and 59 genera in the order based on phylogenetic analyses and divergence time.

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Chaetosphaeriaceae, a genus-rich family, was initially introduced by Locquin (1984) and later validated by Réblová et al. (1999) with acceptance of seven sexual genera and13 asexual genera. Since then, more genera have been added to the family (Locquin 1984, Réblová 1999, Maharachchikumbura et al. 2016, Lin et al. 2019, Zheng et al. 2020). Maharachchikumbura et al. (2016) and Wijayawardene et al. (2018) included 38 genera in the family. While, Lin et al. (2019) accepted 49 genera. Recently, a comprehensive study of *Chaetosphaeriaceae* was provided by Wu & Diao (2022); they further expanded the family to accommodate 89 accepted genera, including 22 new genera and 10 newly assigned genera based on a systematic study with an integrated approach of morphological observation and phylogenetic analyses. In this study, following the treatment of Wu & Diao (2022), a new genus, *Pseudostriatosphaeria* with the type *P. chiangraiensis* and three new records *Codinaea lithocarpi*, *Dinemasporium ambiguum*, and *D. pseudostrigosum* are introduced based on phylogeny and morphology.

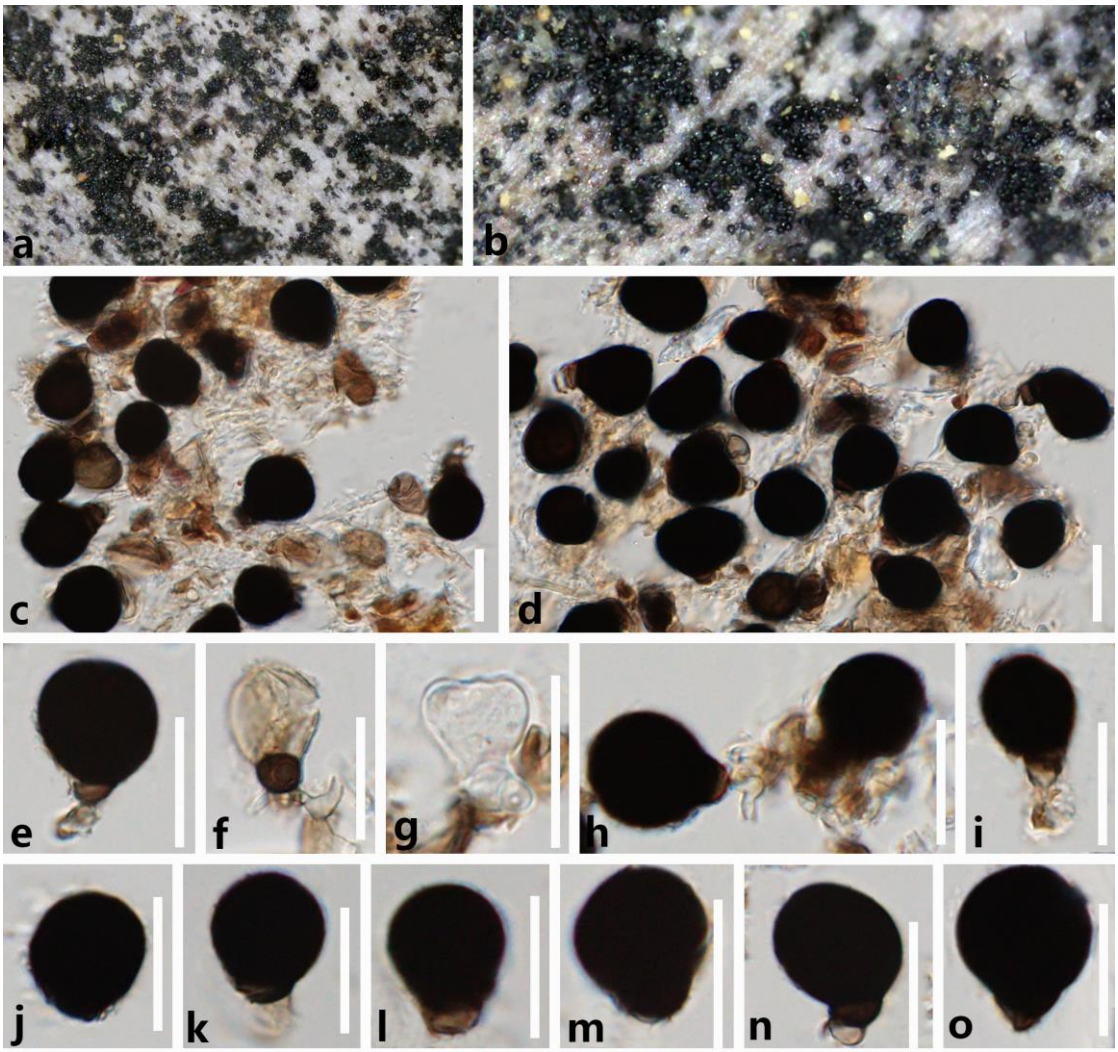

Figure 110 – *Savoryella chiangraiensis* (MFLU 23-0228, holotype). a, b The appearance of conidiomata on the host substrate. c–i Conidia with conidiogenous cells. j–o Conidia. Scale bars: c–o = 20 µm.

Codinaea Maire

Codinaea was introduced by Maire (1937) with *C. aristata* as the type species. Gamundí et al.

(1977) rediscovered *Dictyochaeta* and proposed *Codinaea* as a synonym. However, recent studies suggested that *Codinaea* species with setulate conidia are distinct from those acking conidial setulae (*Dictyochaeta*) (Wu & Diao 2022). The emended concept of the genus was provided in Wu & Diao (2022). There are 79 records listed in Index Fungorum (2023). A new host record species, *Codinaea lithocarpi,* is introduced from *Cocos nucifera* in this study.

64. *Codinaea lithocarpi* (R.H. Perera, E.B.G. Jones & K.D. Hyde) W.P. Wu & Y.Z. Diao, in W.P. Wu & Y.Z. Diao, Fungal Divers. 116: 1–546 (2022) Fig. 111

Index Fungorum number: IF841690; Facesoffungi number: FoF14314

Saprobic on decaying leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate, effuse, hairy, brown, with white conidial masses. *Setae* 160–230 × 4.5–6 µm ($\overline{x}$ = 198 × 5.5 µm, n = 25), solitary or in groups of 2–4, straight or flexuous, septate, unbranched, fertile at apex, with persistent collarettes, dark brown and robust at the base, paler towards the apex, smooth-walled. *Conidiophores* 40–65 × 3–4.5 µm ($\overline{x}$ = 52 × 4 µm, n = 25), macronematous, mononematous, aggregated, in small groups often associated with setae, rarely solitary, straight or flexuous, cylindrical, unbranched, septate, smooth, dark brown to pale brown, paler at apex, smooth-walled. *Conidiogenous cells* 15–25 × 3–5 µm ($\overline{x}$ = 20 × 4 µm, n = 25), mono- to polyphialidic, integrated, terminal, determinate, hyaline or pale brown, with distinct, sub-cylindrical, with funnel-shaped collarettes. *Conidia* 10–15 × 3–4 µm ($\overline{x}$ = 12.5 × 3 µm, n = 25), solitary, aseptate, fusiform, curved, in slimy mass, hyaline, smooth-walled, with single setula at each end, 6−8 µm long, filiform.

Culture characteristics – Conidia germinated on PDA. Colonies circular to irregular, medium dense, flat or effuse, with edge fimbriate and write, white from above and pale brown with time, dark brown below.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, C6-4-1 (MFLU 23-0229), living cultures MFLUCC 23-0155.

Known host and distribution – On dried fruits of *Lithocarpus* sp. (Fagaceae) in Thailand (Perera et al. 2020); on dead culm of *Arundo donax*, on dead fruit of *Camellia* sp., on dead fruit of unidentified tree, on dead leaves of palm in China (Wu & Diao 2022); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – LSU = OR438871, ITS = OR438404

Notes – In a BLASTn search, the closest match of the ITS sequence of the strain with 100% similarity was *Codinaea lithocarpi* (MFLUCC 17-2228), and the closest match to the LSU sequences with 100% similarity was *C. lithocarpi* (MFLUCC 19-0488). In the present phylogenetic analyses, the strain (MFLUCC 23-0155) clustered with *C. lithocarpi* (Fig. 112). The morphology of our strain is similar to *C. lithocarpi* described by Perera et al. (2020). We therefore name our collection as *C. lithocarpi* which is a new host record on *Cocos nucifera* in Thailand.

Dinemasporium Lév.

Dinemasporium was introduced by Léveillé (1846) with *D. strigosum* as the type species. This genus is characterized by superficial conidiomata with setae; “phialidic” conidiogenous cells; and conidia fusiform, aseptate, hyaline to pale brown, smooth, with a single, unbranched, filiform, cellular appendage at each end (not separated from the body via septa); lateral appendages present or absent (Duan et al. 2007, Crous et al. 2012). *Dinemasporium* was revised by Duan et al. (2007) with accepted 24 species and later several new species have been introduced to the genus (Crous et al. 2012, Hashimoto et al. 2015). Recently, Diao et al. (2023) reviewed the genus and accepted 37 species in the genus including seven new species with key to species of *Dinemasporium*. In this study, two new records are introduced with detailed descriptions and illustrations.

65. *Dinemasporium ambiguum* A. Hashim. & Kaz. Tanaka, in Hashimoto et al., Mycoscience 56: 88 (2014) [2015] Fig. 113

Index Fungorum number: IF807969; Facesoffungi number: FoF14315

Saprobic on decaying leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* stromatic, cupulate, superficial, subglobose, unilocular, dark brown to grayish black; composed of dark brown basal stromatic rectangular cells. *Conidiomatal setae* up to 113 µm, arising from the basal stroma, straight, septate, brown, thick-walled. *Conidiophores*, hyaline, lining the basal stroma as palisade layer, cylindrical, smooth, reduce to conidiogenous cells. *Conidiogenous cells* 10–15 × 2–3 µm, ($\overline{x}$ = 10.5 × 2 µm, n = 35), phialidic, lageniform, hyaline, smooth. *Conidia* 8.5–10 × 3–3.5 µm, ($\overline{x}$ = 9 × 3 µm, n = 40), ellipsoid, obtuse at apex, slightly truncate at base, unicellular, hyaline, smooth, guttulate, bearing one or two single unbranched appendages at each end and often with lateral apical appendages arising from slightly below the apex, 5.5–9 µm long ($\overline{x}$ = 7 µm, n = 40).

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 18 September 2020, X.G. Tian, P12-2 (MFLU 23-0230), living cultures MFLUCC 23-0153.

Figure 111 – *Codinaea lithocarpi* (MFLU 23-0229, new host record). a, b Colonies on natural substrate. c–e Setae. f–h conidiogenous cells with conidia. i–o Conidia. p Germinated conidium. q, r Colony on PDA from surface and reverse. Scale bars: c–e = 100 µm, f–h, p = 20 µm, i–o = 10 µm.

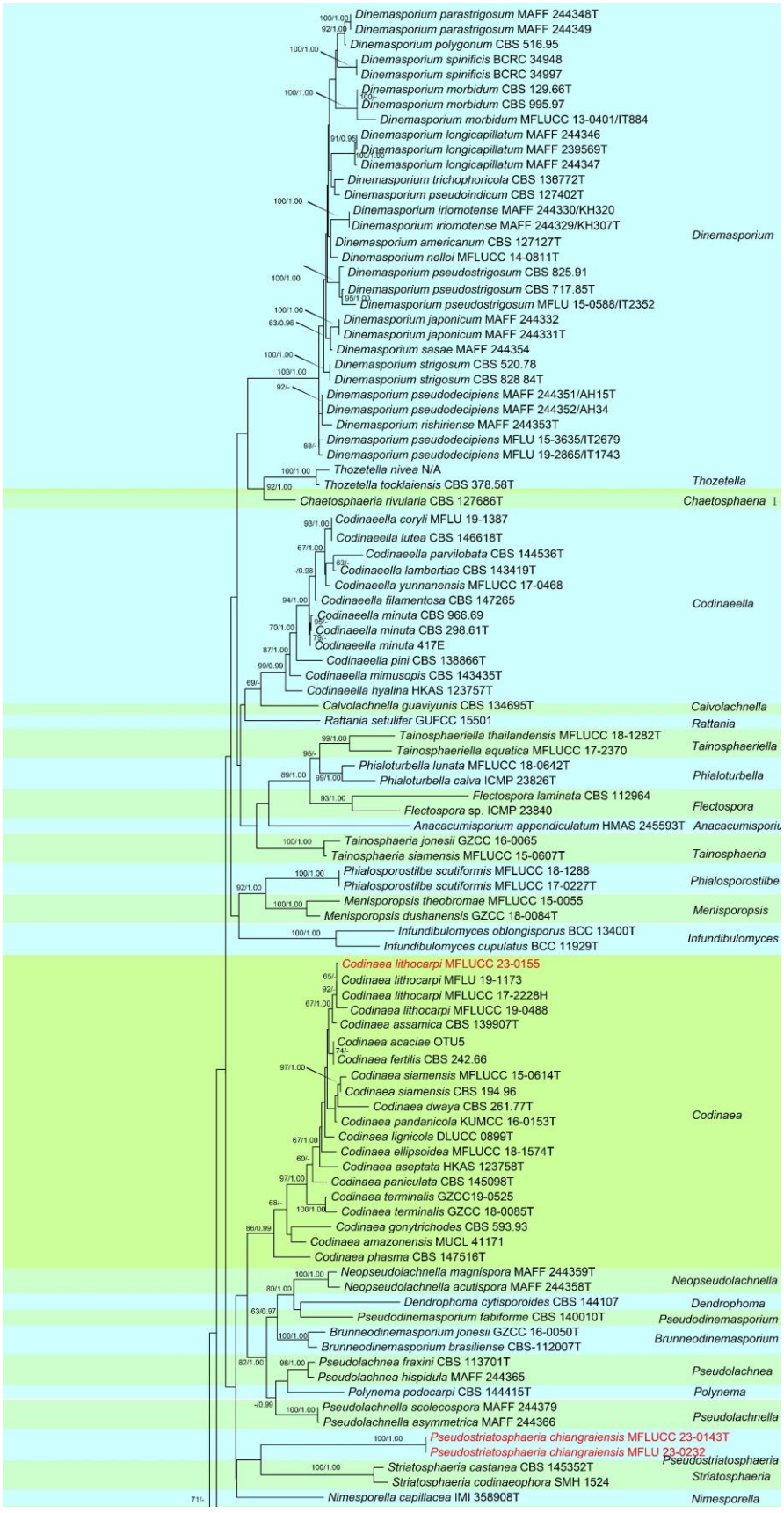

Figure 112 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Wu & Diao (2022). One hundred and ninety strains are included in the combined sequence analysis, which comprise 1608 characters with gaps. *Leptosporella arengae* (MFLUCC 15-0330) and *L. bambusae* (MFLUCC 12-0846) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring

RAxML tree with a final likelihood value of -30626.549853 is presented. The matrix had 953 distinct alignment patterns, with 20.29% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.231652, C = 0.265000, G = 0.298569, T = 0.204779; substitution rates AC = 1.341077, AG = 2.223614, AT = 1.955896, CG = 0.700826, CT = 6.905022, GT = 1.000000; gamma distribution shape parameter 0.298247. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

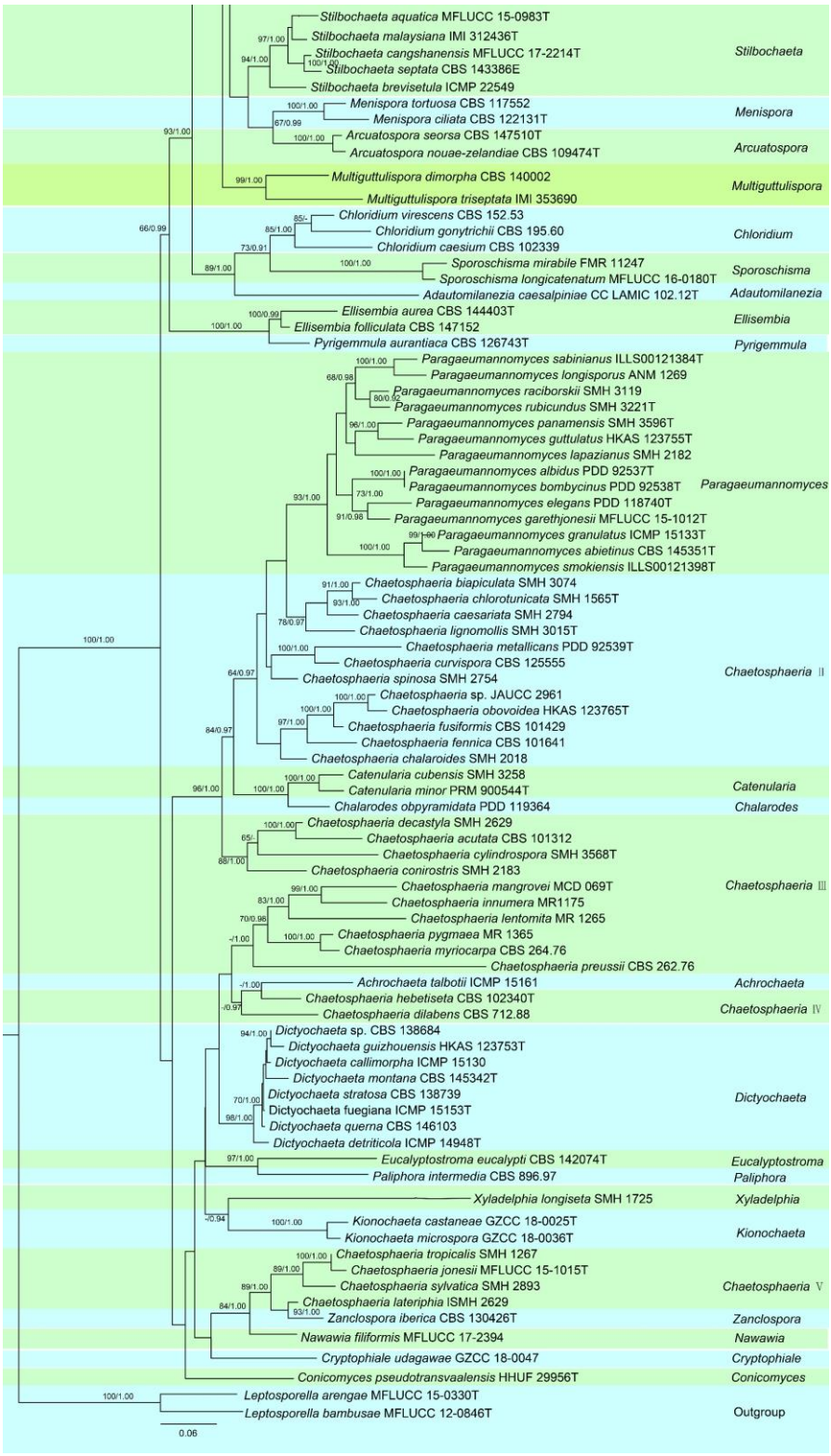

Figure 112 – Continued.

Known host and distribution – On dead culms of *Miscanthus* sp. in Japan (Hashimoto et al. 2015); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438872, ITS = OR438405

Notes – Phylogenetic analyses showed that our strain (MFLUCC 23-0153) clustered with *D. ambiguum* with 60% ML support (Fig. 114). In a BLASTn search, the closest match of the ITS and LSU sequences of the strain with 99.58% and 99.76% similarity, respectively to *D. ambiguum* (NN057382). Our collection (MFLUCC 23-0153) is morphologically similar to the holotype of *D. ambiguum* in having stromatic, scattered, cupulate, superficial, globose to elliptic, unilocular conidiomata with dark brown, smooth-walled, unbranched setae, cylindrical, hyaline, simple or branched conidiophores, phialidic, cylindrical to lageniform conidiogenous cells and naviculate to ellipsoid, unicellular, hyaline, smooth, guttulate conidia that are bearing one or two-branched or unbranched appendages at each end and often lateral (Hashimoto et al. 2015). Therefore, we, identify our isolate as *D. ambiguum*, a new host and geographical record on *Ananas comosus* in Thailand.

Our phylogenetic analysis showed that *D. ambiguum* is closely related to *D. iriomotense*. However, *D. ambiguum* is different from *D. iriomotense* in having simple or branched conidiophores and naviculate to ellipsoid, obtuse at the apex, truncate at the base and larger conidia (8.5–10 × 2–4 µm vs. 6.5–8.5 × 2–3 µm) that are bearing one or two branched or unbranched appendages at each end and often lateral (Hashimoto et al. 2015). While *D. iriomotense* has branched conidiophores and conidia are ellipsoid, obtuse at the apex, slightly truncate at the base and bearing a single unbranched appendage at each end.

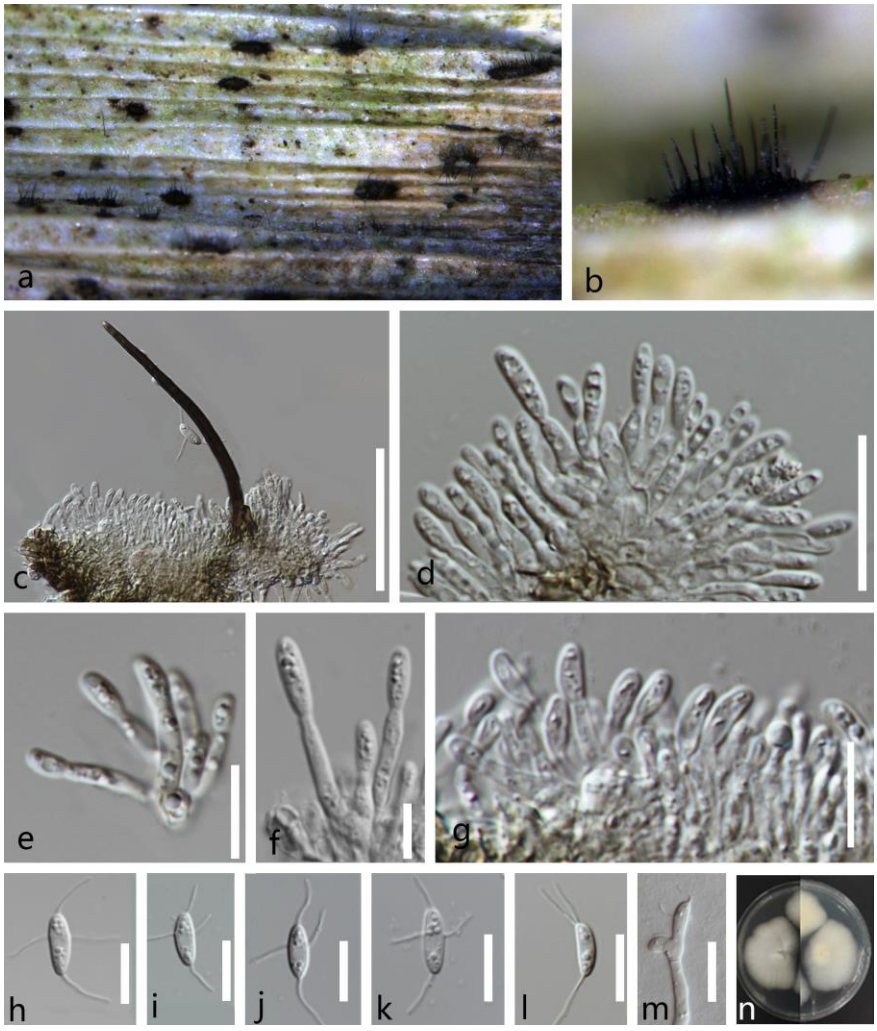

Figure 113 – *Dinemasporium ambiguum* (MFLU 23-0230, new host and geographical record).

a, b Conidiomata on host surface. c Excipulum of conidiomata and setae. d–g Conidiophores, conidiogenous cells and immature conidia. h–l Conidia. m Germinated conidium. n Colonies on PDA from surface and reverse. Scale bares: c = 50 μm, d, e, g = 20 μm, f, h–m = 10 μm.

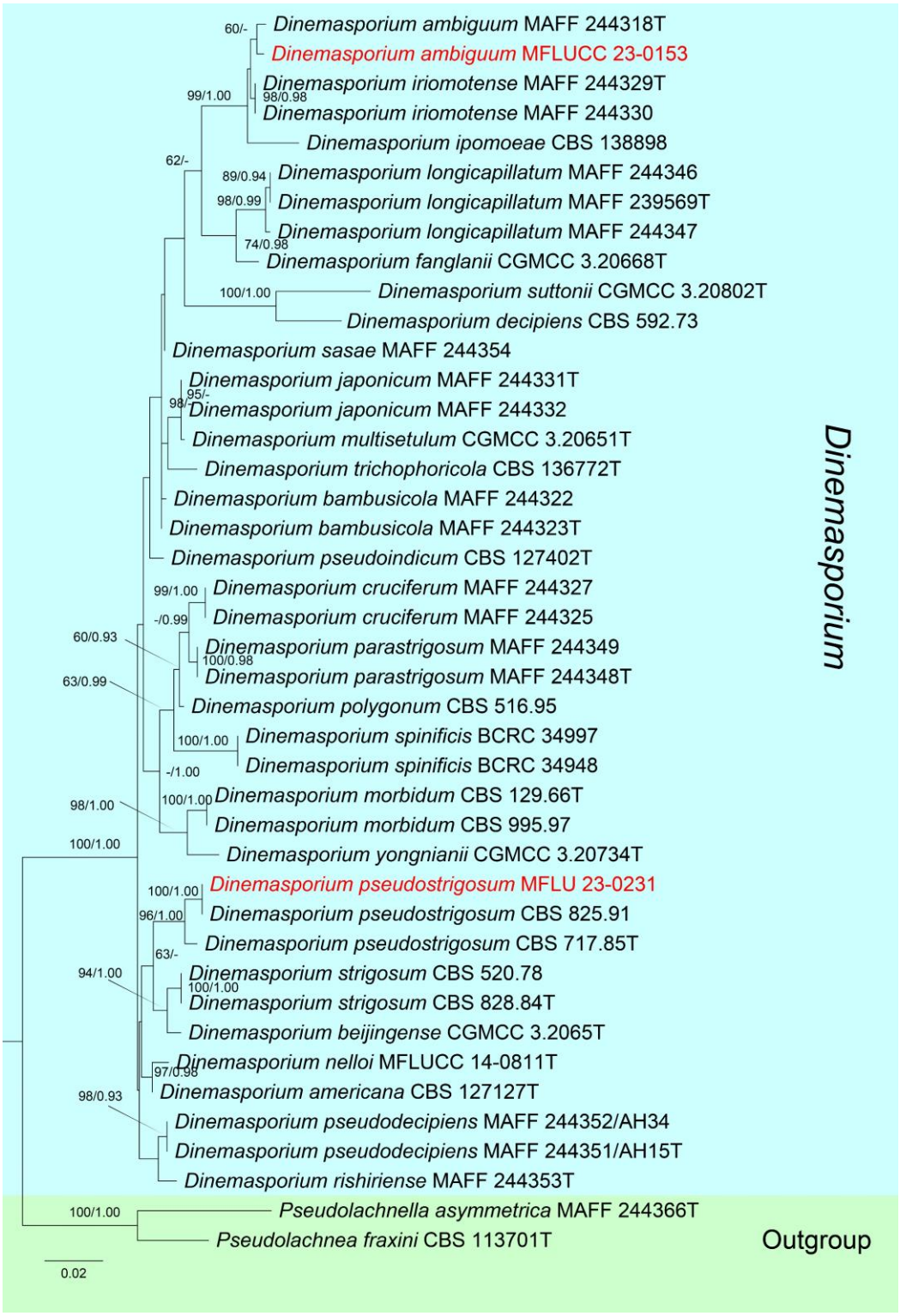

Figure 114 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Wu & Diao (2022). Forty-three strains are included in the combined sequence analysis, which comprise 1663 characters with gaps. *Pseudolachnea fraxini* (CBS 113701) and *Pseudolachnella asymmetrica* (MAFF 244366) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -4874.195394 is presented. The matrix had 306

distinct alignment patterns, with 40.10% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.227517, C = 0.275743, G = 0.292774, T = 0.203965; substitution rates AC = 1.437585, AG = 2.499427, AT = 2.951625, CG = 1.893079, CT = 9.586428, GT = 1.000000; gamma distribution shape parameter 0.100220. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

66. ***Dinemasporium pseudostrigosum*** Crous, in Crous, Verkley, Christensen, Castañeda-Ruíz & Groenewald, in Crous et al. Persoonia 28: 134 (2012) Fig. 115

Index Fungorum number: IF800164; Facesoffungi number: FoF07316.

Saprobic on dead leave of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* brown to dark brown, superficial, solitary to gregarious, pulvinate, oval to rounded in outline setose. *Conidiomatal setae* 190–300 ×5–7 µm ($\overline{x}$ = 245 × 6 µm, n = 15), subulate, brown and blunt at base, becoming paler and acute towards apex, arising from lateral excipulum and basal stroma. *Conidiomatal wall* 10–25 µm thick, composed basal stroma of *textura angularis* with thin-walled, hyaline to pale brown cells, and lateral excipulum of *textura porrecta* with dark brown to hyaline cells. *Conidiophores* hyaline, cylindrical, unbranched, mostly arising from inner layers of basal stroma, occasionally from lateral excipulum. *Conidiogenous cells* 10–15 × 1.5–2 µm ($\overline{x}$ = 11 × 2 µm; n = 20), hyaline, phialidic, integrated or discrete, determinate, subcylindrical, thick and smooth-walled, with moderate periclinal thickenings in the collarette zone. *Conidia* 8–9 ×2–3 µm ($\overline{x}$ = 8 ×2.5 µm; n = 40), hyaline, naviculate to fusiform, rounded at the apex, truncate at the base, unicellular, thick- and smooth-walled, guttulate, bearing 7–9 µm long, unbranched, tubular, with an apical appendage and excentric basal appendage.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 8 December 2020, X.G. Tian, P4-18 (MFLU 23-0231).

Known hosts and distribution – On *Stigmaphyllon sagraeanum* in Cuba (Crous et al. 2012); on *Triticum aestivum* in Germany (Crous et al. 2012); on dead grass (Poaceae) in Thailand (Goonasekara et al. 2022); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438873, ITS = OR438406

Notes – Phylogenetic analyses showed that strain (MFLU 23-0231) grouped between *Dinemasporium pseudostrigosum* with 100% ML and 1.00 PP bootstrap support (Fig. 114). In a BLASTn search of NCBI GenBank, the closest match of the ITS and LSU sequence of our strain with 100% similarity to *D. pseudostrigosum* (JQ889279 and OL824389), respectively and were identical to *D. pseudostrigosum*. Our collection is similar to *D. pseudostrigosum* described by Crous et al. (2012). Therefore, we identified our collection as *D. pseudostrigosum*, a new host record on *Ananas comosus* in Thailand.

67. ***Pseudostriatosphaeria*** X.G. Tian, K.D. Hyde & Tibpromma, gen. nov.

Index Fungorum number: IF900988; Facesoffungi number: FoF14316

Etymology – Genus epithet in reference to the similarity to *Striatosphaeria.*

Saprobic on dead leaves or wood in terrestrial habitats. Sexual morph: Not observed. Asexual morph: *Conidiomata* mostly scattered or sometimes in groups, superficial, cupulate, sporodochial, dark brown to black, setose. *Conidiomatal setae* abundant, brown to black, subcylindrical to cylindrical, straight or slightly curved, septate, wide at base, acute at apex, unbranched, smooth, thick-walled, arising from basal stroma. *Basal stroma* with cells of textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monophialidic, integrated, determinate, hyaline to pale brown, subcylindrical, smooth-walled. *Conidia* fusiform, straight or curved, obtuse to subobtusely rounded at apex, truncate to rounded at the base, hyaline to subhyaline, aseptate, guttulate, smooth-walled, with a single, unbranched, flexuous, tubular appendage at each end.

Type species – *Pseudostriatosphaeria chiangraiensis* X.G. Tian, K.D. Hyde & Tibpromma

Notes – In our multi-loci phylogenetic analyses, *Pseudostriatosphaeria* formed a separate branch and sister to *Striatosphaeria* and *Nimesporella* (Fig. 115). Conidiophores of both

Striatosphaeria and *Nimesporella* are macronematous, mononematous, septate, unbranched, and lack a conidiomatal setae (Réblová et al. 2020b, Wu & Diao 2022). In contrast, *Pseudostriatosphaeria* has conidiomatal setae, and conidiophores are reduced to conidiogenous cells. In addition, the conidia of *Pseudostriatosphaeria* are aseptate, guttulate, fusiform, obtuse to subobtusely rounded at the apex, truncate to rounded at the base conidia with an appendage at each end. While, conidia of *Striatosphaeria* are reniform to ellipsoidal or botuliform, 1-septate, with or sometimes without appendage (Réblová et al. 2020b). Conidiogenuos cells of *Nimesporella* are polyphialidic, extending sympodially (Wu & Diao 2022). In contrast, *Pseudostriatosphaeria* has monophialidic, integrated, determinate conidiogenuos cells. Therefore, a monotypic genus *Pseudostriatosphaeria* is introduced to accommodate *P. chiangraiensis*.

