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# AJOM new records and collections of fungi: 151-200

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**Abstract**

This article is the third in the Asian Journal of Mycology Notes series, wherein we report 50 new fungal collections distributed in two phyla, five classes, 16 orders and 35 families. The present study provides descriptions and illustrations for five new species (*Acrocalymma hyaline*, *Allocryptovalsa aquilariae*, *Alternaria arida*, *Apoharknessia thailandica* and *Tatraea aseptata*) and 21 new host and 23 new geographical records. All these introductions are supported by morphological data and multi-gene phylogenetic analyses. This article provides the platform to disseminate the data on fungal collections with new sequence data, which is vital for future studies. An accurate and timely report of new fungus-host or fungus-country records is necessary for the diagnostics, identification, and management of economically significant fungal groups, especially the phytopathogens.

**Keywords** – 5 new taxa – 44 new records – *Anthracothecium* – *Asterophora* – *Botryosphaeria* – *Camarosporidiella* – *Chlorencoelia* – *Cladosporium* – *Clonostachys* – *Colletotrichum* – *Coniochaeta* – *Cordana* – *Corynespora* – *Diaporthe* – *Discosia* – *Gymnopilus* – *Hymenotorrendiella* – *Lasiodiplodia* – *Lepiota* – *Magnibotryascoma* – *Melanconis* – Molecular phylogeny – *Nigrospora* – *Neoleptosporella* – *Nigrograna* – *Phaeobotryon* – *Phaeoseptum* – *Pleurotus* – *Pochonia* – *Pseudofusicoccum* – *Pseudopithomyces* – *Pulveroboletus* – *Pyrenula* – *Salsuginea* – *Spegazzinia* –Taxonomy – *Translucidithyrium* – *Vaginatispora* – *Vamsapriya* – *Volutella*

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The organization of the taxa in this study is in accordance with the Outline of fungi and fungus-like taxa (Wijayawardene et al. 2022), Refined families of Sordariomycetes (Hyde et al. 2020a), Refined families of Dothideomycetes (Hongsanan et al. 2020a, b) and Notes, outline and divergence times of Basidiomycota (He et al. 2019a).

**Phylum** ***Ascomycota***
**Class** ***Dothideomycetes*** O.E. Erikss. & Winka
**Subclass** ***Dothideomycetidae*** P.M. Kirk et al.
***Cladosporiales*** Abdollahz. & Crous
***Cladosporiaceae*** Chalm. & R.G. Archibald

**01.** ***Cladosporium tenuissimum*** Cooke, Grevillea 6(no. 40), 140 (1878) (Contributed by C Prematunga)

***Mycosphaerellales*** P.F. Cannon
***Phaeothecoidiellaceae*** K.D. Hyde & Hongsanan

**02.** ***Translucidithyrium chinense*** H.X. Wu & X.H. Li, in Li et al., MycoKeys 76, 7 (2020) (Contributed by MWD Sandamali)

**Subclass** ***Pleosporomycetidae*** C.L. Schoch et al.
***Pleosporales*** Luttrell ex M.E. Barr
***Acrocalymmaceae*** Crous & Trakun.

**03**. ***Acrocalymma hyalina*** N. Wu, Jian K. Liu & K.D. Hyde **sp. nov.** (Contributed by N Wu)

**04.** ***Acrocalymma pterocarpi*** Jayasiri, E.B.G. Jones & K.D. Hyde, in Jayasiri et al., Mycosphere 10(1), 20 (2019) (Contributed by AR Rathnayaka)

**05.** ***Acrocalymma walkeri*** (Shoemaker, C.E. Babc. & J.A.G. Irwin) Crous & Trakun., in Trakunyingcharoen et al., IMA Fungus 5(2), 407 (2014) (Contributed by SN Wijesinghe)

***Camarosporidiellaceae*** Wanas., Wijayaw., Crous & K.D. Hyde

**06.** ***Camarosporidiella laburnicola*** (R.H. Perera, Bulgakov & K.D. Hyde) Wanas. & K.D. Hyde, in Wanasinghe et al., Studies in Mycology 87, 234 (2017) (Contributed by D Pem)

***Corynesporascaceae*** Sivan.

**07.** ***Corynespora torulosa*** (Syd. & P. Syd.) Crous, Persoonia 31, 211 (2013) (Contributed by BC Samarakoon)

***Didymosphaeriaceae*** Munk

**08.** ***Pseudopithomyces chartarum*** (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Diversity 75, 27–274 (2015) (Contributed by BC Samarakoon and KWT Chethana)

**09.** ***Spegazzinia radermacherae*** Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10, 73 (2019) (Contributed by G-C Ren)

***Lophiostomataceae*** Sacc.

**10.** ***Vaginatispora palmae*** S.N. Zhang, J.K. Liu & K.D. Hyde, Fungal Diversity 96, 242 (2019) (Contributed by YH Yang)

***Nigrogranaceae*** Jaklitsch & Voglmayr

**11.** ***Nigrograna magnoliae*** Wanas., in Wanasinghe, Wijayawardene, Xu, Cheewangkoon & Mortimer, PLoS One 15(7, e0235855), 10 (2020) (Contributed by MC Samarakoon)

***Phaeoseptaceae*** S. Boonmee, Thambugala & K.D. Hyde

**12.** ***Phaeoseptum thailandicum*** Samarak. & K.D. Hyde in Jayawardena et al., Fungal Diversity 117: 45 (2023) (Contributed by Z Lin Tun and CS Bhunjun)

***Pleosporaceae*** Nitschke

**13.** ***Alternaria arida*** Chaiwan, Jayawardena, Bulgakov & K.D. Hyde, **sp. nov.** (Contributed by N Chaiwan)

***Salsugineaceae*** K.D. Hyde & Tibpromma

**14.** ***Salsuginea phoenicis*** S.N. Zhang, E.B.G. Jones, K.D. Hyde & J.K. Liu, in Jones et al., Botanica Marina 63(2), 158 (2019) (Contributed by ND Kularathnage)

***Teichosporaceae*** M.E. Barr

**15.** ***Magnibotryascoma mali*** Phukhams., Wanas. & K.D. Hyde, Fungal Diversity 87, 105 (2017) (Contributed by N Wu)

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

**16.** ***Botryosphaeria dothidea*** (Moug.) Ces. & De Not., Commentario della Società Crittogamologica Italiana 1(fasc. 4), 212 (1863) (Contributed by AR Rathnayaka)

**17.** ***Lasiodiplodia theobromae*** (Pat.) Griffon & Maubl., Bulletin de la Société mycologique de France 25, 57 (1909) (Contributed by N Huanraluek)

**18.** ***Phaeobotryon negundinis*** Daranagama, Bulgakov, K.D. Hyde, Mycosphere 7, 936 (2016) (Contributed by KWT Chethana)

***Phyllostictaceae*** Fr.

**19.** ***Pseudofusicoccum adansoniae*** Pavlic, T.I. Burgess & M.J. Wingf., Mycologia 100(6), 855 (2008) (Contributed by AR Rathnayaka and AD Madagammana)

**Class** ***Eurotiomycetes*** Tehler ex O.E. Eriksson & K. Winka
**Subclass** ***Chaetothyriomycetidae*** Doweld.
***Pyrenulales*** Fink ex D. Hawksw. & O.E. Erikss.
***Pyrenulaceae*** Rabenh.

**20.** ***Anthracothecium prasinum*** (Hepp) Müll. Arg., Linnaea 43, 44 (1880) (Contributed by V Thiyagaraja)

**21.** ***Pyrenula ochraceoflava*** (Nyl.) R.C. Harris, Memoirs of the New York Botanical Garden 49, 96 (1989) (Contributed by V Thiyagaraja)

**Class** ***Leotiomycetes*** O.E. Erikss. & Winka
**Subclass** ***Leotiomycetidae*** P.M. Kirk, P. Cannon, Minter & Stalpers
***Helotiales*** Nannf.
***Cenangiaceae*** Rehm

**22.** ***Chlorencoelia torta*** (Schwein.) J.R. Dixon, Mycotaxon 1(3), 230 (1975) (Contributed by AS Lestari)

***Helotiaceae*** Rehm

**23.** ***Hymenotorrendiella indonesiana*** Crous & P.R. Johnst., in Crous et al., Persoonia 44, 349 (2020) (Contributed by CY Li)

**24.** ***Tatraea aseptata*** H.L. Su & Q. Zhao, **sp. nov.** (Contributed by HL Su)

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

**25**. ***Apoharknessia thailandica*** N. Wu, Jian K. Liu & K.D. Hyde **sp. nov.** (Contributed by N Wu)

***Diaporthaceae*** Höhn. ex Wehm.

**26.** ***Diaporthe eres*** Nitschke, Pyrenomycetes Germanici 2, 245 (1870) (Contributed by PD

Abeywickrama)

**27.** ***Diaporthe vexans*** (Sacc. & P. Syd.) Gratz, Phytopathology 32, 542 (1942) (Contributed by W Punyaboon)

***Melanconidaceae*** G. Winter

**28.** ***Melanconis stilbostoma*** (Fr.) Tul. & C. Tul., Selecta Fungorum Carpologia (Paris) 2, 115 (1863) (Contributed by SN Wijesinghe)

**Subclass** ***Hypocreomycetidae*** O.E. Erikss. & Winka
***Glomerellales*** Chadef. ex Réblová, W. Gams & Seifert
***Glomerellaceae*** Locq. ex Seifert & W. Gams

**29.** ***Colletotrichum endophytica*** Manamgoda, Udayanga, L. Cai & K.D. Hyde, Fungal Diversity 61, 107–115 (2013) (Contributed A Armand)

**30.** ***Colletotrichum siamense*** Prihast., L. Cai & K.D. Hyde, Fungal Diversity 39, 98 (2009) (Contributed by XY Ma)

***Hypocreales*** Lindau
***Bionectriaceae*** Samuels & Rossman

**31.** ***Clonostachys agarwalii*** (Kushwaha) Schroers [as 'agrawalii'], Studies in Mycology 46, 90 (2001) (Contributed by RH Perera)

**32.** ***Clonostachys ralfsii*** Schroers, Studies in Mycology 46, 135 (2001) (Contributed by SN Wijesinghe)

***Clavicipitaceae*** (Lindau) Earle ex Rogerson

**33.** ***Pochonia chlamydosporia*** (Goddard) Zare & W. Gams, in Gams & Zare, Nova Hedwigia 72(3–4), 334 (2001) (Contributed by WAE Yasanthika)

***Nectriaceae*** Tul. & C. Tul.

**34.** ***Volutella lini*** Mukerji, J.P. Tewari & J.N. Rai, Transactions of the British Mycological Society 51(2), 337 (1968) (Contributed by MS Calabon)

**Subclass** ***Sordariomycetidae*** O.E. Erikss & Winka
***Chaetosphaeriales*** genera *incertae sedis*

**35.** ***Neoleptosporella camporesiana*** R.H. Perera & K.D. Hyde, Fungal Diversity 100, 219 (2020) (Contributed by L Lu, Tibpromma S)

***Coniochaetales*** Huhndorf, A.N. Mill. & F.A. Fernández
***Coniochaetaceae*** Malloch & Cain

**36.** ***Coniochaeta taeniospora*** (Sacc.) Friebes, Jaklitsch & Voglmayr, Sydowia 68, 91 (2016) (Contributed by D Bundhun)

***Cordanaceae*** Nann.

**37.** ***Cordana terrestris*** (Timonin) Hern.-Restr., Gené & Guarro, in Hernández-Restrepo et al., Mycologia 106, 729 (2014) (Contributed by WAE Yasanthika)

**Subclass** ***Xylariomycetidae*** O.E. Erikss & Winka
***Amphisphaeriales*** D. Hawksw. & O.E. Erikss.
***Apiosporaceae*** K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

**38.** ***Nigrospora lacticolonia*** Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39, 131 (2017) (Contributed by H Li)

**39.** ***Nigrospora oryzae*** (Berk. & Broome) Petch, Indian Botanical Society Journal 4, 24 (1924) (Contributed by D Gomdola)

**40.** ***Nigrospora osmanthi*** Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39, 135 (2017) (Contributed by H Zhao)

**41.** ***Nigrospora vesicularifera*** M. Raza & L. Cai, Fungal Diversity 99(1), 1–104 (2019) (Contributed by NP Samaradiwakara)

***Sporocadaceae*** Corda

**42.** ***Discosia celtidis*** Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity, 108 (2021) (Contributed by DS Tennakoon)

***Xylariales*** Nannf.
***Diatrypaceae*** Nitschke

**43.** ***Allocryptovalsa aquilariae*** T.Y. Du & Tibpromma **sp. nov.** (Contributed by TY Du and S Tibpromma).

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

**44.** ***Vamsapriya uniseptata*** N.G. Liu & K.D. Hyde, in Sun et al., Journal of Fungi 7(891), 12 (2021) (Contributed by H Win).

**Phylum** ***Basidiomycota***
**Class** ***Agaricomycetes*** Doweld
**Subclass** ***Agaricomycetidae*** Locq.
***Agaricales*** Underw.
***Agaricaceae*** Chevall.

**45.** ***Lepiota angusticystidiata*** J.F. Liang & Z.L. Yang, in Liang, Yu, Lu, Wang & Song, Mycologia 110, 496 (2018) (Contributed by P Sysouphanthong)

**46.** ***Lepiota venenata*** Zhu L. Yang & Z.H. Chen, in Cai, Chen, He, Luo & Yang, Journal of Fungal Research 16, 67 (2018) (Contributed by P Sysouphanthong)

***Hymenogastraceae*** Vittad.
***Gymnopilus*** P. Karst.

**47.** ***Gymnopilus lepidotus*** Hesler, Mycologia Memoirs 3, 40 (1969) (Contributed by AN Ediriweera, KC Wadduwage and DN Wijayalath)

***Lyophyllaceae*** Jülich

**48.** ***Asterophora lycoperdoides*** (Bull.) Ditmar, Neues Journal Botanik 3(3, 4), 56 (1809) (Contributed by SM Tang)

***Pleurotaceae*** Kühner
***Pleurotus*** (Fr.) P. Kumm.

**49.** ***Pleurotus tuber-regium*** (Fr.) Singer, Lilloa 22, 271 (1951) [1949] (Contributed by AN Ediriweera, KC Wadduwage and DN Wijayalath)

***Boletales*** E.-J. Gilbert
***Boletaceae*** Chevall.

**50.** ***Pulveroboletus fragrans*** Raspé & Vadthanarat, in Raspé et al., Mycol. Progr. 15(4/38): 4 (2016) (Contributed by O Raspé)

## Introduction

The AJOM new records and collections of fungi is a series of publications introduced in 2020, which aims to provide a framework for publishing novel data on the taxonomy and phylogeny of diverse fungal genera, emphasizing novel host and geographical records (Hyde et al. 2020c, Chethana et al. 2021a). To date, there are many series that perform a similar function, yet

with a focus on novel fungal taxa, such as Fungal Diversity Notes (Jayawardene et al. 2023, Boonmee et al. 2021), Fungal Planet (Crous et al. 2020, 2022a), Genera of phytopathogenic fungi (Chen et al. 2022) and Mycosphere notes series (Manawasinghe et al. 2022). However, the most important purpose of our series is to provide space for mycologists to publish new data related to ecology and morphology, including new sequence data necessary to establish stable taxonomy for fungal genera.

Even though the newly described fungal taxa per year has increased dramatically over the past few years (Wang et al. 2023), there are still poorly described species that lack molecular data and are introduced with only one isolate. Therefore, continuous revisions are taking place for different fungal taxa considering their morphology, phylogeny, and ecology. New host and geographical records introduced in this study can facilitate these processes by providing the data and fresh specimens for the mycologists to study and reference and also assist research on population dynamics of ecologically important fungal taxa. Identifying and documenting new records on fungal pathogens can be particularly important to understand their host and geographical ranges for disease management (Dugan et al. 2009).

The current study is the third in the series of Asian Journal of Mycology notes, with entries mainly collected from China, Italy, Laos, Russia, Sri Lanka, and Thailand. We aim to provide new data, including morphological, geographical, and sequence data for fungal taxa, which are instrumental for revising species descriptions and producing taxonomic keys for species. In the current study, we provide detailed morphological descriptions of collections, with listed herbarium material, high-resolution illustrations, sequence data and discussions on fungal taxa. Publication of new host and geographical records as a single entity in a peer-reviewed journal ensures the scientific accuracy and validity of such information and assists the dissemination of these records widely.

## Materials and methods

All the fungal taxa identifications followed the polyphasic approach described in Chethana et al. (2021b). Specimens described in this study were collected from China, Italy, Laos, Russia, and Thailand. Morphological analyses with illustrations were provided following Senanayake et al. (2020), coupled with phylogenetic analyses performed by maximum likelihood (ML), maximum parsimony (MP), and Bayesian posterior probability (BYPP) criteria (Dissanayake et al. 2020). In addition, the pairwise homoplasy index (PHI) test was carried out when necessary, using Split Tree as described by Quaedvlieg et al. (2014) to determine the recombination level within phylogenetically closely related species.

## Taxonomy

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

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

Facesoffungi number: FoF 14145

For Dothideomycetes, we follow the recent treatments of (Liu et al. 2017, Wijayawardene et al. 2022, Hongsanan et al. 2020a, b).

**Subclass *Dothideomycetidae*** P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker, in Schoch et al., Mycologia 98(6), 1045 (2007)

Facesoffungi number: FoF 00025

***Cladosporiales*** Abdollahz. & Crous, in Abdollahzadeh, Groenewald, Coetzee, Wingfield & Crous, Studies in Mycology 95, 390 (2020)

Facesoffungi number: FoF 14146

***Cladosporiaceae*** Chalm. & R.G. Archibald, Yearbook of Tropical Medicine and Hygiene: 25 (1915)

Facesoffungi number: FoF 06966

***Cladosporium*** Link, Mag. Gesell. naturf. Freunde, Berlin 7: 37 (1816) [1815]

Facesoffungi number: FoF 06967

According to Lindau (1907), *Mydonosporium* is synonymous with *Cladosporium*, a conclusion supported by Vries (1952). However, this conclusion could not be confirmed since its type material could not be examined as it is not preserved. Fries (1849) reallocated the type species of *Azosma* (Corda 1831), *A. helminthosporioides*, to *Cladosporium*, whereas Saccardo and Traverso (Saccardo 1913) assigned it to *Macrosporium* (= *Alternaria*). The identity of *Azosma* remains doubtful and could not be proven since the type material is not preserved. Von Arx (1983) considered *Acroconidiella* a synonym of *Heterosporium* and reduced *Stenella* to synonymy with *Cladosporium*. However, *Acroconidiella* possesses tretic conidiogenous cells and conidiogenous loci and hila within the genus. *Stenella s. lat.* is quite distinct from those of *Cladosporium* by being pileate (*Stenella s. str*.) to planate (former species of *Stenella s. lat.* now assigned to *Zasmidium*), i.e., in any case without dome and raised rim. Hence, the two genera proposed to be retained as separate genera (Crous & Braun 2003). The type material of *Acrosporella* (Riedl & Ershad 1977) has recently been examined and shown to be a synonym of *Cladosporium* (Braun 2009, Bensch et al. 2012). An updated phylogeny for the genus is given in Fig. 1.

***Cladosporium tenuissimum*** Cooke, Grevillea 6(no. 40), 140 (1878)

Index Fungorum Number: IF 145672; Facesoffungi number: FoF 09313; Fig. 2

*Saprobic* on an unknown host. **Sexual Morph:** Undetermined. **Asexual Morph:** *Conidiomata* thick, falcate star-like, superficial, solitary, scattered, black. *Colonies* on PDA, reaching 7 cm diameter, after 102 days at 25 ºC, greenish to black wrinkled, regular colony with filiform margin, filamentous form, raised, smooth, reverse greenish brown with a black center. *Mycelium* immersed, septate, unbranched, hyaline to brownish hyphae. *Conidiophore* hyaline to brown, small, short. *Conidiogenous cell* 4–12 µm high × 3–4 µm wide ($\overline{x}$ = 7 × 3 µm, n = 4), hyaline to brown, ellipsoidal to ampulliform, intercalary. *Conidia* 3–7 µm high × 2–5 µm wide ($\overline{x}$ = 4 × 3 µm, n = 24), globose, subglobose to ellipsoidal, aseptate, hyaline to light brown, smooth.

Culture characteristics – Conidia germinated on PDA within 72 hr., reaching 40 mm diam. in 2 weeks at 25 °C. *Colonies* on PDA with velvety, feathery, regular, dark green, or dark olivaceous. Sporulation was observed. The reverse of colony black or dark brown or dark green.

Material examined – Thailand, Chiang Rai Province, Muang District, Mae Fah Luang University, on dead wood of unknown host, 17 February 2021, C. J. Prematunga (MFLU 22-0112), living culture MFLUCC 22-0055.

GenBank accession numbers – ITS: ON860666, *act*: ON952525, *tef-1α*: OP081761.

Known distribution (based on molecular data) – Brazil, China, Korea, Thailand, the USA (Heuchert et al. 2005, Bensch et al. 2018, Rosado et al. 2019, Tennakoon et al. 2021a, this study).

Known hosts (based on molecular data) – *Acacia mangium*, *Anacardium occidentale*, *Carica papaya*, *Capsicum* sp., *Macaranga tanarius*, *Morus australis*, *Passifora edulis*, *Zea mays* (Heuchert et al. 2005, Bensch et al. 2018, Rosado et al. 2019, Tennakoon et al. 2021a).

Notes – Based on BLASTn search results of ITS, *act*, and *tef-1α* sequence data, our strain (MFLUCC 22-0055) showed high similarity (≥ 80%) to several *Cladosporium* taxa in the GenBank. In our phylogenetic analysis (Fig. 1), MFLUCC 22-0055 has shown a close phylogenetic affinity to *C. tenuissimum* (CBS 125995). The dark, erect irregular-branched conidiophores, 15–40 µm long, cylindrical to subclavate conidiogenous cells, and 3–10 × 2–5 µm, dark, subglobose, 0–3-septate conidia of *C. tenuissimum* show similar morphology with our isolate (Bensch et al. 2012). We report *C. tenuissimum* in Chiang Rai, Thailand, as a new record.

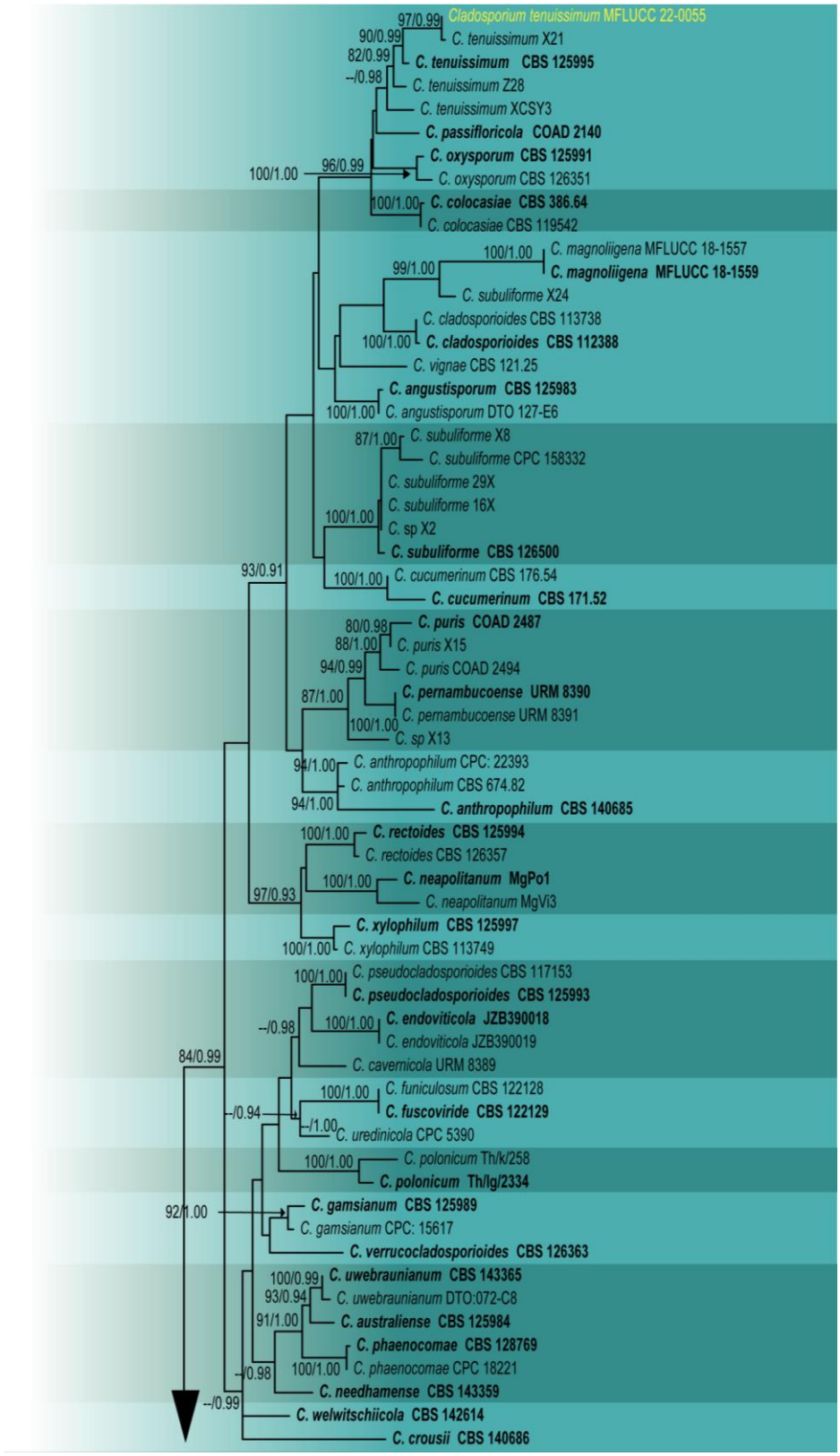


**Fig. 1 –** Maximum likelihood tree revealed by RAxML from an analysis of ITS, *act* and *tef-1α* sequence data of the species of *Cladosporium*, showing the phylogenetic position of *Cladosporium tenuissimum* (MFLUCC 22-0055). Maximum likelihood bootstrap supports (≥ 80%) and Bayesian posterior probabilities (≥ 0.90 BYPP) are given near the branches as ML/BYPP. The tree is rooted with *C. sphaerospermum* (CBS 193.54) and *C. longissimum* (CBS 300.96). Ex-type strains are indicated in **bold**. The newly generated sequences are indicated in yellow. The scale bar represents the expected number of nucleotide substitutions per site.

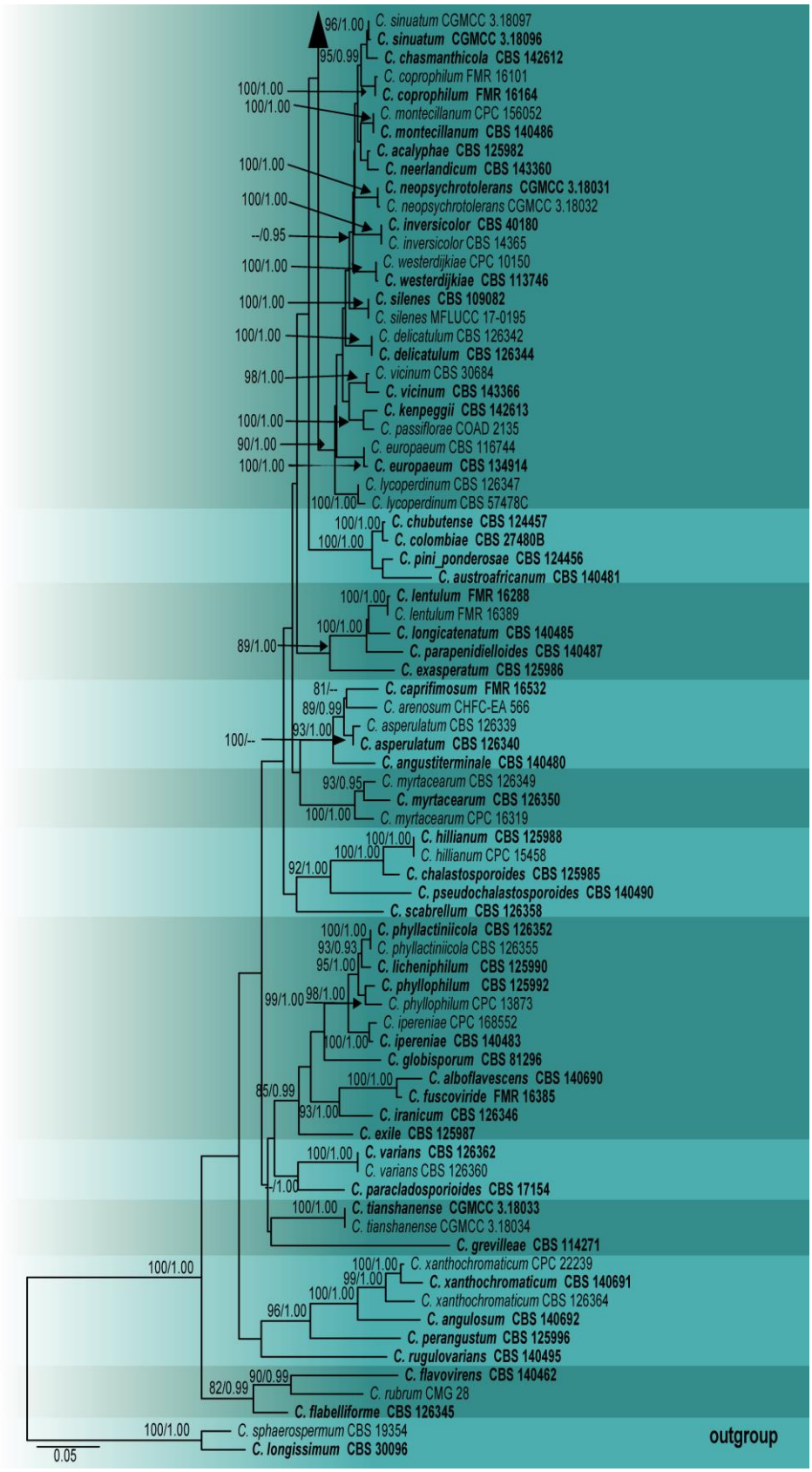


**Fig. 1** – Continued

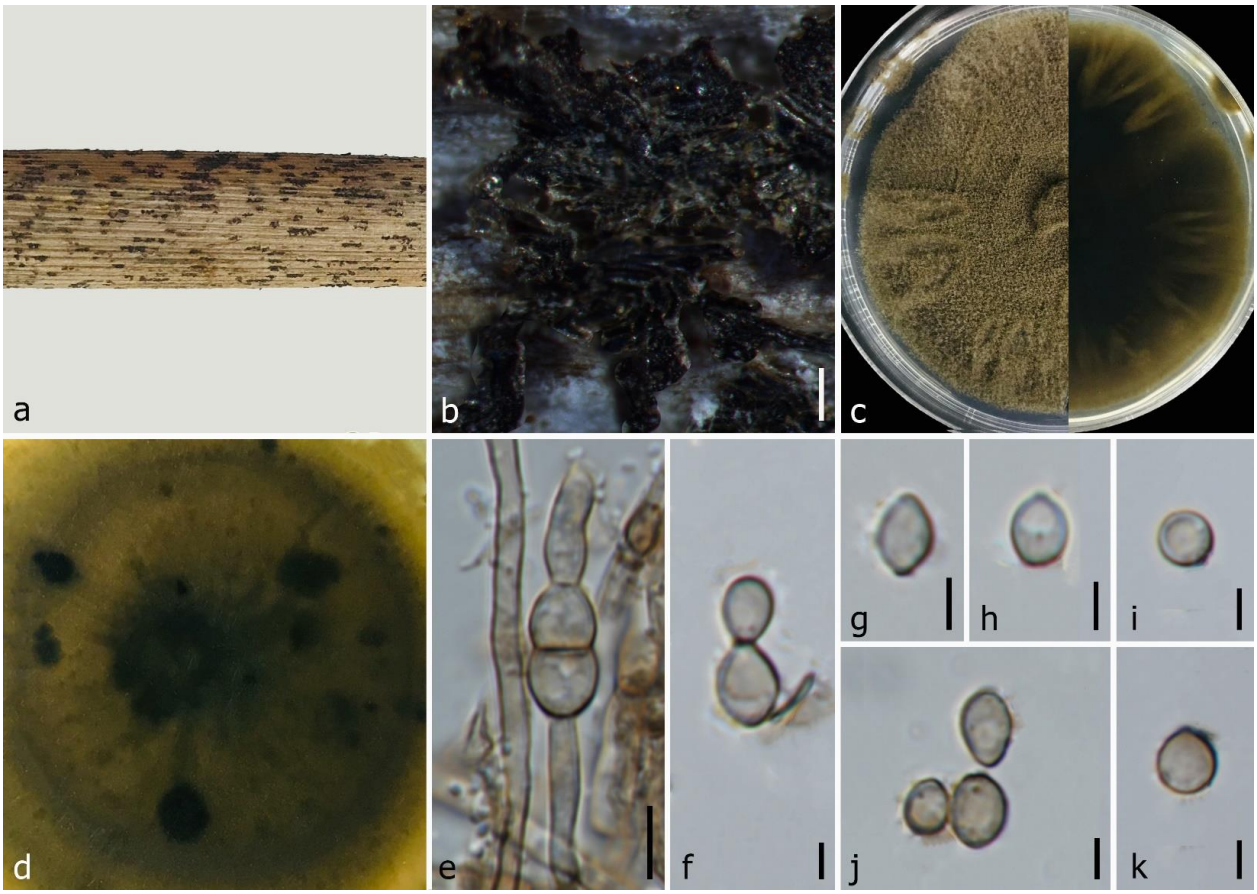


**Fig. 2 – *Cladosporium tenuissimum*** (MFLU 22-0112, **new geographical record**). a Conidiomata on the host. b Close-up of conidiomata on the substrate. c Culture on the PDA (left: top view, right: reverse view). d Sporulating on the PDA. e–f Conidiophore and conidiogenous cells. g–k Conidia. Scale bars: b = 100 µm, e = 10 µm, f = 5 µm, g–k = 3 µm.

***Mycosphaerellales*** P.F. Cannon, in Kirk et al., Ainsworth & Bisby's Dictionary of the Fungi, Edn 9 (Wallingford), x (2001)

Facesoffungi number: FoF 14162

***Phaeothecoidiellaceae*** K.D. Hyde & Hongsanan, in Senanayake et al., Mycosphere 8(1), 140 (2017)

Facesoffungi number: FoF 02883

***Translucidithyrium*** X.Y. Zeng & K.D. Hyde, Mycological Progress 17(9), 1090 (2018)

Facesoffungi number: FoF 04090

*Translucidithyrium* was introduced by Zeng et al. (2018), with *Translucidithyrium thailandicum* as the type species. This genus morphologically resembles the members of *Myriangiaceae* and *Schizothyriaceae* but differs by lacking a network-like structure separating locules in the ascomata and appendaged ascospores (Zeng et al. 2018, Li et al. 2020). This genus is also morphologically very similar to *Lecideopsella* (*Schizothyriaceae*) in having solitary, scattered, grey-coloured ascomata outlined by thin upper walls and globose asci with 1-septate ascospores (Zeng et al. 2018, Li et al. 2020). In contrast to *Translucidithyrium* lacking a network-like structure in ascostromata, ascal pedicels and appendaged, hyaline ascospores, *Lecideopsella* has ascospores that are pale yellowish at both ends (Phookamsak et al. 2016, Zeng et al. 2018). An updated phylogeny for *Phaeothecoidiellaceae* and closely related taxa is shown in Fig. 3.

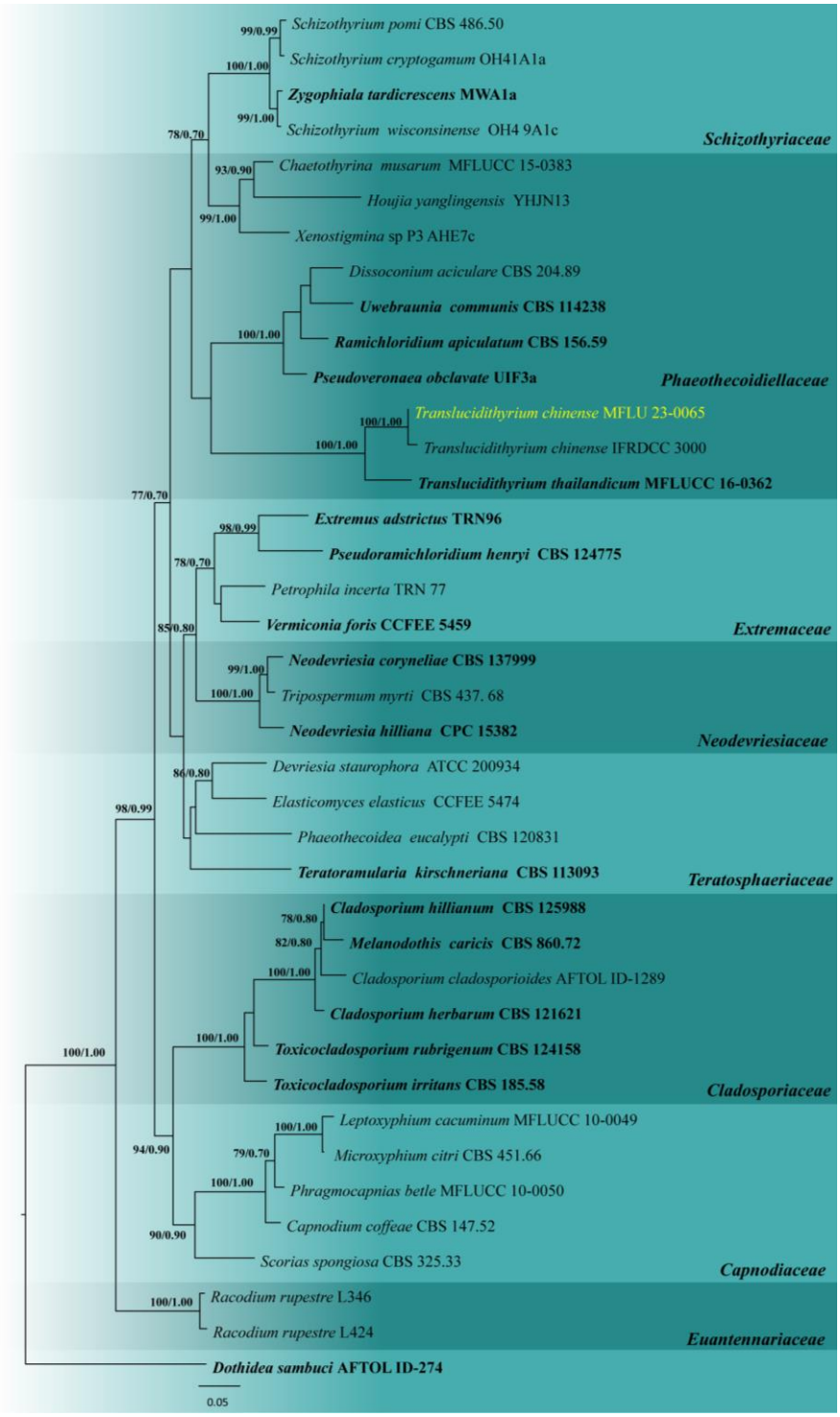


**Fig. 3 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Thirty-nine strains are included in the combined gene analyses comprising 1462 characters after alignment (893 characters for LSU and 569 for ITS). *Dothidea sambuci* (AFTOL ID-274) is used as the outgroup taxon. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. The best RaxML tree with a final likelihood value of -12266.208 is presented. The matrix had 768 distinct alignment patterns, with 19.62% undetermined characters or gaps. Evolutionary models Tn+F+R6 and GTR+G were selected as the best-fit models for the LSU and ITS gene regions, respectively. Bootstrap values for maximum likelihood equal to or greater than 60 and Bayesian posterior probabilities equal to or greater than 0.90 are placed above or below the branches, respectively. Ex-type strains are **in bold**. The newly generated sequences are indicated in yellow.

***Translucidithyrium chinense*** H.X. Wu & X.H. Li, in Li et al., MycoKeys 76, 7 (2020)

Index Fungorum number: IF 557843; Facesoffungi number: FoF 09429; Fig. 4

*Epiphyllous* appearing as brownish lesions on the surface of unidentified leaves. *Mycelium* scarce or not distinct. **Sexual morph:** *Ascomata* 600–700 μm in diam. ($\overline{x}$ = 650 μm, n = 15), solitary, scattered, globose to subglobose, flattened, light brown, without ostiole. *Peridium* poorly developed at the basal, thin at the upper walls, membranous, composed of pale brown, interwoven, irregular, meandering, interwoven arranged cells. *Hamathecium* composed of hyaline interascal tissues. *Asci* 55–70 × 40–70 μm ($\overline{x}$ = 65 × 50 μm, n = 15), bitunicate, 8-spored, globose to subglobose, embedded in interascal tissues, apedicellate. *Ascospores* 35–40 × 10–15 μm ($\overline{x}$ = 37 × 12 μm, n = 20), crowded, irregularly overlapping, hyaline, ovoid at young state, fusiform to inequilateral at maturity, tapering at both ends, 1-septate, constricted at the septum, lower cell longer than the upper, hook-like curve in the upper cell, verrucose to smooth, covering a thin sheath. **Asexual morph:** Undetermined.

Material examined – Thailand, Nan Province, Pua District, unidentified leaf, 4 February 2022, Diana Sandamali, MFLU 23-0065.

GenBank accession numbers – ITS: OQ568947, LSU: OQ568948.

Known distribution (based on molecular data) – China (Li et al. 2020), Thailand (this study).

Known hosts (based on molecular data) – *Alpinia blepharocalyx* (Li et al. 2020).

Notes – The morphology of this species resembles *Translucidithyrium chinense* in having brownish, globose ascomata, globose to subglobose, 8-spored asci, and hyaline, 1-septate, curved ascospores that are initially ovoid, becoming fusiform at maturity (Li et al. 2020). The comparisons of the ITS sequences show four base pair differences across 450 bp (1.1 %). Our ITS and LSU combined phylogenetic analyses (Fig. 3) reveal that our strain clusters with *Translucidithyrium chinense* (IFRDCC 3000) with 100% maximum likelihood and 1.00 posterior probability support. Thus, we report the first geographical record of *T. chinense* in Thailand.

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

Facesoffungi number: FoF 14163

***Pleosporales*** Luttrell ex M.E. Barr, Prodromus to class Loculoascomycetes (Amherst), 67 (1987)

Facesoffungi number: FoF 08715

***Acrocalymmaceae*** Crous & Trakun., in Trakunyingcharoen et al., IMA Fungus 5(2), 404 (2014)

Facesoffungi number: FoF 08135

***Acrocalymma*** Alcorn & J.A.G. Irwin, Transactions of the British Mycological Society 88(2), 163 (1987)

Facesoffungi number: FoF 07097

*Acrocalymma*, the only genus in *Acrocalymmaceae*, was introduced to accommodate *A. medicaginis* Alcorn & J.A.G. Irwin as the type species (Alcorn & Irwin 1987, Wijayawardene et al. 2022). *Acrocalymma medicaginis* was recognized as the asexual morph of *Massarina walkeri* by Shoemaker et al. (1991). However, Trakunyingcharoen et al. (2014) showed that *A. medicaginis* and *M. walkeri* are phylogenetically distinct and introduced a new combination, *A. walkeri*. Both sexual and asexual morphs are recorded for this genus (de Silva et al. 2022). Currently, 11 species are listed under this genus in the Index Fungorum (2022). An updated phylogeny is shown in Fig. 5.


**Fig. 4 – *Translucidithyrium chinense*** (MFLU 23-0065, **new geographical record**). a Leaf specimen. b, c Ascomata on the leaf surface. d Squash mount of ascomata. e Section through ascomata. f Interascal tissue. g Upper cell wall. h Immature ascus. i–k Mature asci. l–q Immature to mature ascospores. r Germinated ascospore. Scale bars: c = 200 μm, d = 100 μm, e, g–j = 20 μm, f, k–r = 10 μm.

***Acrocalymma hyalina*** N. Wu, Jian K. Liu & K.D. Hyde **sp. nov.**

Index Fungorum number: IF 900557; Facesoffungi number: FoF 14276; Fig. 6

Etymology – From the Latin "hyaline" in reference to the hyaline conidia.

Holotype – GZAAS 23-0591

*Saprobic* on decaying branch of an unidentified host. **Asexual morph:** Coelomycetous. *Conidiomata* 160–230 μm high, 190–230 μm diam. ($\bar{x}$ = 190 × 212 μm, n = 10), solitary or aggregated, immersed, partially erumpent when mature, dark brown to black, more or less circular, uniloculate, thick-walled, wall composed of outer layers of thick-walled, dark brown *textura angularis*, inner layers of thin-walled, hyaline *textura angularis*. *Ostiole* circular, central, papillate. *Peridium* 17–27 μm wide, composed of 5–6 layers, with outer 3–4 layers brown, thick-walled cells of *textura angularis* and inner 1–3 layers hyaline, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, arising from all around the basal region of the conidioma. *Conidiogenous cells* 6–12 μm long × 5–8 μm wide, cylindrical, sometimes slightly curved, phialidic, hyaline. *Conidia* 30–38 × 5–9 μm ($\bar{x}$ = 34 × 8 μm, n = 20), oblong to subcylindrical, straight, hyaline, aseptate, guttulate, not constricted or slightly constricted at the middle. **Sexual morph:** Undetermined.

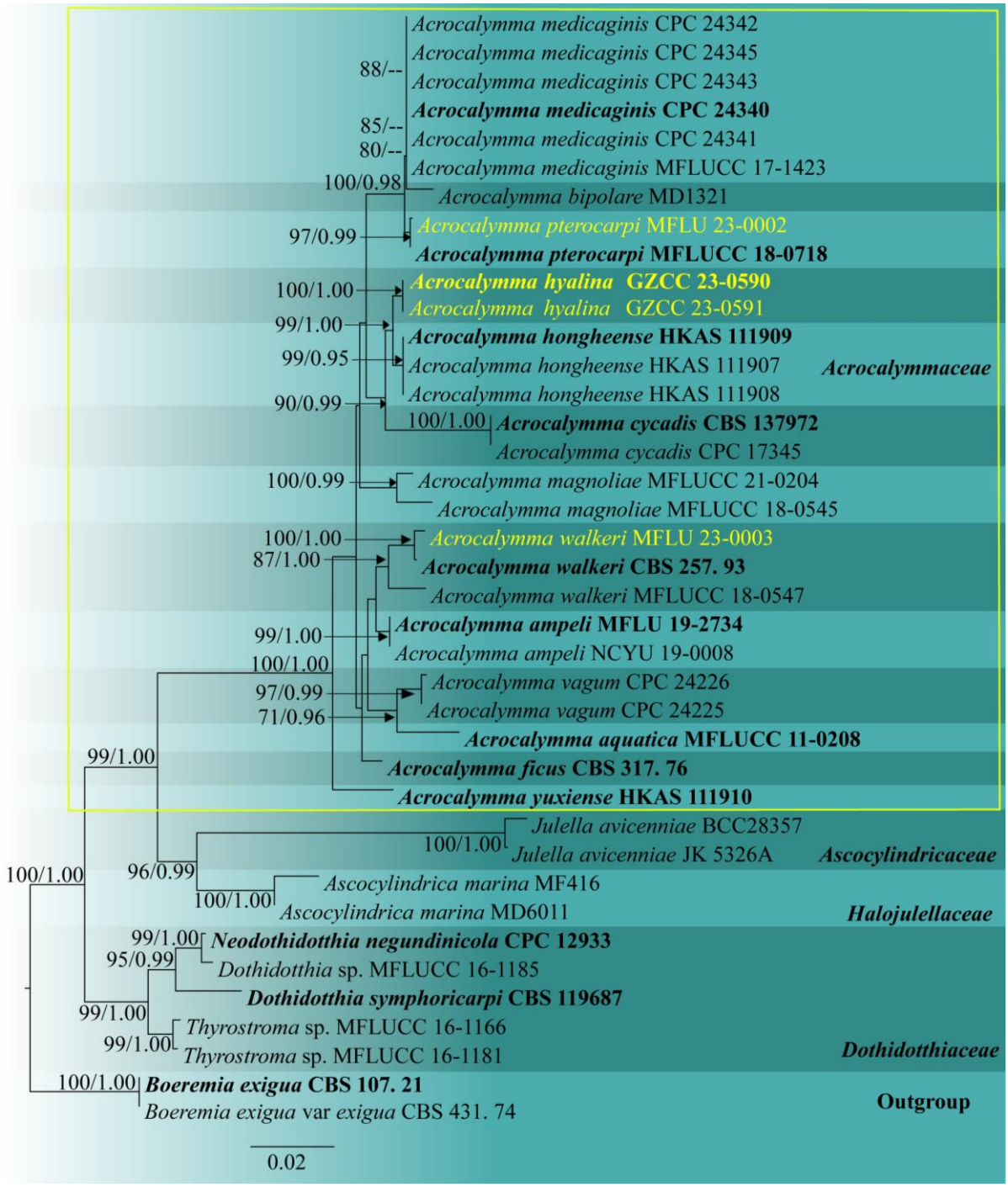


**Fig. 5 –** Phylogram generated from the maximum likelihood analysis based on the combined LSU, SSU and ITS sequence data. Thirty-nine strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -6868.654138 is presented. Evolutionary models applied for all genes are GTR+G. The matrix had 483 distinct alignment patterns, with 28.24% of undetermined characters or gaps. Bootstrap support values for maximum likelihood greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree was rooted with *Boeremia exigua* (CBS 107. 21) and *B. exigua* var *exigua* (CBS 431. 74). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching 10 mm diam. after one week at 20–23 °C, circular, slightly raised, surface smooth, entire margin, white in surface view.

Material examined – Thailand, Chiang Rai Province, Phaya Mengrai District, Mae Pao, 19°53'5"N, 100°5'37"E, on an unidentified dead wood, 7 January 2020, Na Wu, YW285 (GZAAS 23-0591, holotype); ex-type living culture, GZCC 23-0590; *ibid*., YW284 (GZAAS 23-0592), living culture GZCC 23-0591.

GenBank accession numbers – GZCC 23-0590 - ITS: OR052071, LSU: OR052054; GZCC 23-0591 - ITS: OR052072, LSU: OR052055.

Notes – Phylogenetically, this collection resides in the genus *Acrocalymma* and is closely related to *A. hongheense* (Fig. 5). Our isolate is morphologically similar to *A. hongheense* (strain HKAS 111907, HKAS 111908 and HKAS 111909), but *A. hongheense* has 1-septate conidia (Mortimer et al. 2021). In addition, the conidial size of *A. hyalina* (30–38 × 5–9 μm) is bigger than that of the *A. hongheense* ex-type (20–35 × 7–9 μm, HKAS 111909). Regarding the nucleotide comparison, *A. hyalina* and *A. hongheense* differed in five base pairs (bp) in the ITS region, and six in the LSU region. Thus, based on phylogenetic inference supported by morphological observations, we introduce this species as a new *Acrocalymma* species.

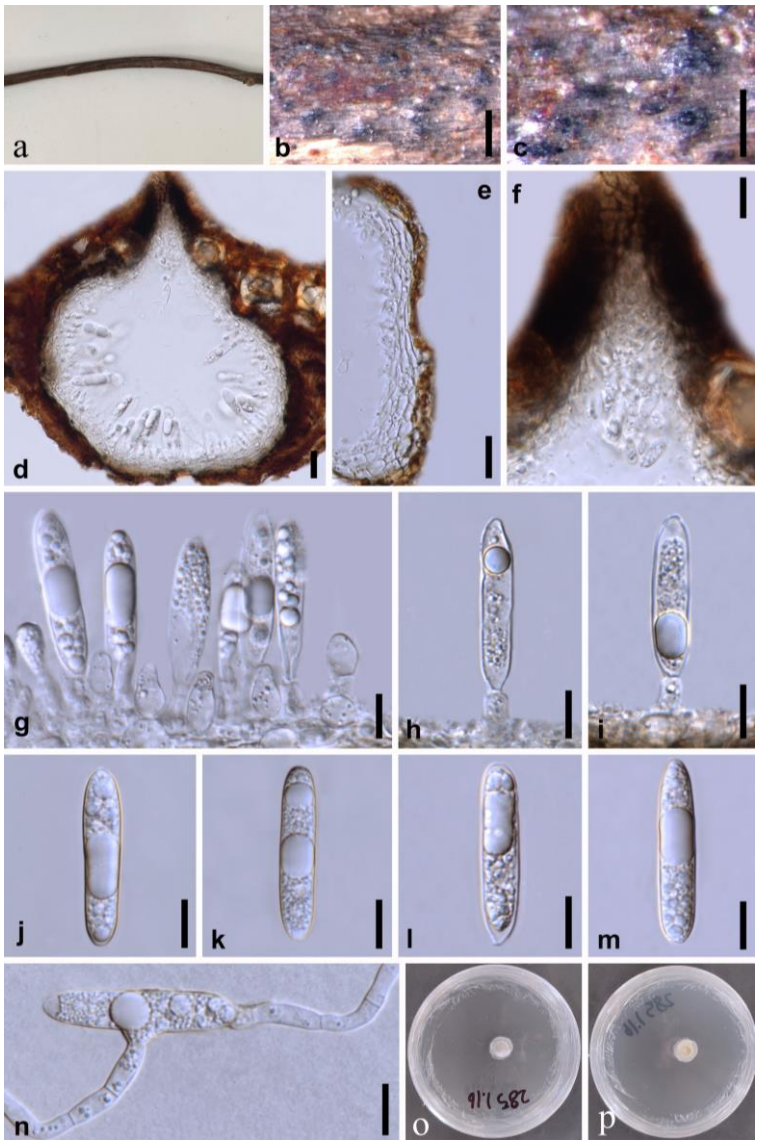


**Fig. 6 – *Acrocalymma hyalina*** (GZAAS 23-0591, **holotype**). a Host substrate. b, c Conidiomata on the host. d Section through a conidioma. e Peridium. f Ostiole with periphyses. g–i Conidiophores and conidia. j–m Conidia. n Germinating conidium. o, p Culture on the PDA from the surface (o) and reverse views (p). Scale bars: b = 50 μm, c–e = 20 μm, f–n = 10 μm.

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

Index Fungorum number: IF 555528; FacesofFungi number: FoF 05228; Fig. 7

*Saprobic* on dead twigs of *Bidens* sp. **Sexual morph:** *Ascomata* 120–130 μm high, 110–130 μm diam. ($\bar{x}$ = 125 × 120 μm, n = 10), scattered, erumpent to nearly superficial, globose to subglobose, dark brown to black, ostiolate with minute papilla. *Ostiole* 34–36 μm diam., central, papillate. *Peridium* 10–30 μm diam., composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, inner cells hyaline, arranged in a *textura angularis*. *Hamathecium* composed of 1–2 μm wide, numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 40–60 × 8–10 μm ($\bar{x}$ = 50 × 9.5 μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, with furcate pedicel, apically rounded with a small ocular chamber. *Ascospores* 16–20 × 5–6 μm ($\bar{x}$ = 19 × 5.5 μm, n = 30), overlapping biseriate, hyaline, fusiform, 1–3-septate, guttulate, with narrowly rounded ends with mucilaginous sheath. **Asexual morph:** Undetermined.

Material examined – Thailand, Chiang Mai Province, Mushroom Research Centre (MRC), on dead twig of *Bidens* sp., 11 November 2020, Pahoua Pasouvang, MFLU 23-0002.

GenBank accession numbers – ITS: OQ184951, LSU: OQ184954, SSU: OQ184984

Known distribution (based on molecular data) – China (de Silva et al. 2022), Thailand (Jayasiri et al. 2019, this study).

Known hosts (based on molecular data) – On a fallen pod of *Pterocarpus indicus* (Jayasiri et al. 2019), dead twigs attached to the *Magnolia* sp. (de Silva et al. 2022), dead twigs of *Bidens* sp. (this study).

Notes – Morphologically, our collection (MFLU 23-0002) is similar to the holotype of *A. pterocarpi* (MFLUCC 17–0926) collected from a fallen pod of *Pterocarpus indicus* (*Fabaceae*) in Thailand (Jayasiri et al. 2019). Both isolates have similar morphology (Fig. 7), with erumpent to nearly superficial, globose or subglobose ascomata, cylindrical asci with a short, narrowed, furcate pedicel and hyaline, fusiform, 1–3-septate ascospores (Jayasiri et al. 2019). However, the size of ascomata ($\bar{x}$ = 125 × 120 μm) and asci ($\bar{x}$ = 50 × 9.5 μm) of our collection are comparatively smaller than the holotype ($\bar{x}$ = 143 × 141 μm *vs*. $\bar{x}$ = 70 × 10 μm) (Jayasiri et al. 2019). According to the phylogenetic analyses (Fig. 5), our collections (MFLU 23-0002) clustered with *A. pterocarpi* strain (MFLUCC 18-0718) with 97% maximum parsimony bootstrap support and 0.99 Bayesian posterior probability. Furthermore, base pair differences between our collection (MFLUCC 17-0926) and the holotype of *A. pterocarpi* (MFLUCC 17-0926) are insignificant (LSU = 0.4% (3/760 bp), SSU = 0.4% (4/985 bp), and ITS = 1.2% (6/468 bp), confirming that they are the same species. Based on the morpho-molecular evidence, we introduced our new collection as a new host record of *A. pterocarpi* from *Bidens* sp. in Thailand.

***Acrocalymma walkeri*** (Shoemaker, C.E. Babc. & J.A.G. Irwin) Crous & Trakun., in Trakunyingcharoen et al., IMA Fungus 5(2), 407 (2014)

≡ *Massarina walkeri* Shoemaker, C.E. Babc. & J.A.G. Irwin 1991

Index Fungorum number: IF 810840, Faces of Fungi number: FoF 12929; Fig. 8

*Saprobic* on dead stems of *Tithonia diversifolia*. **Sexual morph:** *Ascomata* 160–180 μm high, 110–120 μm diam. ($\bar{x}$ = 170 × 115 μm, n = 5), solitary or aggregated, aggregates are scattered on the surface, immersed to semi-immersed, erumpent through the substrate, globose to subglobose, dark brown to black, ostiolate. *Ostiole* central. *Peridium* 10–19 μm wide ($\bar{x}$ = 15 μm, n = 10), composed of several layers, outer layer dark, fusing, indistinguishable from the host tissues, from outer towards inner dark brown or brown pseudoparenchymatous cells to hyaline cells of *textura angularis*. *Hamathecium* comprises numerous, 1.5–2.2 μm wide, filamentous, branched, septate, pseudoparaphyses. *Asci* 47–70 × 8.5–11 μm ($\bar{x}$ = 60 × 9 μm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, with furcate pedicel and a small ocular chamber. *Ascospores* 16–18 × 3–5 μm ($\bar{x}$ = 17 × 4.2 μm, n = 20, l/w = 4.0), biseriate, 1-septate, slightly constricted at the

septum, with wider upper cell, fusiform, acute ends, smooth-walled, hyaline, guttulate, with a sheath. **Asexual morph:** Undetermined.


**Fig. 7 – *Acrocalymma pterocarpi* on a dead twig of *Bidens* sp.** (MFLU 23-0002, **a new host record**). a, b Appearance of ascomata on host surface. c, d Section through an ascoma. e Ostiole. f Section through the peridium. g Pseudoparaphyses. h–k Asci. l–o Ascospores. p An ascospore stained with Indian Ink. Scale bars: a =500 μm, b =100 μm, c, d =50 μm, e =20 μm, f–p =10 μm.

Material examined – Thailand, Chiang Rai Province, Doi Mae Salong, dead stems of *Tithonia diversifolia*, 10 September 2020, Pahoua Pasouvang, PS-CM-258 (MFLU 23-0003).

GenBank accession numbers – ITS: OQ184952, LSU: OQ184955, SSU: OQ184985.

Known distribution (based on molecular data) – Australia (Shoemaker et al. 1991, Trakunyingcharoen et al. 2014), Thailand (de Silva et al. 2022, this study).

Known hosts (based on molecular data) – *Medicago sativa* (Shoemaker et al. 1991, Trakunyingcharoen et al. 2014), *Magnolia* sp. (de Silva et al. 2022), *Tithonia diversifolia* (this study).

Notes – Morphologically, our collection (MFLU 23-0003) resembles the holotype of *Acrocalymma walkeri* (DAOM 198791a; IMI 320072; isotype - CBS:257.93) in having globose or subglobose, dark brown to black ascomata (160–180(225) high, 160–180(225) μm diam *vs*. 160–180 μm high, 110–120 μm diam), peridium with a *textura angularis* cells (12–18 μm *vs*. 10–19 μm), septate, pseudoparaphyses (1–1.5 *vs*. 1.5–2.2 μm), 8-spored, cylindrical, short pedicellate asci (50–80 × 8–11 *vs*. 47–70 × 8.5–11 μm), and biseriate, 1-septate, fusiform, guttulate, hyaline ascospores (19–22 × 4.5–5.5 μm l/w = 4.0 *vs*. 16–18 × 3–5 μm l/w = 4.0) with a sheath (Shoemaker et al. 1991). Also, another collection of *A. walkeri* (MFLUCC 18-0547) was introduced by de Silva et al. (2022) and shares similar characters to our collection (Fig. 8) and CBS 257.93. In the phylogeny, our strain (MFLU 23-0003) grouped with the isotype (CBS 257.93) of *A. walkeri* with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability support (Fig. 5), and MFLUCC 18-0547 forms a distinct lineage sister to our strain and the type strain of the fungus. Therefore, further collections, including additional coding genes, are suggested to clarify the placements of the strains related to *A. walkeri*. Based on morphology and phylogenetic analyses, we conclude that our strai n is *A. walkeri*, the first record of *Tithonia diversifolia* in Thailand.

***Camarosporidiellaceae*** Wanas., Wijayaw., Crous & K.D. Hyde, in Wanasinghe et al., Studies in Mycology 87, 216 (2017)

Facesoffungi number: FoF 03528

***Camarosporidiella*** Wanas., Wijayaw. & K.D. Hyde, in Wanasinghe et al., Studies in Mycology 87, 216 (2017)

Facesoffungi number: FoF 03529

*Camarosporidiella* was introduced by Wanasinghe et al. (2017) with *C. caraganicola* as the type species. It is a well-defined type genus of *Camarosporidiellaceae*. *Camarosporidiella* is characterized by immersed to sub-peridermal conidiomata, enteroblastic, annellidic, integrated macroconidiogenous cells and medium brown to dark brown, phragmosporous to muriform macroconidia, hyaline. The sexual morph is characterized by black, superficial to semi-immersed ascomata, central, short ostioles, fissitunicate, cylindrical, short-pedicellate asci and muriform, mostly ellipsoidal ascospores with 3–8 transverse septa and 2–4 vertical septa. *Camarosporidiella* comprises 23 epithets. An updated phylogeny for the genus and related genera is provided in Fig. 9.

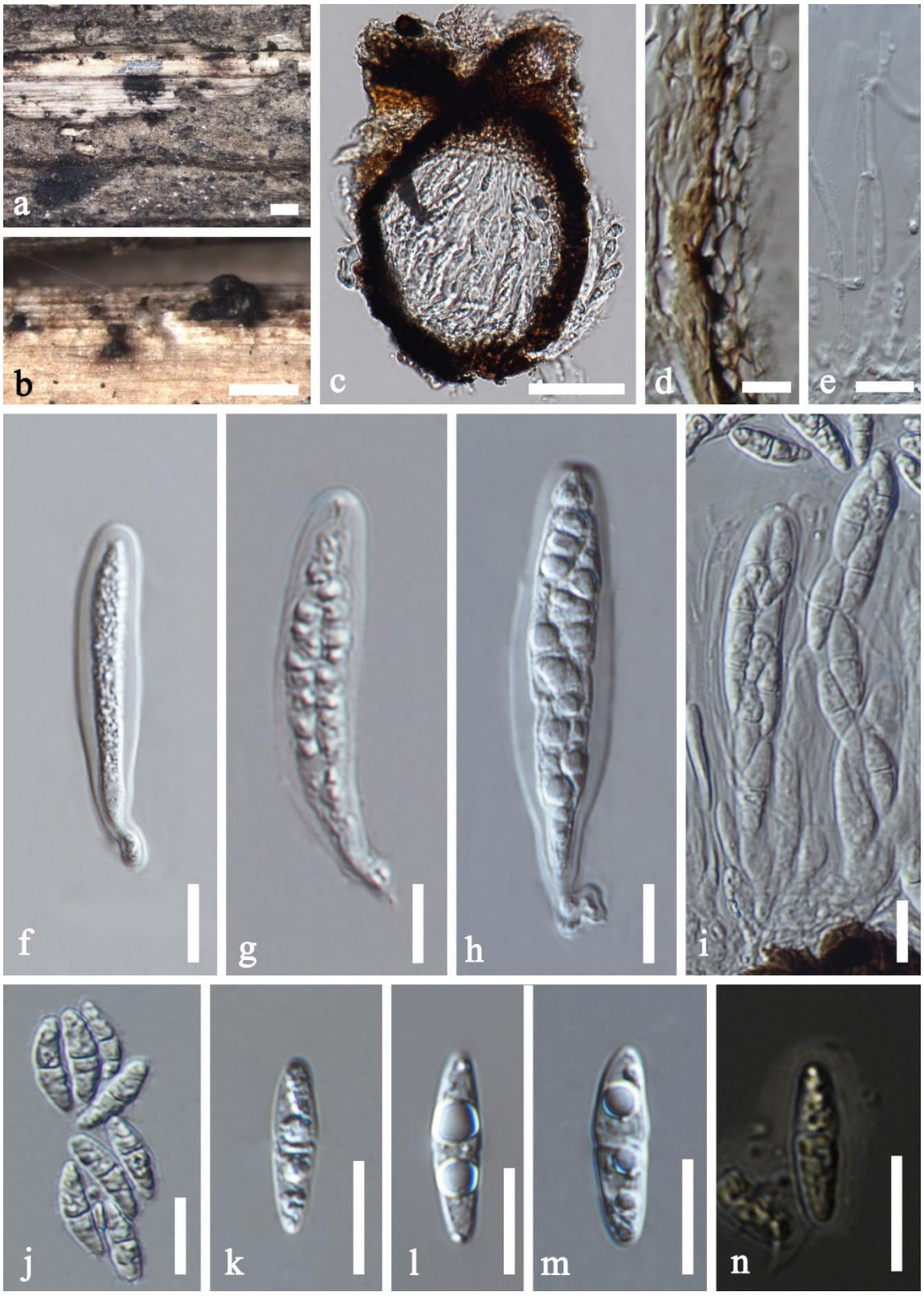


**Fig. 8 – *Acrocalymma walkeri* (**MFLU 23-0003, **a new host record)**. a–b Appearance of ascomata on the host substrate. c Vertical section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–n Ascospores. n An ascospore stained in Indian Ink. Scale bars: a = 500 μm, b = 200 μm, c = 50 μm, d–n = 10 μm.

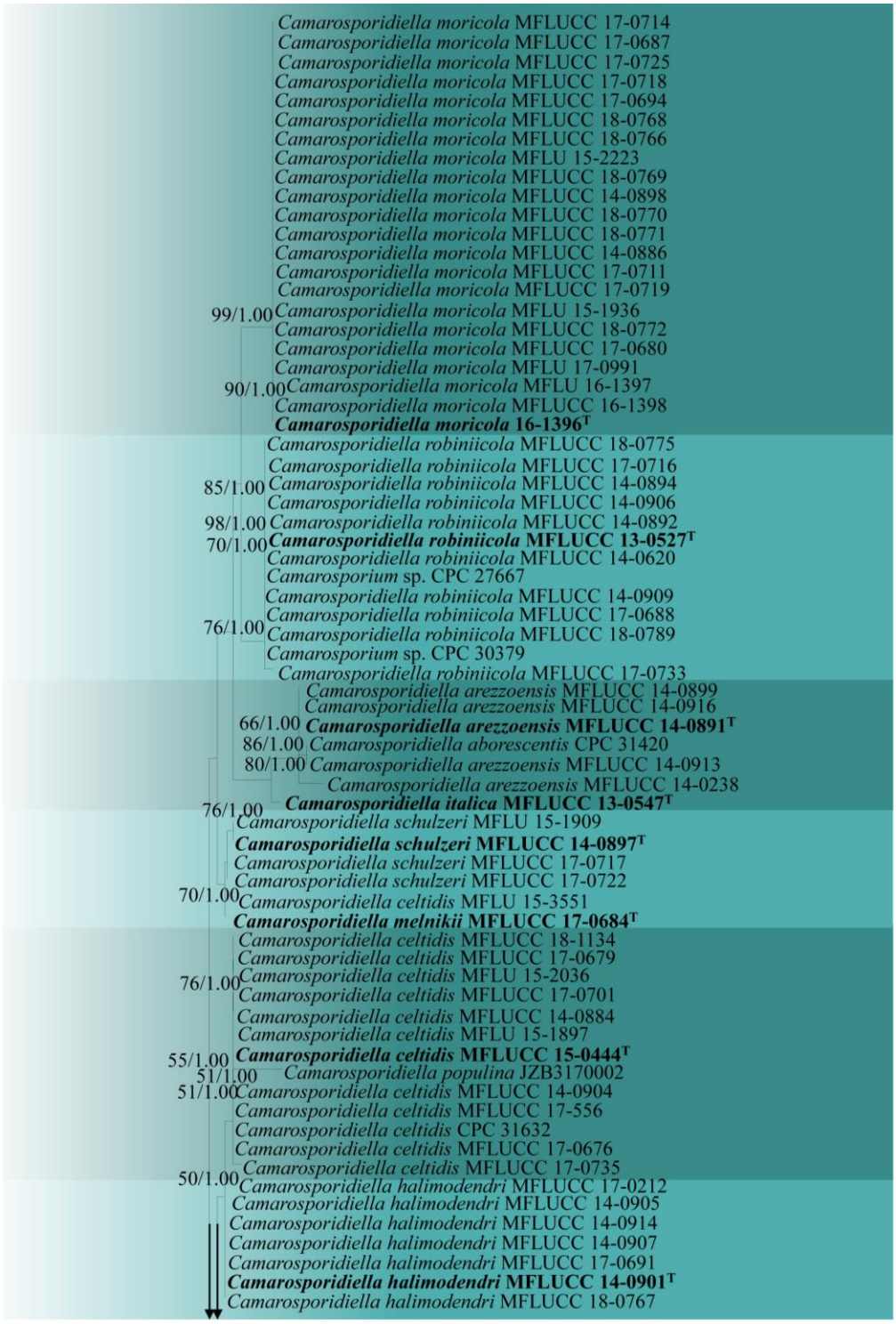


**Fig. 9 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. One hundred and eighteen strains are included in the combined gene analyses comprising 1327 characters after alignment (850 characters for LSU and 477 characters for ITS). *Staurosphaeria lycii* isolates (MFLUCC 17-0211, MFLUCC 17-0210) are used as the outgroup taxa. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. The best RaxML tree with a final likelihood value of -2861.045329 is presented. The matrix had 168 distinct alignment patterns, with 2.83% undetermined characters or gaps. Evolutionary models GTR+I+G and GTR+G were selected as the best-fit models for the LSU and ITS gene regions, respectively. Bootstrap values for maximum likelihood equal to or greater than 50 and Bayesian posterior probabilities equal to or greater than 0.90 are placed above or below the branches, respectively. Ex-type strains are **in bold**. The newly generated sequences are indicated in yellow.

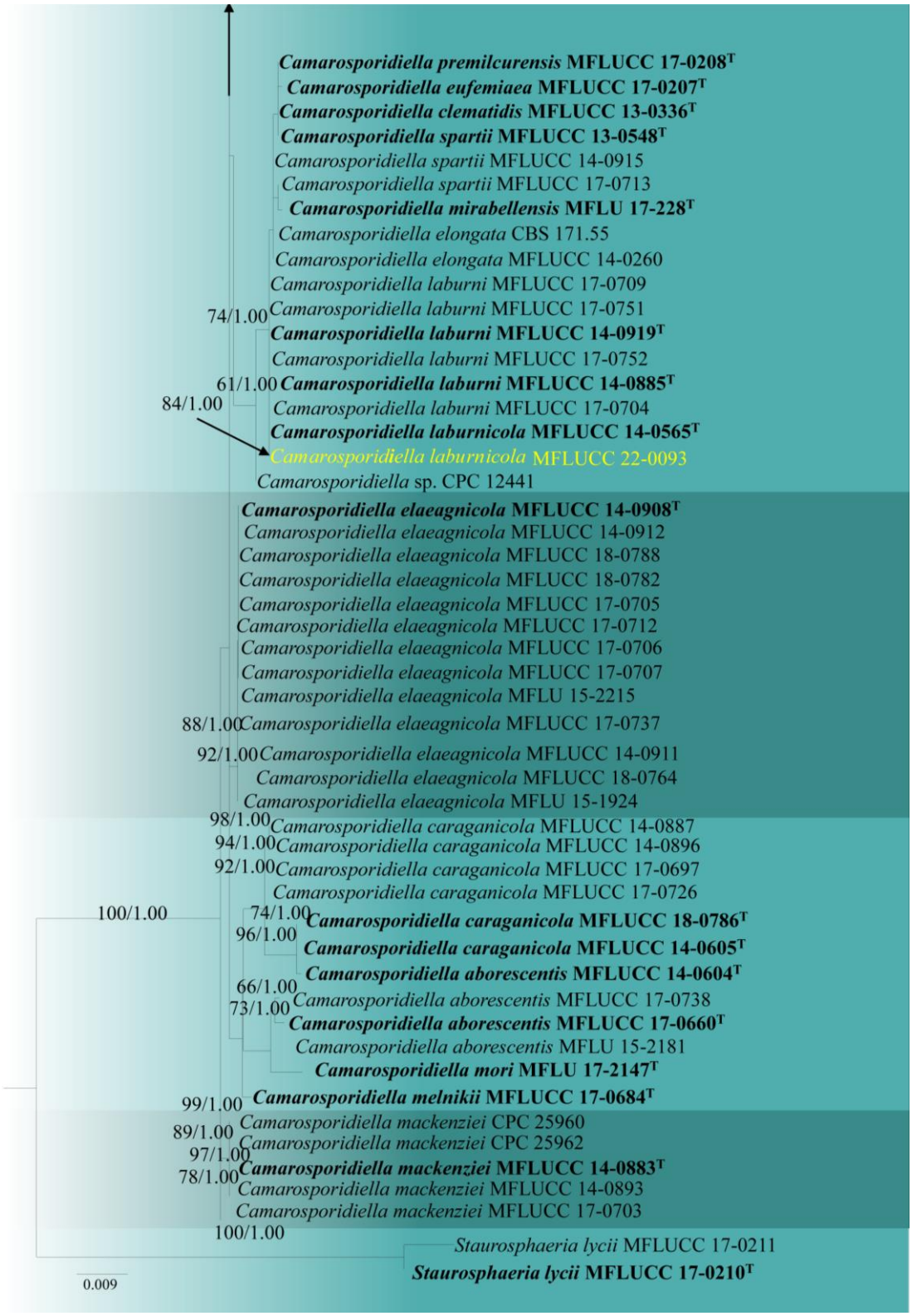


**Fig. 9 –** Continued.

***Camarosporidiella laburnicola*** (R.H. Perera, Bulgakov & K.D. Hyde) Wanas. & K.D. Hyde, in Wanasinghe et al., Studies in Mycology 87, 234 (2017)

Index Fungorum number: IF 821953; Facesoffungi number: FoF 2784; Fig. 10

*Saprobic* on branches of *Laburnum anagyroides*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* 300−350 µm diam., 210−300 µm high, pycnidial, solitary, scattered or grouped, semi-immersed to erumpent, globose, carbonaceous, black, with a papillate ostiole. *Conidiomatal wall* not observed. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, with percurrent annellations, doliiform, hyaline, smooth-walled, formed from the innermost layer of the conidiomatal wall. *Conidia* 13−15 × 5−7 µm ($\bar{x}$ = 14.1 × 6.4 µm, n = 20), oblong, ellipsoidal, straight to slightly curved, at first hyaline turning pale to dark brown at maturity, smooth-walled, rounded at both ends, muriform, 1–3-transversely septate and 1–2 vertical septa.

Culture characteristics – Colonies on MEA reaching 35–45 mm diam. in 4 weeks, powdery white to pinkish grey, spreading with moderate aerial mycelium, slightly irregular, margins smooth, with underneath pinkish grey.

Material examined – Italy, Lago Pontini - Bagno di Romagna, Forlì-Cesena, dead branches of *Laburnum anagyroides*, 3 November 2018, E. Camporesi, (MFLU 18-2630); living culture MFLUCC 22-0093).

GenBank accession numbers – LSU: OP680988, ITS: OP680989.

Known distribution (based on molecular data) – Italy (this study), Russia (Tibpromma et al. 2017).

Known hosts (based on molecular data) – *Laburnum anagyroides* (Tibpromma et al. 2017, this study).

Notes – The sexual morph of *Camarosporidiella laburnicola* was introduced from *Laburnum anagyroides* in Russia (Tibpromma et al. 2017). This study recovered an isolate (MFLUCC 22-0093) from branches of *L. anagyroides* in Italy. This new isolate shares a close phylogenetic affinity to *C. laburnicola* (MFLUCC 14-0565) in our combined LSU and ITS sequence analyses. Our species is characterized by an asexual morph (Fig. 10) and cannot be compared with *C. laburnicola* (MFLUCC 14-0565), which has a sexual morph. A pairwise alignment of the ITS sequence of *C. laburnicola* (MFLU 15-1522) to that of our strain (MFLUCC 22-0093) revealed zero base pair differences. Therefore, we provide the first asexual morph report of *C. laburnicola* and a new geographical record for Italy.