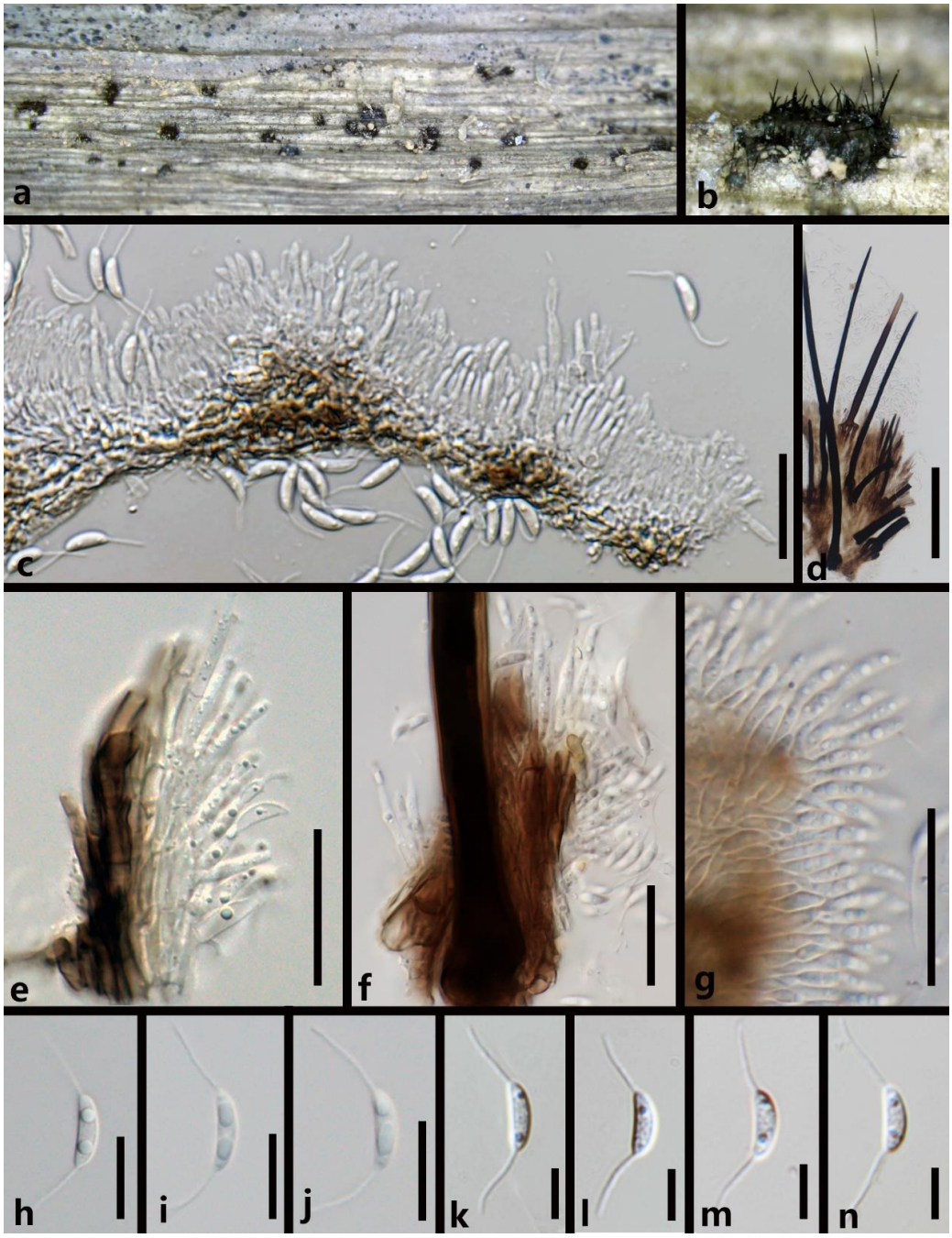

Figure 115 – *Dinemasporium pseudostrigosum* (MFLU 23-0231, new host record). a, b Appearance of black conidiomata on the host. c Vertical section of conidioma. d setae. e–g Conidiophores, conidiogenous cells and developing conidia. h–n Conidia. Scale bars c, d = 100 μm, e–g = 20 μm, h–n = 10 μm.

68. *Pseudostriatosphaeria chiangraiensis* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov.

Fig. 116

Index Fungorum number: IF900989; Facesoffungi number: FoF14317

Etymology – Referring to the location where the specimen was collected, Chiang Rai Province, Thailand.

Holotype – MFLU 23-0233

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* mostly scattered or sometimes in groups, superficial, sporodochial, cupulate, dark brown to black, setose. *Conidiomatal setae* abundant, brown to black, subcylindrical to cylindrical, straight or slightly curved, septate, wide at base, acute at apex, unbranched, smooth, thick-walled, 65–100 µm long, arising from basal stroma. *Basal stroma* with cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 15−20 × 2.5−3 µm ($\overline{x}$ = 18 × 3 µm, n = 30), monophialidic, integrated, determinate, hyaline to pale brown, subcylindrical, smooth-walled. *Conidia* hyaline to subhyaline, aseptate, thin-walled, smooth, fusiform, straight or curved, obtuse to subobtusely rounded at apex, truncate to rounded at the base, guttulate, verruculose, 15−20 × 4−5 µm ($\overline{x}$ = 16 × 4.5, n = 30), with a single, unbranched, flexuous, tubular appendage at each end, 10–15 µm long.

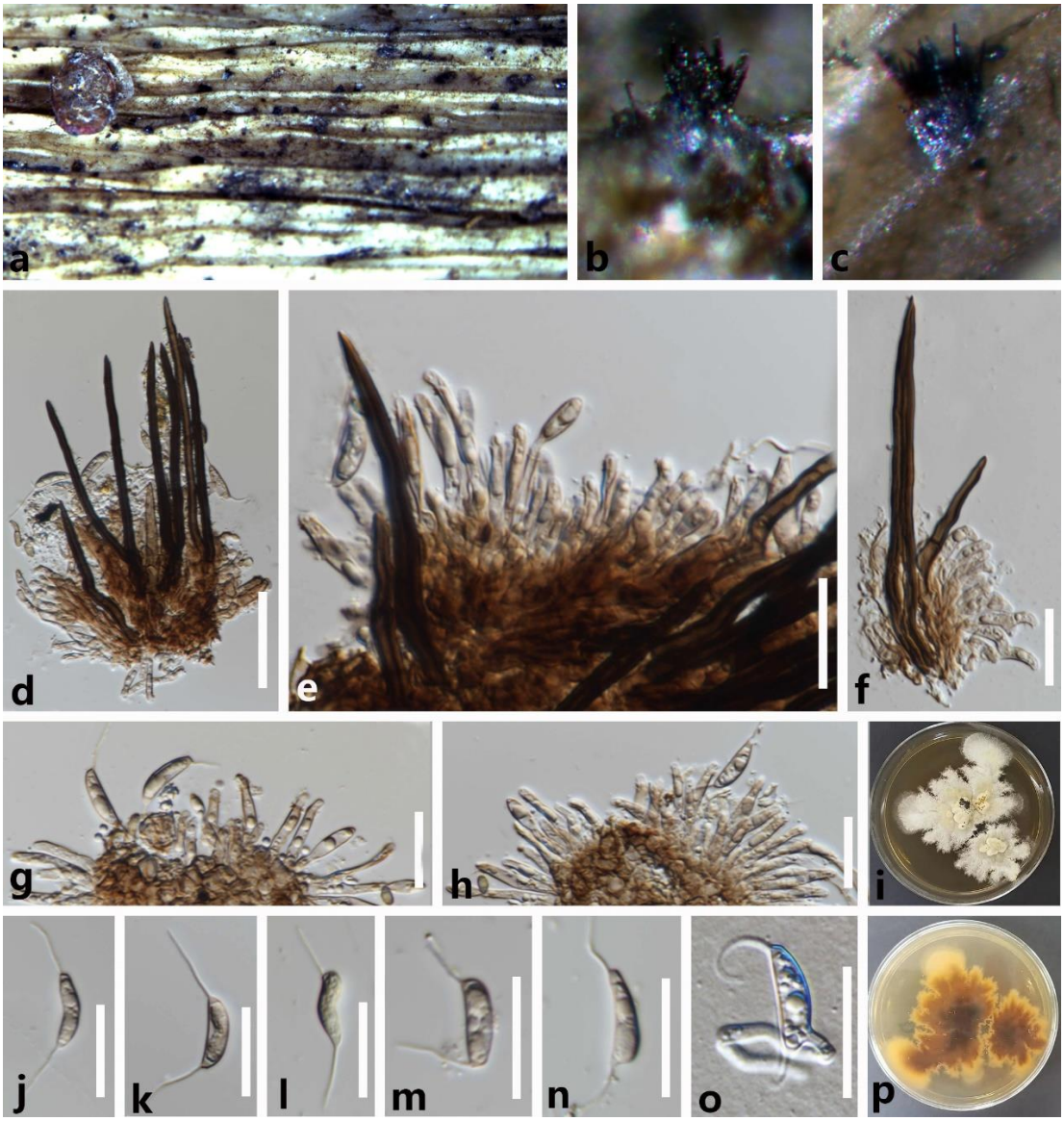

Figure 116 – *Pseudostriatosphaeria chiangraiensis* (MFLU 23-0233, holotype). a–c Colonies on dead leaves of *Ananas comosus*. d, e Section of sporodochium. f Conidiomatal setae.

g, h Conidiogenous cells with attached conidium. j–n Conidia. o Germinated conidium. i, p Colonies on PDA from surface and reverse. Scale bars: d = 40 μm, e–o = 20 μm.

Culture characteristics – Conidia germinating on PDA within 12 h at room temperature. Colonies irregular, mycelium slightly flattened, filamentous, cultures creamy white on surface, brown in reverse.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 17 August 2020, X.G. Tian, p7–2 (MFLU 23-0233, holotype), ex-type culture (MFLUCC 23-0143); *ibid*, 11 November 2020, X.G. Tian, p13–1 (MFLU 23-0232, paratype).

GenBank numbers – MFLU 23-0233: LSU = OR438875, ITS = OR438408. MFLU 23-0232: LSU = OR438874, ITS = OR438407.

Notes – *Pseudostriatosphaeria chiangraiensis* is introduced here as a novel species based on morphological distinctions and phylogenetic analyses. In the multi-loci phylogenetic analyses, *P. chiangraiensis* (MFLUCC 23-0143 and MFLU 23-0232) clustered as a sister lineage to *Striatosphaeria codinaeophora* (MR 1230) and *S. castanea* (CBS 1453520) (Fig. 112). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Fig. 117). The significant recombination between two strains of our strains (MFLUCC 23-0143 and MFLU 23-0232) indicates that they are conspecific (Φw = 1) (Fig. 117). Morphologically, *Pseudostriatosphaeria chiangraiensis* shares similar morphology to *S. codinaeophora* and *S. castanea*, in having monophialidic, hyaline, conidiogenous cells. However, *P. chiangraiensis* differs the two species in having conidiomatal setae, conidiophores reduced to conidiogenous cells, and aseptate, guttulate conidia with appendage at each end. While both *S. codinaeophora* and *S. castanea* lack a conidiomatal setae and have macronematous, mononematous conidiophores and reniform to ellipsoidal, 1-septate conidia (Réblová et al. 2020b). In addition, *S. codinaeophora* lacks conidial appendages which are distinct from *P. chiangraiensis*. Thus, we identified new strains as a novel species, *Pseudochromolaenicola chiangraiensis* based on phylogenetic analyses and morphological characteristics.

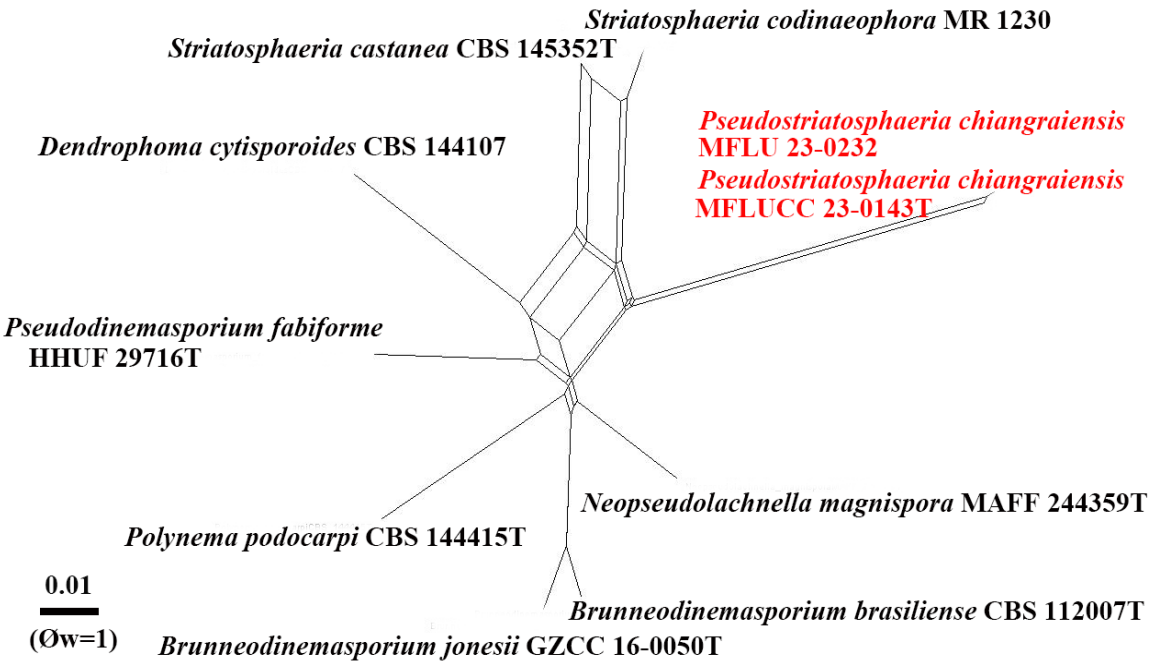

Figure 117 – Results of the PHI test of *Pseudostriatosphaeria chiangraiensis* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxa are in red bold type and T indicates holotype or ex-type strains.

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

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

Amphisphaeriales was introduced by Eriksson (1966). The family consists of 15 families *viz. Amphisphaeriaceae*, *Apiosporaceae*, *Beltraniaceae*, *Castanediellaceae*, *Clypeophysalosporaceae*, *Hyponectriaceae*, *Iodosphaeriaceae*, *Melogrammataceae*, *Oxydothidaceae*, *Phlogicylindriaceae*, *Pseudomassariaceae*, *Pseudosporidesmiaceae*, *Pseudotruncatellaceae*, *Sporocadaceae*, and *Vialaeaceae* (Wijayawardene et al. 2022).

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

Apiosporaceae was introduced by Hyde et al. (1998) to accommodate the genera *Appendicospora* and *Apiospora*, with *Apiospora* as the type genus. Wijayawardene et al. (2022) accepted five genera *viz. Appendicospora*, *Apiospora*, *Arthrinium*, *Dictyoarthrinium* and *Nigrospora* in this family.

Apiospora Sacc.

Apiospora was introduced by Saccardo with *Apiospora montagnei* as the type species (Saccardo 1875). The genus was reported in both sexual and asexual morphs. The sexual morphs are characterized by multi-locular perithecial stromata with hyaline ascospores surrounded by a thick gelatinous sheath (Dai et al. 2016, Pintos & Alvarado 2021). The asexual morph of *Apiospora* was characterized by basauxic conidiogenesis, with globose to subglobose conidia, which are usually lenticular in side view, obovioid and pale-brown to brown (Hyde et al. 1998, Dai et al. 2016). Most *Apiospora* species are associated with plants as endophytes, pathogens or saprobes (Samuels et al. 1981, Dai et al. 2016, Yin et al. 2021). Some species have also been isolated from lichens, air, soil and animal tissues (Sharma et al. 2014, Elissawy et al. 2017, Goodenough et al. 2017, Wang et al. 2017a, Tang et al. 2020).

69. ***Apiospora ananasi*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 118

Index Fungorum number: IF900990; Facesoffungi number: FoF14320

Etymology – Referring to *Ananas comosus*, on which the fungus was collected.

Holotype – MFLU 23-0236

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Colonies* on natural substrate dry, dark brown to black, consisting of a sterile mycelial outer zone and a round, abundantly sporulating center. *Mycelium* superficial, branched, hyaline, smooth-walled hyphae. *Conidiophores* 10–25 µm high × 1.5–3 µm diam. ($\bar{x}$ = 16.5 × 2 µm, n = 10), basauxic, mononematous, branched, flexuous, smooth, hyaline, septate. *Conidiogenous hyphae* develop from conidiogenous mother cells. *Conidiogenous cells* monoblastic or polyblastic, terminal to intercalary, hyaline, smooth, cylindrical to subcylindrical. *Conidia* aseptate, brown to black, 15–20 µm diam. ($\bar{x}$ = 16.5 µm, n = 40), globose to subglobose, with a straight germ-slit along spore length.

Culture characteristics – Conidia germinating on PDA within 24 h at 25 ℃. On PDA, colonies are surface white, lightly yellow, wooly, flat, spreading, filiform, with abundant aerial mycelia, reverse off-white to yellow.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 2 September 2020, X.G. Tian, p9-6, (MFLU 23-0236, holotype); ex-type living culture MFLUCC 23-0101.

GenBank numbers – MFLU 23-0236: LSU = OR438876, ITS = OR438409, *tef1-α* = OR500338, tub2 = OR538086. MFLUCC 23-0101: LSU = OR438877, ITS = OR438410, *tef1-α* = OR500339, *tub*2 = OR538085

Notes – In the phylogenetic analyses, *Apiospora ananasi* formed a distinct lineage and basal to *A. aurea* (CBS 244.83), *A. cordylinae* (GUCC 10026), and *A. hydei* (CBS 114990 and KUMCC 16–0204) with 89% ML and 1.00 PP bootstrap support values (Fig. 119). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 0.08) (Fig. 120). Morphologically, *Apiospora ananasi* is different from *A. aurea* in having smaller conidia

without a hyaline rim (15–20 µm vs. 10–30 × 10–15 µm diam). In addition, conidiogenous hyphae of *A. aurea* are denticulate, which was not observed in *A. ananas* (Calvo & Guarro 1980). *Apiospora ananasi* is distinct from *A. hydei* by micronematous, flexuous, hyaline conidiophores, monoblastic or polyblastic, hyaline, cylindrical to subcylindrical conidiogenous cells and brown to black, globose to subglobose conidia. *Apiospora hydei* has pale brown conidiophores, subcylindrical to doliiform to lageniform conidiogenous cells and brown, roughened, globose in surface view, lenticular in side view conidia *Apiospora cordylinae* has conidiophores reduced to conidiogenous cells, erect, doliiform to ampulliform or lageniform conidiogenous cells and olivaceous to brown conidia. Both phylogenetic analyses and morphological characteristics supported our species as a distinct new species.

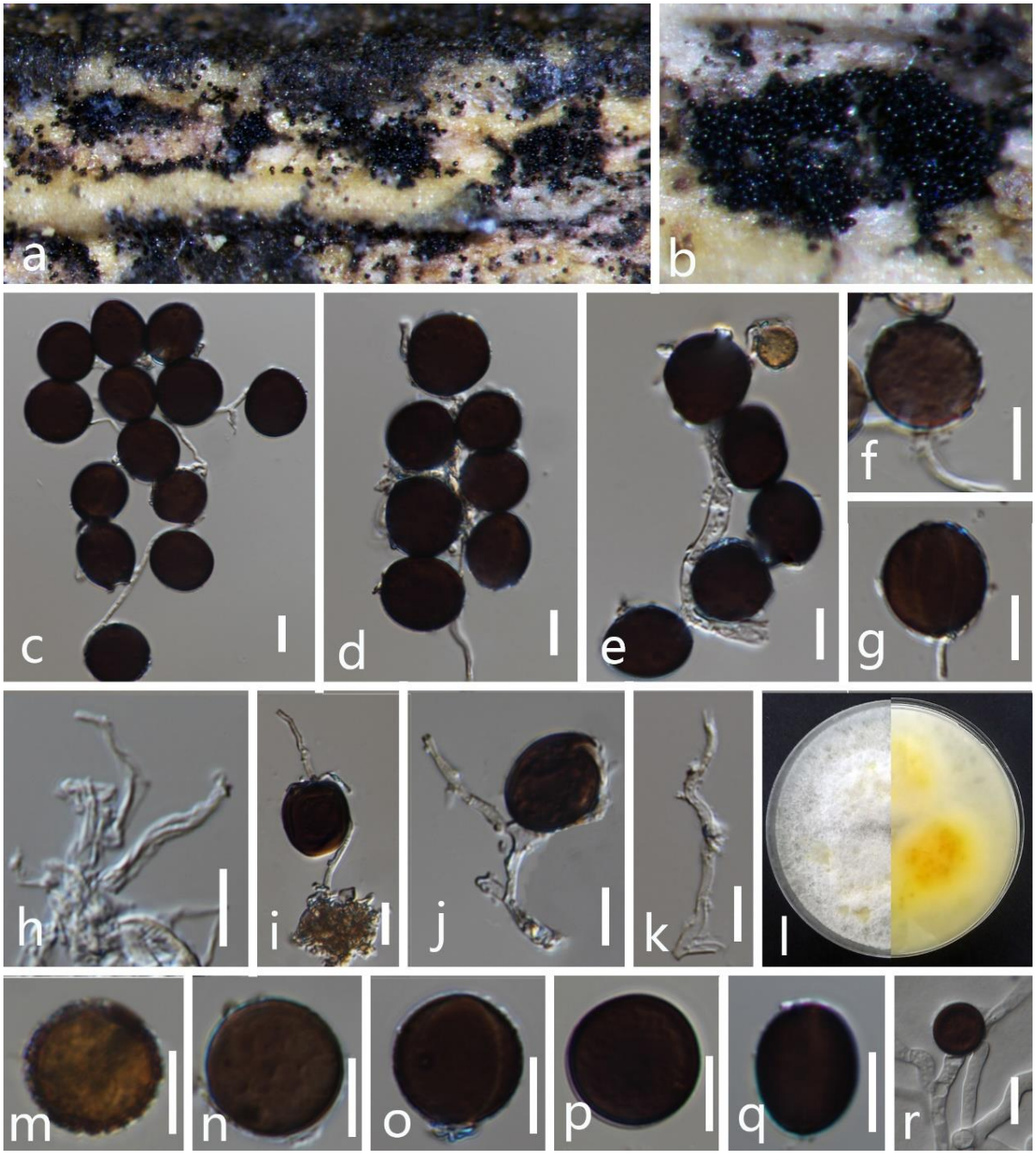

Figure 118 – *Apiospora ananasi* (MFLU 23-0236, holotype). a–b Appearance of the fungus on dead leaves of *Ananasi comosus*. c–g, i, j Conidia with conidiophores. h, k conidiophores. m–q Conidia. r Germinated conidium. l Colonies on PDA from surface and reverse. Scale bars: c–k, m–r = 10 µm.

Figure 119 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1-α*, and *tub2* sequence data. Related sequences were obtained from Tian et al. (2021a). One hundred and thirty-nine strains are included in the combined sequence analysis, which comprise 2799 characters with gaps. *Sporocadus trimorphus* (CBS 114203) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -35836.050389 is presented. The matrix had 1676 distinct alignment patterns, with 34.90% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237659, C = 0.254267, G = 0.253704, T = 0.254370; substitution rates AC = 1.319455, AG = 3.273930, AT = 1.170924, CG = 1.081154, CT = 4.981121, GT = 1.000000; gamma distribution shape parameter 0.292067. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

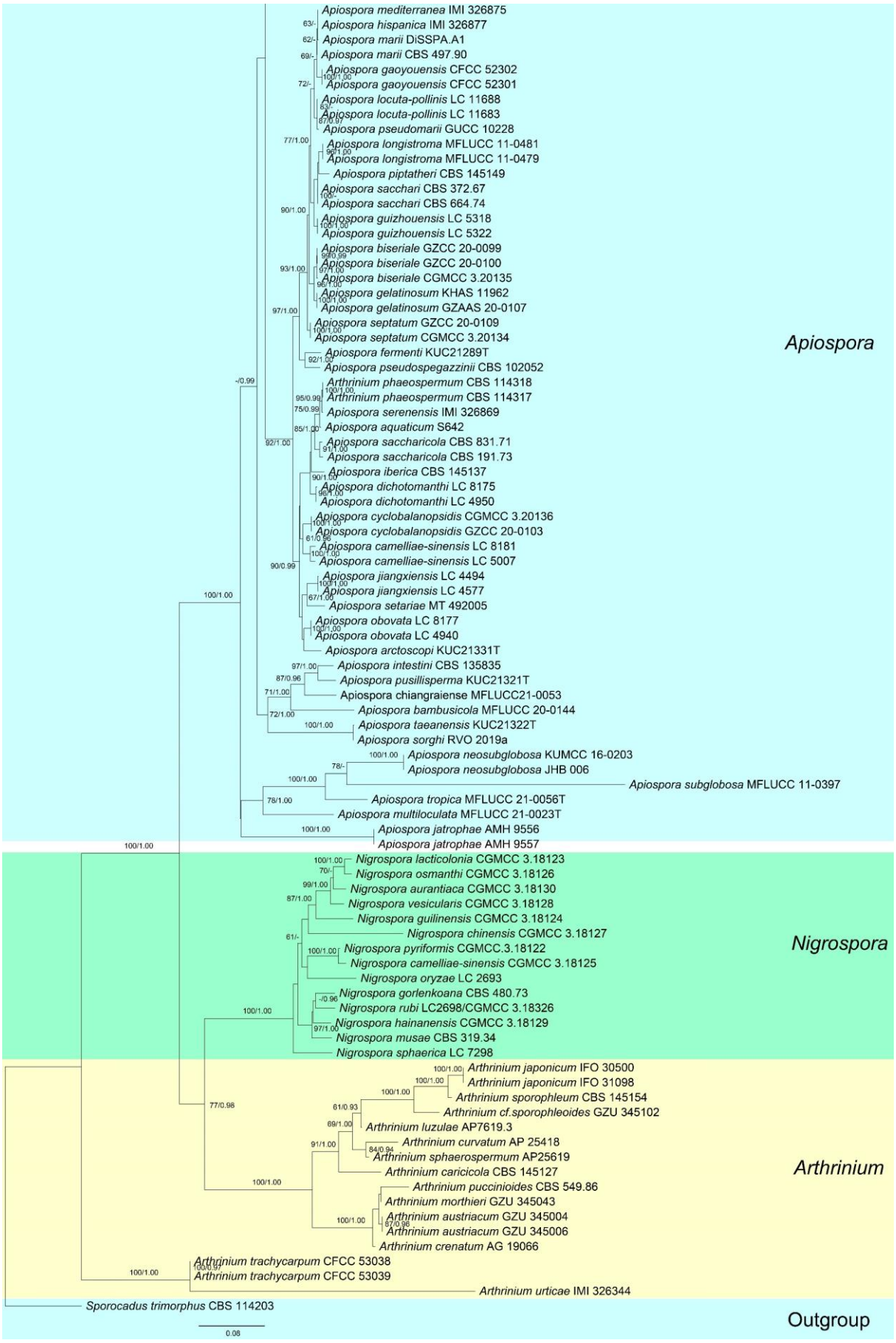

Figure 119 – Continued.

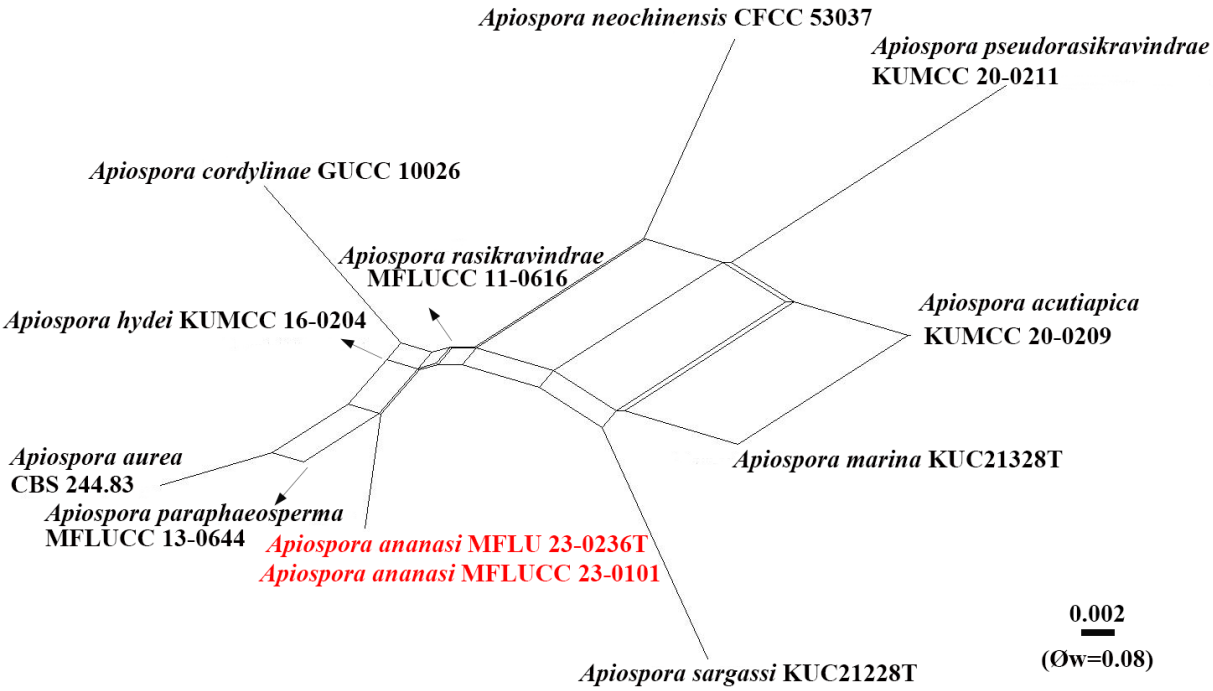

Figure 120 – Results of the PHI test of *Apiospora ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test did not find any statistically significant recombination (Φw = 0.08) in the data set. The new strains are in red bold type, and T indicates holotype or ex-type strains.

70. *Apiospora rasikravindrae* (Shiv M. Singh, L.S. Yadav, P.N. Singh, Rahul Sharma & S.K. Singh) Pintos & P. Alvarado, in Pintos et al., Fungal Systematics and Evolution 7: 207 (2021)

Fig. 121

Index Fungorum number: IF837716; Facesoffungi number: FoF14321

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* pycnidial, scattered, globose to slightly conical, black. *Conidiophores* 10–20 × 1–2 µm ($\overline{x}$ = 14 × 1.5 µm, n = 15), basauxic, mononematous, unbranched, straight or flexuous, hyaline to brown, smooth and thin-walled. *Conidiogenous hyphae* develop from conidiogenous mother cells. *Conidiogenous cells* monoblastic or polyblastic, terminal or intercalary, determinate, cylindrical, hyaline to brown, smooth, aggregated. *Conidia* in surface view 10–11.5µm diam. ($\overline{x}$ = 11 µm, n = 80), in lateral view 10–12 × 6.5–8µm ($\overline{x}$ = 11 × 7.5 µm, n = 30), borne as bunches on conidiophores, lenticular inside view, globose to ovoid, occasionally elongated to ellipsoidal in surface view, brown to dark brown, smooth-walled, thin-walled, with a central scar and straight germ slit spore length.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, p6-15 (MFLU 23-0237); living culture, MFLUCC 23-0110.

Known hosts and distribution – From soil in Svalbard (Singh et al. 2013); on dead culms of bamboo in Thailand (Tian et al. 2022a); from egg masses of *Arctoscopus japonicus* in Korea (Kwon et al. 2022); on *Cissus* sp. in Netherlands (Crous & Groenewald 2013); on *Phyllostachys aurea* in Spain (Pintos et al. 2019); on Bamboo in China (Wang et al. 2018); on rice in Thailand (Crous & Groenewald 2013); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438878, ITS = OR438411, *tef1-α* = OR500340, *tub*2 = OR538087

Notes – Our phylogenetic analyses showed that our strain (MFLUCC 23-0110) group within the lineage of *A. rasikravindrae* (Fig. 119). Morphologically, our new isolate is closely related to the holotype of *A. rasikravindrae* in having lenticular, globose to ovoid, occasionally elongated to

ellipsoidal, brown to dark brown, smooth-walled, germ-slit conidia and micro-semi-macronematous, mononematous, unbranched, straight or flexuous, smooth and thin-walled, hyaline conidiophores. Hence, our strain is identified as *A. rasikravindrae*, a new host record on *Ananas comosus*.

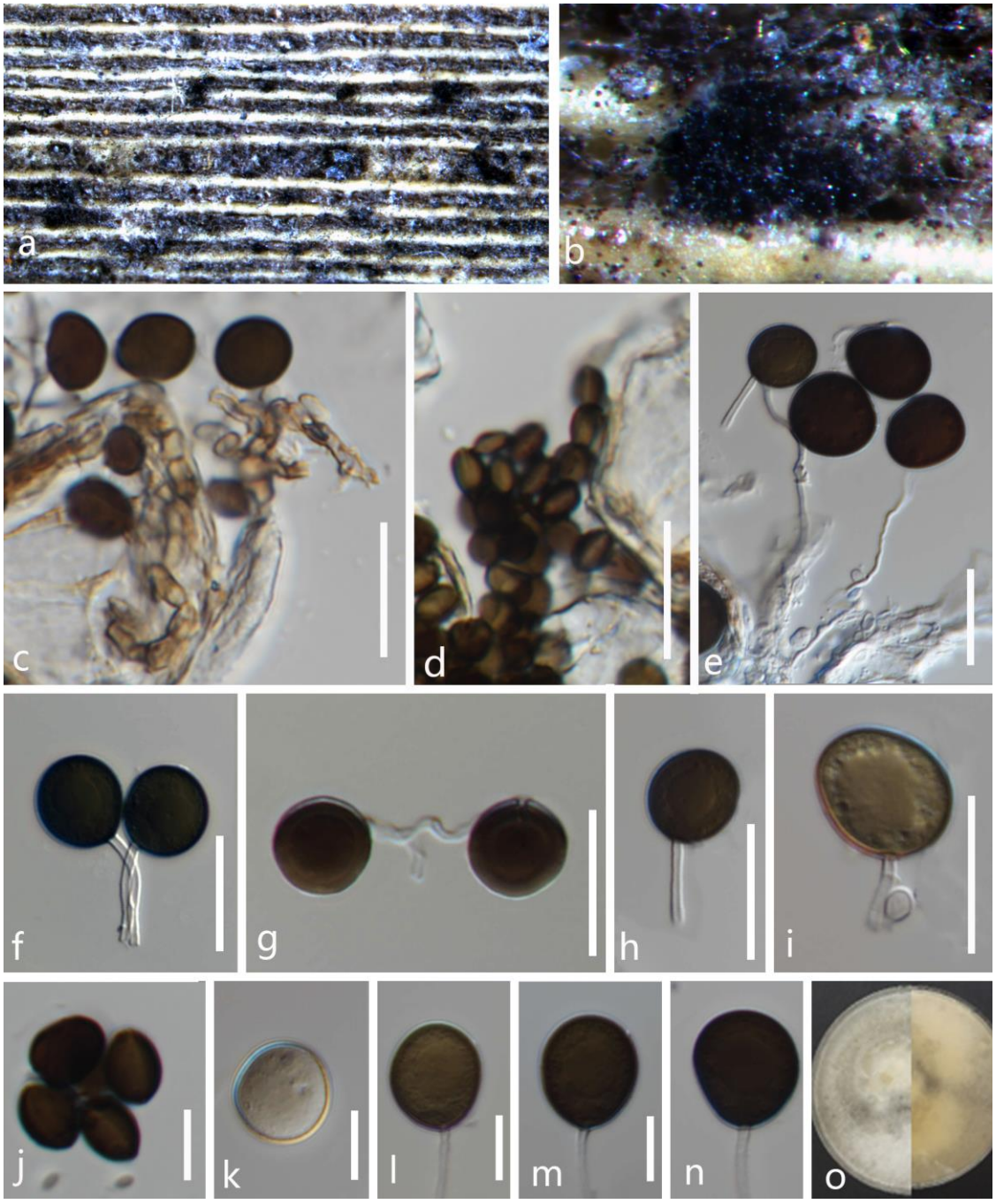

Figure 121 – *Apiospora rasikravindrae* (MFLU 23-0237, new host record). a, b Appearance of the fungus on dead leaves of *Ananas comosus*. c–e Conidia with conidiophores. f–i, l–n Conidiogenous cells bearing conidia. j, k Conidia. o Colonies on PDA from surface and reverse. Scale bars: c–i = 20 µm, j–o = 10 µm.

Nigrospora Zimm.

Nigrospora is a cosmopolitan dematiaceous ascomycetes fungus with a diverse host range. Species in this genus have been reported as pathogens, endophytes, and saprobes from various hosts (Rashmi et al. 2019). The asexual morph of this genus is characterized by branched micronematous or semimacronematous conidiophores, monoblastic conidiogenous cells and black,

shiny, aseptate conidia and sexual morph comprises perithecial ascomata, short–stalked asci with biseriate ascospores (Rashmi et al. 2019, Raza et al. 2019). Forty-one species are listed in Index Fungorum (2023). In this study, *Nigrospora oryzae* was isolated from leave spots of *Oryza sativa.*

71. ***Nigrospora oryzae*** (Berk. & Broome) Petch, J. Indian bot. Soc. 4: 24 (1924) Fig. 122

Index Fungorum number: IF253729; Facesoffungi number: FoF06596

Associated on leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. Hyphae smooth, hyaline to pale brown, branched, septate, 2–4 μm diam. *Conidiophores* micronematous or semi-macronematous, multi-septate, branched, flexuous or straight, pale brown, smooth. *Conidiogenous cells* 10–15 × 3.5–6 μm ($\overline{x}$ = 4.7 × 10.4 μm, n = 15), globose to subglobose, ampulliform, aggregated in clusters on hyphae, monoblastic, pale brown. *Conidia* 10–15 × 10–13 μm ($\overline{x}$ = 12.6 × 11.1 μm, n = 30), solitary, globose or subglobose, dark brown to black, shiny, smooth, aseptate.

Culture characteristics – Colonies on PDA, 30–35 mm diam. after 2 weeks, colonies from above: medium dense, irregular, fat, slightly raised, surface smooth with crenate edge, velvety with smooth aspects, grey to white; reverse: dark brown to grey in the center, grey to pale brown at the margin.

Material examined – Thailand, Chiang Rai Province, Nang Lae Subdistrict, on leaves of *Oryza sativa*, 26 July 2020, X.G. Tian, R(P)2–2 (MFLU 23-0238, dried culture); living culture, MFLUCC 23-0167.

Hosts and distribution – On *Gossypium hirsutum* in China (Zhang et al. 2012a); on *Aloe vera* in China (Zhai et al. 2013); on *Hibiscus mutabilis* in China (Han et al. 2021); on date palm in Iraq (Abass & Mohammed 2014); on *Dendrobium candidum* in China (Wu et al. 2014); on *Arachis hypogaea* in India (Vijayalakshmi et al. 2022); on *Aquilaria sinensis* in China (Li et al. 2014); on *Poa pratensis* in Canada (Zheng et al. 2012); *Tinospora cordifoli*a in India (Vig et al. 2022); on *Oryza sativa* (Rice) in China (Liu et al. 2021a); on cotton in Alabama (Palmateer et al. 2003); on *Aloe vera* in Pakistan (Alam et al. 2017); on Wheat in Kazakhstan (Eken et al. 2016); on *Costus speciosus* in China (Sun et al. 2021); in *Aloe vera* from Bangladesh (Begum et al. 2018); on rice leaves in Sri Lanka and on *Camellia* sp., *Castanopsis* sp., *Cephalotaxus sinensis*, *Cleyera japonica*, *Daphniphyllum macropodum*, *Daphniphyllum oldhamii*, *Nelumbo* sp., on *Neolitsea* sp., *Osmanthus* sp., *Pentactina rupicola*, *Pittosporum illicioides*, *Rhododendron* sp., *Rubus reflexus*, submerged wood, *Symplocos zizyphoides*, *Ternstroemia* sp., *Tutcheria microcarpa* in China (Wang et al. 2017b); on *Bromus inermis* and *Festuca elatior* in Canada (Conners 1967); on *Cercis chinensis*, *Pinus thunbergia* and *Prunus serrulata* in Japan (Watanabe 2010); on *Eucalyptus globulus* in Uruguay (Lupo et al. 2001); on *Quercus* spp. in USSR (Mittal et al. 1990); from *Emblica officinalis* in India (Rathod et al. 2014); on *Camellia sinensis* in China (Manawasinghe et al. 2021); on *E. nitens*, *E. grandis*, *Glycine max*, *Gossypium hirsutum* and *Kigelia pinnata* (Rashmi et al. 2019); on dead leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438879, ITS = OR438412, *tef1-α* = OR500341

Notes – In our phylogenetic analyses, our new isolate (MFLUCC 23-0167) clustered with four strains of *Nigrospora oryzae* with 99% ML and 1.00 PP support (Fig. 123). Morphologically, our new collection is similar to *N. oryzae* in having micronematous or semi-macronematous, multiseptate, flexuous or straight, pale brown, smooth-walled conidiophores, monoblastic, determinate conidiogenous cells and globose or subglobose, black, smooth, aseptate conidia. There are no significant morphological differences between our new isolate and *N. oryzae*. The comparisons of nucleotide of ITS and *tef1-α* gene regions between our new isolate and *N. oryzae* (LC 6759, LC 6766, LC 2689 and LC 7293) revealed 1bp and 5bp differences, respectively. Thus, we identified our new isolate as *N. oryzae* and introduced it as a new geographical record in Thailand.

Beltraniaceae Nann.

Beltraniaceae accepted nine genera, *Beltrania*, *Beltraniella*, *Beltraniopsis*, *Hemibeltrania*,

Parapleurotheciopsis, *Porobeltraniella*, *Pseudobeltrania*, *Pseudosubramaniomyces*, and *Subsessila* (Wijayawardene et al. 2022). Most *Beltraniaceae* species are saprobes, while a few are pathogen (Hyde et al. 2020b).

Beltrania Penz.

Beltrania was introduced to accommodate *B. rhombica* by Penzig (1882). *Beltrania* species are mainly characterized by unbranched setae with radially lobed basal cells, unbranched conidiophores, denticulate conidiogenous cells and biconic conidia (Penzig 1882, Phukhamsakda et al. 2022). A sexual morph has not been reported for this genus. This study introduces a new record of *Beltrania rhombica* from dead leaves of *Ananas comosus* in Thailand.

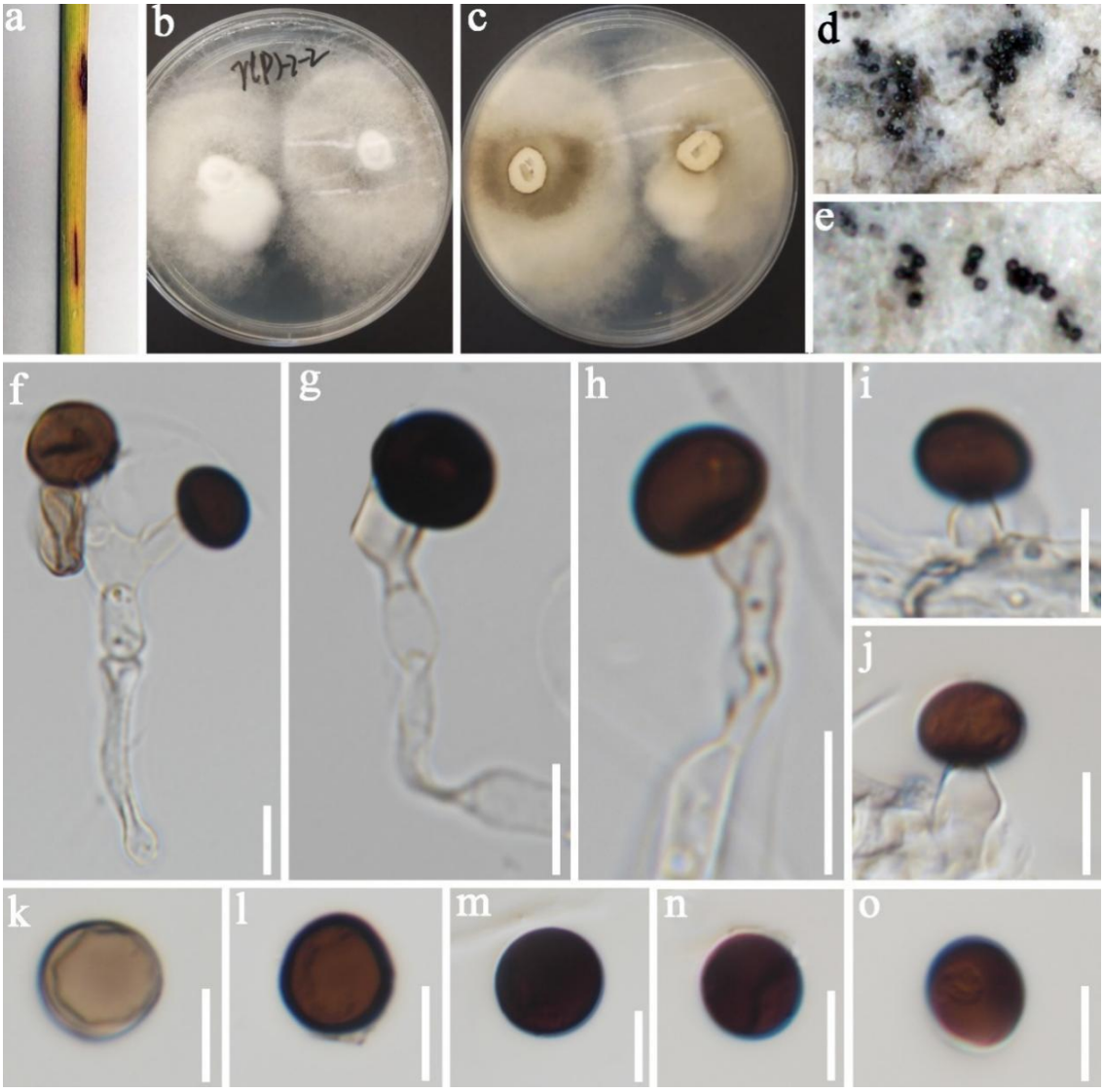

Figure 122 – *Nigrospora oryzae* (MFLU 23-0238, new geographical record). a Symptoms on the leaf of *Oryza sativa*. b Colonies on PDA from surface. c Colonies on PDA from reverse. d, e Hyphae with conidia mass forming on culture. f–j Conidiogenous cells with conidia. k–o Conidia. Scale bars: f–o = 10 μm.

72. *Beltrania rhombica* Penz., Michelia 2(no. 8): 474 (1882) Fig. 124

Index Fungorum number: IF240124; Facesoffungi number: FoF03631

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Mycelium* mostly immersed in the substratum. *Setae* numerous, erect, flexuous, unbranched, single, thick-walled, smooth, pale brown to dark brown, up to 100 μm long, 5–6 μm

wide at the base. *Conidiophores* macronematous, single or in groups, straight or flexuous, septate, smooth, thick-walled, cylindrical or clavate, brown, arising from radially lobed basal cells, 26–40 × 3.5–5.5 µm ($\bar{x}$ = 30 × 7 µm, n = 15). *Conidiogenous cells* polyblastic, integrated, terminal, sympodial, cylindrical or clavate, brown, smooth, 10–20 × 2.5–10 µm ($\bar{x}$ = 15 × 4 µm, n = 15). *Conidia* acrogenous, simple, dry, straight, smooth, biconic, appendiculate, rostrate, pale brown with a hyaline to subhyaline equatorial transverse band, 20–25 µm ($\bar{x}$ = 22 µm, n = 20) long including appendage, 10–15 µm ($\bar{x}$ = 12 µm, n = 20) wide in the broadest part.

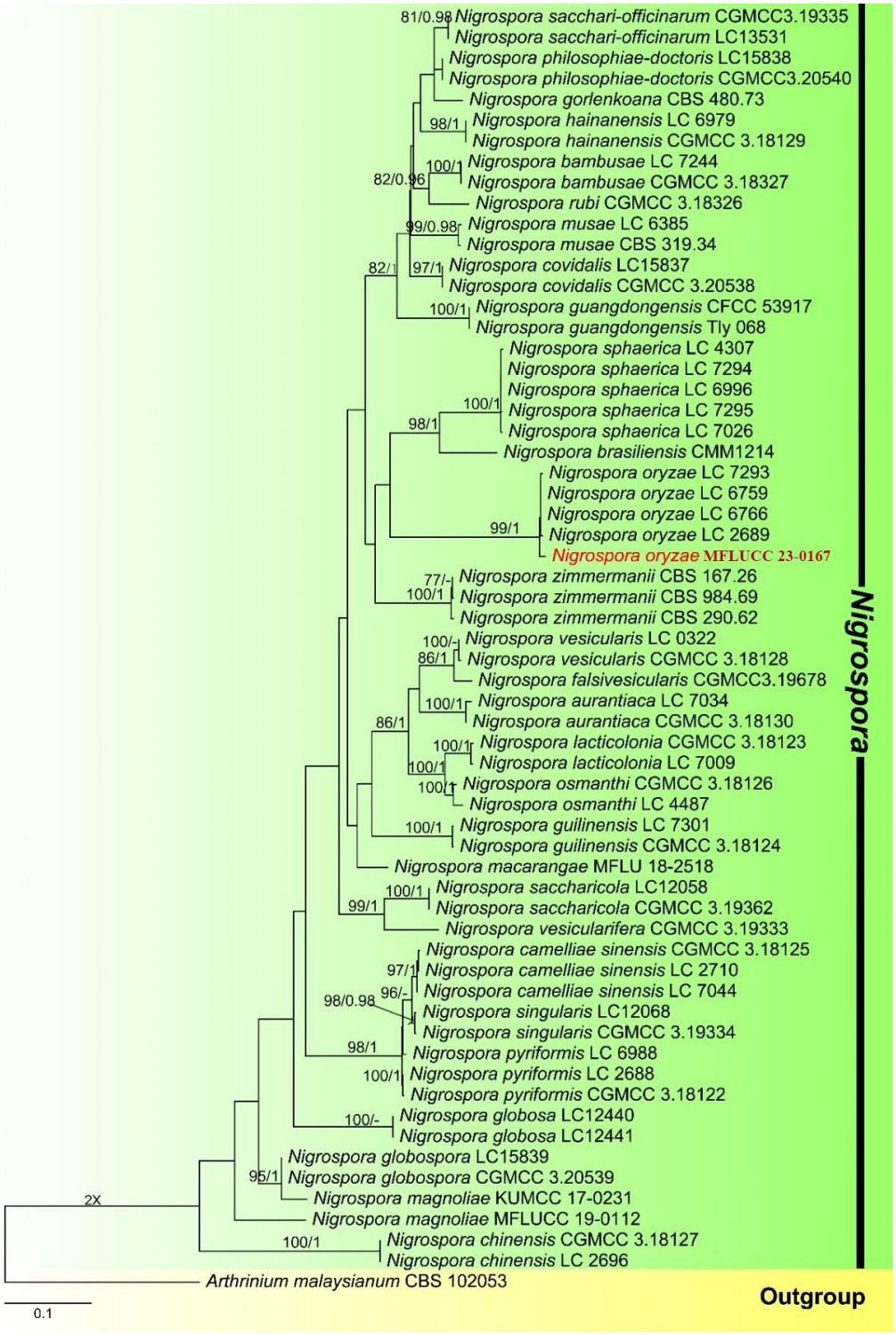

Figure 123 – RAxML tree based on analysis of combined ITS, *tef1-α*, and *tub2* dataset. The combined analysis includes 62 strains with 1441 characters including gaps (ITS: 535bp, *tef1-α*: 480bp, *tub2*: 426bp). The tree is rooted with *Arthrinium malaysianum* (CBS 102053). Tree

topology of the maximum likelihood analysis and Bayesian analysis are similar. The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML likelihood value of –10303.690850. The matrix had 684 distinct alignment patterns, with 14.64% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.249102, C = 0.235801, G = 0.278062, T = 0.237035; substitution rates AC = 3.429408, AG = 3.446748, AT = 1.814192, CG = 1.255022, CT = 8.630115, GT = 1.000000; gamma distribution shape parameter α = 0.117960. Bootstrap values for ML ≥ 75% and Bayesian posterior probabilities (PP) ≥ 0.95 are labelled on the nodes. The newly obtained sequence is indicated in red.

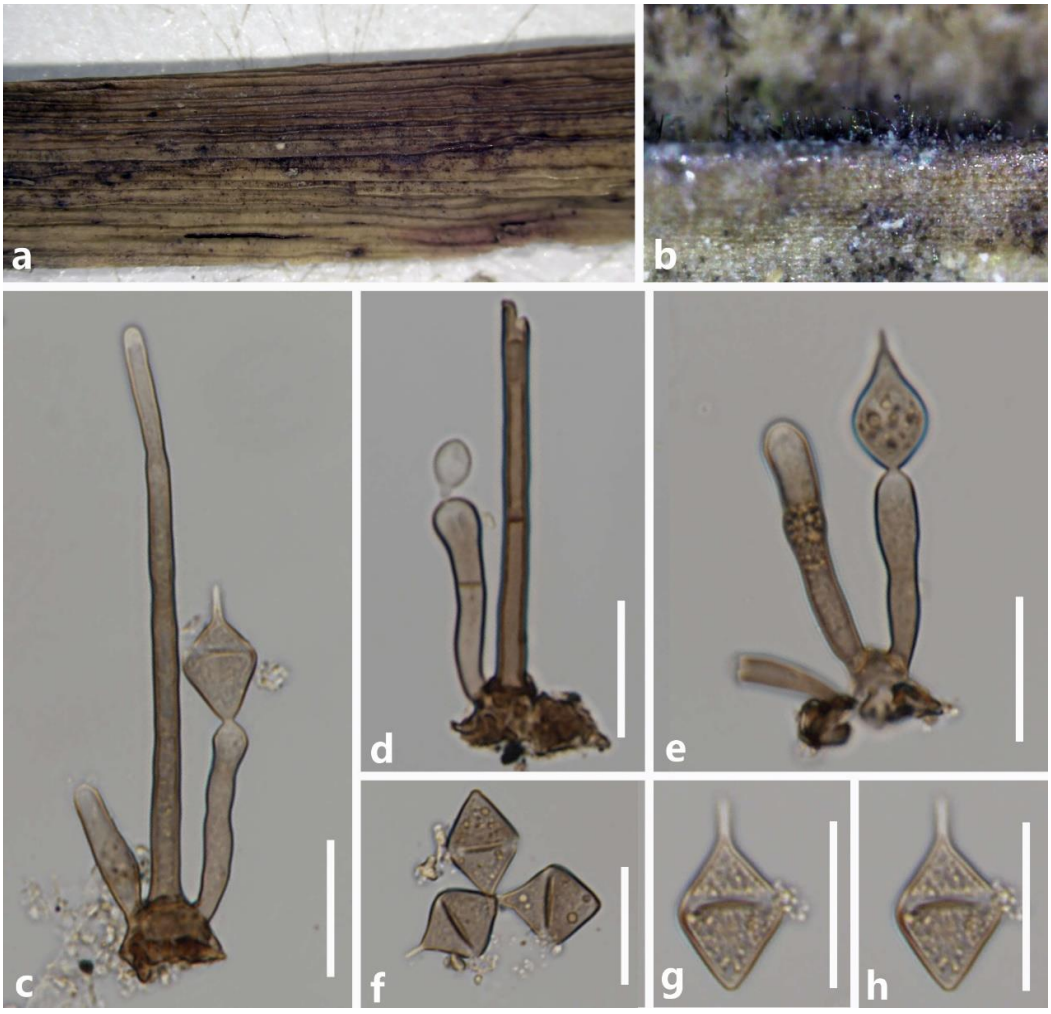

Figure 124 – *Beltrania rhombica* (MFLU 23-0239, new host and geographical record). a, b Colonies on the host surface. c–e Conidiophores. f–h Conidia. Crushed conidium and parts of its content. Scale bars: c–h = 20 μm.

Material examined – Thailand, Chiang Rai Province, Nang Lae Subdistrict, on dead leaves of *Ananas comosus*, 1 August 2020, X.G. Tian, P4-4 (MFLU 23-0239).

Known hosts and distribution – On seeds of sesame in India (Saxena & Mishra 1990); on floating litter in Argentina (Swapna & Nagaveni 2009); on *Quercus ilex* leaf litter in Tuscany (Zucconi & Pasqualetti 2007); on *Poeciloneuron indicum* in Western Ghats (Swapna & Nagaveni 2009); on bark of *Eucalyptus globules* from Faisalabad Pakistan (Abbas et al. 2010); leaf litter of cashew (*Anacardium occidentale*) in India (Shanthi & Vittal 2010); on *Tibouchina semidecandra* in China (Shi et al. 2012); on *Ficus ampelas* in China (Tennakoon et al. 2022); on mango trees in Iran (Dehghani et al. 2023); on leaves of *Acacia* sp. (Fabaceae) in Malaysia (Hernandez-Restrepo et al. 2016); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – LSU = OR438880, ITS = OR438413

Notes – *Beltrania rhombica*, the type species of *Beltrania*, was reported by Penzig (1882). In the multi-loci phylogenetic analyses, our strain (MFLU 23-0239) is grouped in the *Beltrania rhombica* (Fig. 125). Morphologically, our strain shares similar morphology with *Beltrania rhombica* (MFLU 17-1261) in having unbranched, single, setae and conidiophores arising from radially lobed basal cells, polyblastic and sympodial conidiogenous cells, swollen separating cells and biconic, appendiculate conidia *Beltrania rhombica* (MFLU 17-1261) have ellipsoidal, obovoid, thin-walled, smooth, hyaline of separating cells, however, our strain lack separating cells. Thus, we identified new strains as *Beltrania rhombica* based on phylogenetic analyses and morphological characters. Our strain *Beltrania rhombica* (MFLU 23-0239) was introduced as a new host and geographical record on *Ananas comosus* in Thailand.

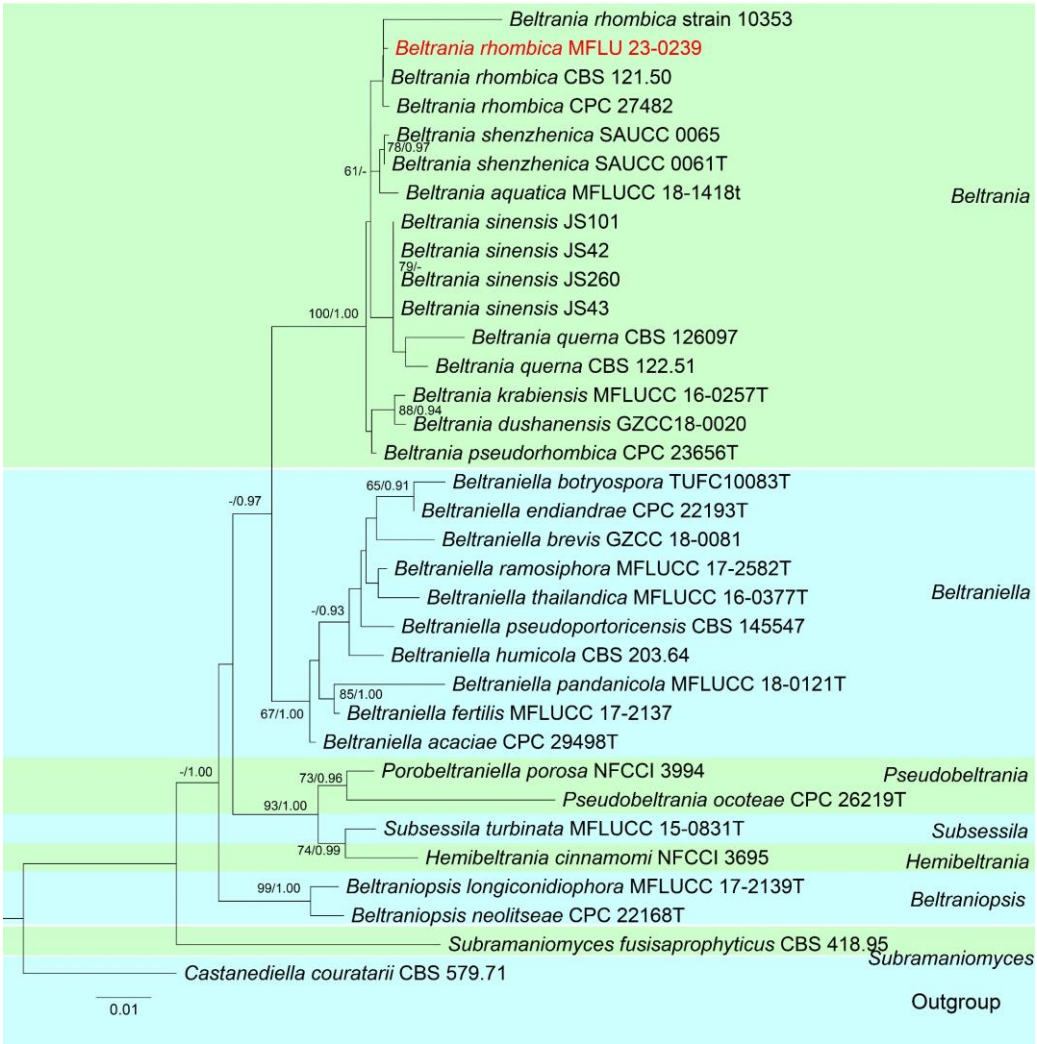

Figure 125 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Related sequences were obtained from Zhang et al. (2022a). Thirty-four strains are included in the combined sequence analysis, which comprise 1386 characters with gaps. *Castanediella couratarii* (CBS 579.71) was used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -4372.103671 is presented. The matrix had 313 distinct alignment patterns, with 8.42% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250406, C = 0.212018, G = 0.268944, T = 0.268632; substitution rates AC = 1.215935, AG = 2.094512, AT = 1.432580, CG = 0.547483, CT = 4.882973, GT = 1.000000; gamma distribution shape parameter 0.083794. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequence is in red, while T indicates holotype or ex-type strains.

Sporocadaceae Corda

Sporocadaceae was introduced by Corda (1842) and typified by *Sporocadus*. Species of this family occur as endophytes, plant pathogens and saprobes on a wide range of host plants (Maharachchikumbura et al. 2013, He et al. 2022, Zhang et al. 2022b). *Sporocadaceae* species are mostly known as pestalotioid fungi which are defined as having multi-septate, fusiform conidia with appendages at one or both ends, frequently with some melanised cells (Liu et al. 2019a). Liu et al. (2019) revised the taxonomy of *Sporocadaceae* based on multi-locus phylogenetic analyses; they accepted 30 genera (including seven new genera) in the family. Hyde et al. (2020a) placed *Doliomyces* and *Annellolacinia* in the family. The recent treatment of *Sporocadaceae* was provided by Wijayawardene et al. (2022) and 35 genera were accepted in the family.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous

Neopestalotiopsis was introduced by Maharachchikumbura et al. (2014b) with *N. protearum* as the type species. There are 84 records listed in Index Fungorum (2023). The asexual morph of *Neopestalotiopsis* is characterized by conidiomata subglobose, globose, clavate, solitary or aggregated, dark brown to black, immersed to erumpent; conidiophores indistinct, often reduced to conidiogenous cells; conidiogenous cells discrete, cylindrical, ampulliform to hyaline, smooth, thin-walled, holoblastic, becoming percurrent to produce additional conidia at slightly higher levels. conidia ellipsoid to subcylindrical, straight to slightly curved, 4-septate; basal cell conic to subcylindrical, with a truncate base, hyaline or pale brown to olivaceous, thin and rugose to smooth-walled; three median cells doliiform, wall rugose to verruculose, versicoloured, septa darker than the rest of the cell; apical cell hyaline, conic to cylindrical, thin- and smooth-walled; with tubular apical appendages, one to many, filiform or attenuated, flexuous, branched or unbranched; basal appendage single, tubular, unbranched, centric (Maharachchikumbura et al. 2014b). *Neopestalotiopsis* are found as saprobes or pathogens on plants, and the sexual morph remains unknown (Liu et al. 2021b). In recent years, the majority of *Neopestalotiopsis* species have been discovered in China and Thailand (Norphanphoun et al. 2019).

73. ***Neopestalotiopsis chiangmaiensis*** Tibpromma & K.D. Hyde, in Tibpromma et al., 93: 1–160, (2018) Fig. 126

Index Fungorum number: IF554515; Facesoffungi number: FoF04525

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 150–450 × 100–270 μm, pycnidial conidiomata variable in shape and size, mostly globose to subglobose, glabrous, solitary. *Conidiomata* pycnidial in culture on PDA at 25 °C after 30 days, globose to oval, solitary or aggregated in clusters, semi-immersed, black, 100–200 μm diam.; exuding globose, black, glistening, conidial masses. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* 5–15 × 1–5 μm ($\overline{x}$ = 8.86 × 3.27 μm, n = 30), phialidic, cylindrical, hyaline to pale brown, smooth, percurrently proliferating. *Conidia* 10–20 × 5–10 μm ($\overline{x}$ = 17.84 × 6.98 μm, n = 30), fusiform, ellipsoid, straight to slightly curved, 4-septate, constricted at the septa, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 1–5 μm long ($\overline{x}$ = 4.15 μm, n = 30); three median cells dolliform, 10–15 μm long ($\overline{x}$ = 11.74 μm, n = 30), smooth-walled, yellow-brown to brown, septa darker than the rest of the cell (second cell from the base pale brown, 1–5 μm long; third cell yellow-brown, 1–7 μm long; fourth cell brown, 1–7 μm long); apical cell 1–6 μm long ($\overline{x}$ = 3.86 μm, n = 30), hyaline, subcylindrical, rugose, thin- and smooth-walled; with 2–3 tubular apical appendages (mostly 3), arising from the apical crest, unbranched, filiform, 5–20 μm ($\overline{x}$ = 12.85 μm, n = 40); basal appendage single, filiform, tubular, unbranched, centric, 2–6 μm long ($\overline{x}$ = 3.95 μm).

Culture characteristics – Colonies on PDA attained after 6 days at room temperature (25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The black conidial mass covered the stromatic colonies after 60 days.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 16 January 2021, X.G. Tian, P15-5 (MFLU 23-0241), living culture (MFLUCC 23-0150).

Known hosts and distribution – On dead leaves of *Pandanus* sp. in Thailand (Tibpromma et al. 2018); in healthy leaves of *Magnolia candolli* (Magnoliaceae) in China (de Silva et al. 2021); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438414, *tef1-α* = OR500347

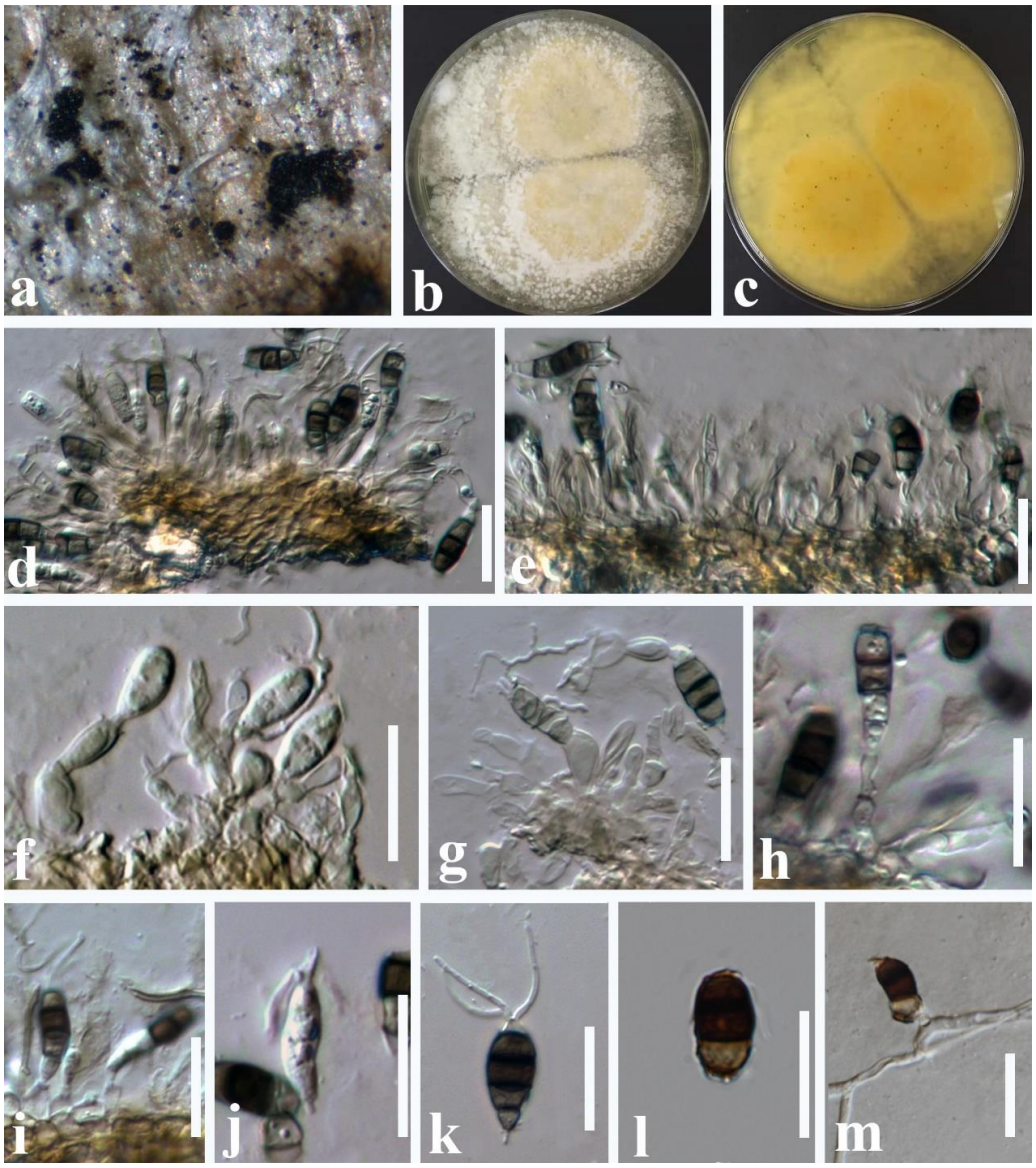

Figure 126 – *Neopestalotiopsis chiangmaiensis* (MFLU 23-0241, new host record). a Conidiomata on the host. b, c Colonies on PDA from surface and reverse. d–i Conidiogenous cells and conidia. j–l Conidia. m Germinated conidium. Scale bars: d–m = 20 µm.

Notes – *Neopestalotiopsis chiangmaiensis* was introduced by Tibpromma et al. (2018) from *Pandanus* sp. in Thailand. Based on multi-gene phylogenetic analyses (ITS, *tef1-α*, and *tub2*), our strain (MFLUCC 23-0150) clustered together with the type strain of *N. chiangmaiensis* (Fig. 127). Morphologically, our strain is similar to the *N. chiangmaiensis* in having fusoid to ellipsoid, straight to slightly curved conidia with 2–3 tubular apical appendages and short basal appendage (Tibpromma et al. 2018). *N. chiangmaiensis* differs from *N. dendrobii* from the latter by having proliferate 1–2 times percurrently conidiogenous cells, slightly smaller conidia (10–20 × 5–10 µm vs. (19–) 20.5–23 (–24.5) × (6–) 6.5–7.5 (–8) µm) with light color, and third cell darker brown than others (Ma et al. 2019). *N. chiangmaiensis* differs from *N. saprophytica* by the latter having bigger conidia (10–20 × 5–10 µm vs. 22–30×5–6 µm) with 2–4 tubular apical appendages and light color second cell (Maharachchikumbura et al. 2012). Based on both phylogeny and morphology, our

strain is identified as *N. chiangmaiensis*. This is the first report of *N. chiangmaiensis* from *Ananas comosus*.