***Corynesporascaceae*** Sivan., Mycol. Res. 100(7), 786 (1996)

Facesoffungi number: FoF 12737

***Corynespora*** Güssow, J. Royal Agric. Soc. England 65, 272 (1905) [1904]

Facesoffungi number: FoF 06663

*Corynesporascaceae*, established by Sivanesan (1996) based on *Corynesporasca*, was accepted in *Pleosporales* by Hyde et al. (2013). The family comprises two genera, *Corynesporasca* and *Corynespora* (Voglmayr & Jaklitsch 2017). *Corynespora* was established by Güssow (1906) to accommodate *Corynespora melonis* (= *Cercospora melonis*). The genus is pathogenic on several agricultural crops (i.e., cotton, papaya, pepper, roselle, rubber, and tomato) worldwide, causing leaf and fruit spots (Kwon et al. 2001, Fulmer et al. 2012, Conner et al. 2013, Salunkhe et al. 2019, Kumar & Singh 2021). In addition, *Corynespora* exhibits saprobic and endophytic nutritional modes (Scomparin et al. 2012, Kumar & Singh 2016). The genus has also been discovered in air, lower plants, lichens and soil in terrestrial environments and aquatic habitats (Hyde et al. 2020c, Kumar & Singh 2021). The updated phylogeny for the genus is provided in Fig. 11.

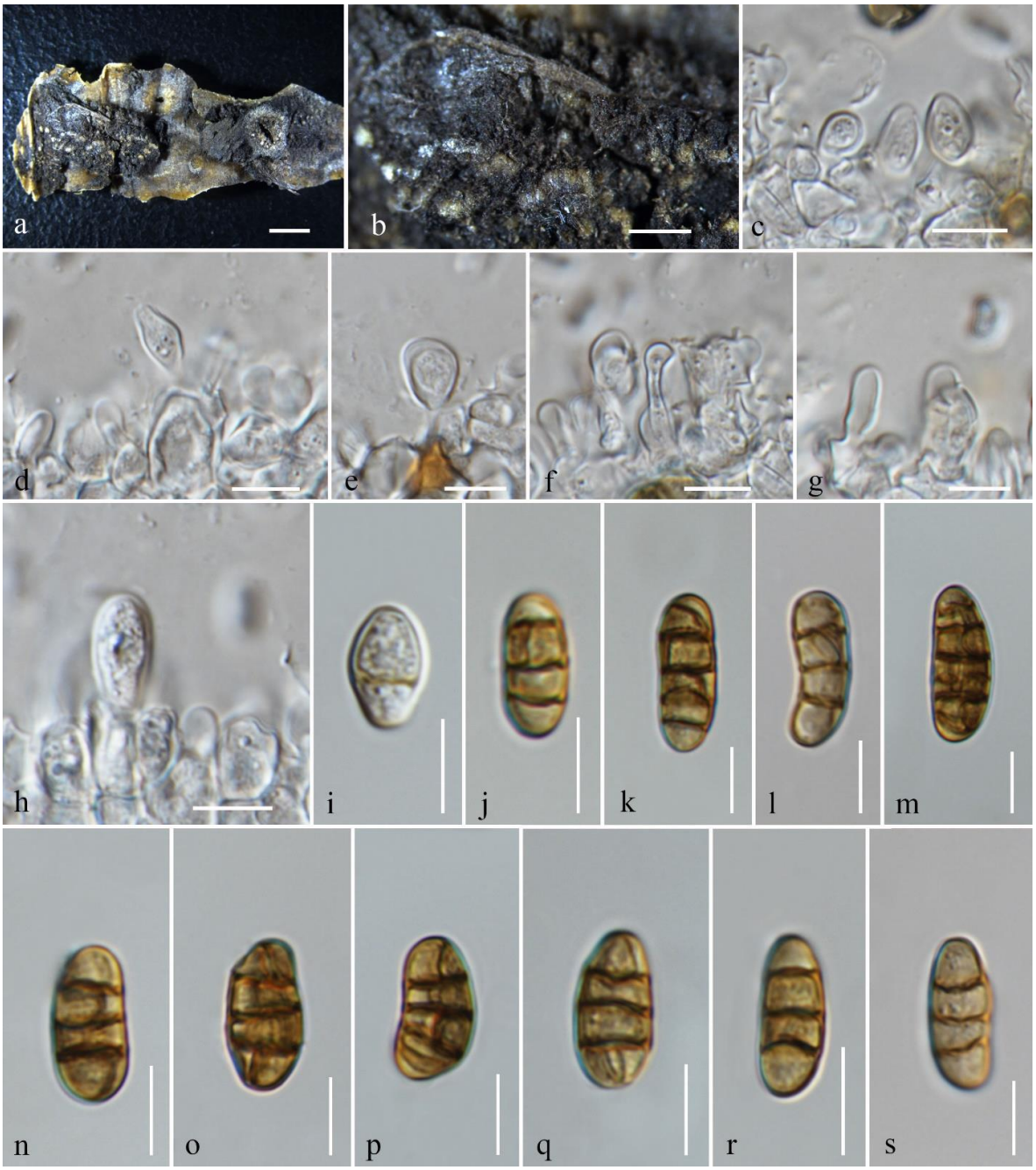


**Fig. 10 – *Camarosporidiella laburnicola*** (MFLU 18-2630, **a new geographical record**). a, b Conidiomata on host surface. c–h Conidiogenous cells and developing conidia. i–s Conidia. Scale bars: a = 2000 µm, b = 1000 µm, c–s = 10 µm.

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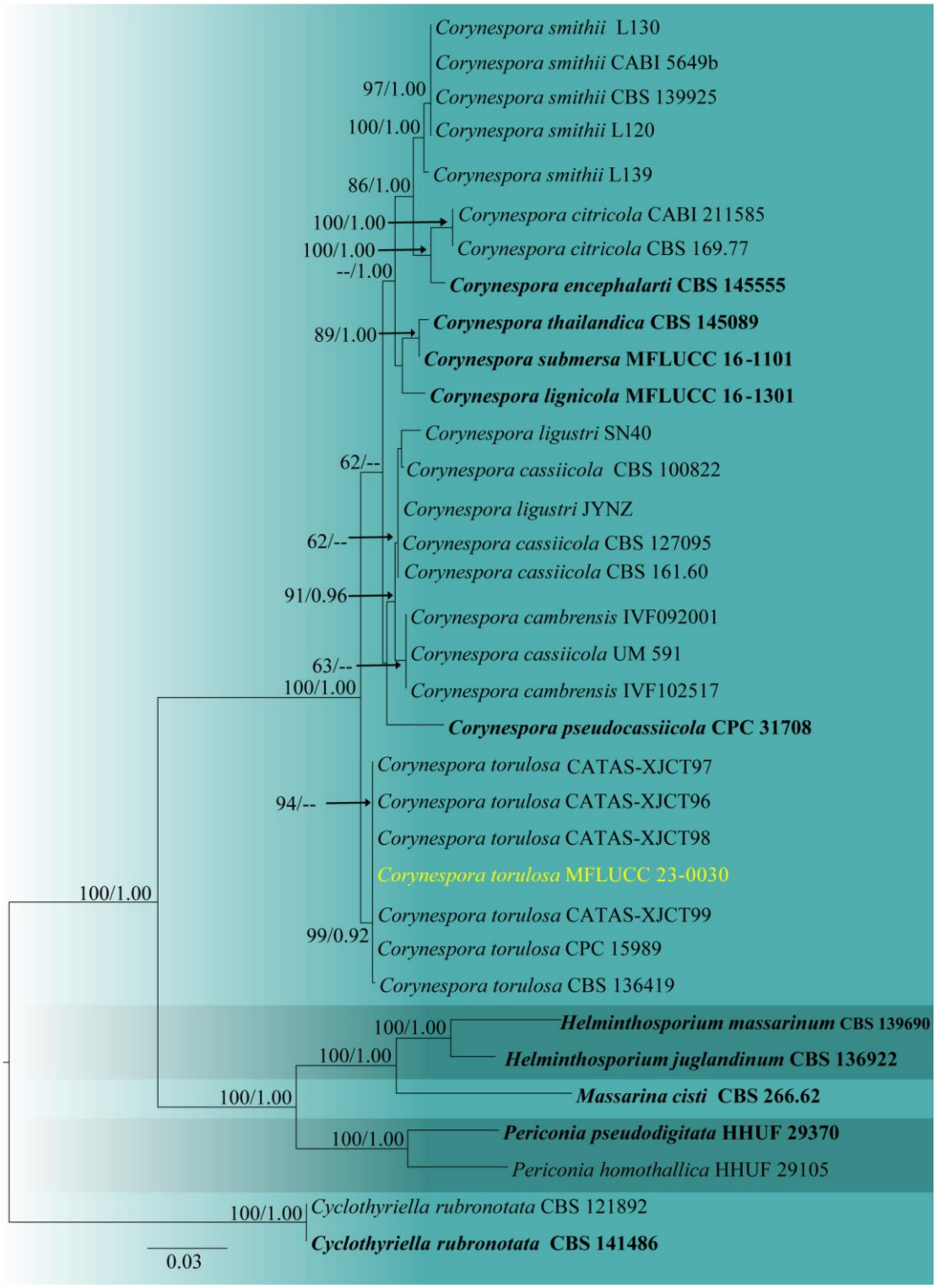


**Fig. 11 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data for selected taxa in *Pleosporales*. Thirty-five strains are included in the combined analyses which comprised 1366 characters (808 characters for LSU and 458 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -21969.93 is presented. The matrix had 1136 distinct alignment patterns, with 35.79% of undetermined characters or gaps. The evolutionary model GTR+I+G applied to both ITS and LSU regions. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree is rooted with *Cyclothyriella rubronotata* (CBS 141486 and CBS 121892). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Corynespora torulosa*** (Syd. & P. Syd.) Crous, Persoonia 31: 211 (2013)

Index Fungorum number: IF 805829; Facesoffungi number: FoF 14164; Fig. 12

*Saprobic* on dead leaves of *Musa* sp. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* effuse, grey, brown or black, often hairy. *Mycelium* immersed, occasionally superficial. *Stroma* none. *Setae* and *hyphopodia* absent. *Conidiophores* erect from the mycelium, 110–220 µm × 1–14 µm ($\overline{x}$ = 137.5 × 9.8 µm, n = 30), 9–12 µm wide at the base, 1–3 µm near the apex, arising singly, simple, torsive, straight or flexuous, unbranched, pale brown to dark brown, septate, 4–5 thin flange tissue parts appearing as wings on the surface. *Conidiogenous cells* monoblastic, integrated, terminal, percurrent, doliiform, collarette, producing hyaline spherical immature conidia at terminal end. *Conidia* 60–80 µm × 10–17 µm ($\overline{x}$ = 65.2 × 12.5 µm, n = 50), with blackish brown scar at the base, formed singly, cylindrical, straight or slightly curved, tapering towards rounded apex, mid brown or golden brown, smooth or verruculose, aseptate or 1–multi transverse pseudosepta, thin flange tissue part attached to the surface of the conidia like a wing at the apex of some conidia.

Culture Characteristics – Colonies on PDA at 25° C and under light reach 5 cm diameter in 6 days, initially greyish white, mouse grey or white and becoming brownish black at maturity. Filamentous, or rhizoid form, raised. Margin entire, lobate or ciliate

Material examined – Thailand, Chiang Rai Province, Nang Lae, on a dead banana leaf, 20 March 2019, Binu C. Samarakoon, BNS213 (MFLU 17-1773), living culture MFLUCC 23-0030.

GenBank accession numbers – LSU: OQ947166, ITS: OQ947171.

Known distribution (based on molecular data) – Cosmopolitan distribution (Kumar & Singh 2021).

Known hosts (based on molecular data) – *Costus comosus*, *Heliconia bihai*, *Ravenala madagascariensis*, *Musa* spp. (Kumar & Singh 2021).

Notes – *Corynespora torulosa*, previously known as *Deightoniella torulosa* (= *Brachysporium torulosum*), was accommodated in the *Corynesporascaceae* by Crous et al. (2013) based on molecular data. The fungus has been reported to cause black leaf spots on banana leaves in Georgia, India, Jamaica, and Thailand (Meredith 1962, Koné et al. 2008). In addition, *C. torulosa* was reported to cause fruit speckles on banana fruits at the pre-harvest stage in Jamaica and Cuba (Meredith 1962, Almenares & Pérez-Vicente 2019). *Corynespora torulosa* also has saprobic and endophytic nutritional modes discovered in terrestrial habitats (Meredith 1962, Photita et al. 2001). In the multi-gene phylogeny (LSU and ITS), our isolates grouped with *C. torulosa* isolates with CATAS-XJCT97, CATAS-XJCT98 and CATAS-XJCT99 (Fig. 11). Our strain (Fig. 12) is similar in morphology to the illustration of Ellis (1971). Based on morphology and solid molecular justifications, we document the occurrence of *Corynespora torulosa* associated with *Musa* sp. as a saprobe from Thailand.

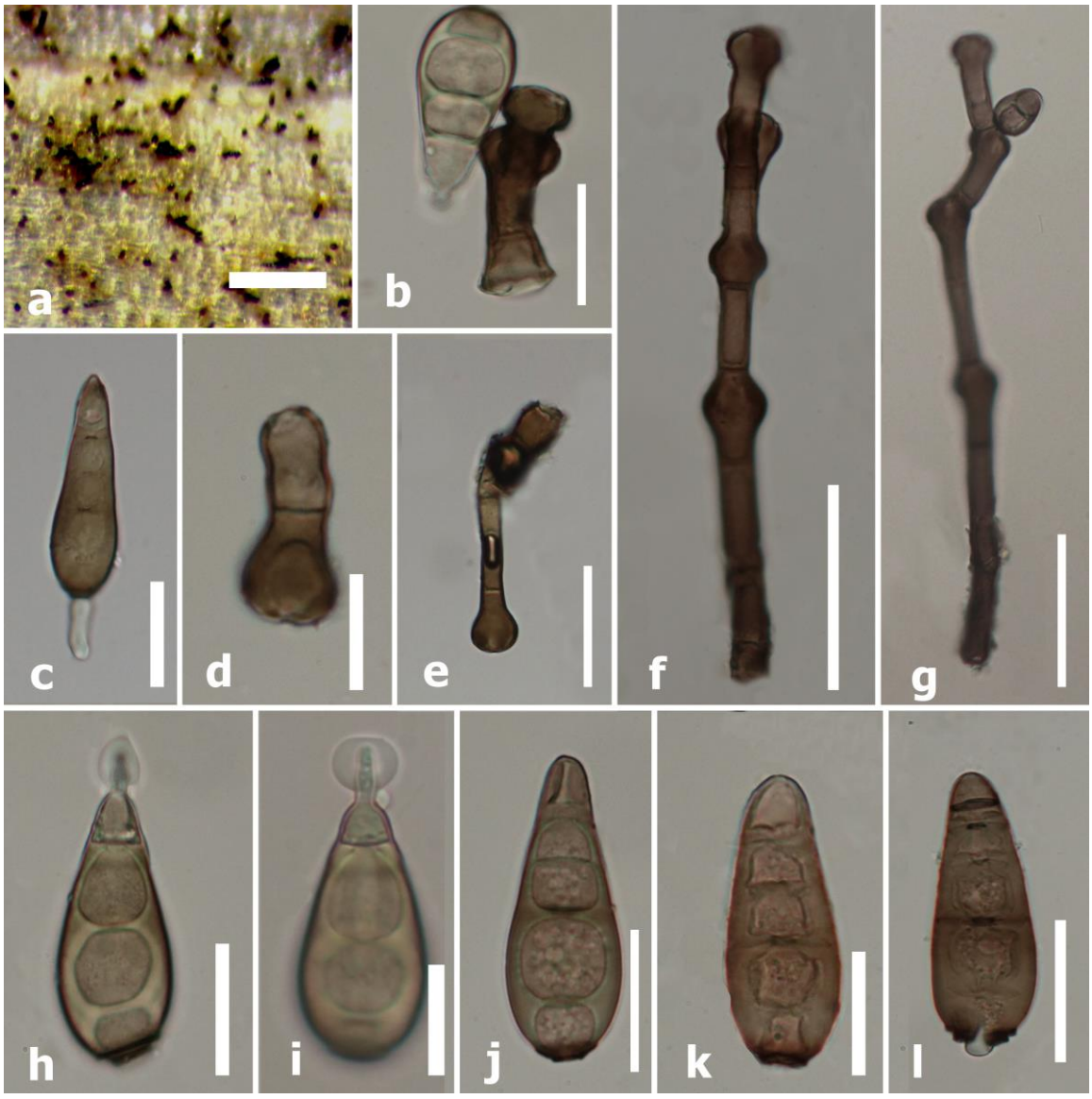


**Fig. 12 – *Corynespora torulosa*** (MFLU 17-1773, **new saprobic collection**). a Colonies on host. b, d, e, f Conidiophores and conidia. g Attachment of conidia. c, h–l Conidia. Scale bars: a = 100 μm, f, g = 30 μm, b, d, e = 15 μm, c, h–l = 20 μm.

***Didymosphaeriaceae*** Munk, Dansk botanisk Arkiv 15, 128 (1953)

Facesoffungi number: FoF 00200

***Pseudopithomyces*** Ariyaw. & K. D. Hyde, in Ariyawansa et al., Fungal Diversity 75, 27–274 (2015)

Facesoffungi number: FoF 00937

*Pseudopithomyces*, introduced by Ariyawansa et al. (2015), is usually associated with dead plant debris. To date, 13 epithets are listed in Index Fungorum (2023). Members of this genus comprise endophytes, saprobes, and pathogens (Promputtha et al. 2007, Duplessis et al. 2011, Stauber et al. 2020). We provided the updated phylogeny for the genus *Pseudopithomyces* in Fig. 13.

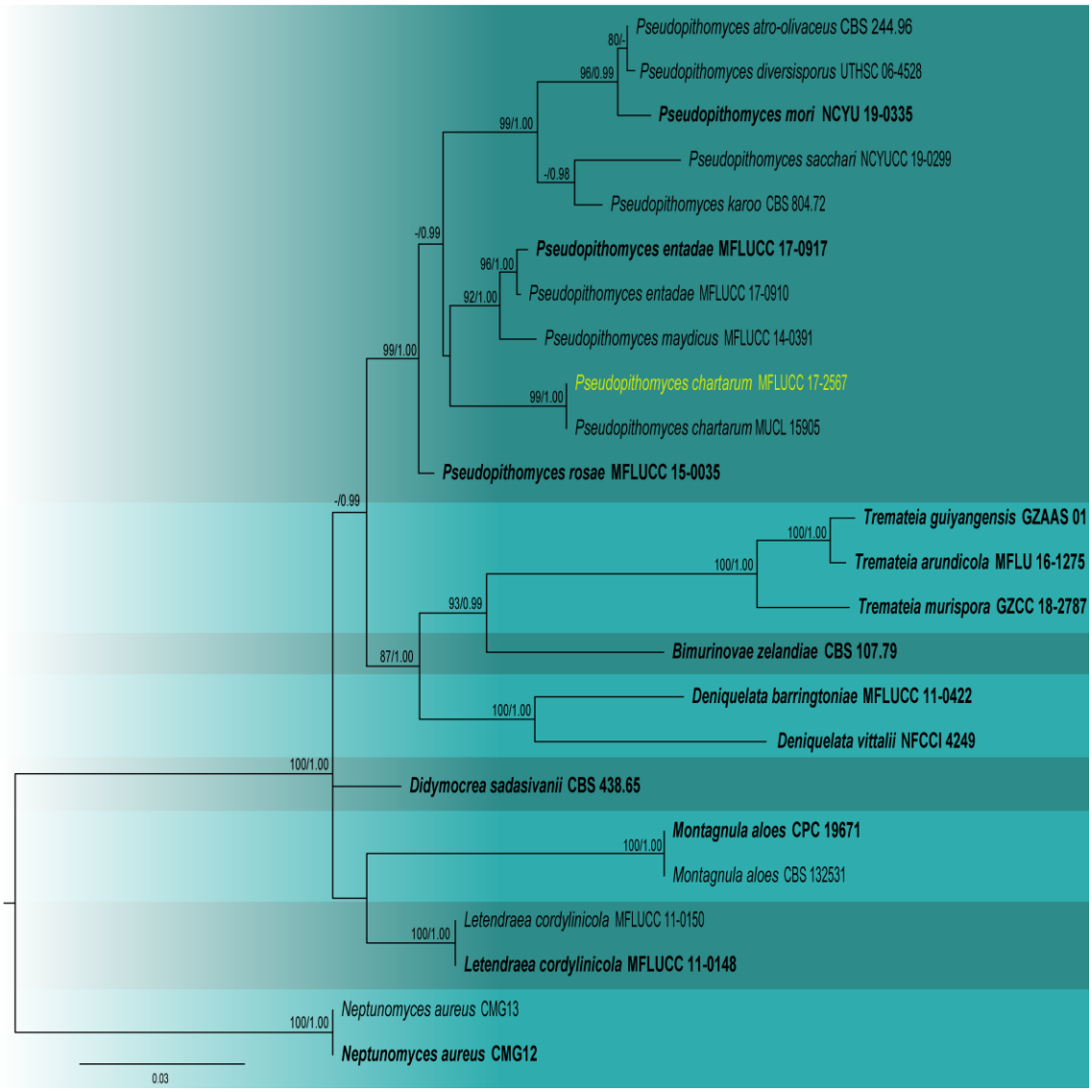


**Fig. 13 –** Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *tef1-α* sequence data for the genus *Pseudopithomyces* and related taxa. Twenty-four strains are included in the combined analyses which comprised 2972 characters (916 characters for SSU, 730 characters for LSU, 400 characters for ITS and 914 characters for *tef1-α*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -14172.708958 is presented. The matrix had 450 distinct alignment patterns, with 34.59% of undetermined characters or gaps. The evolutionary model SYM+I+G applied to LSU sequence data, while GTR+I+G applied to ITS, SSU and *tef1-α* gene regions. Bootstrap support values for ML equal to or greater than 80% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Neptunomyces aureus* (CMG 12, CMG 13). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Pseudopithomyces chartarum*** (Berk. & M. A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Diversity 75, 27–274 (2015)

Index Fungorum number: IF 551393; Facesoffungi number: FoF 00938; Fig. 14

*Saprobic* on the leaves of *Musa* sp. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* scattered, powdery, dark brown to black, effuse. *Vegetative hyphae* hyaline to pale brown, septate, branched. *Conidiophores* 7–10 µm × 4–5 µm ($\overline{x}$ = 9 × 4.5 µm, n = 20), micronematous, mononematous, hyaline, unbranched, septate or aseptate, thin-walled, with

globular base and a truncated apex. *Conidiogenous cells* 5–8 µm × 3–5 µm ($\overline{x}$ = 7.8 × 4.6 µm, n = 20), terminal, hyaline, globose or subglobose, integrated, hyaline. *Conidia* 18–25 µm × 10–15 µm ($\overline{x}$ = 19.5 × 12 µm, n = 20), subglobose, initially light brown, becoming brown to dark brown at maturity, 3–4 transverse septa, 1–3 longitudinal septa, darken and slightly constricted at the septa, verruculose, thick-walled.

Culture characteristics – Colonies on PDA, reaching 5 cm diam. at 14 days at room temperature (25–30 ℃), superficial, cottony, pinkish white, radially striate with a regular edge.

Material examined – Thailand, Chiang Rai Province, Rattana Dormitory, dead leaf of *Musa* sp., 20 May 2020, Binu C. Samarakoon, BNS246 (MFLU 19-0408), living cultures MFLUCC 17-2567.

GenBank accession numbers – ITS: OR186205, LSU: OR186208, *tef 1-α*: OR195686.

Known distribution (based on molecular data) – worldwide (Lumyong et al. 2003, Ariyawansa et al. 2015)

Known hosts (based on molecular data) – dead leaf of *Musa* sp. (Lumyong et al. 2003, Ariyawansa et al. 2015, this study)

Notes – Our isolate was identified as *Pseudopithomyces chartarum* based on the morphology and multi-gene phylogeny of combined SSU, LSU, ITS, and *tef 1-α.* In the multi-gene phylogeny, our isolate MFLUCC 17-2567 clustered with *Pseudopithomyces chartarum* with 99% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 13). However, our species shows similar morphological characters (Fig. 14) to the type species except for a few differences, such as the shapes and sizes of conidiophores and conidia (Ariyawansa et al. 2015). These changes may be due to environmental influences. Here, we provide a saprobic collection of *P. chartarum* from dead *Musa* sp. in Thailand.

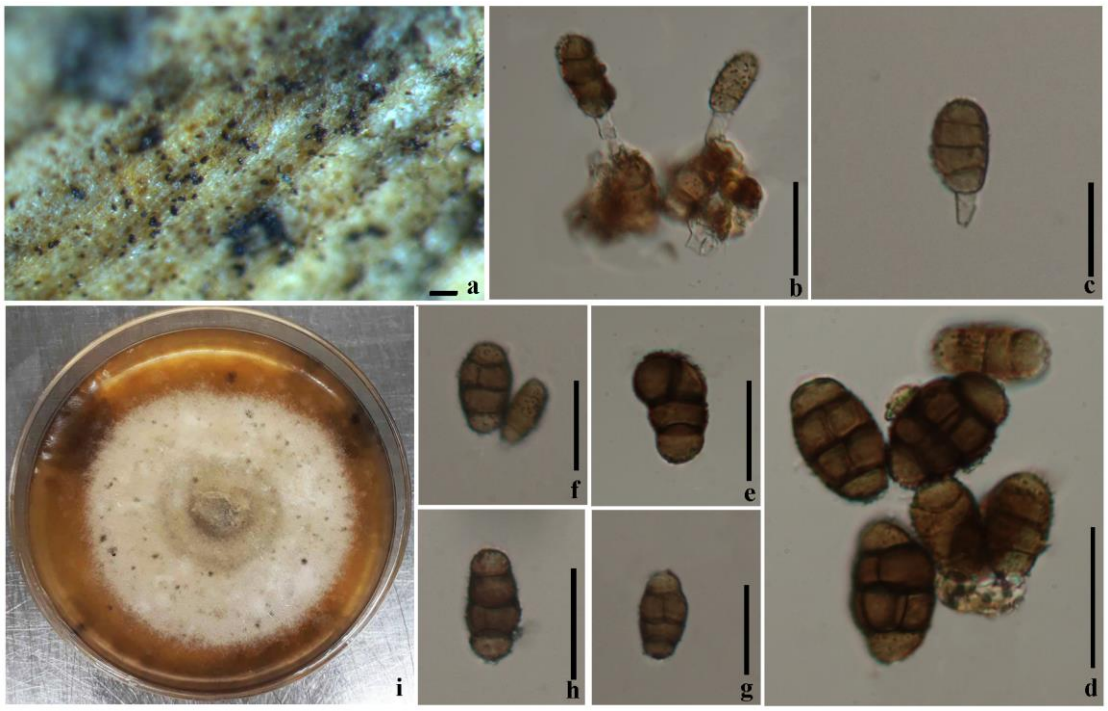


**Fig. 14 – *Pseudopithomyces chartarum*** (MFLU 19-0408, **a new saprobic collection**). a Colonies on dead banana leaf. b–c Conidiophores bearing conidia. d–h Conidia. i Colony on the PDA. Scale bars: a = 0.1 mm, b–g = 15 µm, h = 18 µm.

***Spegazzinia*** Sacc., Michelia 2, 37 (1880)

Facesoffungi number: FoF 08241

*Spegazzinia* was introduced by Saccardo (1880) with *Spegazzinia ornata* as the type species. Currently, there are 33 *Spegazzinia* taxa listed in Index Fungorum (2023). We provided the updated phylogeny for the genus *Spegazzinia* in Fig. 15.

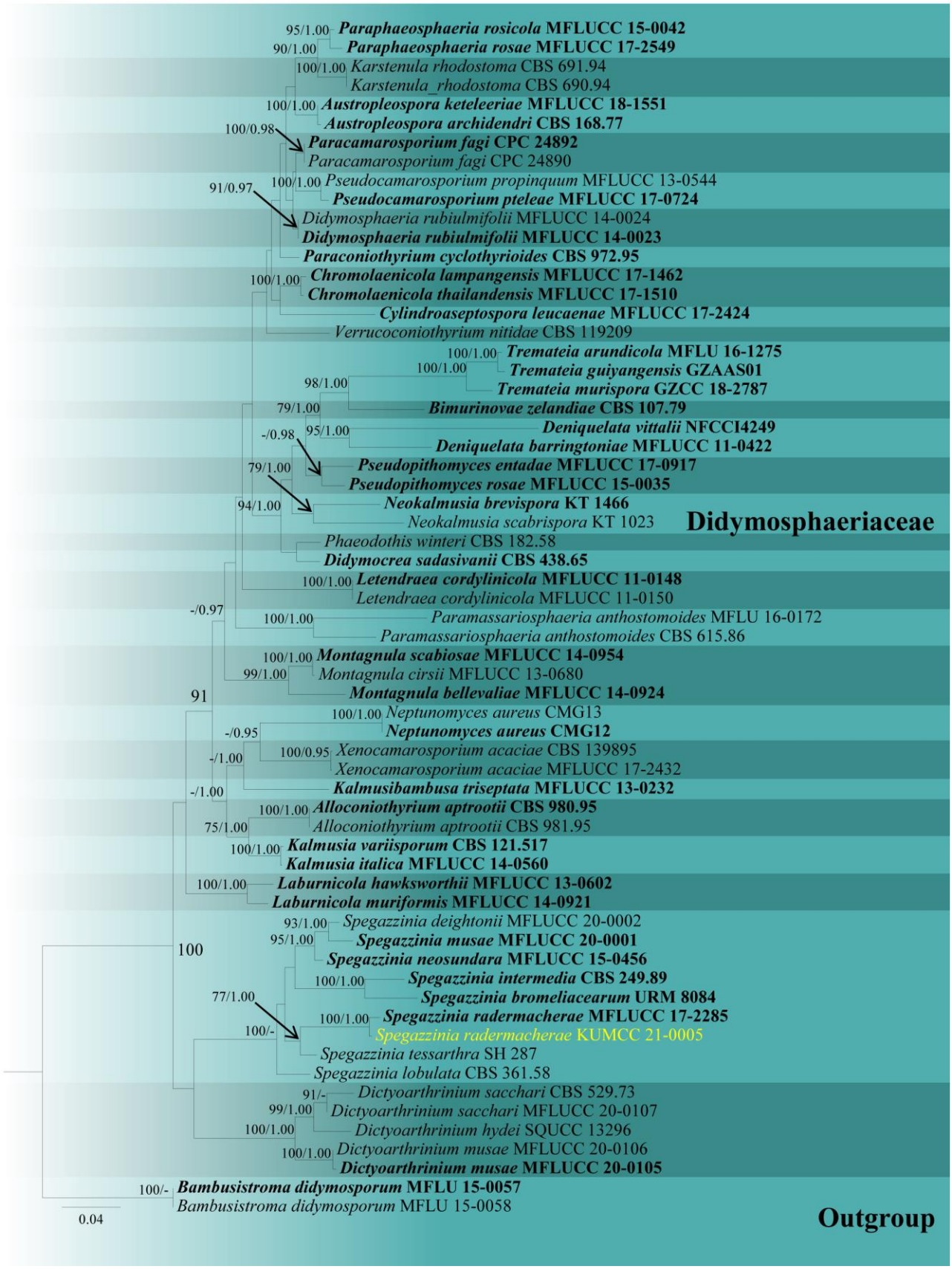


**Fig. 15 –** Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *tef1-α* sequence data. Sixty-three strains are included in the combined analyses which comprised 3512 characters (1010 characters for SSU, 855 characters for LSU, 734 characters for ITS and 913 characters for *tef1-α*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -

20142.962026 is presented. The matrix had 1179 distinct alignment patterns, with 34.45% of undetermined characters or gaps. The evolutionary model SYM+I+G applied to LSU sequence data, while GTR+I+G applied to ITS, SSU and *tef1-α* gene regions. Bootstrap support values for ML equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes respectively. The tree is rooted with *Bambusistroma didymosporum* (MFLU 15-0057, MFLU 15-0058). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Spegazzinia radermacherae*** Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10, 73 (2019)

Index Fungorum number: IF 555547; Facesoffungi number: FoF 05249; Fig. 16

*Saprobic* on dead woody plant. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Sporodochia* dark, dense, dry, powdery, velvety. *Conidiogenous mother cells* 4.5–5 × 4–4.5 μm ($\overline{x}$ = 4.8 × 4.5 μm, n = 10), subspherical, hyaline to light brown. *Conidiophores of α conidia* up to 90–104 × 2.5–3.5 μm ($\overline{x}$ = 95 × 3 μm, n = 10), erect or flexuous, unbranched, dark golden brown. *Conidiophores of β conidia* 7–11 × 3–4 μm ($\overline{x}$ = 10 × 3.5 μm, n = 10), short, erect, unbranched, subhyaline or light brown. *Conidia* of two kinds; *α-conidia* 15.5–18.5 × 14–18 μm ($\overline{x}$ = 17 × 16.5 μm, n = 40), 4-celled, brown to black brown, each cell globose to subglobose with conspicuous spines 2–2.5 μm. *β-conidia* 16.8–19.7 × 16.5–19.5 μm ($\overline{x}$ = 18.3 × 18.2 μm, n = 40), disc-shaped, 4-celled, initially pale brown, becoming brown to dark brown at maturity, crossed septate, smooth to verrucose.

Culture Characteristics – Colonies on PDA, reaching 20–30 mm diam. at 15 days at room temperature (25–30 ℃), superficial, circular, rough, moderately dense, flat, white, reverse pale yellow.

Material examined – China, Yunnan Province, Diqing Autonomous Prefecture, Xianggelila (27.28’8°N, 99.50’45°E), 2958 m, on a dead woody plant, 30 August 2020. Guang-Cong Ren, DQ06 (KUN-HKAS 122871), living culture KUMCC 21-0005.

GenBank accession numbers – LSU: OP002066, ITS: OP002065.

Known distribution (based on molecular data) – China, Yunnan Province (this study), Thailand, Chiang Rai Province (Jayasiri et al. 2019, Chethana et al. 2021a).

Known hosts (based on molecular data) – on a fallen pod of *Radermachera sinica* and dead leaf of *Musa* sp. (Jayasiri et al. 2019, Chethana et al. 2021a).

Notes – *Spegazzinia radermacherae* was introduced by Jayasiri et al. (2019) based on morphology and phylogenetic analyses from a fallen pod of *Radermachera sinica* (*Bignoniaceae*) in Thailand. Based on our phylogenetic analysis of combined SSU, LSU, ITS, and *tef1-α* sequence data, our collection (KUMCC 21-0005) clusters with the type species of *S. radermacherae* (MFLUCC 17-2285) with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 15). Our collection shares similar morphological features with *R. garethjonesii* (MFLUCC 17-2285) in having brown, 4-celled α-conidia and disc-shaped, 4-celled β-conidia (Fig. 16). However, our collection has bigger conidia than *S. radermacherae* (MFLUCC 17-2285). Based on morphological characteristics and phylogenetic analysis, we introduce KUMCC 21-0005 as a new geographical record of *S. radermacherae* from China.

***Lophiostomataceae*** Sacc, Sylloge Fungorum. 2, 672 (1883)

Facesoffungi number: FoF 00796

***Vaginatispora*** K.D. Hyde, Nova Hedwigia 61(1-2), 234 (1995)

Facesoffungi number: FoF 00828

*Vaginatispora* was introduced to accommodate *V. aquatica* as the type specie from a woody plant (Hyde et al. 2019). Initially, this genus, based on the characteristic “massarina-like” ascomata with much longer ostiolar necks and ascospores bearing an entire sheath, was placed in *Massarinaceae* (Hyde 1995). However, Liew et al. (2002) suggested synonymizing *Vaginatispora* under *Lophiostoma* based on ITS phylogeny. Later, *Vaginatispora* was considered a synonym of *Lophiostoma* due to its phylogenetic affinities to *Lophiostoma* (Zhang et al. 2014). Subsequently,

*Vaginatispora* was verified as a separate genus within *Lophiostomataceae* with morphological characteristics and multi-gene phylogeny analysis and also included *V. aquatica* and *V. fucklii* (Thambugala et al. 2015). *Vaginatispora* species are characterized by depressed globose ascomata, immersed, with a slot-like ostiole, numerous filamentous pseudoparaphyses, asci cylindrical to clavate and ellipsoidal, hyaline, 1-septate ascospores, with a mucilaginous collar around its equator, having single large gutless in each cell, and a spreading papilionaceous sheath (Thambugala et al. 2015, Wanasinghe et al. 2017, Hashimoto et al. 2018, Hyde et al. 2020a). Eight species are accepted in this genus (Wijayawardene et al. 2022). An updated phylogeny is provided in Fig. 17.

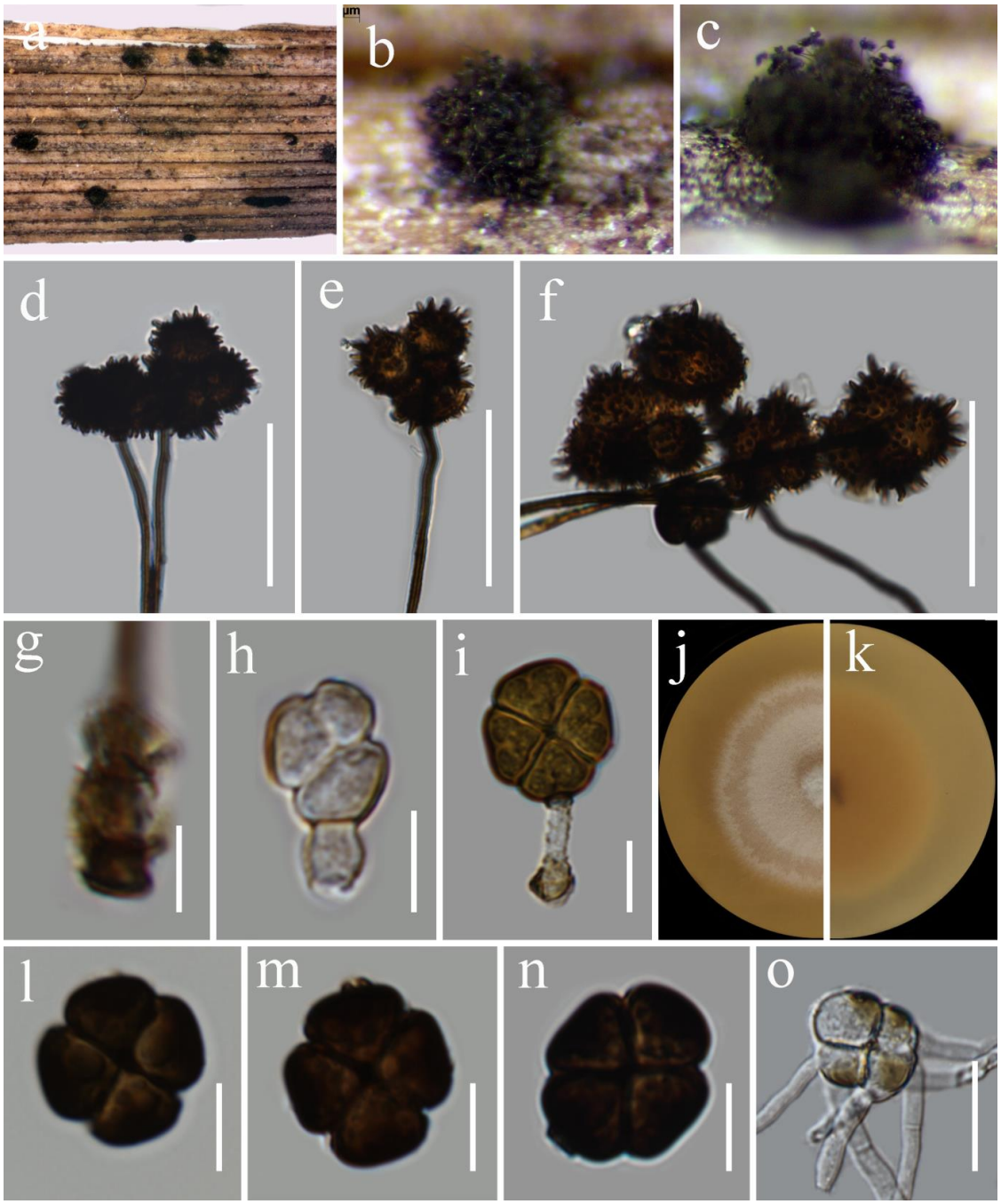


**Fig. 16 – *Spegazzinia radermacherae*** (KUN-HKAS 21-0005, **a new geographical record**). a–c Fungal colonies on host surface. d–f α-conidia. g Conidiophore mother cell of α-conidia. h, i Developmental stages of β-conidia. j, k Colonies on PDA showing sporulation after 15 days. l–n β-conidia. o Germinated conidium. Scale bars: d–f = 50 µm, g–i, l–n = 10 µm, o = 30 µm.

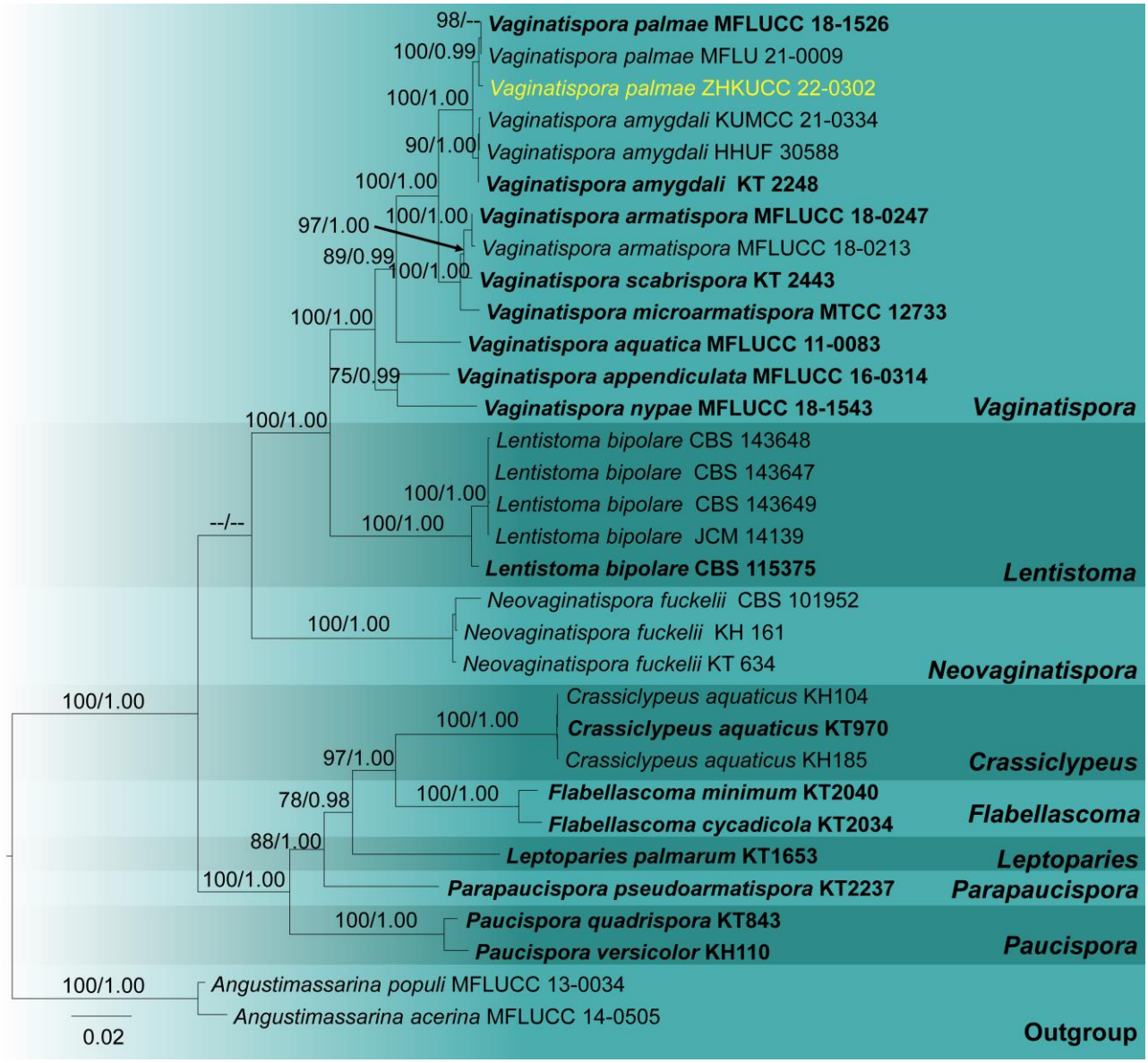


**Fig. 17 –** Phylogram generated from maximum likelihood analysis based on the combined ITS, LSU, SSU, *tef1-α* and *rpb2* sequence data of the genus *Vaginatispora*. Thirty-two isolates are included in the combined analyses which comprised 4575 characters (806 characters for ITS, 853 characters for LSU, 986 characters for SSU, 901 characters for *tef1-α* and 1029 characters for *rpb2*). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -16632.948483 is presented. The matrix had 1094 distinct alignment patterns, with 22.27% of undetermined characters or gaps. The GTR+G evolutionary model was applied to all the genes. Bootstrap support values for ML greater than or equal to 75% and Bayesian posterior probabilities greater than or equal to 0.95 are given near the nodes, respectively. The tree was rooted with *Angustimassarina populi* (MFLUCC 13-0034) and *Angustimassarina acerina* (MFLUCC 14-0505). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Vaginatispora palmae*** S.N. Zhang, J.K. Liu & K.D. Hyde, Fungal Diversity 96, 242 (2019)

Index Fungorum number: IF 556316; Facesoffungi number: FoF 15187; Fig. 18.

*Saprobic* immersed on the dead trunk of *Litchi chinensis*. **Sexual morph**: *Ascomata* 170–270 × 220–400 µm ($\bar{x}$ = 215 × 330 µm, n = 10), semi-immersed, solitary or group, globose to subglobose, dark brown to black, mastoid on top, carbonaceous, ostiolate. *Ostiole* central, narrow bottle pore-like opening, filled with a gelatinous substance, dark brown to black, thick-walled cells. *Peridium* 15–90 µm wide ($\bar{x}$ = 47 µm, n = 25), think-walled, consists of 3–6 strata of slightly flattened *textura angularis* cells, inner layer hyaline, outer layer light brown to dark brown, thick-walled cells fused with host tissue. *Hamathecium* 2–4 µm wide ($\bar{x}$ = 3 µm, n = 40), dense, broadly filiform, septate, thin-walled, smooth-walled, rather branched, pseudoparaphyses. *Asci* 60–130 × 10–20 µm ($\bar{x}$ = 91 × 15 µm, n = 15), 8-spored, bitunicate, cylindrical to clavate, smooth-walled, rounded apex, with an ocular chamber and a bulbous, short pedicel. *Ascospores* 25–30 × 5–10 µm ($\bar{x}$ = 28 × 8 µm, n = 50), overlapping biseriate, hyaline, fusiform, smooth-walled, 1-septate, slightly constricted at the middle septum, broad in the middle, tapering at both ends, apex slightly pointed or obtusely rounded, surrounded by a narrow mucilaginous sheath, with 5–10 µm long, tapering appendages, and mature ascospores with distinct oil droplets. **Asexual morph**: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 hrs. Colonies on PDA reached a 20 mm diameter after two weeks at 25 °C, circular, rough surface, dense hyphae, slightly raised, extending radially outwards, surface view olivaceous brown at the middle, light olivaceous at the margins, reverse view olivaceous to dark brown at the middle, light olivaceous at the margins.

Material examined – China, Guangdong Province, Guangzhou City, Zengcheng District, on the dead trunk of *Litchi chinensis* (23.253964 N, 113.829763 E, 22 m), 21 September 2021, Y. H. Yang, ZGLZ030 (MHZU 22-0162), living culture ZHKUCC 22-0302.

GenBank accession numbers – ITS: OP735537, LSU: OP735541, SSU: OP735559, *tef1-α*: OQ749733, *rpb2*: OQ749734.

Known distribution (based on molecular data) – Thailand (Ranong: Hyde et al. 2019), China (Taiwan: Rathnayaka et al. 2021, Guangdong: this study).

Known hosts (based on molecular data) – *Nypa fruticans* (Hyde et al. 2019), *Swietenia macrophylla* (Rathnayaka et al. 2021), *Litchi chinensis* (this study).

Notes – In the phylogenetic analysis of the combined ITS, LSU, SSU, *tef1-α* and *rpb2* sequence data, our new isolate (ZHKUCC 22-0302) clustered with *V. palmae* as a monophyletic affiliate with 99% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 17). Except for the thicker peridium (15–90 µm *vs*. 15–38 µm) and longer asci (60–130 µm *vs*. 89–115), our collection (Fig. 18) resembles the morphology of the holotype of *V. palmae* (MFLUCC 18-1526) (Hyde et al. 2019). Based on morphological and phylogenetic similarities, we described herein our new isolate (ZHKUCC 22-0302) as a new host record of *V. palmae*, inhabiting the dead trunks of *Litchi chinensis* in China.

***Nigrogranaceae*** Jaklitsch & Voglmayr, Studies in Mycology 85, 54 (2016)

Facesoffungi number: FoF 08317

***Nigrograna*** Gruyter, Verkley & Crous, in Gruyter, Woudenberg, Aveskamp, Verkley, Groenewald & Crous, Studies in Mycology 75, 31 (2012) [2013]

Facesoffungi number: FoF 08318

*Nigrograna* was introduced by De Gruyter et al. (2013) to accommodate the type species *Nigrograna mackinnonii* (Borelli) Gruyter, Verkley & Crous. Currently, the genus includes 18 *Nigrograna* species that are saprobes and endophytes (Tibpromma et al. 2017, Wanasinghe et al. 2020, Zhang et al. 2020). We provide the updated phylogeny for the genus *Nigrograna* in Fig. 19.

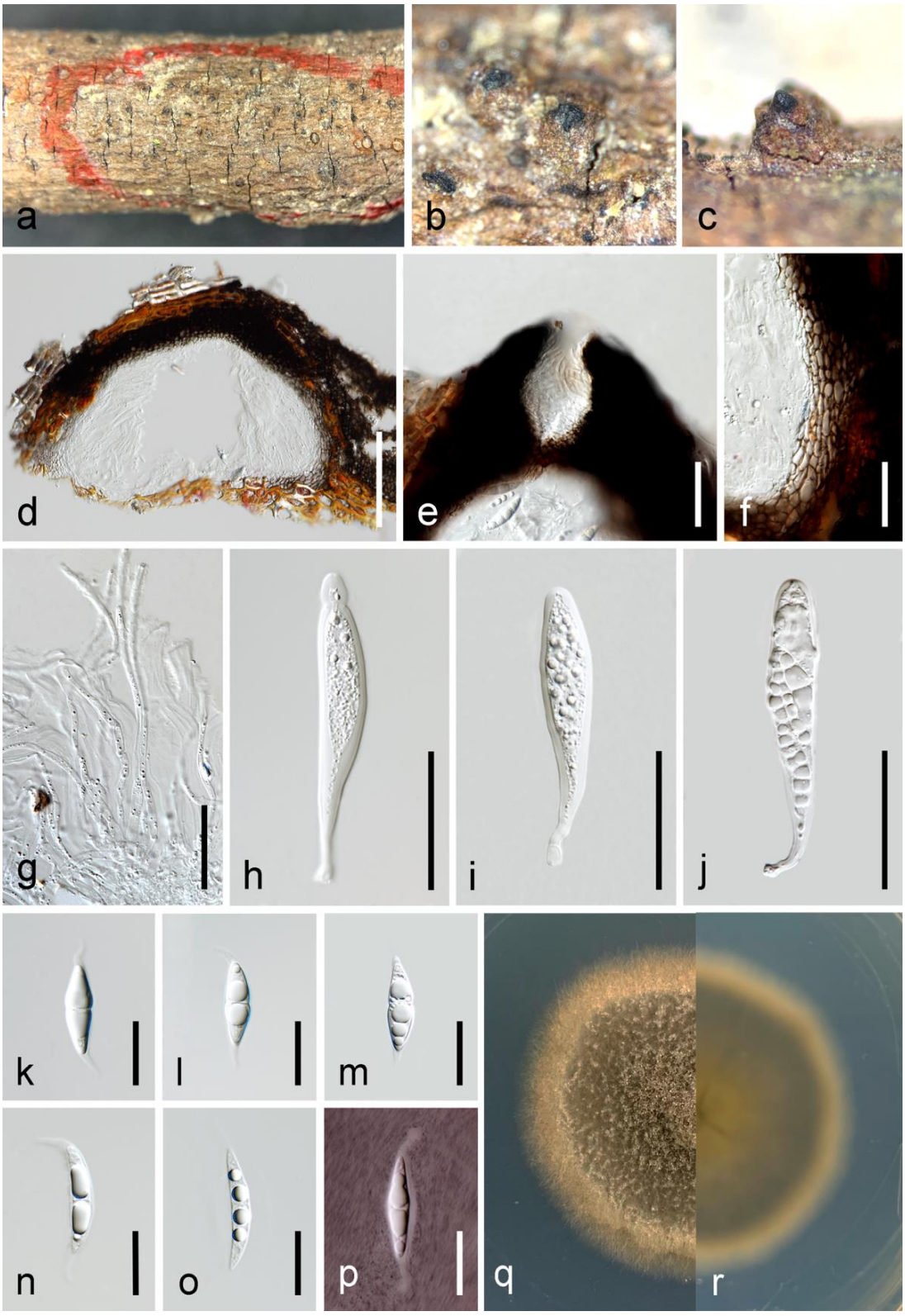


**Fig. 18 – *Vaginatispora palmae*** (MHZU 22-0162, **a new host record**). a–c Ascomata on the host substrate. d Vertical section of an ascoma. e Prolonged neck. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Ascospore stained with Indian Ink. q, r Upper (q) and reverse view (r) of the colony on PDA. Scale bars: d = 100 µm, e, f, h–j = 50 µm, k–p = 20 µm, g = 30 µm.

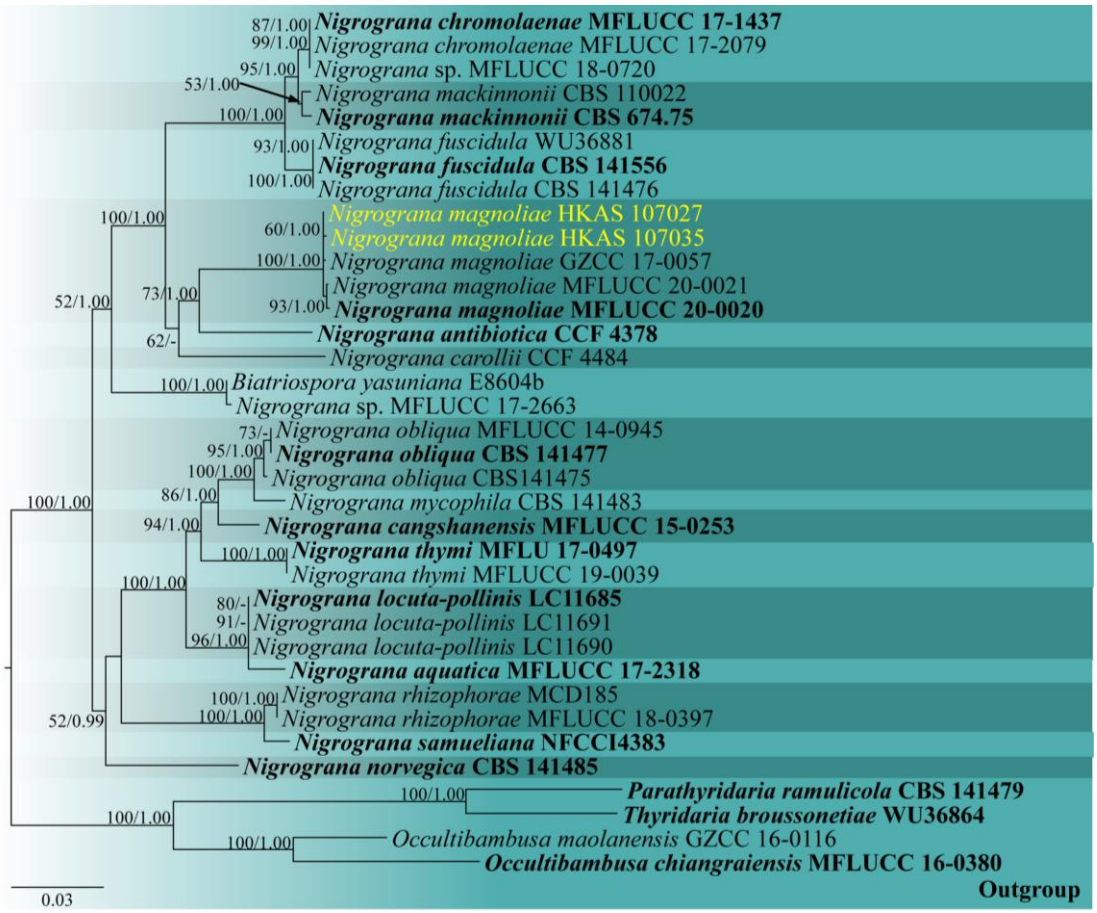


**Fig. 19 –** Phylogram generated from maximum likelihood analysis based on the combined LSU, SSU, *tef1*-α, and *rpb2* sequence data of the genus *Nigrograna*. Thirty-six isolates are included in the combined analyses which comprised 3799 characters (833 characters for LSU, 1023 characters for SSU, 933 characters for *tef1*-α and 1010 characters for *rpb2*). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -14937.288660 is presented. The matrix had 951 distinct alignment patterns, with 25.69% of undetermined characters or gaps. The GTR+G+I evolutionary model was applied for all the genes. Bootstrap support values for ML equal to or greater than 50% and Bayesian posterior probabilities equal to or greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Occultibambusa chiangraiensis* (MFLU 16-0380), *O. maolanensis* (GZCC 16-0116), *Parathyridaria ramulicola* (CBS 141479) and *Thyridaria broussonetiae* (WU36864). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Nigrograna magnoliae*** Wanas., in Wanasinghe, Wijayawardene, Xu, Cheewangkoon & Mortimer, PLoS ONE 15(7, e0235855), 10 (2020)

Index Fungorum number: IF 557331; Facesoffungi number: FoF 09092; Fig. 20

*Saprobic* on dead branches of *Michelia alba*, *Rosa* sp. and fungal fruiting bodies of *Shearia* sp. **Sexual morph:** *Ascomata* 220–365 × 190–285 µm ($\bar{x}$ = 289 × 249 µm, n = 8), perithecioid, singly gregarious, immersed in bark or fungal fruiting bodies, sometimes erumpent, subglobose or ellipsoidal, black, with an ostiole, cylindrical neck. *Ostiole* mostly central, brittle. *Peridium* 15–22 µm ($\bar{x}$ = 18.7 µm, n = 10) wide, 3–4-layered, composed of *textura angularis* cells, outer layer, dark brown, thick-walled, large cells, often surrounded by an olivaceous to dark brown subiculum, middle and inner layers, pale brown, thin-walled small cells. *Hamathecium* composed of 1.5–2.7 µm ($\bar{x}$ = 2.3 µm, n = 25) wide, numerous, tapering distally pseudoparaphyses, rarely trabeculate pseudoparaphyses. *Asci* 70–86 ×8.5–10.5 µm ($\bar{x}$ = 78 × 9.5 µm, n = 20), bitunicate, fissitunicate, 8-spored, clavate to cylindric-clavate, short pedicellate, apically rounded, sometimes with an ocular

chamber. *Ascospores* 13.5–18.5 × 4.4–6.5 µm ($\bar{x}$ = 15.8 × 5.6 µm, n = 25), biseriate, fusoid to clavate, yellowish brown to dark brown, 3-septate, apical cell often acute, second cell usually slightly widened, constricted at the medium, only slightly at other septa, straight or curved, terminal cells often slightly longer than mid cells. **Asexual morph:** Undetermined.

Materials examined – China, Guizhou, Guiyang, Guizhou Academy of Agricultural Sciences (GZAAS) premises, on dead branch of *Michelia alba*, and fruiting bodies of *Shearia* sp., 7 October 2019, MC Samarakoon SAMC266 (HKAS 107035); China, Sichuan, Chengdu, UESTC premises, on dead branch of *Rosa* sp., 30 September 2019, MC Samarakoon SAMC259 (HKAS 107027).

GenBank accession numbers – ITS: OM293747, LSU: OM293741, SSU: OM293752, *rpb2*: OM305055, *β-tubulin*: OM305065, *tef1-a*: OM305059 (HKAS 107035); ITS: OM293746, LSU: OM293740, SSU: OM293751, *β-tubulin*: OM305064, *tef1-a*: OM305058 (HKAS 107027).

Known distribution (based on molecular data) – China (Wanasinghe et al. 2020, Zhang et al. 2020, this study), Thailand (Zhang et al. 2020).

Known hosts (based on molecular data) – *Magnolia denudata* (Wanasinghe et al. 2020), *Michelia alba*, *Rosa* sp. and fruiting bodies of *Shearia* sp. (this study), and several unidentified hosts (Zhang et al. 2020).

Notes – Wanasinghe et al. (2020) discovered *Nigrograna magnoliae* with sexual and asexual morphs on living *Magnolia denudata* branches. Zhang et al. (2020) described two collections of *N. magnoliae* on decaying twigs of an unidentified host and submerged wood from China and Thailand, respectively. The size of the asci and ascospores of the type strain (MFLU 20–0092) overlaps with those of our new collections (asci: 60–100 × 8–12 µm *vs.* 70–86 × 8.5–10.5 µm and ascospores: 12–16 × 5–6.5 µm *vs.* 13.5–18.5 µm × 4.4–6.5 µm). Our new collections are morphologically and phylogenetically similar to *N. magnoliae* and are introduced as new records. Interestingly, we observed some ascomata of *N. magnoliae* immersed in conidiomata and ascomata of *Shearia* sp. (Fig. 20).

***Phaeoseptaceae*** S. Boonmee, Thambugala & K.D. Hyde, Mycosphere 9(2), 323 (2018)

Facesoffungi number: FoF 04462

***Phaeoseptum*** Ying Zhang, J. Fourn. & K.D. Hyde, in Zhang, Fournier, Phookamsak, Bahkali & Hyde, Mycologia 105(3), 606 (2013)

Facesoffungi number: FoF 08326

*Phaeoseptum*, introduced by Zhang et al. (2013) with *Phaeoseptum aquaticum* as the type species, generally occurs as saprobes in freshwater (Phukhamsakda et al. 2019, Hongsanan et al. 2020a, Jayawardena et al. 2023). The genus is characterized by immersed ascomata with bitunicate, 8-spored asci, and fusiform, slightly curved ascospores (Zhang et al. 2013). There are seven species listed in the Index Fungorum (2023), and all of them have been confirmed with molecular data. An updated phylogeny for *Phaeoseptum* is provided in Fig. 21.

***Phaeoseptum thailandicum*** Samarak. & K.D. Hyde in Jayawardena et al., Fungal Diversity 117, 45 (2023)

Index Fungorum number: IF 559754; Facesoffungi number: FoF 11798; Fig. 22

*Saprobic* on decaying branch of *Albizia lebbeck*. **Sexual morph:** *Ascomata* 300–320 × 225–245 µm ($\bar{x}$ = 310 × 227 µm, n = 5), immersed, dark brown to black, globose to oval, appearing as elongated regions on the host surface. *Peridium* 10–37 µm wide, thick-walled, wide at the apical portions with *textura prismatica* cell layers; inner layers pale brown and outer layers more pigmented outwardly, with cells fusing with host tissue. *Hamathecium* comprising 1–2 µm wide, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. *Asci* 82–128 × 15–20 µm ($\bar{x}$ = 97.4 × 17.7 µm, n = 20), 8-spored, bitunicate, club-like, apically rounded, thick-walled, with a short pedicel and a minute ocular chamber. *Ascospores* 24–30 × 7–10 µm ($\bar{x}$ = 27 × 9 mm, n = 20), overlapping uni- or biseriate, ellipsoid, hyaline when young, yellowish to brown at maturity, muriform, 11–13-transversely septate, biseriate, with a vertical septum in nearly all median cells, not constricted at the septa, the septa partly pale brown, having a

thickened and heavily pigmented appearance at maturity, smooth-walled, without a sheath. **Asexual morph:** Undetermined.

Culture characteristics – Colonies on PDA slow-growing, reaching 10 mm diameter after 15 days at 27 °C, from above dark brown to gray radiating outwards, wrinkled folded at the middle, dense, circular, flattened, umbonate, entire edge, fairly fluffy; reverse black in the middle and dark brown at the edges.

Material examined – Thailand, Chiang Rai Province, Mae Fah Luang University, dead branches of *Albizia lebbeck* (Fabaceae), 10 July 2022, ZL Tun 121 (MFLU 23-0260), living culture MFLUCC 23-0236.

GenBank accession numbers – LSU: OR349688, ITS: OR211590, *tef1-α*: OR270931.

Known distribution (based on molecular data) – Thailand (Nan Province: Jayawardena et al. 2023, Chiang Rai Province: this study).

Known hosts (based on molecular data) – unidentified dicotyledonous dead branch (Jayawardena et al. 2023) and *Albizia lebbeck* (this study).

Notes – The new isolate (MFLU 23-0260) formed a clade with *Phaeoseptum thailandicum* isolates with 88% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 21), and is morphologically similar to *Phaeoseptum thailandicum* (MFLU 19-2136) (Jayawardena et al. 2023). *Phaeoseptum thailandicum* was introduced from an unidentified dicotyledonous dead branch, while our new collection was collected from a branch of *Albizia lebbeck* in Thailand. Therefore, we introduce our isolate as a new host record of *Phaeoseptum thailandicum*.


**Fig. 20 – *Nigrograna magnoliae*** (HKAS 107035 and HKAS 107027, **new host records**). a, c, d Ascomata on *Michelia alba* dead branches. b, e, f Ascomata on *Rosa* sp. dead branches (white arrows show ascomata). g Cross section of an ascoma. h Section of the peridium. i Pseudoparaphyses. j–m Asci. n–s Ascospores. Scale bars: a, b = 1 cm, c = 1000 µm, e = 500 µm, d, f = 200 µm, g = 100 µm, h, j–m = 20 µm, n–s = 10 µm, i = 5 µm.

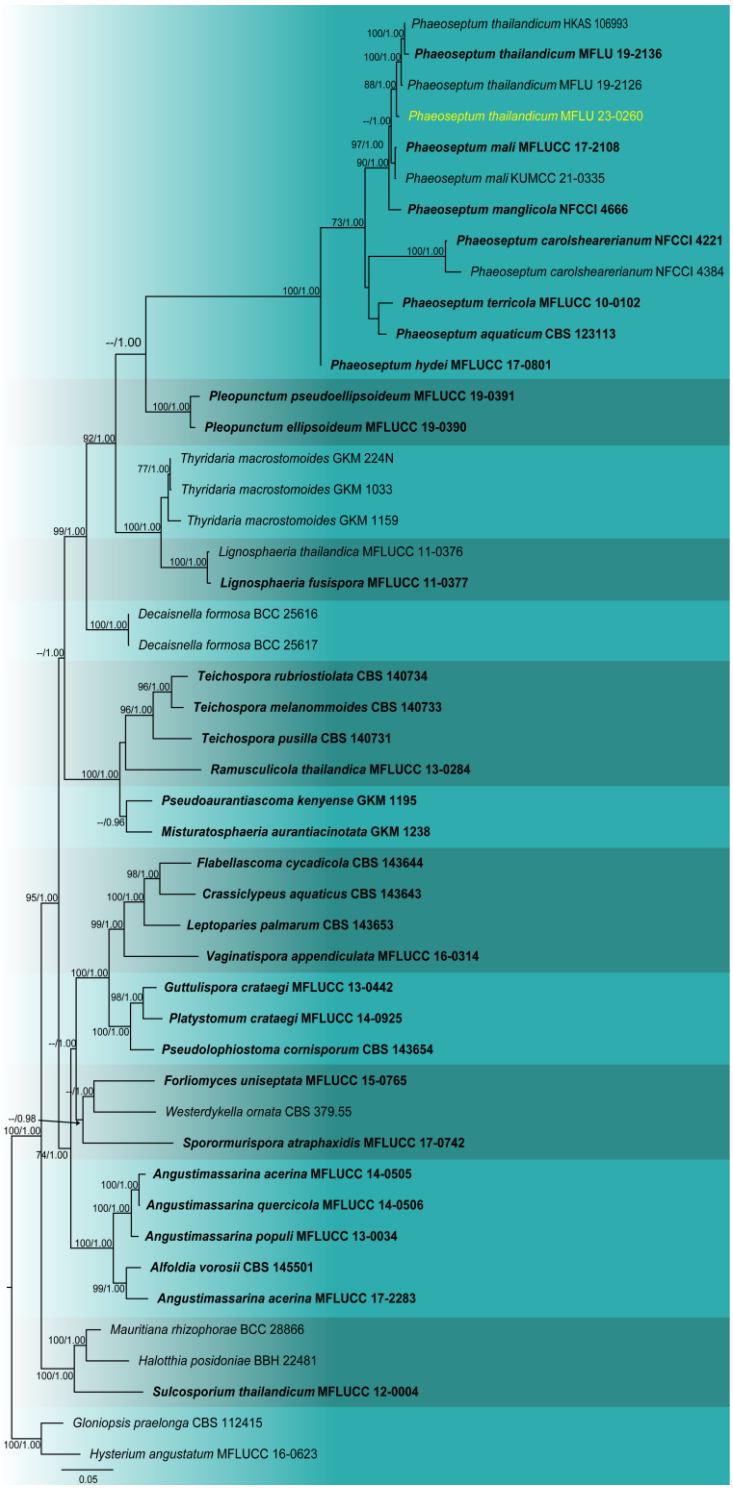


**Fig. 21 –** Phylogram generated from maximum likelihood analysis based on the combined LSU, SSU, ITS and *tef1-α* sequence data of the genus *Phaeoseptum*. Forty-seven isolates are included in the combined analyses which comprised 5850 characters (1134 characters for LSU, 1421 characters for SSU, 1818 characters for ITS and 1477 characters for *tef1-α*). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -28035.586869 is presented. The matrix had 1940 distinct alignment patterns, with 36.56% of undetermined characters or gaps. The GTR+G evolutionary model was applied for each gene region. Bootstrap support values for ML greater than or equal to 70% and Bayesian posterior probabilities greater than or equal to 0.95 are given near the nodes, respectively. The tree was rooted with *Gloniopsis praelonga* (CBS 112415) and *Hysterium angustatum* (MFLUCC 16-0623). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

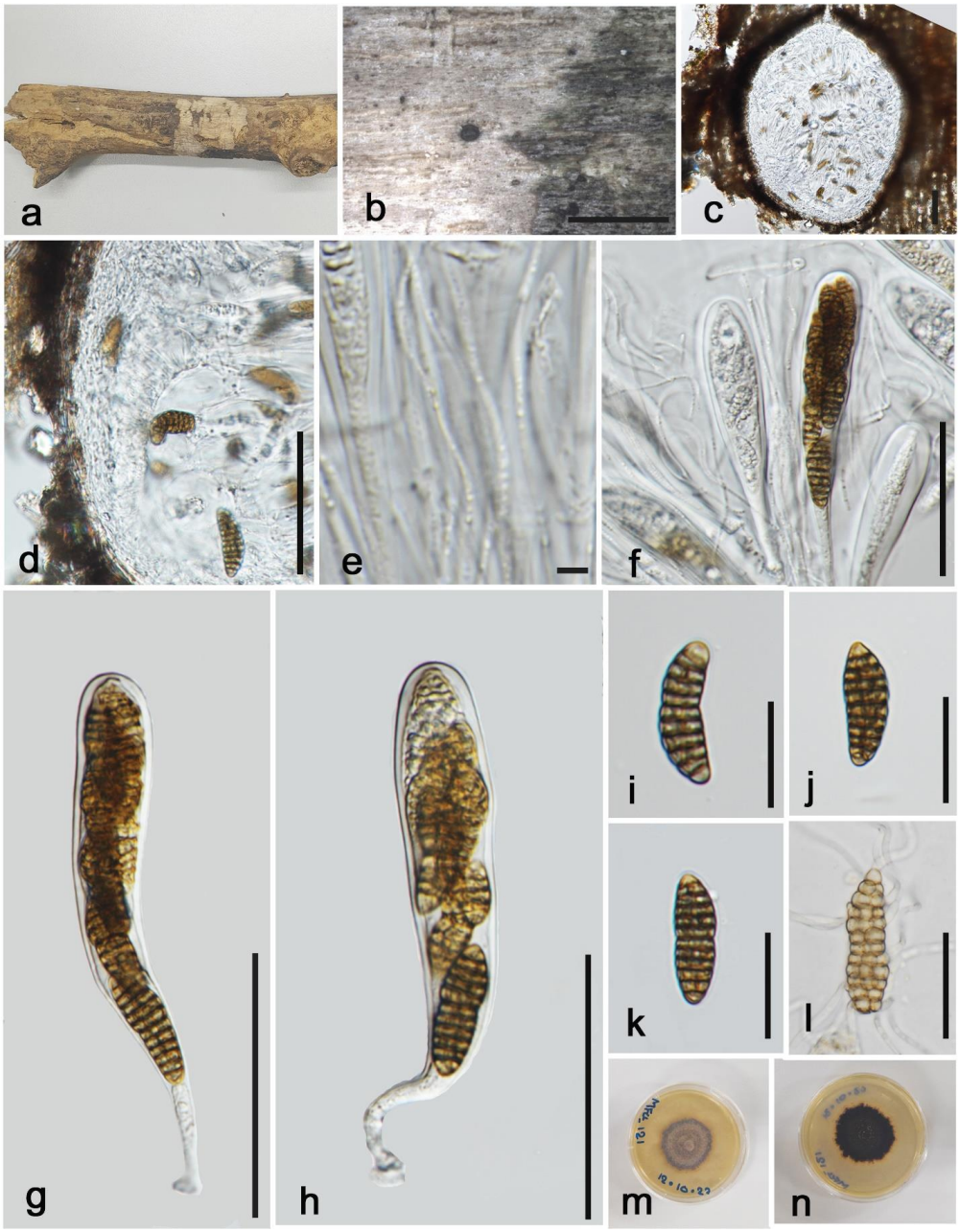


**Fig. 22** – ***Phaeoseptum thailandicum*** (MFLU 23-0260, **a new host record**). a Substrate. b Appearance of ascomata on host. c Vertical section of an ascoma. d Peridium. e Pseudoparaphyses. g–h Asci. i–l Ascospores. m, n Upper (m) and reverse view (n) of the colony on PDA. Scale bars: c = 50 µm, d = 20 µm, e = 5 µm. f–h = 50 µm, i–l = 50 µm.

***Pleosporaceae*** Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26, 74 (1869)

Facesoffungi number: FoF 00500

***Alternaria*** Nees, Syst. Pilze (Würzburg), 72 (1816) [1816-1817]

Facesoffungi number: FoF 00501

Nees (1816) established this genus typified by *Alternaria tenuis* (the synonym of *A. alternata*) and characterized by the muriform and catenulate conidia. Based on the morphology, this genus has been classified into two taxonomic sections, large- and small-spored taxa (Simmons 2007, Tao et al. 2019). The phylogenetic tree is consistent and strongly supported by the morphological sections of Simmons (2007). *Alternaria* species were isolated from necrotic leaf spots and blight symptoms by having conidia with a short or medium body in various patterns of

branched or unbranched chains or solitary (Tao et al. 2019). An updated phylogeny for *Alternaria* is provided in Fig. 23.

***Alternaria arida*** Chaiwan, Jayawardena, Bulgakov & K.D. Hyde, **sp. nov.**

Index Fungorum number: IF 900631; Facesoffungi number: FoF 15188; Fig. 24

*Saprobic* on dead stems of *Artemisia absinthium*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiophores* 10–60 × 4–6 μm ($\bar{x}$ = 35 × 5 μm, n = 30), solitary or terminally erecting from hyphae, straight or slightly curved, pale brown to brown, 1–5-septate, rough, usually with virgariella-like branching patterns. *Conidia* 20–40 × 10–20 μm ($\bar{x}$ = 30 × 15 μm, n = 50), solitary, occasionally 2 in a chain, long ovoid and ellipsoid, erostrate, light brown to dark brown, smooth-walled, 3–6 transverse septa (sometimes up to 7), 0–2 longitudinal septa or oblique in a transverse segment.

Culture characteristics – Colonies on PDA reaching 30.5 mm diam. after 14 days at 25 ºC, covering petri dish in 4 weeks, initially white to gray, circular, flat, slightly wooly, entire margin. Sporulating regions at the centre.

Material examined – Russia, Rostov region, Rostov-on-Don City, Botanical Garden of Southern Federal University, ruderal vegetation, on dead stems of *Artemisia absinthium*, 11 May 2017, Timur S. Bulgakov, T-1833 (MFLU 17-2135, **holotype**); Russia, Donetsk region, Donetsk, Donetsk Botanical Garden, on dead leaves of *Yucca filamentosa*, 20 May 2017, Timur S. Bulgakov, DNK-140 (MFLU 17-2561).

GenBank accession numbers – MFLU 17-2561 - ITS: OR135245, *gapdh*: OR140522, *tef1-α*: OR140524; MFLU 17-2135 - ITS: OR135247, *gapdh*: OR140523, *tef1-α*: OR140525.