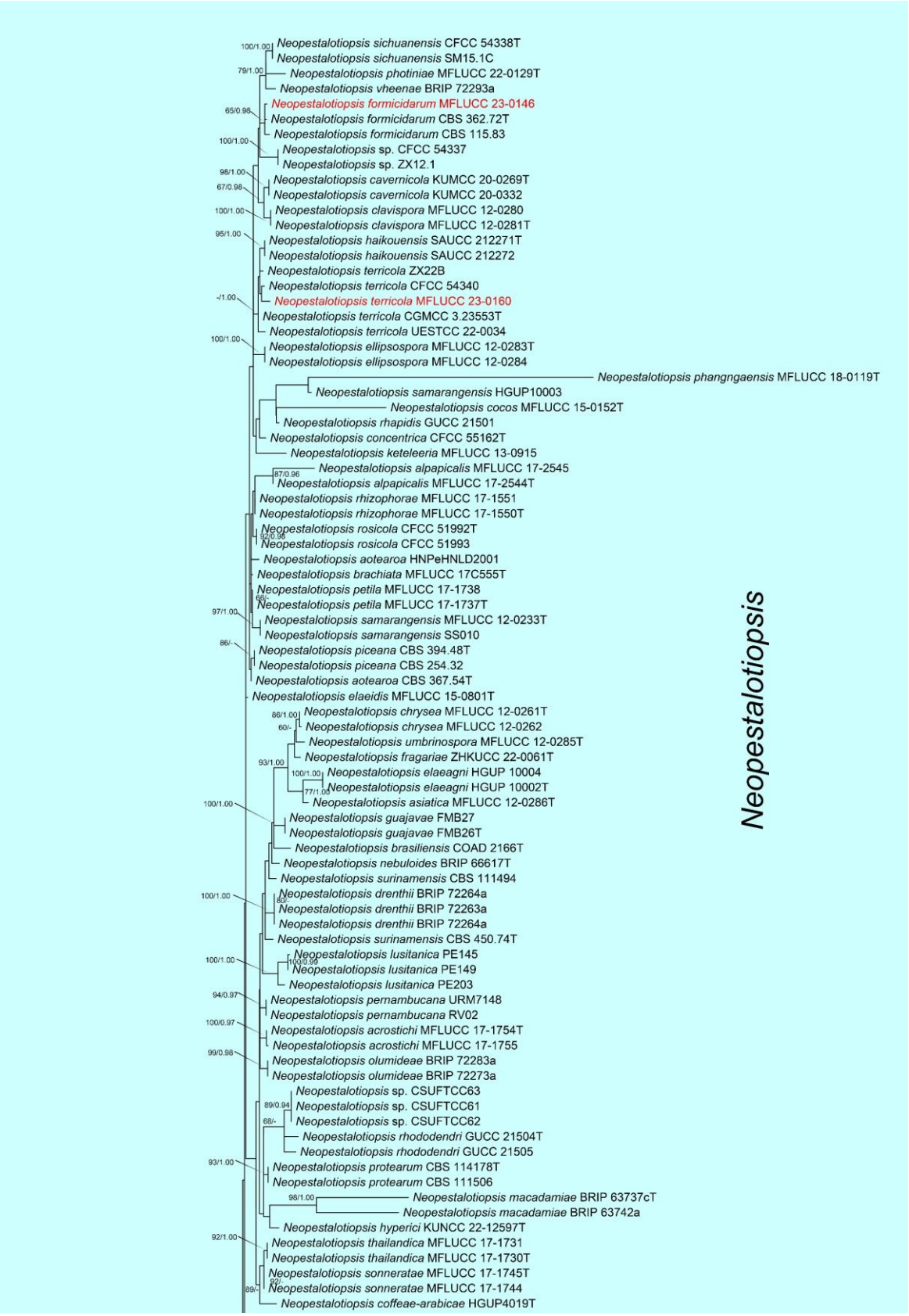

Figure 127 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1-α*, and *tub2* sequence data. One hundred and sixty-three strains are included in the combined sequence analysis, which comprise 2204 characters with gaps. *Pseudopestalotiopsis cocos* (CBS

272.29T), *P. indica* (CBS 459.78) and *P. theae* (MFLUCC 12-0055) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -12934.619333 is presented. The matrix had 940 distinct alignment patterns, with 27.14% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.235454, C = 0.272088, G = 0.218082, T = 0.274376; substitution rates AC = 1.190034, AG = 3.097913, AT = 1.385398, CG = 0.890439, CT = 4.483309, GT = 1.000000; gamma distribution shape parameter α = 0.375358. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

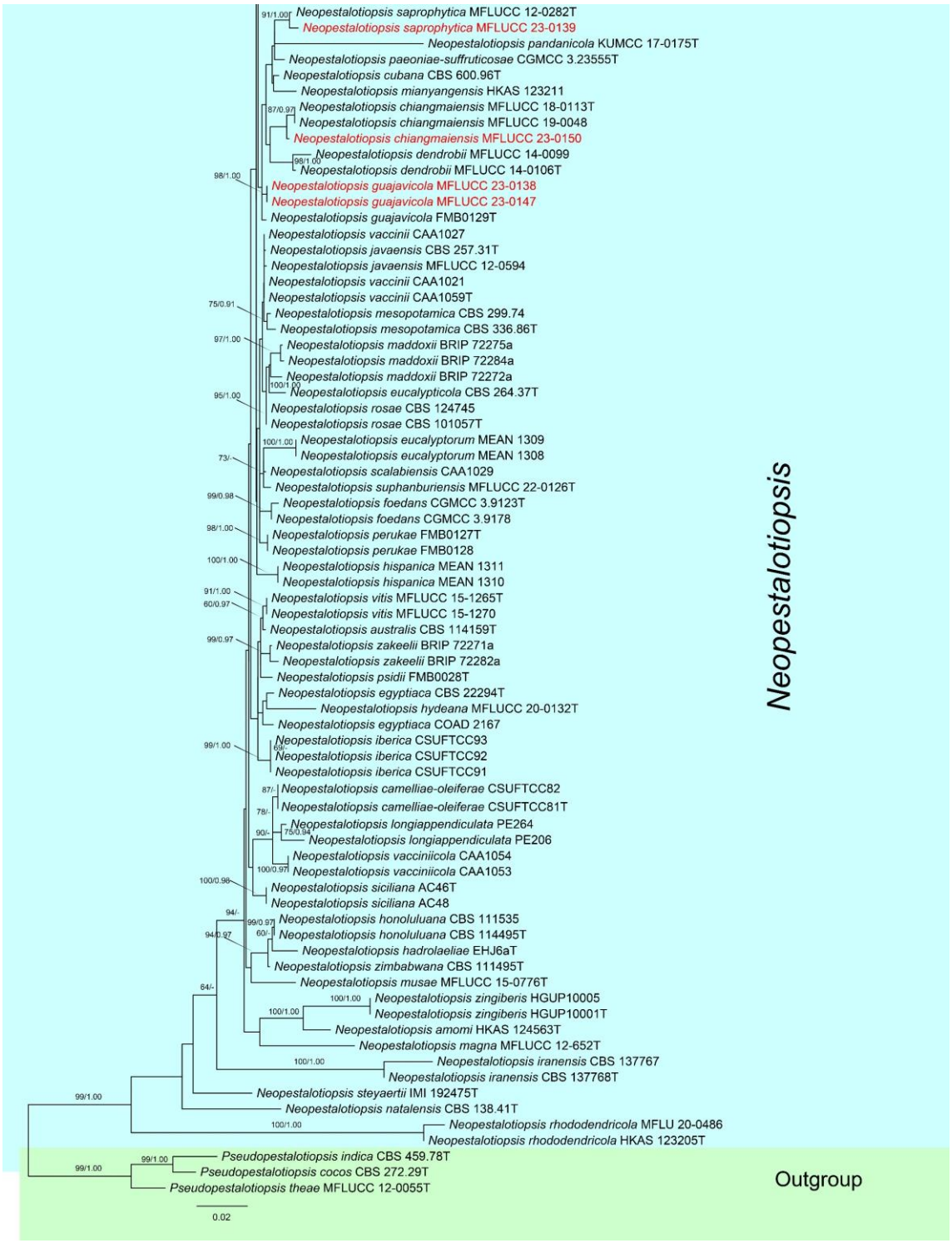

Figure 127 – Continued.

74. *Neopestalotiopsis formicidarum* Maharachch., K.D. Hyde & Crous [as '*formicarum*'], in Maharachchikumbura et al., Stud. Mycol. 79: 140 (2014) Fig. 128

Index Fungorum number: IF821673; Facesoffungi number: FoF10804

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: *Colonies* grow on the host substrate. *Conidiophores* subcylindrical, hyaline to subhyaline. *Conidiogenous cells* 3.5–7 × 2–3.5 μm ($\overline{x}$ = 5 × 2.5 μm, n = 15), phialidic, discrete, cylindrical to ampulliform, hyaline, smooth. *Conidia* 20–25 × 8–10 μm ($\overline{x}$ = 24 × 8.5 μm, n = 30), fusiform, ellipsoid, straight to slightly curved, 4-septate, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 4–5 μm long ($\overline{x}$ = 4.5 μm, n = 25); three median cells, 15–17 μm long ($\overline{x}$ = 15.5 μm, n = 25), smooth-walled, light brown to dark brown, dark brown with septa darker than the rest of the cells, second cell from the base pale brown, 5–6.5 μm long, third cell yellow-brown, 4–5.5 μm long; fourth cell brown, 4.5–5.5 μm long, apical cell 3–5 μm long ($\overline{x}$ = 4 μm, n = 25), hyaline, subcylindrical, rugose, thin- and smooth-walled, with 2–4 tubular apical appendages (mostly 2 and 3, seldom 4), arising from the apical crest, unbranched, filiform, 10–20 μm ($\overline{x}$ = 15 μm, n = 45); basal appendage single, filiform, tubular, unbranched, centric, 3–5 μm long ($\overline{x}$ = 4.5 μm, n = 25).

Culture characteristics – Colonies on PDA, with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Ananas comosus*, 8 December 2020, X.G. Tian, P14-2 (MFLU 23-0242), living cultures MFLUCC 23-0146.

Known hosts and distribution – On dead ants in Ghana and plant debris in Cuba (Maharachchikumbura et al. 2014b); on diseased leaf of *Hevea brasiliensis* in Thailand (Pornsuriya et al. 2020); on *Jabuticaba* in Taiwan Province, China (Lin et al. 2022); on *Paullinia cupana* in Brazil (Gualberto et al. 2021); on *Calamus castaneus* in Malaysia (Azuddin et al. 2022); on *Kadsura coccinea* in China (Liang et al. 2023); on dead leaves of *Ananas comosus* in Thailand (this study).

GenBank numbers – ITS = OR438415, *tef1-α* = OR500345

Notes – Multigene phylogenetic analyses of combined ITS, *tub2* and *tef1-α* sequences dataset indicates that our new collection (MFLUCC 23-0146) are grouped with *Neopestalotiopsis formicidarum* (CBS 362.72 and CBS 115.83) (Fig. 127). The morphological characters of our new collection shares similar characters with *N. formicidarum* (CBS 362.72) in having fusiform, 4-septate, granulate, conic to obconic basal cell conidia with a truncate base (Maharachchikumbura et al. 2014b, Yang et al. 2021). Therefore, our new collection is identified as a new host and geographical record on *Ananas comosus* in Thailand.

75. *Neopestalotiopsis guajavicola* I.U Haq, S. Ijaz & N. A. Khan, Pakist. J. Agric. Sci. 58: 1307 (2021) Fig. 129

Index Fungorum number: IF840639; Facesoffungi number: FoF13402

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Not observed. Asexual morph: Colonies grow on the host substrate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–4.5 μm ($\overline{x}$ = 3.5 μm, n = 20), phialidic, discrete, cylindrical, hyaline, smooth. *Conidia* 20–25 × 8–10 μm ($\overline{x}$ = 22.5 × 9 μm, n = 35), fusiform, ellipsoid, 4-septate, granulate; basal cell conic to obconic with a truncate base, hyaline to yellow, thin-walled, 3.5–4.5 μm long ($\overline{x}$ = 4 μm, n = 35); with three median cells, 14–15.5 μm long ($\overline{x}$ = 15 μm, n = 35), smooth-walled, light brown to dark brown, dark brown with septa darker than the rest of the cells, second cell from the base pale brown, 4–5.5 μm long, third cell yellow-brown, 4.5–5.5 μm long; fourth cell brown, 4.5–5.5 μm long, apical cell 3.5–4.5 μm long ($\overline{x}$ = 4 μm, n = 35), hyaline, subcylindrical, rugose, thin- and smooth-walled, with 3 tubular apical appendages, arising from the apical crest, unbranched, filiform, 25–35 μm ($\overline{x}$ = 30 μm, n = 30); basal appendage single, filiform, tubular, unbranched, centric, 4.5–6.5 μm long ($\overline{x}$ = 5.5 μm).

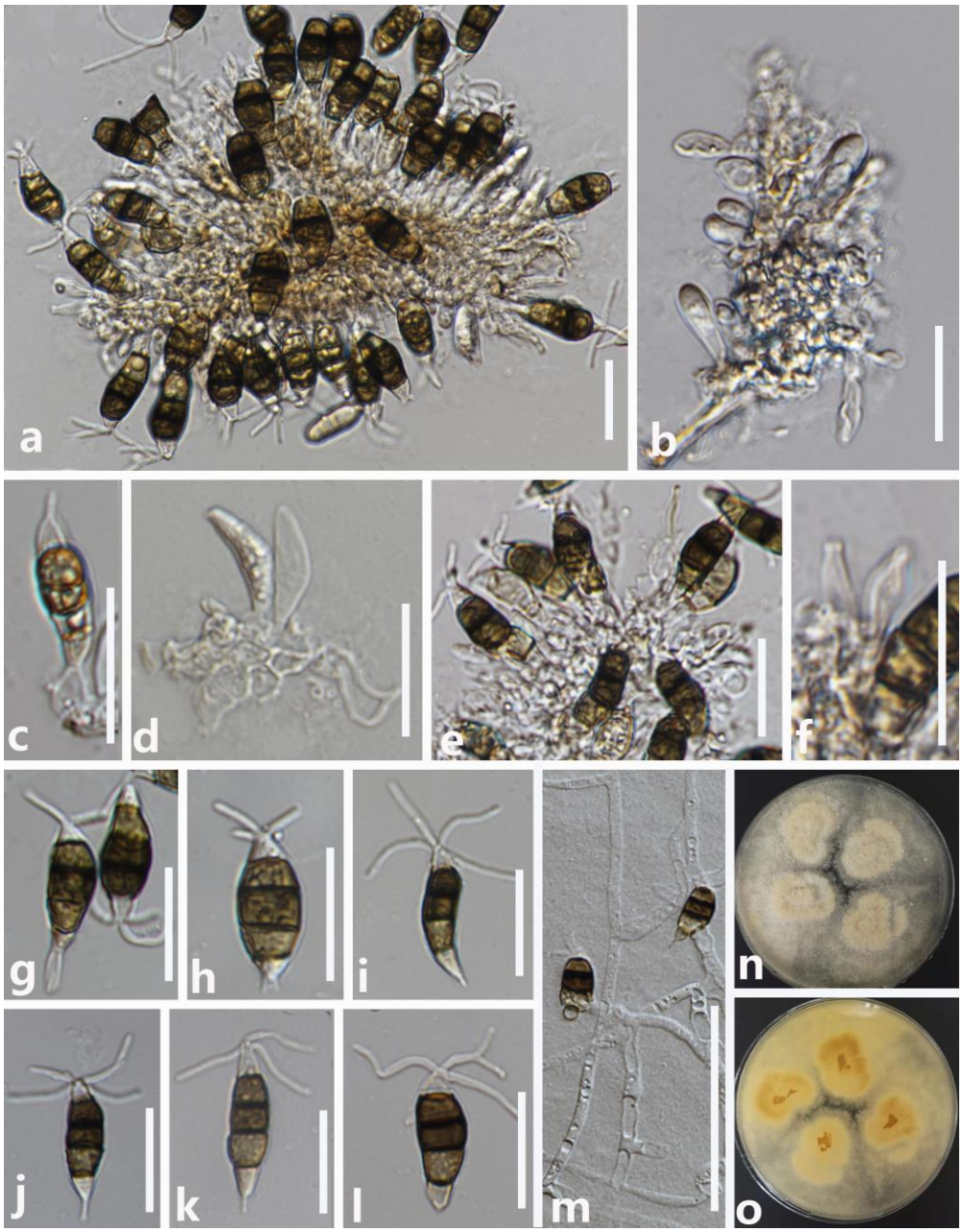

Figure 128 – *Neopestalotiopsis formicidarum* (MFLU 23-0242, new host and geographical record). a–b Colonies grow on the host substrate. a, b conidiophores with conidia. c–f Conidiogenous cells with conidia. g–l Conidia. m Germinated conidium. n–o Colonies on PDA from surface and reverse. Scale bars: m = 40 μm, a–l = 20 μm.

Culture characteristics – Colonies on PDA, with undulate edge, write and yellowish, sparse aerial mycelium on the surface, reverse pale yellow.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Ananas comosus*, 8 December 2020, X.G. Tian, P14-6 (MFLU 23-0244), living cultures MFLUCC 23-0147; *ibid*, on dead leaves of *Cocos nucifera*, 16 December 2020, X.G. Tian, C5-1 (MFLU 23-0243), living cultures MFLUCC 23-0138.

Known hosts and distribution – From fruit and branches of *Psidium guajava* in Pakistan (Haq et al. 2023); on dead leaves of *Ananas comosus* and *Cocos nucifera* in Thailand (this study).

GenBank numbers – MFLUCC 23-0138: ITS = OR438416, *tef1-α* = OR500342. MFLUCC 23-0147: ITS = OR438417, *tef1-α* = OR500346, *tub*2 = OR538090

Notes – NCBI BLASTn search of our new isolate (MFLUCC 23-0147) showed that ITS sequence had 100% similarity to many *Neopestalotiopsis* species, *viz. N. piceana* (CBS367.54),

N. aotearoa (CBS 367.54), *N. cubana* (HNLGMI-2), and *N. formicarum* (ZHKUCC 22-0015); *tef1-α* sequence had 100% similarity to *N. clavispora* (NM16304 and NM16303); *tub2* sequence had 100% similarity to *N. cubana* (GBLZ16PE-002) and *N. saprophytica* (YLWB-FBR01). The phylogenetic analyses showed our strains (MFLUCC 23-0138 and MFLUCC 23-0147) clustered with *N. guajavicola* with low support (Fig. 127). *Neopestalotiopsis guajavicola* was described as a pathogen of *Psidium guajava* by Ul Haq et al. (2021). The nucleotide comparisons showed that our strain (MFLUCC 23-0147) is not significantly different from *N. guajavicola* (FMB0129) in ITS, *tef1-α* and *tub2* sequence data. Morphologically, our strain shares similar morphology with the holotype of *N. guajavicola* (FMB0129) (Ul Haq et al. 2021). Therefore, we identify our collection as new host and geographical record of *N. guajavicola* on *Ananas comosus* and *Cocos nucifera* in Thailand.

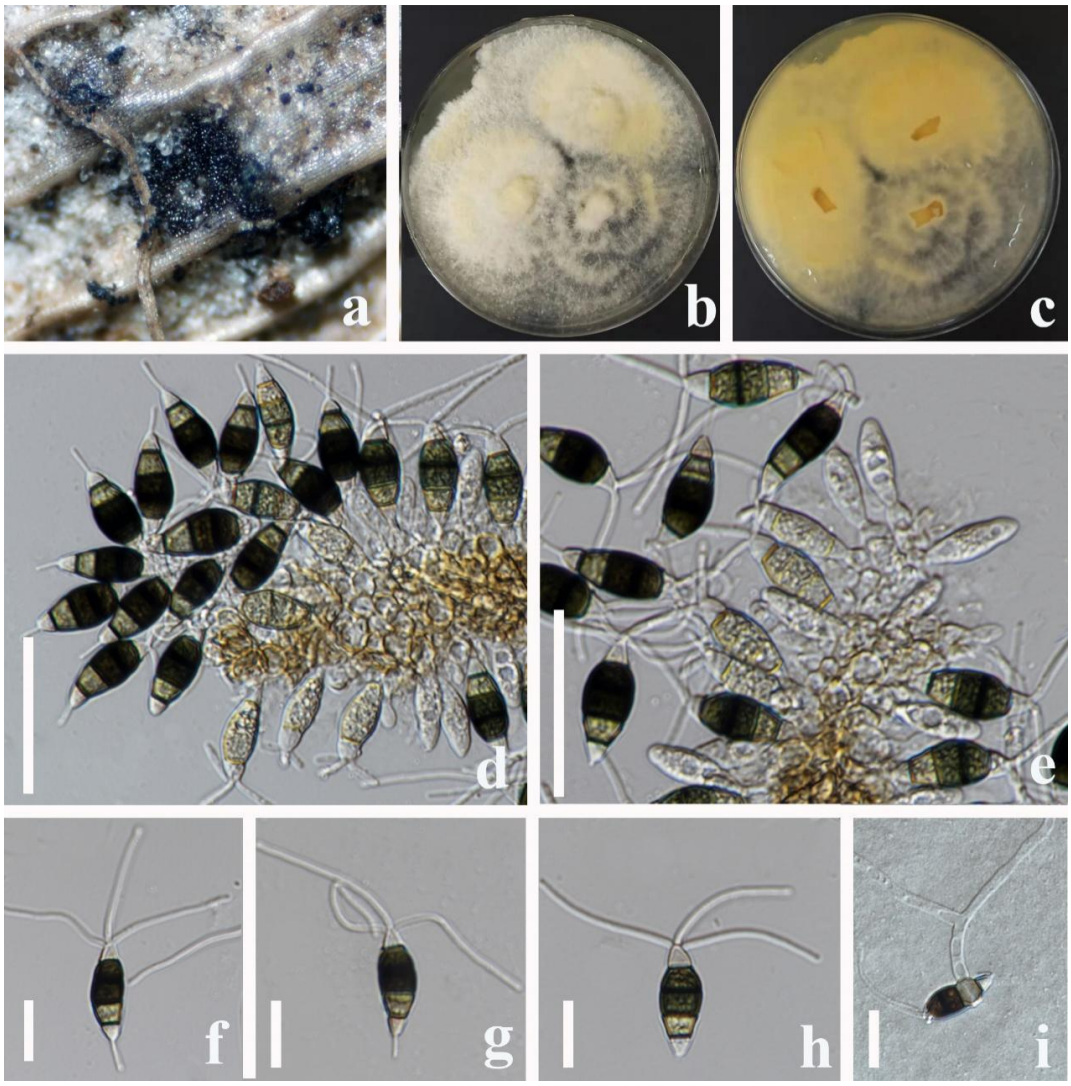

Figure 129 – *Neopestalotiopsis guajavicola* (MFLU 23-0244, new host and geographical record). a Colony on natural substrate. b, c Colonies on PDA from surface and reverse. d, e Conidiophores, conidiogenous cells and developing conidia. f–h Conidia. i Germinated conidium. Scale bars: d, e, i = 20 μm, f–h = 10 μm.

76. ***Neopestalotiopsis terricola*** W.L. Li & J.K. Liu, in Li et al., Journal of Fungi 8 (11, no. 1175): 14 (2022) Fig. 130

Index Fungorum number: IF845408; Facesoffungi number: FoF12748

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 200–400 × 100–300 μm, pycnidial, variable in shape and size, mostly globose to

subglobose, glabrous, solitary. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* 2–10 × 2–3 µm ($\overline{x}$ = 6 × 2 µm, n = 10) holoblastic, mostly integrated, ampulliform, cylindrical, hyaline to light brown, smooth-walled. *Conidia* 15–25 × 5–8 µm ($\overline{x}$ = 18.5 × 6.5 µm, n = 25), ellipsoid to fusiform, straight to slightly curved, 4-septate, constricted at the septa, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 2.3–4 µm long ($\overline{x}$ = 3 µm, n = 20); three median cells dolioform, 10–13 µm long ($\overline{x}$ = 12 µm, n = 20), smooth-walled, yellow-brown to brown, septa darker than the rest of the cell (second cell from the base pale brown, 3.5–4.5 µm long; third cell yellow-brown, 3.5–4.5 µm long; fourth cell brown, 3–4.5 µm long); apical cell 2.5–4 µm long ($\overline{x}$ = 3.5 µm, n = 20), hyaline, subcylindrical, rugose, thin- and smooth-walled; with 1–3 tubular apical appendages, arising from the apical crest, unbranched, filiform, 4.5–8.5 µm ($\overline{x}$ = 6.5 µm, n = 30); basal appendage single, filiform, tubular, unbranched, 2–3.5 µm long ($\overline{x}$ = 3 µm).

Culture characteristics – Colonies on PDA attained after 7 days at room temperature (20–25 ℃), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The black conidial mass covered the stromatic colonies after 40 days.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 16 December 2020, X.G. Tian, c6-21 (MFLU 23-0245), living cultures MFLUCC 23-0160.

Known hosts and Distribution – On *Paeonia suffruticosa* in China (Li et al. 2022); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – ITS = OR438418, *tef1-α* = OR500344, *tub*2 = OR538089.

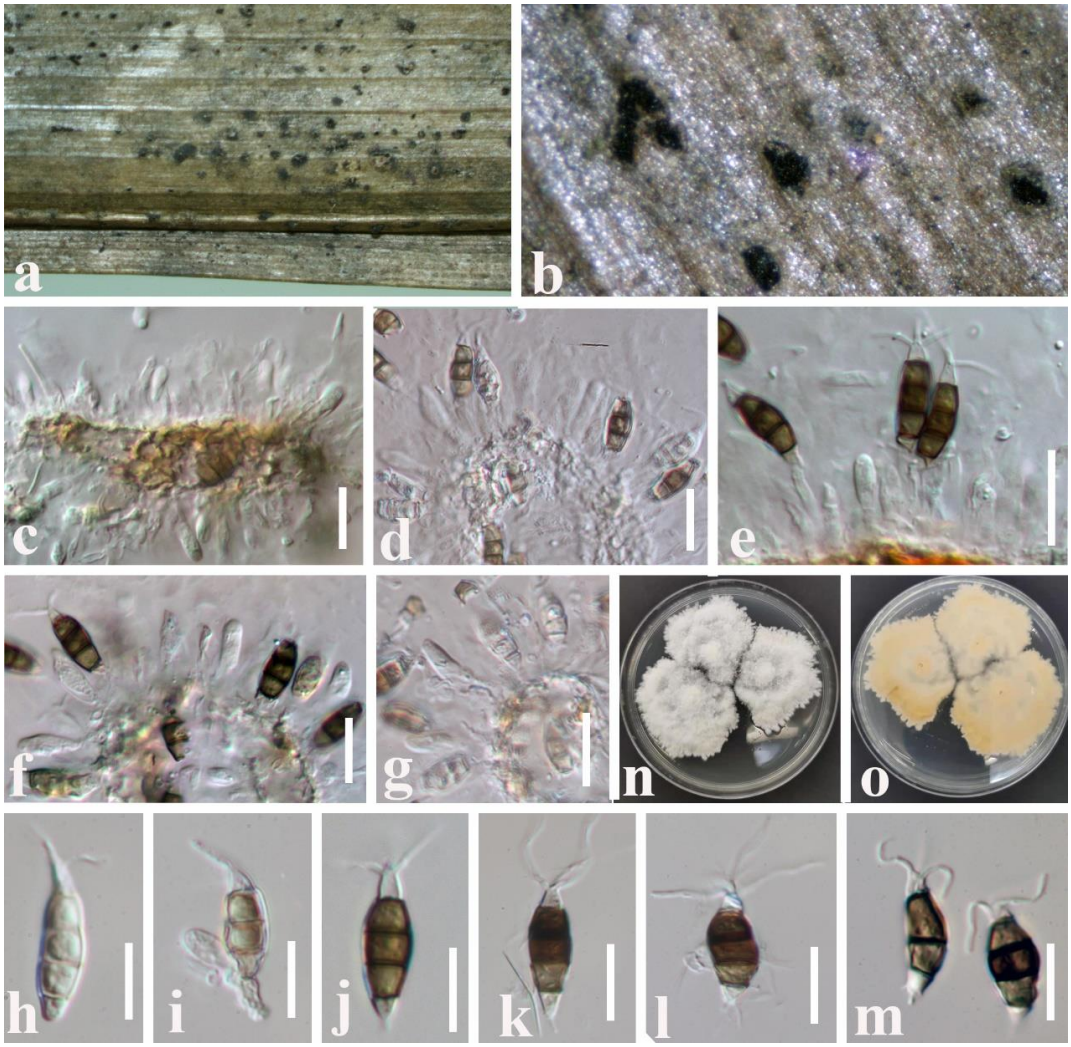

Figure 130 – *Neopestalotiopsis terricola* (MFLU 23-0245, new host and geographical record).

a, b Conidiomata on dead leaves of *Cocos nucifera*. c–g Conidiogenous cells and conidia. h–m Conidia. n, o Colonies on PDA from surface and reverse. Scale bars: c–g = 20 μm, h–m = 10 μm.

Notes – *Neopestalotiopsis terricola* was described as a pathogen on *Paeonia suffruticosa* by Li et al. (2022). In our phylogenetic analyses, our new isolate (MFLUCC 23-0160) clustered with four strains of *N. terricola* (CGMCC3.23553, UESTCC 22.0034, CFCC 54340 and ZX22B) (Fig. 127). Morphologically, our new collection is similar to *Neopestalotiopsis terricola* in having similar conidial size and number of appendages (Li et al. 2022). There are no significant differences between our isolate and *N. terricola* in ITS, *tef1-α*, and *tub2* sequence data. Thus, we identified our new isolate as *N. terricola* based on phylogeny and morphology and this is a new host and geographical record report of *N. terricola* on *Cocos nucifera* in Thailand.

77. *Neopestalotiopsis saprophytica* (Maharachch. & K.D. Hyde) Maharachch., K.D. Hyde & Crous, in Maharachchikumbura et al., Stud. Mycol. 79: 148 (2014) Fig. 131

≡ *Pestalotiopsis saprophyta* Maharachch. & K.D. Hyde, in Maharachchikumbura, Guo, Cai, Chukeatirote, Wu, Sun, Crous, Bhat, McKenzie, Bahkali & Hyde, Fungal Divers. 56(1): 119 (2012).

Index Fungorum number: IF809780; Facesoffungi number: FoF13405

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 200–500 × 150–230 μm, pycnidial conidiomata variable in shape and size, mostly globose to subglobose, glabrous, solitary. *Conidiomata* pycnidial in culture on PDA at 25 °C after 60 days, globose to oval, solitary or aggregated in clusters, semi-immersed, black, up to 200 μm diam.; exuding globose, black, glistening, conidial masses. *Conidiophores* septate, unbranched or irregularly branched, colorless, smooth-walled. *Conidiogenous cells* 2–10 × 1–4 μm ($\overline{x}$ = 6.19 × 2.41 μm, n = 30), holoblastic, discrete or integrated, lageniform, subcylindric to cylindric, hyaline to pale brown. *Conidia* 20–30 × 5–10 μm ($\overline{x}$ = 23.24 × 8.87 μm, n = 60), ellipsoid to fusiform, straight to slightly curved, 4-septate, constricted at the septa, granulate; basal cell conic to obconic with a truncate base, hyaline, thin-walled, 3–7 μm long ($\overline{x}$ = 5.06 μm, n = 30); three median cells dolioform, 11–20 μm long ($\overline{x}$ = 16.22 μm, n = 30), smooth-walled, yellow-brown to brown, septa darker than the rest of the cell (second cell from the base pale brown, 4–7 μm long; third cell yellow-brown, 4–7 μm long; fourth cell brown, 3–7 μm long); apical cell 3–6 μm long ($\overline{x}$ = 4.91 μm, n = 30), hyaline, cylindric to subcylindric, thin- and smooth-walled; with 2–4 tubular apical appendages, arising from the apical crest, unbranched, filiform, 8–30 μm ($\overline{x}$ = 17.33 μm, n = 60); basal appendage single, filiform, tubular, unbranched, 1–8 μm long ($\overline{x}$ = 4.66 μm).

Culture characteristics – Colonies on PDA attained after 7 days at room temperature (20–25 °C), with undulate edge, white, sparse aerial mycelium on the surface; reverse pale yellow. The black conidial mass covered the stromatic colonies after 40 days.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 1 December 2020, X.G. Tian, C5-5 (MFLU 23-0246), living cultures MFLUCC 23-0139.

Known hosts and distribution – From leaves of *Magnolia* in China (Maharachchikumbura et al. 2012); on *Neopestalotiopsis saprophytica* and on royal palm from Malaysia (Ismail et al. 2017, 2022); on *Paphiopedilum micranthum* and *Persimmon* in China (Qin et al. 2020, 2023); on fruits of *Litsea rotundifolia* in Hongkong, China (Maharachchikumbura et al. 2014); on *Cinnamomum dichotoma* in India (Reddy et al. 2016); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – ITS = OR438419, *tef1-α* = OR500343, *tub*2 = OR538088

Notes – *Neopestalotiopsis saprophytica* was initially described as *Pestalotiopsis saprophyta* by Maharachchikumbura et al. (2012). Maharachchikumbura et al. (2014) introduced a new genus *Neopestalotiopsis* to accommodate several *Pestalotiopsis* species based on multi-gene analysis and *N. saprophytica* was transferred to *Neopestalotiopsis* (Maharachchikumbura et al. 2014b). In this study, our new strain (MFLUCC 23-0139) clustered with the ex-type strain of *N. saprophytica* (MFLUCC 12-0282) with high statistical support (Fig. 127). In addition, our strain is similar to

N. saprophytica in having irregularly branched conidiogenous cells and fusiform conidia with 2–4 tubular apical appendages (Maharachchikumbura et al. 2012) (Maharachchikumbura et al. 2014). Thus, based on phylogenetic analyses and morphlogical characters, we identified our new isolate as *N. saprophytica*.

Neopestalotiopsis saprophytica has been reported as a plant pathogen causing leaf spot of *Elaeis guineensis* and *Paphiopedilum micranthum*, guava scab, gray blight disease on *Camellia sinensis*, stem rot of eucalyptus cuttings and stem canker on *Rosa chinensis* (Jayawardena et al. 2016, Jiang et al. 2018, Solarte et al. 2018, Wang et al. 2019a, Qin et al. 2020, Santos et al. 2020) from worldwide. This is a new host and geographical record of *N. saprophyticas* on *Cocos nucifera* in Thailand.