Notes – Based on our phylogenetic analysis of combined ITS, *gapdh*, *rpb2*, *tef1-α*, and *Alt-a* sequence data of *Alternaria* species (Fig. 23), our isolates (MFLU 17-2135 and MFLU 17-2561) clustered with 99% maximum parsimony, 95% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability, confirming that they belong to the same species. However, in the phylogenetic tree, these two isolates formed a branch separated from other *Alternaria* species (Fig. 23). Consistent with the multi-gene phylogenies, this phylogenetically distant group also shows different morphologies compared to the closely related *A. alstroemeriae* (Fig. 24). Our species differs from *A. alstroemeriae* by having smaller conidia (20–40 × 10–20 μm), solitary, pale to medium brown, narrowly ellipsoid to ellipsoid or ovoid, beakless conidia with multiple transverse septa and rarely longitudinal septa, while *A. alstroemeriae* subcylindrical conidia in short chains (Simmons 2007, Yamagishi et al. 2009, Nishikawa & Nakashima 2013). Furthermore, chalastospora and branched primary conidiophores were not observed in our species compared to *A. alstroemeriae* (Woudenberg et al. 2013, Kgatle et al. 2018). Furthermore, our species are slow-growing on PDA, reaching 30.5 mm diam. at 25 ºC after 14 days with white to grey colour colonies and the sporulation can be mostly observed at the center while colonies of *A. alstroemeriae* grows faster (covering petri dish after 7 days at 25 ºC), and sporulation is submerged in agar substrates (Simmons 2007). The mycelial growth on PDA are olivaceous brown to black (Yamagishi et al. 2009).

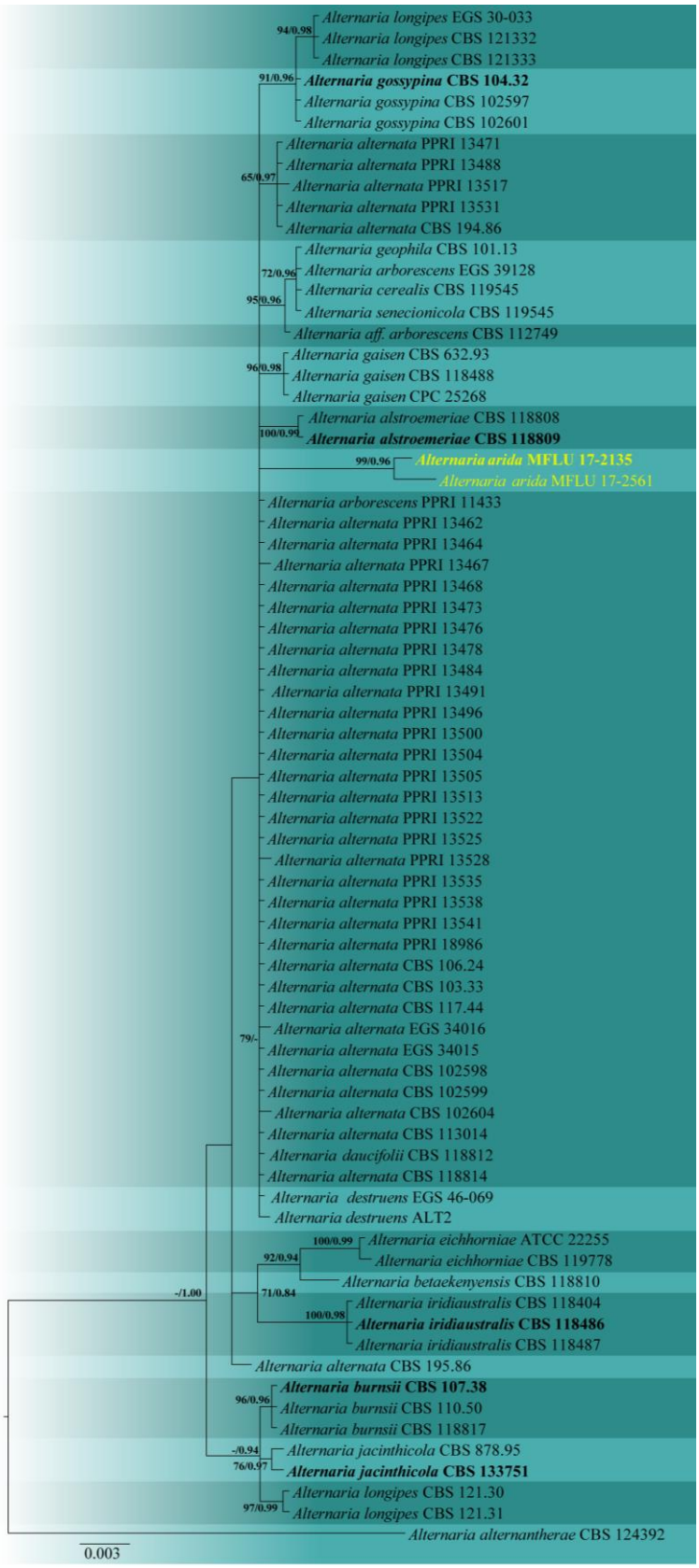


**Fig. 23 –** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *gadph* and *tef1-α* sequence data for *Alternaria* taxa, comprising 1,341 characters (ITS = 522, *gadph* = 579, and *tef1-α* = 240). The best-scoring RAxML tree with a final likelihood value of -5250.975025 is presented. The matrix had 146 distinct alignment patterns, with 4.65% of undetermined characters or gaps. Evolutionary model applied for all genes is GTR+I+G. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and posterior probability

values greater than 0.90 are given at each node. Ex-type strains are in **bold**, while the new isolate is indicated in yellow. The tree is rooted to *Alternaria alternantherae* (CBS 124392).


**Fig. 24** – ***Alternaria arida*** (MFLU 17-2135, **holotype**). a The specimens in the envelop. b Appearance of ectostromata on host surface. c Culture on the PDA. d Conidia. e–g Conidiophores. h Conidia and conidiophores. Scale bars: d, e, f, h = 10 μm, h = 5 μm.

***Salsugineaceae*** K.D. Hyde & Tibpromma, in Hyde et al., Fungal Diversity 63, 227 (2013)

Facesoffungi number: FoF 08364

***Salsuginea*** K.D. Hyde, Botanica Marina 34(4), 315 (1991)

Facesoffungi number: FoF 08365

*Salsuginea* was introduced with the type species *Salsuginea ramicola* on submerged wood of *Aegiceras* sp. in Thailand (Hyde 1991). This genus is morphologically distinct from other similar genera by having ascospores with apical germ pores or extensions and a peridium of *textura porrecta* to *textura epidermoidea* cells (Hyde 1991, Hyde et al. 2013). Currently, there are three species in this genus, viz., *Salsuginea phoenicis*, *S. ramicola*, and *S. rhizophorae*. Species in this genus are saprobes on the decaying, submerged mangrove wood and palms in brackish waters in mangrove forests in Thailand (Hyde 1991, Hyde et al. 2013, Jones et al. 2020). An updated phylogeny is shown in Fig. 25.

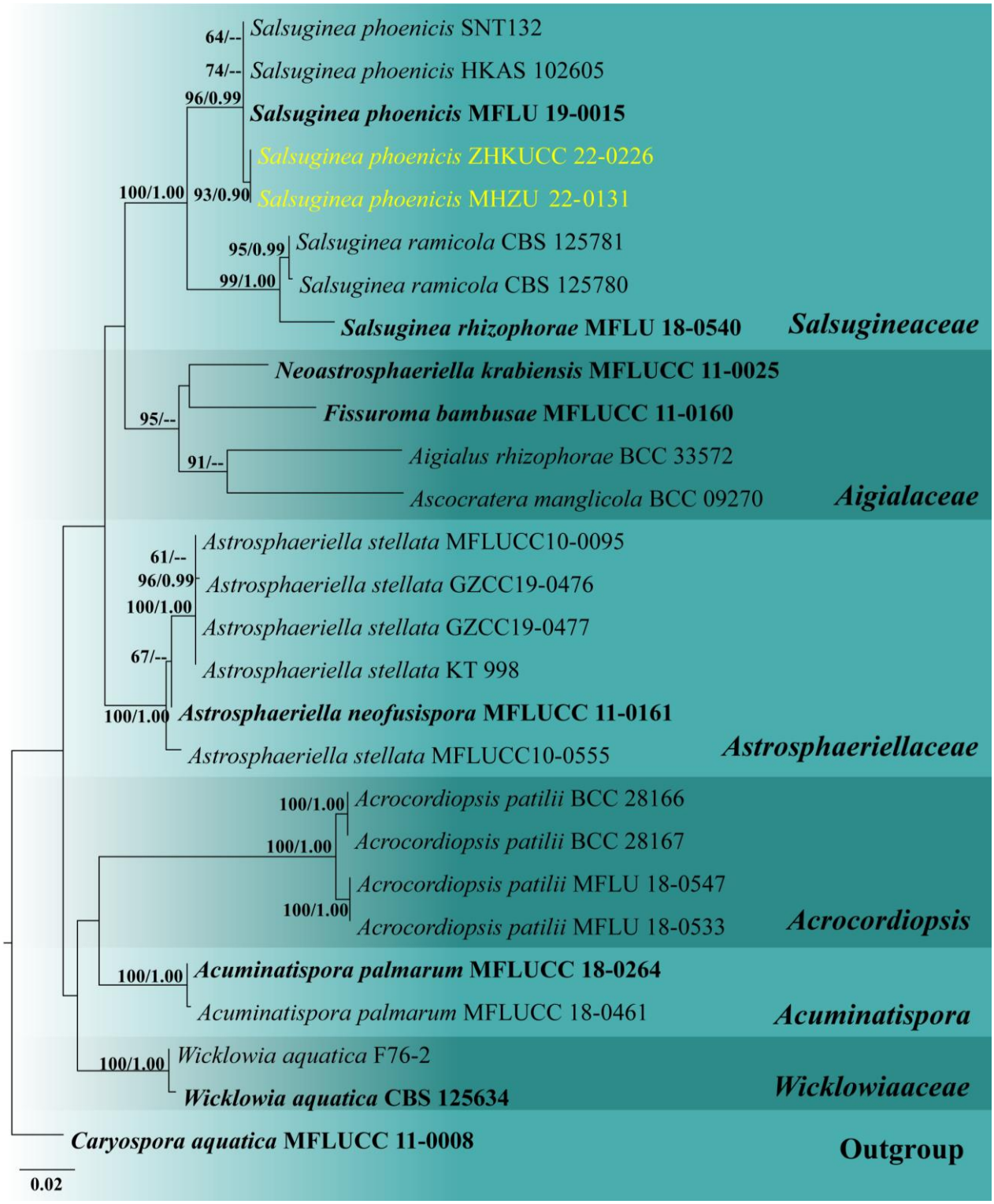


**Fig. 25 –** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, *tef*1-*α*, and *rpb2* sequence data which comprised 3,669 characters (LSU = 899, SSU = 1020, *tef*1-*α* = 930, and *rpb2* = 820). The best scoring RAxML tree with a final likelihood value of -8757.729573 is presented. The matrix had 422 distinct alignment patterns, with 7.32% of undetermined characters or gaps. Evolutionary model applied for all genes is GTR+I. Bootstrap support values for maximum likelihood equal to or greater than 60% and clade credibility values equal to or greater than 0.95 from Bayesian inference analysis are labelled at each node. Ex-type strains are in **bold**, while the new isolate is indicated in yellow. The tree is rooted to *Caryospora aquatica* (MFLUCC 11-0008).

***Salsuginea phoenicis*** S.N. Zhang, E.B.G. Jones, K.D. Hyde & J.K. Liu, in Jones et al., Botanica Marina 63(2), 158 (2019)

Index Fungorum number: IF 829547; Facesoffungi number: FoF 14242; Fig. 26

*Saprobic* on decaying petioles of *Phoenix roebelenii*. **Sexual morph**: *Clypeus* composed of host cells interspersed with darkened fungal tissue. *Ascomata* 400–520 μm high, 640–950 μm in diam. ($\bar{x}$ = 489 × 802 μm, n = 10), solitary, scattered, immersed to erumpent, subglobose, black, carbonaceous, with a central ostiole, papillate, clypeate. *Peridium* thick, up to 50 μm wide, composed of brown cells of *textura epidermoidea*. *Hamathecium* comprising 1–2 μm wide, numerous, anastomosing, branched, septate, filiform, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 145–270 × 20–30 μm ($\bar{x}$ = 229 × 27 μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, with an apical apparatus consisting of a large distinctive ocular chamber. *Ascospores* 45–60 × 15–25 μm ($\bar{x}$ = 55 × 20 μm, n = 20), uniseriate or overlapping uniseriate, hyaline when young, brown at maturity, broad fusiform or ellipsoidal, 2-celled and almost equally, strongly constricted at the central septum, with hyaline apical and basal germ pores, smooth-walled, lacking a mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics – Colonies on PDA attaining 3 cm diam. within 2 weeks at 25 °C under dark, velvety, circular, wavy margin, slightly raised, inner zone white and outer zone darker or pale brown, reverse brown, with a margin of translucent.

Material examined – China, Guangdong Province, Guangzhou City, Baiyun Mountain, near a small fresh water stream, on decaying, submerged petiole of *Phoenix roebelenii*, 16 August 2021, I.C. Senanayake, GZ14 (MHZU 22-0131), living cultures ZHKUCC 22-0226.

GenBank accession numbers – ZHKUCC 22-0226 - LSU: OQ586396, *tef1-α*: OQ590004; MHZU 22-0131 - LSU: OQ586396, *tef1-α*: OQ590004.

Known distribution (based on molecular data) – Thailand (Jones et al. 2020), China (this study).

Known hosts (based on molecular data) – on decaying petiole of *Phoenix paludosa* (Jones et al. 2020), on decaying, submerged petiole of *P. roebelenii* (this study).

Notes – The combined gene analysis of LSU, SSU, *tef1-α*, and *rpb2* showed that our salsuginea-like collection (MHZU 22-0131) grouped with *S. phoenicis* with 96% maximum likelihood bootstrap support and 0.99 Bayesian posterior probability (Fig. 25). Our collection is morphologically very similar to the holotype of *S. phoenicis* (Jones et al. 2020). However, the holotype was collected from the marine environment, while ours' was obtained from a freshwater habitat. Therefore, we identified this collection as *S. phoenicis* based on morphological and phylogenetic analyses (Figs. 25 and 26). This is the first report of *S. phoenicis* in China and the first collection after the holotype.

***Teichosporaceae*** M.E. Barr, Mycotaxon 82, 374 (2002)

Facesoffungi number: FoF 00830

***Magnibotryascoma*** Thambug. & K.D. Hyde, in Thambugala et al., Fungal Diversity 74, 199–266 (2015)

Facesoffungi number: FoF 00835

Based on morphological differences and phylogenetic evidence, Thambugala et al. (2015) introduced a novel genus, *Magnibotryascoma*, with *Magnibotryascoma uniseriate* as the type. Six species are currently accepted in *Magnibotryascoma*, viz., *M. acaciae*, *M. kungmingense*, *M. mali*, *M. melanommoides*, *M. rubriostiolata* and *M. uniseriate* (Hyde et al. 2017, Tennakoon et al. 2021b, Crous et al. 2022b). The morphological characters of *Magnibotryascoma* differ from *Teichospora* by having brown, fusiform to elliptical, 1–3-septate ascospores. An updated phylogeny is shown in Fig. 27.

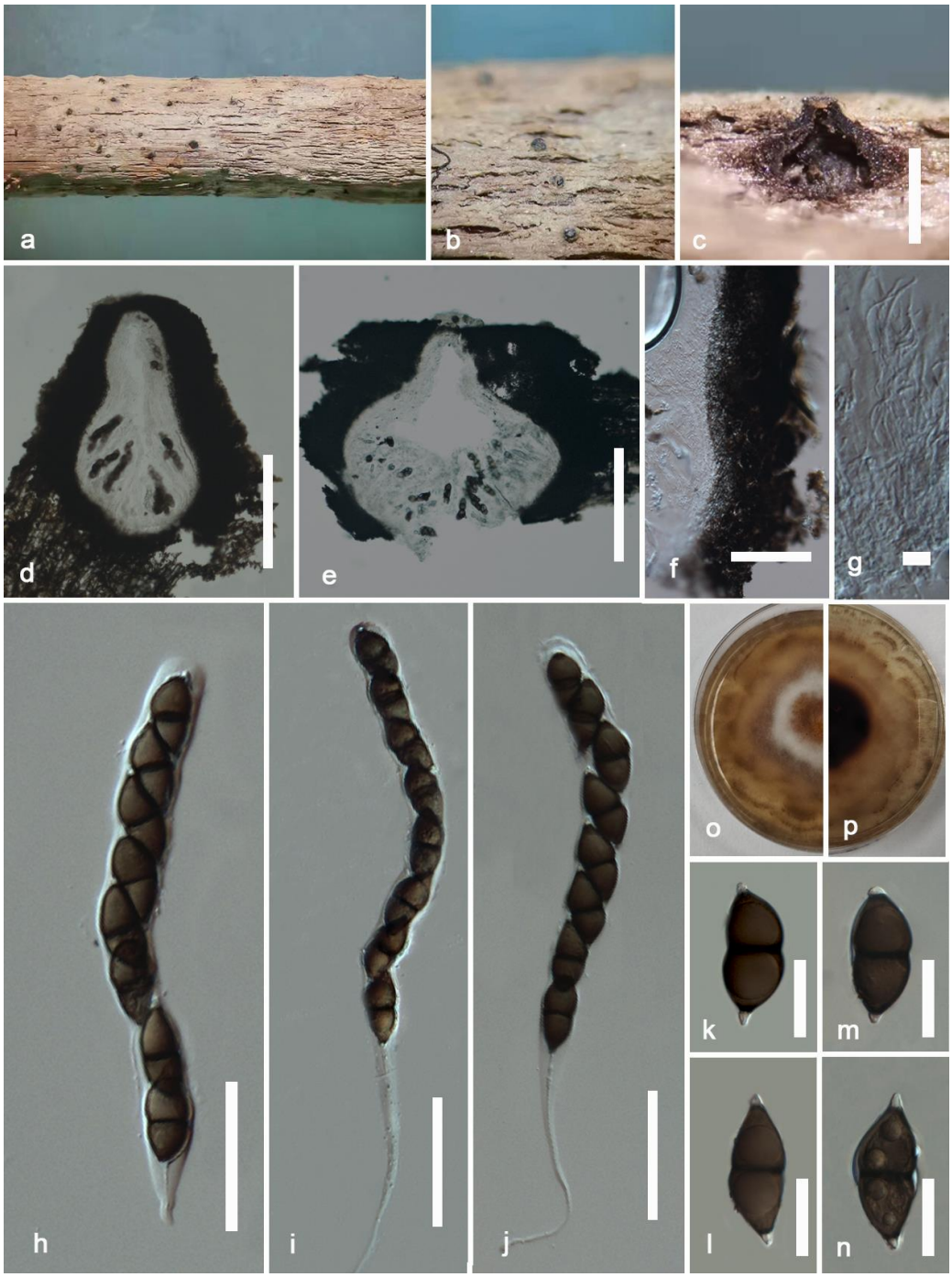


**Fig. 26 – *Salsuginea phoenicis*** (MHZU 22-0131, **a new geographical record**). a, b Ascomata on the substrate. c–e Vertical cross-section of an ascoma. f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. o Surface view of colony on PDA. p Reverse view of colony on PDA. Scale bars: d, e = 300 µm, f = 50 µm, g = 10 µm, h–j = 100 µm, k–n = 25 µm.

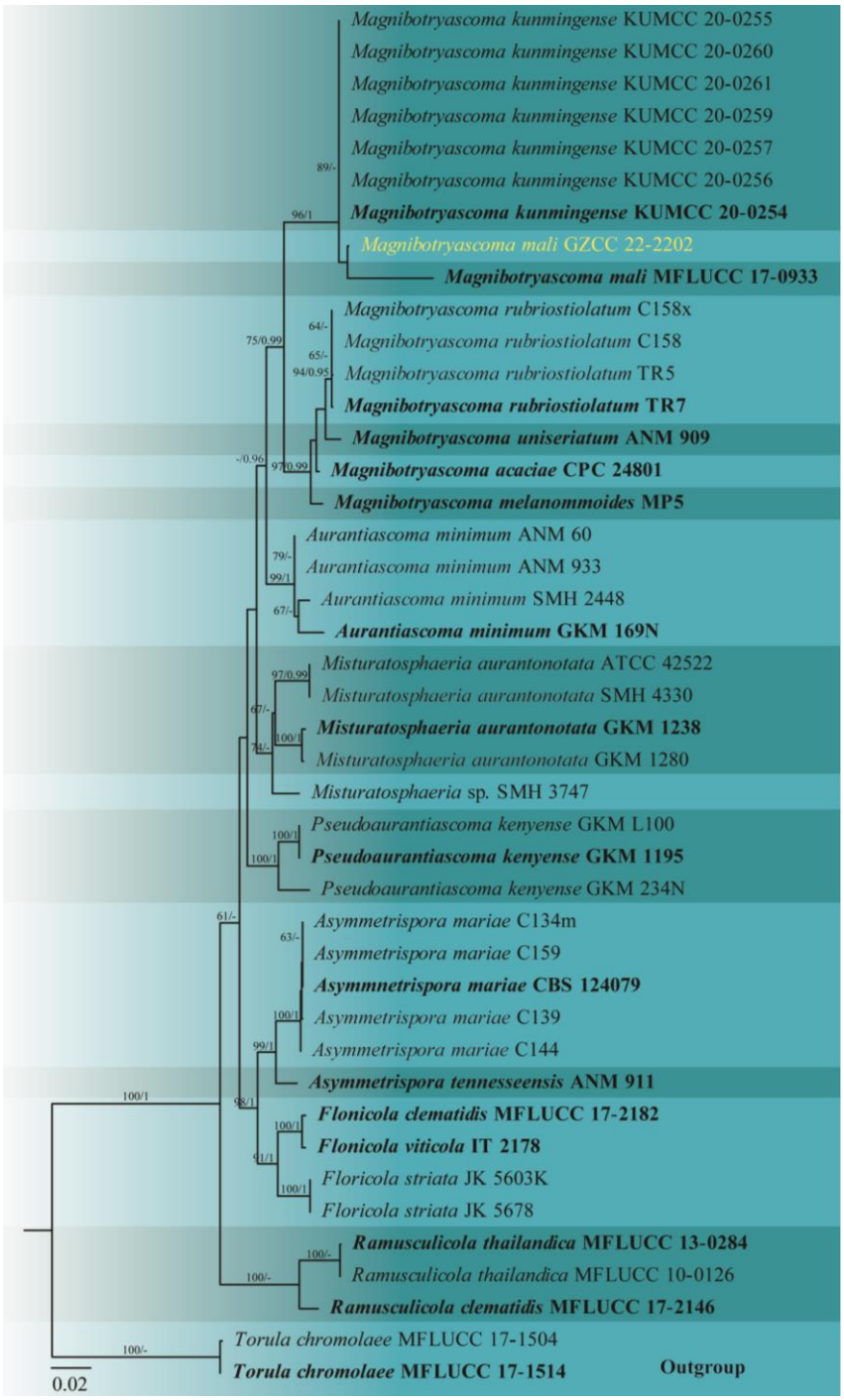


**Fig. 27 –** Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1-α* sequence data for *Teichosporaceae*. Forty-three strains are included in the combined analyses which comprised 3290 characters (546 characters for ITS, 821 characters for LSU, 994 characters for SSU, 929 characters for *tef1-α*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -10312.973943 is presented. Estimated base frequencies were as follows: A = 0.234738, C = 0.259620, G = 0.280304, T = 0.225338; substitution rates AC = 1.342287, AG = 2.282828, AT = 1.707394, CG = 1.224997, CT = 9.169275, GT = 1.000000; gamma distribution shape parameter α = 0.130805. The GTR+I+G evolutionary model was applied to all the genes in the dataset. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree was rooted with *Torula chromolaee* (MFLUCC 17-1504, MFLUCC 17-1514). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Magnibotryascoma mali*** Phukhams., Wanas. & K.D. Hyde, Fungal Diversity 87, 105 (2017)

Index Fungorum number: IF 553255; Facesoffungi number: FoF 003387; Fig. 28

*Saprobic* on dead branch of *Osmanthus fragrans*. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 140–220 × 215–205 μm ($\bar{x}$ = 185 × 250 μm, n = 20), solitary, semi-immersed or immersed in the substrate, globose to subglobose, dark brown to brown, with a short neck and a central ostiole. *Peridium* up to 11–26 μm wide, composed of dark brown to black, thick-walled cells of *textura globosa*, becoming thin-walled and hyaline towards the inner region. *Paraphyses* absent. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells. *Conidiogenous cells* 2–7 × 2–4 μm ($\bar{x}$ = 4 × 2 μm, n = 20), ampulliform to subcylindrical, hyaline, smooth-walled, arising from the inner layer of pycnidium wall. *Conidia* 3–5 × 2–3 μm ($\bar{x}$ = 4 × 2 μm, n = 50), subglobose, oval, guttulate, hyaline when immature, golden brown at maturity, aseptate and smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies slow growing, reaching 30 mm diam. after 2 weeks at 20–25 °C, becoming ash-gray on the surface after one week, with the reverse side of the colonies pale gray to gray, and finally black after two weeks, dense, circular, slightly raised, surface smooth with crenate edge.

Material examined – China, Sichuan Province, Chengdu City, Chengdu Botanical Garden, 30°45'59"N, 104°7'19"E, on dead branch of *Osmanthus fragrans*, 28 March 2021, Na Wu, YW338, (GZAAS 22-2204), living culture GZCC 22-2202.

GenBank accession numbers – ITS: OP927796, LSU: OP926034, SSU: OP927796, *tef1-α*: OQ597716.

Known distribution (based on molecular data) – China (Hyde et al. 2017, this study), New Zealand (Crous et al. 2022b).

Known hosts (based on molecular data) – *Malus halliana* (Hyde et al. 2017), *Metrosideros* sp. (Crous et al. 2022b), *Osmanthus fragrans* (this study).

Notes – Our strain (GZCC 22-2202) clustered with the ex-type strain of *Magnibotryascoma mali* (MFLUCC 17-0933) based on the multi-gene phylogenic analyses (ITS, LSU, SSU, and *tef1-α*) (Fig. 27). Morphologically, our strain is similar to the *M. mali* (MFLU 17-0559) collected from decaying twigs of *Malus halliana* in China in having golden brown, oval, aseptate, smooth-walled conidia (Hyde et al. 2017). Based on morpho-molecular data analysis, we conclude that our new collection is a new host record of *M. mali* on *Osmanthus fragrans* in China.

***Dothideomycetes* orders *incertae sedis***

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

Facesoffungi number: FoF 07659

***Botryosphaeriaceae*** Theiss. & H. Syd., Annales Mycologici 16(1/2), 16 (1918)

Facesoffungi number: FoF 00116

***Botryosphaeria*** Ces. & De Not., Commentario della Società Crittogamologica Italiana 1(fasc. 4), 211 (1863)

Facesoffungi number: FoF 00141

Cesati and De Notaris (1863) introduced *Botryosphaeria* with *Botryosphaeria dothidea* as a type species. *Botryosphaeria* species have worldwide distribution on a wide range of hosts, such as monocotyledonous, dicotyledonous, and gymnosperm hosts (Darge & Woldemariam 2021). Currently, 30 species are accepted in this genus (Wu et al. 2021). An updated phylogeny for the genus is provided in Fig. 29.

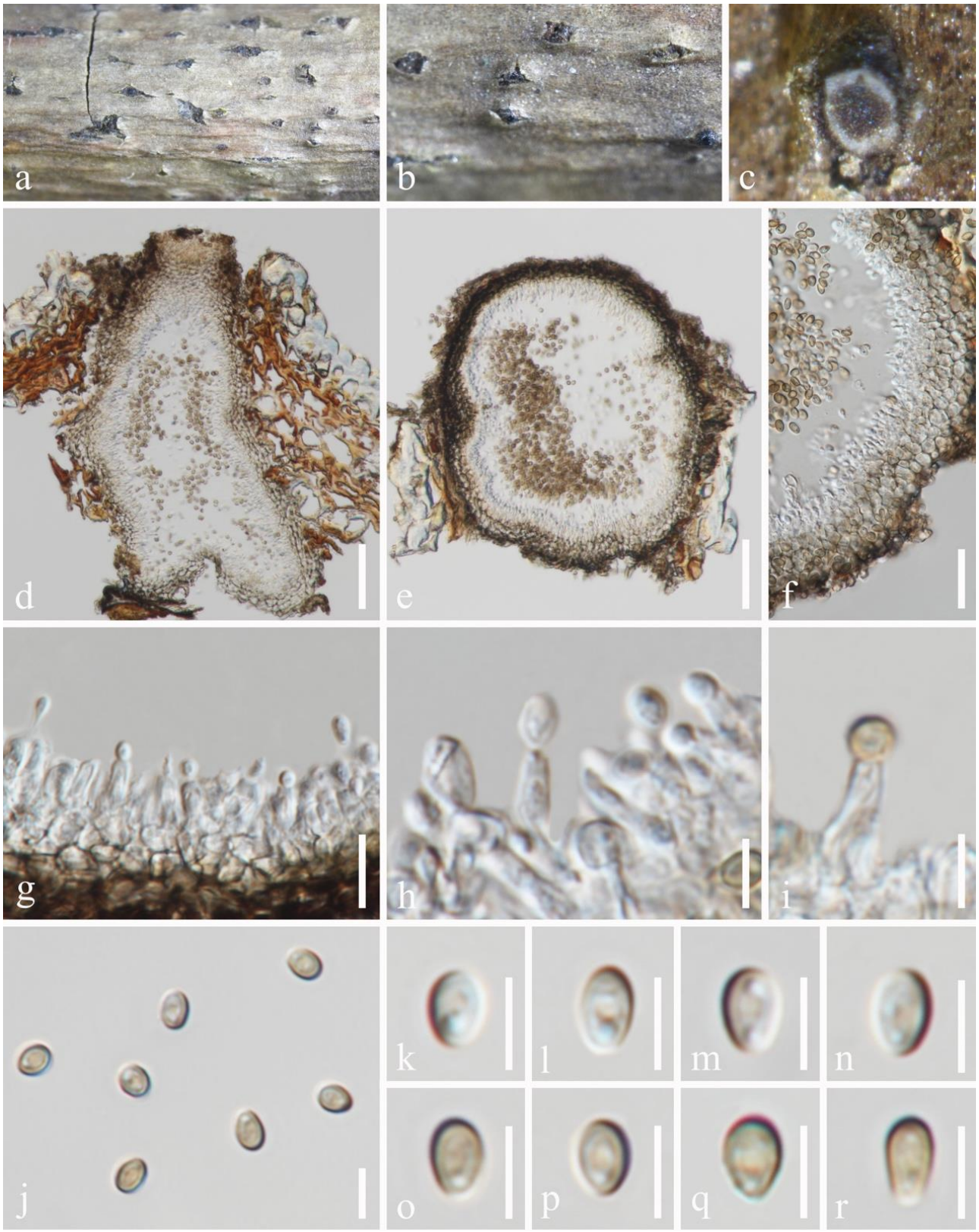


**Fig. 28 – *Magnibotryascoma mali*** (GZAAS 22-2204, **new host record**). a, b Conidiomata on host substrate. c–e Vertical section of a conidioma. f Section of the peridium. g–i Conidiogenous cells and developing conidia. j–r Conidia. Scale bars: d, e = 50 μm, f = 20 μm, g = 10 μm, h–r = 5 μm.

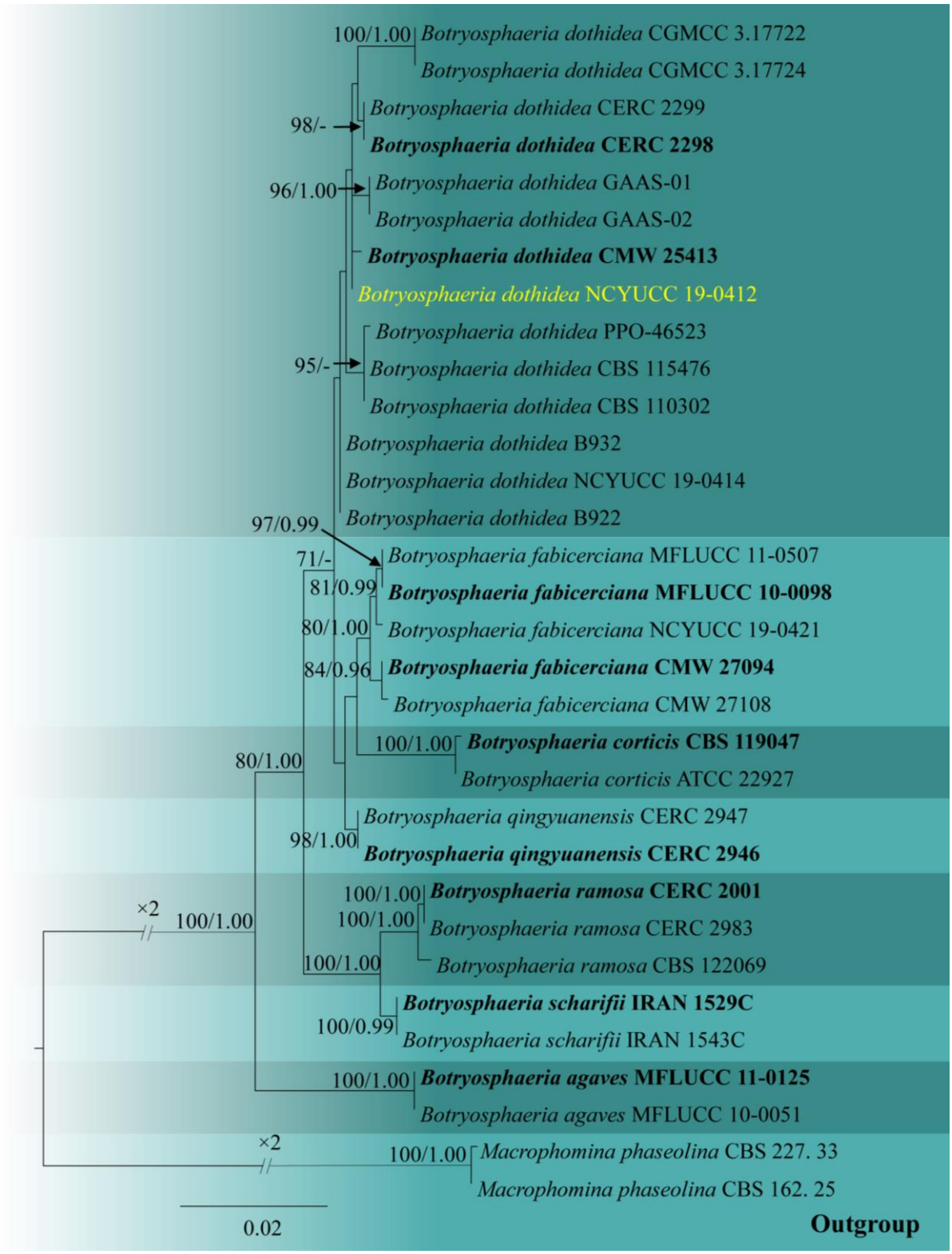


**Fig. 29 –** Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α*, and *β-tubulin* sequence data of the genus *Botryosphaeria*. Thirty-two strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -2993.72 is presented. Evolutionary model applied for all genes is GTR+G. The matrix had 222 distinct alignment patterns, with 14.38% of undetermined characters or gaps. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree was rooted with *Macrophomina phaseolina* (CBS 227.33 and CBS 162.25). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Botryosphaeria dothidea*** (Moug.) Ces. & De Not., Commentario della Società Crittogamologica Italiana 1(fasc. 4), 212 (1863)

Index Fungorum number: IF 183247; Facesoffungi number: FoF 03512; Fig. 30

*Saprobic* on dead twig of *Ficus benghalensis*. **Sexual morph:** *Ascomata* 180–240 μm, high × 210–245 μm diam ($\bar{x}$ = 215 × 230 μm, n = 10), solitary to aggregated, semi-immersed to erumpent under epidermis, coriaceous, uniloculate, globose to subglobose, black, papillate. *Peridium* 25–40 μm wide, two-layered, outer layer composed of thick-walled, brown to dark brown cells of *textura angularis*, inner layer composed of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* comprising numerous, 2–3 μm wide, hypha-like, septate, slightly constricted at septum, cellular pseudoparaphyses. *Asci* 55–85 × 15–20 μm ($\bar{x}$ = 70 × 17 μm, n = 15), bitunicate, fissitunicate, 8-spored, clavate, apically rounded, short-pedicellate, with a well-developed ocular chamber. *Ascospores* 20–25 × 8–10 μm ($\bar{x}$ = 22 × 9 μm, n = 30), uniseriate at the base, overlapping 2–3-seriate at the apex, ellipsoid to fusiform, hyaline, aseptate, broad at the middle, thick and rough-walled. **Asexual morph:** Undetermined in this study, see Rathnayaka et al. (2021) for description.

Culture characteristics – Ascospores germinating on PDA within 6 hours and germ tube produced from both ends of the ascospore. Colonies on PDA fast growing, reaching 5–6.5 cm diam. after 4 days at 25 °C, colonies circular, flattened, fluffy, fairly dense, aerial, grey in upper side and black in lower side.

Material examined – China, Taiwan Province, Fenghuang Mountain, Lugu Township, Nantou County, lives on a dead twig of *Ficus benghalensis*, 17 September 2019, Achala Rathnayaka (MFLU 22-0180), living culture (NCYUCC 19-0412).

GenBank accession numbers – ITS: OP689559, *tef1-α*: OP700655, *β-tubulin*: OP700656.

Known distribution (based on molecular data) – Switzerland (Slippers et al. 2004), China (Alfieri et al. 1984, Kuo et al. 1989, Ni et al. 2010, Huang & Wang 2011, Ko et al. 2011, Mayorquin et al. 2012, Wang et al. 2020, Rathnayaka et al. 2021, this study).

Known hosts (based on molecular data) – *Araucaria cunninghamii* (Huang & Wang 2011), *Camellia sinensis* (Rathnayaka et al. 2021), *Ficus carica* (Alfieri et al. 1984, Wang et al. 2020), *F. benghalensis* (this study), *F. microcarpa* (Mayorquin et al. 2012), *Mangifera indica* (Ni et al. 2010), *Prunus mume*, *P. persica* and *P. communis* (Ko et al. 2011), *Prunus* sp. (Slippers et al. 2004), *Vitis* sp. (Kuo et al. 1989) and several hosts (Jayawardena et al. 2019).

Notes – *Botryosphaeria dothidea*, previously known as *Sphaeria dothidea*, was described from twigs of *Fraxinus* sp. (Fries 1823). The holotype for *S. dothidea* was introduced by von Arx & Müller (1954) from the specimen on *Rosa* sp. in the Fries collection and is not accepted (Slippers et al. 2004). Later, a neotype was designed from the Fries collection (Slippers et al. 2004), which failed due to the immature status of the specimen and the absence of spores (Slippers et al. 2004). Epitype and ex-epitype culture for *B. dothidea* were introduced by Slippers et al. (2004) from *Prunus* sp. collected from Switzerland. According to the phylogenetic analysis, strain NCYUCC 19-0412 clustered with the ex-epitype and other isolates of *B. dothidea* (Fig. 29). Previously, *Botryosphaeria dothidea* has been recorded on several *Ficus* species (Alfieri et al. 1984, Wang et al. 2020, Mayorquin et al. 2012). This is the first record of *B. dothidea* on *Ficus benghalensis* in Taiwan Province in China.


**Fig. 30 – *Botryosphaeria dothidea*** (MFLU 22-0180, **a new host record**). a, b Appearance of ascostromata on host surface. c, d Section through ascoma. e Peridium. f Pseudoparaphyses. g–i Asci. j–m Ascospores. n, o Colony on PDA (n upper, o lower). Scale bars: a = 500 μm, b–d = 100 μm, e, f, j–m = 10 μm, g–i = 20 μm.

***Lasiodiplodia*** Ellis & Everh., in Clendenin, Botanical Gazette 21, 92 (1896)

Facesoffungi number: FoF 00151

*Lasiodiplodia* was introduced with *Lasiodiplodia tubericola* (current name: *L. theobromae*) as the type species (Clendenin 1896). Members of the genus have a cosmopolitan distribution in tropical and subtropical regions and also become more abundant in temperate regions (Slippers et al. 2007). An updated phylogeny is presented in Fig. 31.

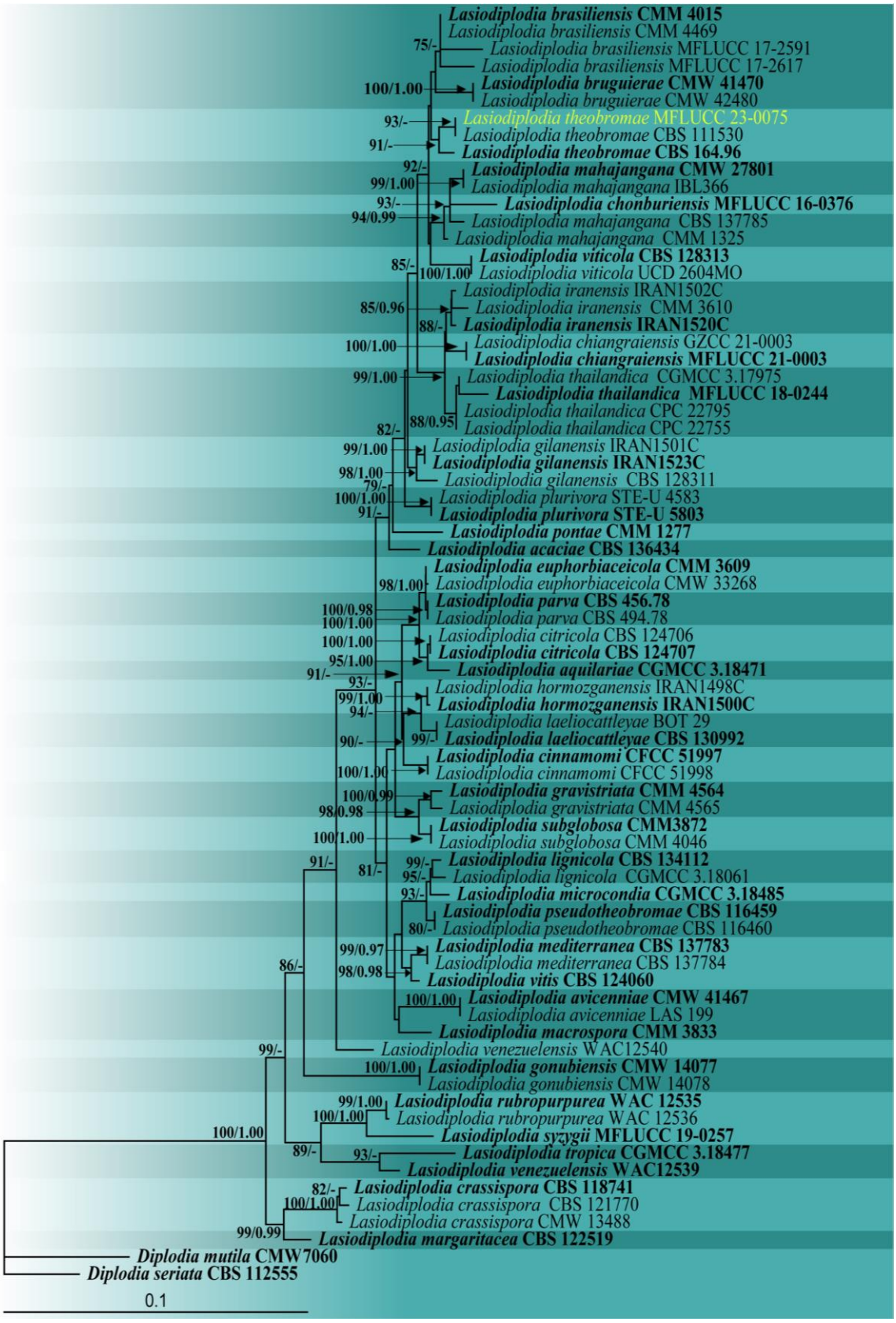


**Fig. 31 –** Phylogram generated from the maximum likelihood analysis based on the combined ITS, *tef1-α*, *β-tubulin* and *rpb2* sequence data of the genus *Lasiodiplodia*. Seventy-four strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -7167.598 is presented. Evolutionary model applied for all genes is GTR+G. The matrix had 492 distinct alignment patterns, with 0.53% of undetermined characters or gaps. Bootstrap support values for ML equal to

or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.90 are given near nodes, respectively. The tree was rooted with *Diplodia seriata* (CBS 112555) and *Diplodia mutila* (CMW 7060). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Lasiodiplodia theobromae*** (Pat.) Griffon & Maubl., Bulletin de la Société mycologique de France 25, 57 (1909)

Index Fungorum number: IF 188476; Facesoffungi number: FoF 00167; Fig. 32

*Saprobic* on the fruit of *Garcinia mangostana*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* pycnidial, unilocular, dark brown to black, immersed in the host. On PDA: *Mycelium* hyaline to dark grey. *Paraphyses* 23–76 µm long, 2–6 µm wide ($\bar{x}$ = 39 × 3 µm, n = 15), hyaline, cylindrical, septate, occasionally branched, with rounded ends. *Conidiogenous cells* holoblastic, hyaline, thin-walled, smooth, percurrent one or two annellations, or proliferating at the same level giving rise to periclinal thickenings. *Conidia* 18–30 × 10–15 µm ($\bar{x}$ = 25 × 13 µm, n = 30, L/W = 2 µm), subovoid to ellipsoid-ovoid, with a broadly rounded apex and a tapering to the truncated base, initially double-layered, hyaline, and unicellular, becoming 1-septate, light to dark brown with typical striate formation at maturity.

Culture characteristics – Colony on PDA have mycelium white to light-cream at seven days at 25 °C, becoming dark grey with fluffy aerial mycelium and produces liquid exudates after one month.

Material examined – Thailand, Chiang Rai Province, Fah Thai Market, on the fruit of *Garcinia mangostana*, 30 September 2021, Ruvishika S. Jayawardena, FUG14 (MFLU 23-0085), living culture MFLUCC 23-0075.

GenBank accession numbers – ITS: OR131265, *β-tubulin*: OR148429, *rpb2*: OR148430, *tef1-α*: OR148431.

Known distribution (based on molecular data) – worldwide distribution: Argentina, Australia, Brazil, Cameroon, China, Costa Rica, Ecuador, Egypt, Ghana, Guyana, India, Iran, Italy, Malaysia, Nigeria, Oman, Peru, Philippines, Puerto Rico, South Africa, Sri Lanka, Thailand, the USA, Venezuela (Salvatore et al. 2020, Farr & Rossman 2023, this study).

Known hosts (based on molecular data) – wide host range (Salvatore et al. 2020, Farr & Rossman 2023), *Garcinia mangostana* (this study).

Notes – *Lasiodiplodia theobromae* has been reported from various economically important crops, *viz*., *Cucumis melo* (Suwannarach et al. 2020), *Dimocarpus longan* (Pipattanapuckdee et al. 2019), *Fragaria* × *ananassa* (Phetphan et al. 2023), *Mangifera indica* (Trakunyingcharoen et al. 2013), *Musa* sp. (Salaemae et al. 2019), and *Syzygium samarangense* (Trakunyingcharoen et al. 2015), causing fruit rot and dieback in Thailand. Diseased mangosteen fruits become hard, and the skin turns to dark colour. The skin of the fruit is covered with black pycnidia immersed in the epidermis. Sangchote and Pongpisutta (1998) reported that *Lasiodiplodia theobromae* was the most common fungus causing fruit rots of mangosteen in eastern and southern Thailand based on morphology. This study provides the first record of *Lasiodiplodia theobromae* from northern Thailand.

***Phaeobotryon*** Theiss. & Syd., Annales Mycologici 13 (3–6), 664 (1915)

Facesoffungi number: FoF 07629

*Phaeobotryon* was initially introduced to accommodate *Phaeobotryon cercidis* (≡ *Dothidea cercidis*) (Theissen & Sydow 1915), but later given the status of an individual genus distinct from all other botryosphaeriaceous genera (Phillips et al. 2008, 2013). According to both Index Fungorum (2023) and MycoBank (2023), nine species have been listed for *Phaeobotryon*, and only four of them are known from their living cultures, including *Phaeobotryon cupressi*, *P. mamane*, *P. negundinis* and *P. rhois* (Liu et al. 2012, Phillips et al. 2013, Slippers et al. 2013, Fan et al. 2015). An updated phylogeny for *Phaeobotryon* was given in Fig. 33.

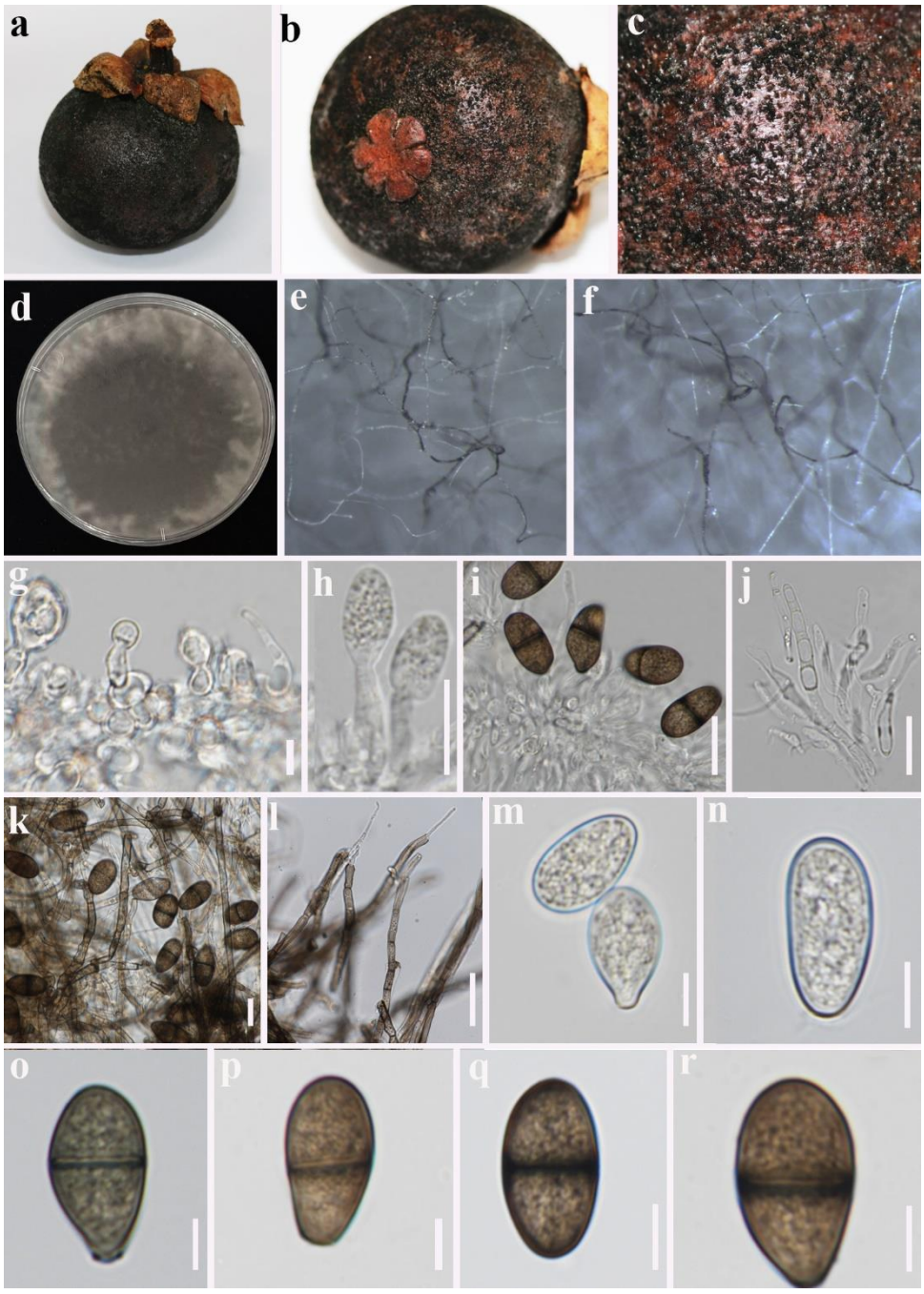


**Fig. 32 – *Lasiodiplodia theobromae*** (MFLUCC 23-0075, **a new geographical record**). a–c Appearance of ascomata on the host surface. d Surface view of the colony on PDA. e, f Mycelia. g–i Conidiogenous cells. j Paraphyses. k, l Conidia among mycelia. m, n Immature conidia. o–r Mature conidia. Scale bars: g, k, m–r = 10 μm, h, j = 20 μm, i = 25 μm, l = 50 μm.

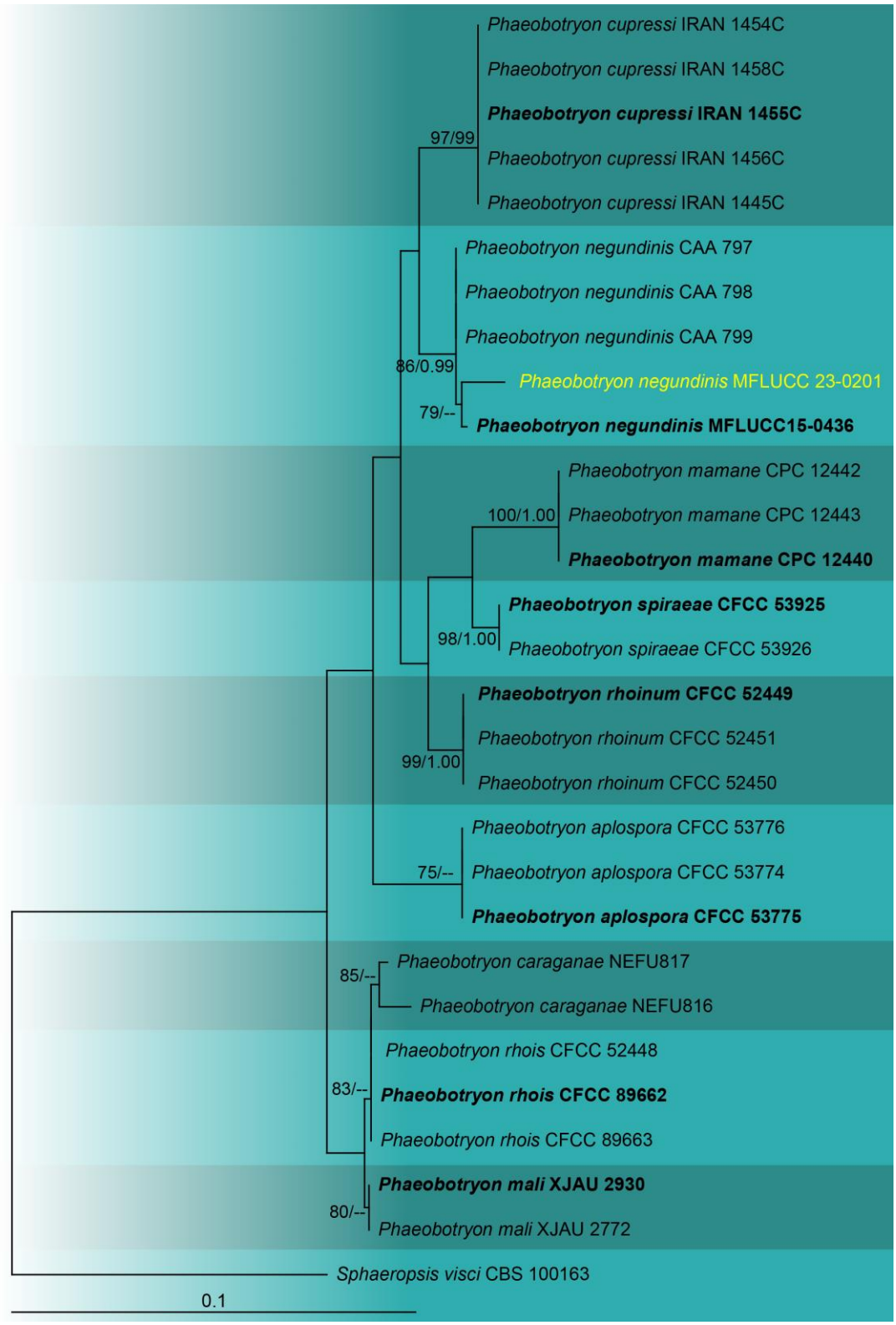


**Fig. 33 –** Phylogram generated from the maximum likelihood analysis based on the combined ITS and *tef1-α* sequence data of the genus *Phaeobotryon*. Twenty-nine strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -2120.952524 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 159 distinct alignment patterns, with 7.70% of undetermined characters or gaps. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 are given near

nodes, respectively. The tree was rooted with *Sphaeropsis visci* (CBS 100163). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Phaeobotryon negundinis*** Daranagama, Bulgakov and K.D. Hyde, Mycosphere 7, 936 (2016)

Index Fungorum number: IF 551954; Facesoffungi number: FoF 15189; Fig. 34

*Saprobic* on dead twigs of *Morus alba*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* 210–330 μm high × 220–315 μm diam. ($\bar{x}$ = 268 × 253 μm, n = 6), solitary, scattered, immersed, becoming erumpent through the host tissue, uniloculate, black, globose to subglobose, ostiolate. *Conidiomatal wall* 28–45 μm ($\bar{x}$ = 37 μm, n = 10), comprising several layers of lightly pigmented to dark brown cells of *textura angularis*, becoming hyaline towards the conidiogenous region. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 12–25 × 3–5 μm ($\bar{x}$ = 17 × 3.2 μm, n = 10), holoblastic, lining the conidiomatal cavity, hyaline, subcylindrical. *Conidia* 12.5–20.7 × 4.6–10.5 μm ($\bar{x}$ = 16 × 7.7 μm, n = 28), ovoid with a broadly rounded apex and truncated base, smooth to finely verruculose, initially aseptate and hyaline, becoming 1-septate and dark brown at maturity.

Cultural characteristics – Conidia germinating on PDA within 18 h. Colonies entire-edged, fast-growing, reaching 9 cm on the PDA at 25 °C after seven days, circular, flat, dense, initially white mycelia, becoming gray in older cultures.

Material examined – Russia, Rostov region, Shakhty City, Alexandrovsky park, on dying and dead twigs and branches of *Morus alba*, 26 November 2017, T.S. Bulgakov, MOR-23 (MFLU 23-0360), living culture MFLUCC 23-0201.

GenBank accession numbers – ITS: OR186220, *tef1-α*: OR195687.

Known distribution (based on molecular data) – Canada (Ilyukhin & Ellouze 2023), Russia (Daranagama et al. 2016, this study), the USA (DeKrey et al. 2022).

Known hosts (based on molecular data) – *Acer negundo*, *Forsythia* × *intermedia*, *Ligustrum vulgare* (Daranagama et al. 2016), *Malus domestica* (Ilyukhin & Ellouze 2023), *Morus alba* (this study), *Vitis vinifera* (DeKrey et al. 2022).

Notes – *Phaeobotryon negundinis* is usually known worldwide as a grapevine trunk disease pathogen (DeKrey et al. 2022). However, in the current study, we isolated this pathogen from dead twigs and branches. The isolate of the current study shows morphological similarities to the ex-type of *Phaeobotryon negundinis* (Daranagama et al. 2016) and clustered to the latter with 70% maximum likelihood bootstrap support and 0.90 Baysian posterior probability (Fig. 33). This study reports the *P. negundinis* from *Morus alba* from Russia.

***Phyllostictaceae*** Fr. [as 'Phyllostictei'], Summa veg. Scand., Sectio Post. (Stockholm), 420 (1849)

Facesoffungi number: FoF 02296

***Pseudofusicoccum*** Mohali, Slippers & M.J. Wingf., Studies in Mycology 55: 249 (2006)

Facesoffungi number: FoF 05299

*Pseudofusicoccum* was introduced with *Pseudofusicoccum stromaticum* as the type species (Crous et al. 2006a). *Pseudofusicoccum* is morphologically related to *Fusicoccum* and *Neofusicoccum*, and phylogenetically differs from the genera mentioned above (Crous et al. 2006a). Most of the species in this genus are recorded from their asexual morph (Senwanna et al. 2020). The conidia of *Pseudofusicoccum* are surrounded by a mucilaginous sheath (Phillips et al. 2019). Currently, nine species belong to this genus (Wijayawardene et al. 2022). Here, we provide the updated phylogeny for the *Pseudofusicoccum* taxa (Fig. 35).

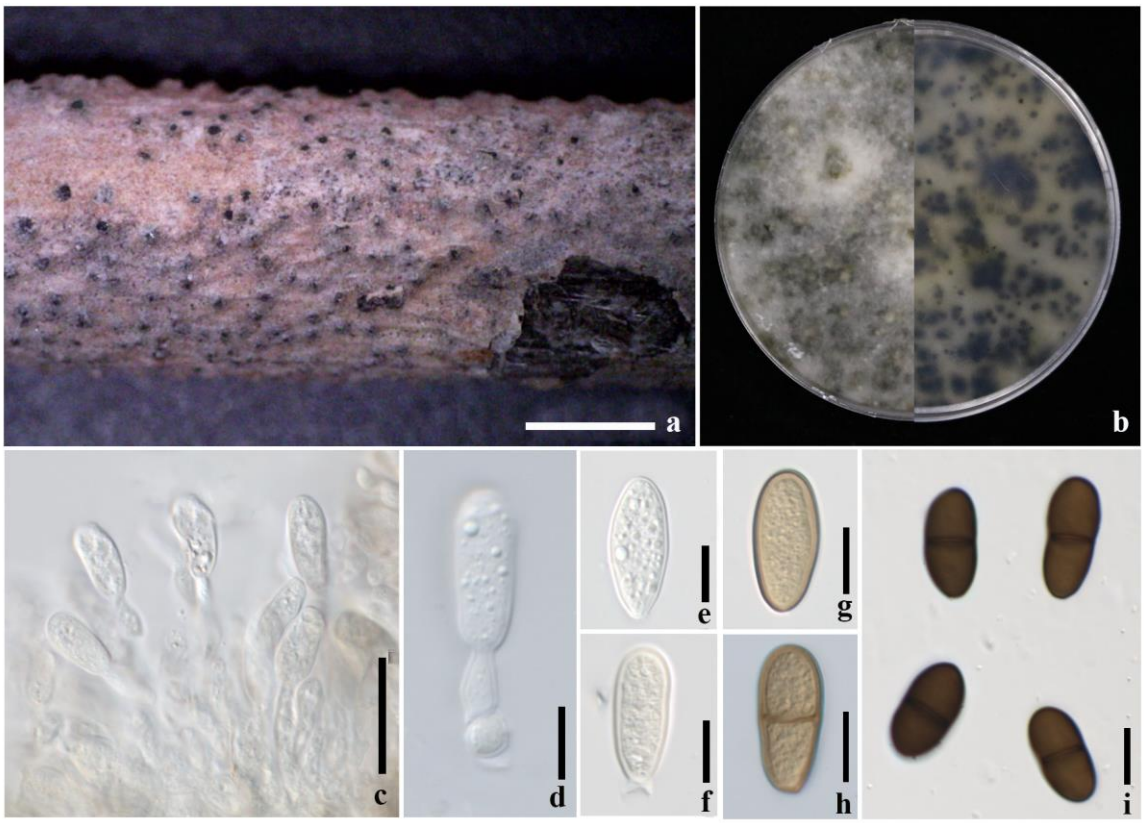


**Fig. 34 – *Phaeobotryon negundinis*** (MFLUCC 23-0201, **a new host record**). a Appearance of conidiomata on the host surface. b Surface (left) and reverse (right) views of the colony on PDA. c–d Conidia developing on conidiogenous cells. e–f Immature conidia. g–i Conidia at different stages of maturity. Scale bars: a = 2 mm, c = 20 μm, d–i = 10 μm.

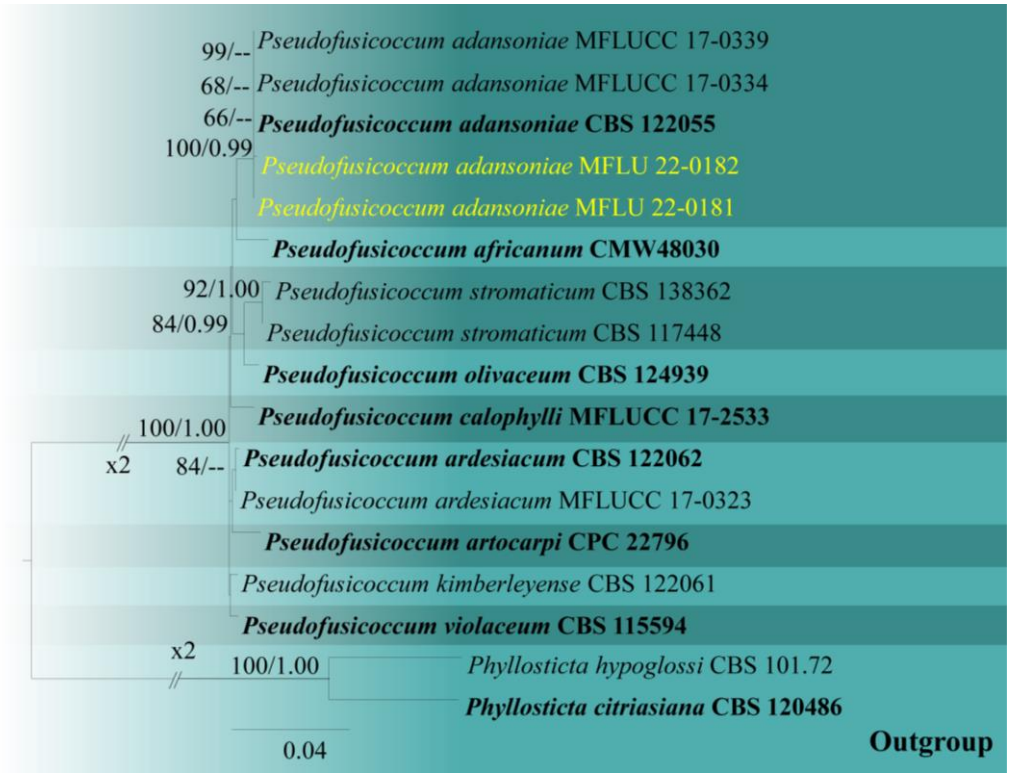


**Fig. 35 –** Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, *tef1-α* and *β-tubulin* sequence data of the genus *Pseudofusicoccum*. Seventeen strains are

included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -4983.29 is presented. Evolutionary model GTR+I+G is applied for all the genes. The matrix had 285 distinct alignment patterns, with 32.63% of undetermined characters or gaps. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are given near nodes, respectively. The tree was rooted with *Phyllosticta citriasiana* (CBS 120486) and *P. hypoglossi* (CBS 101.72). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

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

Index Fungorum number: IF 512048; Facesoffungi number: FoF 00168; Figs. 36, 37

*Saprobic* on dead twig of *Mangifera indica* (sexual morph) and dead leaves of *Epipremnum pinnatum* (asexual morph). **Sexual morph:** *Ascomata* 160–170 μm high × 170–200 μm diam. ($\bar{x}$ = 165 × 182 μm, n = 10), solitary, scattered, immersed, erumpent, globose to subglobose, gregarious, uniloculate. *Peridium* 20–50 μm wide, two-layered, outer layer composed of thick-walled, brown to dark brown cells of *textura angularis*, inner layer composed of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* comprising 3–5 μm wide, hyaline, septate pseudoparaphyses, constricted at septa. *Asci* 50–140 × 20–25 μm ($\bar{x}$ = 85 × 20 μm, n = 20), bitunicate, fissitunicate, 8-spored, cylindric-clavate to clavate, with a long pedicel, apically rounded with a well-developed ocular chamber. *Ascospores* 18–26 × 8–10 μm ($\bar{x}$ = 22 × 9 μm, n = 30), 1–2-seriate, overlapping, hyaline, aseptate, short clavate, straight, smooth-walled, with granular appearance. **Asexual morph**: Coelomycetous. *Conidiomata* 175–200 μm high × 115–130 μm diam. ($\bar{x}$ = 180 × 120 μm, n = 10), pycnidial, solitary, semi-immersed, uniloculate, subglobose to ellipsoid, black. *Conidiomatal wall* 30–38 μm wide, consist of 5–8 layers, outer layer composed of thick-walled, dark brown to brown cells of *textura angularis*, inner layer composed of thin-walled, hyaline to light brown cells of *textura angularis*. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 5–6 × 2–4 μm ($\bar{x}$ = 5.5 × 3 μm, n = 20), lining the pycnidial cavity, holoblastic, cylindrical, hyaline, discrete, determinate, smooth walled tapering to the apex. *Conidia* 18–21 x 5–8 ($\bar{x}$ = 20 × 7 μm, L/W= 2.8, n = 20), aseptate, oblong, straight, occasionally slightly bent, hyaline, smooth-walled, with granular contents.

Material examined – Thailand, Chiang Rai Province, Mueang, Thasud, on a dead twig of *Mangifera indica*, 14 November 2020, Achala Rathnayaka, AN04 (MFLU 22-0181); *ibid*, Nang Lae village, on dead leaves of *Epipremnum pinnatum*, 13 May 2020, Achala Rathnayaka AV002 (MFLU 22-0182).

GenBank accession numbers – MFLU 22-0181: ITS: OP689652, LSU: OP689693; MFLU 22-0182: ITS: OP689653, *β-tubulin*: OP700654.

Known distribution (based on molecular data) – Australia (Pavlic et al. 2008), Thailand (Doilom et al. 2015, Senwanna et al. 2020, this study).

Known hosts (based on molecular data) – *Adansonia gibbosa* (Pavlic et al. 2008), *Tectona grandis* (Doilom et al. 2015), *Hevea brasiliensis* (Senwanna et al. 2020), *Epipremnum pinnatum*, *Mangifera indica* (this study).

Notes – The morphologies of both sexual and asexual morphs of our fungal collections are similar to the holotype of *P. adansoniae* isolated from a canker on branches and twigs of *Hevea brasiliensis* (Senwanna et al. 2020) and dying branches of *Adansonia gibbose* in Australia (Pavlic et al. 2008). However, our sexual morph (MFLU 22-0181) has larger asci and ascospores ($\bar{x}$ = 85 × 20 μm and $\bar{x}$ = 22 × 9 μm) than those of the holotype ($\bar{x}$ = 70 × 18 μm *vs*. $\bar{x}$ = 16.6 × 6.3 μm) (Senwanna et al. 2020). Also, the length of conidia of our asexual morph (MFLU 22-0182) ($\bar{x}$ = 20 × 7 μm, L/W= 2.8) is comparatively smaller than the holotype ($\bar{x}$ = 22.5 × 5.2 μm, L/W= 4.3) (Pavlic et al. 2008). According to the phylogenetic analyses, our collections (MFLU 22-0181 and MFLU 22-0182) clustered with other *P. adansoniae* strains (CBS 122055, MFLUCC 17-0334, MFLUCC 17-0339) with 100% MPBS and 0.99 BYPP (Fig. 35). The current study presents new

host records of *P. adansoniae* on *Epipremnum pinnatum* and *Mangifera indica* in Thailand and the second sexual morph record of *P. adansoniae*.

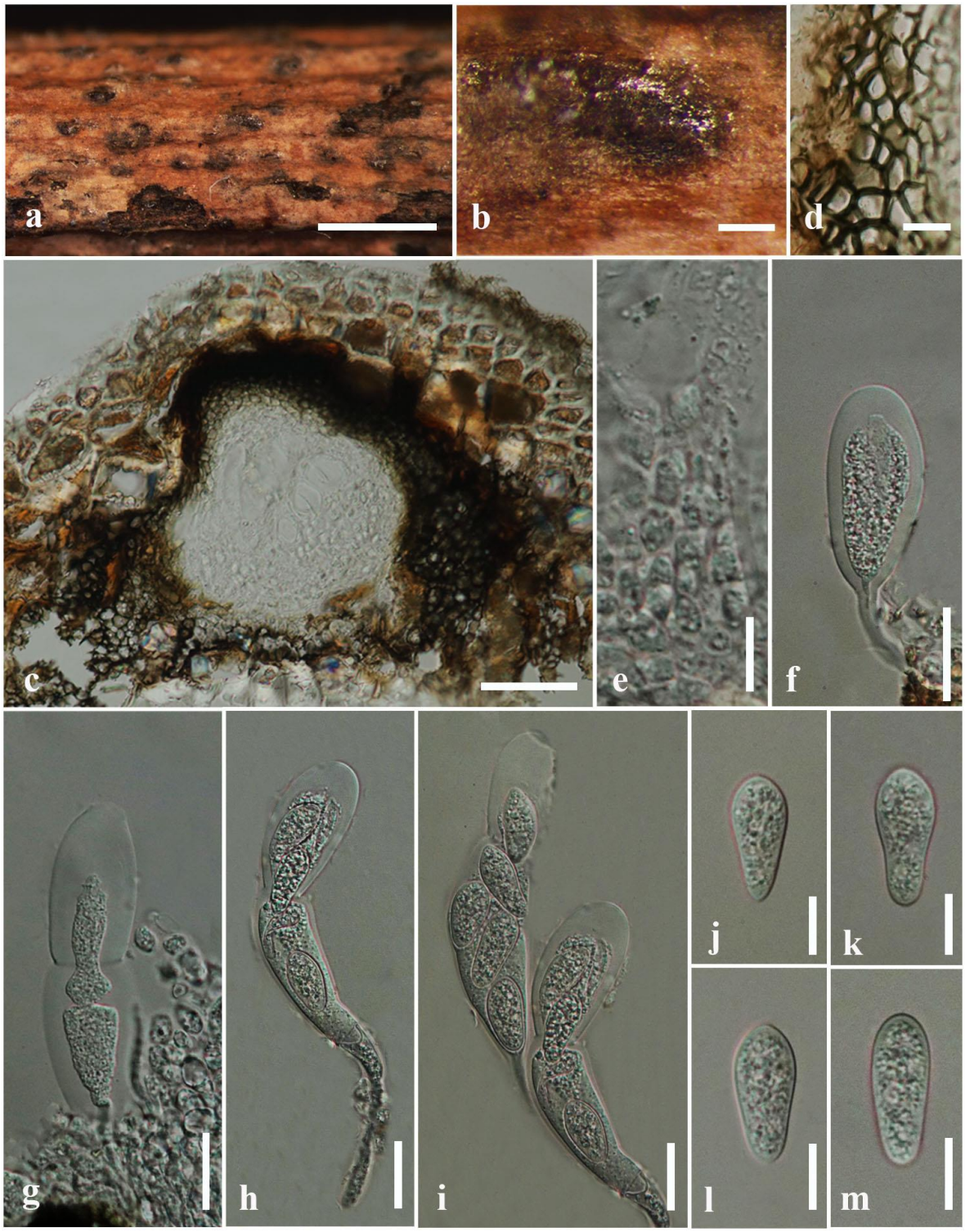


**Fig. 36 – Sexual morph of *Pseudofusicoccum adansoniae*** (MFLU 22-0181, **a new host record**). a, b Appearance of ascostromata on host surface. c Section through ascomata. d Section through peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. Scale bars: a = 1 mm, b = 100 µm, c = 50 µm, d, e, j–m = 10 µm, f–i = 20 µm.

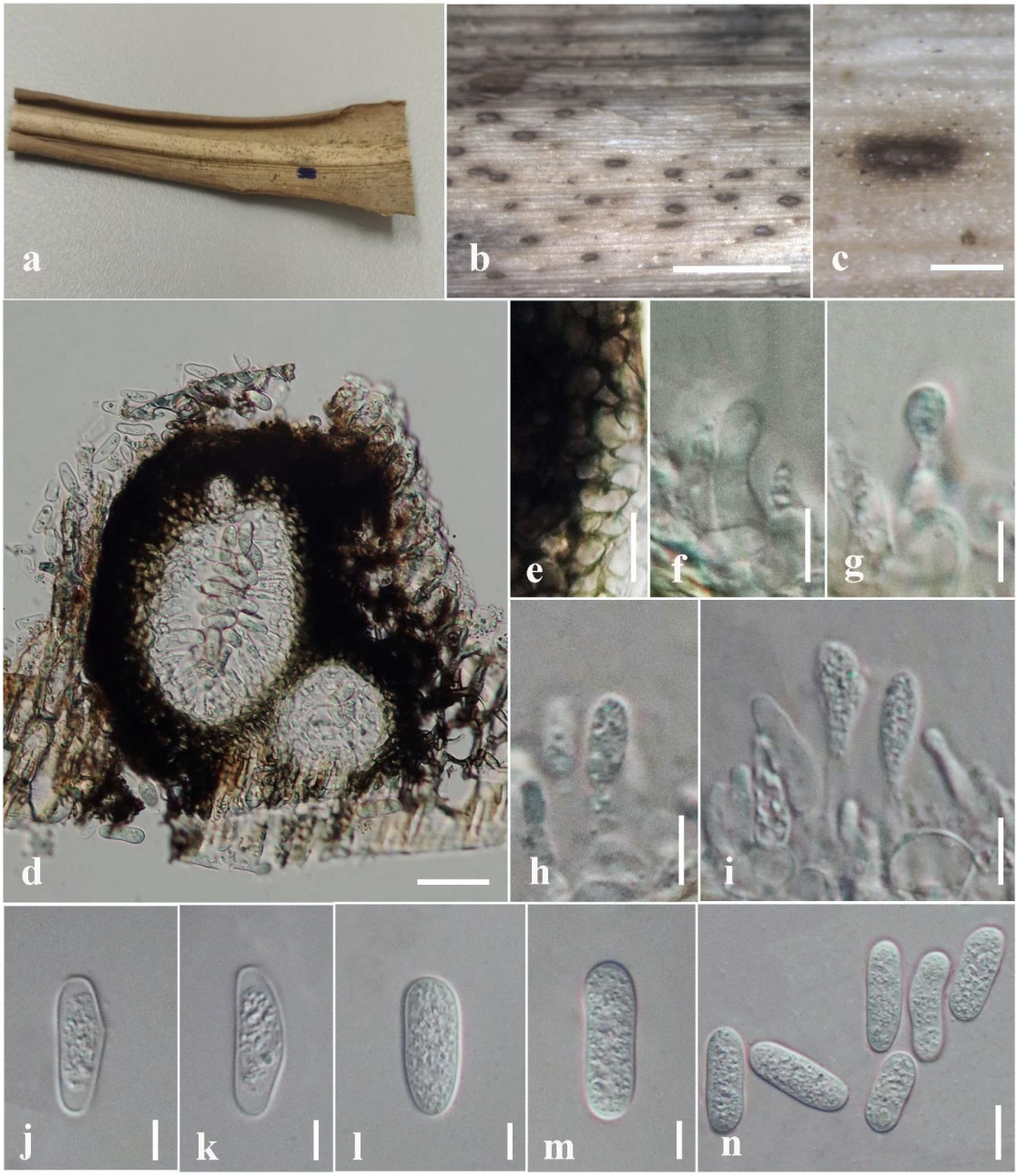


**Fig. 37 – Asexual morph of *Pseudofusicoccum adansoniae*** (MFLU 22-0182, **a new host record**). a Host. b, c Appearance of conidiomata on host tissue. d Vertical section of conidiomata. e Section through peridium. f–i Developing conidia attached to conidiogenous cells. j–n Conidia. Scale bars: b = 1 mm, c = 200 µm, d = 50 µm, e = 5 µm, f–i, n = 10 µm, j–m = 5 µm.