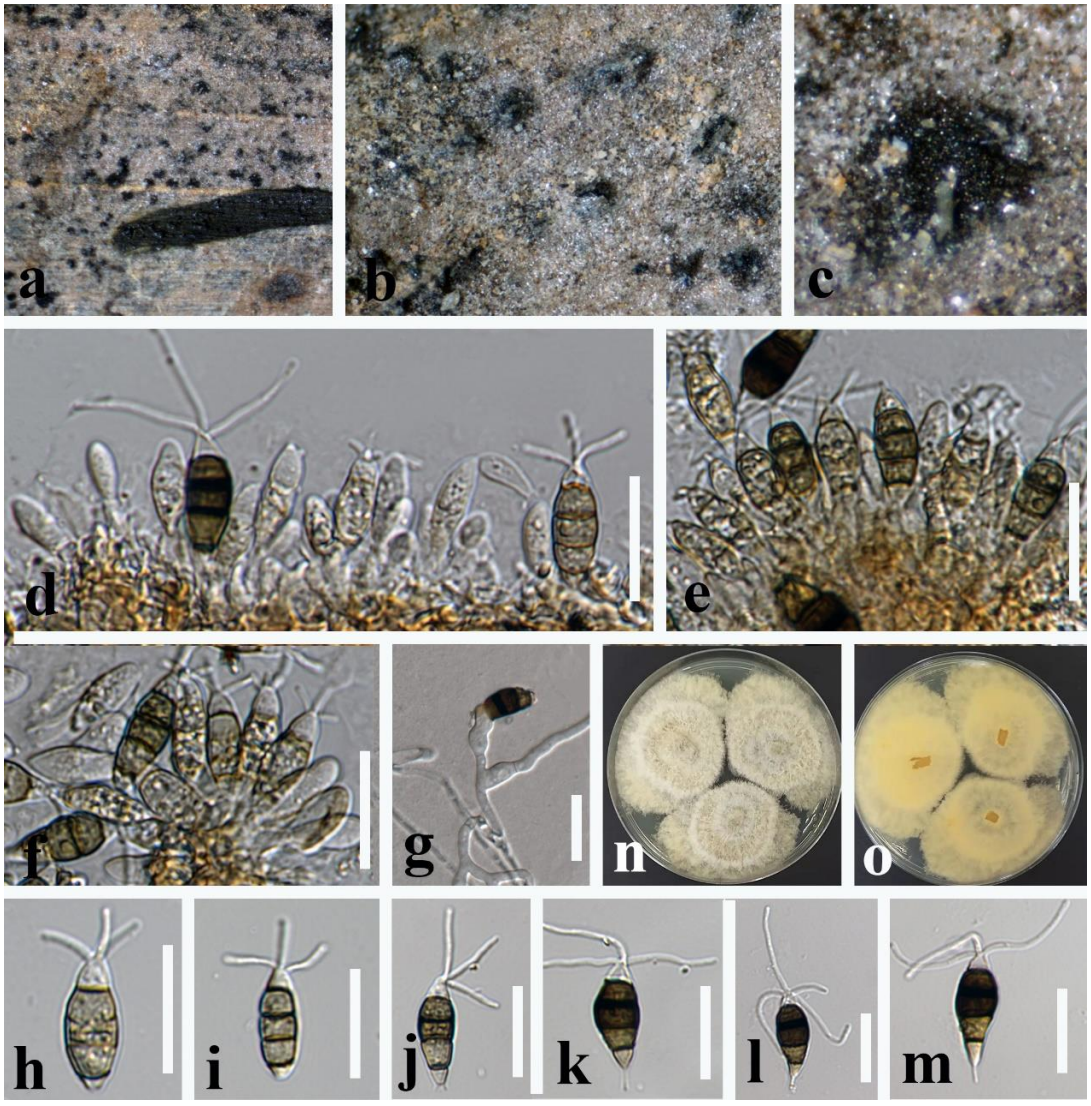

Figure 131 – *Neopestalotiopsis saprophytica* (MFLU 23-0246, new host and geographical record). a–c Colonies on natural substrate. d–f Conidiogenous cells and conidia. g Germinated conidium. n, o Colonies on PDA from surface and reverse. h–m Conidia. Scale bars: d–g, h–m = 20 µm.

Pestalotiopsis Steyaert

Pestalotiopsis was established by Steyaert (1949) with *P. maculans* as the type. The typical characters of *Pestalotiopsis* are fusiform conidia that are usually 5-celled, with 3 colored median cells and 2 colourless end cells as well as two or more apical appendages (Steyaert 1949). Species of *Pestalotiopsis* are widely distributed in various hosts and commonly found in tropical and temperate regions (Maharachchikumbura et al. 2014b). *Pestalotiopsis* species are important plant

pathogens that cause various diseases in many plant species (Maharachchikumbura et al. 2011, Maharachchikumbura et al. 2014a). *Pestalotiopsis* species are also commonly found as endophytes (Watanabe et al. 2010, Rönsberg et al. 2013, Gu et al. 2022) and a few species have been reported as pathogens from humans or animals (Sutton 1999, Monden et al. 2013).

Pestalotiopsis species have overlapping morphological characters thus it is difficult to identify *Pestalotiopsis* species based on morphology only. Studies suggested that the colour intensities of the median conidial cell, the size of conidia and the presence or absence of basal appendages can be used as additional taxonomic characters for interspecific division of *Pestalotiopsis* species (Griffiths & Swart 1974, Jeewon et al. 2003, Hu et al. 2007, Maharachchikumbura et al. 2014a). Jeewon et al. (2003) mentioned that due to the overlapping variation in size and shape of homologous structures, the pigmentation of median cells and the size of appendages are important when identified the *Pestalotiopsis* species. The phylogenetic analyses of combined ITS, *tef1-α*, and *tub2* gene was recommended to delaminate the species boundaries in *Pestalotiopsis* species. There are 403 records of *Pestalotiopsis* listed in the Index Fungroum (2023). In this study, *Pestalotiopsis adusta* is reported from *Cocos nucifera.*

78. *Pestalotiopsis adusta* (Ellis & Everh.) Steyaert, Trans. Br. mycol. Soc. 36: 82 (1953)

Fig.132

Index Fungorum number: IF302600; Facesoffungi number: FoF14323

Saprobic on dead leaves of *Cocos nucifera*. *Colonies* effuse on the natural substrate, scattered, dark brown to dark. Sexual morph: Not observed. Asexual morph: *Conidiomata* acervulus, subepidermal in origin. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, simple, filiform, short. *Conidia* 18–20 × 5.5–6 µm ($\overline{x}$ = 19.5 × 6 µm n = 30), fusiform to ellipsoid, straight to slightly curved, 4-septate, with short basal cell, hyaline, thin-walled, 2.5–4 µm long ($\overline{x}$ = 3.5 µm), basal appendage, 5.5–10 µm long ($\overline{x}$ = 7 µm), filiform; with three median cells, doliiform to subcylindrical, brown to olivaceous, with septa and periclinal walls darker than another cell, together 12–14 µm long ($\overline{x}$ = 13 µm) second cell from base 4–4.5 µm ($\overline{x}$ = 4 µm); third cell 4–5 µm ($\overline{x}$ = 4 µm); fourth cell 4–5 µm ($\overline{x}$ = 4.5 µm); apical cell hyaline, conic, 2–4 µm long ($\overline{x}$ = 3 µm); with two to four appendages, 5.5–10 µm long ($\overline{x}$ = 7 µm), tubular, filiform, arising from the apex of the apical cell.

Culture characteristics – Colonies on PDA reaching 7 cm diam. after 6 days at 25 °C, with undulate edge, whitish, with dense aerial mycelium on surface; reverse of culture white to pale yellow.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 16 January 2021, X.G. Tian, c6-13 (MFLU 23-0247), living culture (MFLUCC 23-0158).

Known hosts and distribution – On leaves of *Prunus cerasus* in USA; refrigerator door PVC gasket in Fiji; on *Syzygium* sp. in Thailand; on leaves of *Prunus cerasus* in the USA (Maharachchikumbura et al. 2012); on leaves of *Clerodendrum canescens* in China (Xu et al. 2016); on stem bark of *Sinopodophyllum hexandrum* in China (Xiao et al. 2017); on immature coconut in Brazil (Rosado et al. 2015); on Chestnut in India (Kumar and Khan 1983); on *Dictyosperma album* in China (Zhu et al. 2015);on Raspberry in China (Yan et al. 2019); on dead leaves of *Cocos nucifera* in Thailand (this study).

GenBank numbers – ITS = OR438420, *tef1-α* = OR500348, *tub*2 = OR538091

Notes – In the multi-loci phylogenetic analyses, our strain (MFLUCC 23-0158) grouped with *Pestalotiopsis adusta* (MFLUCC10-0146 and ICMP6088, ex-type) (Fig. 133). Morphologically, our strain shares similar morphology with the holotype of *P. adusta* (ICMP6088) in having indistinct conidiophores, reduced to conidiogenous cells and fusiform to ellipsoid, straight to slightly curved, 4-septate and similar sized conidia with basal and apical appendage (ref). In pairwise nucleotide comparisons showed that our strain (MFLU 23-0247) is not significantly different from the strains of *P. adusta* (MFLUCC10-0146) and (ICMP6088) strains in ITS, *tef1-α*, and *tub2* gene regions. Thus, we identified our strain as *P. adusta* based on phylogenetic analyses and morphological characters, and we reported it as a geographic record from Thailand.

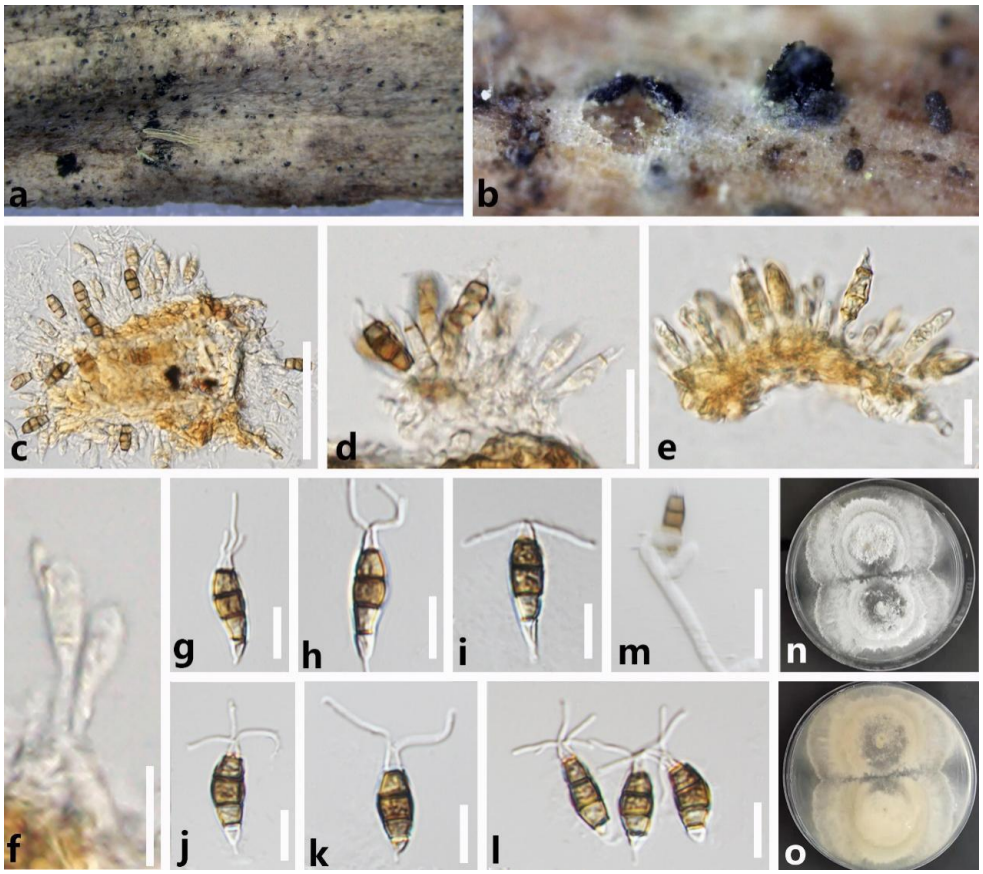

Figure 132 – *Pestalotiopsis adusta* (MFLU 23-0247, new host and geographic report). a, b The appearance of conidiomata on the host substrate. c–f Conidia with conidiogenous cells. g–l Conidia. m Germinated conidium. n, o Colonies on PDA from surface and reverse. Scale bars: c = 50 µm, d–f, m = 20 µm, g–l = 10 µm.

Xylariales Nannf.

Xylariales, is a large order in *Xylariomycetidae*, which was introduced by Nannfeldt (1932). This order has been revised in many studies based on phylogenetic analyses and morphological characters (Nannfeldt 1932, Hongsanan et al. 2017, Voglmayr et al. 2018, Wendt et al. 2018, Samarakoon et al. 2022). The latest treatment of *Xylariales* was provided by Hyde et al. (2022a), where they accepted 15 families and 160 genera in *Xylariales*.

Hypoxylaceae DC.

Hypoxylaceae was validated by Wendt et al. (2018) with accepted 14 genera based on multi-locus phylogeny, morphology and chemotaxonomy studies. Daranagama et al. (2018) accepted 18 genera in the family, however, three genera *Alloanthostomella*, *Neoanthostomella* and *Pseudoanthostomell* clustered as a separate clade in *Xylariaceae sensu stricto* (Daranagama et al. 2018, Voglmayr et al. 2018, Wendt et al. 2018). Hence the three genera were excluded from *Hypoxylaceae* and placed in *Xylariales genera incertae*. The recent treatment of *Hypoxylaceae* was provided by Hyde et al. (2020a) with accepted 19 genera in the family.

Daldinia Ces. & De Not.

Daldinia was erected by de Cesati & de Notaris (1863) and redefined by Stadler et al. (2014) and later included in *Hypoxylaceae*. Most species are characterized by the internal concentric zones below the perithecial layer in their stroma and by the presence of KOH- extractable pigments on and below their stromatal surface. There are 100 records of *Daldinia* listed in the Index Fungroum (2023). In this study, *Daldinia eschscholtzii* is reported as a new record on *Oryza sativa* based on morphology and phylogeny.

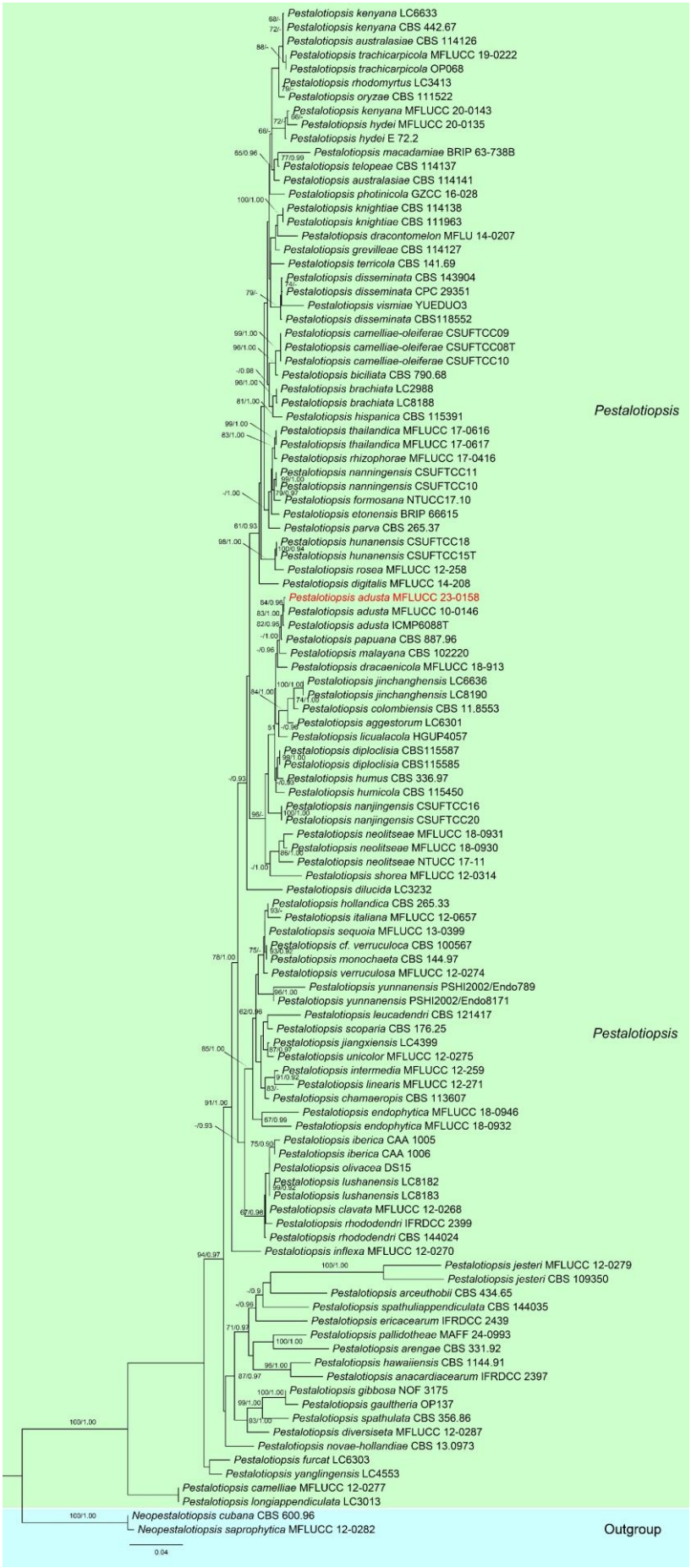

Figure 133 – Phylogram generated from maximum likelihood analysis based on combined ITS,

tef1-α and *tub2* sequence data. Related sequences were obtained from Gu et al. (2021). One hundred and ten strains are included in the combined sequence analysis, which comprise 2268 characters with gaps (ITS: 1–538, *tef1-α*: 539-1487, SSU: 1488-2268, *tub2*: 2953–3862). *Neopestalotiopsis cubana* (CBS 600.96) and *N. saprophytica* (MFLUCC 12-0282*)* were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -14783.698640 is presented. The matrix had 943 distinct alignment patterns, with 31.63% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241744, C = 0.261020, G = 0.249387, T = 0.247849; substitution rates AC = 1.115811, AG = 3.435887, AT = 1.152668, CG = 0.937746, CT = 4.604377, GT = 1.000000; gamma distribution shape parameter α = 0.263353. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

79. *Daldinia eschscholtzii* (Ehrenb.) Rehm, Annls mycol. 2(2): 175 (1904) Fig. 134

Index Fungorum number: IF544992; Facesoffungi number: FoF02990

Endophytic on fresh leaves of *Oryza sativa*. Sexual morph: Not observed. Asexual morph: Observed on eight weeks old culture, hyphomycetes. *Mycelium* superficial, composed of septate, inflated, branched, rough in cultures. *Conidiophores* 3–4 µm diam. ($\overline{x}$ = 3.5 µm, n = 15) hyaline, macronematous, mononematous, with dichotomous to trichotomous conidiogenous structure bearing nodulisporium–like branching pattern, 1–3 conidiogenous cells arising from previous conidiogenous terminus. *Conidiogenous cells* 15–25 ×2.5–3.5 µm ($\overline{x}$ = 18 × 3 µm, n = 35), holoblastic, polyblastic, terminal or intercalary, cylindrical, hyaline, with nodose apices. *Conidia* 4.5–5 µm × 2–3 µm ($\overline{x}$ = 5 × 2.5 µm, n = 25), hyaline, aseptate, obovoid to ellipsoid, smooth, round at apex, truncate at the base.

Culture characteristics – Colonies light, reaching 15 cm on PDA at 25 °C in two weeks, initially white, turning smoke-grey with age, and reverse black in color.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on fresh leaves of *Oryza sativa*, 2 November 2020, X.G. Tian, re2-2 (MFLU 23-0248, dried culture), living culture (MFLUCC 23-0170).

Known hosts and distribution – On *Pogostemon cablin* in China (Liu et al. 2019b); on *Barleria prionitis* in Thailand (Khruengsai et al. 2021); on *Musa paradisiaca* in Anambra state (Chigozie et al. 2020); in a leaf of grapevine (*Vitis vinifera*) from Korea (Lee et al. 2019); from *Psidium guajava* in India (Chutulo & Chalannavar 2020); on fresh leaves of *Oryza sativa* in Thailand (this study).

GenBank numbers – LSU = OR438881, ITS = OR438421, *rpb2* = OR634959, *tub*2 = OR538092

Notes – In the phylogenetic analyses of ITS, LSU, *rpb2*, and *tub2*, our strain clustered together with *Daldinia eschscholtzii* strains (Fig. 135). Morphologically, our collection (MFLUCC 23-0170) is similar to *D. eschscholtzii* in having dichotomous or trichotomous conidiogenous structure bearing nodulisporium–like branching pattern and obovoid to ellipsoid conidia with a truncate at the base. Thus, we identified our strain as *D. eschscholtzii* based on phylogenetic analyses and morphological characters. *Daldinia eschscholtzii* is commonly found as endophyte from various hosts (e.g., *Pogostemon cablin* and *Musa* sp.). Our new isolate is an endophyte and a new host record on *Oryza sativa*.

Hypoxylon Bull.

Hypoxylon is a highly diverse genus with more than 200 species and 1000 epithets (Ma et al. 2022). Species in this genus are mainly reported as saprobes and a few species are endophytes and facultative parasites on diseased hosts (Ju & Rogers 1996, Ma et al. 2022). *Hypoxylon* has a worldwide distribution with a higher diversity in tropical and subtropical regions (ref). Members of this genus have been found to produce highly bioactive secondary metabolite and some *Hypoxylon* species might have beneficial effects on their hosts during their endophytic life stage (Helaly et al.

2018). In this study, a new species *Hypoxylon cocois* is introduced, which was collected from dead leaves of *Cocos nucifera*. As I mentioned in the main commens all of your trees must come after your talk about the genus.

Figure 134 – *Daldinia eschscholtzii* (MFLU 23-0248, new host record). a Conidiophores with conidiogenous cells. b, c Colonies on PDA from surface and reverse. d–f Conidiogenous cells and conidia. g–l conidia. m–o Conidiophores with attached conidia. Scale bars: a, d–f, m–o = 10 µm, g–l = 5 µm.

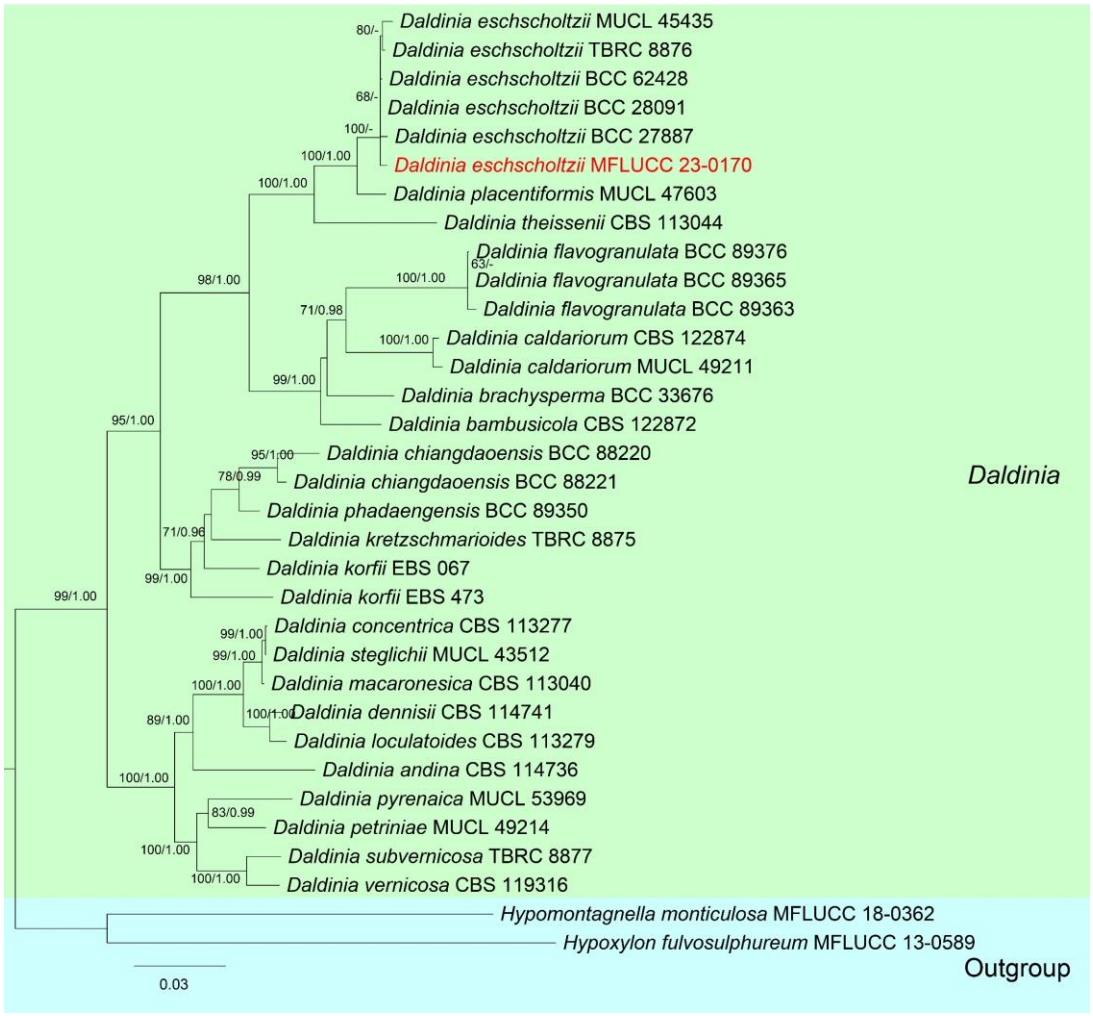

Figure 135 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, and *tub2* sequence data. Related sequences were obtained from Wongkanoun et al. (2020). Thirty-three strains are included in the combined sequence analysis, which comprise 4284 characters with gaps. *Hypomontagnella monticulosa* (MFLUCC 18-0362) and *Hypoxylon fulvosulphureum* (MFLUCC 13-0589) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -40011.480380 is presented. The matrix had 2058 distinct alignment patterns, with 18.28% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237716, C = 0.261980, G = 0.258505, T = 0.241799; substitution rates AC = 1.188806, AG = 4.269345, AT = 1.169781, CG = 0.876795, CT = 6.055059, GT = 1.000000; gamma distribution shape parameter α = 0.216464. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

80. ***Hypoxylon cocois*** X.G, Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 136

Index Fungorum number: IF900991; Facesoffungi number: FoF14324

Etymology – Referring to the host plant *Cocos nucifera*, on which the fungus was collected.

Holotype – MFLU 23-0249

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Stromata* pulvinate to effused-pulvinate, aggregated into groups, with several ascomata, black, ostiolate, mostly with extractable stromal pigments, attached to the surface, conical-dome shaped, raised areas. *Ascomata* 170–260 × 210–360 µm ($\bar{x}$ = 214 × 285 µm, n = 10), globose-subglobose or elongate cylindrical-pyriform, embedded in the stroma, monostichous, interior sometimes filled with a liquid. *Ostiole* umbellate, often opening lower than the stromatal surface. *Peridium* 20–30 µm wide ($\bar{x}$ = 24 µm, n = 10),

comprising 5–12 layers of thin-walled, brown to black cells of textura angularis. *Hamathecium* composed of 2.5–4 µm wide ($\bar{x}$ = 3.5 µm, n = 10), hyaline, filamentous, septate, embedded in a gelatinous matrix, paraphyses. *Asci* 80–90 × 5–10 µm ($\bar{x}$ = 83.5 × 10 µm, n = 20), 8-spored, unitunicate, cylindrical to clavate, straight, short pedicel or sessile, apically rounded, with a J+ apical ring. *Ascospores* 13–15 × 6–7 µm ($\bar{x}$ = 14.5 × 6.5 µm, n = 40), uniseriate, ellipsoidal-subglobose or inequilateral, with narrowly rounded ends, brown to blackish brown, hyaline when young, mostly with a conspicuously straight spore-length germ slit on the convex side. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 12 h at 25 ℃ and germ tubes produced from both cells. Colonies on PDA circular, mycelium velvety with fluffy, filamentous at margin, colony white on PDA from above, colony brown from below.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Cocos nucifera*, 8 December 2020, X.G. Tian, c4-4 (MFLU 23-0249 holotype), ex-type living culture MFLUCC 23-0137.

GenBank numbers – MFLU 23-0249: LSU = OR438882, ITS = OR438422. MFLUCC 23-0137: LSU = OR438883, ITS = OR438423, *rpb2* = OR634960, *tub*2 = OR538093

Notes – In the multi-loci phylogenetic analyses, *Hypoxylon cocois* clustered as a sister taxon to *Hypoxylon begae* with 100% ML and 1.00 PP bootstrap support (Fig. 137). Morphologically, *H. cocois* shares similar morphology to *H. begae* (YMJ 90080707) in having unitunicate, cylindrical asci with apical ring and unicellular, ellipsoid-inequilateral, black blackish brown ascospores. However, the ascospores of *Hypoxylon cocois* are ellipsoidal-subglobose or inequilateral, with narrowly rounded ends. Whereas ascospores of *H. begae* are ellipsoid, nearly equilateral, with broadly rounded ends (Ju & Rogers 1996). Based on the recommendations of Jeewon and Hyde (2016), the nucleotide comparisons showed that *H. cocois* is significantly different from *H. begae* (YMJ 215) in ITS (23/519, 4.43%) and *tub2* (62/763, 8.13%). The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 1) (Fig. 138). Thus, we identified the *Hypoxylon cocois* as a new species based on phylogenetic analyses and morphological characters.

Xylariaceae Tul. & C. Tul.

Xylariaceae was introduced by Tulasne and Tulasne (1863). *Xylariaceae* species are saprobic, pathogenic or endophytic in plant tissues or insects (Hyde et al. 2017, Hongsanan et al. 2015) This family is characterised by well-developed stromata, or lack of stroma, unitunicate, 8-spored, asci, with or without a J+, apical ring, pigmented ascospores with germ slits or pores (Hongsanan et al. 2015, Hyde et al. 2017, Samarakoon et al. 2022). In an updated classification of *Xylariaceae* 38 genera were accepted (Wijayawardene et al. 2022).

Anthostomella Sacc.

Anthostomella, is a polyphyletic genus with a rich species diversity. Members of this genus are characterized by immersed or semi-immersed, clypeate, ascomata with periphysate ostiolar canals, unitunicate, cylindrical asci with or without a J+, apical ring and mostly brown, aseptate ascospores with or without a dwarf cell or appendages at the ends and presence or absence of a germ slit (Lu & Hyde 2000, Daranagama et al. 2015, Samarakoon et al. 2022).

Numerous authors have studied and debated the genus because it was introduced without a ‘type’ (Eriksson 1966, Francis 1975, Lu & Hyde 2000). A comprehensive study of *Anthostomella* was constructed by Daranagama et al. (2015) and they accepted *A. tomicoides* as the generic type and showed that *Anthostomella* is polyphyletic in *Xylariaceae*. Phylogenetic analyses of Hyde et al. (2020a) showed that the genus does not appear to be phylogenetically related to Xylariaceae. Recently, Samarakoon et al. (2022) showed that *Anthostomella* is polyphyletic and formed two clades in Xylariaceales. The two clades are named as “*Anthostomella helicofissa* clade” and “*Anthostomella formosa* clade” (Samarakoon et al. 2022). In this study, we introduce a new species that clustered within the “*Anthostomella formosa* clade”.

Figure 136 – *Hypoxylon cocois* (MFLU 23-0249, holotype). a, b Colonies on dead leaves of *Cocos nucifera*. c, d Section through ascoma. e Peridium. f–h Immature and mature asci. i Pseudoparaphyses. j Apical apparatus in Melzer's reagent. k–n Ascospores. o Germinated ascospore. p, q Colonies on PDA from surface and reverse. Scale bars: c–k = 40 μm, p = 20 μm, l–o = 10 μm.

81. ***Anthostomella cocois*** X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 139

Index Fungorum number: IF900992; Facesoffungi number: FoF14325

Etymology – Referring to the host plant *Cocos nucifera*, on which the fungus was collected.

Holotype – MFLU 23-0250

Saprobic on dead leaves of *Cocos nucifera*. Sexual morph: *Ascomata* 240–310 high × 240–320 μm wide, ($\bar{x}$ = 271 × 276 μm, n = 5), immersed, raised, black, solitary, clypeate, globose to subglobose. *Ostioles* centric, ostiolar canal periphysate. *Peridium* 20–25 μm ($\bar{x}$ = 20 μm, n = 10) wide, with 3-5 cell layers, thick at outer layer, comprising hyaline to yellowish brown cells of *textura angularis*. *Hamathecium* 2.5–3.5 μm ($\bar{x}$ = 3 μm, n = 20) wide, numerous, filamentous, septate, unbranched, apically blunt, paraphyses. *Asci* 70–90 × 6–8 μm ($\bar{x}$ = 76 × 5.7 μm, n = 40), 8-spored, unitunicate, cylindrical, short pedicellate, apically rounded, with a discoid, apical ring. *Ascospores* 10–12 × 3.5–5 μm ($\bar{x}$ = 10.5 × 4 μm, n = 40), uniseriate, brown, ellipsoidal, aseptate, guttulate, with a longitudinally laid germ-slit. Asexual morph: Not observed.

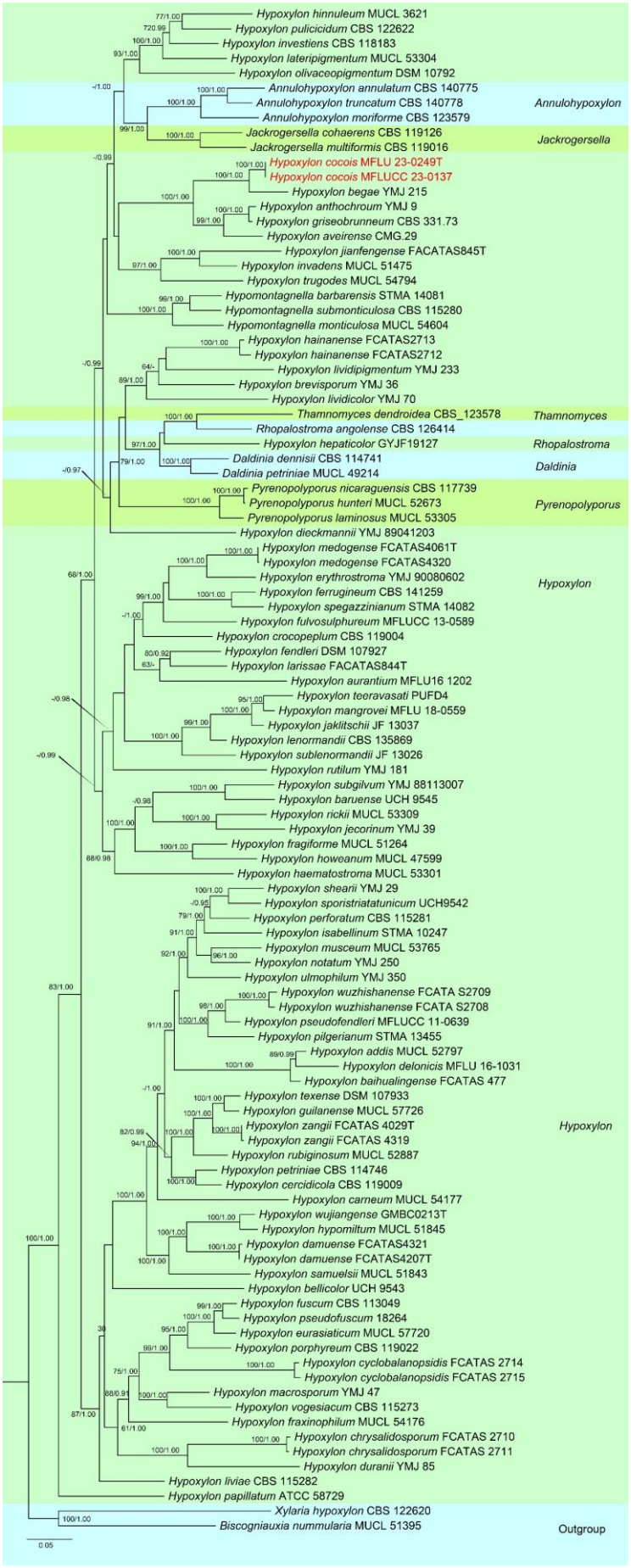

Figure 137 – Phylogram generated from maximum likelihood analysis based on combined ITS,

LSU, *rpb2*, and *tub2* sequence data. Related sequences were obtained from Ma et al. (2022). One hundred and three strains are included in the combined sequence analysis, which comprise 4243 characters with gaps. *Biscogniauxia nummularia* (MUCL 51395) and *Xylaria hypoxylon* (CBS 122620) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -86426.009514 is presented. The matrix had 2349 distinct alignment patterns, with 26.66% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237707, C = 0.269017, G = 0.253026, T = 0.240250; substitution rates AC = 1.224294, AG = 4.297289, AT = 1.489020, CG = 0.930889, CT = 5.571661, GT = 1.000000; gamma distribution shape parameter α = 0.280142. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

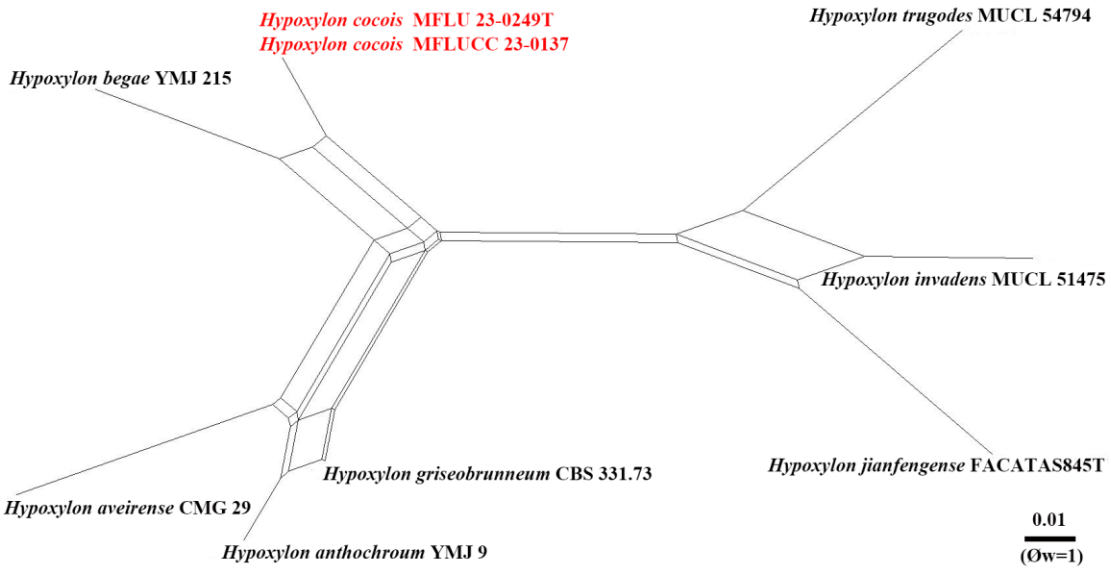

Figure 138 – Results of the PHI test of *Hypoxylon cocois* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

Culture characteristics – Colonies on PDA at 25 °C reaching 10 cm in 2 weeks, at first whitish, felty, with diffuse grey colour margins, reverse turning brown to dark brown.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of *Cocos nucifera*, 3 January 2021, X.G. Tian, C5-12)MFLU 23-0250, holotype(, ex-type living culture MFLUCC 23-0154.

GenBank numbers – MFLU 23-0250: LSU = OR438884, ITS = OR438424. MFLUCC 23-0154: LSU = OR438885, ITS = OR438425, *rpb2* = OR634961

Notes – In the multi-loci phylogenetic analyses of ITS, LSU, *rpb2*, and *tub2*, *Anthostomella cocois* (MFLUCC 23-0154) formed a distinct lineage basal to the genus *Anthostomella* with 97% ML and 1.00 PP, bootstrap support (Fig. 140). *Anthostomella cocois* is phylogenetically close to *A. obesa*. The PHI test revealed no significant recombination event between our strain and the closely related taxa (Φw = 1) (Fig. 141). Morphologically, *A. cocois* is similar to *A. obesa* in having unitunicate, cylindrical, short-pedicellate asci with a discoid, apical ring and uniseriate, globose to equilateral ellipsoidal, unicellular ascospores (Daranagama et al. 2015). However, *A. cocois* is distinct from *A. obesa* in having brown ascospores, while *A. obesa* has brown to black ascospores. *Anthostomella cocois* also has smaller size range of peridium (20–25 µm vs. 25–30 µm wide), ascospores (10–12 × 3.5–5 µm vs. 13–18×6.7–9 µm) and asci (70–90 × 6–8 µm vs. 90–135 × 10–24 µm) than *Anthostomella obesa*. Thus, we identified new strains as new species *Anthostomella cocois* based on phylogenetic analyses and morphological characters.

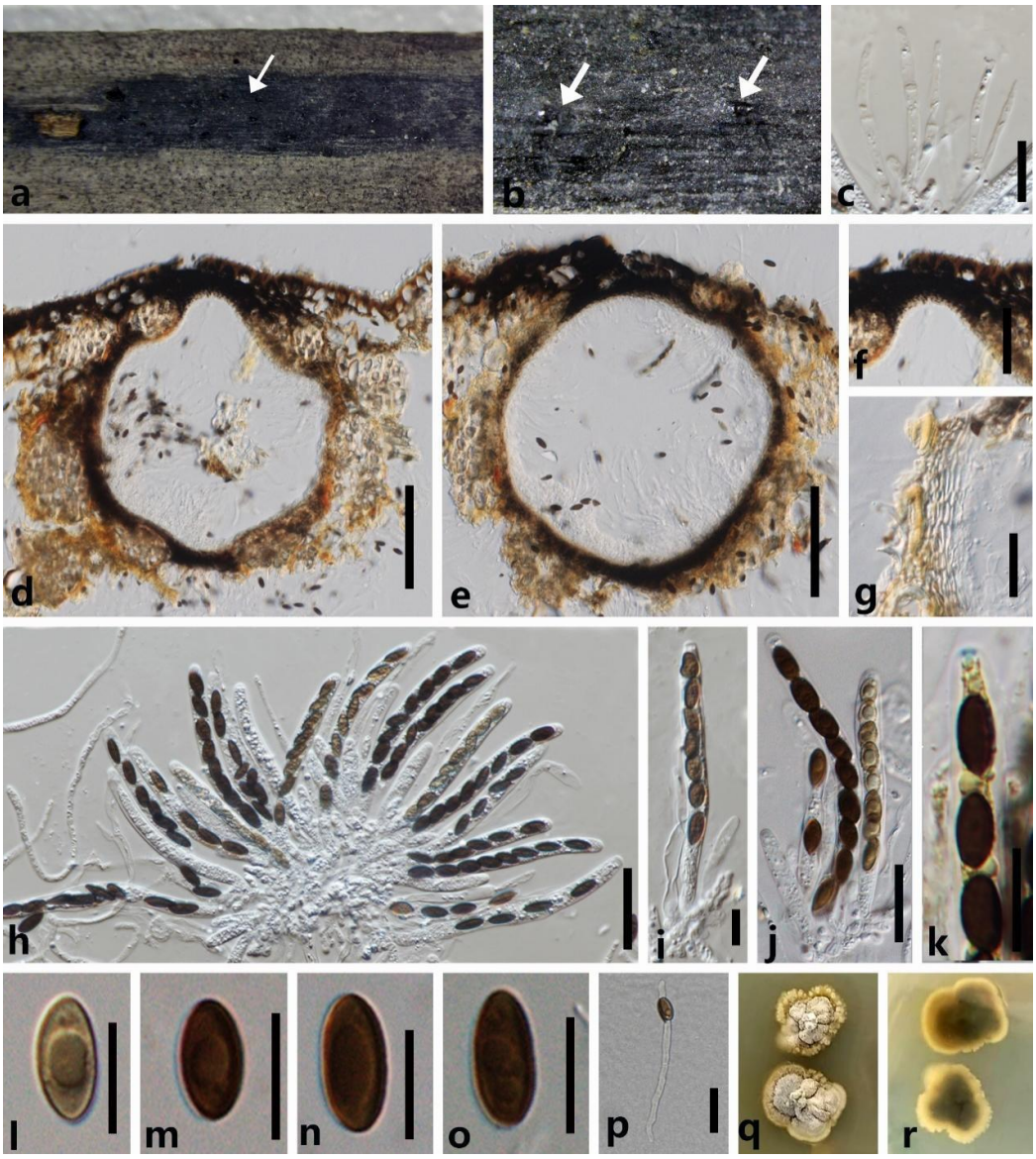

Figure 139 – *Anthostomella cocois* (MFLU 23-0250, holotype). a, b Ascomata in dead substrate. c Paraphyses. d, e Section through ascoma. f Section through ostiole. g Peridium. h–k Asci. (k stained in Melzer's reagent). l–o Ascospores. p Germinated ascospore. q, r Colonies on PDA from surface and reverse. Scale bars: d–e = 100 μm, c, f–j, p = 20 μm, k–o = 10 μm.

Xylariales genera incertae sedis

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

The monotypic genus *Occultitheca* was introduced by Rogers & Ju (2003) with *O. costaricensis* as the type which was isolated from a decaying wood from *Costa Rica*. Samarakoon et al. (2022) introduced the second species *O. rosae* based on morphological characters and provided a tentative phylogenetic placement for the genus. There are only two species accepted in the genus. Members of *Occultitheca* are characterized by immersed ascomata, short pedicellate asci with J+, apical ring, and brown ascospores with hyaline dwarf cells and a straight germ slit (Rogers & Ju 2003, Samarakoon et al. 2022). In this study, we introduce a new species *O. ananasi* based on morphological characters and molecular data.

82. *Occultitheca ananasi* X.G. Tian, K.D. Hyde & Tibpromma, sp. nov. Fig. 142

Index Fungorum number: IF900993; Facesoffungi number: FoF14326

Etymology – Referring to the host plant *Ananas comosus* on which the fungus was collected.

Holotype – MFLU 23-0251

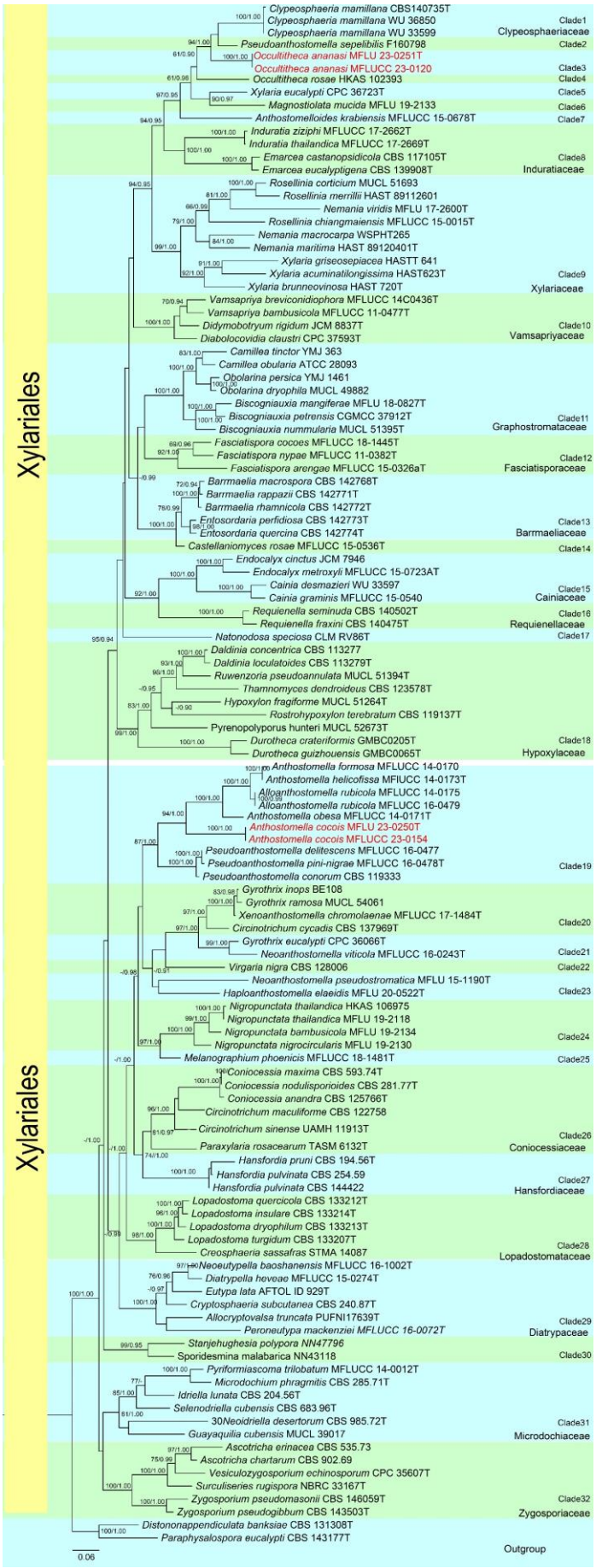

Figure 140 – Phylogram generated from maximum likelihood analysis based on combined ITS,

LSU, *rpb2*, and *tub2* sequence data. Related sequences were obtained from Samarakoon et al. (2022). One hundred and twenty strains are included in the combined sequence analysis, which comprise 3825 characters with gaps. *Distononappendiculata banksiae* (CBS 131308) and *Paraphysalospora eucalypti* (CBS 143177) were used as the outgroup taxa. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of -75216.028056 is presented. The matrix had 2497 distinct alignment patterns, with 41.13% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243237, C = 0.255330, G = 0.262733, T = 0.238701; substitution rates AC = 1.332744, AG = 3.476903, AT = 1.489944, CG = 1.046967, CT = 5.916216, GT = 1.000000; gamma distribution shape parameter α = 0.316819. Bootstrap support values for ML equal to or greater than 60% and PP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red, while T indicates holotype or ex-type strains.

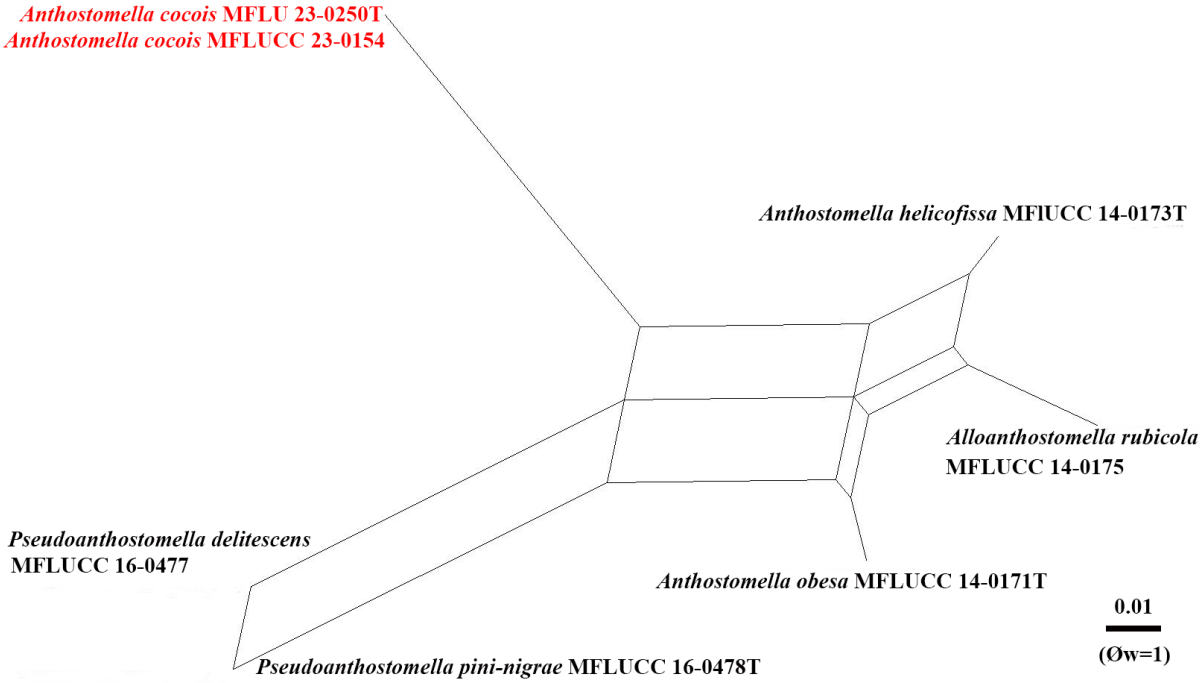

Figure 141 – Results of the PHI test of *Anthostomella cocois* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: *Ascomata* 190–230 × 160–260 µm ($\bar{x}$ = 210 × 209 µm, n = 5), immersed, solitary or aggregated, slightly raising host surface, globose to subglobose. *Clypeus* carbonaceous, black, short, comprising host epidermal cells and dark fungal hyphae. *Ostioles* centric, with ostiolar canal periphysate. *Peridium* 15–20 µm ($\bar{x}$ = 17.5 µm, n = 8) wide, 2-4 cell layers, outer layer thick, comprising brown to dark brown, thick-walled cells of *textura angularis*, with thin inner layer, composed of hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 3–5 µm ($\bar{x}$ = 4 µm, n = 20) wide, longer than the asci, filamentous, septate, slightly constricted at the septa. *Asci* 70–90 × 5–10 µm ($\bar{x}$ = 81.5 × 8 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, apically rounded, rectangular to slightly obconic, with a J+ apical ring. *Ascospores* 10–12.5 × 3.5–4.5 µm ($\bar{x}$ = 11.5 × 4 µm, n = 30), uniseriate, becoming 2-seriate in the middle, olive-greenish to dark olive, inequilaterally oblong-ellipsoidal, apical cell, with large guttules, sometimes covered with a thin mucilaginous sheath, germ slit on ventral side, straight, along the entire spore length, with a small, hyaline, rounded, basal cell. Asexual morph: Not observed.

Material examined – Thailand, Chiang Rai Province, Muang District, on dead leaves of

Ananas comosus, 18 October 2020, X.G. Tian, P12-4)MFLU 23-0251, holotype(, ex-type culture, MFLUCC 23-0120.

GenBank numbers – MFLU 23-0251: LSU = OR438886, ITS = OR438426. MFLUCC 23-0120: LSU = OR438887, ITS = OR438427, *rpb2* = OR634962, *tub*2 = OR538094

Notes – In the phylogenetic analyses of combined ITS, LSU, SSU, and *rpb2* sequence data, our new species *Occultitheca ananasi* (MFLU 23-0251) formed a distinct lineage which is close to *O. rosae* (HKAS 102393) and *Pseudoanthostomella sepelibilis* (Fig. 140). However, *Occultitheca ananasi* can easily be distinguished from *P. sepelibilis* by the ascospores with a germ slit, which were not found in *P. sepelibilis* (Lu & Hyde 2000). Our phylogenetic analyses showed that *P. sepelibilis* formed a distinct lineage within *Xylariales*, far from *Pseudoanthostomella* (Fig. 140). In addition, this species is morphologically different from *Pseudoanthostomella* in having bicellular ascospores, with a large, brown cell and a small, hyaline dwarf cell and a mucilaginous sheath, lack germ slits (Lu & Hyde 2000, Daranagama et al. 2016). Thus, further studies are needed to confirm the taxonomic placement of this species.

Occultitheca ananasi fits well with the morphological concept of the *Occultitheca* in having immersed ascomata, short pedicellate asci with J+, apical ring, and brown ascospores with hyaline dwarf cells and a straight germ slit (Rogers & Ju 2003, Samarakoon et al. 2022). The generic type, *O. costaricensis* lacks sequence data in the GenBank, and morphologically, our species is not significantly distinct from the genus. In addition, limited taxa sampling in the genus provides insufficient information for the genus. Thus, we could not introduce a new genus for our strain *O. ananasi*, and we placed our new species in *Occultitheca* based on the minor differences in morphological characteristics. However, further studies with more molecular and morphological data are required to resolve the taxonomy of *Occultitheca*.

Currently, two species, *O. rosae* and *O. costaricensis* are accepted in *Occultitheca*. Our species *O. ananasi* is quite similar to *O. rosae* in having immersed ascomata, short pedicellate asci, apical ring, and ascospores with hyaline basal cell and a straight germ slit. However, *O. ananasi* mostly has uniseriate, becoming 2-seriate in the middle, olive-greenish ascospores and the paraphyses without guttulate, which differs from *O. rosae* in having uniseriate, brown ascospores and guttulate paraphyses (Samarakoon et al. 2022). *Occultitheca ananasi* mostly has 1–2 individual ascomata, which differs from *O. costaricensis* in having 2–12 ascomata in a cluster. In addition, *O. ananasi* and *O. rosae* differ from *O. costaricensis* in having ascospores with a thin mucilaginous sheath (Samarakoon et al. 2022). The PHI test revealed no significant recombination events between our strain and the closely related taxa (Φw = 1) (Fig. 143). Therefore, we identified our strain as a new species. However, the generic status of these three species needs further studies with more taxa sampling, morphological characteristics, and phylogenetic analyses.

Conclusion

In this study, we described the saprobic fungi associated with three economically important monocotyledons *viz.* Pineapple (*Ananas comosus*), Coconut (*Cocos nucifera*), and Rice (*Oryza sativa*), collected in Thailand and China. A total of 77 species distributed in three classes, 15 orders, 36 families, and 58 genera were identified based on phylogenetic analyses and morphological characteristics (Fig. 144).

In *Dothideomycetes*, three new genera, 10 new species, and 28 new records from coconut, pineapple, and rice were introduced. *Pleosporales* is the dominant order with 29 species, followed by *Botryosphaeriales* (nine species). The dominant family is *Botryosphaeriaceae*, with eight species, followed by *Didymosphaeriaceae* (five species) and *Pleosporaceae* (five species) (Fig. 145). In addition, based on phylogenetic analyses and morphological characteristics, we synonymized *Pseudopithomyces pandanicola* and *P. palmicola* under *P. chartarum*, *P. diversisporus* under *P. atro-olivaceus*.

In *Sordariomycetes*, two new genera, nine new species, and 23 new records were introduced. while *Amphisphaeriales* (10 species) and *Hypocreales* (seven species) were the dominant orders in *Sordariomycetes*. *Sporocadaceae* was the dominant family with six species (Fig. 146). Furthermore,

in *Eurotiomycetes*, two collections were successfully isolated and identified as a new species (Fig. 145).

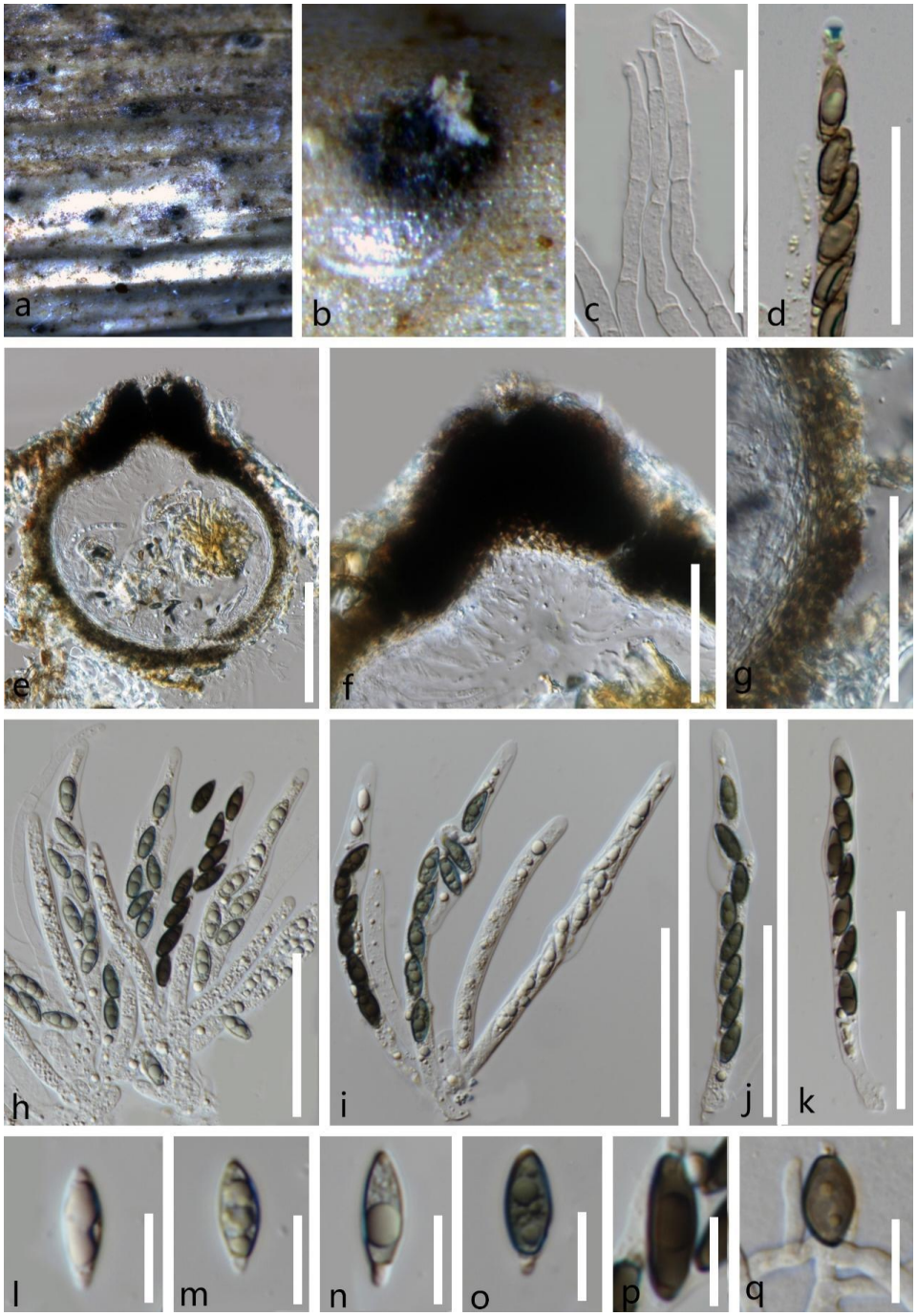

Figure 142 – *Occultitheca ananasi* (MFLU 23-0251, holotype). a, b Ascomata in dead substrate. c Paraphyses. d, h–k Asci (d stained in Melzer's reagent). e Section through ascoma. f Section through ostiole. g Peridium. l–p Ascospores. q Germinated ascospore. Scale bars: e = 100 µm, c, d, f–k = 50 µm, l–q = 10 µm.

Community composition of fungi associated with coconut

Previous studies mostly focused on the fungal pathogens of coconut. Harrison & Jones (2003) reviewed the diseases of coconut and reported 40 pathogens. Vinod (2003) reported six pathogens in coconut. Recently, Vinjusha & Arun Kumar (2022) reported several *Ganoderma* species associated with stem rot of coconut. While endophytic and saprobic fungi on coconut have poorly been studied. China and Thailand are two of the main coconut-growing countries. In this study, we

investigated the saprobic fungi associated with coconut in China and Thailand, and a new genus, six new species, and 21 new records are introduced.

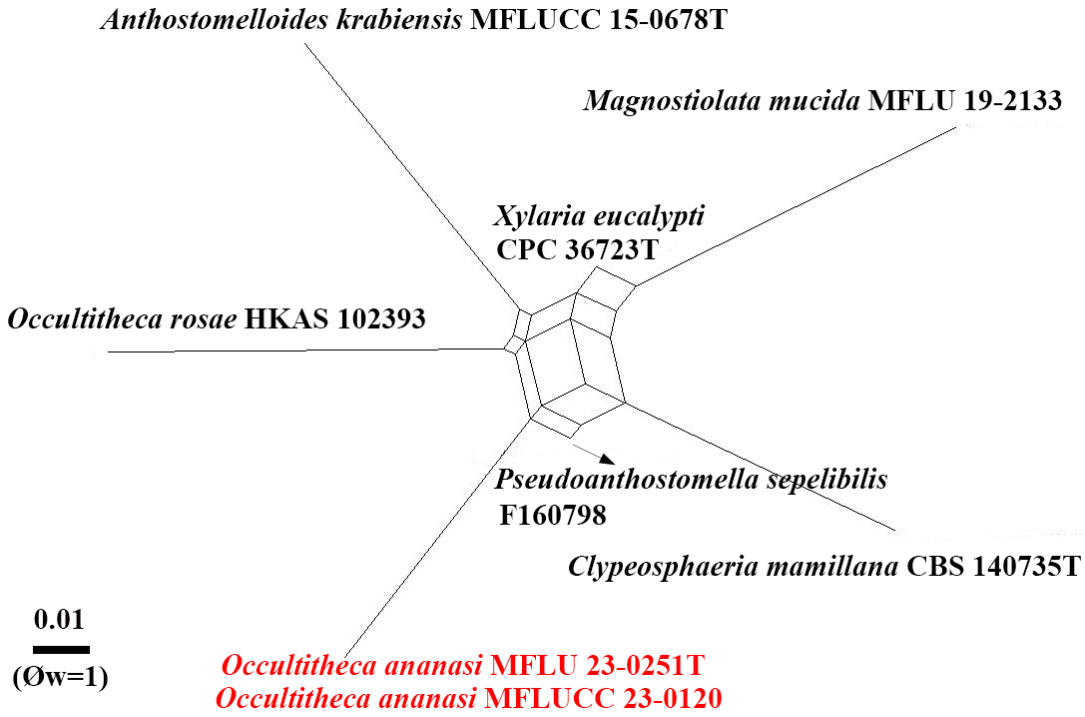

Figure 143 – Results of the PHI test of *Occultitheca ananasi* and closely related species using both LogDet transformation and splits decomposition. The PHI test results (Φw) < 0.05 indicate significant recombination within the dataset. The new taxon is in red bold type and T indicates holotype or ex-type strains.

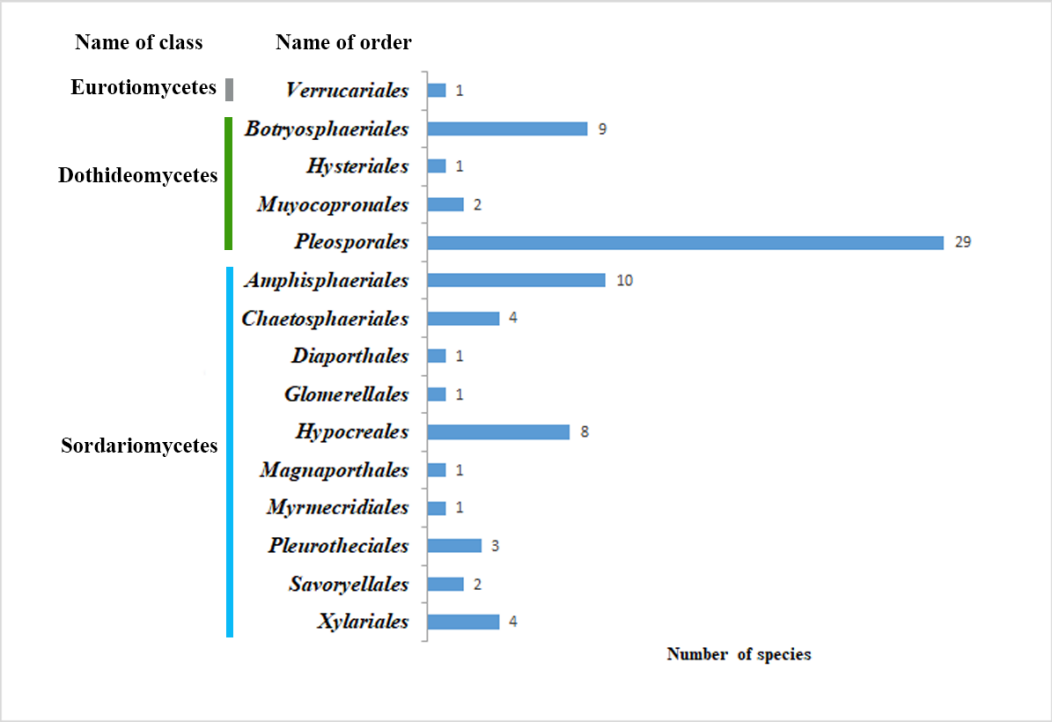

Figure 144 – This study's overview of fungal species in *Dothideomycetes*, *Eurotiomycetes*, and *Sordariomycetes* (Axis X is fungal number, and axis Y is fungal name).

A checklist of fungi associated with coconut is provided based on the previously published literature and this study (Table 2). A total of 120 species belonging to four phyla, 14 classes, 29 orders, and 54 families have been found on coconut (Fig. 148). *Dothideomycetes* and *Sordariomycetes* were the dominant classes with 32 and 45 species respectively, while Hypocreales (*Sordariomycetes*) was the dominant order (Table 2). Among them, 69 pathogens, 51 endophytes, and nine saprobes have been reported from coconut (Fig. 147), which indicates that the saprobic fungi associated with coconut have poorly been studied. Thus, future studies should focus on saprobic fungi associated with coconut. The families *Botryosphaeriaceae*, *Nectriaceae*, *Peronosporaceae*, *Pleosporaceae*, *Polyporaceae*, and *Sporocadaceae* are the main coconut pathogens that cause bud rot, dirty panicle disease, koleroga disease, leaf blight, leaf spots, nut-fall, premature, stem-end rot, and zonate eye-spot disease (Table 2).

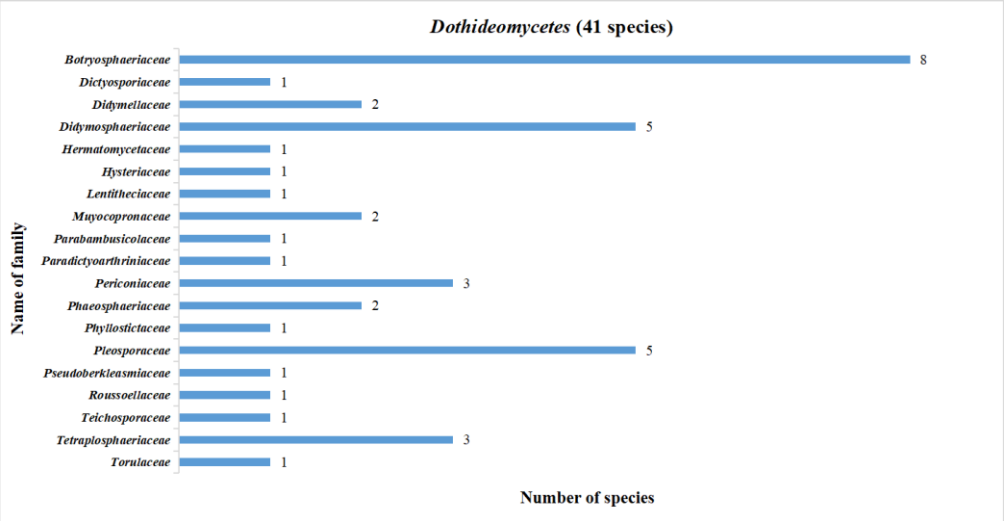

Figure 145 – Numbers of taxa in each family of *Dothideomycetes* (Axis X is fungal number and axis Y is fungal family).