**Class *Eurotiomycetes*** O.E. Erikss. & Winka, Myconet 1(1), 6 (1997)

For *Eurotiomycetes*, we follow the recent treatment of Wijewardena et al. (2022).

**Subclass *Chaetothyriomycetidae*** Doweld, Prosyllabus Tracheophytorum, Tentamen Systematis Plantarum Vascularium (Tracheophyta) (Moscow), LXXVIII (2001)

Facesoffungi number: FoF 14243

***Pyrenulales*** Fink ex D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1), 182 (1986)

Facesoffungi number: FoF 14244

***Pyrenulaceae*** Rabenh., Krypt.-Fl. Sachsen, Abth. 2 (Breslau), 42 (1870)

Facesoffungi number: FoF 14245

***Anthracothecium*** Hampe ex A. Massal., Atti del Reale Istituto Veneto di Scienze, lettere ed Arti, Sér. 3 5, 330 (1860) [1859-1860]

Facesoffungi number: FoF 14246

*Anthracothecium* comprises five species (Aptroot 2012, Wijayawardene et al. 2022), namely *Anthracothecium australiense*, *A. prasinum*, *A. macrosporum*, *A. gregale* and *A. interlatens* (Aptroot 2012). An updated phylogeny for the genus is given in Fig. 38.

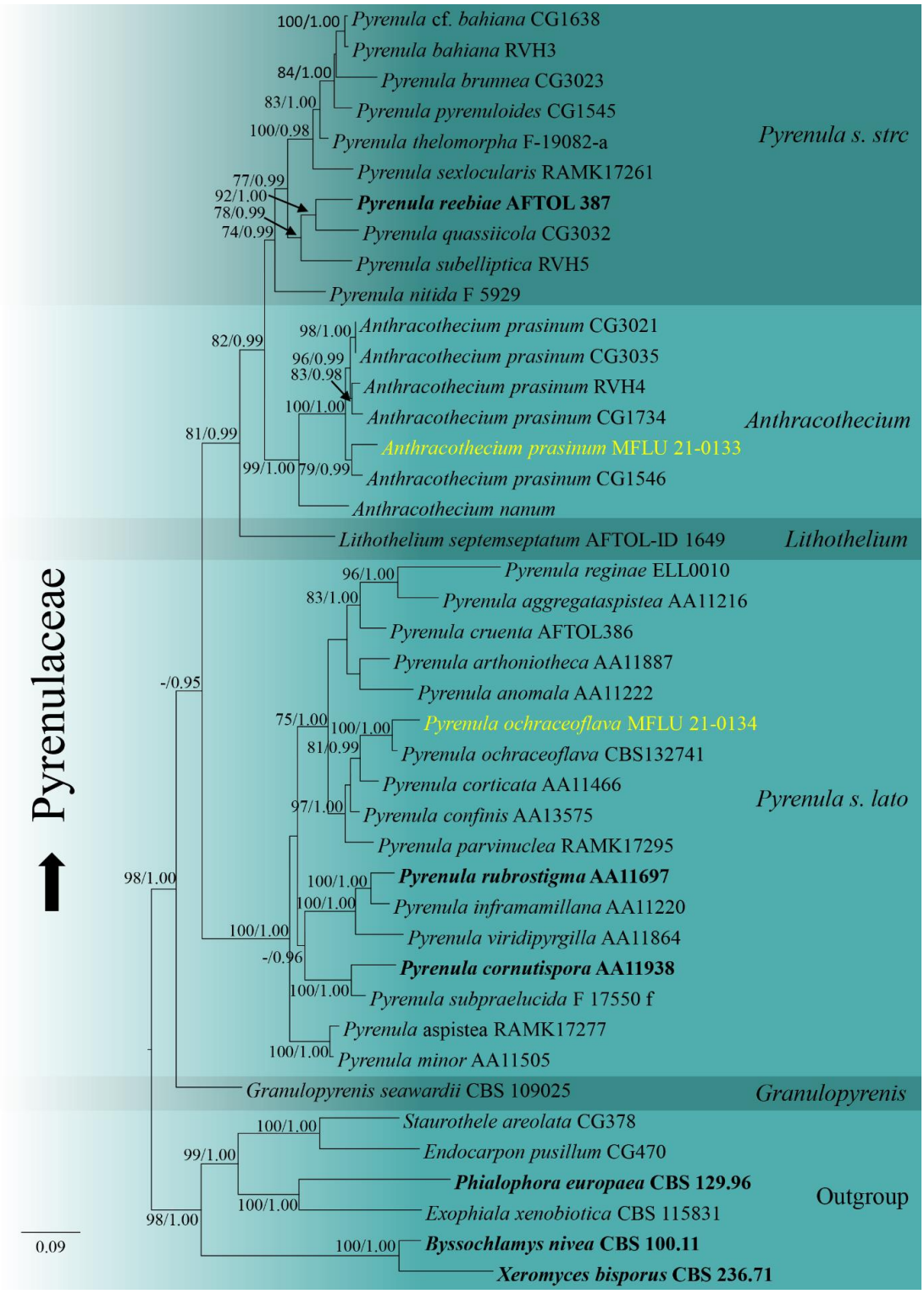


**Fig. 38 –** Phylogram generated from maximum likelihood analysis based on the combined mtSSU, LSU and ITS and sequence data for selected genera in *Pyrenulaceae*. Forty-two strains are included

in the combined analyses, which comprised of 2639 characters (812 characters for mtSSU, 899 characters for LSU, 928 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -23057.85 is presented. The matrix had 1437 distinct alignment patterns, with 27.49% of undetermined characters or gaps. For all the gene regions (mtSSU, LSU, ITS), GTR+G was applied as the evolutionary model. Bootstrap support values for ML equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Byssochlamys nivea* (CBS 100.11), *Endocarpon pusillum* (CG470), *Exophiala xenobiotica* (CBS 115831), *Phialophora europaea* (CBS 129.96), *Phialophora europaea* (CBS 129.96), *Staurothele areolate* (CG378) and *Xeromyces bisporus* (CBS 236.71). The newly generated sequences are indicated in yellow and the type strains in **bold**.

***Anthracothecium prasinum*** (Hepp) Müll. Arg., Linnaea 43, 44 (1880)

Index Fungorum number: IF 132203; Facesoffungi number: FoF 10696; Fig. 39

*Thallus* epi to endoperidermal, pale green, corticated, crustose, continuous, matt to slightly glossy, reflecting bark texture, medulla not apparent. *Prothallus* present, *Photobiont* observed. **Sexual morph:** *Ascomata* perithecial, 1–2 mm wide, semi-immersed to erumpent, solitary, carbonaceous. *Ostiole* distinct, apical, papillate. *Peridium* thickened, carbonaceous, black. *Hamathecium* comprising filamentous paraphyses and asci, hyaline. *Paraphyses* numerous, packed, not branched, aseptate, hyaline, filamentous, 0.8–3 µm thickness, generally exceeding the length of asci. *Asci* 300–340 × 45–55 µm ($\bar{x}$ = 320 × 50 µm, n = 20), bitunicate, fissitunicate, 2-spored, long cylindrical, tholus thickened, tip blunted, with poorly developed stipe, ascus wall apically thickened, inconspicuous ocular chamber. *Ascospores* 120–180 × 25–40 µm ($\bar{x}$ = 150 × 32.5 µm, n = 40), hyaline to brown, oblong to slightly curved, muriform, both ends bluntly tapered, smooth-walled, without gelatinous sheath. **Asexual morph:** Undetermined.

Material examined – Thailand, Phattalung Province, Pa Phayom, Lan khoi, Hat Yai, elevation 80.5 m, 7.89274 (N 7' 53' 33.853") altitude, 99.7895(E 99' 47' 22.206") latitude, on living bark of *Malvaceae*, 11 May 2018, V. Thiyagaraja, MFLU 21-0133.

Known distribution (based on molecular data) – Australia (eastern Queensland) and Thailand (Wolseley et al. 2002, Boonpragob et al. 2009, this study).

Known hosts (based on molecular data) – unknown, living bark of *Malvaceae* (this study).

GenBank accession numbers – ITS: OM320440, LSU: OM296275, mtSSU: OM304350.

Notes – The new collection is phylogenetically closely related to *A. prasinum*. However, the new collection shows differences in the number of ascospores per ascus (2-spored) in comparison to *A. prasinum*, which shows 6-8 ascospores per ascus but shares similarities in the apical ostiole, length of asci, and pantropical habitat. The new strain also shares similar morphological features to *A. interlatens*, in having semi-immersed to immersed, black perithecia, carbonized peridium, 2-spored ascus, and the size of ascospores but differs in the distribution of ascomata (aggregated *vs*. solitary), the shape of ostiole (shared *vs*. apical) and size of asci (200–230 × 45–52 µm *vs*. 300–340 × 45–55 µm) (Joshi et al. 2018). The new collection is recorded on the bark of the *Malvaceae* tree. However, there is no clear evidence for the host substance of *Anthracothecium prasinum*. Thus, we provide a comprehensive illustration (Fig. 39), with a detailed description of this species.

***Pyrenula*** Ach., Kongliga Svenska Vetenskaps Academiens Handlingar, Ny Följd 30, 160 (1809)

Facesoffungi number: FoF 14247

*Pyrenula* is a crustose lichenized genus recorded from smooth and shaded bark that mainly occurs in the tropics but is also distributed in the temperate regions (Cáceres et al. 2013, Ingle et al. 2018). The genus comprises more than 225 species with *Pyrenula nitida* as the type (Wijayawardene et al. 2022). An updated phylogeny for the genus in shown in Fig. 38.


**Fig. 39 – *Anthracothecium prasinum*** (MFLU 21-0133, **a new collection**). a Host. b–d Ascomata on substrate. e Vertical section through an ascoma. f Paraphyses. g Asci. h–m Ascospores. Scale bars: d, e = 500 µm, f, g = 200 µm, h–m = 100 µm.

***Pyrenula ochraceoflava*** (Nyl.) R.C. Harris, Mem. N. Y. bot. Gdn 49: 96 (1989)

Index Fungorum number: IF 134434; Facesoffungi number: FoF 10697; Fig. 40

*Thallus* epi peridermal, whitish, corticated, crustose, pruinose. *Prothallus* present, *Photobiont* observed. **Sexual morph:** *Ascomata* perithecial, 200–300 µm wide, 290–300 µm high, semi-immersed to erumpent, solitary to aggregated, coriaceous. *Ostiole* distinct, filled with paraphysoids. *Peridium* thickened, composed of two layers, outer layer 14–24 µm thickness, brown, thicker at the upper, thinner at the base; inner layer 6–16 µm thickness, black. *Hamathecium* comprising filamentous paraphyses and asci, hyaline. *Paraphyses* 0.6–2 µm thickness, numerous, anastomosing, not branched, septate, hyaline, filamentous, generally exceeding the length of asci. *Asci* 60–80 × 10–24 µm ($\bar{x}$ = 70 × 17 µm, n = 20), bitunicate, fissitunicate, long cylindrical, tholus thickened, tip blunted, with poorly developed stipe, ascus wall apically thickened, inconspicuous ocular chamber. *Ascospores* 10–17 × 6–9 µm ($\bar{x}$ = 13.5 × 7.5 µm, n = 40), overlapping uniseriate to biseriate, 8-spored, ellipsoid, hyaline to pale brown, both ends bluntly tapered, sub-muriform, with 4 tiers of 1–4 each loci, smooth-walled, without a gelatinous sheath. **Asexual morph:** Undetermined.

Material examined – Thailand, Chiang Rai Province, Mae Fah Luang Botanical Garden, on living bark of *Alstonia scholaris*, 24 November 2019, Vinodhini Thiyagaraja, 50L (MFLU 21-0134).

Known distribution (based on molecular data) – India and Thailand (Makhija & Adawadkar 2001, Logesh et al. 2013, Aptroot 2012, Buaruang et al. 2017, this study).

Known hosts (based on molecular data) – *Cocos nucifera* (Makhija & Adawadkar 2001, Logesh et al. 2013, Aptroot 2012, Buaruang et al. 2017), *Alstonia scholaris* (this study).

GenBank accession numbers – ITS: OM320441, LSU: OM296115, mtSSU: OM304349

Notes – The new collection is phylogenetically closely related to *P. ochraceoflava* (Fig. 38). The new collection shares similar morphological characteristics to *P. ochraceoflava* in having perithecial ascomata, ascomatal wall with the orange-brown outer layer and dark brown inner layer, central ostiole, simple paraphyses, absence of periphyses, fissitunicate, 8-spored, elongate cylindrical, 60–80 × 10–24 µm asci with an inconspicuous ocular chamber, and pale to medium brown, ellipsoid, sub-muriform ascospores (Fig. 40). However, the new collection differs by having slight morphological differences, including thallus morphology. For example, most species own pigmented thallus, but a whitish thallus with pruinose was observed in the new strain. Yet the shape and size of asci and ascospores are used as diagnostic characters for *Pyrenula ochraceoflava* (Aptroot 2012). *Pyrenula ochraceoflava* is recorded for the first time from *Alstonia scholaris*, thus, we introduce it as a new host record.

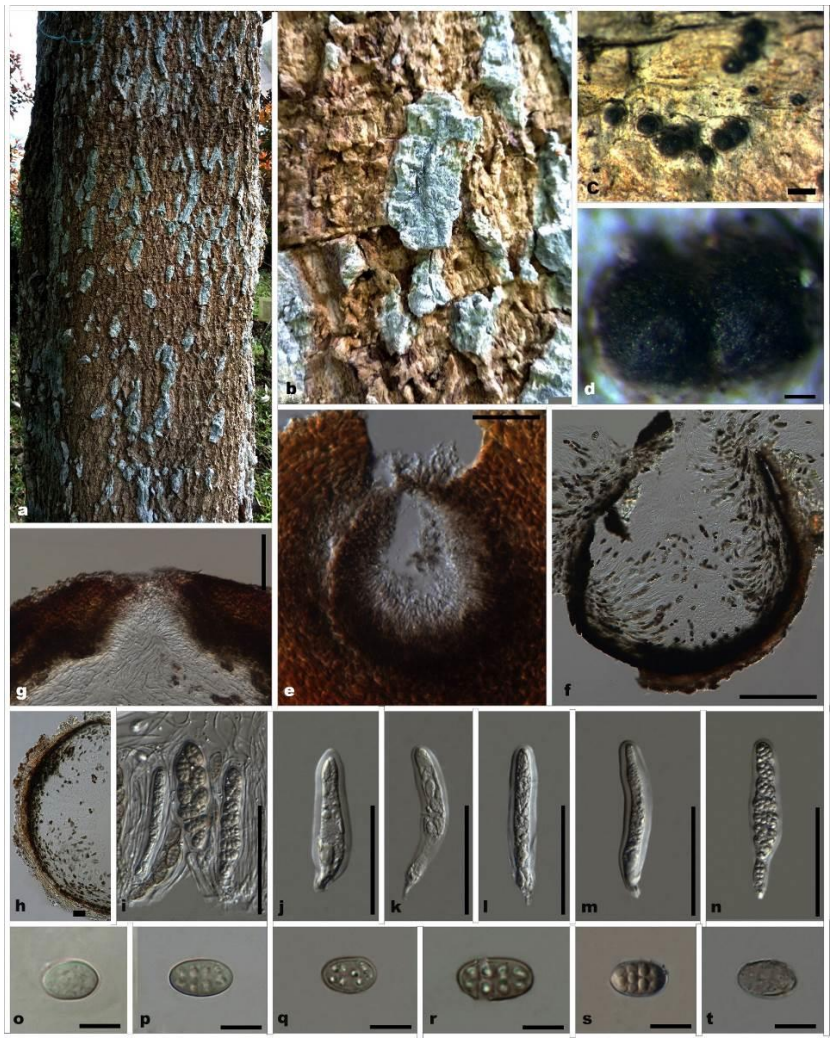


**Fig. 40 – *Pyrenula ochraceoflava*** (MFLU 21-0134, **a new host record**). a–d Ascomata on substrate. e, f Vertical section through an ascoma. g Ostiole. h Peridium. i Paraphyses. j–n Asci. o–t Ascospores. Scale bars: b–d = 100 µm, g–f = 50 µm, h = 30 µm, i–n = 50 µm, o–t = 10 µm.

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

Facesoffungi number: FoF 14248

For Leotiomycetes, we follow the recent treatment of Wijayawardene et al. (2022).

**Subclass *Leotiomycetidae*** P.M. Kirk, P. Cannon, Minter & Stalpers, (2008)

Facesoffungi number: FoF 14249

***Helotiales*** Nannf., Nova acta Regiae Societatis Scientiarum Upsaliensis, Ser. 4 8(no. 2), 68 (1932)

Facesoffungi number: FoF 13859

***Cenangiaceae*** Rehm, Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.3(lief. 31), 213 (1889)

Facesoffungi number: FoF 05955

***Chlorencoelia*** J.R. Dixon, Mycotaxon 1(3), 223 (1975)

Facesoffungi number: FoF 14250

*Chlorencoelia* was introduced by Dixon (1975) with *Chlorencoelia versiformis* (basionym: *Peziza versiformis*) as the type species. This genus is characterized by superficial, medium-sized apothecia, filiform, septate 8-spored, J+, cylindrical asci, and ellipsoid to allantoid ascospores. We provided the updated phylogeny for selected genera in *Cenangiaceae* in Fig. 41.

***Chlorencoelia torta*** (Schwein.) J.R. Dixon, Mycotaxon 1(3), 230 (1975)

Index Fungorum number: IF 311053; Facesoffungi number: FoF 13909; Fig. 42

*Saprobic* on decayed wood barks. **Sexual morph:** *Apothecia* 2–4 × 2–3.1 mm ($\bar{x}$= 3.1 × 2.5 mm, n = 5) in dry condition, arising singly or in small cluster, stipitate. *Receptacle* cupulate, olivaceous dark brown to black. *Stipe* 1.1–1.9 × 0.6–0.9 mm ($\bar{x}$ = 1.5 × 0.8 mm, n = 5) in dry condition, concolorous with receptacle, rugose. *Disc* dark brown, shallow cupulate to infundibuliform convex with enrolling edges upon drying. *Ectal excipulum* 54–106 µm ($\bar{x}$ = 79.5 µm, n = 15), composed of thin to thick-walled, hyaline to dark brown cells of *textura angularis*. *Medullary excipulum* 119–169 µm ($\bar{x}$ = 143.4 µm, n = 15) in lower flanks, composed of thin-walled, hyaline to yellowish cells of *textura intricata*. *Hymenium* 129–181 µm ($\bar{x}$ = 170.6 µm, n = 15). *Paraphyses* 2.4–3.7 µm in diam. ($\bar{x}$ = 2.8 µm, n = 30) at the apex, filiform, occasionally slightly swollen at the apex, septate, sometimes guttulate. *Asci* 95–115 × 4.4–6.9 µm ($\bar{x}$ = 105.3 × 6 µm, n = 15), unitunicate, 8-spored, cylindrical, rounded to subconical apex, amyloid, long substipitate base, arising from croziers. *Ascospores* 6.2–8.4 × 2.4–3.4 µm ($\bar{x}$ = 7.3 × 3 µm, n = 20), uniseriate, ellipsoid, hyaline, biguttulate, rounded at both ends. **Asexual morph:** Undetermined.

Material examined – Thailand, Kew Mae Pan trail, Doi Inthanon, Chomthong District, Chiang Mai Province, bark of an unknown host, 20 October 2021, Pi Usa, KMP3-7B (MFLU 23-0016)

GenBank accession numbers – ITS: OP64490, LSU: OP622874.

Known distribution (based on molecular data) – China (Pärtel et al. 2017, Zhuang et al. 2000), Korea (Han et al. 2014, Kim et al. 2015), New Zealand (unpublished), the USA (Raja et al. 2011, Pärtel et al. 2017), Thailand (this study).

Known hosts (based on molecular data) – *Fuscospora fusca* (unpublished), *Leptospermum scoparium* (unpublished), rotten deciduous wood (Pärtel et al. 2017).

Notes – Our species fit the description of *Chlorencoelia torta* by having black to olivaceous dark apothecia, ectal excipulum of *textura angularis* cells, medullary excipulum of *textura intricata* cells, and ellipsoidal ascospores (Fig. 42). *Chlorencoelia torta* has been previously recorded in Japan, New Zealand, North America, Puerto Rico, the Soviet Union, and Tasmania on decayed wood of *Acer*, *Betula*, *Fagus*, *Quercus*, *Tabebuia*, coniferous and unidentified wood (Dixon 1975, Han et al. 2014, Pärtel et al. 2016). Morphologically, our specimen (MFLU 23-0016) is similar to the holotype of *C. torta* (CUP 51760) designated by Dixon (1975), even though the paraphyses septation in our specimen is irregular. However, the phylogenetic relationship between our species and the holotype cannot be ascertained, as sequence data are unavailable for the type specimen. Phylogenetic comparison can only be assessed for the species to whom sequence data is provided by Pärtel et al. (2017) and Han et al. (2014), as no other studies have been conducted on *C. torta*.

Based on the phylogenetic analysis of combined ITS and LSU sequences, our isolate (MFLU 23-0016) clustered with the isolates of *C. torta* from China, New Zealand, and Korea with 91% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 41).

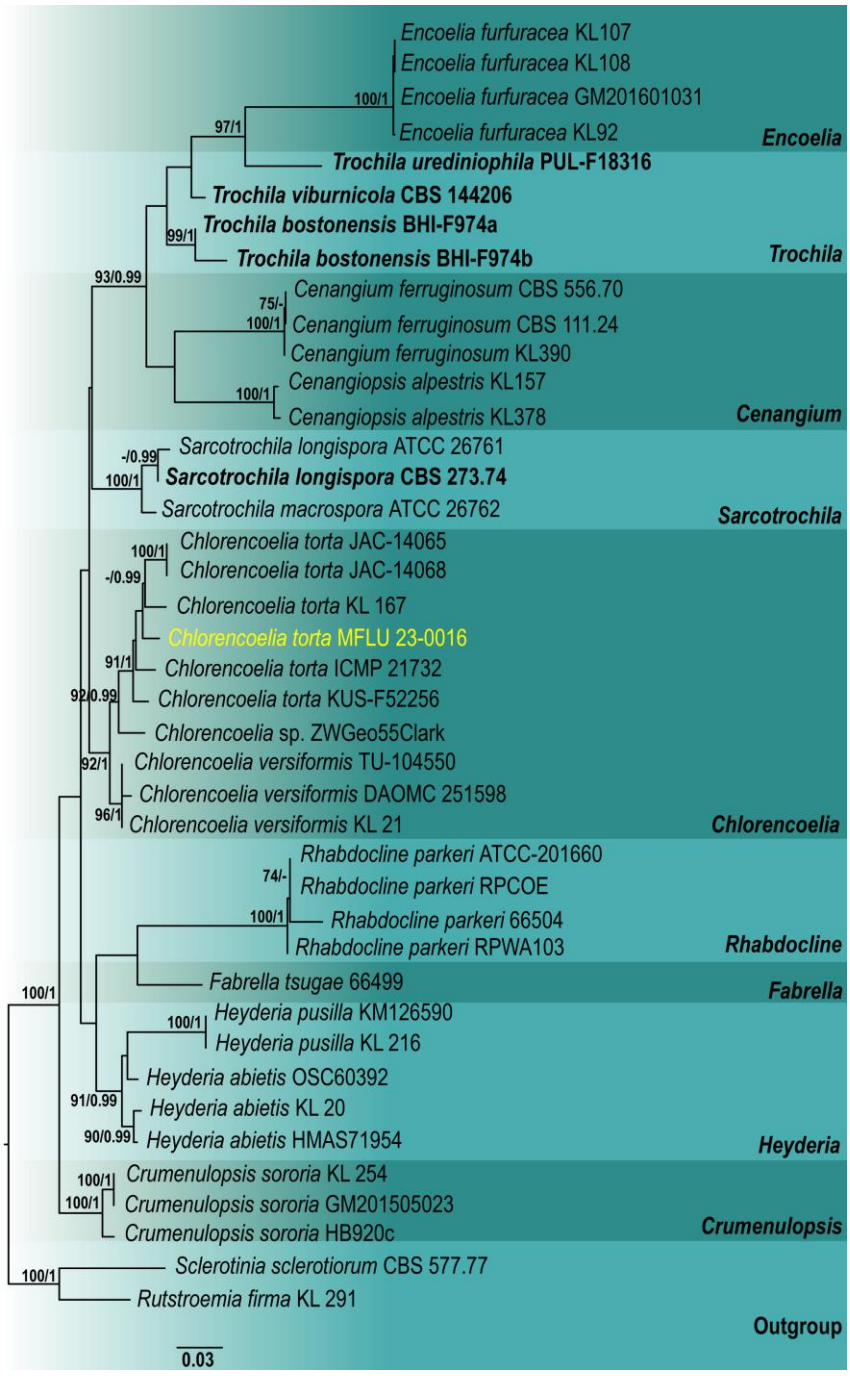


**Fig. 41 –** Phylogram generated from RaxML analysis based on the combined ITS and LSU sequence data of *Cenangiaceae*. Forty-one strains are included in the combined analyses, which comprised of 1303 characters (468 characters for ITS and 835 for LSU). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6924.87 is presented. The matrix had 367 distinct alignment patterns, with 25.9% of undetermined characters or gaps. Evolutionary model applied for both genes is TIM2+I+G. Maximum likelihood bootstrap values equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 (MLBS/BYPP) are given at the nodes, respectively. The tree is rooted to *Sclerotinia sclerotiorum* (CBS 577.77) and *Rutstroemia firma* (KL291). The type strains are indicated in **bold** and newly generated strains are in red.

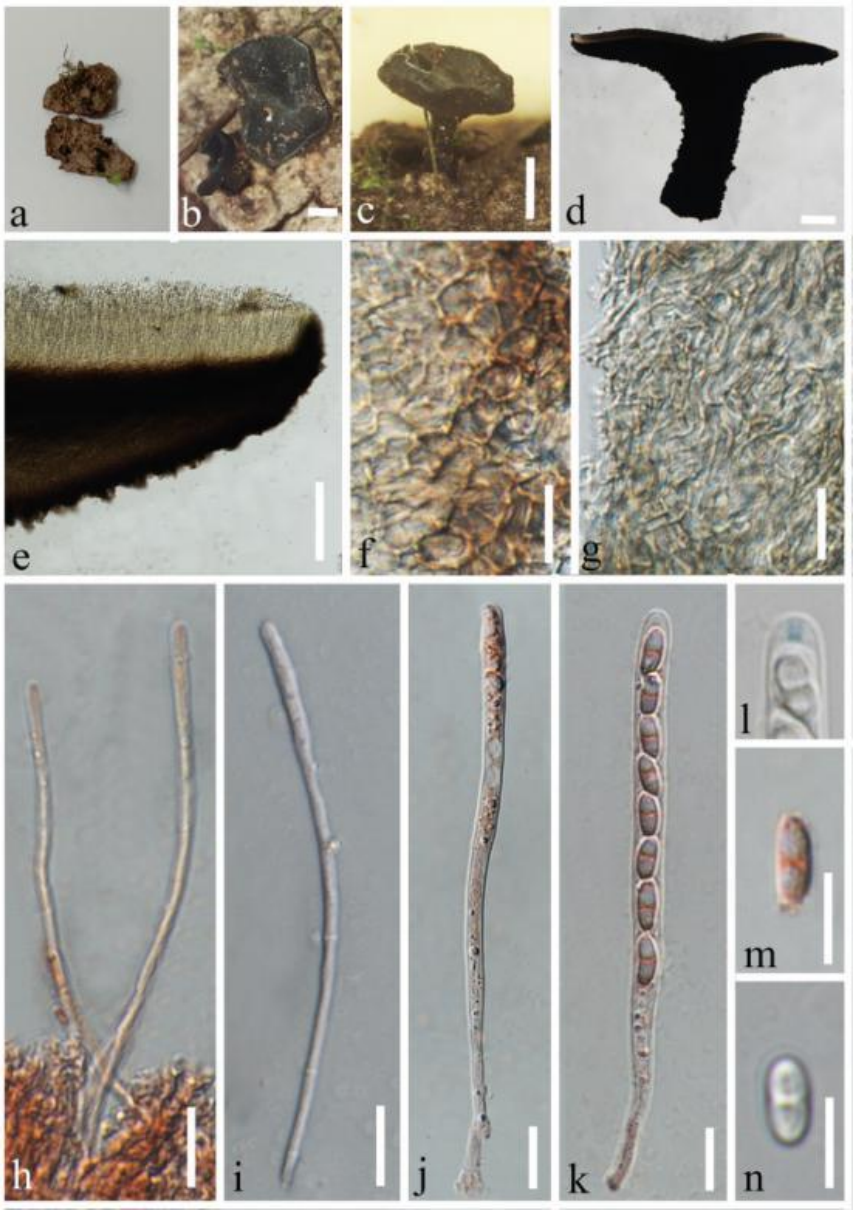


**Fig. 42 – *Chlorencoelia torta*** (MFLU 23-0016, **a new geographical record**). a Bark pieces of a decayed log. b–c Apothecia on the substrate. d Cross section of an apothecium. e Close up of the hymenium at the margin. f Close up of the ectal excipular cells. g Close up of the medullary excipular cells. h–i Slightly apically swollen paraphyses (mounted in Congo red). j–k Asci (mounted in Congo red). l J+ ascal tip (mounted in Melzer agent). m–n Ascospores (m mounted in Congo red). Scale bars: b–c = 1 mm, d = 450 µm, e = 155 µm, f–g = 17 µm, h–k = 15 µm, m–n = 8 µm.

***Helotiaceae*** Rehm [as 'Helotieae'], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.3(lief. 37), 647 (1892) [1896]

Facesoffungi number: FoF 05896

***Hymenotorrendiella*** P.R. Johnst., Baral & R. Galán, in Johnston et al., Phytotaxa 177(1), 9 (2014)

Facesoffungi number: FoF 14251

Johnston et al. (2014) established *Hymenotorrendiella* to accommodate nine species clustered with *Torrendiella*, *Lachnella* and *Zoellneria*. *Hymenotorrendiella eucalypti* is the type species of the genus. *Hymenotorrendiella* taxa can be distinguished from *Torrendiella* by having Calycina- or Hymenoscyphus-type asci apical structure and abundant globose content in living paraphyses (Johnston et al. 2014). The updated phylogeny for *Hymenotorrendiella* taxa is provided in Fig. 43.

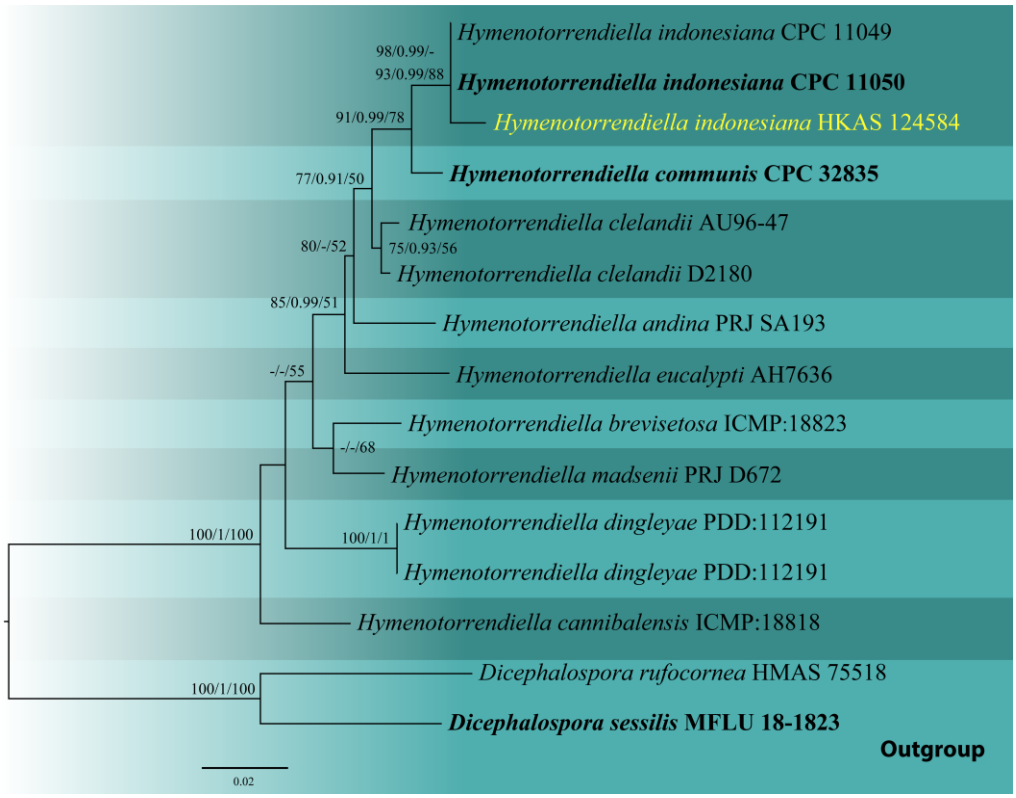


**Fig. 43 –** Phylogram generated from maximum likelihood analysis based on ITS sequence data for the genus *Hymenotorrendiella*. Fifteen strains are included in the analysis which comprised 510 characters for the ITS gene. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -1553.396359 is presented. The matrix had 127 distinct alignment patterns, with 3.74% of undetermined characters or gaps. Evolutionary models applied for the ITS gene is SYM+G. Bootstrap support values for maximum parsimony greater than 50%, maximum likelihood bootstrap support values equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.90 are given near nodes, respectively. The tree is rooted with *Dicephalospora rufocornea* (HAMS 75518), *Dicephalospora sessilis* (MFLU 18-1823). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Hymenotorrendiella indonesiana*** Crous & P.R. Johnst., in Crous et al., Persoonia 44, 349 (2020)

Index Fungorum number: IF 835414, Facesoffungi number: FoF 12899; Fig. 44

*Saprobic* on leaf litters on *Eucalyptus* sp. **Sexual morph:** *Apothecia* 0.4–0.8 mm wide × 0.5–1.0 mm high ($\overline{x}$ = 0.6 × 0.7 mm, n = 20), superficial, scattered or gregarious in groups, stipitate when dry. *Disc* flat to slightly concave when dry, smooth, yellowish central with off-white edge. *Receptacle* cupulate, concolorous at the edge of the disc, covered with dark brown setae. *Stipe* 0.2–0.4 mm ($\overline{x}$ = 0.3 mm, n = 20), short, smooth, dark brown. *Setae* mostly 15–25 per apothecium, 180–270 µm long, smooth, dark brown but paler on apex, 7–8-septate, thick-walled, constricted at the base and connected with the central ectal excipulum cell. *Hymenium* 100–140 µm, hyaline with yellowish brown contents. *Ectal excipulum* 66–74 µm thick, comprised of 3–4 layers, thin-walled, hyaline cells of *textura angularis* with yellowish or brown exudate, inner layer of ectal excipulum comprised of narrow *textura prismatica* cells at stipe, non-gelatinous. *Medullary excipulum* 57–63 µm thick, comprised of thin-walled, loosely hyphae of *textura intricata*, 3.2–4.0 µm wide, hyaline, non-gelatinous. *Paraphyses* 2.8–3.4 µm ($\overline{x}$ = 3.3 µm, n = 30) in the widest, sometimes branched and septate near the base, rounded apex, hyaline. *Asci* 88–110 × 7–10 µm ($\overline{x}$ = 99 × 9 µm, n = 40), 8-spored, cylindric to subclavate, subconical apex with amyloid apical pore in Melzer's reagent, tapering to subtruncate base. *Ascospores* (17.5–)18.0–26.0(–28.0) × (3.7–)4.0–4.9 µm ($\overline{x}$ = 22 × 4.4 µm, n = 100), Q = (3.8–)4.1–6.2(–7.1) µm, Qm = 5.0 ± 0.6 µm, overlapping uni- to bi-seriate,

fusiform with umbrella-shaped, mucilaginous appendage at the ends, slightly curved, hyaline, thin-walled, smooth, aseptate with unipolar or bipolar and irregular guttules. **Asexual morph:** Undetermined.

Material examined – China, Yunnan Province, Puer City, Jingdong County, dead leaf litter of *Eucalyptus* sp., 9 June 2022, Cuijinyi Li LCJY-772 (HKAS 124584).

GenBank accession numbers – ITS: OP321584.

Known distribution (based on molecular data) – Indonesia, Malaysia (Crous et al. 2006b, 2020), China (this study).

Known hosts (based on molecular data) – *Eucalyptus urophylla*, *Eucalyptus* sp. (Crous et al. 2006b, 2020, this study).

Notes – Our collection is found in the subtropical evergreen broad-leaved forest and shares similar morphological features with *Hymenotorrendiella indonesiana* (CPC 11050) by having small cupulate apothecia, distinguishable coloured stipe from the receptacle, dark and long setae arising from the central cells of ectal excipulum and fusiform ascospores with umbrella-shaped mucilaginous appendages at both ends (Crous et al. 2006b). The comparison of the base pairs between our strain and CPC 11050 shows a 0.85% difference in the ITS region (7/823). Based on the phylogenetic analyses of ITS gene fragment (Fig. 43), our collection clustered with *Hymenotorrendiella indonesiana* (CPC 11049 and CPC 11050) with 96% maximum likelihood bootstrap support, 86% maximum parsimony bootstrap support and 0.99 Bayesian probability statistical supports, respectively. This is the first record of this species in China.

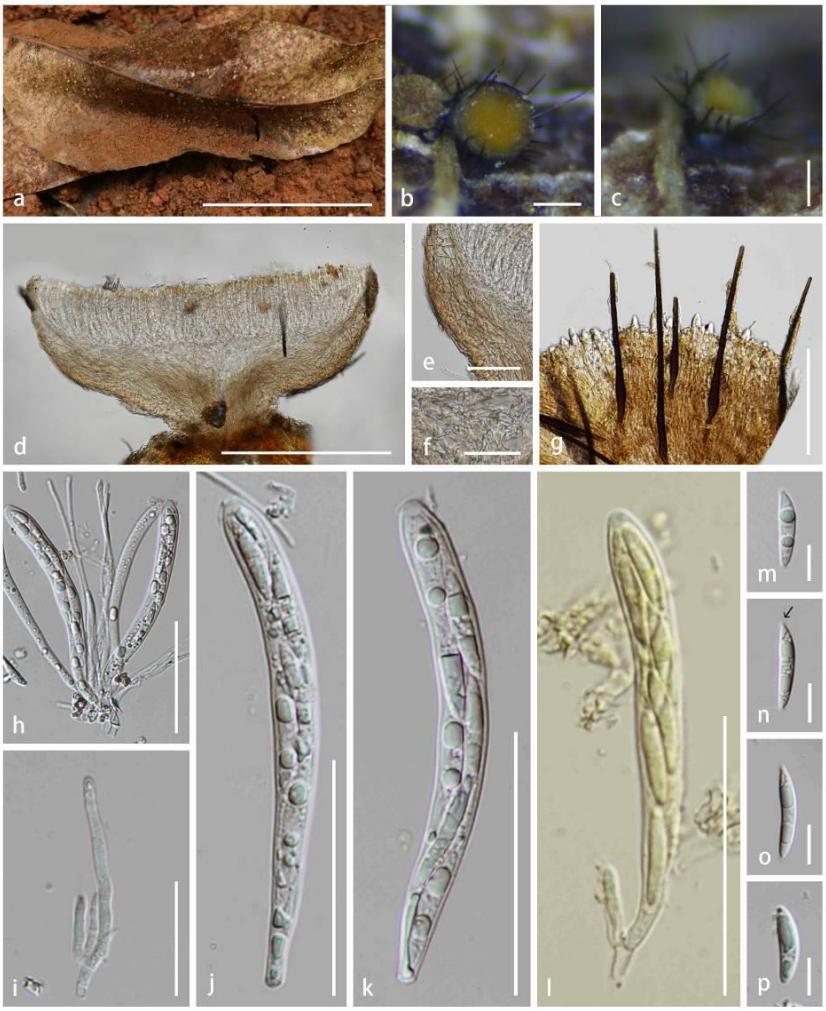


**Fig. 44 – *Hymenotorrendiella indonesiana*** (HKAS 124584, **a new geographical record**). a Fresh ascomata on the leaf. b, c A dried ascoma on the leaf. d Vertical section of an ascoma. e Ectal excipulum. f Medullary excipulum. g Hairs. h Asci and paraphyses. i Paraphyses. j–l Asci (l Ascus

in Meltzer's reagent). m–p Ascospores. Scale bars: a = 4 cm, b–d = 300 µm, e = 70 µm, f = 40 µm, g = 100 µm, h = 50 µm, i = 30 µm, j–l = 50 µm, m, n–p = 10 µm.

***Tatraea*** Svrček, Česká Mykologie 46(3-4), 160 (1993)

Facesoffungi number: FoF 14262

*Tatraea* is a saprobic genus placed in *Helotiaceae* (*Helotiales*, *Leotiomycetes*). The type species of the genus is *Helotium dumbirense*. The genus is characterized by obconical, larger, dark grey to brownish-grey apothecia, tapered, wrinkled stipe, amyloid asci, and reniform, hyaline ascospores with guttules. Besides, *Tatraea* tends to be saprophytic on the dead wood of hard, deciduous trees, rarely conifers (Svrček 1992, Perić 2013). The updated phylogeny for *Tatraea* taxa is provided in Fig. 45.

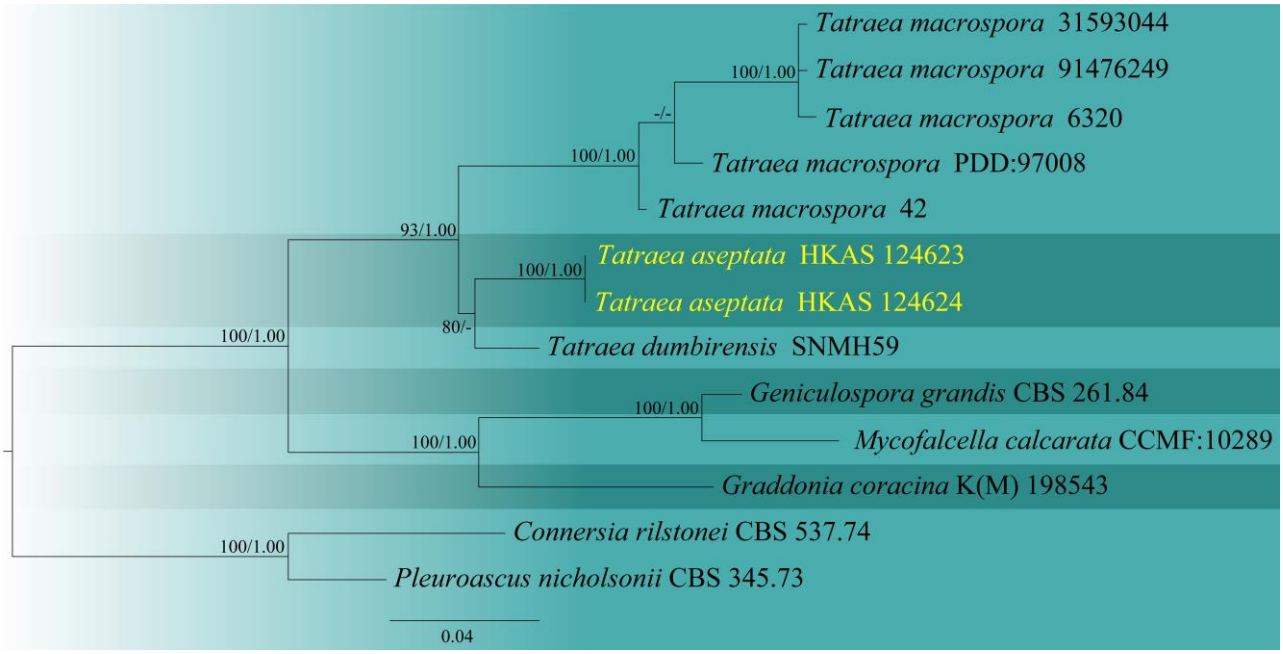


**Fig. 45 –** Phylogram generated from maximum likelihood analysis of *Tatraea* taxa based on ITS sequence data. Thirteen strains are included in the analyses, which comprised of 430 characters. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12735.79 is presented. The matrix had 112 distinct alignment patterns, with 0.14% of undetermined characters or gaps. Evolutionary model applied for ITS gene is GTR+I+G. Maximum likelihood bootstrap values equal to or greater than 80% and Bayesian posterior probabilities equal to or greater than 0.90 (MLBS/BYPP) are given at the nodes. The tree is rooted to *Connersia rilstonii* (CBS 537.74) and *Pleuroascus nicholsonii* (CBS 345.73). The ex-type strains are indicated in **bold** and newly generated strains are in yellow.

***Tatraea aseptata*** H.L. Su & Q. Zhao, **sp. nov.**

Index Fungorum number: IF 559987; Facesoffungi number: FoF 12892; Fig. 46

Etymology – The epithet refers to aseptate ascospores.

*Saprobic* on dead stems. **Sexual morph:** *Apothecia* 0.3–0.6 cm diam., up to 0.3 cm high when fresh, superficial, scattered, slightly leathery, shortly stipitate. *Hymenium* 150–230 µm thick, flat to slightly invaginate, surface smooth, grey to slightly reddish brown when fresh, brown when dry. *Margin* flat to slightly involute, light brown. *Receptacle* discoid to campanulate, light puce when fresh, brown when dry, rough. *Hairs* 40–85 × 6–8 µm ($\bar{x}$ = 64 × 7 µm, n = 20), slightly needle-like with rounded apex, smooth, thick-walled, septate, hyaline, light brown. *Ectal excipulum* 90–290 µm thick, comprised of *textura angularis* cells, 5–20 × 4–13.5 µm ($\bar{x}$ = 12 × 7.5 µm, n = 24), thin-walled, light yellow to light brownish. *Medullary excipulum* 485–725 µm thick,

comprised of *textura intricata* cells, 3.5–7 µm ($\bar{x}$ = 4.4 µm, n = 25) diam., thin-walled, slightly lighter than ectal excipulum. *Paraphyses* 1.5–3.5 µm ($\bar{x}$ = 2.3 µm, n = 25) diam., equal to asci in length, filiform with obtuse apex, septate, unbranched, thin-walled, hyaline. *Asci* 150–185 (–190) × (12–) 13–18 µm ($\bar{x}$ = 171 × 15 µm, n = 24), 8-spored, clavate, hyaline, rounded apex, amyloid at apex, apically thickened and laterally thin wall, with an ocular chamber. *Ascospores* (120/4/2) (18.5–) 21–28 (–32) × 7–9.2 (–10) µm, ($\bar{x}$ = 24.2 × 8.2 µm, n = 119, Q = 2.11–4.38 µm, Qm = 2.97 ± 0.35 µm), uniseriate, reniform with tapered or rounded apices, aseptate, slightly smooth, slightly thick-walled, hyaline, uni- to multi-guttulate, mostly one oil guttule. **Asexual morph:** Undetermined.

Material examined – China, Yunnan, Ailao Mountains, alt. 2428 m, on the bark of a dead branch, 2 September 2021, H.L. Su, SHL206 (HKAS 124623, **holotype**); *ibid*., alt. 2328 m, on the bark of a dead branch, 28 August 2021, H.L. Su, SHL51 (HKAS 124624, **paratype**).

GenBank accession numbers – HKAS 124623: OP538030, HKAS 124624: OP538031.

Notes – Based on the phylogenetic tree obtained from ITS sequence analysis (Fig. 45), our specimen clustered sister to *Tatraea dumbirensis* with 88% maximum likelihood bootstrap and 0.67 Bayesian posterior probability support. *Tatraea* has two accepted species, *T. macrospora* and *T. dumbirensis* (Svrček 1992, Baral et al. 1999, Perić 2013, Van Vooren & Mourgues 2009, Wijayawardene et al. 2022). Compared to our new species, *T. macrospora* and *T. dumbirensis* have different mature ascospore morphologies (Svrček 1992, Baral et al. 1999, Perić 2013, Van Vooren & Mourgues 2009). *Tatraea macrospora* has 3–8-septate ascospores (Baral et al. 1999) and *T. dumbirensis* has 1–2-septate ascospores (Svrček 1992), while our species has aseptate ascospores (Fig. 46). Furthermore, our species has light puce receptacle, while *T. macrospora* and *T. dumbirensis* have shallow cream-colored to grayish receptacle (Fig. 46).

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

Facesoffungi number: FoF 14263

For Sordariomycetes, we follow the recent treatments of Hyde et al. (2020a) and Wijayawardene et al. (2022).

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

Facesoffungi number: FoF 00594

***Diaporthales*** Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis 8, 53 (1932)

Facesoffungi number: FoF 00593

***Apoharknessiaceae*** Senan., Maharachch. & K.D. Hyde, in Senanayake et al., Studies in Mycology 86, 234 (2017)

Facesoffungi number: FoF 03457

***Apoharknessia*** Crous & S.J. Lee, Studies in Mycology 50(1), 239 (2004)

Facesoffungi number: FoF 01428

Lee et al. (2004) established the genus *Apoharknessia* to accommodate its type species, *A. insueta*. To date, three species are accepted under the genus (Wijayawardene et al. 2022, Marin-Felix et al. 2019). An updated phylogeny for the genus in shown in Fig. 47.

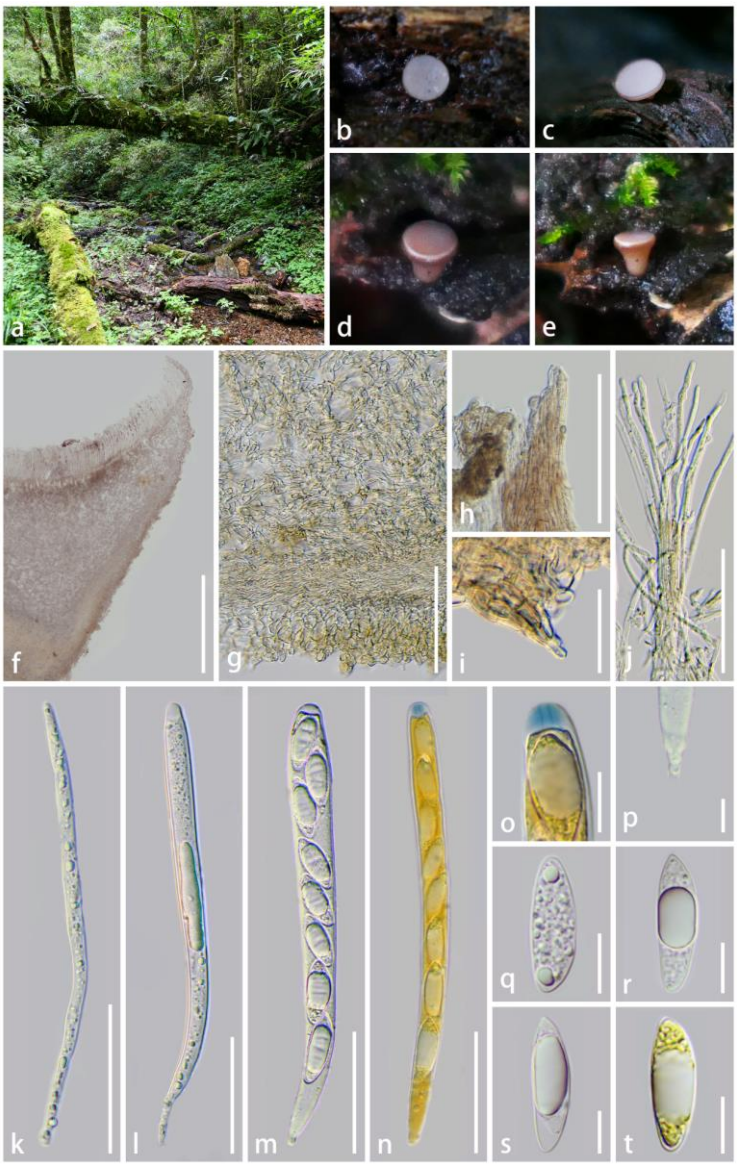


**Fig. 46 – *Tatraea aseptata*** (HKAS 124623, **holotype**). a Habit. b–e Apothecia on the substrate. f Vertical section of the apothecium. g Excipulum. h Ectal excipulum. i Hair. j Paraphyses. k–m Asci. n Ascus in Melzer's reagent. o Apex of the ascus in Melzer's reagent. p Base of the ascus. q–s Ascospores. t Ascospore in Melzer. Scale bars: f = 500 µm, g = 100 µm, h–n = 50 µm, o–t = 10 µm.

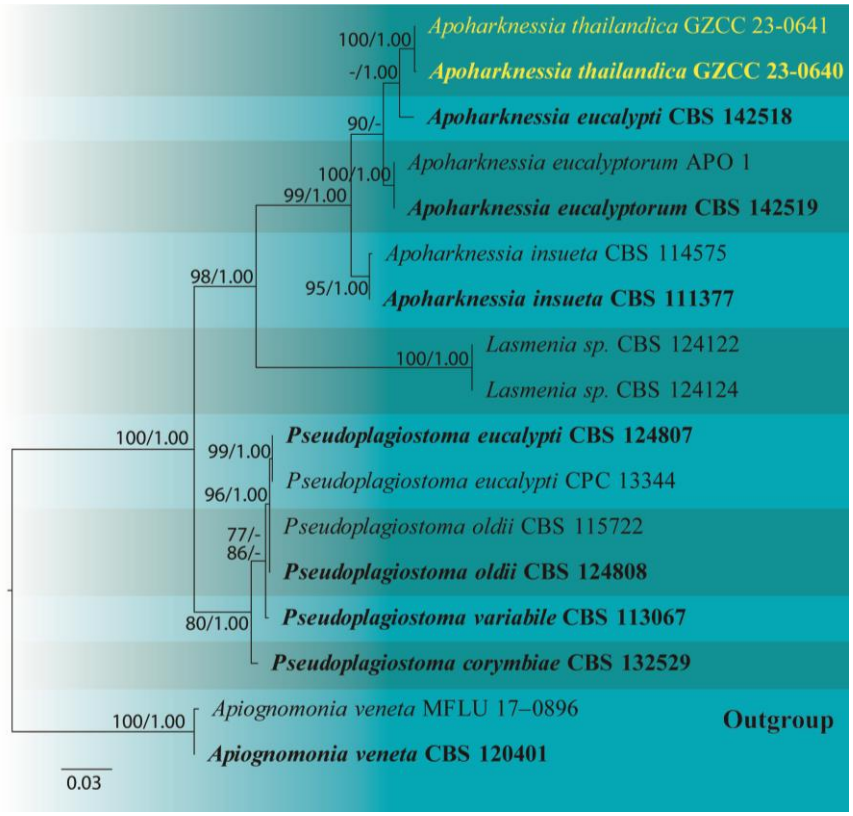


**Fig. 47 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing the species of *Diaporthales*. Seventeen taxa were included in the combined analyses, which comprised 1514 characters (ITS = 664 bp, LSU = 850 bp) after alignment. The best scoring RAxML tree with a final likelihood value of -4419.572824 is presented. The matrix had 274 distinct alignment patterns, with 15.77% of undetermined characters or gaps. Bootstrap support values for maximum likelihood (ML) equal to or greater than 75% and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are indicated above or below the nodes. The newly generated sequence is indicated in yellow. The tree is rooted to *Apiognomonia veneta* (MFLU 17-0896 and CBS 120401). The ex-type strains are indicated in **bold**.

***Apoharknessia thailandica*** N. Wu, Jian K. Liu & K.D. Hyde **sp. nov.**

Index Fungorum number: IF 900618; Facesoffungi number: FoF 14373; Fig. 48

Etymology – Name refers to the country where this fungus was collected, Thailand.

Holotype – GZAAS 23-0645

*Saprobic* on a decaying branch of an unidentified host, forming black spots on the host surface. **Asexual morph**: *Conidiomata* 110–150 × 110–160 µm ($\bar{x}$ = 140 × 130 µm, n = 10), semi-immersed or immersed in the substrate, solitary, globose to subglobose, dark brown, composed of thin-walled cells of *textura angularis*, unilocular, glabrous. *Peridium* up to 6–12 µm wide, consisting of yellow and small *textura angularis* cells. *Conidiophores* micronematous, reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 1–2 µm, lageniform to ampulliform or ampulliform to subcylindrical, hyaline, smooth, percurrently proliferating once or twice near the apex. *Conidia* 9–12 × 6–8 µm ($\bar{x}$ = 10 × 7 µm, n = 30), broadly ellipsoidal to obovoid or obliquely gibbose, apex obtusely rounded, aseptate, non-apiculate, medium brown or brown, with or without a longitudinal hyaline band on flat surface, thick-walled, smooth, with or without striations along the length of conidia, with prominent central guttules, basal and apical appendage absent. **Sexual morph:** Undetermined.

Material examined – Thailand, Chiang Mai Province, Mae Taeng District, Ki Lek Sub-district, Chang Wat, 19°07'08.3"N, 98°44'03.2"E, a decaying branch of an unidentified host, 10 August 2019, Na Wu, YW148 (GZAAS 23-0645, **holotype**), ex-type living culture GZCC 23-

0640; *ibid*., Cho Lae Sub-district, Chang Wat, 19°08'01.3"N, 99°00'29.4"E, on unidentified leaf, 6 August 2019, Na Wu, YW179 (GZAAS 23-0646), living culture GZCC 23-0641.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies are slow growing, reaching 45 mm diam. after one week at 20–23 °C, with moderate aerial mycelium and smooth, lobate margins, greenish black in middle, dirty white in outer region.

GenBank accession numbers – GZCC 23-0640 – LSU: OR147191, ITS: OR147194; GZCC 23-0641 – LSU: OR147192, ITS: OR147195.

Notes – In our phylogeny, we included all species of *Apoharknessia* which have molecular data in the GenBank. Phylogenetically recognized *A. thailandica* is closely related to *A. eucalypti* but formed a distinct linage (Fig. 47). Morphologically, conidia of *A. thailandica* (9–12 × 6–8 µm) are larger than the conidia of *A. eucalypti* ((7–)8–10(–11) × (5–) 6(–7) µm) (Marin-Felix et al. 2019). In addition, conidia of *A. thailandica* do not have any basal and apical appendages. In terms of the nucleotide comparison, *A. thailandica* and *A. eucalypti* differed in twenty base pairs in the ITS region, and three in the LSU region. Therefore, we establish our strain as a novel species in *Apoharknessia*.

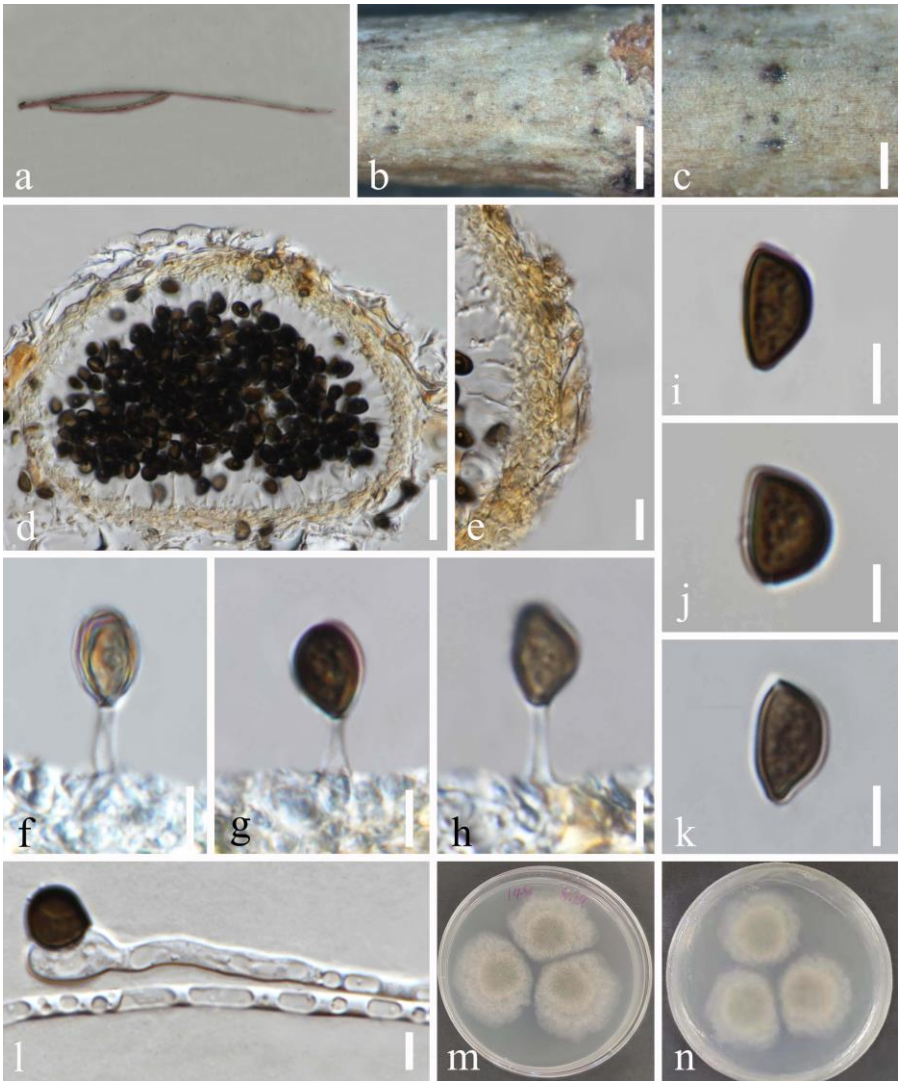


**Fig. 48 – *Apoharknessia thailandica*** (GZAAS 23-0645, **holotype**). a–c Conidiomata on the host substrate. d Cross section of a conidioma. e Peridium. f–h Conidiophores and conidia. i–k Conidia. l Germinating conidium. m, n Colonies on the PDA from above (m) and below (n). Scale bars: b = 50 µm, c, d = 20 µm, e–l = 5 µm.

***Diaporthaceae*** Höhn. ex Wehm., American Journal of Botany 13, 638 (1926)

Facesoffungi number: FoF 01383

***Diaporthe*** Nitschke, Pyrenomycetes Germanici 2, 240 (1870)

Facesoffungi number: FoF 00146

*Diaporthe*, described by Nitschke (1870), is known to have endophytes, saprobes, and pathogens from a wide range of hosts worldwide (Udayanga et al. 2011, Dissanayake et al. 2017, Abeywickrama et al. 2020, 2022, Hyde et al. 2020c, Chethana et al. 2021a). Currently, 1157 names of *Diaporthe* have been stated in the Index Fungorum, and many species lack molecular data (Index Fungorum 2023). We provided the updated phylogeny for *Diaporthe eres* (Fig. 49) and *D. sojae* (Fig. 50) species complexes.

***Diaporthe eres*** Nitschke, Pyrenomycetes Germanici 2, 245 (1870)

Index Fungorum number: IF 172054; Facesoffungi number: FoF 02182; Fig. 51

*Saprobic* on *Arrhenatherum eliatus*. Visible as small black patches on the host surface. **Asexual morph:** Coelomycetous. *Conidiomata* 100–150 µm diam. ($\bar{x}$ = 125 µm, n = 10), visible as black patches, scattered, semi-immersed, pycnidial, globose or sub globose. *Conidiomatal wall* consisting of 2–3 layers of pale brown, thick-walled cells of *textura angularis*. *Conidiophores* hyaline, smooth, unbranched. *Alpha conidia* 6–9 × 1–3 µm ($\bar{x}$ = 7.5 × 2 µm, n = 20), hyaline, smooth-walled, ovate to ellipsoidal, base sub-truncate. *Beta conidia* and *Gamma conidia* not observed. **Sexual morph:** see Udayanga et al. (2014).

Culture characters – Colonies on PDA fast growing at 25 ºC for a week, white, aerial, fluffy mycelium, reverse dark pigmentation developing in centre.

Material examined – Italy, Forlì-Cesena [FC], Predappio, dead aerial stems of *Arrhenatherum eliatus*, 4 November 2018, Camporesi Erio, JZBH320220, living culture: JZB320220.

GenBank accession numbers – ITS: OP002067, *β-tubulin*: OP837430, *cal*: OP837433, *his*: OP837432.

Known distribution (based on molecular data) – wide geographical range, including Africa, Asia, Europe, America (https://nt.ars-grin.gov/fungaldatabases/fungushost), Italy (this study).

Known hosts (based on molecular data) – wide range of host plants, including *Asteraceae*, *Clusiaceae*, *Ebenaceae*, *Ericaceae*, *Fagaceae*, *Juglandaceae*, *Pinaceae*, *Poaceae* (this study), *Rosaceae*, *Sapindaceae*, *Ulmaceae* and *Vitaceae* plant families (https://nt.ars-grin.gov/fungaldatabases/fungushost, Abeywickrama et al. 2022), *Arrhenatherum eliatus* (this study).

Notes – In this study, we recovered a saprobic *Diaporthe* species from dead aerial stems of *Arrhenatherum eliatus* from Italy. Multi-loci phylogeny and morphological characteristics confirmed that this isolate belongs to *Diaporthe eres* species complex. Isolate JZB320220 develops a sister clade to *D. eres* isolate MFLUCC 17-0963 (≡ *D. lonicerae*) with 70% maximum likelihood bootstrap support and 0.96 Bayesian posterior probability (Fig. 49). *Diaporthe lonicerae* was originally described from a dead aerial branch of *Lonicera* sp. from Italy. Recently, it was synonymized as *D. eres* based on multi-loci, haplotype network, and genealogical concordance phylogenetic species recognition data (Dissanayake et al. 2017, Chaisiri et al. 2021, Abeywickrama et al. 2022). Our isolate (JZB320220) shares similar morphological characters with minor dimensional differences (Fig. 51). The mature conidiomata of *D. eres* isolate MFLUCC 17-0963 (≡ *D. lonicerae*) are larger than those of our isolate JZB320220 (up to 680 µm *vs.* 100–150 µm). Furthermore, our isolate has relatively smaller alpha conidia than the MFLUCC 17-0963 isolate (6–9 × 1–3 µm *vs.* 12.5–16 × 3.5–4 µm). When we compare the morphology of our isolate with the ex-epitype strain of *D. eres* (AR5193), our isolate has smaller conidiomata (200–250 µm *vs.* 100–150 µm) and similar size of alpha conidia (6–9 × 1–3 µm *vs.* 6–9 × 3–4 µm). These minor dimensional differences are probably due to environmental variations, host associations or the different growth media. This study provides the first report of *Diaporthe eres* associated with *Arrhenatherum eliatus* in Italy and the first record in the world for the association of *Diaporthe* species with *Arrhenatherum* species.

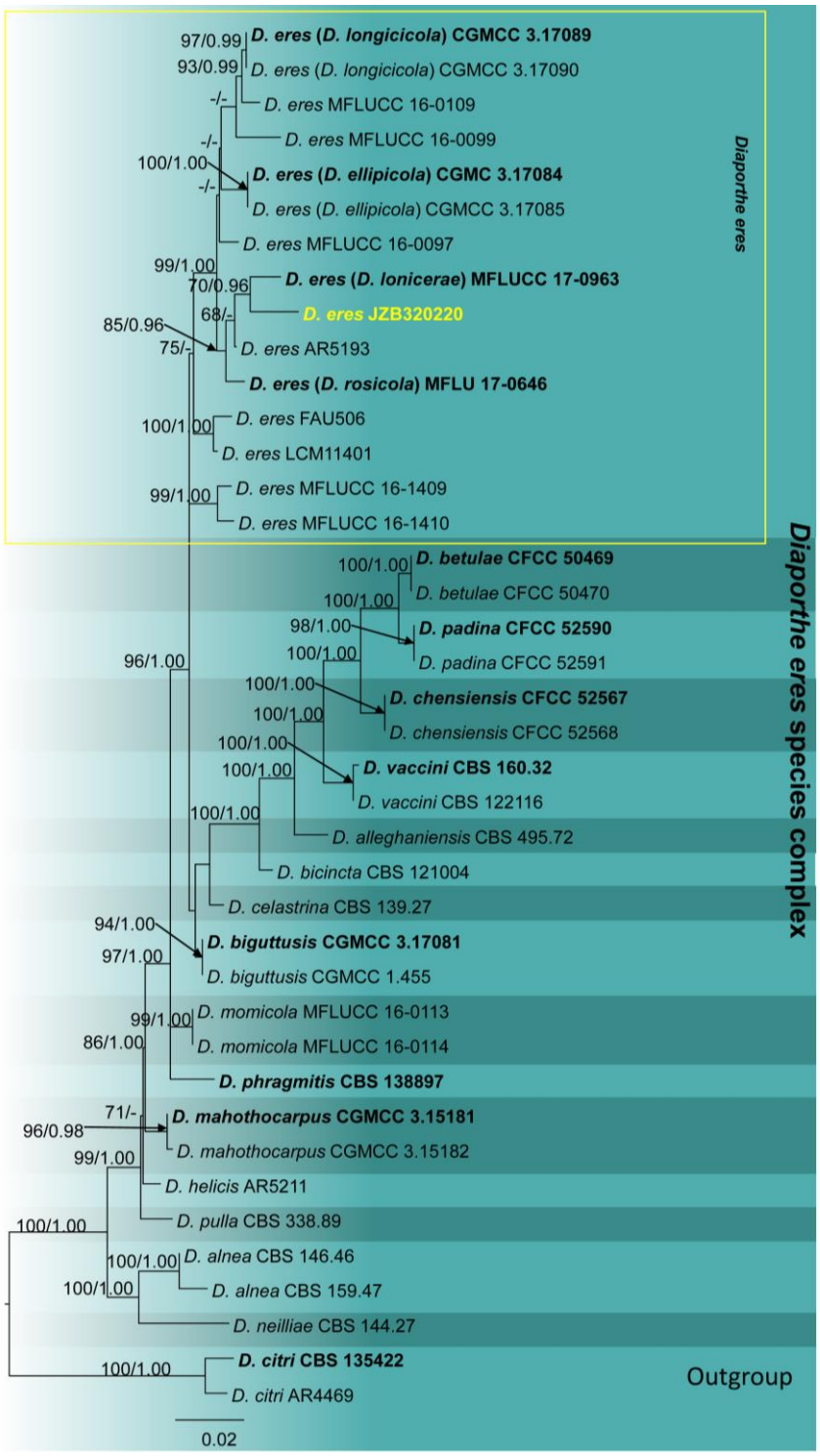


**Fig. 49 –** Phylogram generated from maximum likelihood analysis (RAxML) of *Diaporthe eres* species complex based on ITS, *β-tubulin*, *cal*, *tef1-α*, and *his* sequence data. Forty strains are included in the combined analyses which comprised 1831 characters (442 characters for ITS, 376 characters for *β-tubulin*, 347 characters for *cal*, 224 characters for *tef1-α*, 422 characters for *his*). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12735.79 is presented. The matrix had 353 distinct alignment patterns, with 218 parsimony-informative sites, 127 singleton sites and 1486 constant sites. Evolutionary model GTR+I+G was applied for all genes. Maximum likelihood bootstrap values equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 (MLBS/BYPP) are given at the nodes. The tree is rooted to *Diaporthe citri* (CBS 135422, AR4469). The ex-type strains are indicated in **bold** and newly generated strains are in yellow.

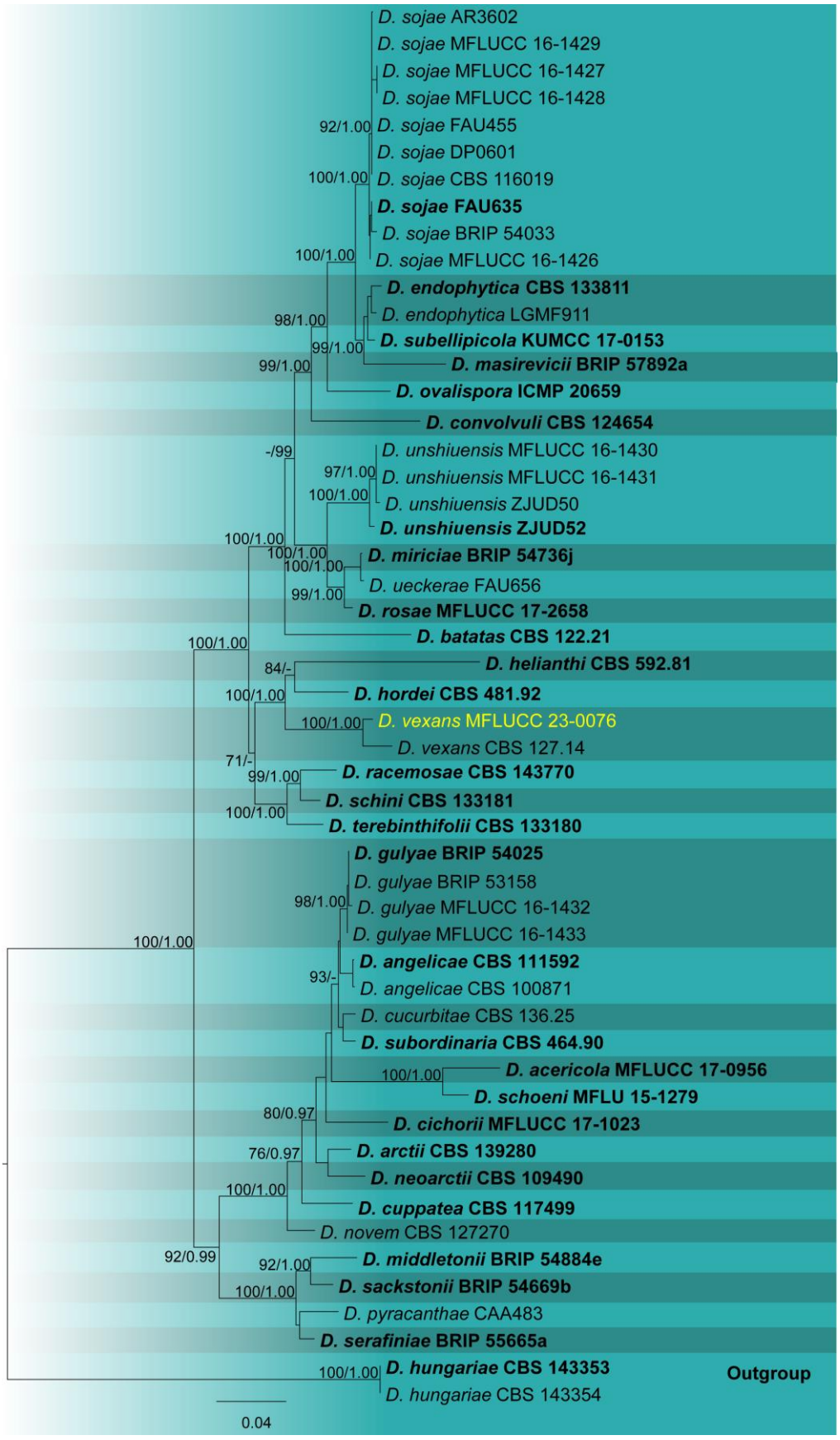


**Fig. 50 –** Phylogram generated from maximum likelihood analysis (RAxML) of *Diaporthe sojae* species complex based on ITS, *β-tubulin*, *cal*, *tef1-α*, and *his* sequence data. Fifty-two strains are included in the combined analyses which comprised 2203 characters (510 characters for ITS, 399 characters for *β-tubulin*, 495 characters for *cal*, 352 characters for *tef1-α*, 427 characters for *his*).

Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -14161.335 is presented. The matrix had 952 distinct alignment patterns, with 669 parsimony-informative sites, 221 singleton sites and 1313 constant sites. Evolutionary model GTR+I+G was applied for all genes. Maximum likelihood bootstrap values equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 (MLBS/BYPP) are given at the nodes. The tree is rooted to *Diaporthe hungariae* (CBS 143353, CBS 143354). The ex-type strains are indicated in **bold** and newly generated strains are in yellow.

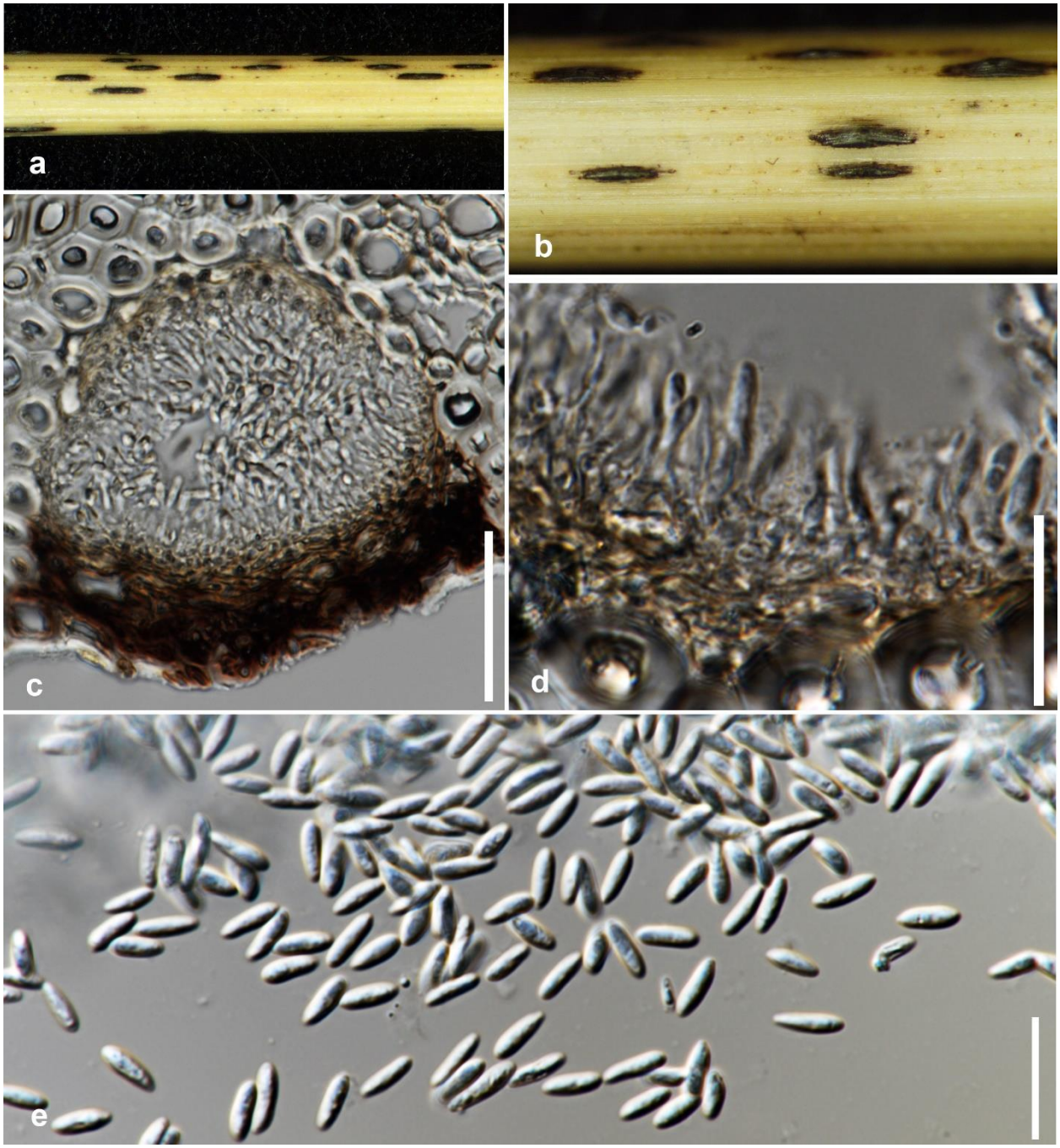


**Fig. 51 – *Diaporthe eres*** (JZBH320220, **new host record**). a, b Conidiomata on host surface. c Section through a conidioma. d Conidia attached to the conidiophores. e Alpha conidia. Scale bars: c = 50 µm, d, e = 10 µm.

***Diaporthe vexans*** (Sacc. & P. Syd.) Gratz, Phytopathology 32, 542 (1942)

Index Fungorum number: IF 286070; Facesoffungi number: FoF 14120; Fig. 52

*Associated* with the fruit rot of *Solanum melongena*. **Asexual morph:** On PDA: *Conidiomata* pycnidial, globose to subglobose, multilocular, dark brownish to black, erumpent or immersed, often with brown to dark brownish exudate from the ostioles. *Conidiophores* hyaline in the upper region, rarely branched, pale brown to greenish at the base, smooth, 2–4-septate, tapering towards the apex. *Conidiogenous cells* 10–18 × 2–3 µm, phialidic, slightly tapering towards the apex. *Alpha conidia* 5–7 × 2–3 µm ($\overline{x}$ = 6.6 × 2.9 µm, n = 30), hyaline, fusiform or oval, usually biguttulate. **Sexual morph:** Undetermined.

Culture characters – Cultures incubated on PDA at 25 °C in darkness, Colony pale yellowish, greenish to brownish at the centre, reverse pale yellowish, becoming brownish at the centre with age. Aerial mycelium yellowish, sparse, and fluffy, with irregular margin and visible conidiomata at maturity.

Material examined – Thailand, Chiang Rai Province, Fah Thai market, on fruit rot of *Solanum melongena*, 1 February 2023, K. C. Mallikarathna, EP03 (MFLU 23-0081), living culture MFLUCC 23-0076.

Known distribution (based on molecular data) – worldwide (Gratz 2006, Mahadevakumar & Janardhana 2016, Keinath et al. 2021, Farr & Rossman 2023), Thailand (this study).

Known hosts (based on molecular data) – species of *Solanaceae* are the main hosts (Gratz 2006, Mahadevakumar & Janardhana 2016, Keinath et al. 2021, Farr & Rossman 2023), *Solanum melongena* (this study).

GenBank accession numbers – ITS: OR131267, *β-tubulin*: OR162309, *cal*: OR162310.

Note – *Diaporthe vexans*, associated with the diseases of eggplants and brinjal (*Solanaceae*), is a serious fungal pathogen causing significant economic losses in terms of production in the world (Mahadevakumar & Janardhana 2016, Keinath et al. 2021). This species produces different disease symptoms, such as damping-off, leaf blight, fruit rot, and stem blight on the brinjal crop (Mahadevakumar & Janardhana 2016). Initially, brown, soft, sunken lesions appear on fruits. With the disease progression, these lesions enlarge and merge, covering a larger portion of the fruit surface with concentric rings of small black pycnidia on the margins (Keinath et al. 2021). Pycnidia on fruits were commonly observed, and in severe infection with dry weather conditions, the infected fruit becomes shriveled, dry, and mummified (Pawar & Patel 1957, Plantix 2023). Based on morphology and phylogenetic analyses (Fig. 50), we identified the fungus we isolated from the fruit rot of eggplant as *Diaporther vexans* (Fig. 52). Hence, herein we provide the first report of *D. vexans* associated with eggplant fruit rot in Thailand.

***Melanconidaceae*** G. Winter [as 'Melanconideae'], Rabenhorst's Kryptogamen-Flora, Edn 2 (Leipzig) 1.2, 764 (1886)

Facesoffungi number: FoF 01395

***Melanconis*** Tul. & C. Tul., Selecta fungorum carpologia (Paris) 2, 115 (1863)

Facesoffungi number: FoF 06512

*Melanconis*, described by Tulasne (1856), was typified with *Melanconis stilbostoma* without a generic diagnosis. This genus with a cosmopolitan distribution mainly occurs on plants belonging to *Betuloideae* (Jaklitsch & Voglmayr 2020). Taxa in *Melanconis sensu stricto* are characterised by white to yellowish, ectostromatic discs that project distinctly and continue as stromatic central columns downwards, entostroma differ from internal bark tissue, long, cylindrical ostiolar necks that converge in the discs, hyaline, bicellular ascospores with or without appendages, lacking paraphyses at maturity and asci with an apical ring that are released from the subhymenium at maturity (Jaklitsch & Voglmayr 2020). Asexual morphs of *Melanconis* produce acervular conidiomata, with two types of conidia, Melanconium-like brown α-conidia and narrow hyaline to brownish β-conidia (Jaklitsch & Voglmayr 2020). An updated phylogeny for *Melanconidaceae* is shown in Fig. 53.

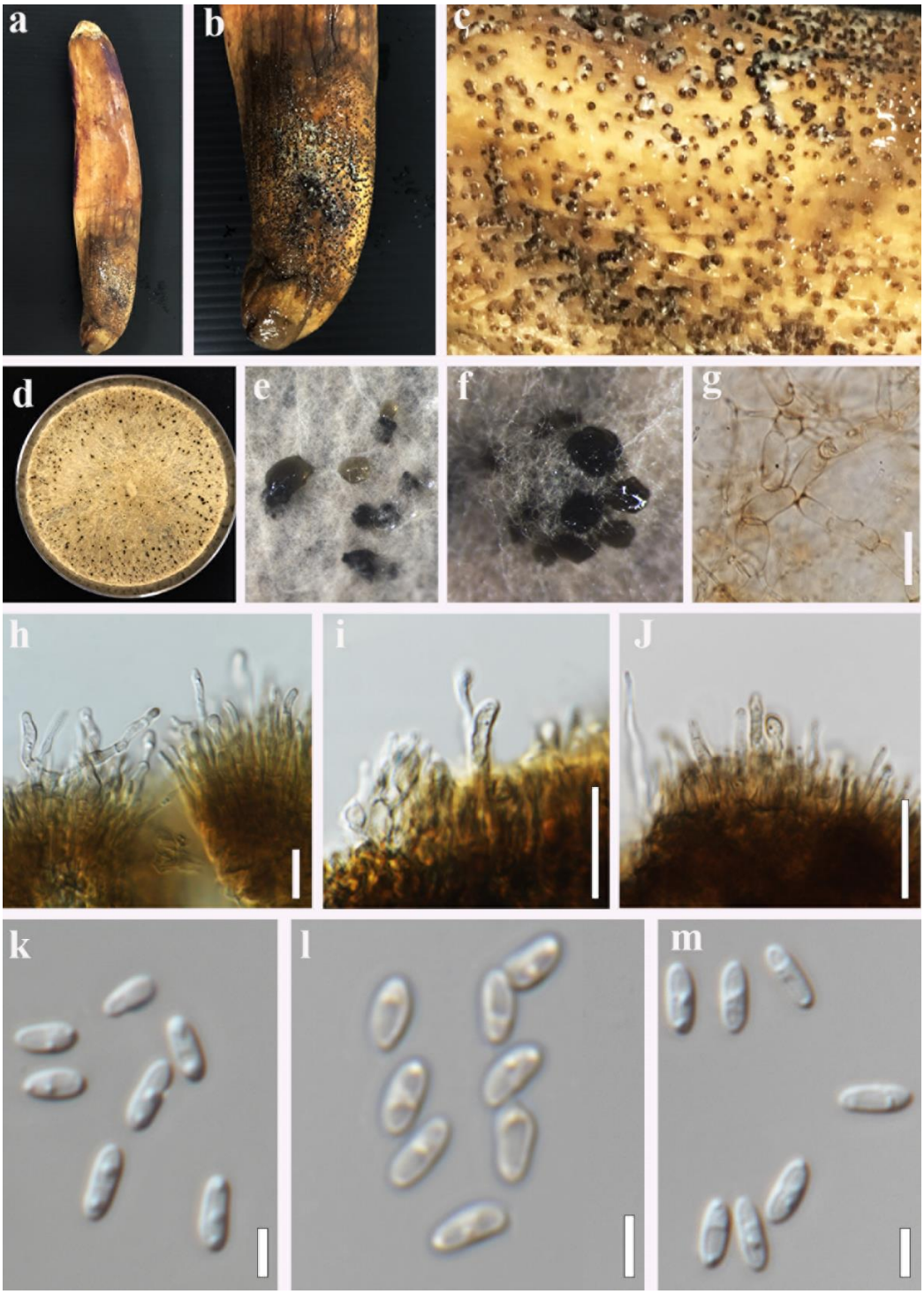


**Fig. 52 –** ***Diaporthe vexans*** (MFLU 23-0081, **a new host record**). a–c Conidiomata on the fruit. d–f Sporulating conidiomata on PDA. g Mycelia on PDA. h–j Conidiogenous cells. k–m Alpha conidia. Scale bars: g = 50 µm, h–j = 10 µm, k–m = 5 µm.

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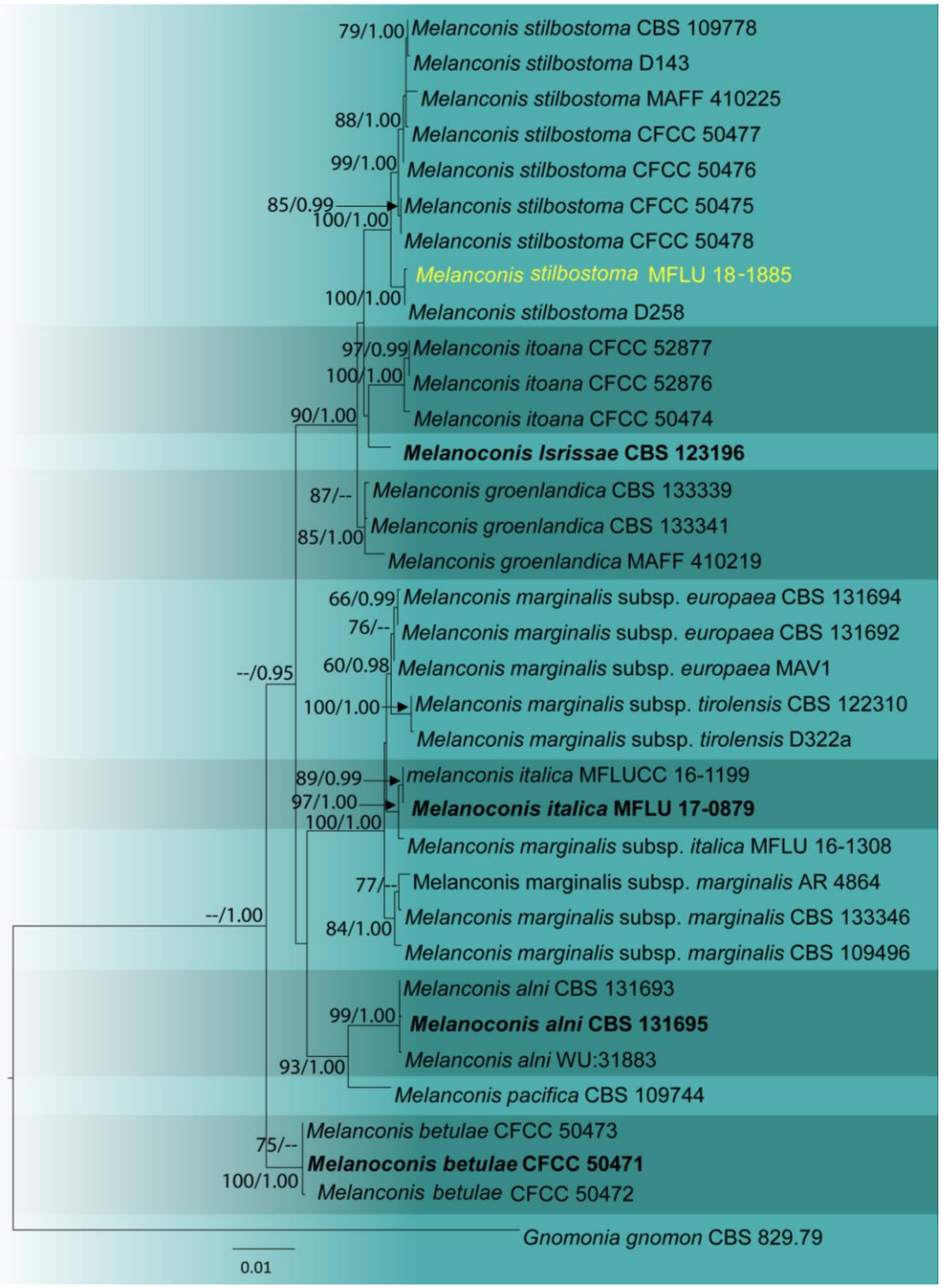


**Fig. 53 –** Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb*2 and *tef1-α* sequence data. Thirty-five strains were included in the combined sequence analyses, which comprised 3268 characters with gaps (ITS = 528, LSU = 858, *rpb*2 = 1161, *tef1-α* = 721). Single gene analyses were also performed, and topology and clade stability compared with the combined gene analyses. *Gnomonia gnomon* (CBS 829.79) strain was used as the outgroup taxon. Final ML optimization likelihood is -7101.950102. The matrix included 311 distinct alignment patterns, with 11.83 % undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.247189, C = 0.263714, G = 0.268910, T = 0.220187; substitution rates AC = 1.490211, AG = 3.125914, AT = 1.908995, CG = 0.756262, CT = 9.270114, GT = 1.0; gamma distribution. Bootstrap support values for ML (first set) equal to or greater than 65%, BYPP equal to or greater than 0.95 are given above or below the nodes. The strain from the current study is in yellow and the type strains are in **bold**.

***Melanconis stilbostoma*** (Fr.) Tul. & C. Tul., Selecta fungorum carpologia (Paris) 2, 115 (1863)

Index Fungorum number: IF 243057; Facesoffungi number: FoF 04448; Fig. 54

*Plant pathogenic* on the twigs of *Betula pubescens*. **Asexual morph:** *Conidiomata* 1100–1300 × 550–650 µm ($\bar{x}$ = 1257 × 592 µm, n = 10), stromatic, acervular or pulvinate, solitary to aggregated, immersed to semi-immersed, unilocular with circular covering disc, slightly convex, yellowish-white. *Conidiomatal wall* 80–200 µm wide, surrounded and intermingled with host cells, thick-walled. *Hymenium* comprises dense, hyaline hyphae with the cells of *textura intricata*. *Conidiophores* start from a pseudoparenchymatous base, filiform, aseptate, branched at the base, smooth-walled, strongly aggregated, hyaline at the beginning, and turn brown from the tips. *Conidiogenous cells* highly dense, originating from the terminal of conidiophores, annellidic, enteroblastic, cylindrical, repetitive, producing hyaline α-conidia. *Conidia* 15–25 × 8–15 µm ($\bar{x}$ = 20 × 11 µm, n = 20, l/w = 1.8), oval, ellipsoidal to subglobose, aseptate, thick-walled, smooth, hyaline at immaturity, pale brown to brown at maturity without β-conidia. **Sexual morph:** see Jaklitsch & Voglmayr (2020).

Material examined – Russia, Rostov region, Shakhty City District, Lenin Street, urban trees, on dying (dieback) twigs of *Betula pubescens*, 8 May 2018, Timur S. Bulgakov, T-7510 (MFLU 18-1885).

Known distribution (based on molecular data) – Austria, China, Italy, Japan, Poland, Russia, Sweden, United States and Ukraine (Zhuang 2005, Sogonov et al. 2008, Voglmayr et al. 2012, Fan et al. 2016, Hyde et al. 2020c, Jaklitsch & Voglmayr 2020, Farr & Rossman 2023, this study).

Known hosts (based on molecular data) – *Betula* spp. (*B. aetnensis*, *B. pendula*, *B. platyphylla* var. *japonica*, *B. platyphylla*, *B. papyrifera*, *B. rotundifolia* and *B. tianschanica*) (Zhuang 2005, Sogonov et al. 2008, Voglmayr et al. 2012, Fan et al. 2016, Hyde et al. 2020c, Jaklitsch & Voglmayr 2020, Farr & Rossman 2023), *Betula pubescens* (this study).

GenBank accession numbers – ITS: OQ629853, LSU: OQ629854, *rpb2*: OQ653555, *tef1-α*: OQ653556

Notes – In the multi-gene phylogeny, our strain MFLU 18-1885 clustered with strains of *Melanconis stilbostoma* (CBS 109778, D 143, MAFF 410225, CFCC 50477, CFCC 50476, CFCC 50475, CFCC 50478 and D 258) with 100 % maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 53). Our collection shares similar morphologies to the asexual morph of *M. stilbostoma* described by Jaklitsch & Voglmayr (2020). *Melanconis stilbostoma* is widespread in European and Asian parts of Russia and adjacent countries in natural habitats of *Betula* species (Sinadsky 1973, Cherepanova & Cherepanov 2003, Rebriev et al. 2012). Previously, *M. stilbostoma* was recorded and confirmed on *B. pendula* in Donetsk (Hyde et al. 2020c) and Lugansk regions (Ordynets et al. 2013). Based on morphology (Fig. 54) and molecular data analysis (Fig. 53), we conclude our collection is the first record of *M. stilbostoma* on *Betula pubescens* in Rostov region, Russia.

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

Facesoffungi number: FoF 06512

***Glomerellales*** Chadef. ex Réblová, W. Gams & Seifert, Studies in Mycology 68, 170 (2011)

Facesoffungi number: FoF 09687

***Glomerellaceae*** Locq., Mycologia 98(6), 1083 (2007)

Facesoffungi number: FoF 01100

***Colletotrichum*** Corda, in Sturm, Deutschlands Flora, 3 Abt. (Pilze Deutschl.) 3(12), 41 (1831)

Facesoffungi number: FoF 00144

The genus *Colletotrichum* was established by Corda (1831) with *C. lineola* as the type species (Jayawardena et al. 2016). Being the sole genus in the *Glomerellaceae* (*Glomerellales*, *Sordariomycetes*) and comprises approximately 270 species that constitute 15 complexes at present (Talhinhas & Baroncelli 2021, Yu et al. 2022). The genus includes endophytes, pathogens, and saprobes in a wide range of hosts worldwide (Jayawardena et al. 2016). These plant pathogens cause severe anthracnose on various economically important crops, such as apples, beans, cotton,

grape, strawberry, etc. (Bernstein et al. 1995, Dean et al. 2012, Sharma & Kulshrestha 2015). The epitypification and use of multi-locus phylogeny to delimit species are advocated for a better understanding of the genus (Hyde et al. 2009, Damm et al. 2012). The recommended barcoding genes for *Colletotrichum* species resolution include ITS, *actin*, *ApMat*, *chs-1*, *gapdh*, *his* and *β-tubulin* (Hyde et al. 2014). We provide the updated phylogeny for *Colletotrichum* taxa in Fig. 55.

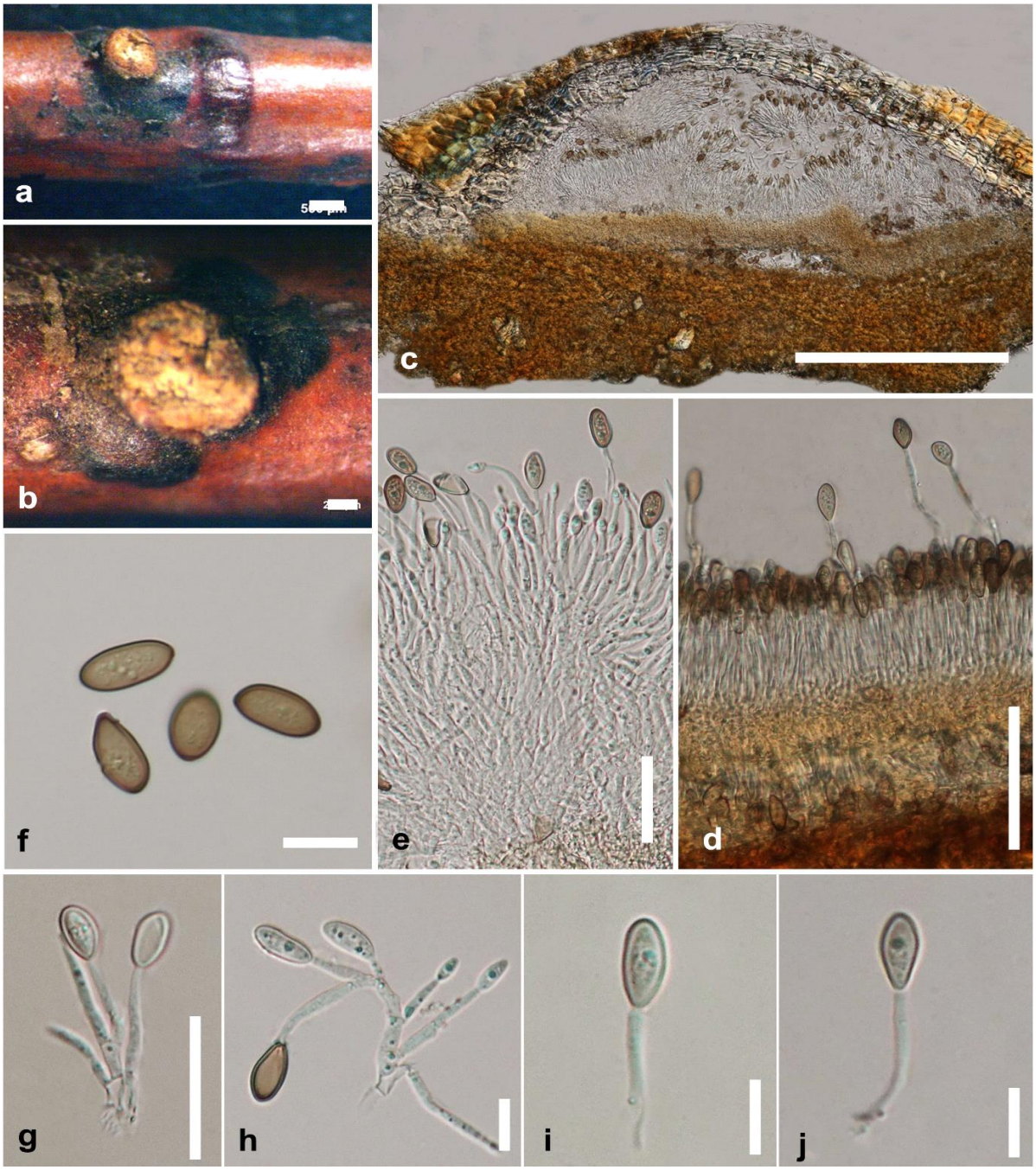


**Fig. 54 – *Melanconis stilbostoma*** (MFLU 18-1885, **a new host record**). a–b A conidioma on twigs of *Betula pendula*. c Longitudinal section of a conidioma. d–e Arrangement and development of conidiospores and conidiogenous cells inside conidiomata. g–j Conidia. Scale bars: a, c = 500 μm, b = 200 μm, d = 100 μm, e, g = 50 μm, f, h–j = 20 μm.

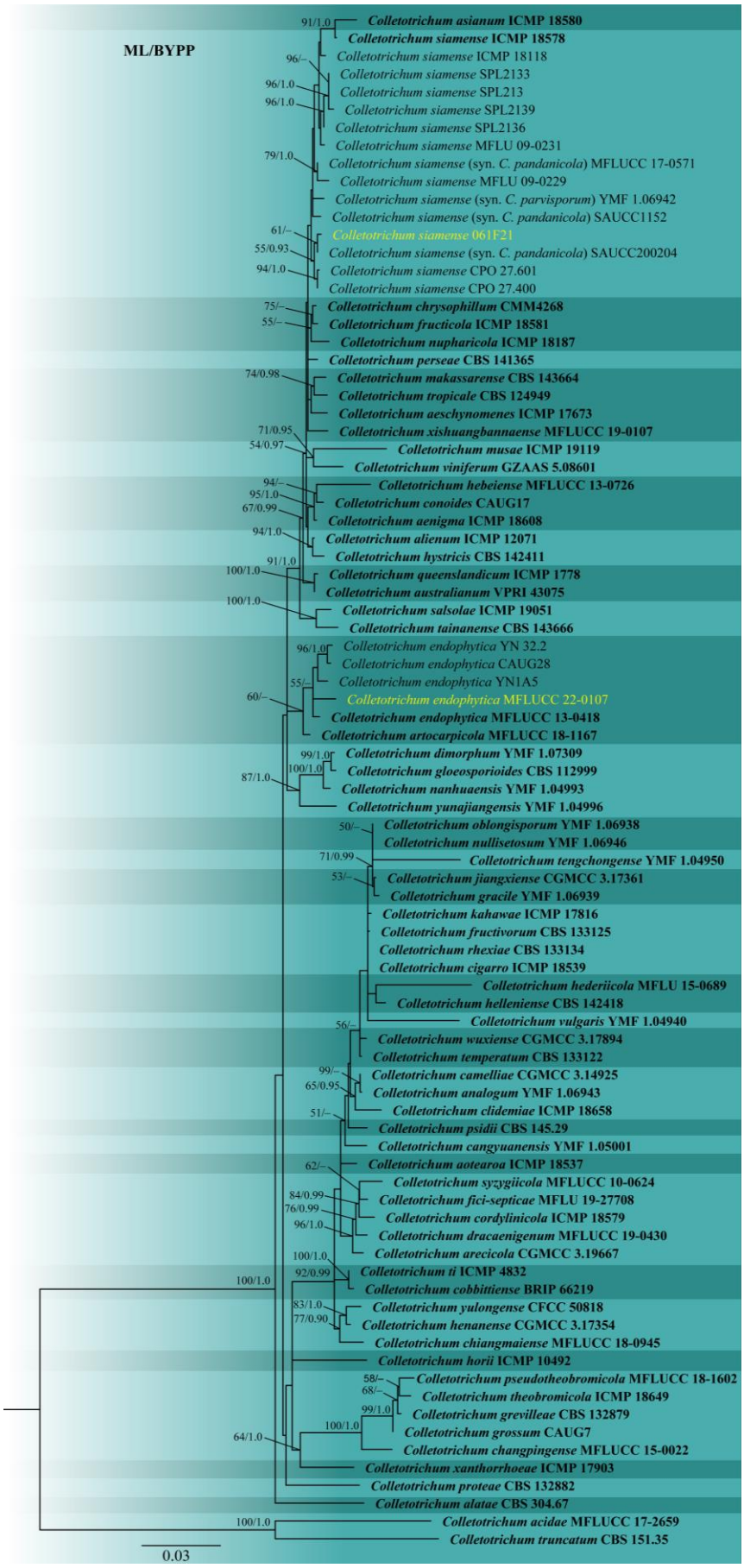


**Fig. 55 –** Phylogram generated from maximum likelihood analysis based on the combined ITS, *actin*, *chs-1*, *gapdh* and *β-tubulin* sequence data of *Colletotrichum* taxa. Eighty-six strains are

included in the combined analyses which comprised 1667 characters (516 characters for ITS, 259 characters for *actin*, 239 characters for *chs-1*, 246 characters for *gapdh*, 407 *β-tubulin*) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -10238.057479 is presented. The matrix had 766 distinct alignment patterns, with 5.46% undetermined characters or gaps. Evolutionary models applied for ITS, *actin*, *chs-1*, *gapdh* and *β-tubulin* genes are TIM2+I, TPM1uf+G, TIM1+G, TrN+I and TIM2ef+G models, respectively. Bootstrap support values for ML equal to greater than 50% and Bayesian posterior probabilities equal to greater than 0.90 are given near nodes, respectively. The tree is rooted with *Colletotrichum acidae* (MFLUCC 17-2659) and *C. truncatum* (CBS 151.35). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Colletotrichum endophytica*** Manamgoda, Udayanga, L. Cai & K.D. Hyde, Fungal Diversity 61, 107–115 (2013)

Index Fungorum number: IF 565248; Facesoffungi number: FoF 14040; Fig. 56

Associated with the symptomatic leaf of *Dalbergia*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* acervuli, solitary, superficial, rounded and dark in color, setae not observed. *Conidiophores* (16.5–) 19–26 (–28) × 3–4 µm ($\bar{x}$ = 22.5 × 3.3 µm, n = 25), hyaline, smooth-walled, aseptate, unbranched, cylindrical to clavate. *Conidia* 13–17 × 4–5 µm ($\bar{x}$ = 14.5 × 4.8 µm, n = 25), straight, abundantly cylindrical, rarely ovoid with rounded ends.

Culture characteristics – Colonies on PDA reaching 70–77 mm diam. after 7 days at 25–28 °C, aerial mycelia medium dense, cottony, circular, undulate, white to olivaceous grey, reverse black color. *Appressoria* formed in slide culture on PDA measured 6–11.5 (−13) × 3–6.5 µm ($\bar{x}$ = 8.5 × 4.5 µm, n = 20), formed from mycelia, terminal, brown, variable in shape, irregular unlobed or lobed, appressoria complex formation present.

Materials examined – Thailand, Chiang Rai Province, Mueang, Huai Sak, Ang Kep Nam Nong Buak Tao Reservoir, from a symptomatic leaf of *Dalbergia*, 27 September 2021, A. Armand (MFLU 22-0172), living culture MFLUCC 22-0107.

GenBank accession numbers – ITS: OP648261, *β-tubulin*: OP712674, *gapdh*: OP712673, *chs-1*: OP712672, *act*: OP712671.

Known distribution (based on molecular data) – Thailand (Manamgoda et al. 2013, this study), China (Zhang et al. 2022), Sri Lanka (Dissanayake et al. 2021).

Known hosts (based on molecular data) – *Pennisetum purpureum* (Manamgoda et al. 2013), unidentified wild fruit (Udayanga et al. 2013), *Philodendron bipinnatifidum* (Zhang et al. 2022), Mango (Li et al. 2019), Coffee (Cao et al. 2019), Chili (Diao et al. 2017), *Dalbergia* sp. (this study).

Notes – This species was distributed in tropical regions (Manamgoda et al. 2013, Dissanayake et al. 2021, Zhang et al. 2022a). Our strain shares similar colony and micro-morphology with the type material and is in agreement with the morphology of *Colletotrichum endophytica*. Multi-loci analyses using ITS, *act*, *gapdh*, *chs-1*, and *β-tubulin* reveal that our strain clusters with other *C. endophytica* strains reported from different hosts (Fig. 55). Manamgoda et al. (2013) described *C. endophytica* (MFLUCC 13-0418) as a new species from Thailand and this is the first known record of the occurrence of *C. endophytica* on *Dalbergia*.

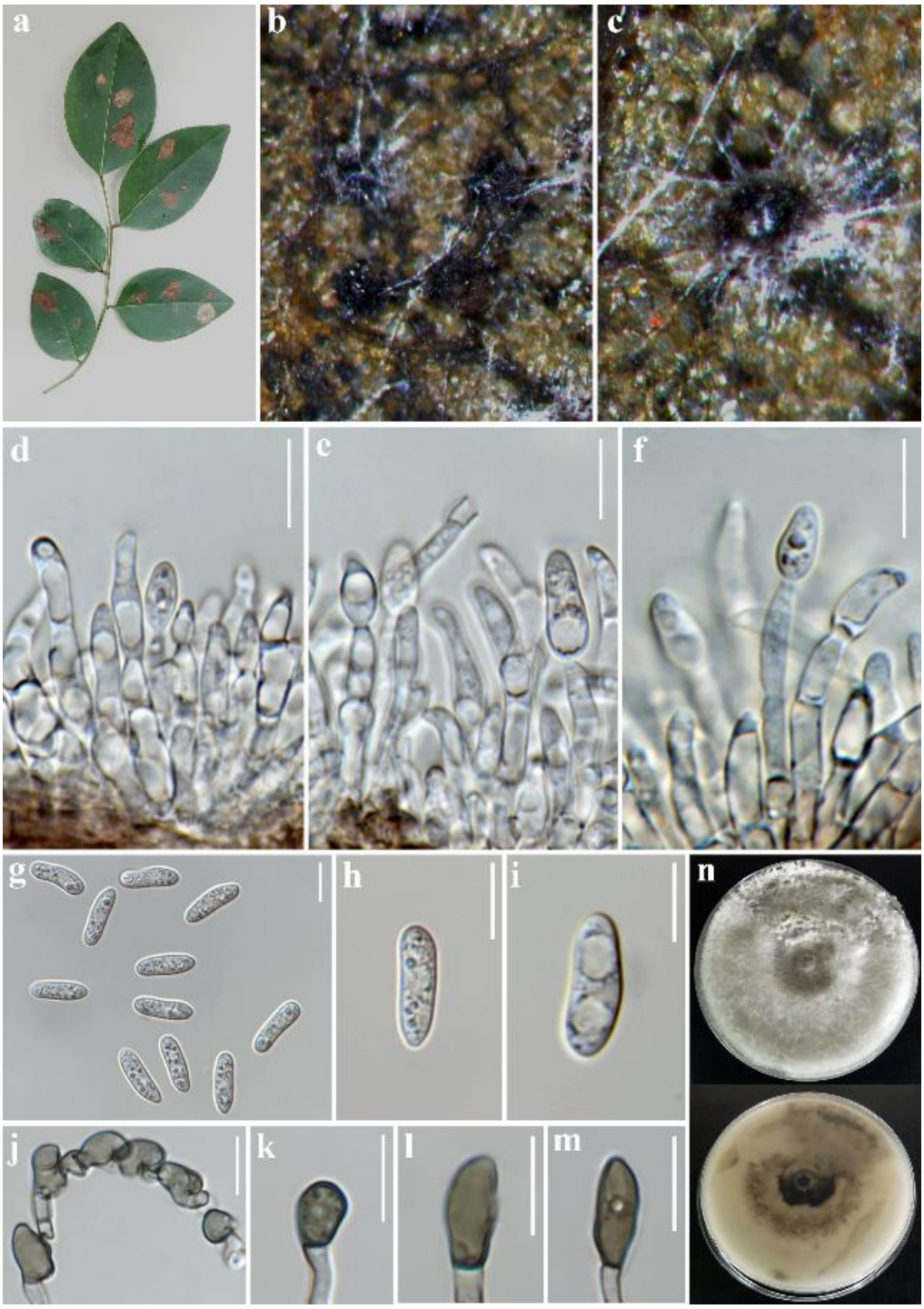


**Fig. 56 – *Colletotrichum endophytica*** (MFLUCC 22-0107, **a new host record**). a Host leaves. b–c Acervuli on the host. d–f Conidiogenous cells and conidia. g–i Conidia. j–m Appressoria. n Upper and reverse side of culture. Scale bars: d–m = 10 µm.

***Colletotrichum siamense*** Prihast., L. Cai & K.D. Hyde, Fungal Diversity 39, 98 (2009)

Index Fungorum number: IF 515410; Facesoffungi number: FoF 03599; Fig. 57

*Endophytic* in the flowers of *Dendrobium* sp. **Sexual morph:** Undetermined. **Asexual morph:** *Vegetative hyphae* 1.5–3µm, hyaline to brown, smooth-walled, branched, septate. *Setae* hyaline to brown, cylindrical to fusiform, with apical tip and rounded base, septate, straight or slightly curved. *Conidiophores* hyaline to pale brown, septate, cylindrical to clavate, smooth-walled, branched or unbranched, slightly-curved, formed on a cushion brown-coloured cells. *Conidiogenous cells* phialidic, hyaline to pale brown, cylindrical to clavate, guttulate. *Conidia* 14–

18 × 4–6 µm ($\bar{x}$ = 15.18 × 4.8 µm, n = 20), one-celled, aseptate, hyaline, subglobal to cylindrical, with one rounded and another truncated ends, smooth-walled, guttulate.

Culture characteristics – Colony on PDA surface superficial, with flat margin, rough, grained, radiated, dense, jungle green; reverse greenish black. Growth rate: 2.5 mm/day at 28 °C.

Material examined – Thailand, Chiang Rai Province, Chiang Rai University Garden, from flowers of *Dendrobium* sp., 6 July 2019, Xiao-Ya Ma (GZAC O61F21), living cultures O61F21.

GenBank accession numbers – ITS: MW084361, *gapdh*: MW160395, *act*: MW092169, *β-tubulin*: MW160394.

Known distribution (based on molecular data) – worldwide (Than et al. 2008, Prihastuti et al. 2009, Sharma & Shenoy 2014, James et al. 2014, Liu et al. 2014, Jayawardena et al. 2016, Feng et al. 2019, Tang et al. 2021), Thailand (this study).

Known hosts (based on molecular data) – *Artocarpus heterophyllus*, *A. sericicarpus*, *Bauhinia variegata*, *Camellia sinensis*, *Capsicum annuum*, *Capsicum* sp., *Carica papaya*, *Cassia fisculata*, *Citrus* sp., *Cocos nucifera*, *Coffea arabica*, *C. canephora*, *Commelina* sp., *Cymbopogon citrates*, *Dioscorea rotunda*, *Eriobotrya japonica*, *Fragaria ananassa*, *Ficus elastic*, *Hymenocallis* sp., *Jasminum sambac*, *Malus domestica*, *Mangifera indica*, *Mentha* sp., *Murraya* sp., *Olea europaea*, *Passiflora eduli*, *Pennisetum purpureum*, *Persea americana*, *Piper nigrum*, *Pistacia vera*, *Rosmarinus officinalis*, *Saraca indica*, *Theobroma cacao*, *Vaccinium macrocarpon*, and *Vitis vinifera* (Than et al. 2008, Prihastuti et al. 2009, Sharma & Shenoy 2014, James et al. 2014, Liu et al. 2014, Jayawardena et al. 2016, Feng et al. 2019, Tang et al. 2021), *Dendrobium* sp. (this study).

Notes – *Colletotrichum siamense* was introduced from diseased tissues of *Coffea arabica* in Thailand (Prihastuti et al. 2009). Since then, it has been reported as a pathogen on a wide range of hosts worldwide (Than et al. 2008, Prihastuti et al. 2009, Sharma & Shenoy 2014, James et al. 2014, Liu et al. 2014, Jayawardena et al. 2016, Feng et al. 2019, Tang et al. 2021). The morphology of this isolate (Fig. 57) is the same as the description in Liu et al. (2014) and James et al. (2014). This is the first report of endophytic *C. siamense* in orchids from Thailand. To determine whether this species could cause the disease to *Dendrobium* sp. need further evidence.

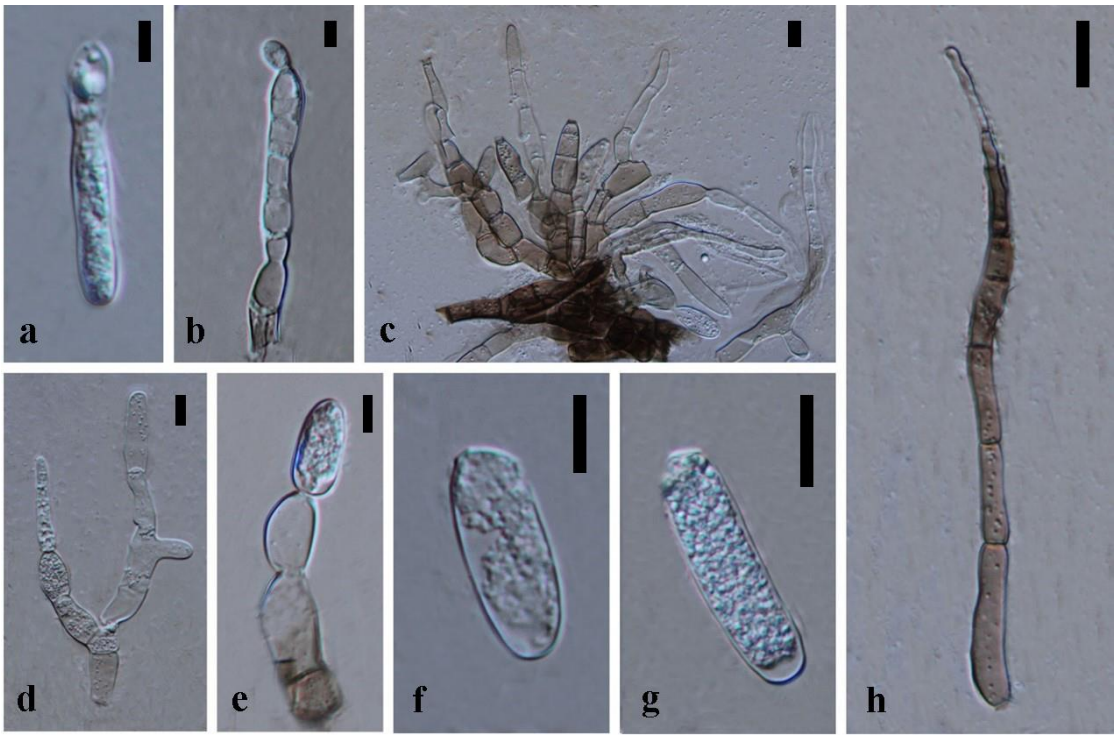


**Fig. 57 – *Colletotrichum siamense*** (GZAC O61F21, **a new host record**). a–e Conidiophores with conidia. f–g Conidia. h Setae. Scale bars: a–h = 10 µm.

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

Facesoffungi number: FoF 02091

***Bionectriaceae*** Samuels & Rossman, Studies in Mycology 42, 15 (1999)

Facesoffungi number: FoF 01367

***Clonostachys*** Corda, Pracht - Flora. Europaeischer Schimmel-Bildungen, 31 (1839)

Facesoffungi number: FoF 02102

Currently, 100 species are listed under *Clonostachys* in Index Fungorum (2023). We provide the updated phylogeny for selected taxa in *Clonostachys* with a new host and a geographical records of *C. ralfsii* and *C. agarwalii* in Fig. 58.

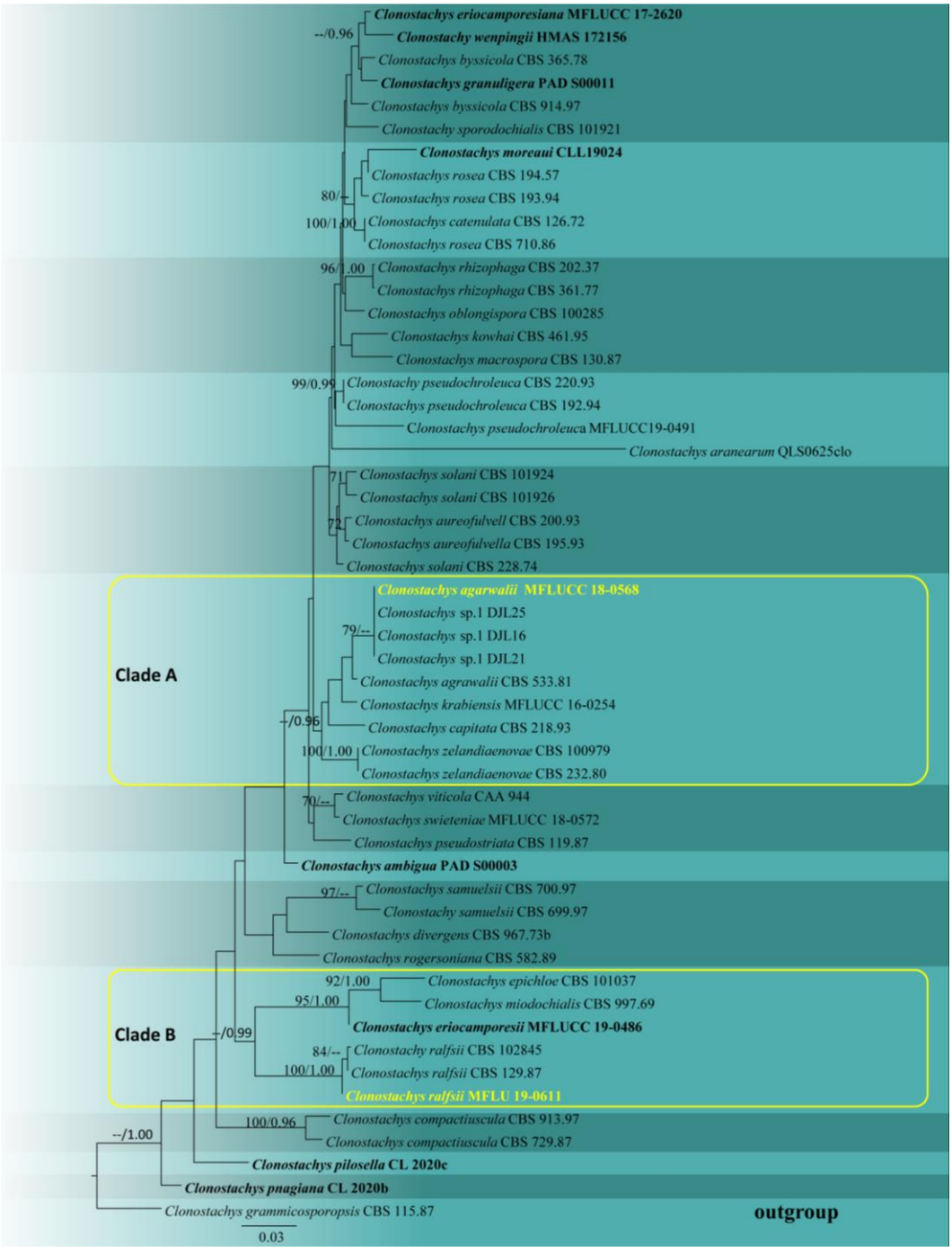


**Fig. 58 –** Phylogram generated from maximum likelihood analysis based on the combined ITS, LSU, *β-tubulin* and *tef1-α* sequence data of *Clonostachys* taxa. Fifty-three strains are included in the

combined analyses which comprised 2376 characters (493 characters for ITS, 850 characters for LSU, 648 characters for *β-tubulin*, 385 characters for *tef1-α*) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -10039.778526 is presented. The matrix had 632 distinct alignment patterns, with 51.62% undetermined characters or gaps. Evolutionary models applied for ITS, LSU, *β-tubulin* and *tef1-α* genes are SYM+I+G, GTR+I+G, HKY+I+G and K80+I models, respectively. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Clonostachys grammicosporopsis* (CBS 115.87). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Clonostachys agarwalii*** (Kushwaha) Schroers [as 'agrawalii'], Studies in Mycology 46, 90 (2001)

Basionym: *Gliocladium agarwalii* Kushwaha, Current Science 49(2), 74 (1980)

Index Fungorum number: IF 485123; Facesoffungi number: FoF 14270; Fig. 59

*Saprobic* on dead twigs of *Lagerstroemia* sp. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* sporodochial. *Sporodochia* somewhat synnematous, short stipitate, scattered or arranged in small groups on the substrate. *Stipe* up to 145 μm tall, 95–250 μm wide. *Conidiophores* 23–30 × 2–2.5 μm ($\bar{x}$ = 27 × 2.2 μm, n = 15), monomorphic, penicillate, mononematous, densely aggregated, hyaline, septate, short stipitate. *Conidiogenous cells* 10–15 × 2.1–3.3 μm ($\bar{x}$ = 12.7 × 2.8 μm, n = 25), phialidic, arranged in groups of 2 at the tip of conidiophores, narrowly flask-shaped, hyaline, straight to slightly curved, smooth-walled, periclinal thickening at the tip, with a visible collarette. *Conidia* 3.5–5.1 × 2.2–2.7 μm ($\bar{x}$ = 4 × 2.5 μm, n = 55), ovoidal to ellipsoidal, somewhat curved or straight, mostly with a slightly flattened side, aseptate, hilum laterally displaced, arranged in imbricate white to pale orange columns, can breakdown into slimy masses, smooth-walled.

Material examined – Thailand, Chiang Mai Province, Mae Rim Sub-district, dead twigs of *Lagerstroemia* sp., 18 September 2017, RH Perera, Rim15 (MFLU 19-0976), living culture MFLUCC 18-0568.

GenBank accession numbers – ITS: OM276726, LSU: OM276821, *tef1-α*: OM283276.

Known distribution (based on molecular data) – India (Schroers 2001), Thailand (this study).

Known hosts (based on molecular data) – decomposing buffalo horn pieces (Schroers 2001), *Lagerstroemia* sp. (this study).

Notes – Our new isolate (MFLUCC 18-0568) grouped with *Clonostachys agarwalii* (CBS 533.81) and three endophytic *Clonostachys* isolates (DJL25, DJL21, and DJL16) obtained from root samples of *Changnienia amoena* (Orchidaceae) in China (Fig. 58). No morphological data have been provided for those endophyte isolates (Jiang et al. 2011). Our collection (MFLU 19-0976) fits the description of conidiogenous cells and conidial measurements of *C. agarwalii* provided by Schroers (2001). With the evidence from the phylogenetic analysis and morphology, we identify our isolate as *C. agarwalii*. We collected sporodochia from the natural substrate, but none were reported from *in vitro* cultures (Schroers 2001). This paper illustrates *Clonostachys agarwalii* as a new host of *Lagerstroemia* sp. and a new geographical record from Thailand.

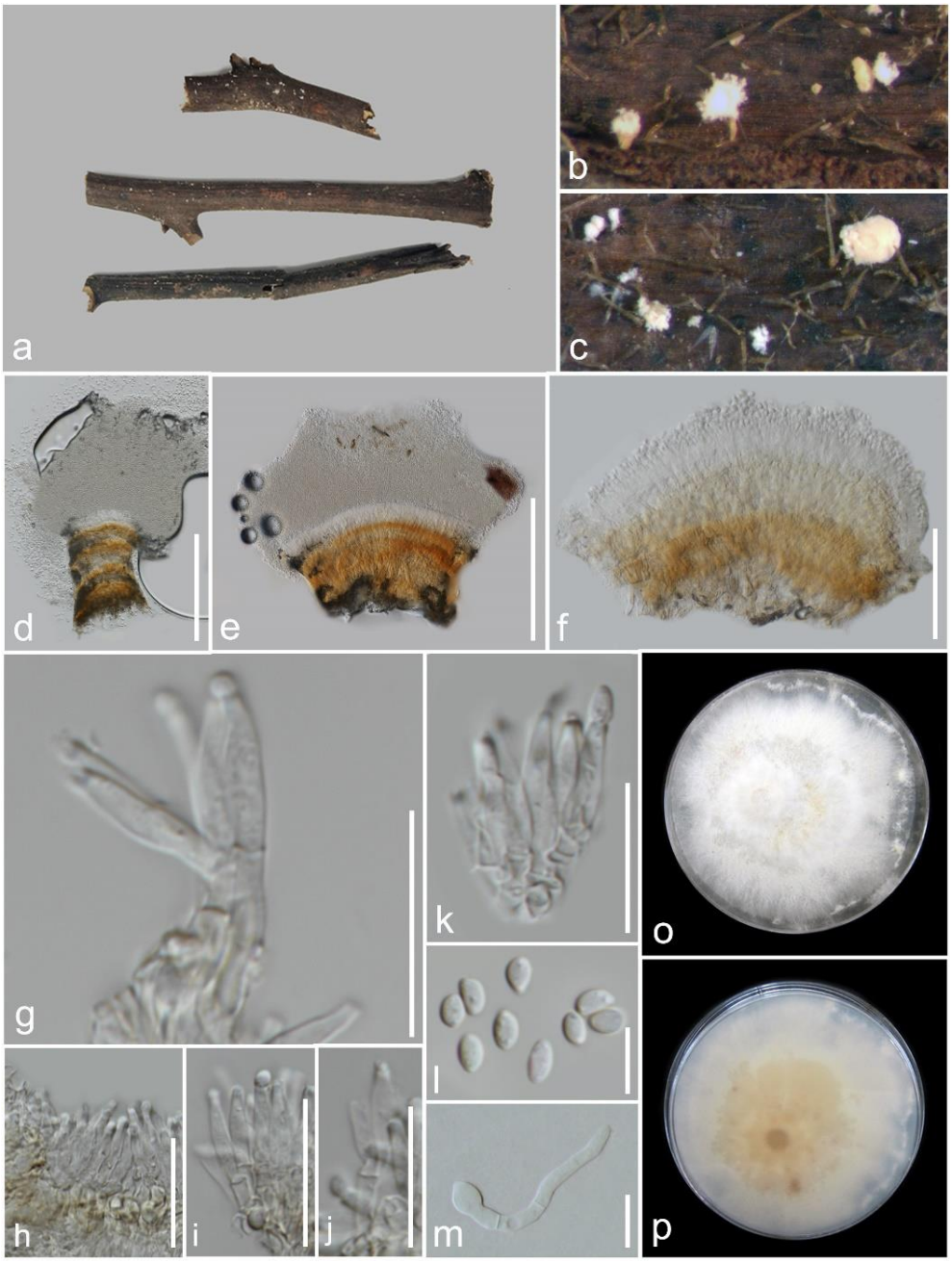


**Fig. 59 – *Clonostachys agarwalii*** (MFLU 19-0976, **new host and geographical record**). a Herbarium material. b, c Sporodochia on the substrate. d–f Sporodochia mounted in water. g–k Conidiophores with phialides and conidia. l Conidia. m Germinating conidium. o, p Colony on PDA. Scale bars: d, e = 200 µm, f = 50 µm, g–i = 20 µm, j, k = 10 µm.

***Clonostachys ralfsii*** Schroers, Studies in Mycology 46, 135 (2001)

Synonyms: *Bionectria ralfsii* (Berk. & Broome) Schroers & Samuels 2001

Index Fungorum number: IF 485142; Facesoffungi number: FoF 14271; Fig. 60

*Saprobic* on the dead branch of *Corylus avellana*. **Sexual morph:** see (Schroers 2001). **Asexual morph:** *Sporodochium* 250–350 µm high, 400–690 at widest sides µm diam. ($\bar{x}$ = 290 × 550 µm, n = 10), solitary, weakly erumpent, widening in upper part, densely packed subhymenial hyphae or synnematous, yellowish-white patches on the host surface. *Conidiophores* 3–5.9 µm wide ($\bar{x}$ = 5.4 µm, n = 20), monomorphic, penicillate, intercalary phialides present, adpressed, in sporodochial aggregates or conidiomata, cylindrical or sub-cylindrical, formed below solitary terminal phialides, apically bearing conidiogenous cells. *Conidiogenous cells* 5–8 µm wide ($\bar{x}$ = 6.5 µm, n = 20), enteroblastic, phialidic, arising from a single cell, narrowly flask-shaped, gradually

tapering towards the tip with a short collar, conspicuous periclinal thickening, wide near aperture. *Conidia* 8–13 × 6–8.5 µm ($\bar{x}$ = 12.1 × 7.5 µm, n = 30), broadly ellipsoidal to limoniform, aseptate, slightly curved, protruding, tapering at both ends, with collarette-like remains of the phialidic tip, deeply pigmented, olive-black conidial mass, hyaline at the beginning, pale green at maturity, finely rough-walled.

Material examined – Italy, Forlì-Cesena Province, Tontola-Predappio, on a dead hanging branch of *Corylus avellana*, 20 January 2019, Erio Camporesi, IT 4214 (MFLU 19-0611).

GenBank accession numbers – ITS: OP740990, LSU: OP741010.

Known distribution (based on molecular data) – Australia, New Zealand (Schroers 2001), Italy (this study).

Known hosts (based on molecular data) – bark of unknown dead hosts (Schroers 2001), *Corylus avellana* (this study).

Notes – In the multi-gene phylogeny (ITS, LSU, *β-tubulin* and *tef1-α*) of our study, novel strain (MFLU 19-0611) and other strains of *Clonostachys ralfsii* (CBS 102845 and CBS 129.87) clustered together with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability in Clade B (Fig. 58). These isolates were collected from unquoted dead hosts from different localities. Detailed sexual and asexual morphology with illustrations of this fungus were provided by Schroers (2001). When comparing the morphology of the asexual morph of *C. ralfsii* (Schroers 2001), sporodochium, conidiophores, and conidia are slightly larger in our collection (Table 1, Fig. 60). Also, we considered the nucleotide differences within the rRNA gene regions of those strains for further clarification. When comparing the ITS region (ITS1-5.8S-ITS2) of 485 nucleotides, there is one bp (0.20 %) difference in CBS 102845 and CBS 129.87 with our strain (MFLU 19-0611). The LSU rDNA region of MFLU 19-0611 (516 nucleotides) is identical to that of CBS 129.87. Considering the molecular data analysis, we conclude that our new collection is *Clonostachys ralfsii*. The current study presents a new host record on *Corylus avellana* and the first record from Italy.

**Table 1 –** Synopsis of morphology in asexual morphs of *Clonostachys ralfsii*

| Character | Schroers (2001) | This study |
|---|---|---|
| Sporodochium | 350–600 µm wide at top | 250–350 µm high, 400–690 at widest sides µm diam. |
| Conidiophores | (2.2–)3.4–4–4.6(–5.4) µm at the widest point | 2.5–5.9 µm wide |
| Conidia | (7.4–)11.6–12.6–13.6(–17.8) × (4.8–)6.4–7–7.6(–11) µm | 8–13 µm × 6–8.5 µm |

***Clavicipitaceae*** (Lindau) Earle ex Rogerson, Contributions from the United States National Herbarium 6, 170 (1901)

Facesoffungi number: FoF 01313

***Pochonia*** Bat. & O.M. Fonseca, Publicações Instituto de Micologia, Recife 462, 4 (1965)

Facesoffungi number: FoF 13104

*Pochonia*, typified by *Pochonia humicola*, currently has three accepted species (Mongkolsamrit et al. 2020, Hyde et al. 2020a, Wijayawardene et al. 2022, Species Fungorum 2023). Subsequent to the initial phylogeny provided by Zare et al. (2001), several studies revisited this genus; however, taxonomic ambiguities remained (Sung et al. 2007, Nonaka et al. 2012, Kepler et al. 2014). Sung et al. (2007) introduced *Metacordyceps* to accommodate several *Metarhizium* and *Pochonia* species. However, in a later revision, Kepler et al. (2014) proposed the suppression of *Metacordyceps* and retained *Pochonia*. Mongkolsamrit et al. (2020) provided the most recent taxonomic explanation for *Pochonia.* Species of *Pochonia* are well-known as nematode parasites, and some have been isolated from soil environments (Mongkolsamrit et al. 2020, Hyde et al. 2020a). Some *Pochonia* species produce sexual and asexual morphs, while most produce

dictyochlamydospores or irregularly swollen hyphae (Mongkolsamrit et al. 2020, Hyde et al. 2020a). We provide the updated phylogeny for taxa in *Clavicipitaceae* in Fig. 61.

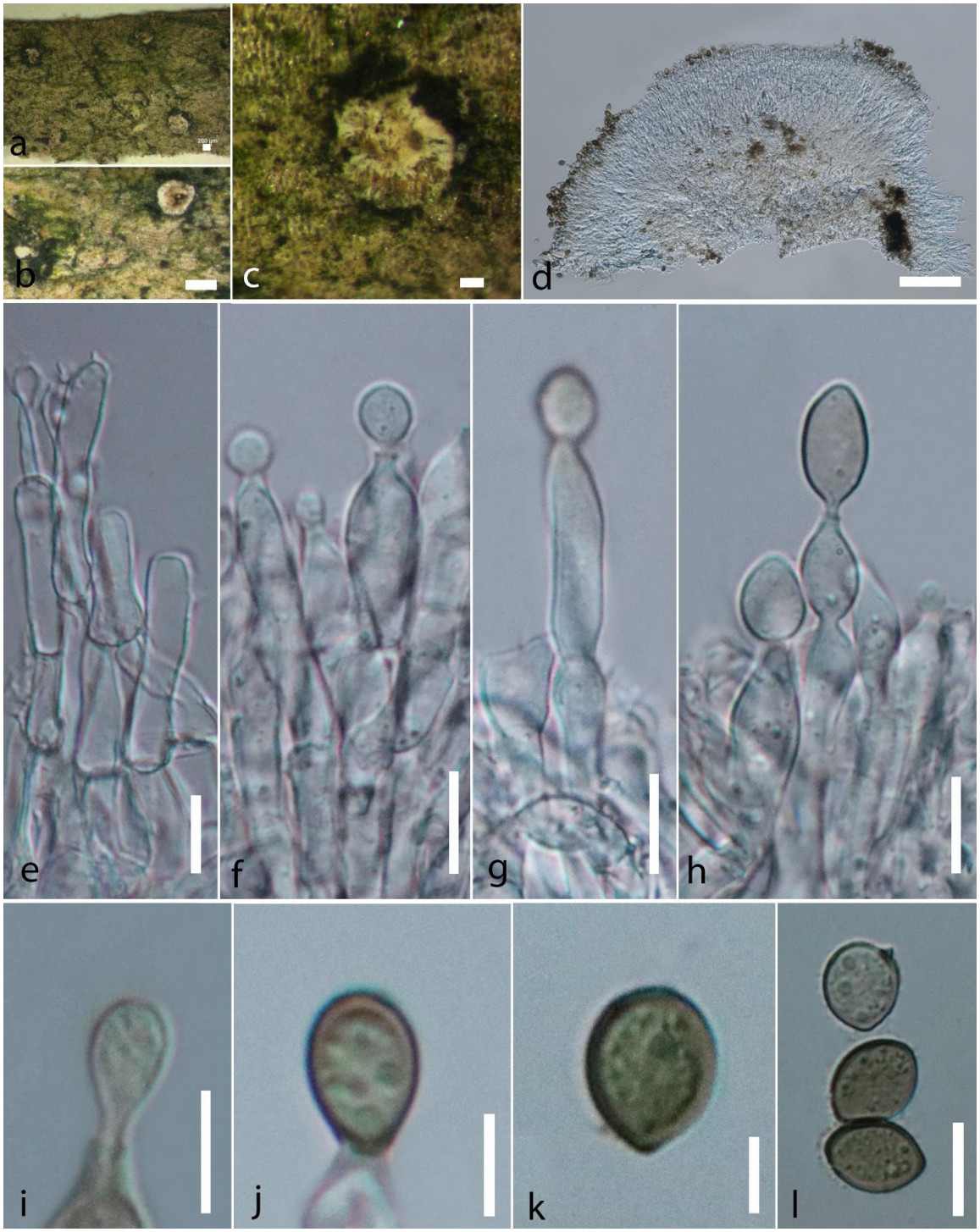


**Fig. 60 – *Clonostachys ralfsii*** (MFLU 19-0611, **a new host and geographical record**). a–c Appearance of sporodochium on the host substrate. d Longitudinal section of a sporodochium. e Appearance of conidiophores in the sporodochium. f–h Different stages of conidiogenesis. i–l Conidia. Scale bars: a, b = 200 μm, c, d = 100 μm, f–h, l = 10 μm, e, i–k = 5 μm.

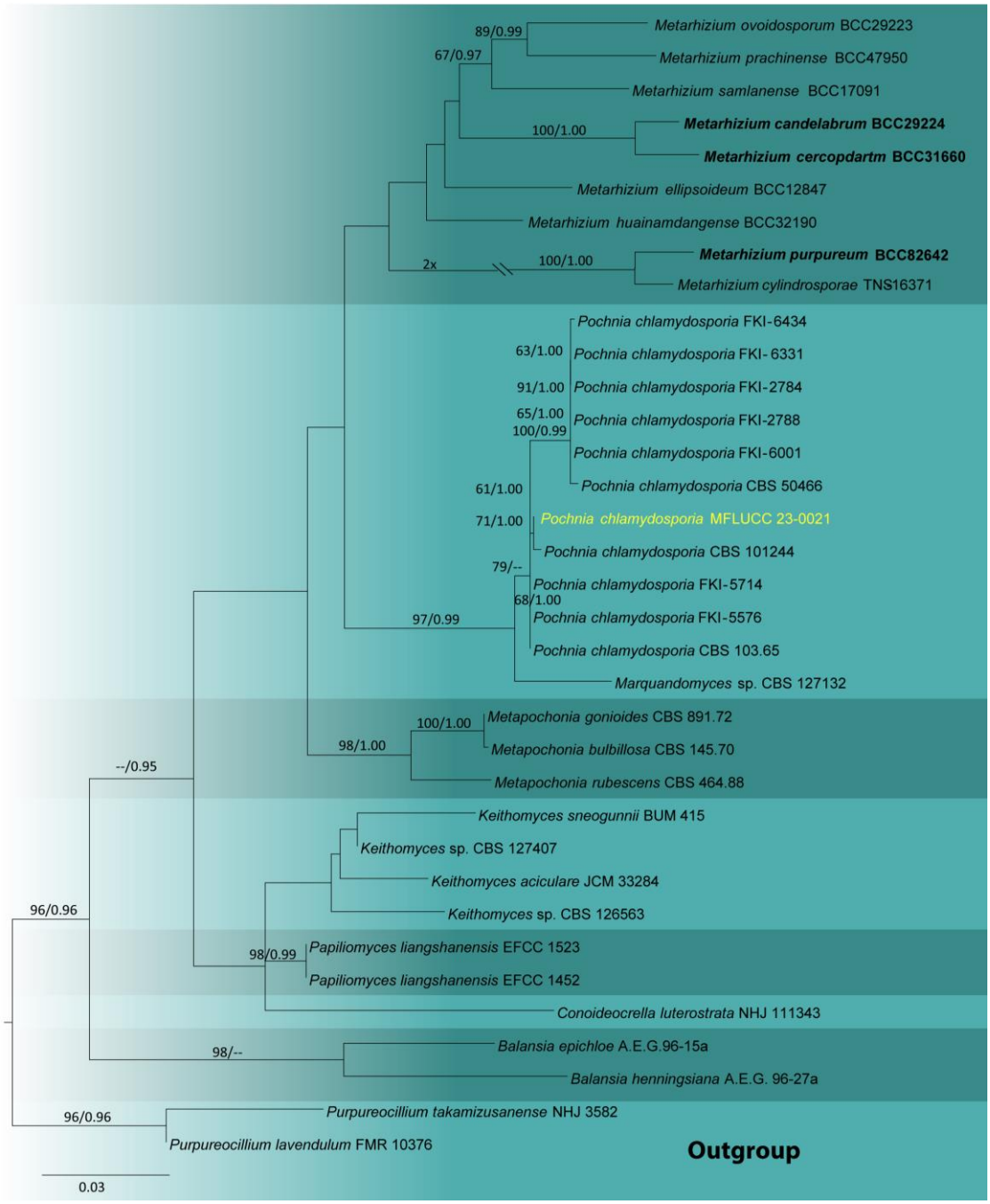


**Fig. 61 –** Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Clavicipitaceae* taxa. Thirty-four strains are included in the combined analyses which comprised 1594 characters (539 characters for ITS and 1055 characters for LSU) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5725.389280 is presented. The matrix had 476 distinct alignment patterns, with 33.06% undetermined characters or gaps. Evolutionary models applied for ITS and LSU are SYM+I+G and GTR+I+G models, respectively. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Purpureocillium takamizusanense* (NHJ 3582) and *P. lavendulum* (FMR 10376). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Pochonia chlamydosporia*** (Goddard) Zare & W. Gams, in Gams & Zare, Nova Hedwigia 72(3–4), 334 (2001)

Basionym: *Cordyceps chlamydosporia* H.C. Evans in Zare et al., Nova Hedwigia 73(1–2), 51–86 (2001)

Index Fungorum number: IF 474783; Facesoffungi number: FoF 14272; Fig. 62

*Hyphae* hyaline, aseptate, smooth-surfaced, becoming course-surfaced when mature. **Asexual morph:** *Conidiophores* 12–30 × 1–1.5 μm ($\overline{x}$ = 22 × 1 μm, n = 20), mononematous, micronematous, erect, straight or slightly curved, smooth-walled, unbranched terminal or intercalary. *Phialides* 3–7 × 1–4 μm ($\overline{x}$ = 6 × 2.5 μm, n = 20), solitary on apices of conidiophores, ellipsoid to sub-cylindrical, bearing conidial chains at the apex. *Conidia* 2.5–5.5 × 1.5–4 μm ($\overline{x}$ = 3 × 2 μm, n = 20), globose or subglobose to ovoid, smooth-walled, hyaline, aseptate. **Sexual morph:** Undetermined.

Culture characteristics – *Colonies* on PDA become 30 mm diam. after 14 days at 25 ℃, appearing in white, becoming yellow to deep-yellow, cottony, slightly raised when mature, entire margined, reverse yellowish brown at the center and whitish yellow at the rind.

Material examined – Thailand, Chiang Rai Province, 19°53'2"N, 100°5'37"E, 440 m, on forest soil, 7 January 2020, W.A.E. Yasanthika, living culture MFLUCC 23-0021.

GenBank accession numbers – ITS: OQ690713, LSU: OQ690716.

Known distribution (based on molecular data) – Canada, Germany, Japan and Thailand (Mensin et al. 2012, Nonaka et al. 2013, Mongkolsamrit et al. 2020, Jaihan et al. 2021, this study).

Known hosts (based on molecular data) – *Nymph of Cicadidae* and soil (Mensin et al. 2012, Nonaka et al. 2013, Kim et al. 2016, Mongkolsamrit et al. 2020, Jaihan et al. 2021), forest soil (this study).

Notes – *Pochonia chlamydosporia* has been identified as an association of four varieties, which were synonymized under *P. chlamydosporia* based on the latest classification (Nonaka et al. 2013, Species Fungorum 2023). This species has been subjected to revision in several studies and synonymized recently by Mongkolsamrit et al. (2020). Both sexual and asexual morphs are reported from this species, and the sexual morph is observed in the nymphs of *Cicadidae* in Thailand (Jaihan et al. 2021). This species is commonly found in soils and is a nematode parasite used as a biocontrol agent (Nonaka et al. 2013). Our collection (MFLUCC 23-0021) is clustered with other *P. chlamydosporia* with 68% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability in the combined ITS and LSU phylogenetic tree (Fig. 61) and also agrees with Mongkolsamrit et al. (2020). Our isolate is morphologically similar to *P. chlamydosporia* (CBS 101244) in having globose or subglobose to ovoid, smooth-walled, hyaline, aseptate conidia produced on phialides (Nonaka et al. 2013). Based on both morphological characteristics (Fig. 62) and multigene phylogenetic analyses (Fig. 61), the current study reports the first collection of *P. chlamydosporia* from the forest soils in Thailand.

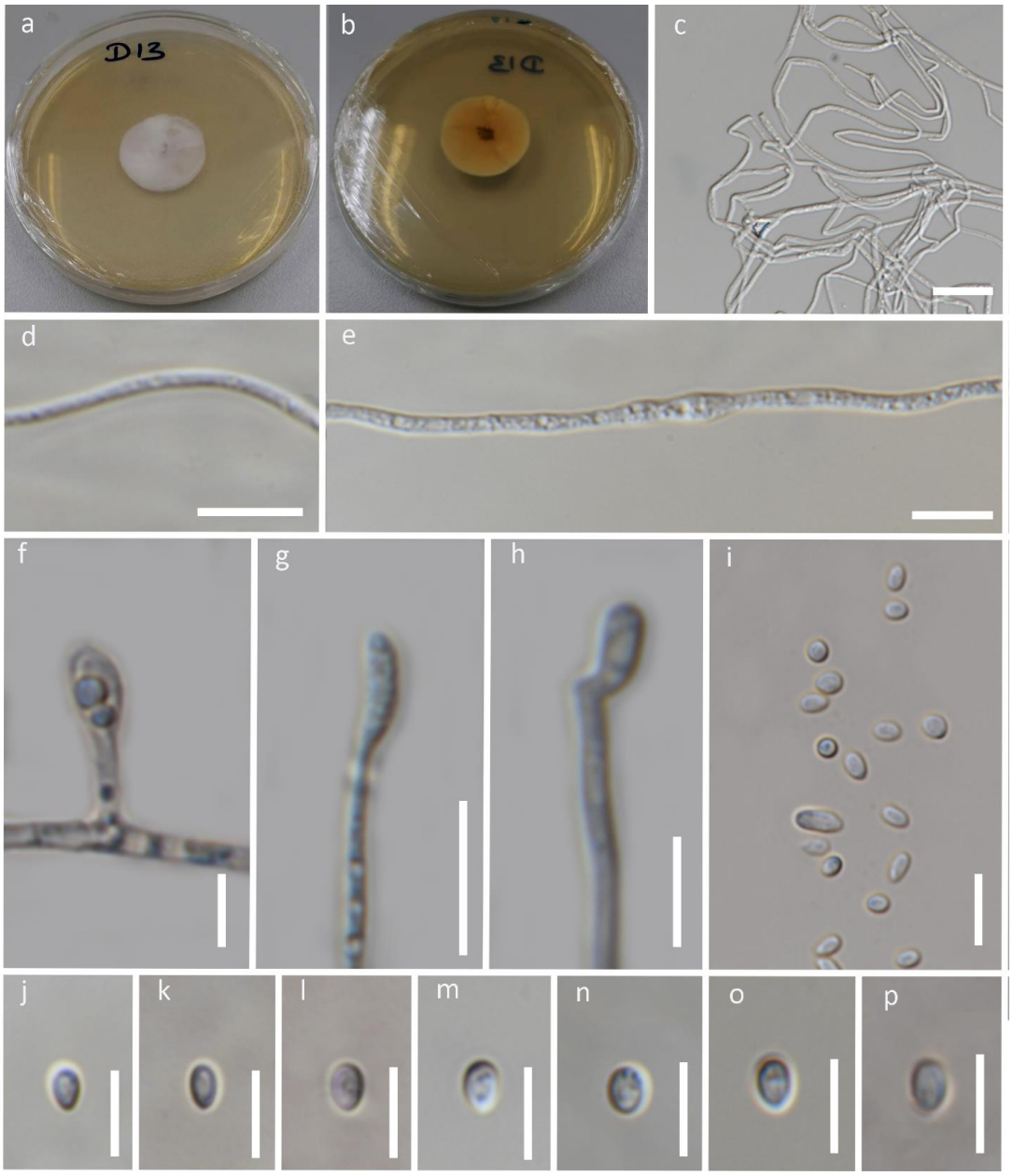


**Fig. 62 – *Pochonia chlamydosporia*** (MFLUCC 23-0021, **a new habitat record**). a Colony from above (on the PDA). b Colony from below (on the PDA). c–e Hyphae. f Conidiogenesis on phialides. g, h Conidiophores. i–p Conidia. Scale bars: c = 20 μm, d, e, h–p = 10 μm, f = 5 μm.

***Nectriaceae*** Tul. & C. Tul. [as 'Nectriei'], Selecta fungorum carpologia (Paris) 3, 3 (1865)
Facesoffungi number: FoF 01396

***Volutella*** Fr., Systema Mycologicum (Lundae) 3(2), 458, 466 (1832)
Facesoffungi number: FoF 10672

*Volutella*, typified by *V. ciliata*, is a cosmopolitan genus with members isolated from plants, soil, and air (Tibpromma et al. 2018). Thirty-two morphological *Volutella* species are listed in Species Fungorum (2023) with 12 species supported by molecular data. We provide the updated phylogeny for *Volutella* species and related taxa in *Nectriaceae* in Fig. 63.