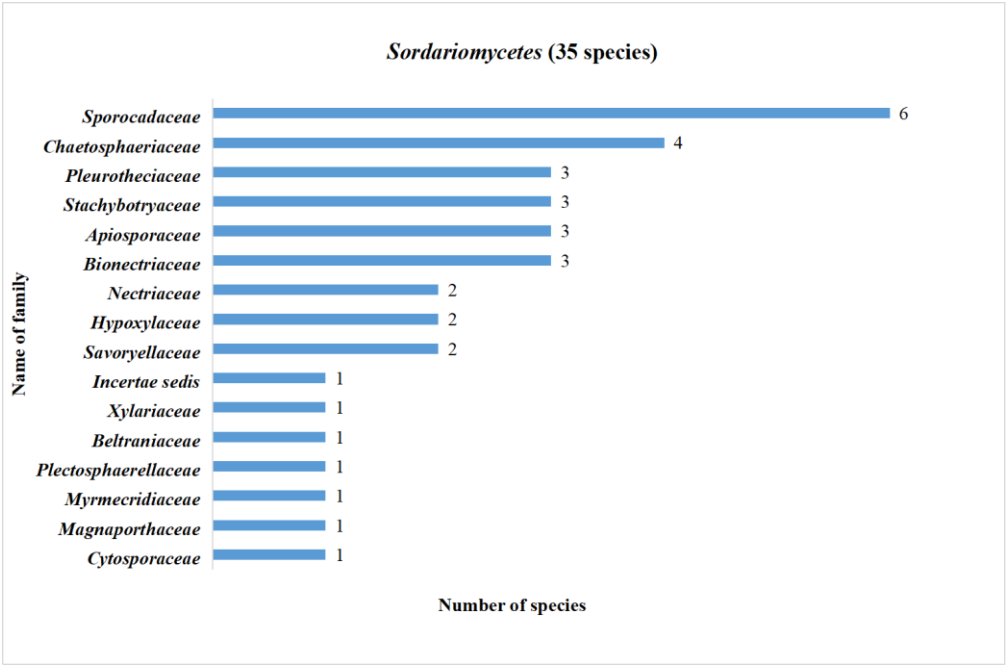

Figure 146 – Numbers of taxa in each family of *Sordariomycetes* (Axis X is fungal number and axis Y is fungal family).

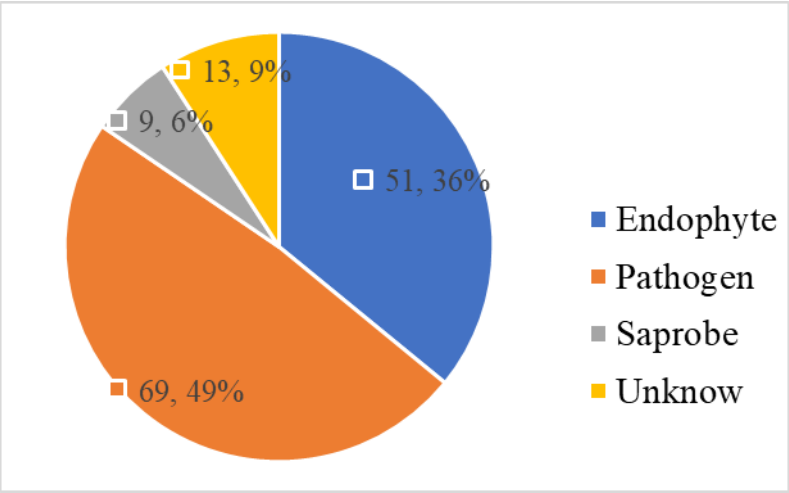

Figure 147 – Numbers and percentages of different life modes of fungi reported in coconut.

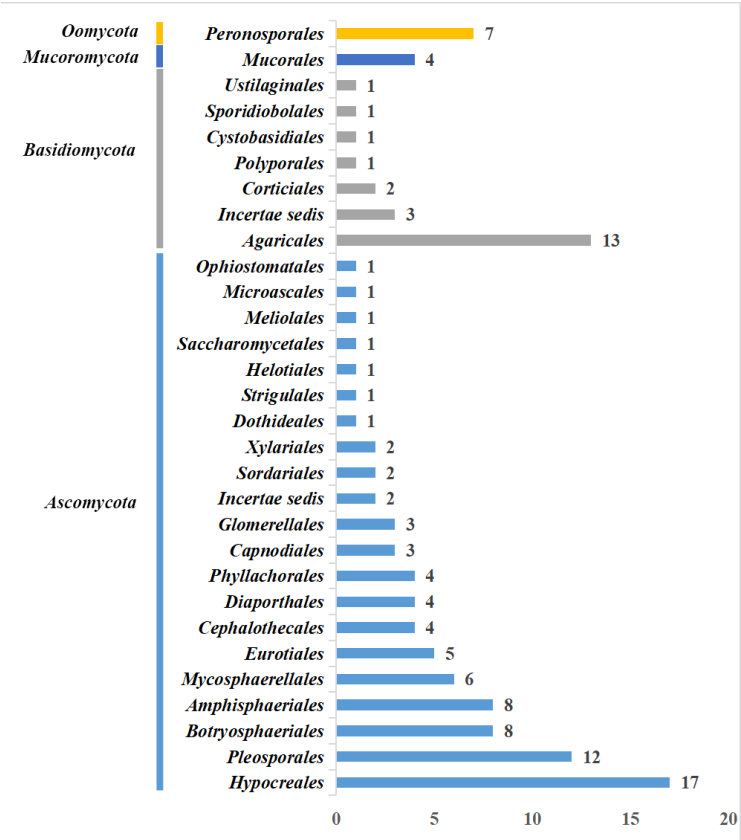

Figure 148 – Numbers of different fungal orders reported in coconut (Axis X is fungal number and axis Y is fungal name).

Several species have been reported as endophytes, pathogens, or saprobes on coconut, for example *Pestalotiopsis palmarum*, *Ceratocystis paradoxa*, and *Ganoderma lucidum* (Table 2), which suggested that fungi may switch their lifestyles from endophytes to pathogens or saprobes (Bhunjun et al. 2023). In addition, Tian et al. (2022c) introduced three new species of *Tubeufiaceae* viz, *Tubeufia cocois* (from coconut), *Neohelicosporium bambusicola* (from Bambusoidea), *Parahelicomyces chiangmaiensis* (from dead wood) but those species are now Nom. inval., Art. 5.4.1 (Shenzhen), as the identifiers associated with the new names were not registered. Therefore, in this study, Index Fungorum numbers for those three species: *Tubeufia cocois* (IF 901123), *Neohelicosporium bambusicola* (IF 901121), and *Parahelicomyces chiangmaiensis* (IF 901122).

Table 2 A check list of fungi associated with coconut (based on published literatures).

Phylum	Class	Order	Family	Species	Lifestyle	References
Ascomycota	*Coryneliomycetidae*	*Eurotiales*	*Aspergillaceae*	*Monascus* sp.	Endophyte	Padmaja (2011)
	Dothideomycetes	*Botryosphaeriales*	*Botryosphaeriaceae*	*Botryosphaeria cocogena*	Pathogen	Harrison & Jones (2003), Dollet et al. (2012), Silva et al. (2017)
				Botryosphaeria disrupta	Pathogen	Harrison & Jones (2003)
				Lasiodiplodia brasiliensis	Pathogen	Rosado et al. (2016), Coelho et al. (2022)
				Lasiodiplodia egyptiacae	Pathogen	Rosado et al. (2016)
				Lasiodiplodia pseudotheobromae	Pathogen	Rosado et al. (2016), Coelho et al. (2022)
				Lasiodiplodia subglobosa	Pathogen	Coelho et al. (2022)
				Lasiodiplodia theobromae (*Botryodiplodia theobromae*)	Endophyte/ Saprobe/ Soil/ Pathogen	Peries (1968), Ram (1989), Thomas et al. (2010), Venkatesagowda et al. (2012), Rosado et al. (2016)
				Macrophoma sp.	Pathogen	Harrison & Jones (2003)
		Capnodiales	*Cladosporiaceae*	*Cladosporium dominicanum*	Endophyte	Oliveira et al. (2021)
			Capnodiaceae	*Fumago vagans*	Endophyte	(Singh & Barde (1985)
			Incertae sedis	*Pseudoepicoccum cocos*	Pathogen	Hyde & Fröhlich (1995), Fröhlich et al. (1997), Harrison & Jones (2003)
		Dothideales	*Saccotheciaceae*	*Aureobasidium* sp.	Soil	Oliveira et al. (2021)
		Incertae sedis	*Incertae sedis*	*Radulidium apiculatum*	Endophyte	Oliveira et al. (2021)
		Mycosphaerellales	*Mycosphaerellaceae*	*Cercospora apii*	Endophyte	Oliveira et al. (2021)
				Cercospora sp.	Pathogen	Harrison & Jones (2003)
				Mycosphaerella palmicola	Pathogen	Hyde & Fröhlich (1995), Fröhlich et al. (1997), Harrison & Jones (2003)
				Scolecostigmina palmivora (*Stigmina palmivora*)	Pathogen	Harrison & Jones (2003)
				Periconiella cocoes	Pathogen	Hyde & Fröhlich (1995), Harrison & Jones (2003)
				Zasmidium musae	Endophyte	Oliveira et al. (2021)
		Pleosporales	*Didymosphaeriaceae*	*Paraphaeosphaeria arecacearum*	Endophyte	Oliveira et al. (2021)

Table 2 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
			Pleosporaceae	*Alternaria burnsii*	Pathogen	Sunpapao et al. (2022)
				Bipolaris gigantea (*Drechslera gigantea*)	Pathogen	Harrison & Jones (2003), Vurro (2007)
				Bipolaris incurvata (Drechslera incurvata)	Pathogen	Mahindapala (1979), Harrison & Jones 2003, Niu et al. (2014)
				Cochliobolus setariae (Bipolaris setariae)	Pathogen	Niu et al. (2014)
				Curvularia eragrostidis	Pathogen	Mahindapala (1979)
				Curvularia lunata (Cochliobolus lunatus)	Pathogen	Mahindapala (1979), Harrison & Jones (2003)
				Curvularia spp.	Endophyte/ Soil/ Pathogen	Peries (1968), Deden et al. (2018), Oliveira et al. (2021)
				Exserohilum rostratum (*Helminthosporium halodes*)	Pathogen	Koshy (2000), Thomas et al. (2010)
			Phaeosphaeriaceae	*Phaeosphaeria nodulispora*	Endophyte	Oliveira et al. (2016), Oliveira et al. (2021)
			Cucurbitariaceae	*Pyrenochaetopsis indica*	Endophyte	Oliveira et al. (2021)
				Pyrenochaetopsis microspora	Endophyte	Oliveira et al. (2021)
		Strigulales	*Strigulaceae*	*Strigula virescens (Cephaleuros virescens)*	Pathogen	Harrison & Jones (2003)
	Eurotiomycetes	*Eurotiales*	*Aspergillaceae*	*Aspergillus flavus*	Endophyte	Fuego et al. (2021)
				Aspergillus niger	Endophyte	Venkatesagowda et al. (2012), Fuego et al. (2021)
				Aspergillus spp.	Saprobe /Soil	Peries (1968), Padmaja (2011)
				Penicillium spp.	Endophyte/ Saprobe/ Soil	Padmaja (2011), Morales-Lizcano et al. (2017), Oliveira et al. (2021)
	Incertae sedis	*Incertae sedis*	*Incertae sedis*	*Capitorostrum cocoes*	Pathogen	Hyde & Fröhlich (1995), Harrison & Jones (2003)
	Leotiomycetes	*Helotiales*	*Erysiphaceae*	*Oidium* sp.	Pathogen	Harrison & Jones (2003)
	Saccharomycetes	*Saccharomycetales*	*Debaryomycetaceae*	*Yamadazyma cocois*	Endophyte	Maksimova et al. (2020)
	Sordariomycetes	*Amphisphaeriales*	*Apiosporaceae*	*Arthrinium* sp.	Endophyte	Calvo et al. (2005)

Table 2 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
			Sporocadaceae	*Pestalotiopsis adusta*	Pathogen	Fröhlich et al. (1997), Rosado et al. (2015)
				Pestalotiopsis elastica	Pathogen	Hyde & Fröhlich (1995), Fröhlich et al. (1997), Karthikeyan & Bhaskaran (1997), Ramos et al. (1998), Rahman et al. (2013)
				Pestalotiopsis palmarum	Endophyte/ Pathogen	Hyde & Fröhlich (1995), Fröhlich et al. (1997), Karthikeyan & Bhaskaran (1997), Ramos et al. (1998), Rahman et al. (2013)
				Pestalotiopsis phoenicis	Pathogen	Fröhlich et al. (1997)
				Pestalotiopsis sp.	Endophyte/ Pathogen	Eris et al. (2017), Oliveira et al. (2021)
				Pseudopestalotiopsis theae (*Pestalotiopsis theae*)	Pathogen	Fröhlich et al. (1997)
		Cephalothecales	*Ceratocystidaceae*	*Ceratocystis paradoxa* (*Chalaropsis thielavioides*, *Thielaviopsis paradoxa*)	Endophyte/ Pathogen	Peries (1968), Harrison & Jones (2003), Vinod (2003), Thomas et al. (2010)
				Phialemonium sp.	Endophyte	Thomas et al. (2010), Venkatesagowda et al. (2012), Morales-Lizcano et al. (2017)
				Rhizoctonia solani (*Pellicularia filamentosa*)	Pathogen	Harrison & Jones (2003), Vinod (2003)
				Rhixoctonia spp.	Endophyte/ Soil	Peries (1968)
		Diaporthales	*Cytosporaceae*	*Cytospora palmarum*	Pathogen	Harrison & Jones (2003)
			Diaporthaceae	*Diaporthe* spp.	Endophyte	Oliveira et al. (2021)
				Epicoccum nigrum	Pathogen	Harrison & Jones (2003)
			Melanconidaceae	*Melanconium* sp.	Pathogen	Harrison & Jones (2003)
		Glomerellales	*Glomerellaceae*	*Colletotrichum gloeosporioides* (*Glomerella cingulate*)	Pathogen	Harrison & Jones (2003), Thomas et al. (2010)
			Graphiolaceae	*Graphiola phoenicis*	Pathogen	Harrison & Jones (2003)
			Plectosphaerellaceae	*Verticillium* sp.	Saprobe	Padmaja (2011)

Table 2 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
		Hypocreales	*Cordycipitaceae*	*Cordyceps* sp.	Endophyte	Morales-Lizcano et al. (2017)
			Hypocreaceae	*Trichoderma hamatum*	Endophyte	Karthikeyan et al. (2006)
				Trichoderma spp.	Endophyte/ Saprobe	Karthikeyan & Bhaskaran (1997), Ramos et al. (1998), Padmaja (2011), Rahman et al. (2013), Morales-Lizcano et al. (2017)
				Trichoderma viride	Endophyte/ Soil/ Pathogen	Peries 1968, Thomas et al. (2010)
			Nectriaceae	*Calonectria pteridis (Cylindrocladium pteridis)*	Pathogen	Harrison & Jones (2003)
				Cylindrocarpon spp.	Endophyte/ Soil	Peries (1968)
				Cylindrocladium spp.	Endophyte	Peries (1968)
				Fusarium clavus	Pathogen	Sunpapao et al. (2022)
				Fusarium fujikuroi (*Fusarium moniliforme*)	Pathogen	Srinivasan & Gunasekaran (1999)
				Fusarium solani	Pathogen	Srinivasan & Gunasekaran (1999)
				Fusarium spp.	Endophyte/ Soil/ Pathogen	Peries (1968), Harrison & Jones (2003), Oliveira et al. (2021)
				Fusarium proliferatum	Pathogen	Padhi et al. (2016)
				Fusarium tricinctum	Pathogen	Sunpapao et al. (2022)
				Nectria pseudotrichia	Endophyte	Oliveira et al. (2021)
			Ophiocordycipitaceae	*Hirsutella thompsonii*	unknown	Edgington et al. (2008)
				Purpureocillium lilacinum	Endophyte	Oliveira et al. (2021)
			Sarocladiaceae	*Sarocladium* sp.	Endophyte	Oliveira et al. (2021)
		Meliolales	*Meliolaceae*	*Asteridiella* sp.	Pathogen	Fröhlich et al. (1997)
		Microascales	*Microascaceae*	*Pseudallescheria* spp.	Endophyte	Fuego et al. (2021)
		Ophiostomatales	*Ophiostomataceae*	*Raffaelea* sp.	Endophyte	Fuego et al. (2021)
		Phyllachorales	*Phaeochoraceae*	*Phaeochoropsis mucosa* (*Catacauma mucosum*)	Pathogen	Harrison & Jones (2003)

Table 2 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Camarotella acrocomiae (*Sphaerodothis acrocomiae*)	Pathogen	Dollet et al. (2012), Silva et al. (2017)
				Camarotella costaricensis	Pathogen	Viana et al. (2005)
				Camarotella torrendiella (*Phyllachora torrendiella*)	Pathogen	Harrison & Jones (2003), Silva et al. (2017), Oliveira et al. (2021)
		Sordariales	*Chaetomiaceae*	*Chaetomium* spp.	Endophyte/ Saprobe	Padmaja (2011), Morales-Lizcano et al. (2017), Fuego et al. (2021), Oliveira et al. (2021)
			Sordariaceae	*Gelasinospora* sp.	Endophyte	Oliveira et al. (2021)
		Xylariales	*Xylariaceae*	*Ascotricha* sp.	Endophyte	Oliveira et al. (2021)
				Xylaria sp.	Endophyte	Oliveira et al. (2021)
		Amphisphaeriales	*Apiosporaceae*	*Nigrospora* sp.	Endophyte/ Soil	Peries (1968), Oliveira et al. (2021)
Basidiomycota	*Agaricomycetes*	*Agaricales*	*Agaricaceae*	*Agaricus* sp.	Saprobe	Padmaja (2011)
			Pleurotaceae	*Pleurotus* sp.	Endophyte	Padmaja (2011)
				Ganoderma applanatum	Pathogen	Vinod (2003)
				Ganoderma australe (*Ganoderma tornatum*)	Pathogen	Steyaert (1975), Pilotti (2005)
				Ganoderma boninense	Saprobe /Pathogen	Abdullah (2000), Pilotti et al. (2004) Pilotti (2005), Vinjusha & Arun Kumar (2021)
				Ganoderma keralense	Pathogen	Vinjusha & Arun Kumar (2021)
				Ganoderma lucidum	Saprobe/ Pathogen	Vinod (2003), Thomas et al. (2010), Thiribhuvanamala & Krishnamoorthy (2021)
				Ganoderma sp.	Endophyte	Zakaria et al. (2005), Purba et al. (2011), Rajendran et al. (2014)
				Ganoderma pseudoapplanatum	Pathogen	Vinjusha & Arun Kumar (2021)
				Ganoderma zonatum	Pathogen	Vinjusha & Arun Kumar (2021)
			Marasmiaceae	*Marasmius palmivorus*	Pathogen	Tey & Chan (1980)
				Helminthosporium sp.	Pathogen	Harrison & Jones (2003)
			Omphalotaceae	*Marasmiellus cocophilus*	Pathogen	Jackson & Firman (1979)

Table 2 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
		Corticiales	*Corticiaceae*	*Corticium penicillatum*	Pathogen	Harrison & Jones (2003)
				Corticium koleroga (*Pellicularia koleroga*)	Pathogen	Harrison & Jones (2003)
		Polyporales	*Polyporaceae*	*Trametes* sp.	Saprobe	Padmaja (2011)
	Cystobasidiomycetes	*Cystobasidiales*	*Cystobasidiaceae*	*Occultifur externus*	Endophyte	Oliveira et al. (2021)
		Incertae sedis	*Symmetrosporaceae*	*Symmetrospora marina*	Endophyte	Oliveira et al. (2021)
				Syncephalastrum racemosum	Endophyte	Oliveira et al. (2021)
				Syncephalastrum sp.	Saprobe	Padmaja (2011)
	Microbotryomycetes	*Sporidiobolales*	*Sporidiobolaceae*	*Rhodotorula glutinis*	Endophyte	Akhtyamova & Sattarova (2013)
	Ustilaginomycetes	*Ustilaginales*	*Ustilaginaceae*	*Pseudozyma hubeiensis*	Endophyte	Oliveira et al. (2021)
Mucoromycota	*Mucoromycetes*	*Mucorales*	*Mucoraceae*	*Mucor racemosus*	Endophyte	Venkatesagowda et al. (2012)
				Mucor spp.	Endophyte/ Soil	Peries (1968), Padmaja (2011)
			Rhizopodaceae	*Rhizopus* spp.	Endophyte/ Soil	Peries (1968), Padmaja (2011)
				Rhizopus stolonifer	Endophyte	Venkatesagowda et al. (2012)
Oomycota	*Peronosporomycetes*	*Peronosporales*	*Peronosporaceae*	*Phytophthora castaneae* (*Phytophthora katsurae*)	Pathogen	Dollet et al. (2012)
				Phytophthora cocois	Pathogen	Weir et al. (2015)
				Phytophthora nicotianae	Pathogen	Dollet et al. (2012), Panabieres et al. (2016)
				Phytophthora palmivora (*Phytophthora arecae*)	Pathogen	Blaha et al. (1994), Harrison & Jones (2003), Vinod (2003), Thomas et al. (2010), Dollet et al. (2012)
				Phytophthora spp.	Pathogen/ Soil	Peries (1968), Harrison & Jones (2003)
				Pythium palmivorum	Pathogen	Butler (1925)
				Pythium spp.	Pathogen	Harrison & Jones (2003)

Note: Most of the fungi reported as pathogens in previous studies were not confirmed by the pathogenicity test.

Community composition of fungi associated with pineapple

Earlier studies on fungi associated with pineapple were mostly focused on pathogens and endophytes (Table 3). Whereas, no studies reported saprobic fungi associated with pineapple. In this study, we collected pineapple litter samples from China and Thailand, and three new genera, 11 new species and 26 new records of fungi are introduced. Among them, about 29% are new species indicating the high diversity of fungi in pineapple and many new species on pineapple are yet to be discovered. *Dothideomycetes* was the dominant class with 21 taxa, while *Botryosphaeriaceae* was the dominant family.

In addition, a check list of fungi associated with pineapple is provided. A total of 71 taxa have been reported from pineapple. Fungi on pineapple were mainly distributed in Ascomycota (61 86%) and most of the species are pathogens (51, 72%) and endophytes (32, 45%) (Table 3, Fig. 149). *Nectriaceae* is the dominant family with 19 taxa (Fig. 149).

Studies suggested that endophytes may switch their life modes from endophytes to pathogens or saprobes when environmental and physiological conditions become suitable, for example, when the host becomes stressed (Bhunjun et al. 2023). We found that several species have been reported as both pathogens and endophytes in pineapple (e.g. *Aspergillus flavus*, *A. niger*, *Epicoccum sorghinum*, *Fusarium ananatum*, *F. chlamydosporum*, *F. equiseti*, *F. fujikuroi*, *F. incarnatum*, *F. napiforme*, *F. proliferatum*, *F. solani*, *Lasiodiplodia theobromae*, *Phialemoniopsis curvata*, *Talaromyces amestolkiae*, *T. funiculosus*, *T. purpureogenus*, *T. stollii*, and *Trichoderma paraviridescens*). In this study, *Lasiodiplodia mahajangana* was isolated as a saprobe on pineapple, while, a previous study reported it as an endophyte on pineapple (Vignassa et al. 2021). Bhunjun et al. (2023) argued that fungi may have ancestors with endophytic life mode and endophytes may switch their life modes to pathogens or saprobes. Our study reports the same phenomenon for fungi in pineapple.

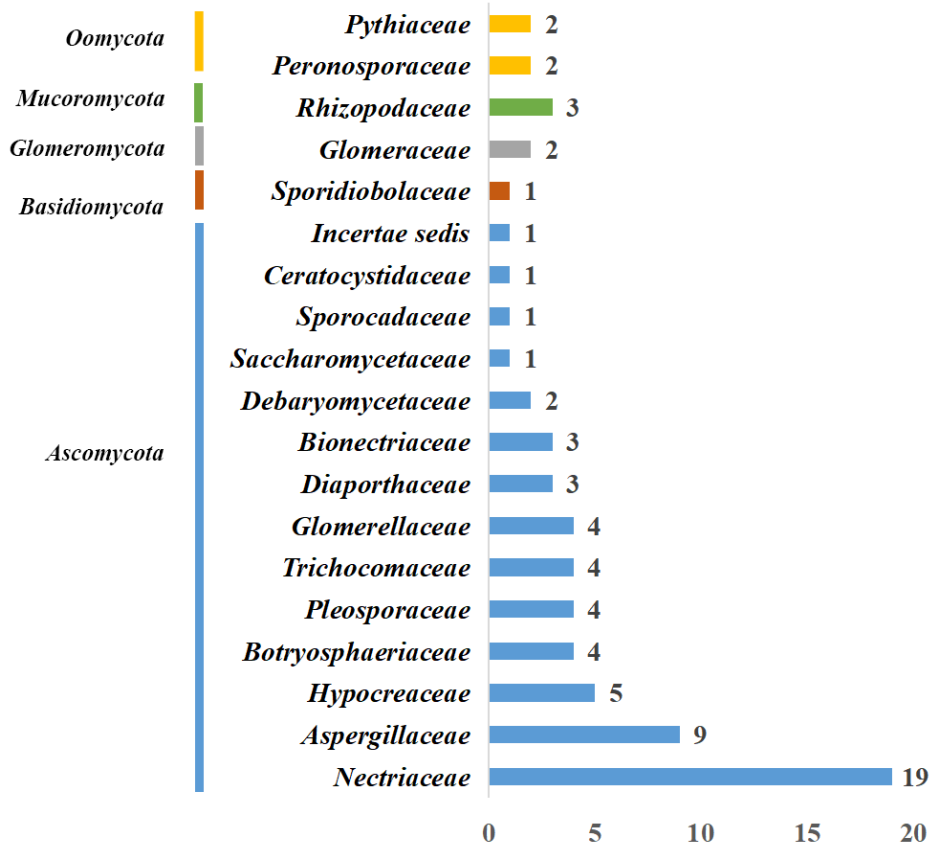

Figure 149 – Numbers of different fungal families reported on pineapple (Axis X is fungal numbers and axis Y is fungal families of each phylum).

Table 3 A check list of fungi associated with pineapple (based on the published literatures).

Phylum	Class	Order	Family	Species	Lifestyle	References
Ascomycota	*Dothideomycetes*	*Botryosphaeriales*	*Botryosphaeriaceae*	*Lasiodiplodia citricola*	Endophyte	Vignassa et al. (2021)
				Lasiodiplodia mahajangana	Endophyte	Vignassa et al. (2021)
				Lasiodiplodia theobromae	Endophyte/Pathogen	Vignassa et al. (2021)
				Neoscytalidium dimidiatum	Pathogeno	Zhong et al. (2016)
		Pleosporales	*Pleosporaceae*	*Curvularia clavata*	Unknown	Zhong et al. (2016)
				Curvularia eragrostidis	Pathogen	Ferreira et al. (2014)
				Curvularia lunata	Pathogen	Vignassa et al. (2021)
				Exserohilum rostratum	Pathogen	Luo et al. (2012)
	Eurotiomycetes	*Eurotiales*	*Aspergillaceae*	*Aspergillus awamori*	Endophyte	Vignassa et al. (2021)
				Aspergillus flavus	Endophyte/ Pathogen	Vignassa et al. (2021)
				Aspergillus fumigatus	Pathogen	Vignassa et al. (2021)
				Aspergillus niger	Endophyte/Pathogen	Mailafia et al. (2017), Vignassa et al. (2021)
				Aspergillus novoparasiticus	Pathogen	Vignassa et al. (2021)
				Aspergillus welwitschiae	Endophyte	Vignassa et al. (2021)
				Penicillium citrinum	Store	Leneveu-Jenvrin et al. (2020)
				Penicillium oxalicum	Pathogen	Wu et al. (2022)
				Talaromyces funiculosus (*Penicillium funiculosum*)	Pathogen	Rohrbach & Schmitt (2003), Petty et al. (2005)
			Trichocomaceae	*Talaromyces amestolkiae*	Endophyte/ Pathogen/ Store	Leneveu-Jenvrin et al. (2020), Vignassa et al. (2021)
				Talaromyces funiculosus	Endophyte/Pathogen	Barral et al. (2020), Vignassa et al. (2021)

Table 3 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Talaromyces stollii	Endophyte/Pathogen	Barral et al. 2(020), Vignassa et al. (2021)
				Talaromyces purpureogenus	Endophyte/Pathogen	Vignassa et al. (2021)
	Saccharomycetes	*Saccharomycetales*	*Debaryomycetaceae*	*Meyerozyma caribbica*	Store	Leneveu-Jenvrin et al. (2020)
				Meyerozyma guilliermondii (*Candida guilliermondii*)	Pathogen	Rohrbach & Schmitt (2003)
			Saccharomycetaceae	*Saccharomyces cerevisiae*	Store	Leneveu-Jenvrin et al. (2020)
	Sordariomycetes	*Amphisphaeriales*	*Sporocadaceae*	*Pestalotiopsis vismiae*	Pathogen	Vignassa et al. (2021)
		Diaporthales	*Diaporthaceae*	*Diaporthe kongii*	Pathogen	Vignassa et al. (2021)
				Diaporthe masirevicii	Pathogen	Vignassa et al. (2021)
				Epicoccum sorghinum	Pathogen/ Endophyte	Vignassa et al. (2021)
		Glomerellales	*Glomerellaceae*	*Colletotrichum ananas*	Pathogen	Armand et al. (2023)
				Colletotrichum gloeosporioides	Pathogen	Armand et al. (2023)
				Colletotrichum sp.	Endophyte	Zhong et al. （2016）
				Colletotrichum truncatum	Pathogen	Armand et al. (2023)
		Hypocreales	*Bionectriaceae*	*Bionectria ochroleuca*	Endophyte	Vignassa et al. (2021)
				Clonostachys rosea	Endophyte	Vignassa et al. (2021)
				Clonostachys wenpingii	Pathogen	Vignassa et al. (2021)
			Nectriaceae	*Cosmospora butyri*	Endophyte	Vignassa et al. (2021)
				Fusarium ananatum	Endophyte/Pathogen	Gu et al. (2015), Barral et al. (2019, 2020), Vignassa et al. (2021)
				Fusarium avenaceum	Unknown	Mailafia et al. (2017)

Table 3 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Fusarium chlamydosporum	Endophyte/Pathogen	Vignassa et al. (2021)
				Fusarium circinatum	Pathogen	Vignassa et al. (2021)
				Fusarium cortaderiae	Pathogen	Vignassa et al. (2021)
				Fusarium dlamini	Endophyte	Vignassa et al. (2021)
				Fusarium equiseti	Endophyte/ Pathogen	Vignassa et al. (2021)
				Fusarium falciforme	Endophyte	Vignassa et al. (2021)
				Fusarium ficicrescens	Endophyte	Vignassa et al. (2021)
				Fusarium fujikuroi (*Fusarium subglutinans, Fusarium verticillioides*)	Endophyte/Pathogen	Bartholomew & Malézieux (1994), Petty et al. (2005), Ibrahim et al. (2017, 2020), Vignassa et al. (2021)
				Fusarium graminearum	Pathogen	Vignassa et al. (2021)
				Fusarium guttiforme	Pathogen	Rohrbach & Schmitt (2003)
				Fusarium incarnatum	Endophyte/ Pathogen	Vignassa et al. (2021)
				Fusarium napiforme	Endophyte/ Pathogen	Vignassa et al. (2021)
				Fusarium oxysporum	Pathogen	Wang et al. (2015a), Vignassa et al. (2021)
				Fusarium proliferatum	Endophyte/Pathogen	Barral et al. (2020), Vignassa et al. (2021), López-García et al. (2012), Ibrahim et al. (2020)
				Fusarium sacchari	Pathogen	Ibrahim et al. (2017, 2020), Vignassa et al. (2021)
				Fusarium solani	Endophyte/Pathogen	Mailafia et al. (2017), Vignassa et al. (2021)
			Hypocreaceae	*Trichoderma asperellum*	Pathogen	Vignassa et al. (2021)

Table 3 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Trichoderma erinaceum	Pathogen	Vignassa et al. (2021)
				Trichoderma harzianum	Pathogen	Vignassa et al. (2021)
				Trichoderma paraviridescens	Endophyte/Pathogen	Vignassa et al. (2021)
				Trichoderma trixiae	Pathogen	Vignassa et al. (2021)
		Microascales	*Ceratocystidaceae*	*Ceratocystis paradoxa* (*Chalara paradoxa, Thielaviopsis paradoxa*)	Pathogen	Bartholomew & Malézieux (1994), Damayanti et al. (1996), Rohrbach & Schmitt (2003), Wijesinghe et al. (2011), Mailafia et al. (2017)
		Incertae sedis	*Incertae sedis*	*Phialemoniopsis curvata*	Endophyte/ Pathogen	Vignassa et al. (2021)
Basidiomycota	*Microbotryomycetes*	*Sporidiobolales*	*Sporidiobolaceae*	*Rhodotorula mucilaginosa*	Store	Leneveu-Jenvrin et al. (2020)
Glomeromycota	*Glomeromycetes*	*Glomerales*	*Glomeraceae*	*Glomus pellucidum*	Endophyte	Guillemin et al. (1992)
				Rhizophagus clarus (*Glomus clarum*)	Endophyte	Guillemin et al. (1992), Zain et al. (2021)
Mucoromycota	*Mucoromycetes*	*Mucorales*	*Rhizopodaceae*	*Rhizopus oryzae*	Pathogen	Zain et al. (2021)
				Rhizopus stolonifer	Pathogen	Vignassa et al. (2021), Zain et al. (2021)
				Rhizopus sp.	Endophyte	Zhong et al. (2016)
Oomycota	*Peronosporomycetes*	*Peronosporales*	*Peronosporaceae*	*Phytophthora cinnamomi*	Pathogen	Green & Nelson (2015, Lu et al. (2019)
				Phytophthora nicotianae (*Phytophthora parasitica*)	Pathogen	Oculi et al. (2020)
			Pythiaceae	*Pythium arrhenomanes*	Pathogen	Green & Nelson (2015)
				Pythium arrhenomanes (*Nematosporangium rhizophthoron*)	Pathogen	Ibrahim et al. (2020)

Note: Most of the fungi reported as pathogens in previous studies were not confirmed by the pathogenicity test.