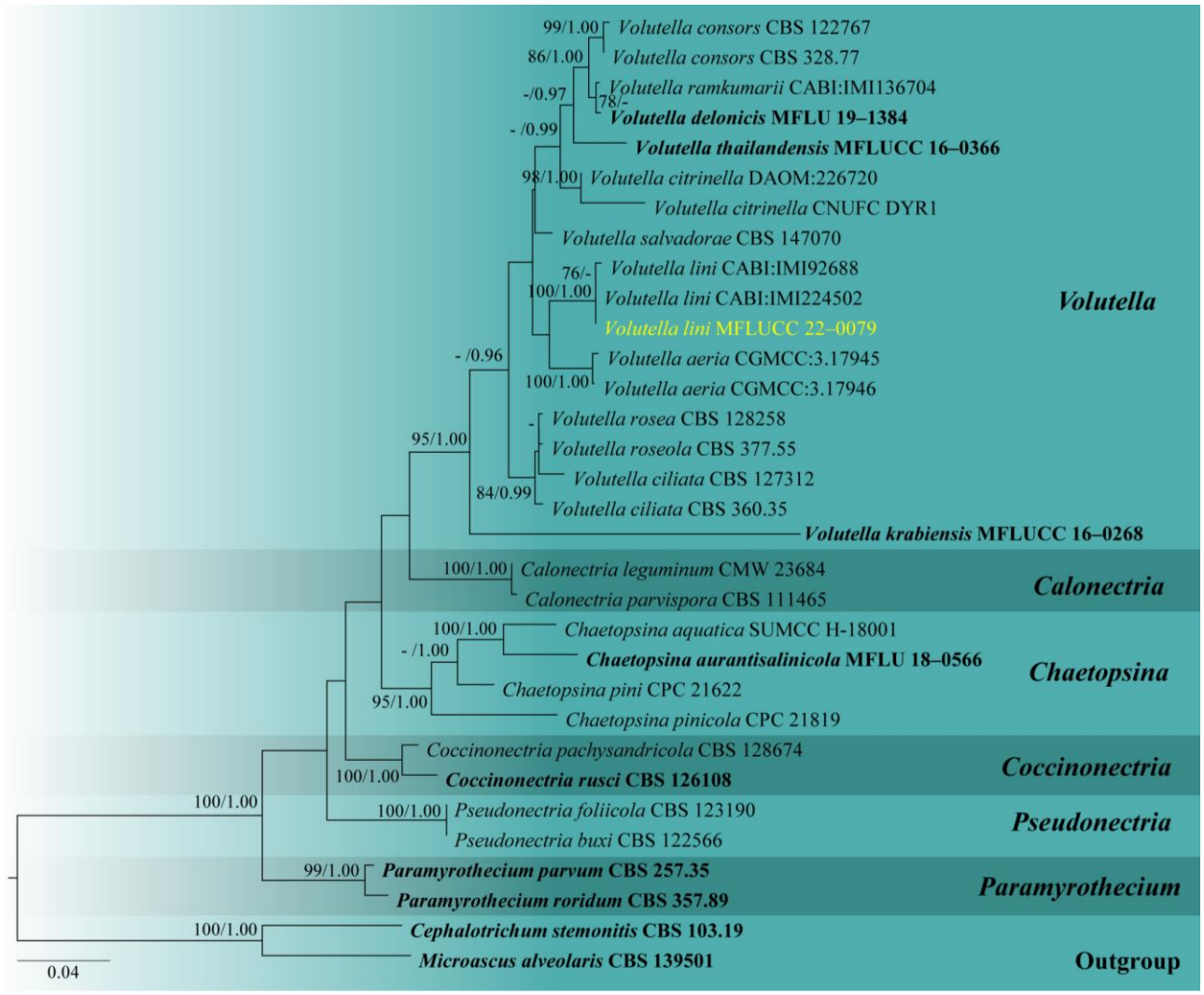


**Fig. 63 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data for selected genera in *Nectriaceae*. Thirty-two strains are included in the combined analyses which comprised 1391 characters (818 characters for LSU, 573 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of –7336.851768 is presented. The matrix had 468 distinct alignment patterns, with 9.24% of undetermined characters or gaps. The best-fit evolutionary models for individual and combined datasets resulted to the GTR+I+G model. Bootstrap support values for ML equal to or greater than 75% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Cephalotrichum stemonitis* (CBS 103.19) and *Microascus alveolaris* (CBS 139501). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Volutella lini*** Mukerji, J.P. Tewari & J.N. Rai, Transactions of the British Mycological Society 51(2), 337 (1968)

Index Fungorum number: IF 283327; Facesoffungi number: FoF 10673; Fig. 64

*Saprobic* on submerged decaying wood in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Colonies* on the substrate effuse, scattered, whitish at first, becoming light yellow at maturity. *Mycelium* mostly immersed, composed of branched, septate, smooth, thin-walled, brown hyphae. *Sporodochia* with setae, 160–265 × 62–78 µm ($\bar{x}$ = 198.6 × 69.7 µm, n =10), sessile with slimy spore mass at the apex, swollen at the apex, hyaline, aseptate, subcylindrical to ovoid, with long acuminate setae arising from the base and margin. *Setae* 95–255 µm long ($\bar{x}$ = 157 µm, n = 30), 5.5 µm thick at the base tapering to 2 µm, erect, straight to curved, flexuous, unbranched, irregular in length, smooth, thick-walled, aseptate,

cylindrical, tapering towards apex into an acute tip. *Conidiophores* aggregated into sporodochia, verticillate, with hyaline, thick setae around the side of conidiomata. *Conidiogenous cells* 8–12 × 1.5–3.0 μm ($\bar{x}$ = 10.3 × 2.1 μm, n = 20), hyaline, subulate. *Conidia* 6–9 × 1–2.5 μm ($\bar{x}$ = 7.5 × 1.7 μm, n = 50), produced at large numbers from the tips of the phialides, slimy, aseptate, hyaline, cylindrical or bacillar, guttulate with rounded or acute ends, smooth, thin-walled, without mucilaginous sheath.

Culture characteristics – Ascospores germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 25–30 mm in 4 weeks at 25 °C. Mycelia superficial, circular, with entire margin, flat, smooth, slimy, moist, from above light brown; reverse, light yellowish orange.

Material examined – Thailand, Tak Province, Tha Sing Yang, Ban Mae Ja Wang on decaying wood submerged in a freshwater river, 17 October 2019, O. Padaruth, CC63 (MFLU 22–0117), living culture, MFLUCC 22–0079.

GenBank accession numbers – LSU: OP216401, ITS: OP216406.

Known distribution (based on molecular data) – India (Cannon et al. 2012), Thailand (this study).

Known hosts (based on molecular data) – Unidentified host (Cannon et al. 2012, this study).

Notes – *Volutella lini*, introduced by Mukerji et al. (1968), was isolated from the rhizosphere and rhizoplane of *Linum usitatissimum* in India. The latest report of the species was by Cannon et al. (2012) from an unknown host in India and also provided the ITS sequence data of the two *Volutella lini* strains (CABI: IMI224502 and CABI: IMI92688). Our isolate, MFUCC 22–0079, is morphologically similar to other *Volutella* species and clustered with the strains of *V. lini* with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 63). *Volutella lini* MFLUCC 22–0079 has larger conidiomata (160–265 × 62–78 μm *vs.* up to 160 × 18.7–45.8 μm), longer setae (95–255 μm *vs.* 50–200 μm), and shorter conidia 6–9 × 1–2.5 μm *vs.* 8–14 × 1.2–1.6 μm) than the type strain, *V. lini* IMI 92688. The latter has a sporodochium with highly branched hyphae that become longer at mature stages and have sclerotia in the culture. The morphological differences observed may be due to the adaptation of *V. lini* to various environmental conditions in different habitats (Fig. 64). There are no differences in the ITS sequence data of the three strains of *V. lini*. Therefore, we introduce this isolate as a new geographical record of *V. lini* in Thailand and a new record also from freshwater habitat. *Volutella lini* is the second species of this genus reported from freshwater habitats, with *V. citronella* as the first one in Korea (Pangging et al. 2021).

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

Facesoffungi number: FoF 06513

***Chaetosphaeriales*** *genera incertae sedis*

***Neoleptosporella*** Phukhams. & K.D. Hyde, Fungal Diversity 102, 147 (2020)

Facesoffungi number: FoF 07246

*Neoleptosporella* was proposed as a new genus by Phukhamsakda et al. (2020) and typified by *N. clematidis*. *Neoleptosporella* species are characterized by subglobose to depressed globose ascomata, shiny black, visible ostioles and immersed beneath a small clypeus, ostioles with periphyses, peridium of dark brown to black cells of *textura angularis*, hyaline, branched and septate paraphyses, broad cylindrical and long-pedicellate asci, with J- apical ring, fusiform and aseptate ascospores (Hyde et al. 2020d, Phukhamsakda et al. 2020). *Neoleptosporella* can be distinguished from *Leptosporella* in having immersed, subglobose to depressed globose ascomata, which are partially carbonaceous at the apex. The apical part of the asci is wedge-shaped and J-, with fusiform, aseptate ascospores with acute ends (Huhndorf & Miller 2011, Dai et al. 2017, Konta et al. 2017, Hyde et al. 2020d). The updated phylogeny for the genus is provided in Fig. 65.

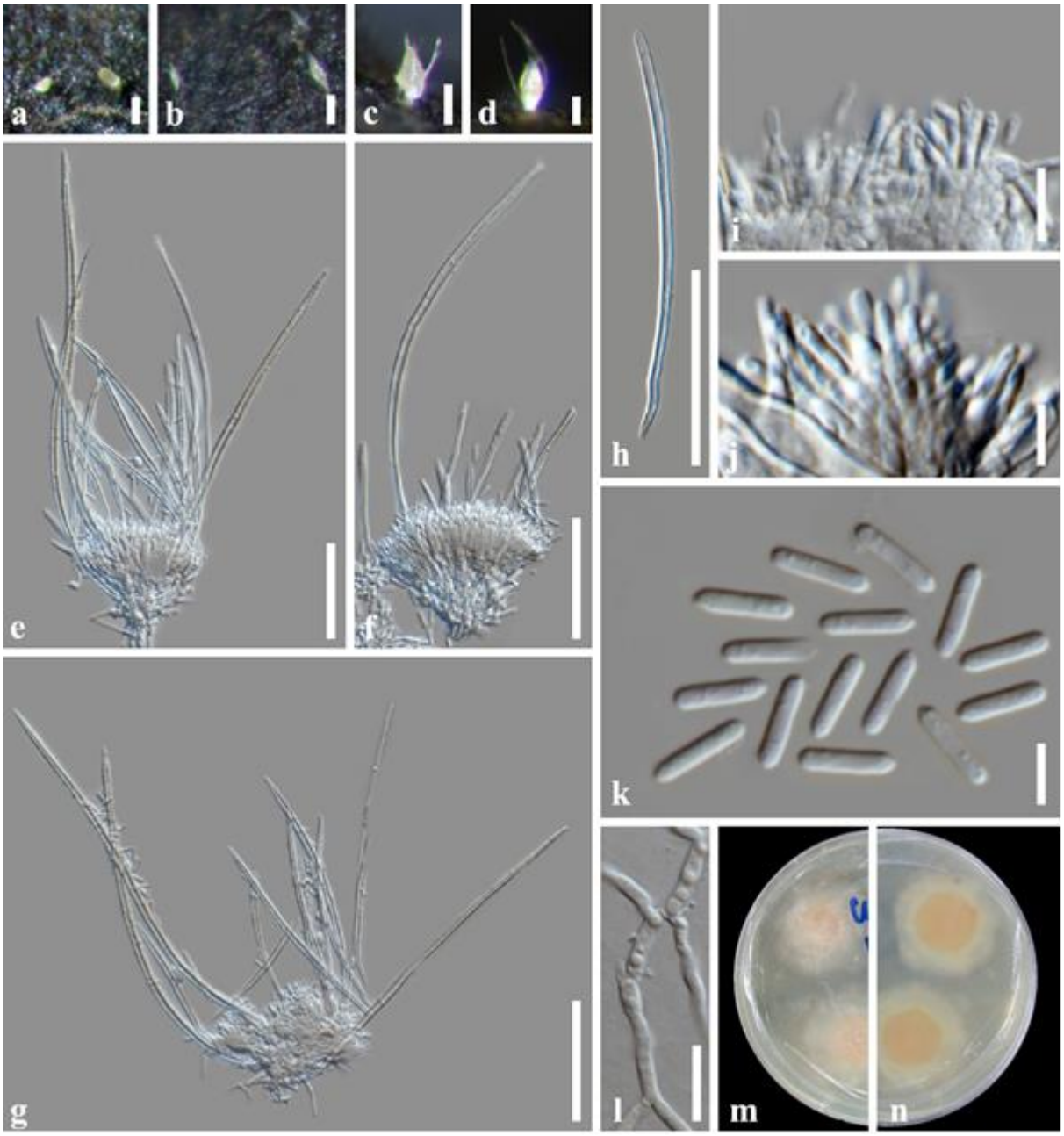


**Fig. 64 – *Volutella lini*** (MFLU 22–0117, **new geographical record and habitat record**). a–d Appearance of sporodochial conidiomata on host. e–g Conidiophores, conidiogenous cells and conidium. h Setae. i, j Conidiogenous cells. k Conidia. l Germinated conidium. m, n Colonies on MEA from above and below. Scale bars: a–g = 50 μm, h–k = 5 μm, l = 20 μm.

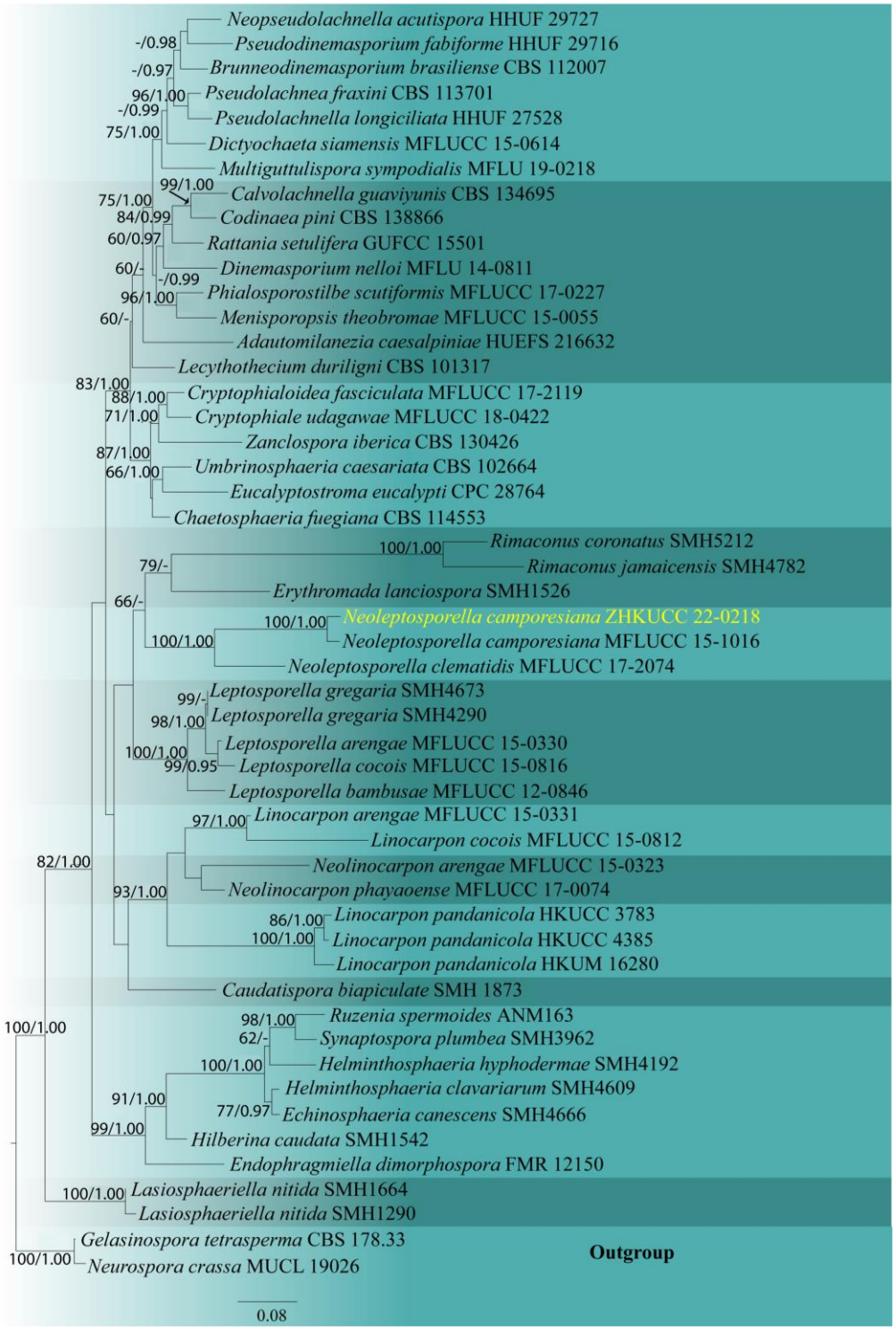


**Fig. 65** – Phylogram generated from a combined LSU-ITS-*rpb*2-*tef1-α* sequence data of *Neoleptosporella* taxa. Fifty-one strains are included in the combined analyses, which comprised 3373 characters (952 characters for LSU, 615 characters for ITS, 990 characters for *rpb*2, 816 characters for *tef1-α*). The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -24625.51 is presented. The matrix had 1510 distinct alignment patterns, with 58.77% of undetermined characters or gaps. Evolutionary model GTRGAMMA was applied for all the genes. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree was rooted with *Gelasinospora tetrasperma* (CBS 178.33) and *Neurospora crassa* (MUCL 19026). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Neoleptosporella camporesiana*** R.H. Perera & K.D. Hyde, Fungal Diversity 100, 219 (2020)

Index Fungorum number: IF 556898; Facesoffungi number: FoF 06962; Fig. 66

*Saprobic* on dead branch of an unidentified plant. **Sexual morph:** *Ascomata* 200–300 μm high, 280–350 μm wide ($\bar{x}$ = 264 × 307 μm, n = 15), solitary or aggregated, immersed beneath small clypeus, uniloculate, subglobose to depressed globose, ostiolate, black shiny ostioles visible. *Peridium* 30–50 μm wide ($\bar{x}$ = 39 μm, n = 15), outer cells fused with the host epidermal cells, composed of dark brown to black cells of *textura angularis*, inner cells hyaline, composed of 2–3 layers of *textura angularis* cells. *Paraphyses* 3–6 μm wide ($\bar{x}$ = 3.9 μm, n = 20), hyaline, branched, septate. *Asci* 90–120 × 8–12 μm ($\bar{x}$ = 100 × 10 μm, n = 20), unitunicate, 8-spored, cylindrical, straight or slightly curved, apex rounded with a wedge-shaped, J- apical ring. *Ascospores* 50–80 × 2.5–4 μm ($\bar{x}$ = 64 × 2.8 μm, n = 20), fusiform, straight or curved, hyaline, aseptate, rounded at the apex, pointed at the base, smooth-walled, without appendages. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on PDA within 12 h. Colonies on PDA, reaching 5 cm diam. after two months at 22 °C, circular, flat, margin filiform, surface with strong wrinkled, yellowish in the center, white at the edge, reverse cracked, light brown to yellowish.

Material examined – China, Yunnan Province, Kunming Botanical Garden, on a dead branch of an unidentified plant, 12 July 2021, Li Lu LL89 (MHZU 22-0125), living culture ZHKUCC 22-0218.

GenBank accession numbers – ITS: OP681141, LSU: OP658918, *rpb2*: OP684007, *tef1-α*: OP684008.

Known distribution (based on molecular data) – Thailand (Hyde et al. 2020d, Phukhamsakda et al. 2020), China (this study).

Known hosts (based on molecular data) – dead stems of *Clematis subumbellata* (Phukhamsakda et al. 2020), a dead branch of an unidentified plant (Hyde et al. 2020d).

Notes – Our specimen is morphologically similar to *Neoleptosporella camporesiana* by having ascomata with black shiny ostioles, cylindrical asci with J- apical ring and filiform ascospores (Hyde et al. 2020d). The comparison of base pairs in ITS showed 2.5 % differences (13/515 bp), while LSU showed 1% difference (10/884 bp). Phylogenetic analyses of combined ITS, LSU, *rpb2* and *tef1-α* revealed that our strain (ZHKUCC 22-0218) clusters with *N. camporesiana* (MFLUCC 15-1016) with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 65). Hyde et al. (2020d) described *N. camporesiana* from Thailand, and this study reports the first geographical record of *N. camporesiana* from China (Fig. 66).

***Coniochaetales*** Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96, 378 (2004)

Facesoffungi number: FoF 01379

***Coniochaetaceae*** Malloch & Cain, Canadian Journal of Botany 49, 878 (1971)

Facesoffungi number: FoF 01332

***Coniochaeta*** (Sacc.) Cooke, Grevillea 16(no. 77), 16 (1887)

Facesoffungi number: FoF 01333

*Coniochaeta* was initially described as a subgenus in *Rosellinia* (Saccardo 1882) until it was raised to genus level by Cooke (1887). Taxa of the genus are distributed worldwide and are either endophytes, pathogens, or saprobes (García et al. 2006, Damm et al. 2010, Samarakoon et al. 2018, Harrington et al. 2019, Chethana et al. 2021a, Mehrabi et al. 2022). The sexual morph of the genus is characterised by dark brown to black, perithecial or cleistothecial ascomata. The ascomatal wall is often membranaceous to pseudoparenchymatous or sometimes coriaceous (Friebes et al. 2016, Samarakoon et al. 2018, Jones et al. 2019). A paraphysate hamathecium is usually present, and the asci are unitunicate, with an inamyloid apical ring. Ascospores are aseptate, often laterally compressed, and comprise a germ slit (García et al. 2006, Friebes et al. 2016). The asexual morph is hyphomycetous (Damm et al. 2010; Si et al. 2021, Mehrabi et al. 2022). While novel taxa have recently been introduced in the genus (Kabtani et al. 2022, Mehrabi et al. 2022), new records have

also been reported (Chethana et al. 2021a, Manawasinghe et al. 2022). An updated phylogeny for the genus is shown in Fig. 67.

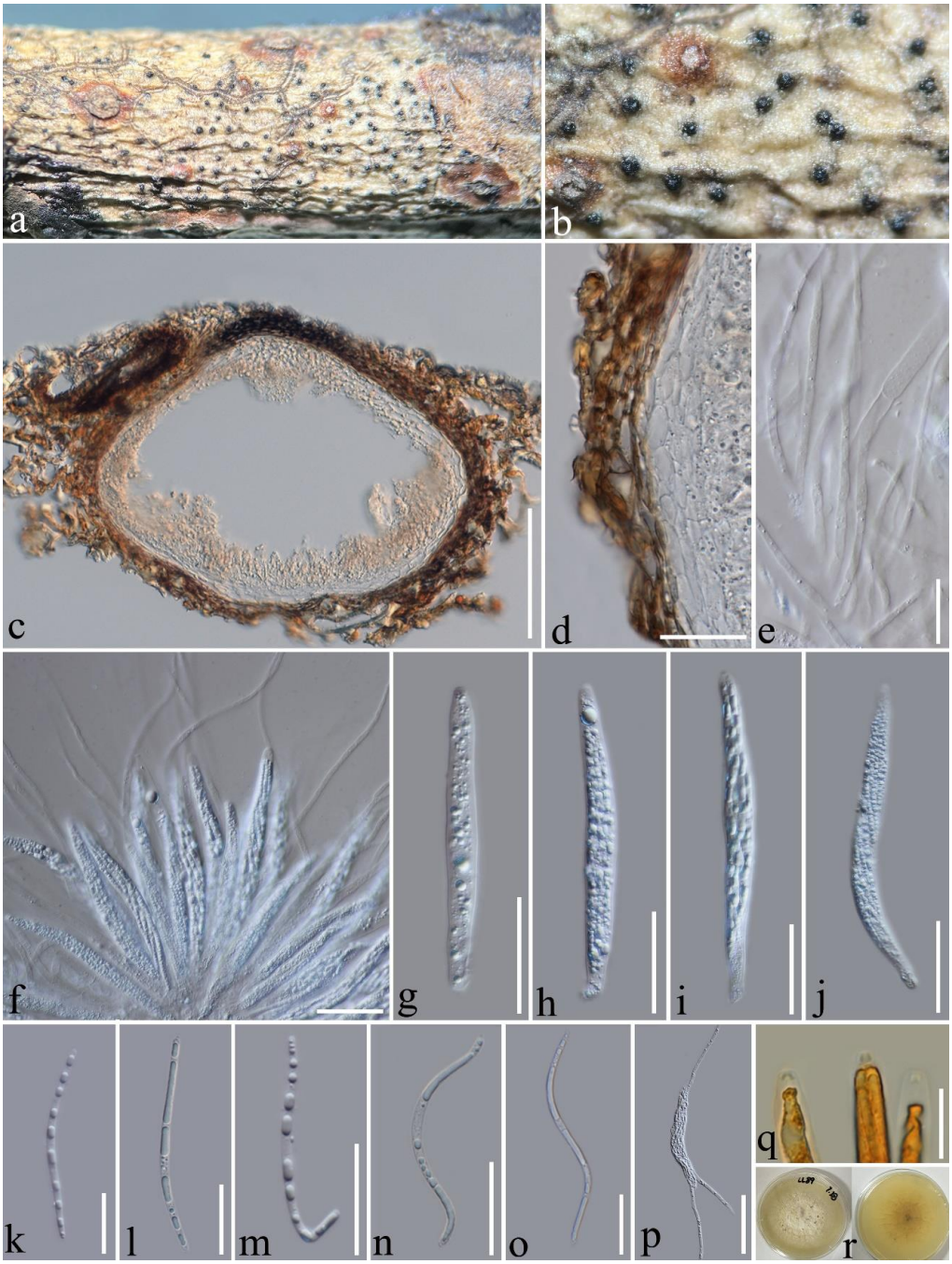


**Fig. 66 – *Neoleptosporella camporesiana*** (MHZU 22-0125, **new geographical record**). a, b Ascomata on the substrate. c Vertical section of an ascoma. d Peridium. e Paraphyses. f–j Asci. k–o Ascospores. p Germinating ascus. q Asci in Melzer's reagent presenting J- reaction of the apical ring. r Colonies on PDA (produced black spot, but no spores). Scale bars: c = 100 µm, d, e = 20 µm, f–j = 30 µm, k–o = 10 µm, p = 50 µm, q = 10 µm.

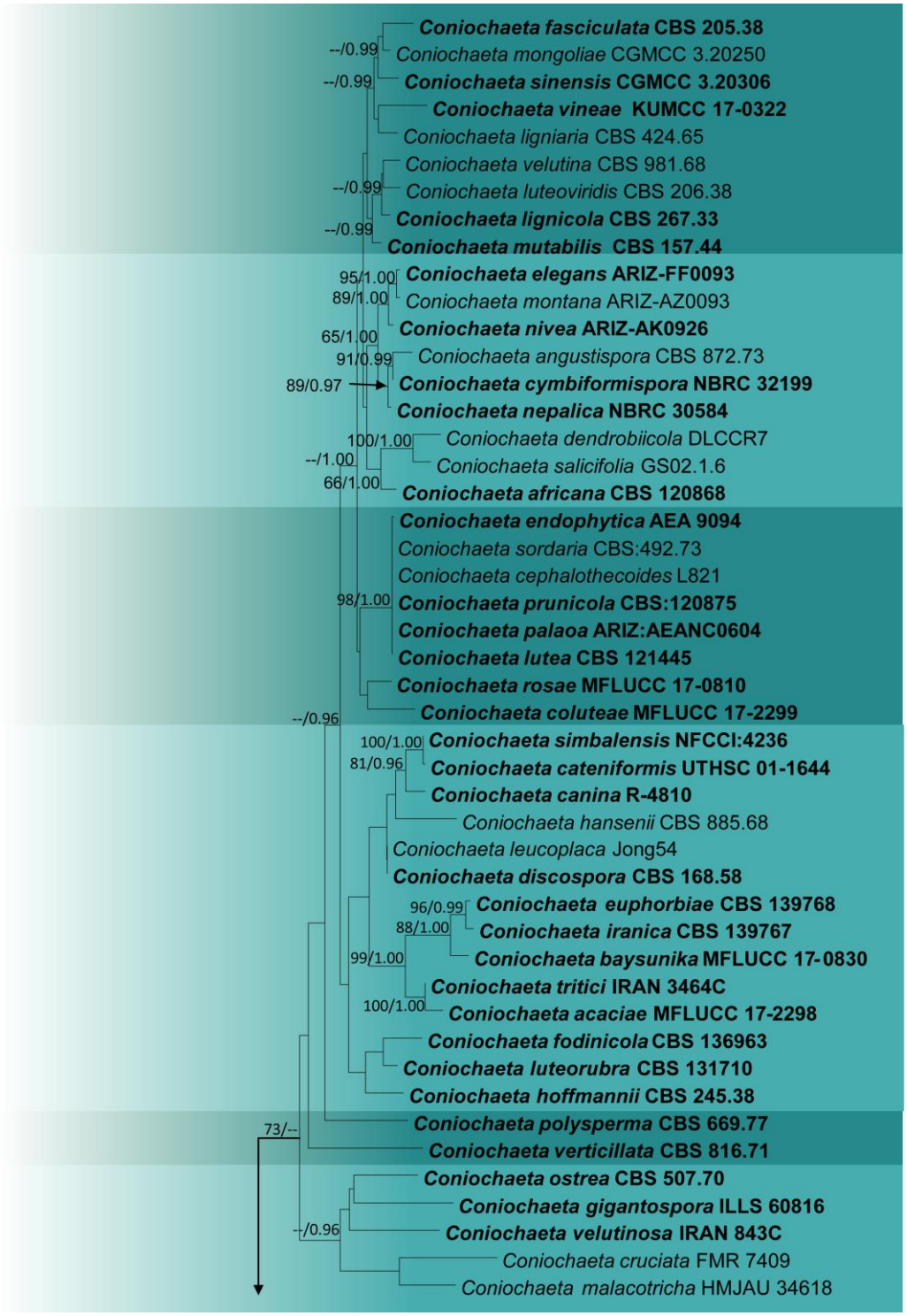


**Fig. 67 –** Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of the genus *Coniochaeta*. Seventy-four strains are included in the combined analyses, which comprised 1572 characters (583 characters for ITS and 989 characters for LSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -10196.808205 is presented. Evolutionary models GTR+I+G is applied for both ITS and LSU genes. The matrix had 662 distinct alignment patterns, with 30.10% of undetermined characters or gaps. Bootstrap support values for ML greater than or equal to 65% and Bayesian posterior probabilities greater than or equal to 0.95 are given near nodes, respectively. The tree was rooted with *Chaetosphaeria innumera* (SMH 2748) and *C. pygmaea* (MR 1365). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

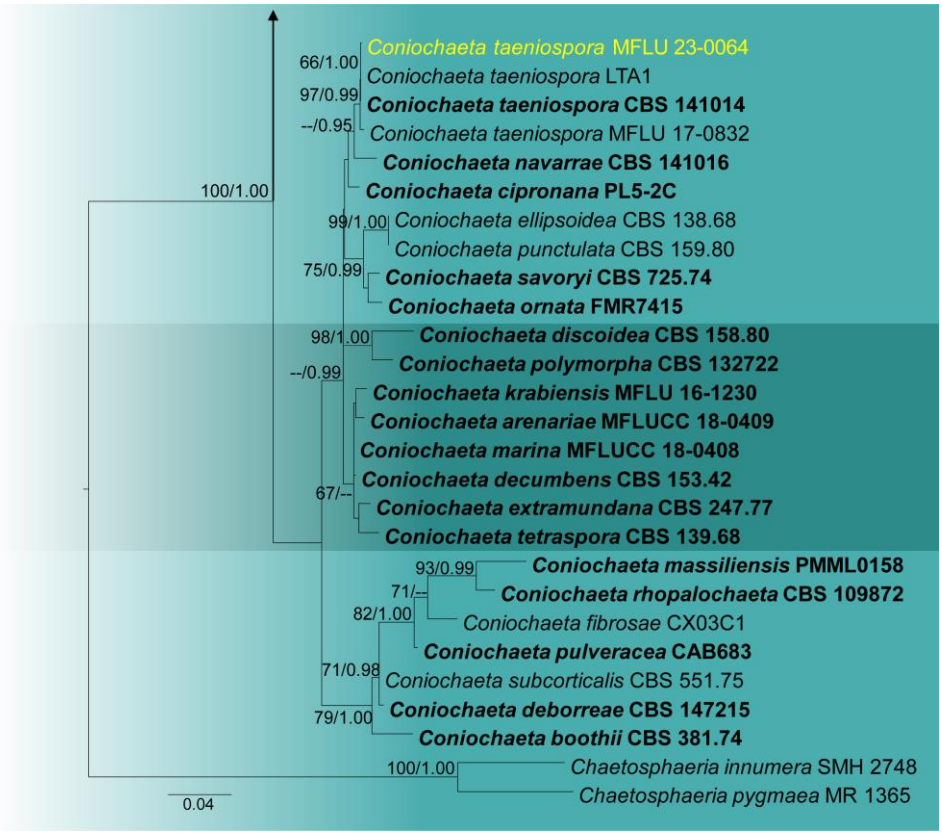


**Fig. 67 –** Continued.

***Coniochaeta taeniospora*** (Sacc.) Friebes, Jaklitsch & Voglmayr, Sydowia 68, 91 (2016)

Index Fungorum number: IF 815856; Facesoffungi number: FoF 06779; Fig. 68

*Saprobic* on dead land branch of *Ostrya carpinifolia*. **Sexual morph:** *Ascostromata* growing in inconspicuous groups or solitary, erumpent through the bark. *Ascomata* 230–370 high, 240–410 µm diam. ($\bar{x}$ = 316.8 × 288.3 µm, n = 6), perithecial, erumpent or semi-immersed, with only the ostioles visible, subglobose, sometimes ampulliform, black, surface smooth to slightly rough, hyaline hyphae often present at the base. *Ostiolar* necks 70–160 µm diam., papillate, hyaline, periphysate. *Ascomatal walls* brittle when dry, softer after rehydrated, 40–65 µm wide near the ostiole, 40–50 µm thick at the base, two-layered, outer layer 15–35 µm thick, comprising compact, relatively thick-walled, brown cells of *textura angularis*, darker towards the outside; inner layer 10–20 µm thick, consisting of compressed, hyaline cells, mostly of *textura prismatica*, turning green in 5% KOH. *Paraphyses* 2.5–4.5 µm wide, hyaline, filiform, septate. *Asci* 150–195 × 9–15 µm ($\bar{x}$ = 178.1 × 13.1 µm, n = 20), unitunicate, often 8-spored, rarely 4-spored, cylindrical, straight to gently flexuous, pedicel slender, with inconspicuous, J- apical ring, more clearly visible in Congo Red. *Ascospores* 15–19 × 7–12 µm ($\bar{x}$ = 17.3 × 10.3 µm, n = 50), l/w 1.7, uniseriate, sub-hyaline when immature, dark brown at maturity, darker brown in 5% KOH, ellipsoid to ovoid, slightly laterally compressed, with a conspicuous straight germ slit expanding the entire length, multi-guttulate, smooth-walled, without sheath or appendages. **Asexual morph:** Undetermined.

Material examined – Italy, Province of Forlì-Cesena [FC], Camposonaldo - Santa Sofia, on dead land branch of *Ostrya carpinifolia*, 10 July 2019, Erio Camporesi IT-4405 (MFLU 23-0064).

GenBank accession numbers – ITS: OQ588788, LSU: OQ588800.

Known distribution (based on molecular data) – Austria (Friebes et al. 2016), Italy (Chethana et al. 2021a, this study).

Known hosts (based on molecular data) – *Quercus petraea* (Friebes et al. 2016), *Quercus* sp. (Chethana et al. 2021a), *Ostrya carpinifolia* (this study).

Notes – The strain MFLU 23-0064 clustered with strains of *Coniochaeta taeniospora* with 66% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 67).

Nucleotide differences between strain MFLU 23-0064 and the ex-epitype strain (CBS 141014) of ITS and LSU sequences are insignificant to differentiate these two strains. Our strain also morphologically resembles the epitype of *Coniochaeta taeniospora* in possessing hyaline hyphae at the base of the ascomata, 2-layered ascomatal wall, whose inner layer turns green in KOH, 4–8-spored, cylindrical asci with slender pedicels and dark brown, guttulate ascospores with a straight germ slit extending the entire length. Moreover, among our isolate and the epitype, sizes of ascomata (230–370 × 240–410 µm *vs.* 200–410 µm × 200–450 µm), paraphyses (2.5–4.5 µm *vs.* 2.5–3.5 µm), asci (150–195 × 9–15 µm *vs.* 169–184 × 9–14 µm), and ascospores (15–19 × 7–12 µm *vs.* 15.5–19.2 × 9.5–12.3) are slightly similar (Friebes et al. 2016). Therefore, this strain MFLU 23-0064 is described as *Coniochaeta taeniospora*. Previous strains of *Coniochaeta taeniospora* have been recorded from *Quercus* spp. (Friebes et al. 2016, Chethana et al. 2021a), while this study reports the strain from *Ostrya carpinifolia* for the first time, representing a new host record from Italy. Furthermore, *Coniochaeta taeniospora* strain COTA72 did not cluster with the other strains of the taxon in our phylogeny, thus, was excluded. Further studies should confirm the definite identity of this strain.

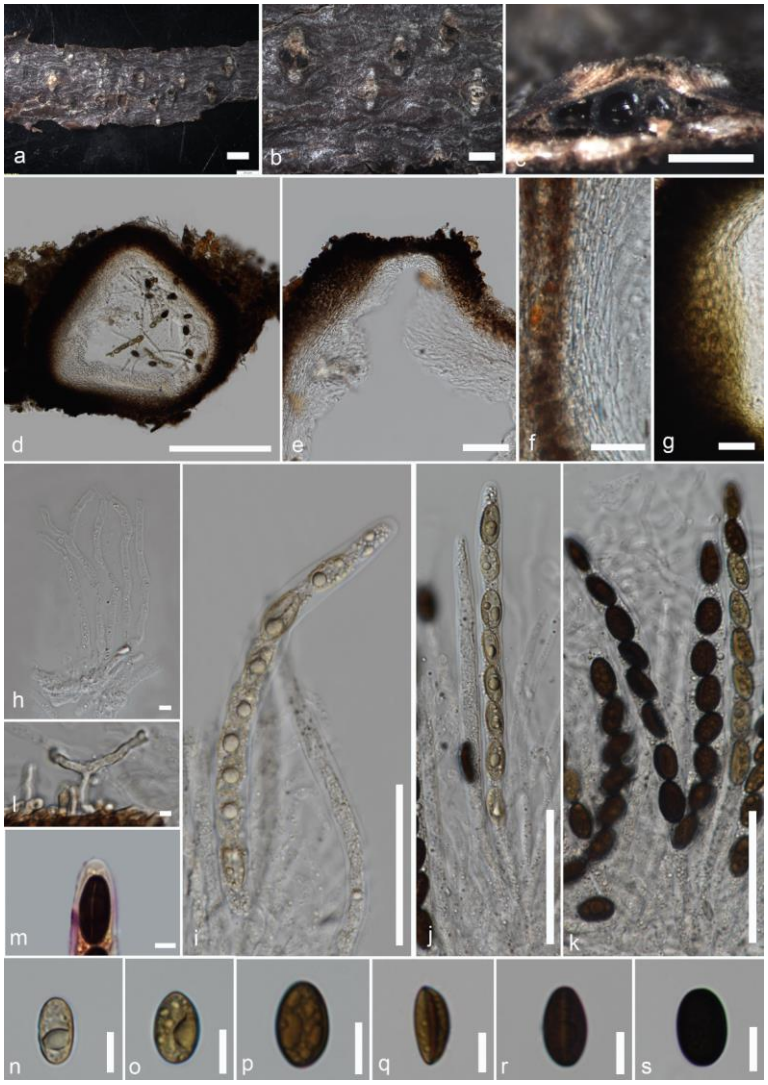


**Fig. 68 – *Coniochaeta taeniospora*** (MFLU 23-0064, **a new host record**). a Appearance of ascostromata on host substrate. b–c Close-up of ascostromata. d Vertical section of an ascoma. e Cross section of an ostiole. f, g Ascomatal walls (g in 5% KOH). h Paraphyses. i–k Asci. l Hyaline hypha. m Apical ring in Congo Red. n–s Ascospores (s in 5% KOH). Scale bars: a, d = 200 µm, b, c = 500 µm, e, i–k = 50 µm, f, g = 20 µm, h, l, m = 5 µm, n–s = 10 µm.

***Cordanaceae*** Nann., Repert. Mic. Uomo, 498 (1934)

Facesoffungi number: FoF 01673

***Cordana*** Preuss, Linnaea 24, 129 (1851)

Facesoffungi number: FoF 01674

Preuss (1851) established this genus with *C. polyseptata, C. pauciseptata*, and *C. pedunculata*. Later, Saccardo (1877) and Hughes (1955) suggested *Cordana pauciseptata as* the lectotype. *Cordana* is a dematiaceous, hyphomycetous genus. Currently, *Porosphaerella cordanophora* is considered the sexual morph of *C. pauciseptata* (Müller & Samuels 1982, Hernández-Restrepo et al. 2014). *Cordana* is recorded in Africa, South and Central America, Spain, South East Asia, and New Zealand on decaying plant matter, other fungi, or in soil (Fernández & Huhndorf 2004, Hernández-Restrepo et al. 2014, Zelski et al. 2014, Ai et al. 2019). Most of the species in this genus are recorded as saprobes and pathogens (Hyde et al. 2020a). We provide the updated phylogeny for taxa in *Cordanaceae* in Fig. 69.

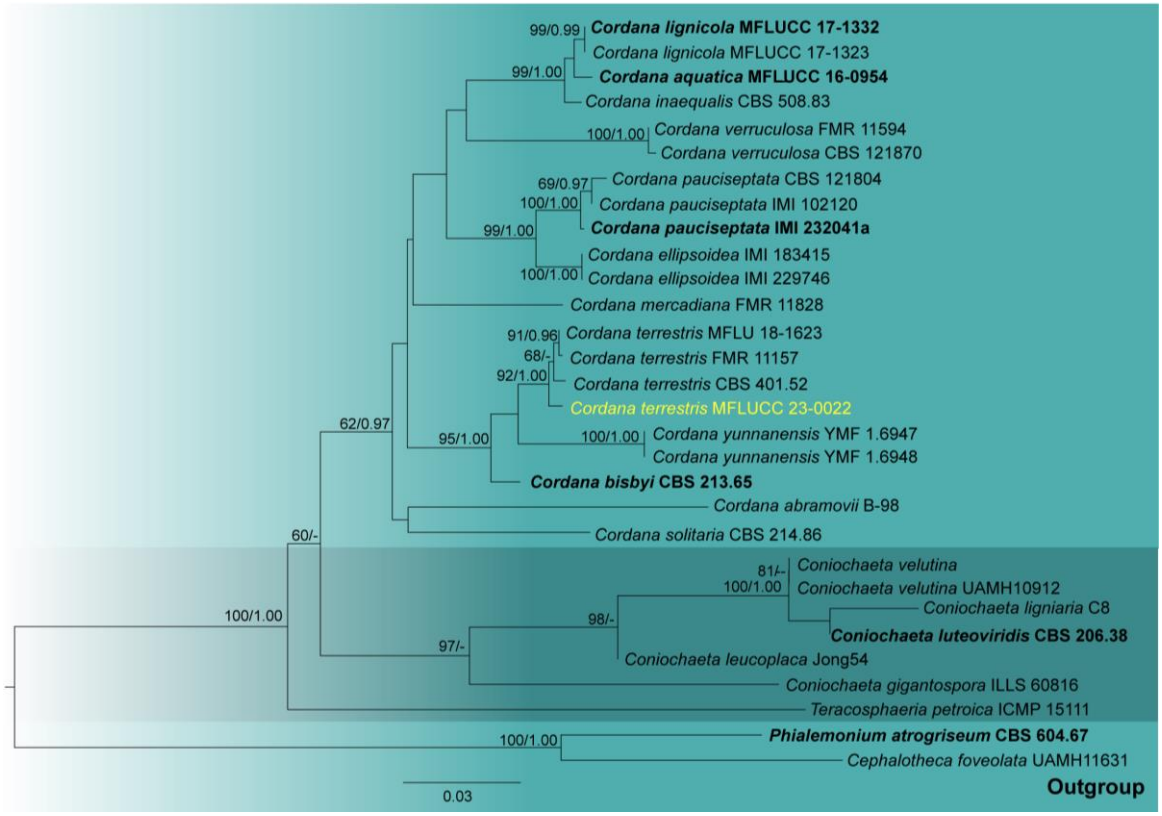


**Fig. 69 –** Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Coniochaetales* taxa. Twenty-nine strains are included in the combined analyses, which comprised 1452 characters (595 characters for ITS and 857 characters for LSU) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5536.915184 is presented. The matrix had 427 distinct alignment patterns, with 28.19% undetermined characters or gaps. Evolutionary models applied for ITS and LSU are SYM+I+G and GTR+I+G models, respectively. Bootstrap support values for ML equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Cephalotheca foveolata* (UAMH11631), *Phialemonium atrogriseum* (CBS 604.67) and *Teracosphaeria petroica* (ICMP 15111). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Cordana terrestris*** (Timonin) Hern.-Restr., Gené & Guarro, in Hernández-Restrepo et al., Mycologia 106, 729 (2014)

Index Fungorum number: IF 807979; Facesoffungi number: FoF 05475; Fig. 70

*Hyphae* septate, branched, smooth, subhyaline to hyaline, becoming rough and brown when mature. **Asexual morph**: *Conidiophores* 25–73 × 1.5–3.5 μm ($\overline{x}$ = 44 × 2 μm, n = 20), micronematous, mononematous, solitary, erect, unbranched or branched, septate, straight or flexuous, cylindrical, hyaline to sub-hyaline. *Conidiogenous cells* holoblastic, polyblastic, terminal, discrete, hyaline. *Conidia* 4–7 × 2.5–4.5 μm ($\overline{x}$ = 5 × 3.5 μm, n = 20), terminal, mostly oblong, sometimes ellipsoid or sub-cylindrical, guttulate, sometimes mid-region slightly constricted, hyaline, smooth-walled. **Sexual morph**: Undetermined.

Culture characteristics – *Colonies* on PDA become 30 mm in diam. after 14 days at 25 ℃, flat, effuse, dark gray to black-brown, undulate margined, reverse grayish brown at the center and become dark brown to brown at the margin.

Material examined – Thailand, Chiang Rai Province, May Yao, from forest soil, 20.0478N 99.7619 E, 863m, 23 September 2019, W.A.E. Yasanthika, living culture, MFLUCC 23-0022.

GenBank accession numbers – ITS: OQ690712, LSU: OQ690715.

Known hosts (based on molecular data) – Soil, *Cecropia* leaves, decaying, submerged wood (Timonin 1940, Fernández & Huhndorf 2004, Luo et al. 2019, this study).

Known distribution (based on molecular data) – China, Brazil, Canada, Cuba, Democratic Republic of Congo (Zaire), Jamaica, Japan, India, New Zealand, Panama, Poland, Puerto Rico, the USA (Georgia, Iowa) (Fernández & Huhndorf 2004, Luo et al. 2019), Thailand (this study).

Notes – *Cordana terrestris* is widespread and has been identified in various aquatic and terrestrial habitats (Hyde et al. 2020a). This species was previously recorded from the soil in Georgia (Timonin 1940). *Spicularia terrestris* and *Pseudobotrytis fusca* were synonymized as *C. terrestris* by Hernández-Restrepo et al. (2014). Our collection (MFLUCC 23-0022) phylogenetically clustered with other *C. terrestris* isolates with 92% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability in LSU-ITS multigene phylogenetic analyses (Fig. 69). The asexual morph of our isolate (Fig. 70) is similar to *C. terrestris* in having terminal, mostly oblong, ellipsoidal or sub-cylindrical, guttulate conidia (Fernández & Huhndorf 2004, Hernández-Restrepo et al. 2014, Luo et al. 2019). Conidial septation and macronematous conidiophores are absent in our isolate in contrast to *C. terrestris* described in Fernández & Huhndorf (2004) and Luo et al. (2019). These morphological differences can result from environmental adaptations (Francisco et al. 2019). Based on the biphasic approach, we report our collection (MFLUCC 23-0022) of *C. terrestris* as the first record on Thailand soil.

**Subclass *Xylariomycetidae*** O.E. Erikss & Winka, Myconet 1, 12 (1997)

Facesoffungi number: FoF 06514

***Amphisphaeriales*** D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1), 177 (1986)

Facesoffungi number: FoF 00672

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

Facesoffungi number: FoF 00629

***Nigrospora*** Zimm., Centbl. Bakt. ParasitKde, Abt. I 8, 220 (1902)

Facesoffungi number: FoF 14273

*Nigrospora* was established to accommodate *N. panici* (Zimmerman et al. 1902, Hyde et al. 2020a). The species of *Nigrospora* found to be filamentous and cosmopolitan in its distribution reporting in diverse hosts and habitats (Hyde et al. 2020a, Wang et al. 2017). Wide distribution of *Nigrospora* species attributed to their lifestyle switches (Sun et al. 2011). Here, we provide the updated phylogeny for the taxa in *Nigrospora* (Fig. 71).

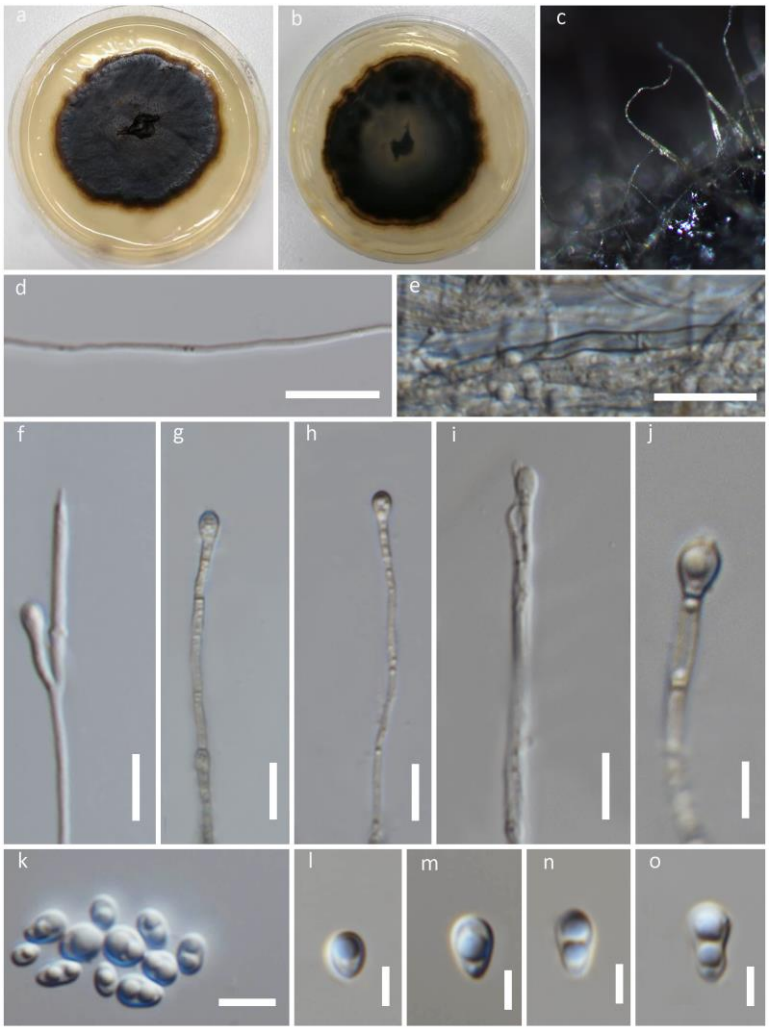


**Fig. 70 – *Cordana terrestris*** (MFLUCC 23-0022, **a new habitat record**). a Colony from above (on PDA). b Colony from below (on PDA). c Conidial attachments. d Immature hyphae. e Mature, pigmented hyphae. f–j Conidiogenesis on the conidiophores. k–o Conidia. Scale bars: d = 20 μm, e = 15 μm, f–i = 10 μm, j, k–o = 5 μm.

***Nigrospora lacticolonia*** Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39, 131 (2017)

Index Fungorum number: IF 820735; Facesoffungi number: FoF 141323; Fig. 72

*Endophytic* on *Acrostichum aureum* leaves. **Sexual morph:** Undetermined. **Asexual morph:** *Hyphae* 3–6 μm diam. ($\overline{x}$ = 3.67 ± 0.83 μm, n = 30), septate, hyaline, smooth, branched. *Conidiomata* immersed, scattered, globose, black. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–12 × 5.5–9 μm ($\overline{x}$ = 8.35 × 6.75 μm, n = 30), aggregated in clusters on hyphae, globose to clavate to bean-shaped, pale brown, verrucous. *Conidia* spherical diameter 11–15 μm ($\overline{x}$ = 13.38 ± 1.03 μm, n = 30), elliptic 12.5–16 × 9–14 μm ($\overline{x}$ = 14.13 ± 0.85 × 11.56 ± 1.22 μm, n = 30), solitary, spherical or slightly elliptical, black, shiny, smooth, aseptate.

Culture characteristics – Colonies on PDA reaching 8 cm diam. after 3 days in the dark at 25℃, circular, woolly in the center, darker in the center, the mycelium covering becomes thinner towards the edge, flocculent, surface view white, reverse view white to off-white, without pigmentation.

Material examined – China, Guangdong Province, Guangzhou city, from leaves of *Acrostichum aureum*, 15 September 2021, Li Hua (MHZU 23-0006, dried culture), living culture ZHKUCC 23-0023, ZHKUCC 23-0024, ZHKUCC 23-0025.

GenBank accession numbers – ZHKUCC 23-0023 - ITS: OQ799024, *tef1-α*: OQ858593, *β-tubulin*: OQ858596; ZHKUCC 23-0024 - ITS: OQ799025, *tef1-α*: OQ858594, *β-tubulin*: OQ858597; ZHKUCC 23-0025 - ITS: OQ799026, *tef1-α*: OQ858595, *β-tubulin*: OQ858598.

Known distribution (based on molecular data) – China, Jiangxi Province (Wang et al. 2017, Kee et al. 2019), Hainan Province (Wang et al. 2017), Guangxi Province (Raza et al. 2019), Guangdong Province (this study).

Known hosts (based on molecular data) – *Acrostichum aureum* (this study), *Camellia sinensis* (Wang et al. 2017), *Hylocereus polyrhizus* (Kee et al. 2019), *Musa paradisiaca* (Wang et al. 2017), *Saccharum officinarum* (Raza et al. 2019).

Notes – *Nigrospora lacticolonia* was introduced by Wang et al. (2017) from Jiangxi Province, China on *Camellia sinensis* leaves. In the present study, we isolated three *Nigrospora* strains from *Acrostichum aureum* leaves. Based on the BLASTn results from the NCBI database, *N. lacticolonia* was given as the closest match. In the multigene phylogenetic analysis of the concatenated ITS, *β-tubulin*, and *tef1-α*, our isolates (ZHKUCC 23-0023, ZHKUCC 23-0024, and ZHKUCC 23-0025) cluster with *N. lacticolonia* strains with 100% maximum likelihood support and 1.00 Bayesian posterior probability (Fig. 71). The morphology of our isolates is similar to that of the ex-type of *N. lacticolonia.* Based on multigene phylogeny and morphological description, we provide a new host record of *N. lacticolonia* from *Acrostichum aureum*, collected from Jiangxi Province, China.

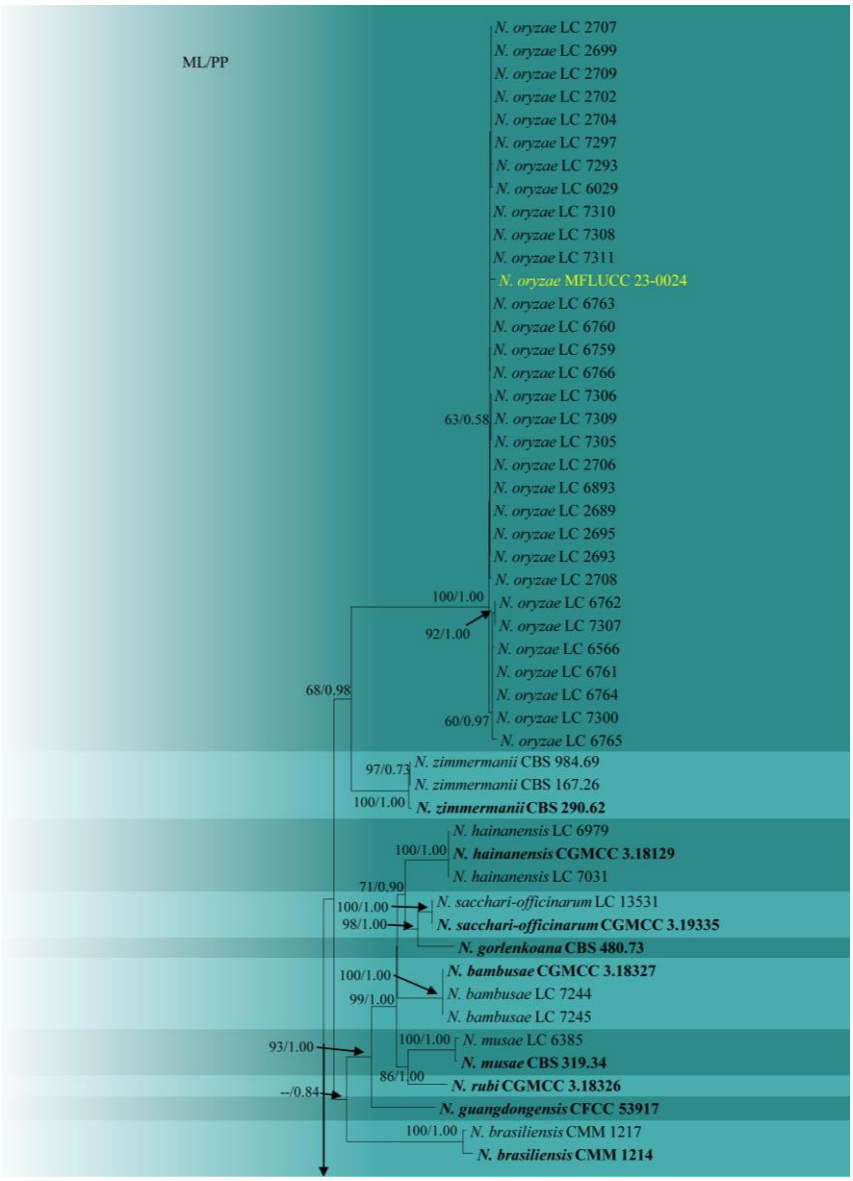

**Fig. 71 –** Phylogram generated from maximum likelihood analysis based on the combined ITS, *β-tubulin* and *tef-1α* sequence data of *Nigrospora*. Ninety-three strains of *Nigrospora* are included in the combined analyses, which comprised 1164 characters (444 characters for ITS, 384 characters for *β-tubulin*, 334 characters for *tef-1α*). The RAxML analysis yielded the best scoring tree, which was used as the backbone tree, with a final likelihood value of -8177.485492. The matrix had 526 distinct alignment patterns with 7.86% of undetermined characters or gaps. Under the Akaike Information Criterion (AIC) the evolutionary model HKY+G is applied to ITS and *β-tubulin* genes, and GTR+I+G is applied to *tef-1α* gene. Maximum likelihood (ML) with bootstrap support greater than or equal to 50% and Bayesian posterior probabilities (PP) values greater than or equal to 0.8 are given near nodes, respectively. The tree is rooted with *Apiospora vietnamensis* (IMI 99670) and *A. sichuanensis* (HKAS 107008). Ex-type strains are in **bold** and the species described herein are denoted in yellow. Hyphen (-) represents support values below 50% (ML) and below 0.80 (PP).

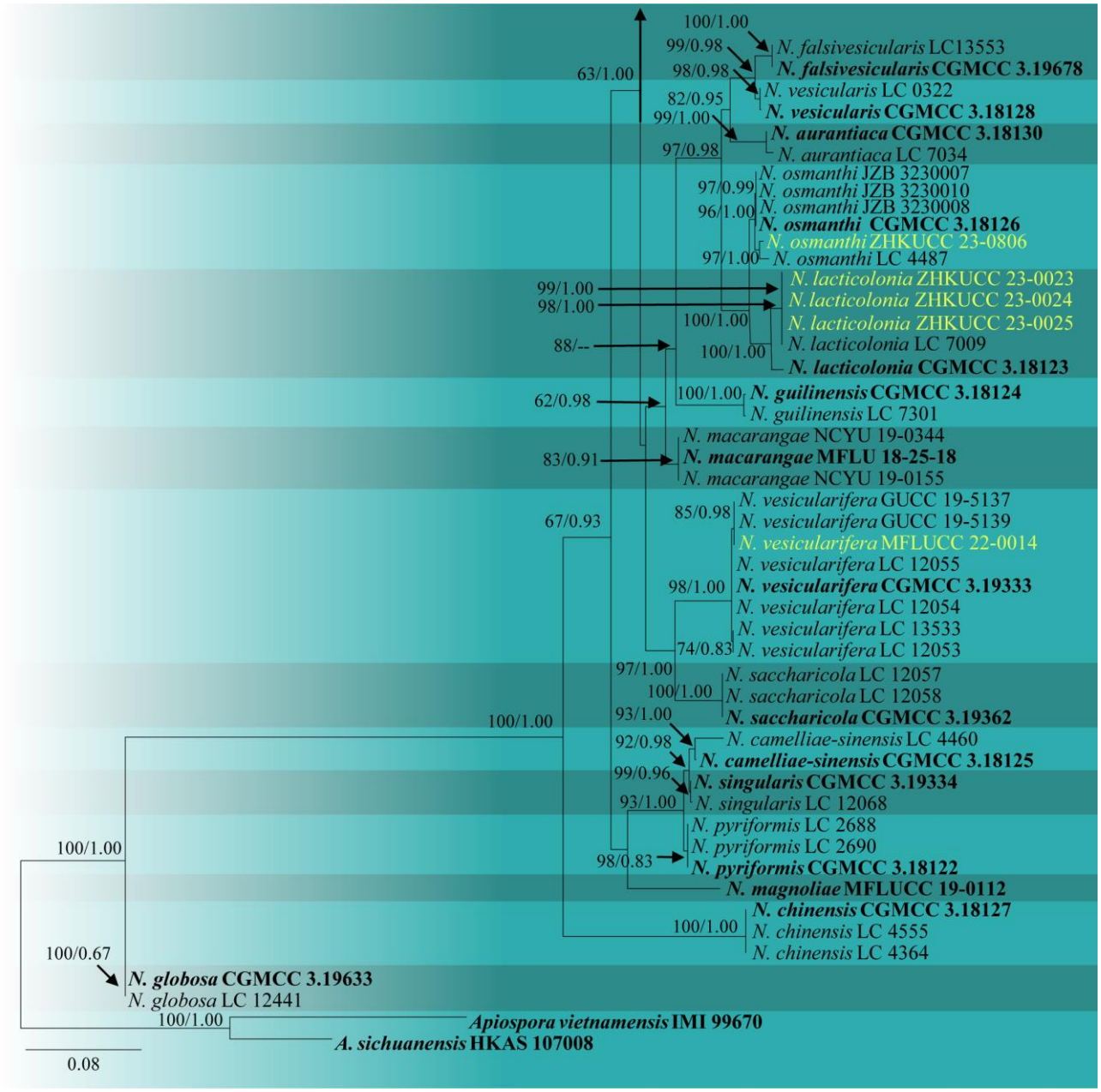


**Fig. 71 –** Continued.

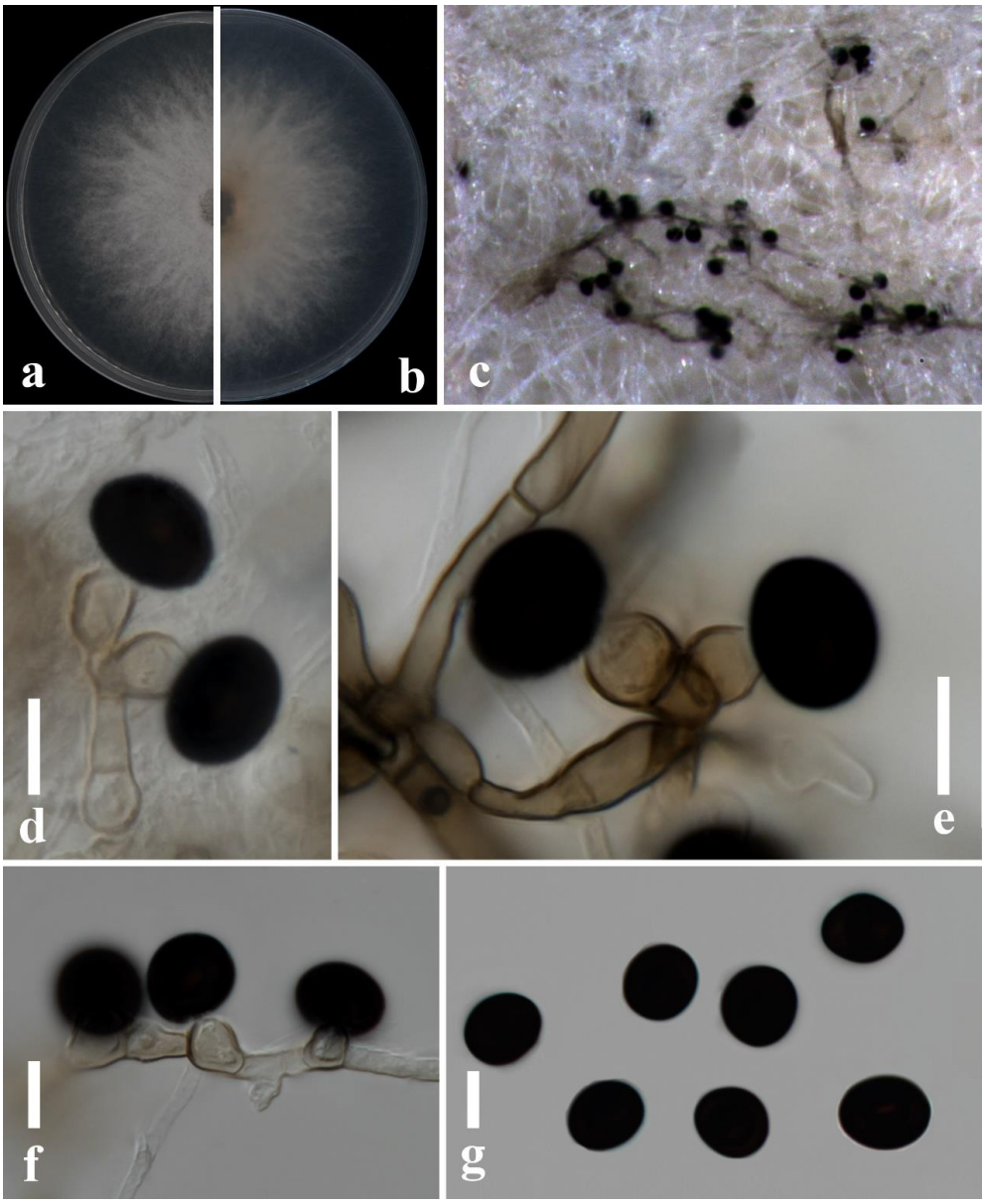


**Fig. 72** – ***Nigrospora lacticolonia*** (ZHKUCC 23-0023, **a new host record**). a Colony on PDA from front view. b Colony on PDA from reverse view. c Conidial mass forming on the culture. d–f Conidia attached to conidiogenous cells. g Conidia. Scale bars: d–g = 10 μm.

***Nigrospora oryzae*** (Berk. & Broome) Petch, Journal of Indian Botanical Society 4, 24 (1924)

Index Fungorum number: IF 253729; Facesoffungi number: FoF 06596; Fig. 73

Associated with leaf spots of *Alpinia purpurata*. Leaf spots irregular, dark brown. **Sexual morph:** Undetermined. **Asexual morph:** *Pycnidia* semi-immersed or partly erumpent on MEA, globose to subglobose, brown to black. *Hyphae* 2.3–3.5 μm diam. ($\overline{x}$ = 2.66 μm, n = 10), septate, hyaline, becoming brown when aged, smooth. *Conidiophores* 71.2–100.7 × 5.4–7 μm ($\overline{x}$ = 81.7 × 6.2 μm, n = 5), micronematous or semi-macronematous, flexuous or straight, ovoid or cylindrical, smooth, pale brown, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 7.1–17.9 × 5.4–9.2 μm ($\overline{x}$ = 12.2 × 6.7 μm, n = 5), monoblastic, ovoid to ampulliform, hyaline, smooth-walled. *Conidia* 11.5–14.2 × 8.8–13.3 μm ($\overline{x}$ = 13 × 11.5 μm, n = 10), solitary, globose to subglobose, sub-spherical, aseptate, single-celled, guttulate, brown to black, with a germ slit of 1.7 μm diam., curved, obtuse-ends, smooth-walled.

Culture characteristics – Colonies on MEA reaching approximately 90 mm diam. after 5 days at 25 °C, covering entire margins, margin circular, fast-growing, initially greyish-white, becoming greyish black with age, and reverse olivaceous grey with black patches, abundantly sporulated.

Material examined – Thailand, Chiang Mai Province, Omkoi, Yang Piang, on leaves of *Alpinia purpurata*, 16 October 2019, D Gomdola (MFLU 23-0066), living culture MFLUCC 23-0024.

GenBank accession numbers – ITS: OQ674508, *tef1-α*: OQ850146.

Known distribution (based on molecular data) – Worldwide, including Alabama, Argentina, Australia, Bangladesh, China, Colombia, Europe, Hongkong, India, Iran, Iraq, Kazakhstan, Ontario, Pakistan, Peninsular Malaysia, Sri Lanka, and USA (Salazar & De García 2005, Widmer et al. 2007, Khodke & Khodke 2009, Zhang et al. 2012, Zheng et al. 2012, Sharma et al. 2013, Abass & Mohammed 2014, Kalati et al. 2014, Li et al. 2014, Rathod et al. 2014, Wu et al. 2014, Thanabalasingam et al. 2015, Cosoveanu et al. 2016, Eken et al. 2016, Li et al. 2017, Begum et al. 2018, Zakaria & Aziz 2018, Zhang et al. 2018, Chen et al. 2019, He et al. 2019b, Zhai et al. 2019, Zhang et al. 2019, Borrelli et al. 2020, Farid et al. 2020, Sun et al. 2020, Anjum et al. 2021, Han et al. 2021, Liu et al. 2021, Rolling et al. 2021, Luo & Jiang 2022, Qiu et al. 2022, Vig et al. 2022, Vijayalakshmi et al. 2022, Wang et al. 2022, Liu et al. 2022, Yang et al. 2022, Zhang et al. 2022b, Lu et al. 2023, Xu et al. 2023), Thailand (this study).

Known hosts (based on molecular data) – a wide range of hosts, including *Aloe vera* (Begum et al. 2018), *Alpinia purpurata* (this study), *Aquilaria sinensis* (Li et al. 2014), *Arachis hypogaea* (Vijayalakshmi et al. 2022), *Artemisia* spp. (Cosoveanu et al. 2016), *Arundo donax* (Widmer et al. 2007), *Avicennia marina* (Rolling et al. 2021), *Bassia scoparia* (Anjum et al. 2021), *Brassica juncea* (Sharma et al. 2013), *Calibrachoa hybrida* (Borrelli et al. 2020), *Centranthera cochinchinensis* (Zhai et al. 2019), *Citrullus lanatus* (Chen et al. 2019), *Coccinia grandis* (Thanabalasingam et al. 2015), *Commelina communis* (Qiu et al. 2022), *Costus speciosus* (Sun et al. 2020), *Davidia involucrata* (Yang et al. 2022), *Dendrobium candidum* (Wu et al. 2014), *Dioscorea* spp. (Lu et al. 2023), *Emblica officinalis* (Rathod et al. 2014), *Euonymus japonicus* (Xu et al. 2023), *Ficus religiosa* (Khodke & Khodke 2009), *Gossypium hirsutum* (Zhang et al. 2012), *Hibiscus mutabilis* (Han et al. 2021), Kiwifruit (Li et al. 2017), *Mentha spicata* (Farid et al. 2020), *Musa* spp. (Zakaria & Aziz 2018), *Nelumbo nucifera* (Zhang et al. 2018), *Nicotiana tabacum* (Wang et al. 2022), *Oryza sativa* (Liu et al. 2021), *Pennisetum americanum* (Kalati et al. 2014), *Phaseolus vulgaris* (Luo & Jiang 2022), *Phoenix dactylifera* (Abass & Mohammed 2014), *Photinia serrulate* (He et al. 2019b), *Poa pratensis* (Zheng et al. 2012), *Populus* spp. (Zhang et al. 2022b), *Rosa hybrida* (Salazar & De García 2005), *Tinospora cordifolia* (Vig et al. 2022), *Triticum aestivum* (Eken et al. 2016), *Vaccinium corymbosum* (Zhang et al. 2019), *Zingiber officinale* (Liu et al. 2022).

Notes – Based on the multigene phylogenetic analyses of the concatenated ITS, *β-tubulin*, and *tef1-α* matrices of *Nigrospora*, our isolate *N. oryzae* (MFLUCC 23-0024) clusters with other species of *N. oryzae* with 100% maximum likelihood support and 1.00 Bayesian posterior probability (Fig. 71). Our phylogram is consistent with those of Wang et al. (2017). Excluding gaps, in pairwise nucleotide comparisons of *N. oryzae* (LC 7311 and LC 6763) and our taxon *N. oryzae* (MFLUCC 23-0024), no base pair differences was observed in ITS, while 2 bp differences were observed across *tef1-α* (200 nucleotides). The conidial shape and sizes of our isolate are similar to those of Zhang et al. (2012), Zhai et al. (2013), Alam et al. (2017), Li et al. (2017), Wang et al. (2017), Begum et al. (2018), and Han et al. (2021). Herein, based on multigene phylogeny and morphological description, we provide a new record of *N. oryzae* associated with leaf spots of *Alpinia purpurata* collected from northern Thailand.

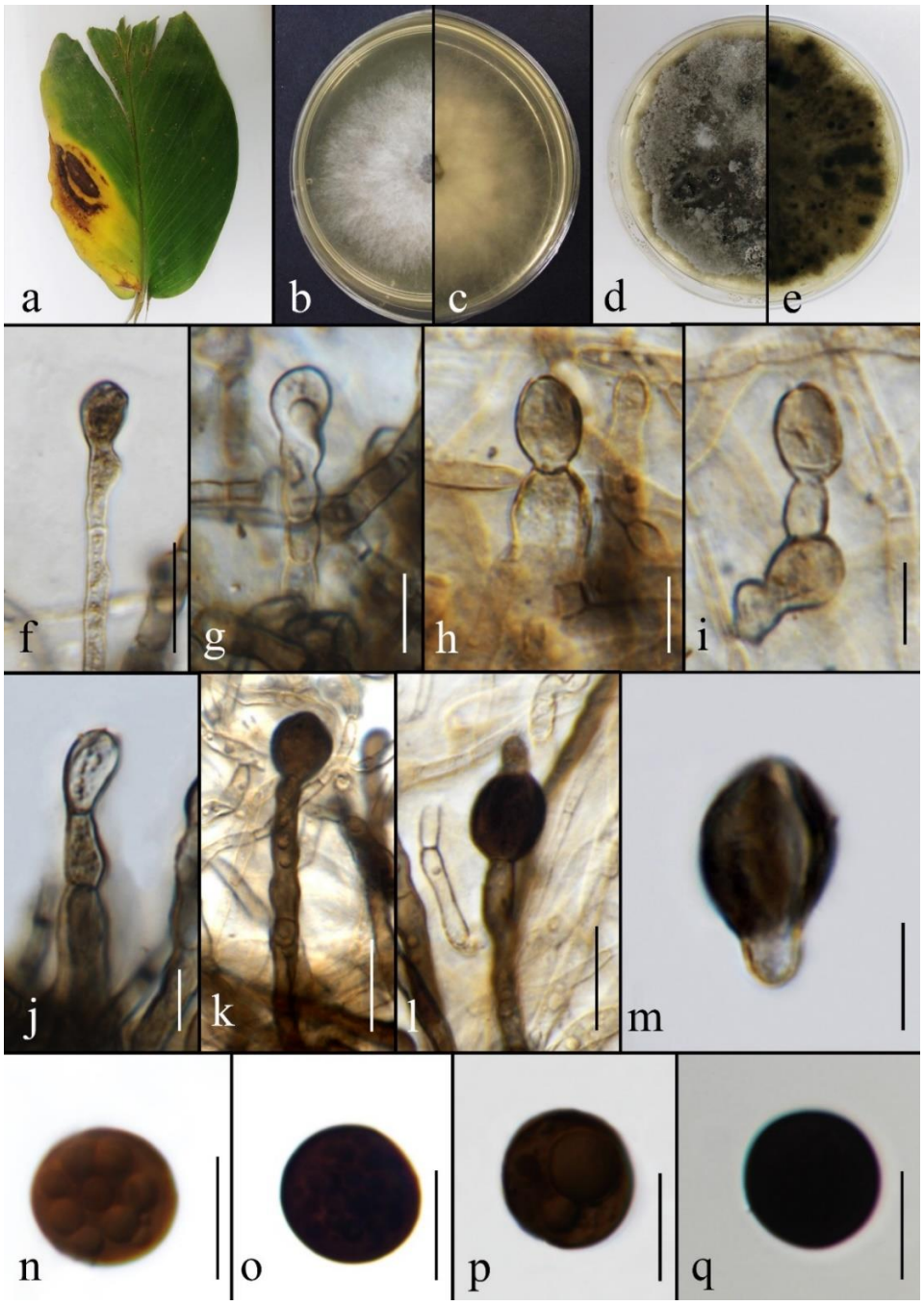


**Fig. 73** – ***Nigrospora oryzae*** (MFLUCC 23-0024, **a new host record**). a Leaf spot on the host. b–c Colony on MEA after 3 days of incubation at 25 °C (front and reverse view). d–e Colony on MEA after 45 days of incubation at 25 °C (front and reverse view). f–g Mycelium. h–j Conidiogenous cells giving rise to conidia. k, l Conidiophores. m Conidium generating a germ tube and exhibiting germ slit. n–q Conidia. Scale bars: g–j, m–q = 10 μm, f, k, l = 20 μm.