Community composition of fungi associated with rice

Fungal diseases of rice have been studied for a long time and many studies reported fungal pathogens (Table 4). In this study, we investigated saprobic fungi on rice and 12 species are described and illustrated based on morphological characteristics and phylogenetic analyses. The 12 species consist of one new genus, three (25%) new species and six new records, which indicates the high undiscovered saprobic fungal diversity on rice. *Pleosporales* was the dominant order with 8 (66%) taxa.

A checklist of fungi associated with rice is also provided. Totally, 335 species associated with rice have been reported, however, most taxa were identified based on only morphology, thus the sequence data of those species are required to confirm their taxonomic placements. Fungi on rice were mainly distributed in *Ascomycota* (268, 80%) (Table 4). *Eurotiales* and *Hypocreales* are the dominant orders (Fig. 150), belonging to *Eurotiomycetes* and *Sordariomycetes*, respectively. *Aspergillaceae* was the dominant family with 78 taxa. The main rice pathogens are mostly from the families *Achlyaceae*, *Ceratobasidiaceae*, *Didymellaceae*, *Mycosphaerellaceae*, *Nectriaceae*, *Pleosporaceae* and *Pythiaceae*.

Figure 150 – Numbers of different fungal orders reported on rice in the literatures (Axis X is fungal numbers and axis Y is fungal orders of each phylum).

Table 4 A checklist of fungi associated with rice (based on the published literatures).

Phylum	Class	Order	Family	Species	Lifestyle	References
Ascomycota	*Dothideomycetes*	*Botryosphaeriales*	*Botryosphaeriaceae*	*Lasiodiplodia theobromae*	Pathogen	Notteghem et al. (1995)
		Cladosporiales	*Cladosporiaceae*	*Cladosporium herbarum*	Endophyte/Soil	Seephueak et al. (2019)
				Cladosporium oxysporum	Soil	Ou (2023)
				Cladosporium sp.	Endophyte	Ou (2023)
				Cladosporium tenuissimum	Endophyte/ Saprobe/Soil	Lapmak et al. (2009), Atugala & Deshappriya (2015), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
		Dothideales	*Saccotheciaceae*	*Aureobasidium pullulans*	Endophyte	Dutta & Ghosh (1965)
				Aureobasidium sp.	Endophyte	Dutta & Ghosh (1965)
		Mycosphaerellales	*Teratosphaeriaceae*	*Hortaea werneckii* (*Cladosporium werneckii*)	Saprobe	Dutta & Ghosh (1965)
			Mycosphaerellaceae	*Mycovellosiella oryzae*	Pathogen	Dutta & Ghosh (1965)
				Passalora janseana (*Cercospora janseana*)	Pathogen/Soil	Dutta & Ghosh (1965)
				Sphaerulina oryzina	Pathogen	Notteghem et al. (1995)
		Pleosporales	*Coniothyriaceae*	*Ochrocladosporium elatum* (*Cladosporium elatum*)	Soil	Taligoola et al. (2004)
			Corynesporascaceae	*Corynespora cassiicola*	Unknown	Ashfaq et al. (2015)
			Didymellaceae	*Ascochyta mycoparasitica*	Pathogen	Taligoola et al. (2004), Lapmak et al. (2009), Naik et al. (2009), Leewijit et al. (2016), Seephueak et al. (2019)
				Epicoccum nigrum (*Epicoccum purpurascens*)	Endophyte/ Pathogen	Taligoola et al. (2004)
				Epicoccum sorghinum (*Phoma sorghina*)	Endophyte/ Pathogen	Ou (2023)
				Phoma spp.	Endophyte	Sharma & Arora (2010), Ou (2023)
			Didymosphaeriaceae	*Pseudopithomyces sacchari*	Unknown	Manandhar (1999)
			Phaeosphaeriaceae	*Phaeosphaeria oryzae*	Pathogen	Dutta & Ghosh (1965)
				Phaeosphaeriopsis musae	Endophyte	Makun et al. (2007)
			Pleosporaceae	*Alternaria alternata*	Endophyte/ Pathogen	Bokhary (1991)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Alternaria chlamydospora	Unknown	Ashfaq et al. (2015)
				Alternaria infectoria (*Pleospora infectoria*)	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Alternaria juxtiseptata	Unknown	Bokhary (1991)
				Alternaria padwickii (*Trichoconiella padwickii*)	Pathogen	Zakaria et al. (2010), Wijesooriya & Deshappriya (2016)
				Alternaria tenuissima	Unknown	Atugala & Deshappriya (2015)
				Bipolaris gigantea (*Drechslera gigantea*)	Endophyte/ Pathogen	Dutta & Ghosh (1965), Sunariasih et al. (2014)
				Bipolaris oryzae (*Cochliobolus miyabeanus*, *Helminthosporium oryzae*)	Pathogen/Soil	Fisher & Petrini (1992), Leewijit et al. (2016)
				Curvularia affinis	Unknown	Ou (2023)
				Curvularia australiensis (*Drechslera australiensis*)	Unknown	Dutta & Ghosh (1965), Seephueak et al. (2019)
				Curvularia beasleyi	Unknown	Dutta & Ghosh (1965), Bokhary (1991), Makun et al. (2007), Kamaluddeen & Abhilasha (2013), Leewijit et al. (2016), Seephueak et al. (2019), Safari Motlagh et al. (2022)
				Curvularia clavata	Unknown	Ou (2023)
				Curvularia dactyloctenicola	Unknown	Dutta & Ghosh (1965)
				Curvularia fallax	Unknown	Ou (2023)
				Curvularia hawaiiensis	Pathogen	Ou (2023)
				Curvularia lunata (*Cochliobolus lunatus*)	Endophyte/ Pathogen/ Saprobe/Soil	Dutta & Ghosh (1965), Lapmak et al. (2009), Zakaria et al. (2010), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Curvularia muehlenbeckiae	Unknown	Ou (2023)
				Curvularia pallescens	Soil	Bokhary (1991), Ou (2023)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Curvularia plantarum	Unknown	Atugala & Deshappriya (2015)
				Curvularia pseudobrachyspora	Unknown	Seephueak et al. (2019)
				Curvularia spicifera (Curvularia tetramera)	Soil	Ou (2023)
				Curvularia spp.	Endophyte/Soil	Ou (2023)
				Curvularia tuberculata	Pathogen/ Saprobe	Ou (2023)
				Curvularia verruculosa	Pathogen	Ou (2023)
				Exserohilum rostratum (*Setosphaeria rostrata*)	Pathogen	Dutta & Ghosh (1965), Ou (2023)
				Pyrenophora biseptata (*Drechslera biseptata*)	Unknown	Fisher & Petrini (1992)
				Stemphylium botryosum	Endophyte	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Stemphylium lycopersici	Unknown	Taligoola et al. (2004)
				Stemphylium vesicarium (*Pleospora herbarum*)	Endophyte	Kumar et al. (2008)
			Pyrenochaetopsidaceae	*Pyrenochaetopsis indica*	Unknown	Dutta & Ghosh (1965)
			Torulaceae	*Dendryphion vinosum* (*Curvularia interseminata*)	Soil	Bokhary (1991), Seephueak et al. (2019)
				Hormiscium gelatinosum	Soil	Ou (2023)
			Trematosphaeriaceae	*Trematosphaeria clarkii*	Endophyte	Dutta & Ghosh (1965)
			Incertae sedis	*Pyrenochaeta oryzae*	Pathogen	Dutta & Ghosh (1965)
		Tubeufiales	*Wiesneriomycetaceae*	*Speiropsis pedatospora*	Endophyte	Ou (1985), Groth (1991), Elazegui & Islam (2003)
	Eremascaceae	*Chaetothyriales*	*Herpotrichiellaceae*	*Phialophora verrucosa*	Endophyte	Sunariasih et al. (2014)
		Eurotiales	*Aspergillaceae*	*Aspergillus amstelodami* (*Eurotium amstelodami)*	Endophyte	Dutta & Ghosh (1965)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Aspergillus awamori (*Aspergillus luchuensis*)	Endophyte/Soil	Dutta & Ghosh (1965)
				Aspergillus candidus	Endophyte/Soil	Dutta & Ghosh (1965), Bokhary (1991), Makun et al. (2007), Seephueak et al. (2019), Safari Motlagh et al. (2022)
				Aspergillus carneus	Soil	Makun et al. (2007)
				Aspergillus clavatus	Soil	Dutta & Ghosh (1965)
				Aspergillus ficuum	Unknown	Dutta & Ghosh (1965)
				Aspergillus flavipes	Soil	Dutta & Ghosh (1965)
				Aspergillus flavus	Pathogen/ Saprobe/Soil	Dutta & Ghosh (1965)
				Aspergillus foetidus	Soil	Dutta & Ghosh (1965)
				Aspergillus fumaricus	Soil	Mishra & Srivastava (1971), Kumar et al. (2008)
				Aspergillus fumigatus	Endophyte/Soil	Taligoola et al. (2004), Lapmak et al. (2009), Selvaraj & Annamalai (2011), Doni et al. (2013), Leewijit et al. (2016), Seephueak et al. (2019)
				Aspergillus glaucus	Saprobe	Dutta & Ghosh (1965)
				Aspergillus gracilis	Soil	Dutta & Ghosh (1965, Makun et al. (2007), Naik et al. (2009)
				Aspergillus humicola	Soil	Dutta & Ghosh (1965), Makun et al. (2007)
				Aspergillus japonicus	Soil	Taligoola et al. (2004)
				Aspergillus miyakoensis	Soil	Dutta & Ghosh (1965)
				Aspergillus neoniveus (Aspergillus niveus)	Soil	Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Aspergillus nidulans (Emericella nidulans)	Endophyte/Soil	Dutta & Ghosh (1965), Mishra & Srivastava (1971), Sunariasih et al. (2014) Ashfaq et al. (2015)
				Aspergillus niger	Endophyte/Soil	Dutta & Ghosh (1965)
				Aspergillus ochraceus	Endophyte/ Saprobe/Soil	Dutta & Ghosh (1965), Makun et al. (2007), Selvaraj & Annamalai (2011), Leewijit et al. (2016)
				Aspergillus parasiticus	Saprobe/Soil	Dutta & Ghosh (1965)
				Aspergillus penicillioides	Endophyte	Dutta & Ghosh (1965)
				Aspergillus repens (Eurotium repens, Eurotium rubrum)	Endophyte	Taligoola et al. (2004), Bertuzzi et al. (2019)
				Aspergillus sclerotiorum	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Aspergillus sp.	Endophyte/Soil	Fisher & Petrini (1992)
				Aspergillus spelunceus	Unknown	Atugala & Deshappriya (2015), Wijesooriya & Deshappriya (2016)
				Aspergillus sydowii	Endophyte/Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Aspergillus tamarii	Soil	Ou (1985)
				Aspergillus terreus	Saprobe/Soil	Ou (1985)
				Aspergillus unguis	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Aspergillus ustus	Endophyte/Soil	Ou (1985)
				Aspergillus versicolor	Saprobe/Soil	Dutta & Ghosh (1965)
				Aspergillus wentii	Endophyte	Sunariasih et al. (2014)
				Emericella sp.	Endophyte	Taligoola et al. (2004)
				Paecilomyces sp.	Endophyte	Atugala & Deshappriya (2015)
				Paecilomyces varioti	Endophyte	Naik et al. (2009)
				Penicillium adametzi	Soil	Lapmak et al. (2009)
				Penicillium albidum	Soil	Dutta & Ghosh (1965)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Penicillium aurantiogriseum (*Penicillium cyclopium, Penicillium viridicatum*)	Endophyte/ Saprobe	Dutta & Ghosh (1965)
				Penicillium brevicompactum	Soil	Dutta & Ghosh (1965)
				Penicillium camemberti	Soil	Naik et al. (2009)
				Penicillium canescens (*Penicillium kapuscinskii*)	Soil	Dutta & Ghosh (1965), Taligoola et al. (2004), Makun et al. (2007)
				Penicillium capsulatum	Soil	Selvaraj & Annamalai (2011)
				Penicillium chermesinum	Soil	Dutta & Ghosh (1965)
				Penicillium chrysogenum	Endophyte	Dutta & Ghosh (1965)
				Penicillium citrinum (*Penicillium steckii*)	Endophyte/ Saprobe/Soil	Dutta & Ghosh (1965), Makun et al. (2007)
				Penicillium commune	Soil	Dutta & Ghosh (1965), Naik et al. (2009)
				Penicillium corylophilum	Soil	Bokhary (1991)
				Penicillium daleae	Soil	Dutta & Ghosh (1965)
				Penicillium decumbens	Endophyte/Soil	Dutta & Ghosh (1965)
				Penicillium dierckxii (*Penicillium charlesii, Penicillium fellutanum*)	Soil	Dutta & Ghosh (1965), Lapmak et al. (2009)
				Penicillium digitatum	Unknown	Dutta & Ghosh (1965), Selvaraj & Annamalai (2011)
				Penicillium glabrum (*Penicillium terlikowskii, Penicillium frequentans*)	Soil	Dutta & Ghosh (1965)
				Penicillium humicola	Unknown	Dutta & Ghosh (1965)
				Penicillium janczewskii (*Penicillium nigricans*)	Soil	Dutta & Ghosh (1965)
				Penicillium melinii	Soil	Ou (2023)
				Penicillium oxalicum	Saprobe	Dutta & Ghosh (1965)
				Penicillium phoeniceum	Soil	Sunariasih et al. (2014)
				Penicillium purpurogenum	Soil	Dutta & Ghosh (1965)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Penicillium raistrickii	Soil	Dutta & Ghosh (1965)
				Penicillium restrictum	Soil	Dutta & Ghosh (1965)
				Penicillium rolfsii	Soil	Dutta & Ghosh (1965)
				Penicillium roseopurpureum	Soil	Dutta & Ghosh (1965)
				Penicillium simplicissimum (*Penicillium janthinellum*)	Endophyte/Soil	Dutta & Ghosh (1965), Potshangbam et al. (2017)
				Penicillium spp.	Endophyte/Soil	Zakaria et al. (2010), Atugala & Deshappriya (2015), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Penicillium thomii	Soil	Dutta & Ghosh (1965)
				Penicillium turbatum	Soil	Dutta & Ghosh (1965)
				Penicillium variabile	Soil	Dutta & Ghosh (1965)
				Penicillium velutinum	Soil	Dutta & Ghosh (1965)
				Penicillium vinaceum	Soil	Dutta & Ghosh (1965)
				Penicillium vulpinum (*Penicillium claviforme*)	Soil	Dutta & Ghosh (1965)
				Penicillium waksmani	Soil	Dutta & Ghosh (1965)
				Talaromyces funiculosus (*Penicillium funiculosum*)	Soil	Bokhary (1991)
				Talaromyces islandicus (*Penicillium islandicum*)	Endophyte/Soil	Fisher & Petrini (1992)
				Talaromyces pinophilus (*Penicillium pinophilum*)	Endophyte	Naik et al. (2009)
				Talaromyces rugulosus (*Penicillium tardum*, *Penicillium rugulosum*)	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Talaromyces stipitatus	Soil	Naik et al. (2009)
	Eurotiomycetes	*Eurotiales*	*Trichocomaceae*	*Ascospirella lutea* (*Talaromyces luteus*)	Soil	Ashfaq et al. (2015)
				Talaromyces varians (*Penicillium varians*)	Soil	Ou (2023)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
	Eurotiomycetes	*Onygenales*	*Gymnoascaceae*	*Arachniotus punctatus* (*Pseudoarachniotus punctatus*)	Soil	Cartwright et al. (1997)
				Mallochia echinulata (*Pseudoarachniotus echinulatus*)	Soil	Ou (2023)
	Leotiomycetes	*Helotiales*	*Discinellaceae*	*Varicosporium* sp.	Endophyte	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Incertae sedis	*Dactylaria* sp.	Unknown	Dutta & Ghosh (1965)
			Incertae sedis	*Scytalidium flavobrunneum* (*Geotrichum flavobrunneum*)	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Incertae sedis	*Scytalidium lignicola*	Endophyte	Ou (2023)
	Leotiomycetes	*Thelebolales*	*Pseudeurotiaceae*	*Pseudeurotium hygrophilum* (*Pseudeurotium zonatum*)	Endophyte	Notteghem et al. (1995)
	Orbiliomycetes	*Orbiliales*	*Orbiliaceae*	*Arthrobotrys foliicola*	Endophyte	Dutta & Ghosh (1965), Taligoola et al. (2004)
				Arthrobotrys sp.	Endophyte	Dutta & Ghosh (1965)
	Saccharomycetes	*Saccharomycetales*	*Dipodascaceae*	*Galactomyces geotrichum*	Endophyte	Fisher & Petrini (1992)
				Geotrichum candidum	Soil/Saprobe	Zakaria et al. (2010)
		Amphisphaeriales	*Apiosporaceae*	*Nigrospora oryzae*	Endophyte/ Pathogen/ Saprobe	Mishra & Srivastava (1971)
			Sporocadaceae	*Pestalotiopsis oryzae*	Unknown	Dutta & Ghosh (1965)
				Pseudopestalotiopsis myanmarina	Unknown	Leewijit et al. (2016)
		Cephalothecales	*Cephalothecaceae*	*Phialemonium* sp.	Endophyte	Ou (2023)
		Chaetosphaeriaceae	*Chaetosphaeriaceae*	*Gonytrichum macrocladum*	Soil	Dutta & Ghosh (1965)
		Cladosporiales	*Cladosporiaceae*	*Cladosporium cladosporioides*	Endophyte/Soil	Ou (2023)
		Coniochaetales	*Coniochaetaceae*	*Coniochaeta velutina*	Unknown	Dutta & Ghosh (1965)
			Ceratostomataceae	*Harzia palmara* (*Chlamydomyces palmarum*)	Unknown	Dutta & Ghosh (1965)
		Diaporthales	*Diaporthaceae*	*Diaporthe arecae*	Unknown	Ashfaq et al. (2015)
				Diaporthe arengae	Unknown	Kardin et al. (1982)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Diaporthe liquidambaris (*Phomopsis liquidambaris*)	Endophyte/Soil	Dutta & Ghosh (1965)
				Diaporthe millettia	Unknown	Atugala & Deshappriya (2015)
				Diaporthe tectonendophytica	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Phomopsis oryzae	Pathogen	Kandar et al. (2018)
				Phomopsis oryzae-saticae	Pathogen	Naik et al. (2009)
		Glomerellales	*Glomerellaceae*	*Colletotrichum fructicola*	Endophyte	Ou (2023)
				Colletotrichum graminicola	Soil	Naik et al. (2009)
				Colletotrichum karstii	Unknown	Phutela et al. (2011)
				Colletotrichum plurivorum	Unknown	Ou (2023)
				Colletotrichum spp.	Endophyte	Ou (2023)
				Colletotrichum truncatum	Unknown	Makun et al. (2007)
			Plectosphaerellaceae	*Verticillium cellulosae*	Soil	Atugala & Deshappriya (2015)
		Hypocreales	*Bionectriaceae*	*Acremonium hansfordii*	Unknown	Lombard et al. (2016)
				Acremonium luzulae	Unknown	Seephueak et al. (2019)
				Acremonium sp.	Endophyte	Seephueak et al. (2019)
				Acremonium strictum	Endophyte	Naik et al. (2009), Atugala & Deshappriya (2015), Wijesooriya & Deshappriya (2016)
				Bionectria pseudostriata	Unknown	Seephueak et al. (2019)
			Clavicipitaceae	*Balansia oryzae-sativae*	Pathogen	Gunnell & Webster (1987)
				Ustilaginoidea virens	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Cordycipitaceae	*Beauveria bassiana* (*Botrytis bassiana*)	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Hypocreaceae	*Gliocladium atrum*	Soil	Dutta & Ghosh (1965)
				Gliocladium penicillioides	Soil	Dutta & Ghosh (1965), Atugala & Deshappriya (2015), Leewijit et al. (2016)
				Gliocladium sp.	Endophyte/Soil	Doni et al. (2013)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Hypomyces chrysospermus (*Sepedonium chrysospermum*)	Soil	Ou (2023)
				Mycogone nigra	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Sepedonium flavidum	Soil	Ou (2023)
				Trichoderma asperelloides	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Trichoderma deliquescens (*Gliocladium deliquescens*)	Soil	Fisher & Petrini (1992)
				Trichoderma glaucum	Soil	Ou (2023)
				Trichoderma harzianum	Endophyte/Soil	Ou (2023)
				Trichoderma koningii	Soil	Dutta & Ghosh (1965)
				Trichoderma reesei	Saprobe	Fisher & Petrini (1992), Taligoola et al. (2004), Leewijit et al. (2016), Safari Motlagh et al. (2022)
				Trichoderma spp.	Endophyte/Soil	Selvaraj & Annamalai (2011)
				Trichoderma virens (*Gliocladium virens*)	Endophyte	Phutela et al. (2011), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Trichoderma viride	Endophyte/Soil	Doni et al. (2013), Safari Motlagh et al. (2022)
			Nectriaceae	*Calonectria morganii*	Pathogen	Dutta & Ghosh (1965)
				Cylindrocladium sp.	Endophyte	Ou (2023)
				Fusarium andiyazi	Unknown	Dutta & Ghosh (1965)
				Fusarium asiaticum	Pathogen	Fisher & Petrini (1992)
				Fusarium chlamydosporum	Soil	Ou (1985, 2023)
				Fusarium coeruleum	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Fusarium equiseti	Endophyte	Ashfaq et al. (2015)
				Fusarium falciforme	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Fusarium fujikuroi (*Fusarium verticillioides*)	Endophyte/ Pathogen	Dutta & Ghosh (1965), Taligoola et al. (2004), Ou (2023)
				Fusarium globosum	Unknown	Fisher & Petrini (1992), Lapmak et al. (2009), Naik et al. (2009), Leewijit et al. (2016), Seephueak et al. (2019)
				Fusarium graminearum	Pathogen	Fisher & Petrini (1992), Makun et al. (2007), Lapmak et al. (2009)
				Fusarium incarnatum (*Fusarium semitectum*)	Endophyte/Soil	Taligoola et al. (2004), Leewijit et al. (2016), Seephueak et al. (2019)
				Fusarium longipes	Unknown	Ou (2023)
				Fusarium moniliforme	Endophyte	Zakaria et al. (2010), Atugala & Deshappriya (2015), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Fusarium oxysporum	Endophyte/Soil	Ou (2023)
				Fusarium solani	Endophyte/Soil	Makun et al. (2007), Lapmak et al. (2009)
				Fusarium spinosum	Unknown	Al-Hatmi et al. (2019)
				Fusarium spp.	Endophyte/Soil	Dutta & Ghosh (1965)
				Fusarium tanahbumbuense	Unknown	Kandar et al. (2018)
				Fusidium viride	Soil	Potshangbam et al. (2017)
				Fusarium volatile	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Ophiocordycipitaceae	*Purpureocillium lilacinum (Penicillium lilacinum, Paecilomyces lilacinus)*	Endophyte/Soil	Bokhary 1991, Fisher & Petrini 1992)
			Sarocladiaceae	*Sarocladium oryzae*	Endophyte/ Pathogen	Mishra & Srivastava (1971), Bokhary (1991)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Sarocladium sparsum	Pathogen	Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Sarocladium spirale	Unknown	Mishra & Srivastava (1971)
				Sarocladium terricola	Unknown	Dutta & Ghosh (1965)
			Stachybotryaceae	*Achroiostachys aurantispora*	Unknown	Dogma Jr & Santos (1980)
				Albifimbria verrucaria (*Myrothecium verrucaria*)	Endophyte/ Pathogen	Dutta & Ghosh (1965), Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Paramyrothecium roridum (Myrothecium roridum)	Soil	Addison et al. (2021)
				Striaticonidium cinctum (Myrothecium striatisporum)	Soil	Dutta & Ghosh (1965)
		Magnaporthales	*Magnaporthaceae*	*Gaeumannomyces amomi*	Endophyte	Dutta & Ghosh (1965), Makun et al. (2007)
				Gaeumannomyces graminis	Endophyte/ Pathogen	Dutta & Ghosh (1965)
				Nakataea oryzae (*Magnaporthe salvinii*)	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Pyriculariaceae	*Pyricularia grisea* (*Magnaporthe grisea*)	Pathogen	Dutta & Ghosh (1965)
				Pyricularia oryzae (*Magnaporthe oryzae*)	Pathogen	Ou (2023)
		Microascales	*Graphiaceae*	*Graphium comatrichoides*	Soil	Limtong et al. (2020)
			Microascaceae	*Microascus gracilis*	Unknown	Ou (1985), Groth (1991), Manandhar (1999), Elazegui & Islam (2003)
		Myrmecridiales	*Myrmecridiaceae*	*Myrmecridium schulzeri*	Unknown	Dutta & Ghosh (1965)
		Pleosporales	*Coniothyriaceae*	*Coniothyrium fuckelii*	Endophyte	Bokhary (1991)
		Sordariales	*Chaetomiaceae*	*Acrophialophora fusispora* (*Acrophialophora nainiana*)	Soil	Taligoola et al. (2004)
				Arcopilus cupreus (*Chaetomium cupreum*)	Endophyte/Soil	Dutta & Ghosh (1965), Safari Motlagh et al. (2022)
				Chaetomium bostrychodes	Soil	Dutta & Ghosh (1965)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Chaetomium brasiliense	Endophyte	Ou (2023)
				Chaetomium elatum	Endophyte	Dutta & Ghosh (1965)
				Chaetomium fimeti	Soil	Naik et al. (2009)
				Chaetomium funicola	Soil	Dutta & Ghosh (1965), Mishra & Srivastava (1971)
				Chaetomium globosum (*Chaetomium olivaceum*)	Endophyte/Soil	Fisher & Petrini (1992), Naik et al. (2009), Seephueak et al. (2019)
				Chaetomium spirale	Soil	Fisher & Petrini (1992)
				Chaetomium spirochaete	Endophyte	Seephueak et al. (2019)
				Chaetomium spp.	Endophyte/Soil	Atugala & Deshappriya (2015)
				Chaetomium trigonosporum	Soil	Seephueak et al. (2019, Ou (2023)
				Chaetomium undulatulum	Soil	Makun et al. (2007)
				Corynascus sepedonium	Unknown	Ou (2023)
				Humicola fuscoatra	Endophyte	Kumar et al. (2008), Wijesooriya & Deshappriya (2016)
				Humicola homopilata (*Chaetomium homopilatum*)	Soil	Ou (2023)
				Humicola spp.	Endophyte/Soil	Ou 2023)
				Pseudothielavia terricola (Thielavia terricola)	Soil	Mohd et al. (2017)
				Trichocladium griseum (*Humicola grisea*)	Soil	Dutta & Ghosh (1965)
			Sordariaceae	*Sordaria macrospora*	Endophyte	Sunariasih et al. (2014)
		Xylariales	*Lopadostomataceae*	*Creosphaeria sassafras*	Endophyte	Ou (2023)
			Hypoxylaceae	*Daldinia eschscholtzii*	Endophyte	Ito & Nagai (1931)
				Hypoxylon pulicicidum	Unknown	Ahn et al. (2005)
				Hypoxylon sublenormandii	Unknown	Jeon et al. (2020)
			Microdochiaceae	*Microdochium albescens*	Pathogen/Soil	Ou 2023)
				Microdochium poae	Unknown	Atugala & Deshappriya (2015)
			Xylariaceae	*Xylaria arbuscula*	Unknown	Ou (2023)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Xylaria badia	Unknown	Ou (2023)
				Xylaria curta	Unknown	Ou (2023)
				Xylaria papulis	Unknown	Ou (2023)
				Xylaria sp.	Soil	Leewijit et al. (2016)
		Incertae sedis	*Incertae sedis*	*Mycothermus thermophilus* (*Scytalidium thermophilum*)	Endophyte	Ou (2023)
Basidiomycota	*Agaricomycetes*	*Agaricales*	*Lyophyllaceae*	*Calocybe indica*	Endophyte	Dutta & Ghosh (1965)
			Psathyrellaceae	*Hormographiella aspergillata*	Unknown	Ou (2023)
				Hormographiella verticillata	Unknown	Naik et al. (2009)
			Schizophyllaceae	*Schizophyllum commune*	Endophyte	Makun et al. (2007)
			Atheliaceae	*Athelia rolfsii*	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
		Cantharellales	*Ceratobasidiaceae*	*Ceratobasidium setariae* (*Ceratobasidium oryzae-sativae*)	Pathogen	Dutta & Ghosh (1965), Fisher & Petrini (1992)
				Ceratorhiza hydrophila (*Sclerotium hydrophilum*)	Pathogen	Dutta & Ghosh (1965), Fisher & Petrini (1992)
				Rhizoctonia fumigata	Pathogen/Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Rhizoctonia oryzae-sativae	Pathogen/Soil	Tzean et al. (2019)
				Rhizoctonia solani	Pathogen/Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003), Naik et al. (2009), Seephueak et al. (2019)
				Rhizoctonia spp.	Endophyte/Soil	Atugala & Deshappriya (2015), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
		Corticiales	*Corticiaceae*	*Waitea circinata* (*Rhizoctonia oryzae*)	Pathogen/Soil	Dutta & Ghosh (1965), Ou (1985), Groth (1991), Elazegui & Islam (2003)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
		Polyporales	*Irpicaceae*	*Ceriporia lacerata*	Endophyte	Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
			Meruliaceae	*Phlebia brevispora*	Endophyte	Ou (2023)
			Polyporaceae	*Trametes versicolor* (*Coriolus versicolor*)	Saprobe	Dutta & Ghosh (1965)
			Incertae sedis	*Phanerodontia chrysosporium (Sporotrichum pruinosum, Phanerochaete chrysosporium)*	Endophyte/Soil	Mishra & Srivastava (1971), Ou (2023)
		Sebacinales	*Serendipitaceae*	*Serendipita indica* (*Piriformospora indica*)	Endophyte	Ou (2023)
	Exobasidiomycetes	*Entylomatales*	*Eballistraceae*	*Entyloma oryzae*	Pathogen	Taligoola et al. (2004)
		Tilletiales	*Tilletiaceae*	*Tilletia barclayana*	Pathogen	Dutta & Ghosh (1965)
	Leotiomycetes	*Helotiales*	*Sclerotiniaceae*	*Sclerotium oryzicola*	Pathogen	Ito & Nagai (1931)
		Sporidiobolales	*Sporidiobolaceae*	*Rhodotorula mucilaginosa* (*Rhodotorula rubra*)	Saprobe	Atugala & Deshappriya (2015), Leewijit et al. (2016), Wijesooriya & Deshappriya (2016)
				Saprolegnia anisospora	Saprobe	Ashfaq et al. (2015)
				Saprolegnia diclina	Saprobe	Ou (2023)
	Pucciniomycetes	*Pucciniales*	*Pucciniaceae*	*Uromyces coronatus*	Pathogen	Dutta & Ghosh (1965), Nzojiyobiri et al. (2003), Selvaraj & Annamalai (2011), Doni et al. (2013)
	Tremellomycetes	*Tremellales*	*Cryptococcaceae*	*Cryptococcus neoformans*	Saprobe	Bokhary (1991)
Blastocladiomycota	*Blastocladiomycetes*	*Blastocladiales*	*Blastocladiaceae*	*Allomyces arbusculus*	Soil	Dutta & Ghosh (1965)
				Allomyces cystogenus	Soil	Fisher & Petrini (1992), Makun et al. (2007), Seephueak et al. (2019), Ou (2023)
Chytridiomycota	*Chytridiomycetes*	*Chytridiales*	*Chytriomycetaceae*	*Podochytrium clavatum*	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Podochytrium lanceolatum	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
Mucoromycota	*Mucoromycetes*	*Mortierellales*	*Mortierellaceae*	*Mortierella* sp.	Endophyte	Bokhary (1991)
		Mucorales	*Choanephoraceae*	*Choanephora cucurbitarum*	Soil	Ou (2023)
				Cunninghamella elegans (*Cunninghamella bertholletiae*)	Soil	Ou (2023)
				Gongronella butleri	Soil	Dutta & Ghosh (1965)
			Mucoraceae	*Mucor circinelloides*	Unknown	Dutta & Ghosh (1965)
				Mucor fragilis	Soil	Dutta & Ghosh (1965)
			Rhizopodaceae	*Rhizopus arrhizus* (*Rhizopus oryzae*)	Soil	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Rhizopus microsporus	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Rhizopus sp.	Endophyte/Soil	Kimiharu (2004)
				Rhizopus stolonifer	Unknown	Ou (1985), Groth (1991), Elazegui & Islam (2003)
			Syncephalastraceae	*Syncephalastrum racemosum*	Soil	Dutta & Ghosh (1965)
Oomycota	*Peronosporomycetes*	*Peronosporales*	*Peronosporaceae*	*Phytophthora drechsleri*	Pathogen	Sharma & Arora (2010)
				Phytophthora japonica (*Pythiomorpha oryzae*)	Saprobe	Fisher & Petrini (1992)
				Phytophthora sp.	Endophyte/Soil	Atugala & Deshappriya (2015), Wijesooriya & Deshappriya (2016)
				Phytophthora megasperma (*Pythiomorpha miyabeana*)	Saprobe	Ou (2023)
				Sclerophthora macrospora	Pathogen	Ito & Nagai (1931)
				Globisporangium spinosum (*Pythium spinosum*)	Pathogen	Dutta & Ghosh (1965), Ou (1985), Groth (1991), Elazegui & Islam (2003), Seephueak et al. (2019)

Table 4 Continued.

Phylum	Class	Order	Family	Species	Lifestyle	References
				Pythiogeton ramosum	Saprobe	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Pythium afertile	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Pythium aristosporum	Pathogen	Ito & Nagai (1931)
				Pythium arrhenomanes	Pathogen	Ito & Nagai (1931)
				Pythium dissotocum	Pathogen	Ito & Nagai 1931)
				Pythium elongatum	Pathogen	Dutta & Ghosh (1965)
				Pythium heteroogonium	Endophyte	Tzean et al. (2019)
				Pythium longipapillum	Endophyte	Tzean et al. (2019)
				Pythium spp.	Endophyte	Tzean et al. (2019)
	Saprolegniomycetes	*Saprolegniales*	*Achlyaceae*	*Absidia* sp.	Endophyte	Atugala & Deshappriya (2015)
				Achlya americana	Unknown	Ito & Nagai (1931)
				Achlya conspicua	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Achlya debaryana	Soil	Dutta & Ghosh 1965)
				Achlya diffusa	Pathogen	Dogma Jr & Santos (1980)
				Achlya flagellata	Saprobe/Soil/Pathogen	Ito & Nagai (1931), Dutta & Ghosh (1965), Dogma Jr & Santos (1980)
				Achlya klebsiana	Pathogen	Ou (1985), Groth (1991), Elazegui & Islam (2003)
				Achlya oryzae	Unknown	Ito & Nagai (1931)
				Achlya proliferoides	Pathogen	Ito & Nagai (1931)
				Dictyuchus sterile	Saprobe	Ou (1985), Groth (1991), Fisher & Petrini (1992), Elazegui & Islam (2003)
				Newbya megasperma (*Achlya megasperma*)	Saprobe	Mishra & Srivastava (1971), Naik et al. (2009), Ou (2023)
		Saprolegniales	*Saprolegniaceae*	*Pythiopsis cymosa*	Soil	Rossman et al. (1990), Chen et al. (2001)

Note: Most of the fungi reported as pathogens in previous studies were not confirmed by the pathogenicity test.

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