***Nigrospora osmanthi*** Mei Wang & L. Cai, in Wang, Liu, Crous & Cai, Persoonia 39, 135 (2017)

Index Fungorum number: IF 820736; Facesoffungi number: FoF 06597; Fig. 74

*Endophytic* on a dead branch of *Phyllostachys sulphurea* var. *viridis*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiophores* mostly reduced to conidiogenous cells. *Conidiogenous cells* 0.6–10.6 × 2.5–7.1 μm ($\overline{x}$ = 6.5 × 4.4 μm, n = 20), monoblastic, discrete, solitary, determinate, initially hyaline, subspherical, becoming brown, ampulliform to cylindrical. *Conidia* 10.4–14.3 × 10–13 μm ($\overline{x}$ = 12.8 × 12 μm, n = 30), solitary, globose or subglobose, brown to black, aseptate, smooth.

Culture characteristics – Colonies on PDA reaching 56 mm diam. after 5 days at 25 ºC, initially white, circular, flat, entire margined, becoming slightly black with age and reverse initially white, and turning black when mature.

Material examined – China, Guangdong Province, Guangzhou City, Tianhe District, South China Botanical Garden, healthy leaves of *Phyllostachys sulphurea* var. *viridis*, 17 June 2021, H.J. Zhao HNZW176 (MHZU 23-0108), living culture ZHKUCC 23-0806.

GenBank accession numbers – ITS: OR054071, *tef1-α*: OR058851, *β-tubulin*: OR058850

Known distribution (based on molecular data) – China (Wang et al. 2017, Mei et al. 2019, this study), Croatia (unpublished), Malaysia (unpublished), USA (unpublished).

Known hosts (based on molecular data) – *Hedera nepalensis* (Wang et al. 2017), *Olea europaea* (unpublished), *Orthosiphon stamineus* (unpublished), *Phyllostachys edulis* (unpublished), *Phyllostachys sulphurea* (this study), *Stenotaphrum secundatum* (Mei et al. 2019).

Notes – Our collection shares the characteristic features, including monoblastic conidiogenous cells in agreement with *Nigrospora osmanthi* (Hyde et al. 2020a). The comparison of base pairs between our strain and the ex-type shows 0.1 % differences (1/545 bp) in the ITS and 0.4 % differences (2/472) in *tef1-α*. Our phylogeny based on the combined ITS, *β-tubulin*, and *tef1-α* analyses reveals that our strain clusters with *Nigrospora osmanthi* (LC 4487) with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 71). Wang et al. (2017) described *N. osmanthi* from China, and this is the first known record of the occurrence of *N. osmanthi* on *Hedera nepalensis*.

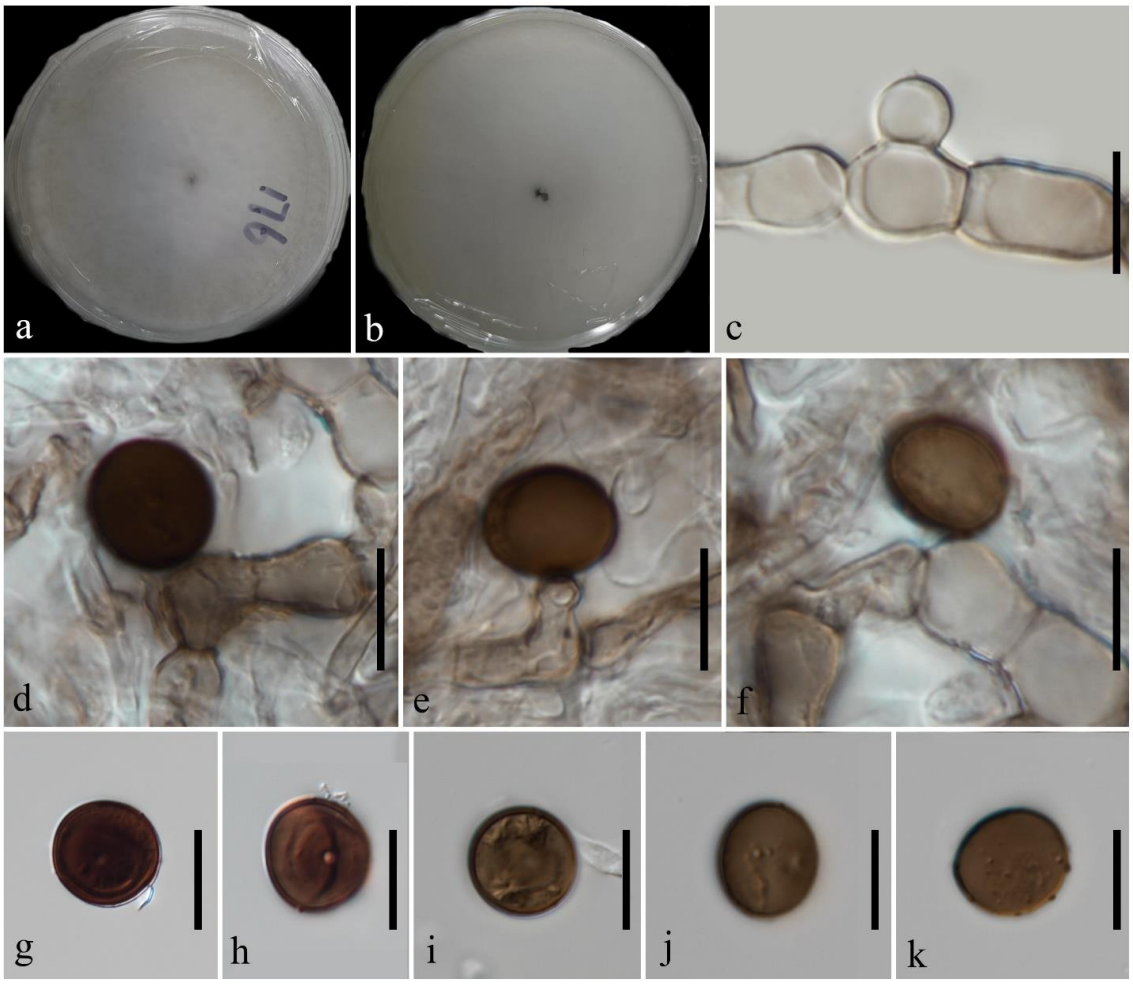


**Fig. 74 – *Nigrospora osmanthi*** (ZHKUCC 23-0806, **a new host record**). a Surface view of the colony, b Reverse view of the colony. c–f Conidiogenous cells giving rise to conidia. g–k Conidia. Scale bars: c–k = 10 μm.

***Nigrospora vesicularifera*** M. Raza & L. Cai, Fungal Diversity 99(1), 1–104 (2019)

Index Fungorum number: IF 556686; Facesoffungi number: FoF 06175; Fig. 75

*Saprobic* on the dead leaf of *Litchi chinensis*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies on the natural substrate black to brown. *Mycelium* composed of smooth, branched, septate, and rarely brown to hyaline hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7.5–10 × 12.5–15.5 μm ($\overline{x}$ = 8.7 × 13.9 μm, n = 20), monoblastic without proliferation, solitary, pale brown, discrete, determinate, short ampulliform, with liberated base and hyaline vesicles, delimiting the conidia from conidiogenous cells. *Conidia* 11.5–19 × 13–17 μm ($\overline{x}$ = 15.25 × 15 μm, n = 20), solitary, globose or subglobose, black, shiny, smooth, aseptate.

Culture characteristics – Colonies on PDA fast-growing reaching 7.2 cm diam. after eight days of incubation at 25 ºC, covering the petri dish in three weeks. Colony circular, entire to filiform margin, medium sparse, flat with fimbriate edge, downy, aerial mycelium, rough surface, colony from above initially white, turning dark grey when mature, and reverse initially white and produces dark brown to black pigment in PDA when mature.

Material examined – Thailand, Chiang Rai Province, Nang Lae, a dead leaf of *Litchi chinensis*, 20 June 2021, NP Samaradiwakara NPSC05 (MFLU 22-0081), living culture MFLUCC 22-0014.

GenBank accession numbers – ITS: ON211313, *tef1-α:* ON622464, *β-tubulin*: ON622465.

Known distribution (based on molecular data) – China (Raza et al. 2019), Thailand (this study).

Known hosts (based on molecular data) – *Saccharum officinarum* (Raza et al. 2019), *Litchi chinensis* (this study).

Notes – *Nigrospora* species are cosmopolitan in distribution and associated with a wide range of crops of economic significance. They comprise endophytes, pathogens, and saprobes (Sun et al. 2011, Rashmi et al. 2019). Raza et al. (2019) recently erected *Nigrospora vesicularifera* to accommodate six pathogenic strains isolated from sugarcane in China. *Nigrospora vesicularifera* is distinguished by vesicles surrounded by the septum between its conidiogenous cells and conidia (Raza et al. 2019). Even though the presence of a vesicle is relevant to *N. musae*, *N. sphaerica*, and *N. vesicularis*, those three species are phylogenetically distant from *N. vesicularifera.* The multi-gene (ITS, *tef1-α*, and *β-tubulin*) phylogenetic analyses revealed that our strain clusters within the *N. vesicularifera* clade with 85% maximum likelihood bootstrap support and 0.98 Bayesian posterior probability (Fig. 71). This is the first record of *N. vesicularifera* as a saprobe on dead leaves of *Litchi chinensis* and the first geographical record of *N. vesicularifera* in Thailand.

***Sporocadaceae*** Corda [as 'Sporocadeae'], Icon. fung. (Prague) 5, 34 (1842)

Facesoffungi number: FoF 06111

***Discosia*** Lib. Pl. crypt. Arduenna, fasc. (Liège) 4(301–400), 346 (1837)

Facesoffungi number: FoF 01777

*Discosia* is one of the widely distributed genera in *Sporocadaceae*. Mostly, they occur as endophytes, pathogens, or saprobes on various vascular plants in tropical, subtropical, and temperate regions (Nag Raj 1993, Okane et al. 1998, Tanaka et al. 2011, Li et al. 2015, Liu et al. 2019). *Discosia* species have uni- to multilocular conidiomata, monoblastic, phialidic to annellidic conidiogenous cells, and hyaline to pale brown conidia with polar or subpolar appendages in the median part of the end cells (Sutton 1980, Nag Raj 1993, Li et al. 2015, Mortimer et al. 2015, Chaiwan et al. 2022). Currently, 51 *Discosia* species are accepted in the Index Fungorum (2023). An updated phylogeny for the genus and its related taxa is provided in Fig. 76.

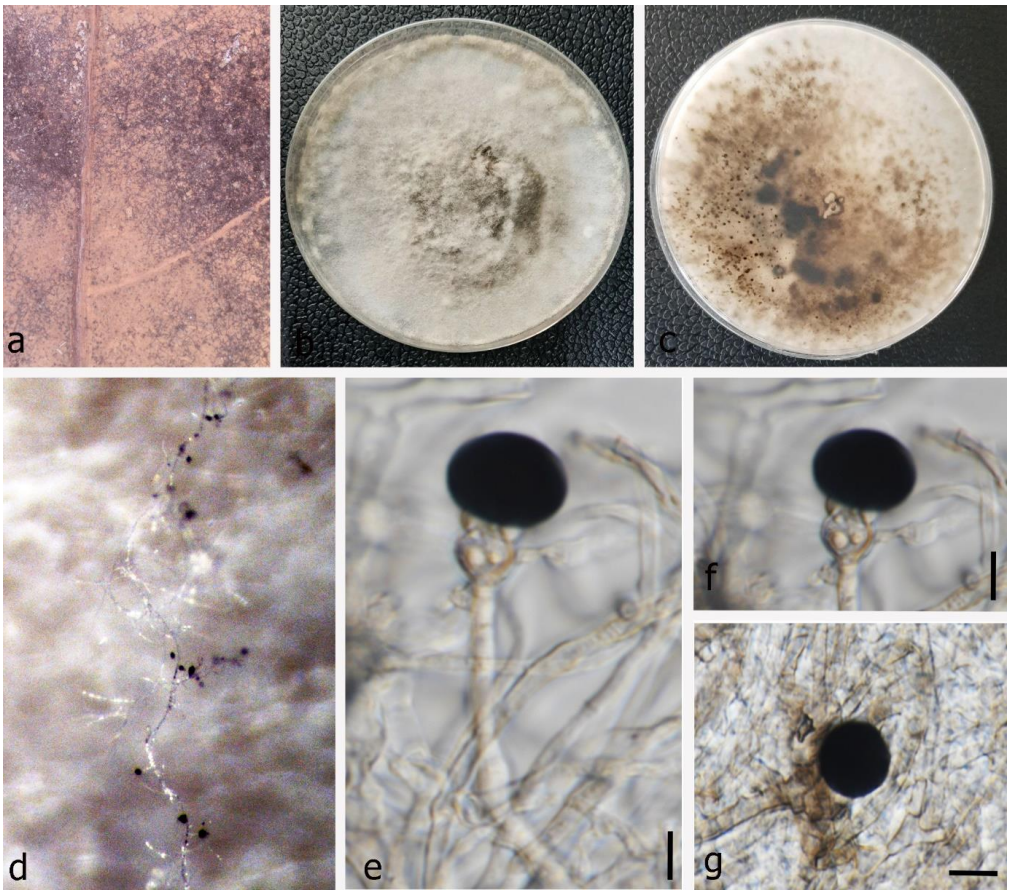


**Fig. 75 – *Nigrospora vesicularifera*** (MFLU 22-0081, **a new geographical and host record**). a Appearance of fungal colonies on host substrate. b–c Colony on PDA (b from above, c from below). d Sporulation on PDA medium. e–f Conidiogenous cells. g Conidia. Scale bars: e–g = 10 μm.

***Discosia celtidis*** Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity 108, 108 (2021)

Index Fungorum number: IF 555455; Facesoffungi number: FoF 09345; Fig. 77

*Saprobic* on the dead leaves of *Trema orientale*. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 50–100 × 250–400 μm ($\overline{x}$ = 71 × 348 μm, n = 10), conspicuous, pycnidial, stromatic, amphigenous, scattered or aggregated, black, flattened or concave at the centre with a convex margin and a relatively thin stromatic base, rounded, glabrous, epidermal, unilocular or multilocular. *Conidiomata wall* 10–15 μm wide, thin-walled, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, cells towards the inside light brown, arranged in a *textura angularis*, with outer layers intermixed with the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–10 × 1–3 μm ($\overline{x}$ = 8.7 × 2.4 μm, n = 20), holoblastic to phialidic, ampulliform, integrated, hyaline, smooth-walled. *Conidia* 18–25 × 3–4 μm ($\overline{x}$ = 23 × 3.5 μm, n = 40), hyaline, fusiform to cylindrical, thick-walled, smooth, straight or slightly curved, 3-septate, slightly constricted at one septum at apex, with cells of equal width, basal cell obconic, with a truncate base, apical cell subconical with a rounded apex, unbranched, filiform, flexuous or straight appendage; presence of both ends, apical and basal appendages 10–12 μm ($\overline{x}$ = 10.8 μm).

Culture characteristics – *Colonies* on PDA, 20–25 mm, diam. after 2 weeks, colony from above medium dense, raised, surface smooth with entire edge, fluffy to velvety with smooth aspects, light brown to dark brown at the margin, dark brown to dark grey in the centre; colony from below light brown at the margin, dark brown to black in the centre, pigmentation not produced in media.

Material examined – China, Taiwan Province, Chiayi, Fanlu Township area, Dahu Forest, dead leaves of *Trema orientale*, 25 August 2019, D.S. Tennakoon, TAP015 (MFLU 18-2604), living culture MFLUCC 19-0132.

GenBank accession numbers – LSU: OP647860, ITS: OP650239.

Known distribution (based on molecular data) – China (Tennakoon et al. 2021a, this study).

Known hosts (based on molecular data) – *Celtis formosana* (Tennakoon et al. 2021a), *Trema orientale* (this study).

Notes – In this study, our isolate (MFLUCC 19-0132) shares similar morphological characteristics with *Discosia celtidis* in having hyaline, fusiform to cylindrical conidia with apical and basal appendages (Tennakoon et al. 2021a). In particular, they have conidia (19–24 × 3–4 µm *vs.* 18–25 × 3–4 µm) and conidiogenous cells (7–9 × 1–3 µm *vs.* 7–10 × 1–3 µm) of overlapped size ranges. Phylogeny also shows that our collection is grouped with *Discosia celtidis* isolates with 96% maximum likelihood bootstrap support and 0.98 Bayesian posterior probability (Fig. 76). Therefore, we introduce our isolate as a new host record of *Discosia celtidis* from *Trema orientale* (Cannabaceae). *Discosia celtidis* was initially introduced by Tennakoon et al. (2021a) from *Celtis formosana* (Cannabaceae). Interestingly, this record was also collected from another species from the same family.

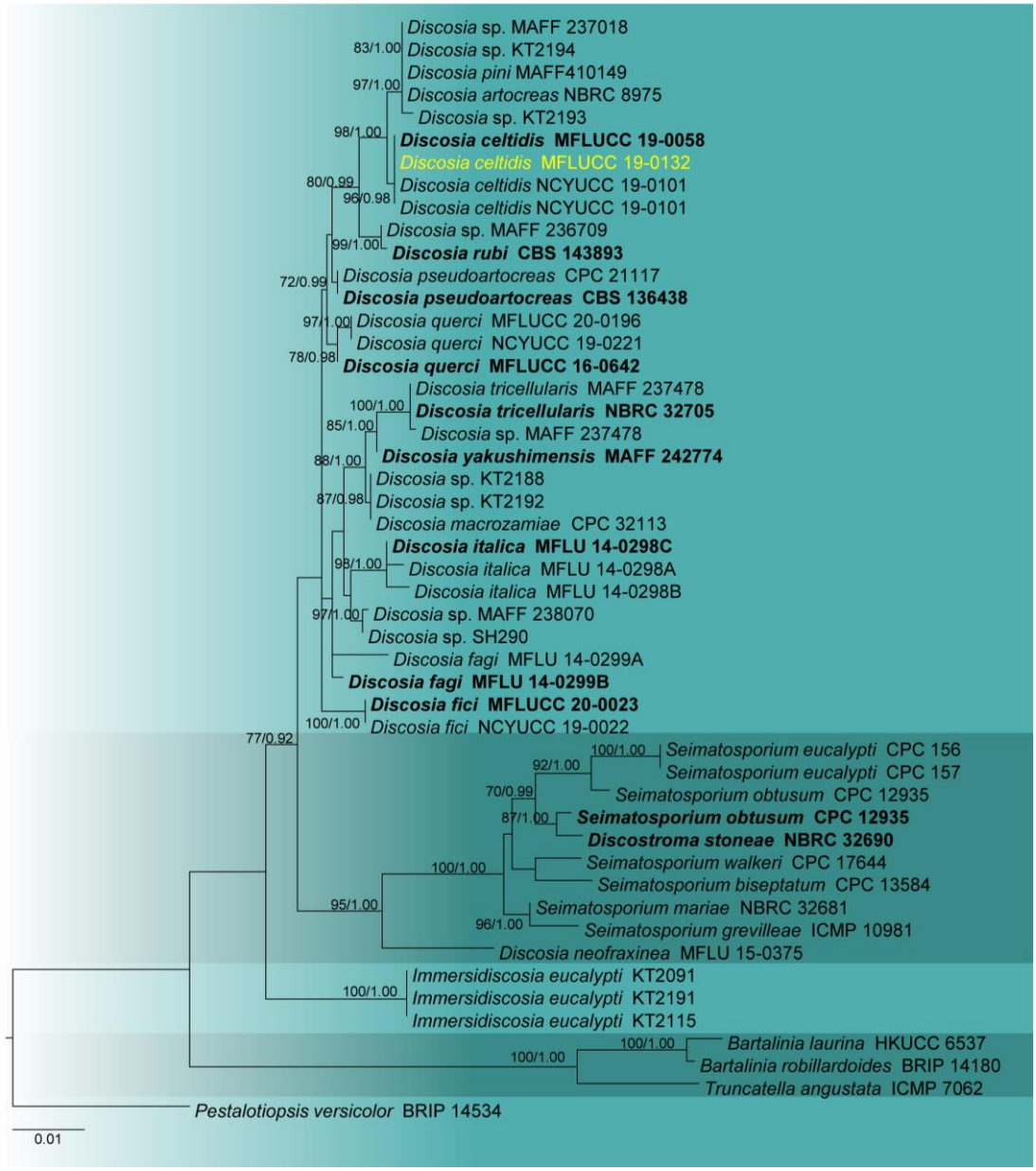

**Fig. 76 –** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Forty-nine strains are included in the combined analyses which comprised 1447 characters (879 characters for LSU and 568 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of - 4353.810124 is presented. The matrix had 315 distinct alignment patterns with 5.74 % of undetermined characters or gaps. The evolutionary model GTR+I+G is applied to LSU and ITS genes. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.95 are given near nodes, respectively. The tree is rooted with *Pestalotiopsis versicolor* (BRIP 14534). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

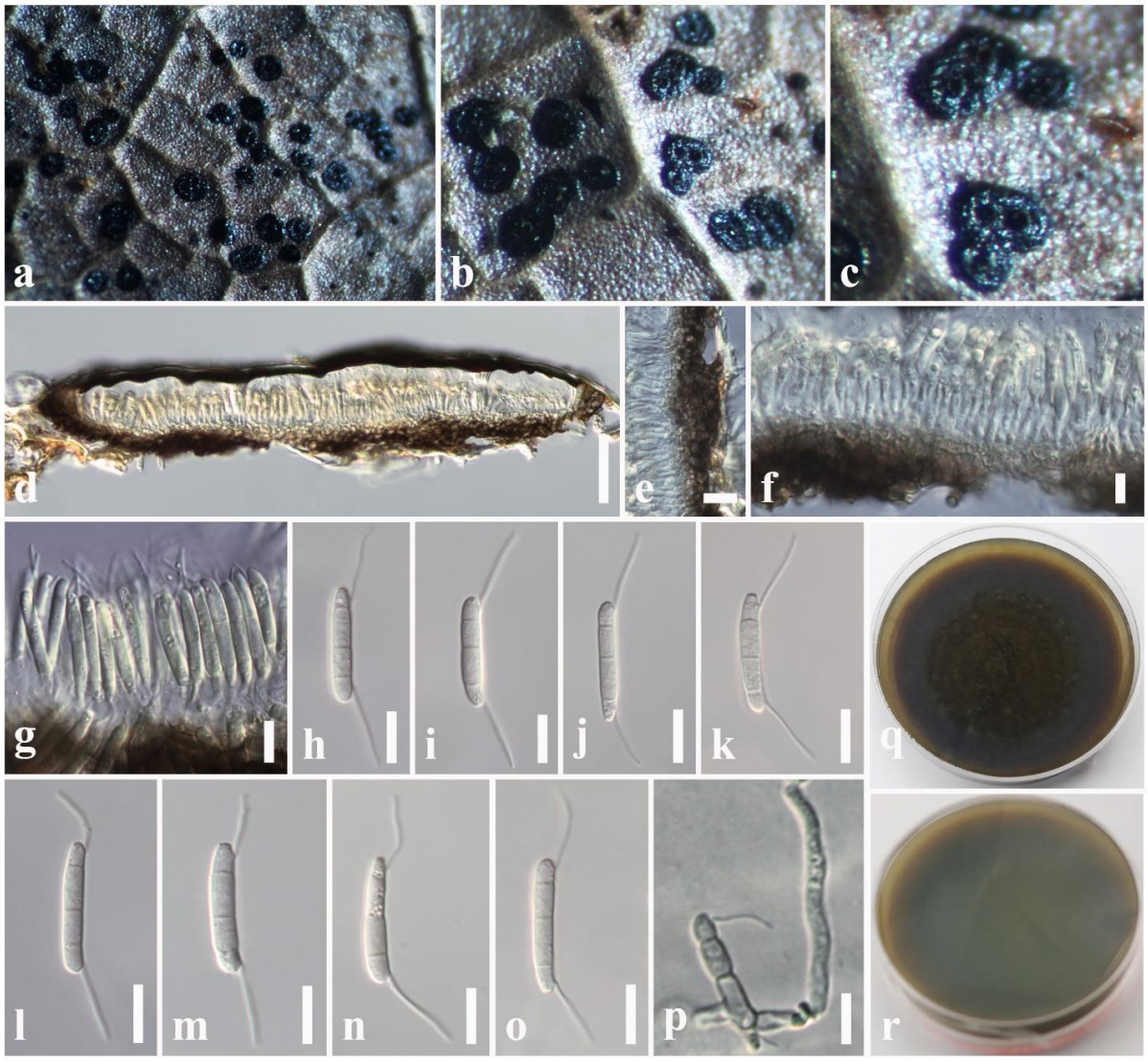


**Fig. 77 – *Discosia celtidis*** (MFLU 18-2604, **a new host record)**. a Appearance of conidiomata on the host. b, c Close-up of conidiomata. d Section of a conidioma. e Conidioma wall. f, g Conidiogenous cells. h–o Conidia. p Germinated conidium. q Colony from above. r Colony from below. Scale bars: d = 50 µm, e–p = 10 µm.

***Xylariales*** Nannf., Nova acta Regiae Societatis Scientiarum Upsaliensis, Ser. 48 (no. 2), 66 (1932)
Facesoffungi number: FoF 12988

***Diatrypaceae*** Nitschke [as 'Diatrypeae'], Verh. naturh. Ver. preuss. Rheinl. 26, 73 (1869)
Facesoffungi number: FoF 00679

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

Facesoffungi number: FoF 03773

*Allocryptovalsa* was introduced by Senwanna et al. (2017) with *Allocryptovalsa polyspora* as the type species. Senwanna et al. (2017) transferred *Eutypella cryptovalsoidea* and *Cryptovalsa rabenhorstii* to *Allocryptovalsa* based on morphological and phylogenetic analyses. The general features of this genus are immersed stromata, ostiolar with periphyses, unbranched, septate paraphyses, polysporous asci and oblong to allantoid ascospores, while the asexual morph was reported with hyaline, elongate-allantoid conidia (Senwanna et al. 2017, Zhu et al. 2021). To date, nine species have been recorded in Index Fungorum (2023). Here, we provide the updated phylogeny for *Allocryptovalsa* taxa (Fig. 78) and the PHI test (Fig. 79).

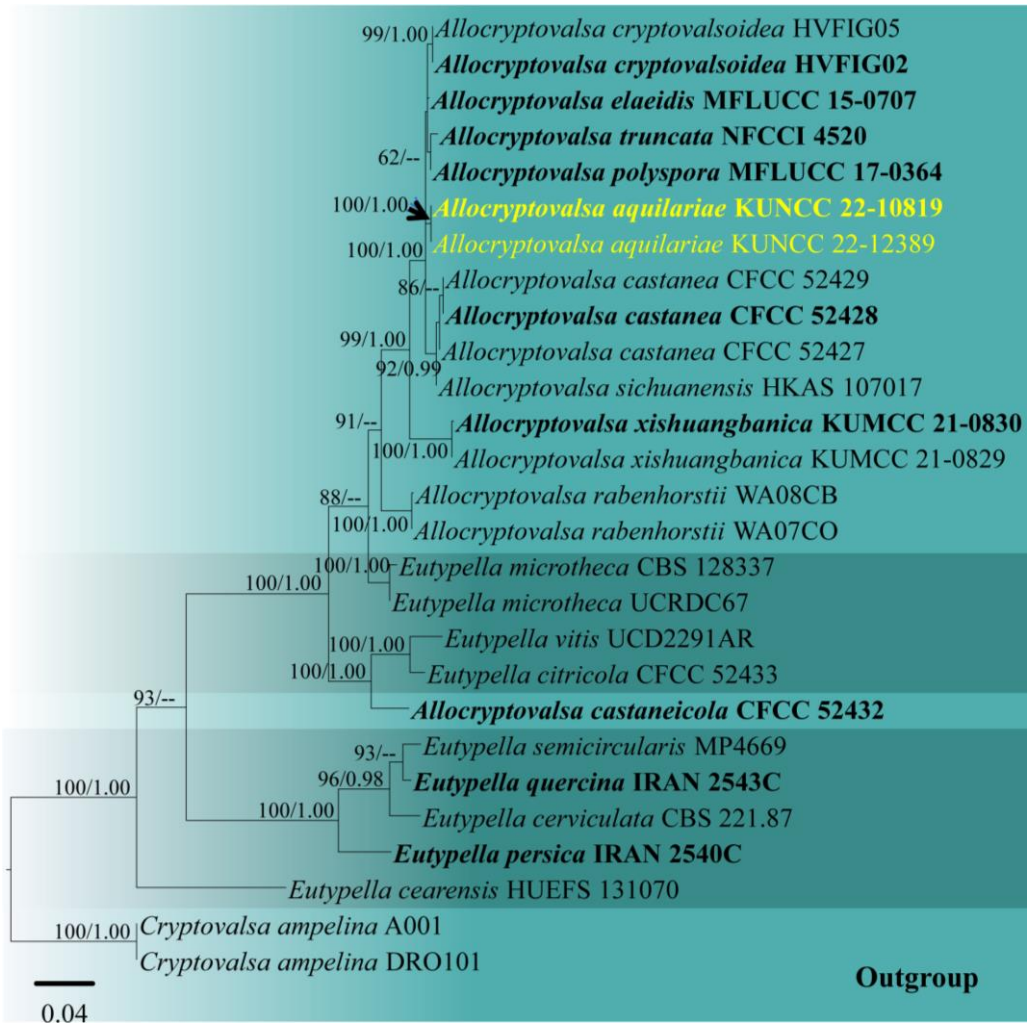


**Fig. 78 –** Phylogram generated from maximum likelihood analysis based on combined ITS and *β-tubulin* sequence data of the genus *Allocryptovalsa*. Twenty-seven strains are included in the combined analyses, which comprised 817 characters (472 characters for ITS, 345 characters for *β-tubulin*). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -3183.305213 is presented. The matrix had 253 distinct alignment patterns with 20.06% of undetermined characters or gaps. The evolutionary model GTR+I+G is applied to both ITS and *β-tubulin* genes. Bootstrap support values for ML analysis equal to or greater than 60% and Bayesian posterior probabilities equal to or greater than 0.90 are given near nodes, respectively. The tree was rooted with *Cryptovalsa ampelina* (A001 and DRO101 strains). Ex-type strains are in black **bold**. The newly generated sequences are indicated in yellow.

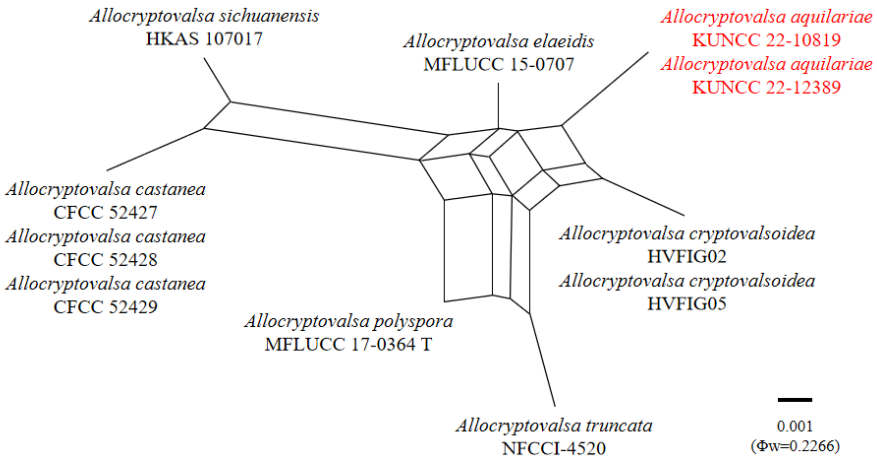


**Fig. 79 –** Split graphs showing the results of PHI test of *Allocryptovalsa aquilariae* and closely related taxa using LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicates that there is significant recombination within the dataset. Application of the PHI test to the concatenated tree-locus sequences (ITS and *β-tubulin*) revealed the recombination level within phylogenetically related species. The test results show Φw = 0.2266 for the combined sequence data, Φw = 0.6455 for ITS data, while *β-tubulin* data is not significant. Therefore, no significant recombination events were observed between *Allocryptovalsa aquilariae* and phylogenetically closely related species. The new taxa are in red.

***Allocryptovalsa aquilariae*** T.Y. Du & Tibpromma **sp. nov.**

MycoBank number: MB 846167; Facesoffungi number: FoF 12954; Fig. 80

Etymology – Named after the host genus, *Aquilaria* from which it was collected.

Holotype – HKAS 124187

*Saprobic* on dead twigs of *Aquilaria sinensis* (Lour.) Spreng. **Sexual morph:** *Ascostromata* gregarious with small black dots, immersed, the surrounding white host tissue without bark, 1–12-loculate. *Ascomata* (excluding the neck) 320–550 µm high × 250–650 µm diam. ($\bar{x}$ = 380 × 410 µm, n = 10), perithecial, solitary to gregarious, immersed in substrate, globose to ampuliform, dark brown to black, not wrapped in white entostroma, the surrounding tissue is black after sectioning, ostiolate, papillate. *Ostiolar canal* 150–330 µm high × 85–150 µm diam. ($\bar{x}$ = 203 × 112 µm, n = 10), central, not protrude or protrude slightly to outside from the substrate, cylindrical or irregular, straight, dark brown to black, periphysate. *Peridium* 35–95 µm wide, composed of several layers of thick-walled, hyaline to brown cells of *textura angularis* to *textura prismatica*, which are not fully fused with the host tissue. *Hamathecium* 2–9 µm wide, hyaline, with granulate, filamentous, unbranched, septate paraphyses, slightly constricted at the septa. *Asci* 130–190 × 10–20 µm ($\bar{x}$ = 167.8 × 15.4 µm, n = 30), spore-bearing part length 65–100 µm ($\bar{x}$ = 87 µm, n = 30), unitunicate, thin-walled, polysporous, clavate, J- apical ring, with 64–102 µm, apically rounded, narrowing towards lower region, with long and fragile pedicels, and some pedicels with subglobose or irregular structure. *Ascospores* (8–)9.5–11.5 × 2–3.5 µm ($\bar{x}$ = 10.2 × 2.8 µm, n = 30), crowded, oblong to allantoid, pale yellowish at maturity, aseptate, slightly curved, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 6 cm diam., after seven days at 28 °C, flattened, filiform margin, with white aerial mycelia, flossy, velvety, reverse white, smooth.

Material examined – China, Yunnan Province, Xishuangbanna, dead twigs of *Aquilaria sinensis*, 13 September 2021, T.Y. Du, YNA27 (HKAS 124187, **holotype**), ex-type culture, KUNCC 22-10819, KUNCC 22-12389.

GenBank accession numbers – KUNCC 22-10819 – ITS: OP454035, *β-tubulin*: OP572197; KUNCC 22-12389 – ITS: OP456373, *β-tubulin*: OP572198.

Notes – In the phylogenetic tree (Fig. 78), our isolates formed an inconspicuous branch with no support similar to *Allocryptovalsa cryptovalsoidea*, *A. elaeidis*, *A. polyspora* and *A. truncata*.

However, the morphology of our isolates differs from the ones related to *A. aquilariae* (Fig. 80). *Allocryptovalsa cryptovalsoidea* has ostioles often perforated, emerging through the bark, while our species do not protrude or protrude slightly to the outside from the substrate, mostly immersed (Trouillas et al. 2011). The ascomata of our collection are 1–12-loculate, wrapped in white powder, which differs from the ascomata of *A. elaeidis* which has 1–2-loculate ascomata, delimited by a black zone in host tissues (Konta et al. 2020). Also, our species differs from *A. polyspora* by having 1–12-loculate, larger ascomata (320–550 × 250–650 µm *vs*. 80–425 × 100–400 µm), whereas the ascomata of *A. polyspora* are 1–3-loculate (Senwanna et al. 2017). *Allocryptovalsa truncata* has superficial ascostromata and individual ascomata, which differ from our collection by having 1–12-loculate, immersed ascostromata (Hyde et al. 2020). In addition, a PHI test (Fig. 79) conducted based on the combined ITS and *β-tubulin* dataset showed that our *Allocryptovalsa aquilariae* isolates form a separate branch with Φw = 0.2266 (Φw > 0.05). Based on the multi-gene phylogenetic tree, PHI test results, and its unique morphological characteristics, *Allocryptovalsa aquilariae* is identified as a new species.

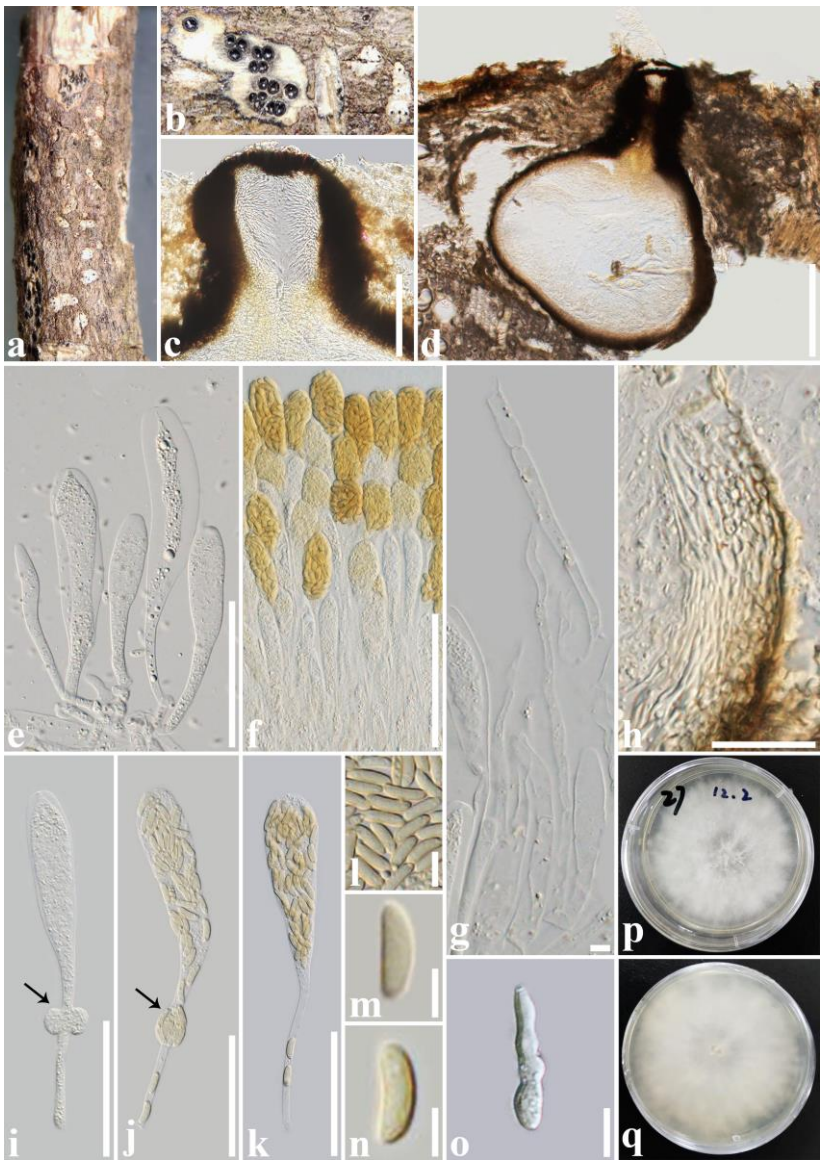


**Fig. 80 – *Allocryptovalsa aquilariae*** (HKAS 124187, **holotype**). a, b Appearance of ascostromata on the host. c Ostiolar periphysate. d Section through an ascoma. e, f, i–k Asci (arrows pointed towards subglobose structures at the pedicel). g Paraphyses. h Peridium. l–n Ascospores. o Germinated ascospore. p, q Culture characteristics on PDA after seven days (p front view, q reverse view). Scale bars: c, f = 100 µm, d = 200 µm, e, h–k = 50 µm, g, m, n = 5 µm, l, o = 10 µm.

***Vamsapriyaceae*** Y.R. Sun, Yong Wang bis & K.D. Hyde, in Sun, et al., Journal of Fungi 7(891), 7 (2021)

Facesoffungi number: FoF 09926

***Vamsapriya*** Gawas & Bhat, Mycotaxon 94, 150 (2006)

Facesoffungi number: FoF 00372

Gawas and Bhat (2005) reported a new genus, *Vamsapriya*, in *Xylariaceae* with *Vamsapriya indica* as the type species. Recently, Sun et al. (2021) investigated the morphological characters and multi-gene phylogeny of *Vamsapriya* and transferred to a newly introduced family, *Vamsapriyaceae*, based on the distinct morphology and multi-gene phylogeny (Sun et al. 2021). There are twelve species listed in the Index Fungorum (2023). The updated phylogeny for the genus is shown in Fig. 81.

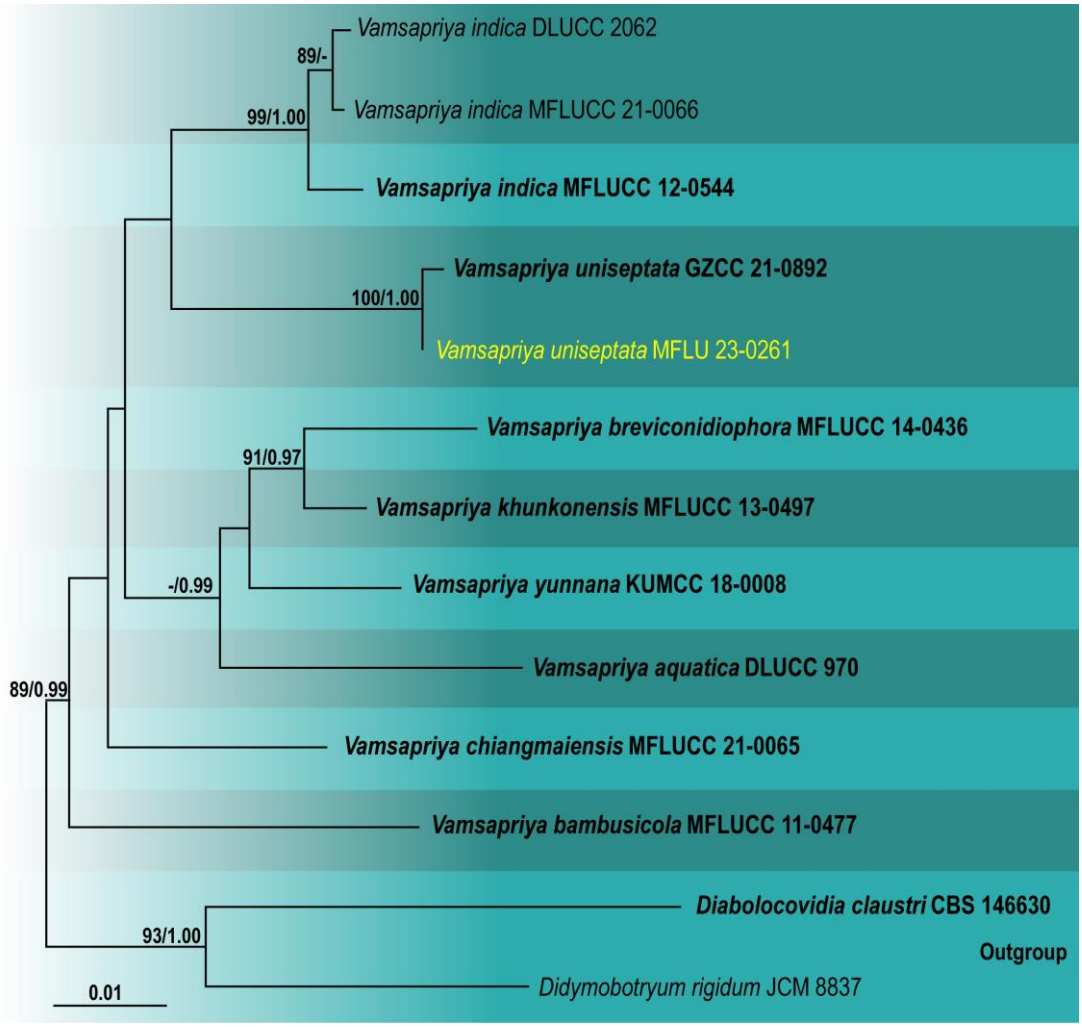


**Fig. 81 –** Phylogram generated from maximum likelihood analysis based on the combined LSU, *rpb2*, *β-tubulin* and ITS sequence data for *Vamsapriya*. Thirteen strains are included in the combined analyses, which comprised 2634 characters after alignment (including gaps). Tree topology derived from the Bayesian analysis was similar to that derived from the maximum likelihood analysis. The best RaxML tree with a final likelihood value of -5802.949387 is presented. The matrix had 312 distinct alignment patterns with 33.30% of undetermined characters or gaps. The evolutionary model GTRGAMMA is applied to all genes. Bootstrap values of maximum likelihood analysis greater than or equal to 80% and Baysian posterior probabilities greater than or equal to 0.95 are given near the nodes. The tree is rooted with *Didymobotryum rigidum* (JCM 8837) and *Diabolocovidia claustra* (CBS 146630). Ex-type strains are in black **bold**. The newly generated sequences are indicated in yellow.

***Vamsapriya uniseptata*** N.G. Liu & K.D. Hyde, in Sun et al., Journal of Fungi 7(891), 12 (2021)

Index Fungorum number: IF 558619; Facesoffungi number: FoF 09928; Fig. 82

*Saprobic* on decaying bamboo. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies black, effuse. *Conidiophores* are macronematous, synnematous, erect, rigid, straight or slightly curved, cylindrical, dark brown, septate. *Synnemata* erect, straight or slightly flexible, dark brown, and comprise compactly positioned conidiophores. *Conidiogenous cells* monotretic, integrated, terminal, clavate, brown to dark brown. *Conidia* catenated, acrogenous, oblong, olivaceous brown, rough, guttulate, 1-septate in the middle, subtunicate at the base and rounded at the apex.

Culture characteristics – Colonies on PDA reaching 90 mm diam. after 14 days at 25 ºC, white in surface, pale brown in reverse and dark to dark brown in the center, circular, flat, cottony, entire margin.

Material examined – Thailand, Chiang Rai Province, Mae Fah Luang University, dead bamboo, 10 July 2022, Hsan Win, MFLU 23-0261, living culture MFLUCC 23-0265.

GenBank accession number – ITS: OR259106, LSU: OR259087, *β-tubulin*: OR269618.

Known distribution (based on molecular data) – China (Sun et al. 2021), Thailand (this study).

Known hosts (based on molecular data) – Decaying wood (Sun et al. 2021) and bamboo (this study).

Notes – *Vamsapriya uniseptata* is distinguished by having 1-septate conidia, while other *Vamsapriya* species have multi-septate conidia (Sun et al. 2021). According to the BLAST results, ITS and LSU sequences of our isolate showed 100 % similarity to the ITS and LSU sequences of the ex-type of *V. uniseptata* (GZAAS 21-0378). In the multi-gene phylogenetic analyses, our isolate clustered with the ex-type of *V. uniseptata* (GZAAS 21-0378) with 100% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Fig. 81). Based on similar morphology (Sun et al. 2021) and multi-gene phylogeny, we introduce our isolate as *Vamsapriya uniseptata*, a new geographical record for Thailand.

**Phylum *Basidiomycota*** R.T. Moore, Botanica Marina 23(6), 371 (1980)

**Class *Agaricomycetes*** Doweld, Prosyllabus Tracheophytorum, Tentamen Systematis Plantarum Vascularium (Tracheophyta) (Moscow), LXXVIII (2001)

Facesoffungi number: FoF 14340

**Subclass *Agaricomycetidae*** Locq., Mycologie générale et structurale, 97 (1984)

Facesoffungi number: FoF 14341

***Agaricales*** Underw., Moulds, mildews and mushrooms. A guide to the systematic study of the Fungi and Mycetozoa and their literature (New York), 97 (1899)

Facesoffungi number: FoF 14342

***Agaricaceae*** Chevall. Fl. gén. env. Paris (Paris) 1, 121 (1826)

Facesoffungi number: FoF 14343

***Lepiota*** (Pers.) Gray, Natural Arrangement of British plants (London) 1, 601 (1821)

Facesoffungi number: FoF 14344

*Lepiota*, which belongs to the family *Agaricaceae*, consists of 450 white-spored species distributed across six sections, which were classified based on their morphological characters and distribution in tropical and temperate zones (Dennis 1952, He et al. 2019a, Vellinga 2001). According to molecular studies, the species and sections are not monophyletic (Vellinga 2003, Liang et al. 2011, Hou & Ge 2020, Hyde et al. 2020b, c). The genus is studied rarely in Laos, and three species have been recorded from Laos, including *Lepiota aureofulvella*, *L. citrophylla*, *L. macrocarpa* and *L. thailandica* (Sysouphanthong et al. 2017, 2020). An updated phylogeny for the genus is illustrated in Fig. 83.

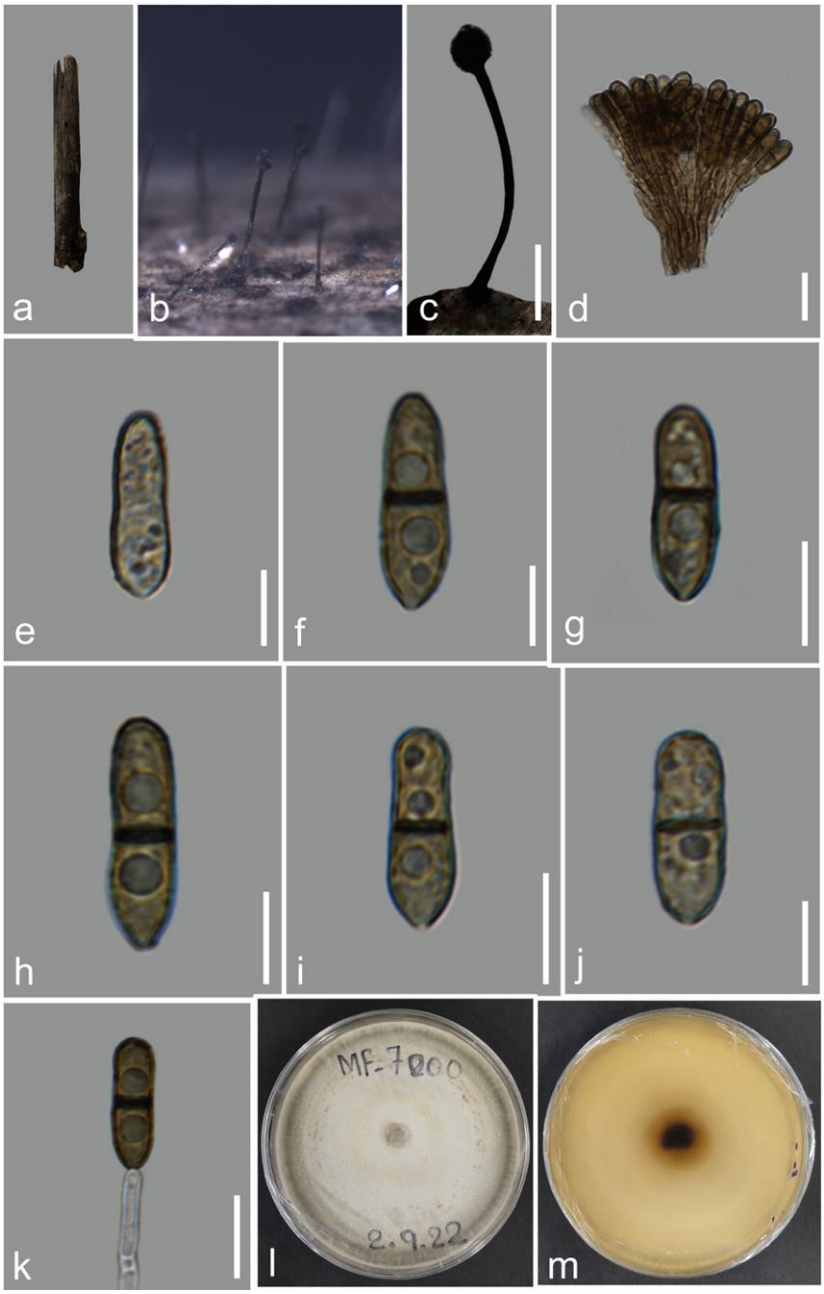


**Fig. 82 – *Vamsapriya uniseptata*** (MFLUCC 23-0265, **a new geographical record**). a Dead bamboo specimen. b Fungal structures on the host substrate. c Conidiophores. d Conidiogenous cells and conidia. e–j Conidia. k Germinating conidium. l, m Front (l) and reverse (m) views of the colony on the PDA. Scale bars: c = 200 µm, d, e–k = 10 µm.

***Lepiota angusticystidiata*** J.F. Liang & Z.L. Yang, in Liang, Yu, Lu, Wang & Song, Mycologia 110, 496 (2018)

Index Fungorum number: IF 819510; Facesoffungi number: FoF 06198; Figs. 84, 85

*Pileus* 10–45 mm diam., first irregular subglobose to conical, expanding to parabolic to campanulate, umbonate, becoming plano-convex to concave when fully mature, with straight or slightly inflexed margin; covered with light brown to dark brown (6D7-6, 6E6–7, 6F6-8) granulose when young, surface breaking up and living concolorous granulose umbo, with light brown to brown (6D7-6, 6E6–7) squamules around umbo towards the margin on white to yellowish white (4A2) background; margin cortinate, with concolorous squamules, sometimes fringed. *Lamellae* free, white, crowded, ventricose, 2–5 mm wide, with concolorous eroded edge. *Stipe* 20–80 × 4–8

mm, cylindrical, narrow at apex, slightly wider at base; with concolorous squamules as those on pileus from annular zone towards base on with white to yellowish white (4A2) background. *Annulus* an annular zone, not well-defined, with white fibrillose and concolorous squamules. *Context* white in pileus, 2–4 mm wide; concolorous with surface in stipe, hollow. *Smell* and *Taste* not observed. *Spore* print white.

*Basidiospores* [50,2,2] 6.3–7.2 × 4.0–5.3 μm, avl × avw = 6.81 × 4.50 μm, Q = 1.36–1.63, avQ = 1.51, ellipsoid ovoid in sideview, ellipsoid in frontal view, thick-walled, hyaline, dextrinoid, congophilous, cyanophilous, not metachromatic. *Basidia* 19–23 × 8–10 μm, clavate, thick-walled, hyaline, 4-spored, rarely 2-spored. *Pleurocystidia* absent. *Cheilocystidia* 10–30 × 5–11 μm, abundant, mostly utriform to narrowly utriform or fusiform, sometimes clavate, branched and septate, hyaline, thick-walled. *Pileus* covering a trichoderm made up of cylindrical elements with attenuated apex, 100–270 × 7–18 μm, septate and branch at base, thick-walled, intracellular and with parietal pale brown pigment, with concolorous narrowly clavate elements under long elements, 35–60 × 10–23 μm. *Stipe* covering a trichoderm similar to pileus covering. *Clamp-connections* present in all tissues.

Material examined – Laos, Vientiane Capital, Xaythany District, Houynhang Preserve Forest, 9 July 2016, P. Sysouphanthong (HNL503160); *ibidem*., 7 July 2016, P. Sysouphanthong (HNL503157); *ibidem*., 04 Aug. 2016, P. Sysouphanthong (HNL503163).

GenBank accession numbers – HNL503160 - ITS: MZ717725.

Known habitat – grow solitary to a large group, terrestrial on soil mixed with decayed leaves and branches (Liang et al. 2018, Hyde et al. 2020b).

Known distribution (based on molecular data) – China (Liang et al. 2018), northern Thailand (Hyde et al. 2020b), central Laos (this study).

Note – According to the morphological characteristics, Lao specimens of *Lepiota angusticystidiata* are similar to type specimens from China (Liang et al. 2018). Thai specimens have longer pileus and stipe covering, but other characters are similar to Lao and China specimens (Hyde et al. 2020b). The phylogenetic analysis of nrITS sequences indicated that specimens of China, Laos and Thailand are clustered with 98% bootstrap support (Fig. 83). Our species is related to the clade of *Lepiota* sect. *Ovissporae*, which consists of species with long elements, and species with short clavate elements in *Lepiota* sect. *Lepiota* (Figs. 84 & 85). Some species related to *L. angusticystidiata* were discussed in Liang et al. (2018) and Hyde et al. (2020b). Current study presents a new geographical record of *Lepiota angusticystidiata* from central Laos.

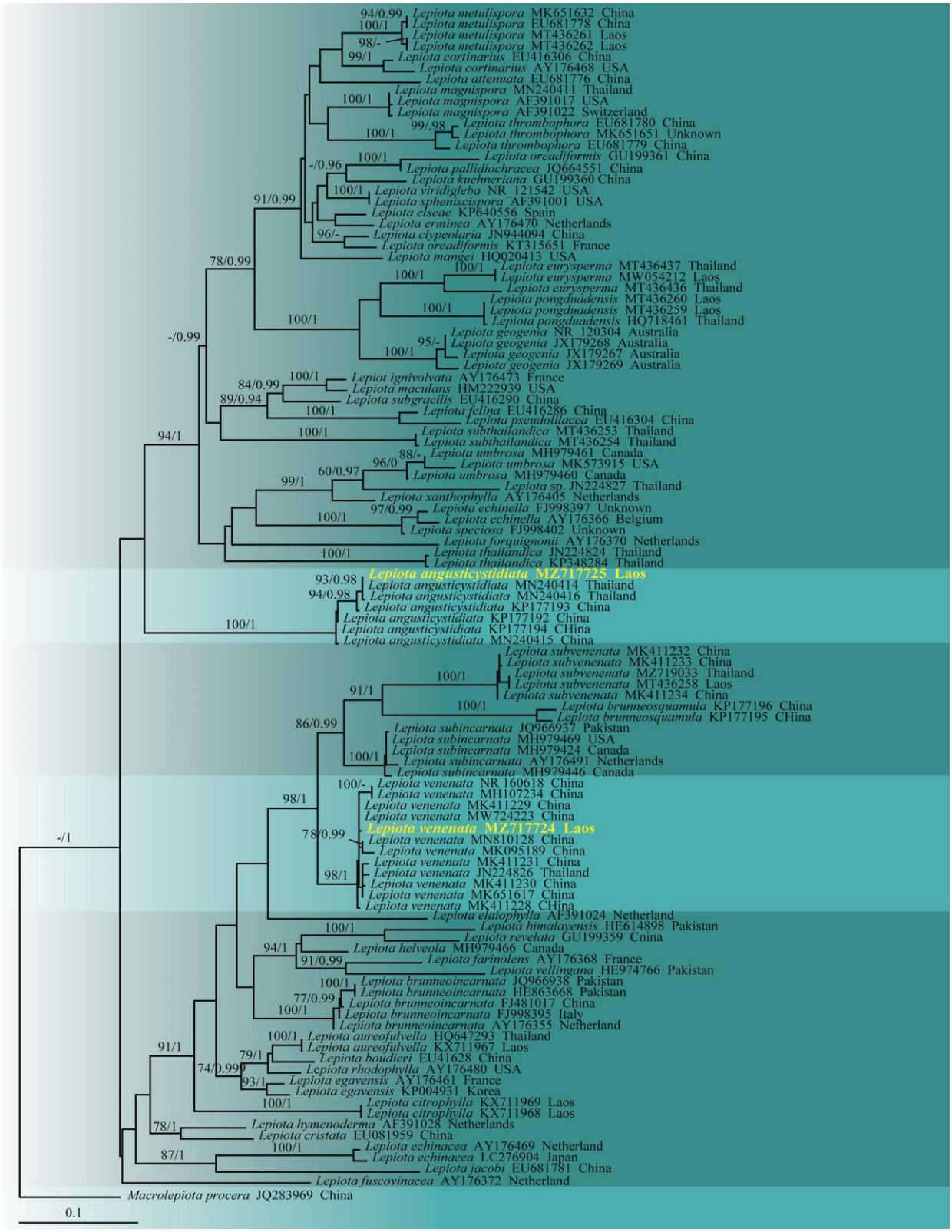


**Fig. 83 –** Maximum likelihood phylogenetic tree (ML) of *Lepiota* based on nrITS sequences. One hundred and eight strains consisting of 683 characters after alignment (including gaps). The tree topology derived from the Bayesian analysis was similar to that derived from the ML analysis. The best RaxML tree with a final likelihood value of -11952.807294 is presented. The matrix had 474 distinct alignment patterns, with 7.95% undetermined characters or gaps. Evolutionary model applied is GTRGAMMA. Bootstrap values of ML equal to greater than 70% and Baysian posterior probabilities equal to greater than 0.94 are given above branches. The tree is rooted with *Macrolepiota procera* (JZB2115036). Newly generated sequence is indicated in yellow.


**Fig. 84 – Basidiomata of *Lepiota angusticystidiata in situ*** (HNL503160, **new country record**). a–b HNL503163. c HNL503160. d–e HNL503157.

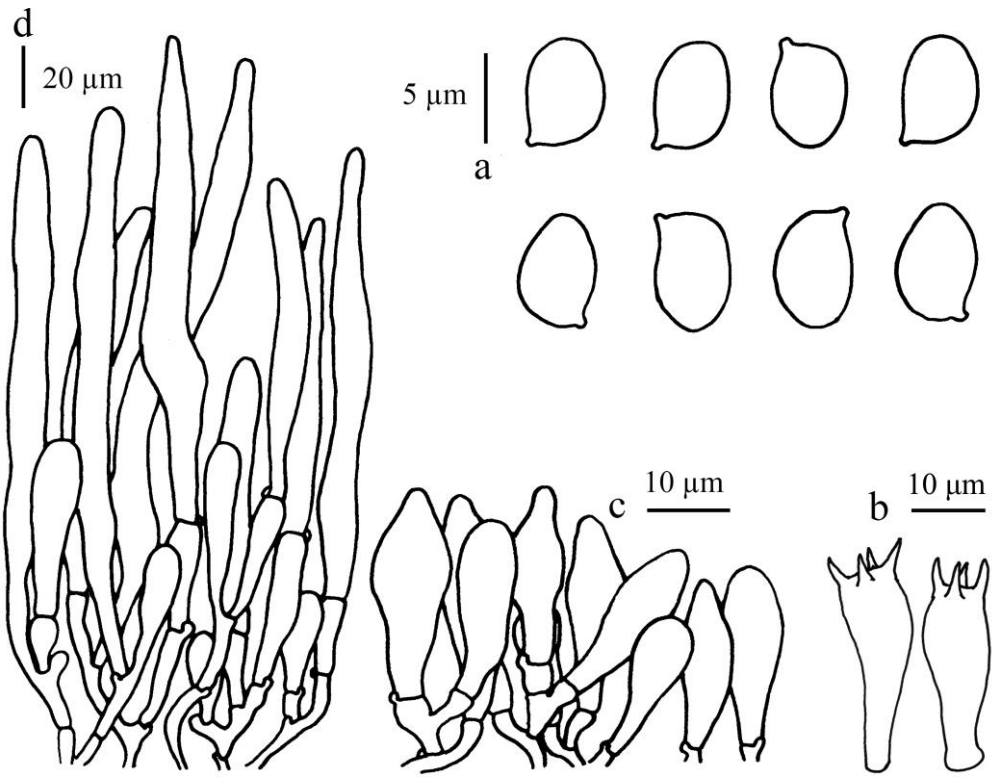


**Fig. 85 – Micro-characteristics of *Lepiota angusticystidiata*** (HNL503160). a Basidiospores. b Basidia. c Cheilocystidia. d. Elements structure on pileus covering.

***Lepiota venenata*** Zhu L. Yang & Z.H. Chen, in Cai, Chen, He, Luo & Yang, J. Fungal Res. 16, 67 (2018)

Index Fungorum number: IF 824765; Facesoffungi number: FoF 10409; Figs. 86, 87

*Pileus* 17–20 mm diam., first parabolic, expanding to umbonate with high umbo, with inflexed margin; fibrillose squamules and squamules at umbo towards margin, light brown to brown (7D6–8), slightly darker at umbo, on white fibrillose background; marginal zone with brown concolorous fibrillose squamules and white thin fibrillose. *Lamellae* free, crowded, ventricose, 2–3 mm wide, white, with concolorous eroded edge. *Stipe* 25–32 × 3–4 mm, cylindrical, with slightly tapering to apex; covered with light brown to brown (7D6–8) squamules from annular zone toward base on white background. Annular zone, with white fibrillose and concolorous squamules. Context white in pileus, 1.5–2 mm wide; white and hollow in stipe. *Smell* and *taste* not observed. *Spore print* white.

*Basidiospores* [50,1,1] 5.5–7.5 × 3.5–4.5 µm, avl × avw = 6.5 × 4.0 µm, Q=1.5–1.8, Qav= 1.6, oblong ovoid in side view, oblong in frontal view, hyaline, slightly thick-walled, dextrinoid, congophilous, cyanophilous, not metachromatic in Cresyl Blue. *Basidia* 15–18× 5.0–6.5 µm, clavate, thin-walled, hyaline, 4-spored. *Pleurocystidia* absent. *Cheilocystidia* 15–25 × 5.0–8.0 µm, mostly clavate, often utriform, rarely cylindrical, hyaline, thin-walled. *Pileus* covering a trichoderm made up of cylindrical elements, always tapering to apex, 55–275 × 6.0–13 µm, slightly thick-walled, with brown intracellular and parietal pigment, without short clavate or clavate elements under long elements, branched and septate. *Clamp connections* present in all tissues.

Material examined – Laos, Xekong Province, Tha Teng District, 30 September 2015, P. Sysouphanthong (HNL503248).

GenBank accession numbers – HNL503248 - ITS: MZ717724.

Known habitat – grow solitary to a small group, terrestrial on rich humus soil (Cai et al. 2018, this study).

Known distribution (based on molecular data) – China (Cai et al. 2018), central Laos (this study).

Notes – *Lepiota venenata* was originally described in the Hubei Province of China (Cai et al. 2018). The type specimen differs from the Laos specimen by having larger basidiomata (30–60 mm diam. of pileus), brown to reddish-brown squamules on pileus and stipe, white to cream lamellae, and longer cheilocystidia (20–38 µm). However, other characters are similar. The phylogenetic tree showed that *Lepiota venenata* is identical to those specimens from China (Cai et al. 2018) and a specimen from Thailand (JN224862, unpublished). Our collection is clustered in the *Lepiota* sect. *Ovisporae* clade with species that have long elements of pileus and stipe coverings, without short clavate elements, and *Lepiota* sect. *Stenosporae*. The southern Laos collection of *Lepiota venenata* exhibits similar morphology to the type specimen (Cai et al. 2018) and is the first record of the species reported.


**Fig. 86 – Basidiomata of *Lepiota venenata in situ* (new country record)**. a–c HNL503248.

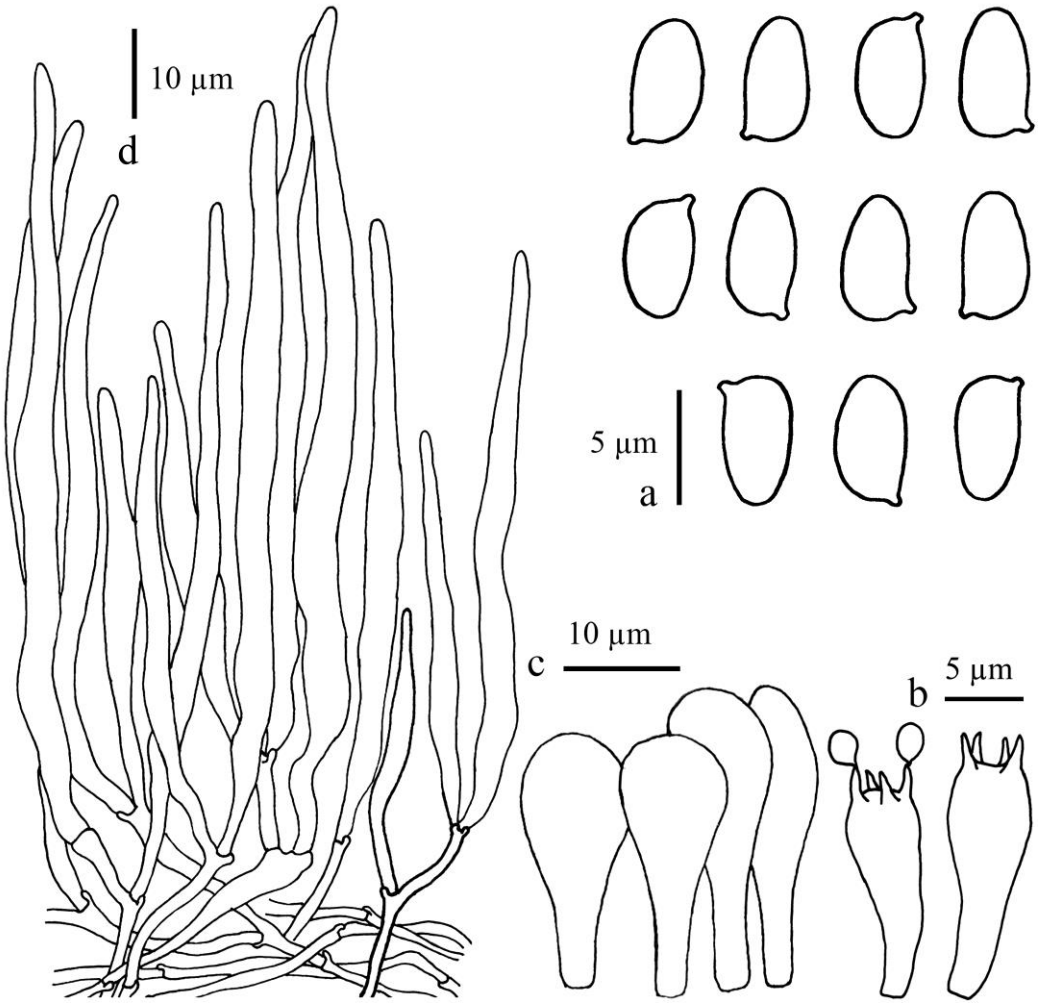


**Fig. 87 – Micro-characters of *Lepiota venenata*** (HNL503248). a Basidiospores. b Basidia. c Cheilocystidia. d Elements structure on pileus covering.

***Hymenogastraceae*** Vittad. [as 'Hymenogastereae'], Monogr. Tuberac. (Milano), 11 (1831)

Facesoffungi number: FoF 14365

***Gymnopilus*** P. Karst., Bidrag till Kännendom af Finlands Natur och Folk 32, XXI (1879)

Facesoffungi number: FoF 14366

*Gymnopilus*, typified by *Gymnopilus liquiritiae* (Guzmán-Dávalos 2003), stands with approximately 200 taxa (Holec 2005, Campi et al. 2021, Hesler 1969). The genus is characterized by yellow to ferruginous or purple basidiomata and lamellae, central to the eccentric stipe, partial cortinoid to fibrillose veil, generally fugacious ring, bitter flesh, ferruginous spore print, ellipsoidal basidiospores with warty to rugose ornamentation, with no germ pore, with dextrinoid walls in some taxa, and the presence of sub-capitulated cheilocystidia and clamp connections in hyphae (Holec 2005, Campi et al. 2021, Hesler 1969). Ecologically, *Gymnopilus* is characterized by a lignicolous habit, growing on wood at different levels of decomposition with no preference for the substrate (Hesler 1969). Many taxa are common in the tropics and are associated with angiosperms, while they are associated with conifers in temperate zones (Holec 2005). The updated phylogeny for the genus is shown in Fig. 88.

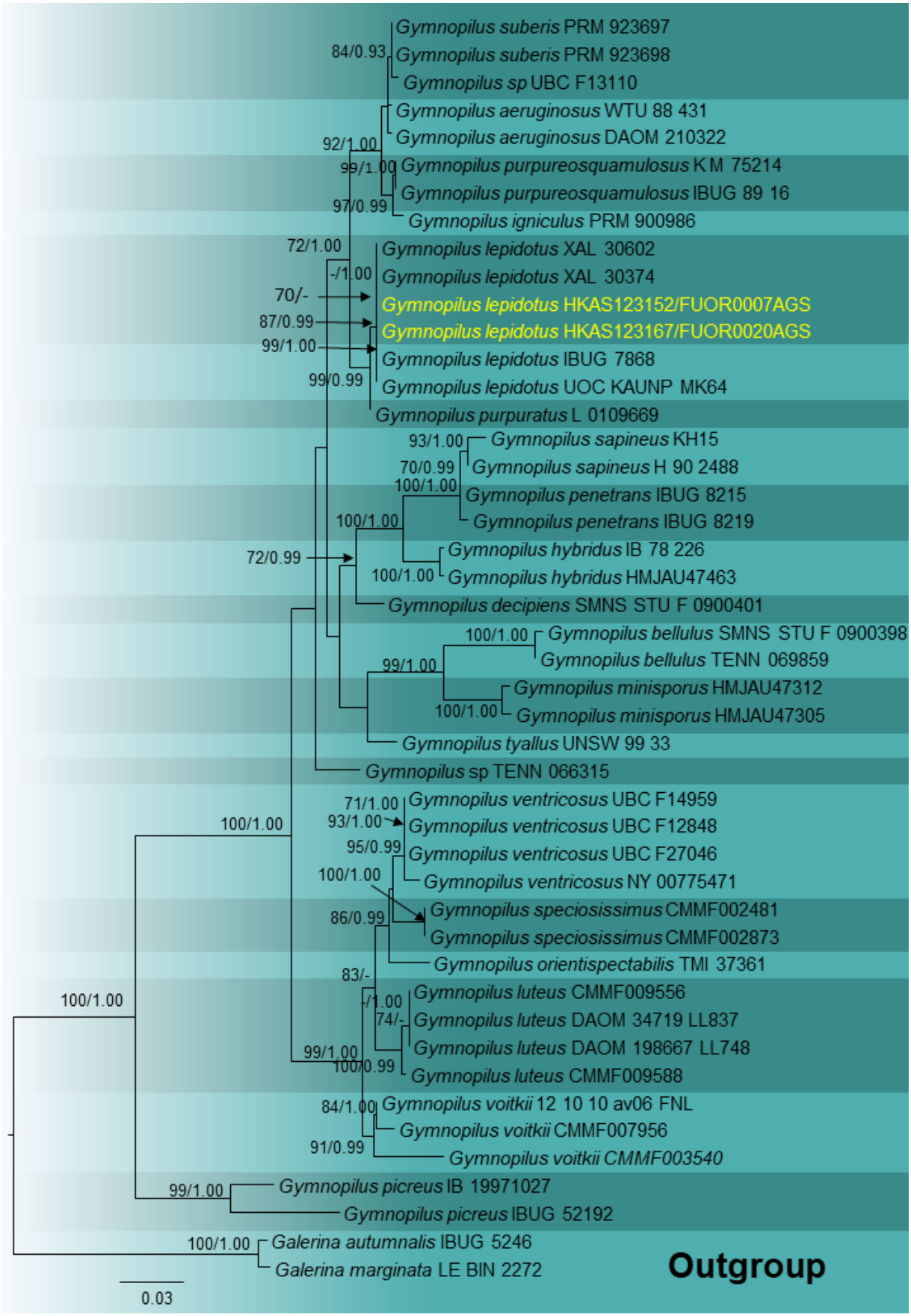


**Fig. 88 –** Phylogram generated from maximum likelihood analysis based on ITS sequence data of taxa in *Gymnopilus*. Forty-six strains are included in the phylogenetic analyses which comprised 1766 characters after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -4446.715724. The matrix

had 311 distinct alignment patterns, with 58.76% of undetermined characters or gaps. Evolutionary model applied for ITS is GTR+I+G. Bootstrap support values for ML equal to or greater than 65% and Bayesian posterior probabilities equal to or greater than 0.95 are indicated near the branches. The tree is rooted with *Galerina autumnalis* (IBUG 5246) and *G. marginata* (LE BIN 2272). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

***Gymnopilus lepidotus*** Hesler, Mycologia Memoirs 3, 40 (1969)

Index Fungorum number: IF 314787; Facesoffungi number: FoF 14367; Fig. 89

*Saprotrophic*, solitary, growing on the rotting bark of a trunk of *Cocos nucifera. Basidiomata* small. *Pileus* 3–5 cm across, covex when young, plano-convex at maturity. *Surface* smooth, wet, yolk yellow (4B8) closer to the periphery, reddish yellow (4A8) to orange (5A7) middle and center, covered reddish orange (7B8) erect scales, densely arranged at center and scattered towards margin. *Margin* rimose, hairy, edge slightly undulating at maturity, translucent sulcate, lamellae; deep yellow (4A8), deep orange (5A8), sub-decurrent, crowded with intermingled lamellulae of three lengths. *Lamellulae* smooth and thick, edge equal. *Stipe* 2.5–4.5 × 0.3–0.5 cm, surface reddish yellow (4A8) to dark orange (5B8) cylindric, slightly curved, flexible, pubscent, striated, flexible, tapering down, hollow, context: thin, 0.2–0.4 cm thick, deep yellow (4A8). *Basidiospores* 6.2–7.3 × 4.8–5.3 µm, ellipsoidal to amygdaliform, rounded to sub-acute apex, thin-walled, hyaline, warty. *Basidia* 18–23 × 6.2–7 µm, claviform, 2-4 spored, hyaline or sub-hyaline. *Pleurocystidia* 20–27 × 6.5–7.2 µm, utriform. *Cheilocystidia* lageniform with obtuse or sub-capitate apex, hyaline to sub-hyaline, hymenoophoral trama; thin-walled, clamp connections present.

Material examined – Sri Lanka, Southern Province, Matara District, growing on a rotting bark of a *Cocos nucifera*, 22 March 2021, A.N Ediriweera, FUOR0020AGS (HKAS123167); *ibid*., FUOR0076AGS (HKAS123152).

GenBank accession numbers – HKAS123152 - ITS: OQ607123; HKAS123167 - ITS: OQ607128.

Known habitat – Decomposing wood or occasionally terrestrial with buried or decomposed wood (Wright & Wright 2005, Lechner et al. 2006, Wright et al. 2008, Vasco-Palacios & Franco-Molano 2013, Grassi et al. 2016), rotting bark (this study).

Known distribution (based on molecular data) – Argentina (Lechner et al. 2006, Wright et al. 2008, Grassi et al. 2016), Colombia, Mexico (Vasco-Palacios & Franco-Molano 2013), USA (Wright & Wright 2005), Sri Lanka (this study).

Notes – This taxon has been recorded from Argentina in Misiones Province (Lechner et al. 2006, Wright et al. 2008, Grassi et al. 2016), Colombia and Mexico in the states of Jalisco and Veracruz (Guzmán-Dávalos 1996) and Florida, United States of America (Wright & Wright 2005). Our new strain is clustered with *G. lepidotus* isolates (XAL 30602 and XAL30374) with 70% maximum likelihood bootstrap support. *Gymnopilus lepidotus* formed a sister clade with *G. purpuratus* with 99% maximum likelihood bootstrap support and 0.99 Bayesian posterior probability. Fernando et al. (2015) reported *G. lepidotus* from Sri Lanka and studied its pharmacological properties. This study reports a new strain of *G. lepidotus* from Sri Lanka, which is phylogenetically closely related to the records from Mexico. The new strain differs by having a smaller pileus, a lower umbo at the center, absence of scales, presence of striates radiating up to the margin, and smaller basidiospores. Our new collection differs from the USA specimen in their basidiomata dimensions and the pileus size recorded as 4–8 mm. Guzmán-Dávalos et al. (2003) revised the taxa and found that the pileus diameter ranged from 6–18 (26) mm even in dried samples from Florida, while samples from Mexico extended up to 7 mm. *Gymnopilus lepidotus* reported from Paraguay showed very similar morphological characteristics to our new record.

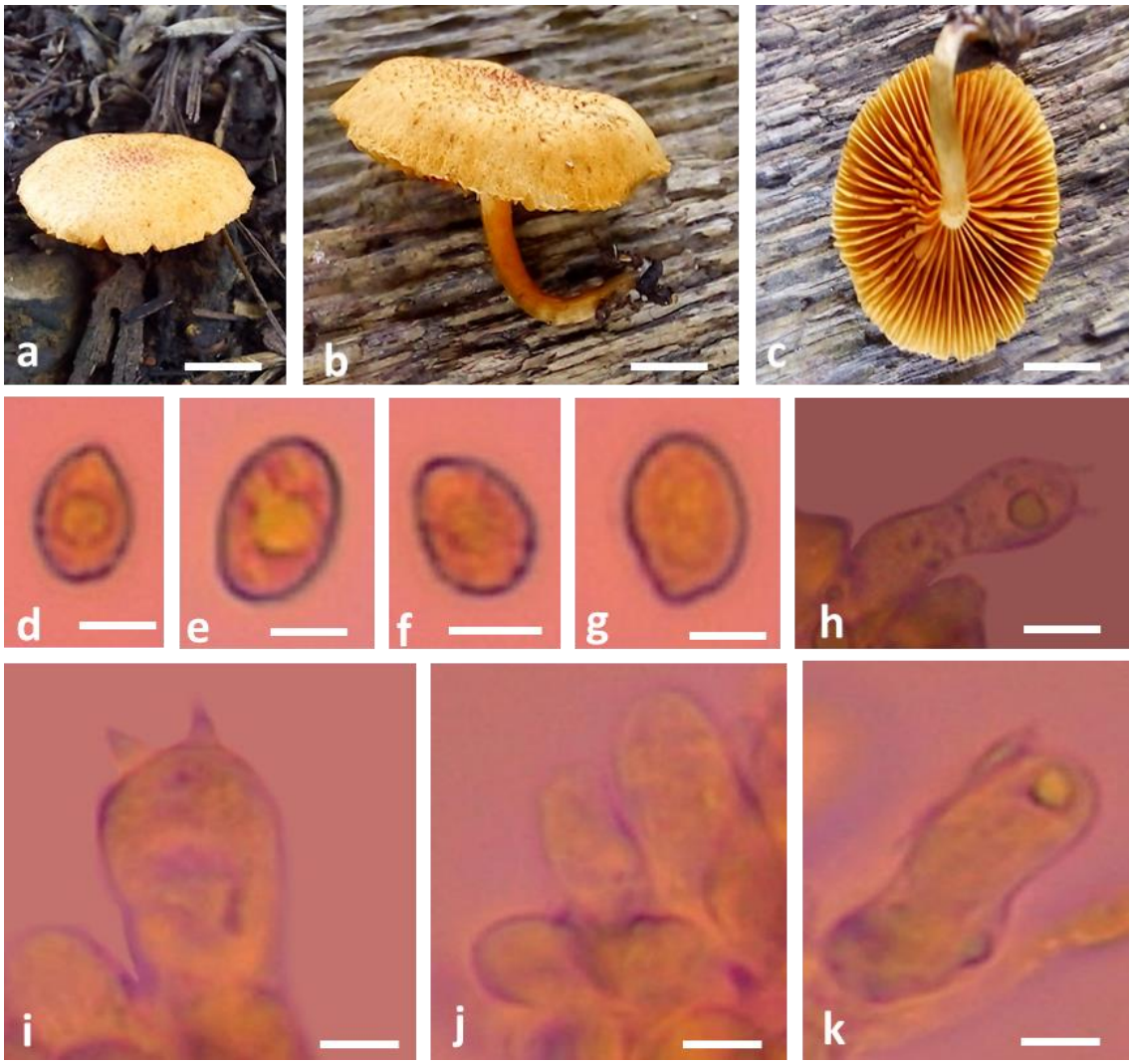


**Fig. 89 – *Gymnopilus lepidotus*** (HKAS123167). a–c Mature basidiome. d–g Basidiospores. h, i Basidia. j, k Cheilocystidia. Scale bars: a–c = 0.5 cm, d–g = 2 μm, h–k = 5 μm.

***Lyophyllaceae*** Jülich, Biblthca mycology 85, 378 (1982)

Facesoffungi number: FoF 14368

***Asterophora*** Ditmar Neues Journal Botanik 3, 56 (1809)

Facesoffungi number: FoF 14369

This genus was introduced by Ditmar (1809) and typified by *A. lycoperdoides*. Currently, only four species are accepted in this genus (Blanco-Dios 2011), *viz.*, *A. salvaterrensis*, *A. lycoperdoides*, *A. mirabilis* and *A. parasitica*. An updated phylogeny for the genus *Asterophora* is illustrated in Fig. 90.

***Asterophora lycoperdoides*** (Bull.) Ditmar, Neues Journal Botanik 3(3, 4), 56 (1809)

Index Fungorum number: IF 233153; Facesoffungi number: FoF 14370; Fig. 91

*Pileus* 2–4 cm diam., hemispherical to convex or plane, white (1A1), powdery, slightly depressed to the depressed shape of center, reflexed aspects of margin. *Chlamydospores* pile on the pileus, light yellow (1A5); context 1–2 mm diam., white (1A1) to pale white (1A2). *Lamellae* white (1A1) when young, becoming yellowish white (1A2) to pale yellow (1A3), lamella edge eroded, lamellulae in 2–3 tiers, 2–3 mm wide. *Stipe* 1.1–2.0 × 0.3–0.4 cm, cylindrical, solid, fiber. *Odor* and taste not distinctive.

*Basidiospores* [50/2/2] 4.2–5.2 × 2.9–3.8 μm, av. 4.6 × 3.3 μm, Q=1.1–1.6, $Q_{av}$=1.4, ovoid to ellipsoid, sparse, thin-walled, smooth under light microscope. *Basidia* 22–24 × 5–7 μm, av. 23.5–

6.2 µm, sparse, broadly clavate, 4-spored. *Chlamydospores* 18.8–24.7 × 12.1–19.9 µm, av. 20.9–15.0 µm, numerous on the pileus surface, subcylindrical, echinulate. *Cystidia* not seen.

Material examined – Thailand. Chiang Mai Province, Pha Deng Village, Pa Pae Sub District, 14 July 2020, S.M. Tang 2020071470 (HKAS 117644); *ibid*., Pa Pae Sub District, S.M. Tang 2020071429 (HKAS 117645).

GenBank accession numbers – HKAS 117644 - ITS: MZ914396, LSU: MZ914399; HKAS 117645 – ITS: MZ914397, LSU: MZ914400.

Known distribution (based on molecular data) – China (Wang et al. 2004), India (Sharma et al. 2007), Turkish (Uzun et al. 2010), Thailand (this study).

Known hosts (based on molecular data) – *Russula nigricans* (Homma et al. 2006).

Notes – *Asterophora lycoperdoides* is recognized by its white pileus, chlamydospores formed on the pileus and echinulate. *Asterophora* has four species, *A. salvaterrensis*, *A. lycoperdoides*, *A. mirabilis* and *A. parasitica*. However, *A. salvaterrensis* has zonate, greenish brown to brownish pileus and smooth chlamydospores (Blanco-Dios 2011). *Asterophora mirabilis* has a smooth pileus, and chlamydospores formed in the lamellar trama and pileal trama above the lamellae (Blanco-Dios 2011). *Asterophora parasitica* has relatively larger basidiospores (5–6 × 3–4 µm) and smooth chlamydospores (Blanco-Dios 2011).

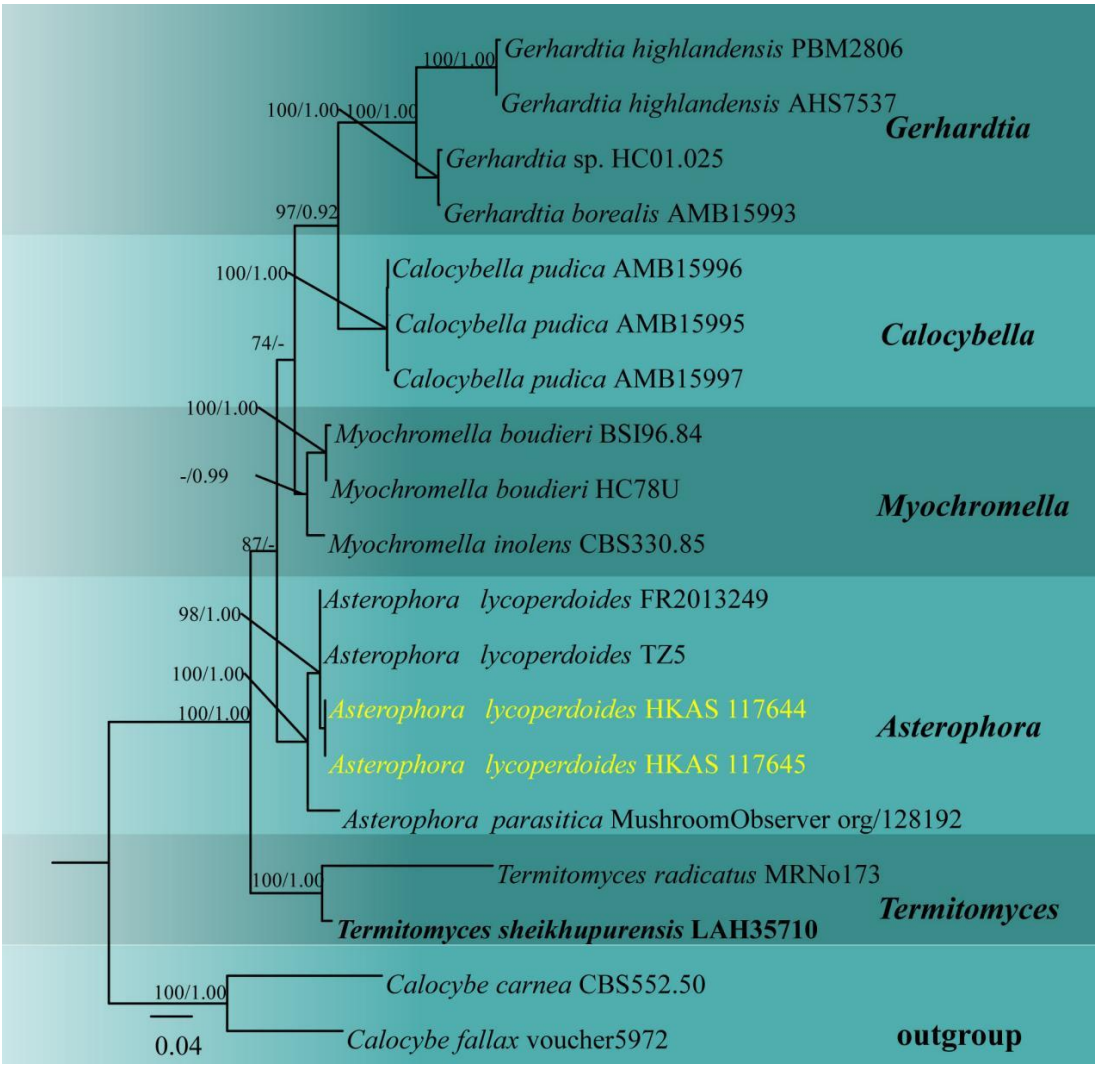


**Fig. 90 –** Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of taxa in *Lyophyllaceae*. Seventeen strains are included in the combined analyses which comprised 1576 characters (691 characters for ITS, 885 characters for LSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best RaxML tree with a final likelihood value of -6583.545571. The matrix had 418 distinct alignment patterns, with 30.40% of undetermined characters or gaps. Evolutionary models applied for ITS and LSU genes are HKY+G and GTR+I models, respectively. Bootstrap support values for ML and MP equal to or greater than 70% and Bayesian posterior probabilities equal to or greater than 0.90 are indicated near the branches. The tree is rooted with *Calocybe carnea* (CBS 552.50) and *C. fallax* (voucher 5972). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

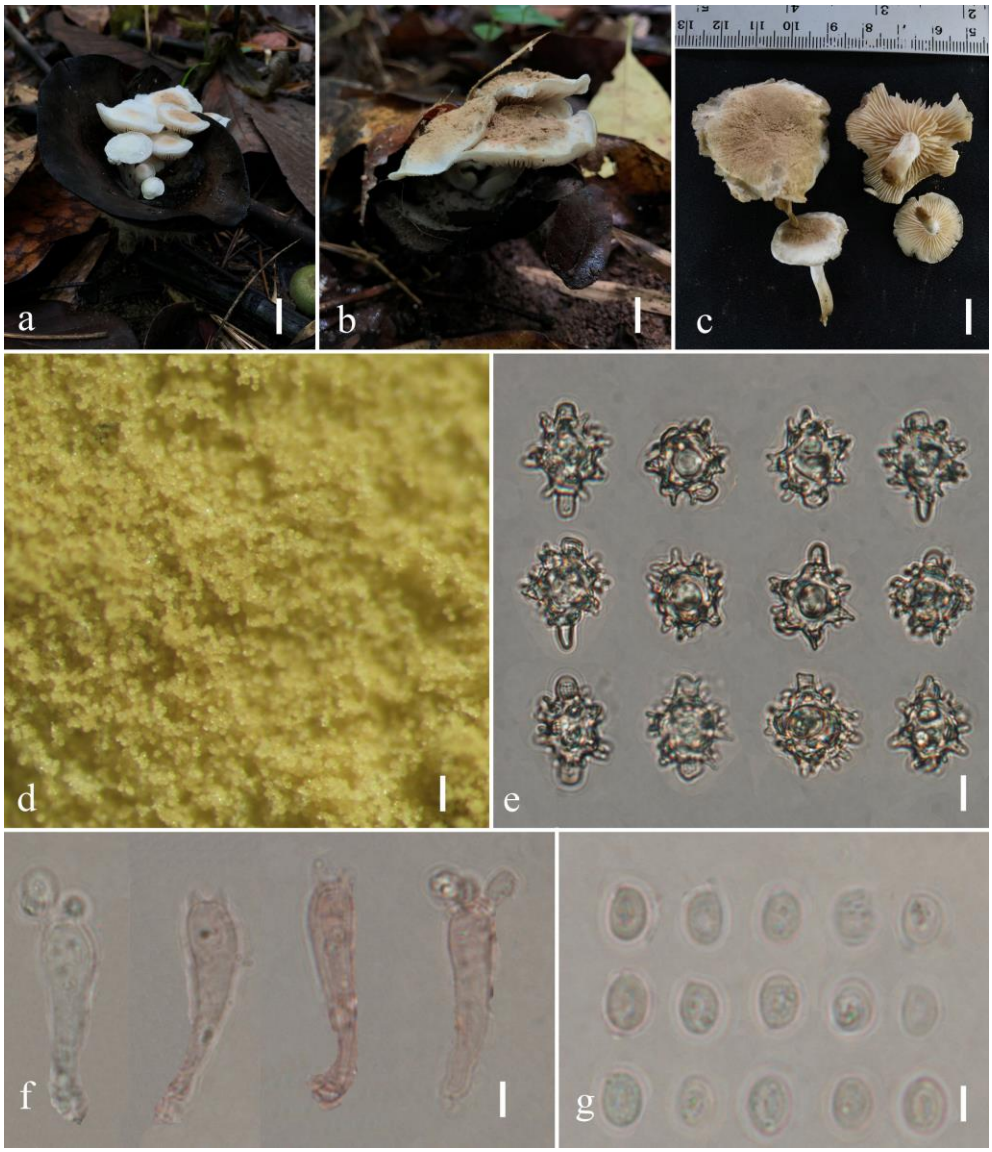


**Fig. 91 – *Asterophora lycoperdoides*** (HKAS 117644 & HKAS 117645, **additional collections**). a–c Basidiomata (a HKAS 117644, b–c HKAS 117645). d Chlamydospores on the surface of pileus. e Chlamydospores. f Basidia. g Basidiospores. Scale bars: a–c = 1 cm, d = 100 μm, e = 10 μm, f, g = 5 μm.

***Pleurotaceae*** Kühner, Bull. mens. Soc. linn. Lyon 49, 184 (1980)

Facesoffungi number: FoF 14080

***Pleurotus*** (Fr.) P. Kumm., Führ. Pilzk. (Zerbst), 24 (1871)

Facesoffungi number: FoF 14081

Genus *Pleurotus*, typified by *Pleurotus ostreatus* comprises oyster mushrooms, which play a major role as basic decomposers of wood and plant residues. Some taxa have also been recorded as

parasites on living trees, causing white rot infections (Hibbet & Vilgalys 1993). Members of *Pleurotus* are distributed broadly in tropical and temperate regions (Corner 1981, Lechner et al. 2005). The taxa in this genus are characterized by pleurotoid basidiomata, ellipsoidal or cylindrical basidiospores, white spore print and hyphae with clamp connections (Cohen et al. 2002, Lechner et al. 2005). Approximately 20 *Pleurotus* taxa are tested for commercial cultivations to check their potential edible and medicinal properties (Mandeel et al. 2005, Pawlik et al. 2012). An updated phylogeny for the genus is provided in Fig. 92.

***Pleurotus tuber-regium*** (Fr.) Singer, Lilloa 22, 271 (1951) [1949]

Index Fungorum number: IF 303985, Facesoffungi number: FoF 13861; Fig. 93

*Saprotrophic*, solitary, growing on a buried decaying wood branch of a tree in moist humus soil. *Basidiomata* medium. *Pileus* 3–12 cm wide, infundibuliform, surface; yellow (2A7) to Pastel yellow (3A4) when young, mustard yellow (3B6) or citron (3B8) at maturity, fuliginous and minutely scurfy squamulose, not scaly. *Margin* incurved, tightly incurved and wavy at maturity, with small floccose fragments of the veil. *Stipe* 2–7 × 0.4–0.9 cm, central, sub-cylindrical to cylindrical, concolorous with the pileus, surface minutely scurfy squamulose. *Lamellae* deeply decurrent, heavily crowded, thin, narrow, 0.2–0.6 mm wide, dichotomous, pastel yellow (2A4) to subochraceous, with entire fuscous-grey edge, very sinuous on drying; no hyphal pegs. *Context* 1.3 mm thick in the centre of the pileus, at first cheesy and hard, then coriaceous, white. *Odour* mushroomy, taste; pleasant. Basidiospores 6.8–11 × 2.7–4.8 µm, brown in water and congo red, smooth, subcylindric to inamyloid, thin-walled. *Basidia* four spored, 20–37 × 3.7–8 µm, thin-walled, hyaline, granules present. *Cheilocystidia* 23–40 × 3.5–7.5 µm, subcylindric to subclavate, subventricose, projecting, elongated, thin-walled, hyaline, smooth, as a sterile edge. *Pleurocystidia* absent. *Hyphae* dimitic skeletal and generative hyphae present. *Generative hyphae* 2–7 µm, not inflating, thickened-wall, frequently branching, clamp connections present. *Skeletal hyphae* 2–5 µm, hyaline, thickened-wall, poorly branched. Gill-trama with radiate construction.

Material examined – Sri Lanka, Sabaragamuwa Province, Ratnapura District, on a buried decaying wood branch of a tree, 1 August 2021, D. Nimthara, HKAS123161/FUOR0023AGS.

GenBank accession number – ITS: OQ607414.

Known distribution (based on molecular data) – Australia, Chad Republic, India, Ivory Coast, Kenya, Liberia, Madagascar, Malaysia, Middle Congo, Nigeria, Papua New Guinea, Samoa, Sierra Leone, Solomon Islands, Sri Lanka, Tanzania, Thailand, Uganda, Zaire Republic, Zambia, Zanzibar, and Zimbabwe (Karunarathna et al. 2016, Readhead et al. 2021, Miriyagalla & Manamgoda 2022).

Known hosts (based on molecular data) – *Daniellia* spp. (Karunarathna et al. 2016, Miriyagalla & Manamgoda 2022).

Notes – *Pleurotus* is a common edible mushroom genus (Karunaratha et al. 2016). On a taxonomy basis, we introduce *P. tuber-regium* from Sri Lanka, which is closely related to records from Thailand (MK894134) and Papua New Guinea (AY450344). Morphologically, the new strain shares common macro and micro characteristics of *P. tuber-regium* recorded from China (Readhead et al. 2021), such as deeply infundibuliform pileus, scufsquamulosese surface and deeply decurrent, crowded lamellae while the new strain differs with 3 – 12 diam. of pileus, yellow, pastel yellow or mustard yellow surface, 68–11 × 2.7–4.8 µm of basidiospores, 20–37 × 3.7–8 of basidia and cheilocystidia of 23–40 × 3.5–7.5 µm. *Pleurotus tuber-regium* is well-recognized as an edible mushroom and has been reported from Sri Lanka in several studies on its edible value and cultivation potential. This study provides a new collection of *P. tuber-regium* with molecular data and a photo plate with a description from Sri Lanka.

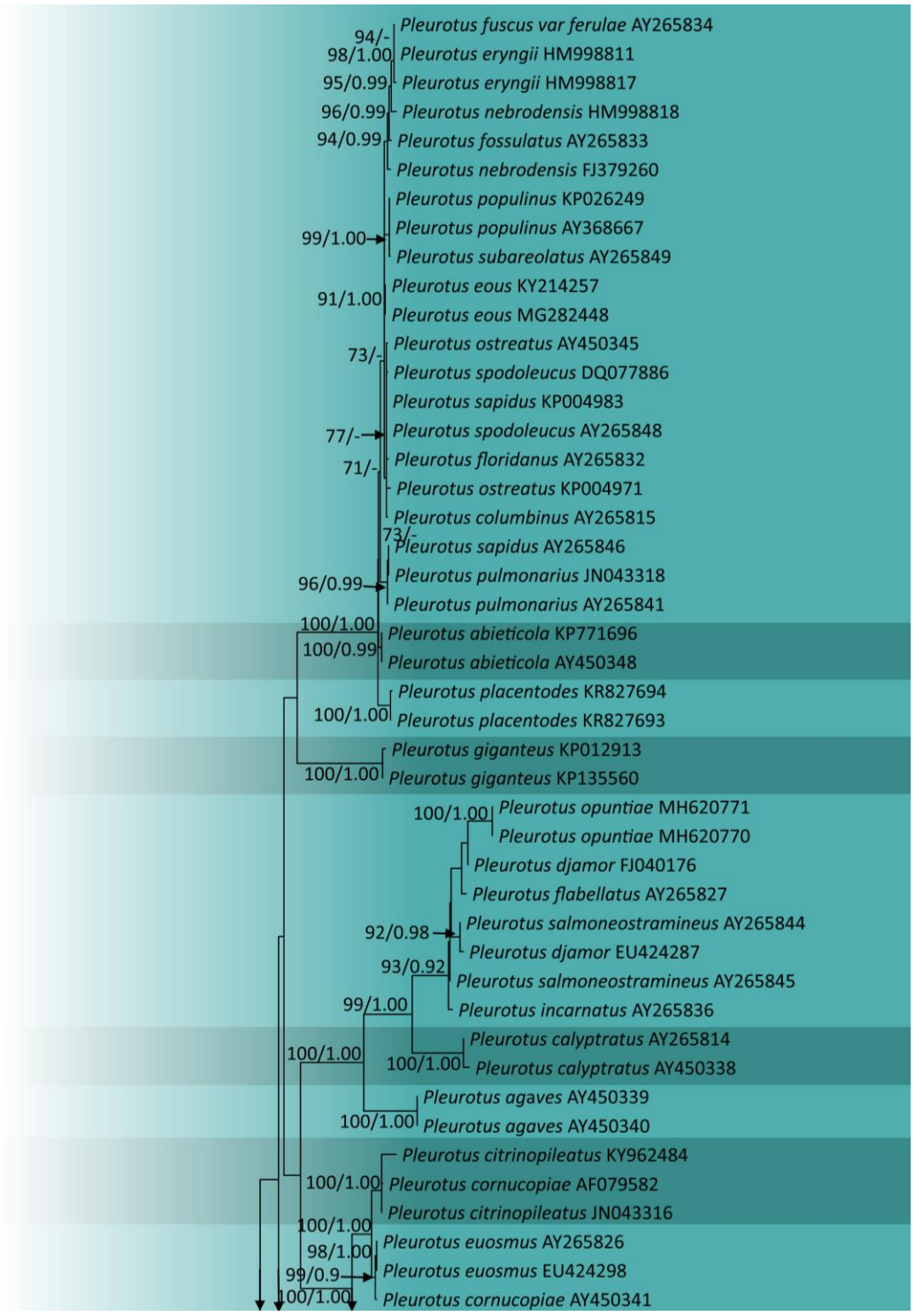


**Fig. 92 –** RAxML analysis based on the ITS sequence data of *Pleurotus* taxa. Forty-five strains are included in the phylogenetic analyses which comprised 1723 characters after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -5553.639272. The matrix had 360 distinct alignment patterns, with 3.72% of undetermined characters or gaps. Evolutionary model applied for ITS is GTR+I+G. Bootstrap support values for ML equal to or greater than 65% and Bayesian posterior probabilities equal to or greater than 0.95 are indicated near the branches. Bootstrap support values for ML equal to or greater than 65%, and Bayesian posterior probabilities (BP) equal to or greater than 0.95 are indicated near the nodes. The tree is rooted with *Hohenbuehelia petalodes* (strain T-104) and *Hohenbuehelia thornii* (AMB 18086). Ex-type strains are in **bold**. The newly obtained strain is indicated in yellow.

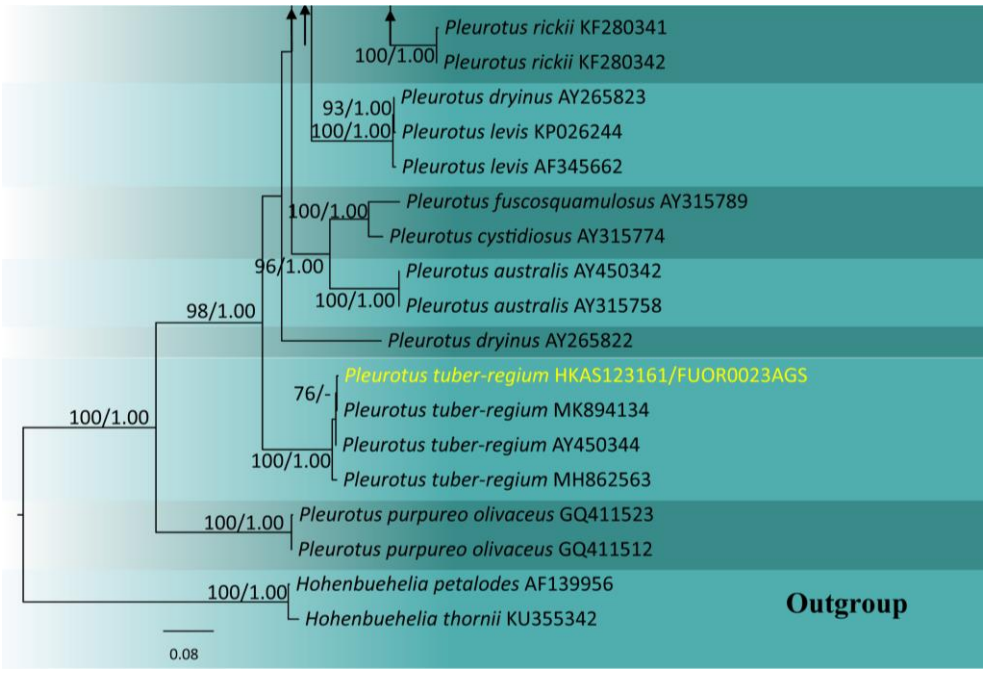


**Fig. 92 –** Continued.

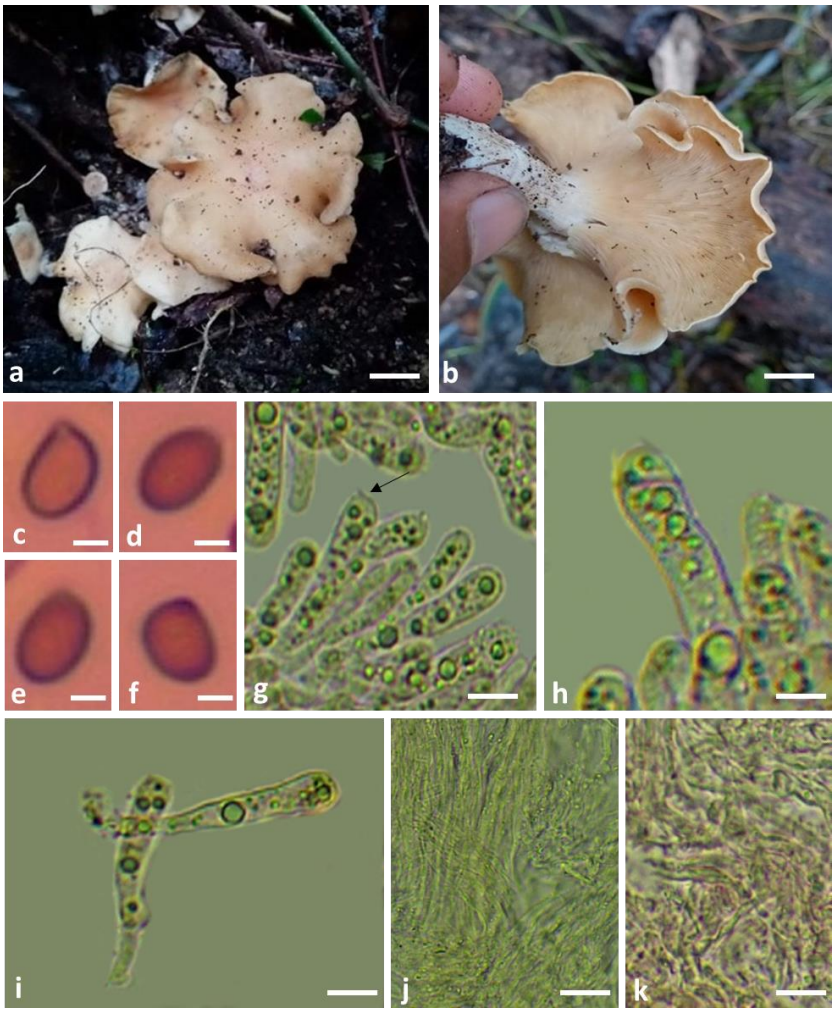


**Fig. 93 – *Pleurotus tuber-regium*** (FUOR0023AGS). a, b Mature basidiome. c–f Basidiospores. g, h Basidia. i Cheilocystidia. j Generative hyphae. k Skeletal hyphae. Scale bars: a, b = 2 cm, c–f = 3 µm, g–k = 5 µm.

***Boletales*** E.-J. Gilbert, Les Livres du Mycologue Tome I-IV, Tom. III: Les Bolets, 83 (1931)

Facesoffungi number: FoF 14371

***Boletaceae*** Chevall., Flore Générale des Environs de Paris 1, 248 (1826)

Facesoffungi number: FoF 09165

***Pulveroboletus*** Murrill, Mycologia 1(1): 9 (1909)

Facesoffungi number: FoF 15031

*Pulveroboletus*, typified with the North American *Pulveroboletus ravenelii*, is a genus of stipitate-pileate, ectomycorrhizal boletes. It currently comprises 38 species, some of which need to be revised (He et al. 2019a) and possibly transferred to other genera. *Pulveroboletus* species are characterized by a mostly yellow general veil (sometimes mixed with olivaceous, brown or various reddish tinges), which can be pulverulent, dry or more or less viscid, olive-brown spore print, and smooth basidiospores (Raspé et al. 2016, Zeng et al. 2017).

***Pulveroboletus fragrans*** Raspé & Vadthanarat, in Raspé et al., Mycological Progress 15(4/38): 4 (2016)

Index Fungorum number: IF 814679, Facesoffungi number: FoF 01917; Fig. 94

*Basidiomata* immature, enclosed in a mostly yellow general veil, bearing slightly viscid, pinkish orange scales on the pileus and to a lesser extent on the stipe, with olivaceous-brown fibrillose patches near the stipe base. *Partial veil* metablematic, cortina-like, pale yellowish white, filling the space enclosed by the general veil, between the stipe and cap. *Hymenophore* white, quickly and intensely bluing when cut. *Pileus* context yellowish white, strongly and quickly bluing when cut. *Stipe* context yellow marbled with white, except at the base, which is entirely yellow, slightly bluing when cut (mainly in the white areas). *Basal mycelium* yellowish white to yellow, cottony, with numerous rhizoids. *Odour* strong, aromatic. *Taste* not recorded.


**Fig. 94 – *Pulveroboletus fragrans*** (CMU-SDBR SV455). Immature basidiomes photographed in the lab.

Material examined – Thailand, Chiang Mai Province, Mae On District, Huay Kaew, on the soil in mixed Dipterocarp-Fagaceae forest, 6 June 2018, Santhiti Vadthanarat & Olivier Raspé, SV455 (CMU-SDBR).

GenBank submissions – *atp6*: MT468186 (CMU-SDBR SV455), *ef1-α*: MT468187 (CMU-SDBR SV455), *rpb2*: MT468188 (CMU-SDBR SV455).

Known distribution (based on molecular data) – Known only from Chiang Mai Province, Thailand.

Notes – The basidiomes found were all immature, but they exhibited the unique odour that is characteristic of the species. The identity of the collection was confirmed by the *atp6* and *ef1-α* sequences, which were 100% identical to the sequence of the holotype. The *rpb2* sequence differed only by two intra-individual heteromorphisms at positions 487 and 783. The *rpb2* sequence of the holotype also contained three intra-individual heteromorphisms that were not present in SV455, at positions 7, 41, and 538. Our collection represents the second record and locality of this rare species. It was found much earlier in the rainy season than all the collections made in the other known locality, i.e., in July (Raspé et al. 2016).

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**References**

Abass MH, Mohammed NH. 2014 – Morphological, molecular and pathological study on *Nigrospora oryzae* and *Nigrospora sphaerica*, the leaf spot fungi of date palm. Basra Journal for Date Palm Researches 13, 26–38.

Abeywickrama PD, Wanasinghe DN, Karunarathna SC, Jayawardena RS, et al. 2020 – A new host report of *Diaporthe manihotia* (*Diaporthales*, *Ascomycota*) from *Camellia* sp. in Yunnan province, China. Asian Journal of Mycology 3, 473–489.

Abeywickrama PD, Camporesi E, Jayawardena RS, Hyde KD, et al. 2022 – Novel and surprising host associations of *Diaporthe* (*Diaporthaceae*, *Diaporthales*) species from Italy. Chiang Mai Journal of Science 49, 1–25.

Ai CC, Ma J, Zhang K, Castañeda-Ruíz RF, Zhang X-G. 2019 – *Cordana meilingensis* and *C. lushanensis* sp. nov. from Jiangxi, China. Mycotaxon 134, 329–334.

Alam MW, Rehman A, Saira M, Kan NA et al. 2017 – First report of leaf spots in *Aloe vera* caused by *Nigrospora oryzae* in Pakistan. Plant Disease 101, 841.

Alcorn JL, Irwin JAG. 1987 – *Acrocalymma medicaginis gen. et.* sp. nov. causing root and crown rot of *Medicago sativa* in Australia. Transactions of the British Mycological Society 88, 163–167.

Alfieri Jr SA, Langdon KR, Wehlburg C, Kimbrough JW. 1984 – *Index of plant diseases in Florida* (Revised). Florida Department of Agriculture and Consumer Services, Division of Plant Industry, Bulletin 11, 1–389.

Almenares M, Pérez-Vicente L. 2019 – Speckle by *Corynespora torulosa* (Syd.) Crous: a pre-harvest fruit disease of *Musa* spp. in Cuba. Revista de Protección Vegetal 34, e06.

Anjum R, Khan IA, Afzal M, Yousaf M, et al. 2021 – First report of *Nigrospora oryzae* causing wilt in Summer Cypress (*Bassia scoparia*) in Pakistan. Plant Disease 105, 4167.

Aptroot A. 2012 – A world key to the species of *Anthracothecium* and *Pyrenula*. Lichenologist 44, 5.

Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B et al. 2015 – Fungal diversity notes 111–252–taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 75, 27–274.

Arx JA von. 1983 – *Mycosphaerella* and its anamorphs. In: Proceedings of Koninklijke Nederlandse Akademie van Wetenschappen C, Vol. 86, pp. 15–54.

Arx JA von, Muller E. 1954 – Die Gattungen der amerosporen Pyrenomyceten. Beiträge zur Kryptogamenflora der Schweiz 11, 1–434.

Baral HO, Galàn Màrquez R, Krisai-Greilhuber I, Matočec N, Palmer JT. 1999 – *Tatraea dumbirensis*, new records of a rare Leotialean discomycete in Europe. Osterreichische Zeitschrift fur Pilzkunde 8, 71–72.

Begum M, Hamza A, Tanny T, Das KC, et al. 2018 – First report of leaf spot disease in *Aloe vera* caused by *Nigrospora oryzae* in Bangladesh. Plant disease 102, 1461.

Bensch K, Braun U, Groenewald JZ, Crous PW. 2012 – The genus *Cladosporium.* Studies in Mycology 72, 1–401.

Bensch K, Groenewald JZ, Meijer M, Dijksterhuis J et al. 2018 – *Cladosporium* species in indoor environments. Studies in Mycology 89, 177–301.

Bernstein B, Zehr EI, Dean RA, Shabi E. 1995 – Characteristics of *Colletotrichum* from peach, apple, pecan, and other hosts. Plant Disease 79, 478–482.

Blanco-Dios JB. 2011 – *Asterophora salvaterrensis* (*Basidiomycota*, *Agaricales*), a new species from Galicia (Spain). Mycotaxon 118, 83–88.

Boonpragob K, Homchantara N, Coppins BJ, McCarthy PM, Wolseley PA. 1998 – An introduction to the lichen flora of Khao Yai National Park, Thailand. Botanical Journal of Scotland 50, 209–219.

Borrelli NP, Stancanelli S, Papone ML, et al. 2020 – Leaf spots of Calibrachoa caused by *Nigrospora oryzae*. Ornamental Horticulture 26, 591–597.

Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N et al. 2021 – Fungal diversity notes 1387–1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 111, 1–335.

Braun U. 2009 – New species, combinations and records of hyphomycetes. Schlechtendalia 19, 63–71.

Buaruang K, Boonpragob K, Mongkolsuk P, Sangvichien E, et al. 2017 – A new checklist of lichenized fungi occurring in Thailand. MycoKeys 23, 1.
Cáceres ME, Aptroot A, Nelsen MP, Lücking R. 2013 – *Pyrenula sanguinea* (lichenized *Ascomycota*: *Pyrenulaceae*), a new species with unique, trypethelioid ascomata and complex pigment chemistry. The Bryologist 116, 350–357.
Cai Q, Chen Z, He Z, Luo H, Yang Z. 2018 – *Lepiota venenata*, a new species related to toxic mushroom in China. Journal of Fungal Research 16, 63–69.
Campi M, Maubet Y, Grassi E, Niveiro N, Guzmán-Dávalos L. 2021 – First contribution to the genus *Gymnopilus* (*Agaricales*, *Strophariaceae*) in Paraguay. Rodriguesia 72, 1–13.
Cannon P, Cannon P, Buddie A, Bridge P et al. 2012 – *Lectera*, a new genus of the *Plectosphaerellaceae* for the legume pathogen *Volutella colletotrichoides*. MycoKeys 3, 23–36.
Cao XR, Xu XM, Che HY, West JS, Luo DQ. 2019 – Characteristics and distribution of *Colletotrichum* species in coffee plantations in Hainan, China. Plant Pathology 68, 1146–1156.
Cesati V, De Notaris G. 1863 – Schema di classificazione degle sferiacei italici aschigeri piu' o meno appartenenti al genere Sphaeria nell'antico significato attribuitoglide Persono. Commentario della Società Crittogamologica Italiana 1, 177–420.
Chaisiri C, Liu X, Lin Y, Fu Y, Zhu F, Luo C. 2021 – Phylogenetic and haplotype network analyses of *Diaporthe eres* species in China based on sequences of multiple loci. Biology 10, 179.
Chaiwan N, Jeewon R, Pem D, Jayawardena RS, et al. 2022 – New Species of *Discosia rhododendricola*, *Neopestalotiopsis rhododendricola* and new geographical record of *Diaporthe nobilis* from *Rhododendron* sp. Journal of Fungi 8, 907.
Chen X, Wang N, Yang MF, Li HX. 2019 – First report of *Nigrospora* leaf spot caused by *Nigrospora oryzae* on Watermelon in China. Plant disease 103, 1019.
Chen Q, Bakhshi M, Balci Y, Broders KD, et al. 2022 – Genera of phytopathogenic fungi: GOPHY 4. Studies in Mycology 101, 417–564.
Cherepanova NP, Cherepanov PS. 2003 – Ascomycefes on *Betulaceae* species on North-West of European Russia. Biological Communications 1, 20–25. (in Russian)
Chethana KWT, Niranjan M, Dong W, Samarakoon MC, et al. 2021a – AJOM new records and collections of fungi: 101–150. Asian Journal of Mycology 4, 113–260.
Chethana KW, Manawasinghe IS, Hurdeal VG, Bhunjun CS, et al. 2021b – What are fungal species and how to delineate them? Fungal Diversity 109, 1–25.
Clendenin I. 1896 – *Lasiodiplodia* E. & E., gen., In: Botanical Gazette 21, 92
Cohen L, Persky Y, Hadar R, Persky L, Hadar Y. 2002 – Biotechnological applications and potential of wood-degrading mushrooms of the genus *Pleurotus*. Applied Microbiology and Biotechnology 58, 582–594.
Conner KN, Hagan AK, Zhang L. 2013 – First report of *Corynespora cassiicola*-incited target spot on cotton in Alabama. Plant Disease 97, 1379.
Cooke MC. 1887 – New Australian fungi. Grevillea 16, 1–6.
Corda ACJ. 1831 – Die pilze deutschlands. In: Sturm J (ed), Deutschlands fora in Abbildungen nach der Natur mit Beschreibungen Sturm, Nürnberg vol. 3, Abt 12, pp 33–64.
Corner EJH. 1981 – The agaric genera *Lentinus*, *Panus* and *Pleurotus* with particular reference to Malaysian species?. Beihefte zur Nova Hedwigia 69, 1–1.
Cosoveanu A, Hernandez M, Iacomi-Vasilescu B, Zhang X, et al. 2016 – Fungi as endophytes in Chinese *Artemisia* spp.: juxtaposed elements of phylogeny, diversity and bioactivity. Mycosphere 7, 102–117.
Crous PW, Braun U. 2003 – *Mycosphaerella* and its anamorphs: 1. Names published in *Cercospora* and *Passalora*: Centraalbureau voor Schimmelcultures (CBS).
Crous PW, Slippers B, Wingfield MJ, Rheeder J, et al. 2006a – Phylogenetic lineages in the *Botryosphaeriaceae*. Studies in Mycology 55, 235–253.

Crous PW, Verkley GJ, Groenewald JZ. 2006b – *Eucalyptus* microfungi known from culture. 1. *Cladoriella* and *Fulvoflamma* genera nova, with notes on some other poorly known taxa. Studies in Mycology 68, 57–78.
Crous PW, Wingfield MJ, Guarro J, Cheewangkoon R, et al. 2013 – Fungal Planet description sheets: 154–213. Persoonia: Molecular Phylogeny and Evolution of Fungi 31, 188–256.
Crous PW, Wingfield MJ, Chooi YH, Gilchrist CL, et al. 2020 – Fungal planet description sheets: 1042–1111. Persoonia: Molecular Phylogeny and Evolution of Fungi 44, 301–459.
Crous PW, Boers J, Holdom D, Osieck ER, et al. 2022a – Fungal Planet description sheets: 1383–1435. Persoonia: Molecular Phylogeny and Evolution of Fungi 48, 261– 371.
Crous PW, Begoude BAD, Boers J, Braun U, et al. 2022b – New and interesting fungi. 5. Fungal Systematics and Evolution 10, 19–90.
Dai DQ, Phookamsak R, Wijayawardene NN, Li WJ, et al. 2017 – Bambusicolous fungi. Fungal Diversity 82, 1–105.
Damm U, Fourie PH, Crous PW. 2010 – *Coniochaeta* (*Lecythophora*), *Collophora* gen. nov. and *Phaeomoniella* species associated with wood necroses of *Prunus* trees. Persoonia - Molecular Phylogeny and Evolution of Fungi 24, 60–80.
Damm U, Cannon PF, Woudenberg JHC, Crous PW. 2012 – The *Colletotrichum acutatum* species complex. Studies in mycology 73, 37–113.
Daranagama DA, Thambugala KM, Campino B, Alves A, et al. 2016 – *Phaeobotryon negundinis* sp. nov. (*Botryosphaeriales*) from Russia. Mycosphere 7, 933–941.
Darge WA, Woldemariam SS. 2021 – *Botryosphaeria* tree fungal pathogens and their diversity. International Journal of Phytopathology 10, 49–56.
Dean R, Van Kan JA, Pretorius ZA, Hammond-Kosack KE, et al. 2012 – The top 10 fungal pathogens in molecular plant pathology. Molecular plant pathology 13, 414–430.
De Gruyter J, Woudenberg JHC, Aveskamp AA, Verkley GJM, et al. 2013 – Redisposition of Phoma-like anamorphs in *Pleosporales*. Studies in Mycology 75, 1–36.
De Silva NI, Hyde KD, Lumyong S, Phillips AJL, et al. 2022 – Morphology, phylogeny, host association and geography of fungi associated with plants of *Annonaceae*, *Apocynaceae* and *Magnoliaceae*. Mycosphere 13, 955–1076.
DeKrey DH, Klodd AE, Clark MD, Blanchette RA. 2022 – Grapevine trunk diseases of cold-hardy varieties grown in Northern Midwest vineyards coincide with canker fungi and winter injury. Plos one 17, e0269555.
Dennis RWG. 1952 – *Lepiota* and allied genera in Trinidad, British West Indies. Kew Bulletin 7, 459– 499.
Diao Y-Z, Zhang C, Liu F, Wang W-Z, et al. 2017 – *Colletotrichum* species causing anthracnose disease of chili in China. Persoonia-Molecular Phylogeny and Evolution of Fungi 38, 20–37.
Dissanayake AJ, Phillips AJL, Hyde KD, Yan JY, et al. 2017 – The current status of species in *Diaporthe*. Mycosphere 8, 1106–1156.
Dissanayake AJ, Bhunjun CS, Maharachchikumbura SSN, Liu JK. 2020 – Applied aspects of methods to infer phylogenetic relationships amongst fungi. Mycosphere 11, 2652–2676.
Dissanayake DMS, Adikaram NKB, Yakandawala DMD, Jayasinghe L. 2021 – Molecular phylogeny-based identification of *Colletotrichum endophytica* and *C. siamense* as causal agents of Avocado anthracnose in Sri Lanka. Ceylon Journal of Science 50, 449–458.
Ditmar LPF. 1809 – Duo genera fungorum. Neues Journal of Botany 3, 55–57.
Dixon JR. 1975 – *Chlorosplenium* and its segregates II. The genera *Chlorociboria* and *Chlorencoelia.* Mycotaxon I, 193–237.
Doilom M, Shuttleworth LA, Roux J, Chukeatirote E, Hyde KD. 2015 – *Botryosphaeriaceae* associated with *Tectona grandis* (teak) in Northern Thailand. Phytotaxa 233, 1–26.
Dugan FM, Glawe DA, Attanayake RN, Chen W. 2009 – The importance of reporting new host-fungus records for ornamental and regional crops. Plant Health Progress 10, 34.

Duplessis S, Cuomo CA, Lin YC, Aerts A, et al. 2011 – Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences 108, 9166–9171.
Ellis MB. 1971 – Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew.
Eken C, Spanbayev A, Tulegenova Z, Yechshzhanov T. 2016 – First report of *Nigrospora oryzae* on wheat in Kazakhstan. Plant disease 100, 861.
Fan XL, Hyde KD, Liu JK, Liang YM, Tian CM. 2015 – Multigene phylogeny and morphology reveal *Phaeobotryon rhois* sp. nov. (*Botryosphaeriales*, *Ascomycota*). Phytotaxa 205, 90–98.
Fan XL, Du Z, Liang YM, Tian CM. 2016 – *Melanconis* (*Melanconidaceae*) associated with *Betula* spp. in China. Mycological Progress 15, 1–9.
Farid K, Zafari D, Soleimani MJ, Bagherabadi S. 2020 – First report of *Nigrospora oryzae* causing brown leaf spot on *Mentha spicata*. Journal of Plant Pathology 102, 1281.
Farr DF, Rossman AY. 2023 – Fungal Databases, Systematic Mycology and Microbiology Laboratory, US National Fungus Collections, ARS, USDA, Beltsville, MD, USA. Accessed on February 17, 2023, http://nt.arsgrin.gov/fungaldatabases/)
Feng FS, Zhou GY, Li H. 2019 − First report of *Colletotrichum siamense* causing anthracnose on *Rosa chinensis* in China. Plant Disease 103, 1422.
Fernández FA, Huhndorf SM. 2004 – Neotropical pyrenomycetes: *Porosphaerella borinquensis* sp. nov. and its *Pseudobotrytis terrestris* anamorph. Fungal Diversity 17, 11–16.
Fernando D, Wijesundera R, Soysa P, De Silva, Nanayakkara DC. 2015 – Strong radical scavenging macrofungi from the dry zone forest reserves in Sri Lanka. Frontiers in Microbiology 1, 32–38.
Francisco CS, Ma X, Zwyssig MM. 2019 – Morphological changes in response to environmental stresses in the fungal plant pathogen *Zymoseptoria tritici*. Scientific Reports 9, 9642.
Friebes G, Jaklitsch WM, García S, Voglmayr H. 2016 – *Lopadostoma taeniosporum* revisited and a new species of *Coniochaeta*. Sydowia 68, 87–97.
Fries EM. 1823 – *Systema Mycologicum*, Volume 2, Sumtibus Ernesti Mauritii: Gryphiswald, Germany, 423–424.
Fries EM. 1849 – Summa vegetabilium scandinaviae, vol 2., Typographia Academica, Uppsala, pp 259–572
Fulmer AM, Walls JT, Dutta B, Parkunan V, et al. 2012 – First report of target spot caused by *Corynespora cassiicola* on cotton in Georgia. Plant disease 96, 1066.
García D, Stchigel AM, Cano J, Calduch M, et al. 2006 – Molecular phylogeny of *Coniochaetales*. Mycological Research 110, 1271–1289.
Gawas P, Bhat DJ. 2005 – *Vamsapriya indica* gen. et sp. nov., a bambusicolous, synnematous fungus from India. Mycotaxon 94, 149–154.
Grassi EM, Romano GM, Schenone NF. 2016 – Macrohongs presentes en un area de manejo regenerativo de bosque de Mata Atlantica (Misiones, Agentina). Boletin de la Sociedad Argentina de Botanica 51, 223–233
Gratz D. 2006 – Distribution maps of plant diseases. Indian Phytopathology 59, 475–481.
Güssow HT. 1906 – Über eine neue Krankheit an Gurken in England (*Corynespora* Mazei, Güssow gen. et spec. nov.). Zeitschrift für Pflanzenkrankheiten 16, 10–13.
Guzmán-Dávalos L. 1996 – New records of the genus *Gymnopilus* (*Agaricales*, *Cortinariaceae*) from Mexico. Mycotaxon 59, 61–78.
Guzmán-Dávalos L. 2003 – Type studies of *Gymnopilus* (*Agaricales*) I. Mycotaxon 86, 395–423.
Guzmán-Dávalos L, Mueller GM, Cifuentes J, Miller AN, Santerre A. 2003 – Traditional infrageneric classification of *Gymnopilus* is not supported by ribosomal DNA sequence data. Mycologia 95, 1204–1214.
Han JG, Hosoya T, Sung GH, Shin HD. 2014 – Phylogenetic reassessment of *Hyaloscyphaceae* sensu lato (*Helotiales*, *Leotiomycetes*) based on multigene analyses. Fungal Biology 2, 150–67.

Han S, Yu S, Zhu T, Li S, et al. 2021 – *Nigrospora oryzae* causing Black Leaf Spot disease of *Hibiscus mutabilis* in China. Plant disease 105, 169.
Harrington AH, Olmo-Ruiz M, U'Ren JM, Garcia K, Arnold AE. 2019 – *Coniochaeta endophytica* sp. nov., a foliar endophyte associated with healthy photosynthetic tissue of *Platycladus orientalis* (*Cupressaceae*). Plant and Fungal Systematics 64, 65–79.
Hashimoto A, Hirayama K, Takahashi H, Matsumura M, et al. 2018 – Resolving the *Lophiostoma bipolare* complex: generic delimitations within *Lophiostomataceae*. Studies in mycology 90, 161–189.
He MQ, Zhao RL, Hyde KD, Begerow D, et al. 2019a – Notes, outline and divergence times of Basidiomycota. Fungal Diversity 99, 105–367.
He BY, Cernava T, He HD, et al. 2019b – First report of leaf spots on *Photinia serrulata* caused by *Nigrospora oryzae* in China. Plant disease 103, 2480.
Hernández-Restrepo M, Gené J, Mena-Portales J, Cano J, et al. 2014 – New species of *Cordana* and epitypification of the genus. Mycologia 106, 723–734.
Hesler LR. 1969 – North American species of *Gymnopilus*. Mycological Memoir no. 3. Hafner, New York, 1–117.
Heuchert B, Braun U, Schubert K. 2005 – Morpho-taxonomic revision of fungicolous *Cladosporium* species (hyphomycetes). Schlechtendalia 13, 1–78.
Hibbett DS, Vilgalys R. 1993 – Phylogenetic relationships of the *Basidiomycete* genus *Lentinus* inferred from molecular and morphological characters. Systematic Botany 18, 409–443.
Holec J. 2005 – The genus *Gymnopilus* (*Fungi*, *Agaricales*) in the Czech Republic with respect to collections from other European countries. Acta Musei Nationalis Pragae, Series B – Historia Naturalis 61, 1–52.
Homma H, Shinoyama H, Tanibe M, Amachi S, et al. 2006 – Fruiting-body formation, cultivation properties, and host specificity of a fungicolous fungus, *Asterophora lycoperdoides*. Mycoscience 47, 269–276.
Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN, et al. 2020a – Refined families of *Dothideomycetes*: *Dothideomycetidae* and *Pleosporomycetidae*. Mycosphere 11, 1553–2107.
Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN, et al. 2020b – Refined families of *Dothideomycetes*: Orders and families *incertae sedis* in *Dothideomycetes*. Fungal Diversity 24, 1–302.
Hou Y-J, Ge Z-W. 2020 – New species of *Echinoderma* and *Lepiota* (*Agaricaceae*) from China. Phytotaxa 447, 221–236.
Huang C, Wang Y. 2011 – New records of endophytic fungi associated with the *Araucariaceae* in Taiwan. Collection and Research 24, 87–95.
Hughes SJ. 1955 – Microfungi. I. *Cordana*, *Brachysporium*, *Phragmocephala*. Canadian Journal of Botany 33, 259–268.
Huhndorf SM, Miller AN. 2011 – A molecular re-appraisal of taxa in the *Sordariomycetidae* and a new species of *Rimaconus* from New Zealand. Studies in Mycology 68, 203–210.
Hyde KD. 1991 – *Helicascus kanaloanus*, *Helicascus nypae* sp. nov. and *Salsuginea ramicola* gen. et sp. nov. from intertidal mangrove wood. Botanica Marina 34, 311–318.
Hyde KD. 1995 – The genus *Massarina*, with a description of *M. eburnea* and an annotated list of *Massarina* names. Mycological Research 3, 291–296.
Hyde KD, Cai L, McKenzie EHC, Yang YL, Zhang JZ, Prihastuti H. 2009 – *Colletotrichum*: a catalogue of confusion. Fungal Diversity 39, 1–17.
Hyde KD, Jones EBG, Liu J-K, Ariyawansa H, et al. 2013 – Families of *Dothideomycetes*. Fungal Diversity 63, 1–313.
Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA, et al. 2014 – One stop shop: backbones trees for important phytopathogenic genera: I (2014). Fungal Diversity 67, 21–125.
Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A, et al. 2017 – Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species. Fungal Diversity 87, 1–235.

Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ, et al. 2019 – Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 96, 1–242.
Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ, et al. 2020a – Refined families of *Sordariomycetes*. Mycosphere 11, 305–1059.
Hyde KD, Jeewon R, Chen YJ, Bhunjun CS, et al. 2020b – The numbers of fungi: Is the descriptive curve flattening? Fungal Diversity 103, 219–271.
Hyde K, de Silva NI, Jeewon R, Bhat DJ, et al. 2020c – AJOM new records and collections of fungi: 1–100. Asian Journal of Mycology 3, 22–294.
Hyde KD, Dong Y, Phookamsak R, Jeewon R, et al. 2020d – Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100, 5–277.
Ilyukhin E, Ellouze W. 2023 – First report of *Phaeobotryon negundinis* associated with twig and branch dieback of *Malus domestica* trees in southern Ontario, Canada and worldwide. Journal of Plant Pathology 105, 355–356.
Index Fungorum. 2023 – http://www.indexfungorum.org/Names/Names.asp. (Accessed on December 4, 2022)
Ingle KK, Uppadhyay V, Nayaka S, Trivedi S, et al. 2018 – New records and an updated key of *Pyrenula* from India. Cryptogam Biodiversity and Assessment, 37–46.
Jaihan P, Sangdee K, Sangdee A. 2021 – Combined multiple genes phylogenetic analysis and morphological characteristic description of entomopathogenic fungi infecting *Cicada* nymph from northeast of Thailand. Biologia 76, 1635–1650.
Jaklitsch WM, Voglmayr H. 2020 – The genus *Melanconis* (*Diaporthales*). MycoKeys 63, 69–117.
James RS, Ray J, Tan YP, Shivas RG. 2014 – *Colletotrichum siamense*, *C. theobromicola* and *C. queenslandicum* from several plant species and the identification of *C. asianum* in the Northern Territory, Australia. Australasian Plant Disease Notes 9, 1–6.
Jayasiri SC, Hyde KD, Jones EBG, McKenzie EH, et al. 2019 – Diversity, morphology and molecular phylogeny of *Dothideomycetes* on decaying wild seed pods and fruits. Mycosphere 10, 1–186.
Jayawardena RS, Hyde KD, Damm U, Cai L, et al. 2016 – Notes on currently accepted species of *Colletotrichum*. Mycosphere 7, 1192–1260.
Jayawardena RS, Hyde KD, Wang S, Sun YR, et al. 2023 – Fungal diversity notes 1512–1610: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 117, 1–272.
Jiang W, Yang G, Zhang C, Fu C. 2011 – Species composition and molecular analysis of symbiotic fungi in roots of *Changnienia amoena* (*Orchidaceae*). African Journal of Microbiology Research 5, 222–228.
Johnston P, Park D, Baral HO, Galan R, et al. 2014 – The phylogenetic relationships of *Torrendiella* and *Hymenotorrendiella* gen. nov. within the *Leotiomycetes*. Phytotaxa 177, 1–25.
Jones EBG, Pang KL, Abdel-Wahab MA, Scholz B, et al. 2019 – An online resource for marine fungi. Fungal Diversity 96, 347–433.
Jones EBG, Devadatha B, Abdel-Wahab MA, Dayarathne MC, et al. 2020 – Phylogeny of new marine *Dothideomycetes* and *Sordariomycetes* from mangroves and deep-sea sediments. Botanica Marina 63, 155–181.
Joshi S, Upreti DK, Hur JS. 2018 – Key to the lichen families *Pyrenulaceae* and *Trypetheliaceae* in Vietnam, with eight new records. Mycotaxon 132, 957–969.
Kabtani J, Militello M, Ranque S. 2022 – *Coniochaeta massiliensis* sp. nov. isolated from a clinical sample. Journal of Fungi 8, 999.
Kalati TH, Jahani M, Zare R, Mirzaee MR. 2014 – First report of *Nigrospora* leaf spot on *Pennisetum americanum* in Iran. Journal of Plant Pathology 96, 606.

Karunarathna SC, Mortimer PE, Chen J, Li GJ, et al. 2016 – Correct names of two cultivated mushrooms from the genus *Pleurotus* in China. Phytotaxa 260, 36–46.
Kee YJ, Hafifi ABM, Huda-Shakirah AR, et al. 2019 – First report of reddish-brown spot disease of red-fleshed dragon fruit (*Hylocereus polyrhizus*) caused by *Nigrospora lacticolonia* and *Nigrospora sphaericain* Malaysia. Crop Protection 122, 165–170.
Keinath AP. 2021 – Differences in susceptibility to *Phomopsis* blight of seven eggplant cultivars with different fruit types. Plant Health Progress 23, 57–64.
Kepler RM, Humber RA, Bischoff JF, et al. 2014 – Clarification of generic and species boundaries for *Metarhizium* and related fungi through multigene phylogenetics. Mycologia 106, 811–829.
Kgatle MG, Truter M, Ramusi TM, Flett B, Aveling TAS. 2018 – *Alternaria alternata*, the causal agent of leaf blight of sunflower in South Africa. European Journal of Plant Pathology 151, 677–688.
Khodke SW, Khodke S. 2009 – A new leaf spot of *Ficus religiosa* by *Nigrospora oryzae*. Indian Phytopathology 62, 274.
Kim CS, Jo JW, Kwag YN, Sung GH, et al. 2015 – Mushroom flora of Ulleung-gun and a newly recorded *Bovista* species in the Republic of Korea. Mycobiology 43, 239–257.
Kim HS, Adhikari M, Yadav DR, Kim SW, et al. 2016 – First report of *Metacordyceps chlamydosporia* (*Cordyceps chlamydosporia*) isolated from soil in Korea. The Korean Journal of Mycology 44, 48–50.
Ko Y, Liu CW, Chen SS, Chiu KY, et al. 2011 – First report of gummosis disease of Japanese apricot caused by *Botryosphaeria dothidea* in Taiwan. Plant Disease 95, 77.
Koné D, Ji P, Fonsah GE, Csinos AS. 2008 – First report of black leaf spot of banana caused by *Deightoniella torulosa* in Georgia. Plant Disease 92, 1470.
Konta S, Hongsanan S, Eungwanichayapant PD, Liu JK, et al. 2017 – *Leptosporella* (*Leptosporellaceae* fam. nov.) and *Linocarpon* and *Neolinocarpon* (*Linocarpaceae* fam. nov.) are accommodated in *Chaetosphaeriales*. Mycosphere 8, 1943–1974.
Konta S, Maharachchikumbura SSN, Senanayake IC, McKenzie EHC, et al. 2020 – A new genus *Allodiatrype*, five new species and a new host record of diatrypaceous fungi from palms (Arecaceae). Mycosphere 11, 239–268.
Kumar S, Singh R. 2016 – Biodiversity, distribution and taxonomy of conidial fungus *Corynespora* (*Corynesporascaceae*) associated with *Malvaceae*. Journal of Biodiversity & Endangered Species 20, 1–3.
Kumar S, Singh R. 2021 – Global diversity and distribution of distoseptosporic micromycete *Corynespora* Güssow (*Corynesporascaceae*): An updated checklist with current status. Studies in Fungi 6, 1–63.
Kuo KC, Kao CW, Leu LS. 1989 – Grape cluster rot induced by *Botryosphaeria ribis*. Plant Protection Bulletin (Taiwan) 31, 238–247.
Kwon JH, Kang SW, Kim JS, Park CS. 2001 – First report of *Corynespora* leaf spot in pepper caused by *Corynespora cassicola* in Korea. The Plant Pathology Journal 17, 180–183.
Lee S, Groenewald JZ, Crous PW. 2004 – Phylogenetic reassessment of the coelomycete genus *Harknessia* and its teleomorph *Wuestneia* (*Diaporthales*), and the introduction of *Apoharknessia* gen. nov. Studies in Mycology 50, 235–252.
Lechner BE, Wright JE, Alberto E. 2005 – The genus *Pleurotus* in Argentina: mating tests. Sydowia 57, 233–245.
Lechner BE, Wright JE, Popoff O. 2006 – New taxa and new records for Argentina of fungi from Iguazú National Park, Misiones. Fungal Diversity 21, 131–139.
Li D, Chen Y, Pan Q, Tao M, Zhang W. 2014 – A new Eudesmane Sesquiterpene from *Nigrospora oryzae*, an endophytic fungus of *Aquilaria sinensis*. Records of Natural Products 8, 330–333.
Li WJ, Liu JK, Bhat DJ, Camporesi E, et al. 2015 – Molecular phylogenetic analysis reveals two new species of *Discosia* from Italy. Phytotaxa 203, 37–46.

Li L, Pan H, Chen MY, Zhang SJ, Zhong CH. 2017 – First report of *Nigrospora oryzae* causing Brown/Black Spot disease of Kiwifruit in China. Plant disease 102, 243.
Li Q, Bu J, Shu J, Yu Z, et al. 2019 – *Colletotrichum* species associated with mango in southern China. Scientific Reports 9, 1–10.
Li X, Wu HX, Li J, Chen H, et al. 2020 – The insights into the evolutionary history of *Translucidithyrium*: based on a newly-discovered species. MycoKeys 76, 1.
Liang JL, Yu F, Lu JK, Wang SK, Song J. 2018 – Morphological and molecular evidence for two new species in *Lepiota* from China. Mycologia 110, 494– 501.
Liew EC, Aptroot A, Hyde KD. 2002 – An evaluation of the monophyly of *Massarina* based on ribosomal DNA sequences. Mycologia 94, 803–813.
Lindau G. 1907 – Dr. L. Rabenhorst's Kryptogamen-Flora von Deutschland, Oesterreich und der Schweiz. Zweite Auflage. Erster Band: Die Pilze Deutschlands, Österreichs und der Schweiz. VIII. Abteilung: Fungi imperfecti: Hyphomycetes (erste Hälfte), Mucedinaceae, Dematiaceae (Phaeosporae und Phaeodidymae) Leipzig, 1–852.
Liu J-K, Phookamsak R, Doilom M, Wikee S, et al. 2012 – Towards a natural classification of *Botryosphaeriales*. Fungal Diversity 57, 149–210.
Liu F, Cai L, Crous PW, Damm U. 2014 – The *Colletotrichum gigasporum* species complex. Persoonia-Molecular Phylogeny and Evolution of Fungi 33, 83–97.
Liu JK, Hyde KD, Jeewon R, Phillips AJ, et al. 2017 – Ranking higher taxa using divergence times: a case study in Dothideomycetes. Fungal Diversity 84, 75–99.
Liu F, Bonthond G, Groenewald JZ, Cai L, et al. 2019 – Sporocadaceae, a family of coelomycetous fungi with appendage-bearing conidia. Studies in Mycology 92, 287–415.
Liu LM, Zhao KH, Zhao Y, et al. 2021 – *Nigrospora oryzae* causing panicle branch rot disease on *Oryza sativa* (Rice). Plant disease 105, 169.
Liu Z, Zhou S, Qi L, et al. 2022 – First report of *Nigrospora oryzae* causing leaf spot on Ginger in China. Plant disease 106, 355.
Logesh AR, Kalaiselvam M, Upreti DK, Nayaka S, et al. 2013 – Mangroves - An abode for unique lichens. Coastal Ecosystems of India, special publication. Annamalai University: Parangipettai 39–44.
Lu X, Xiao C, Zhou K, Fu L, Shen D, Dou D. 2023 – First report of *Nigrospora oryzae* causing Leaf Spot on Yam in China. Plant disease. https://doi.org/10.1094/pdis-11-22-2545-pdn
Lumyong P, Photita W, McKenzie EHC, Hyde KD, Lumyong S. 2003 – Saprobic fungi on dead wild banana. Mycotaxon 85, 345–346.
Luo MY, Jiang YL. 2022 – First report of Leaf Spot on Kidney Bean caused by *Nigrospora oryzae* in China. Plant disease 106, 1064.
Luo Z-L, Hyde KD, Liu J-K (Jack), Maharachchikumbura SS, et al. 2019 – Freshwater Sordariomycetes. Fungal Diversity 99, 451–660.
Mahadevakumar S, Janardhana GR. 2016 – Leaf blight and fruit rot disease of brinjal caused by *Diaporthe vexans* (*Phomopsis vexans*) in six agro-ecological regions of South West India. Plant Pathology & Quarantine 6, 5–12.
Makhija U, Adawadkar B. 2001 – Contributions to the lichen flora of the Lakshadweep (Laccadive) Islands, India. Lichenologist 33, 507–512.
Manamgoda DS, Udayanga D, Cai L, Chukeatirote E, Hyde KD. 2013 – Endophytic *Colletotrichum* from tropical grasses with a new species *C. endophytica*. Fungal Diversity 61, 107–115.
Manawasinghe IS, Calabon MS, Jones EBG, Zhang YX, et al. 2022 – Mycosphere notes 345–386. Mycosphere 13, 454–557.
Mandeel QA, Al-Laith AA, Mohamad SA. 2005 – Cultivation of oyster mushrooms (*Pleurotus* spp.) on various lignocellulosic wastes. World Journal of Microbiology and Biotechnology 21, 601–607.
Marin-Felix Y, Hernández-Restrepo M, Wingfield MJ, Akulov A, et al. 2019 – Genera of phytopathogenic fungi: GOPHY 2. Studies in Mycology 92, 47–133.

Mayorquin JS, Eskalen A, Downer AJ, Liu A. 2012 – First report of multiple species of the *Botryosphaeriaceae* causing Bot Canker disease of Indian Laurel-Leaf Fig in California. Plant Disease 96, 459.
Mehrabi M, Asgari B, Zare R. 2022 – Novel endophytic species of *Coniochaeta* and *Preussia* from the botanical tribe *Triticeae* in Iran. Nova Hedwigia 114, 141–169.
Mei SS, Wang ZY, Zhang J, Rong W. 2019 – First report of leaf blight on *Stenotaphrum secundatum* caused by *Nigrospora osmanthi* in China. Plant Disease 103, 1783.
Mensin S, Soytong K, McGovern RJ, To-Anun C. 2012 – Selection of efficient nematophagous fungi against root-knot nematodes in the highland cultivated area. Journal of Agricultural Technology 8, 2259–2272.
Meredith DS. 1962 – Some components of the air-spora in Jamaican banana plantations. Annals of Applied Biology 50, 577–594.
Miriyagalla SD, Manamgoda DS, Udayanga D. 2022 – Molecular characterization and cultivation of edible wild mushrooms, *Lentinus sajor-caju*, *L. squarrosulus* and *Pleurotus tuber-regium* from Sri Lanka. Current Research in Environmental & Applied Mycology (Journal of Fungal Biology) 12, 28–43.
Mongkolsamrit S, Khonsanit A, Thanakitpipattana D, Tasanathai K., et al. 2020 – Revisiting *Metarhizium* and the description of new species from Thailand. Studies in Mycology 95, 171–251.
Mortimer E, Xu JC, Hyde KD, Chomnunti P. 2015 – Molecular phylogenetic analysis reveals two new species of *Discosia* from Italy. Phytotaxa 203, 37–46.
Mortimer PE, Jeewon R, Xu JC, Lumyong S, Wanasinghe DN. 2021 – Morpho-phylo taxonomy of novel dothideomycetous fungi associated with dead woody twigs in Yunnan Province, China. Frontiers in Microbiology 12, 654683.
Müller E, Samuels GJ. 1982 – Anamorphs of pyrenomycetous ascomycetes II. *Porosphaerella* gen. nov. and its *Cordana* anamorph. Sydowia 35, 150–154.
Mukerji KG, Tewari JP, Rai JN. 1968 – *Volutella lini* sp.nov. from India. Transactions of the British Mycological Society 51, 337–339.
Nag Raj TR. 1993 – Coelomycetous anamorphs with appendage-bearing conidia. Mycologue Publications, Waterloo, Canada, pp 1101.
Nees von Esenbeck CG. 1816 – *Das system der Pilze und Schwämme*. Würzburg, Germany, 1–334.
Ni HF, Liou RF, Hung TH, Chen RS, et al. 2010 – First report of fruit rot disease of mango caused by *Botryosphaeria dothidea* and *Neofusicoccum mangiferae* in Taiwan. Plant Disease 94, 1–128.
Nishikawa J and Nakashima C. 2013 – Taxonomic characterization and experimental host ranges of four newly recorded species of *Alternaria* from Japan. Journal of Phytopathology 161, 604–616.
Nitschke T. 1870 – Pyrenomycetes germanici. Verlag von Eduard Trewendt, Breslau 1, 1–160.
Nonaka K, Ōmura S, Masuma R, Kaifuchi S, et al. 2013 – Three new *Pochonia* taxa (*Clavicipitaceae*) from soils in Japan. Mycologia 105, 1202–1218.
Okane I, Nakagiri A, Ito T. 1998 – Endophytic fungi in leaves of ericaceous plants. Canadian Journal of Botany 76, 657–663.
Ola ARB, Lapailaka T, Wogo HE, Henuk JBD, et al. 2021 – Bioactive secondary metabolites from the mangrove endophytic fungi *Nigrospora oryzae*. Indonesian Journal of Chemistry 21, 1016–1022.
Ordynets O, Akulov O, Helleman S. 2013 – First data about fungal diversity of the "Trekhizbenskyi Step" division of the Luhansk Nature Reserve. Chernomorski Botanical Journal 9, 57–83.
Pangging M, Nguyen TTT, Lee HB. 2021 – Nine new records of ascomycetes from different niches in Korea. The Korean Journal of Mycology 49, 259–283.

Pärtel K, Baral HO, Tamm H, Põldmaa. 2017 – Evidence for the polyphyly of *Encoelia* and *Encoelioideae* with reconsideration of respective families in *Leotiomycetes*. Fungal Diversity 82, 183–219.

Pavlic D, Wingfield MJ, Barber P, Slippers B, Hardy GESJ, Burgess TI. 2008 – Seven new species of the *Botryosphaeriaceae* from baobab and other native trees in Western Australia. Mycologia 100, 851–866.

Pawar VH, Patel MK. 1957 – *Phomopsis* blight and fruit rot of brinjal. Indian Phytopathology 10, 115–120.

Pawlik A, Janusz G, Koszerny J, Małek W, Rogalski J. 2012 – Genetic diversity of the edible mushroom *Pleurotus* sp. by amplified fragment length polymorphism. Current Microbiology 65, 438–445.

Perić B. 2013 – Première récolte monténégrine d'une espèce rare en Europe: *Tatraea dumbirensis*. Mycologia Montenegrina 16, 49–59.

Phetphan C, Supakitthanakorn S, Phuakjaiphaeo C, Pipattanapuckdee A, et al. 2023 – Biological and molecular characterization of *Lasiodiplodia theobromae* causing dieback disease of strawberry in Thailand. Journal of Phytopathology. https://doi.org/10.1111/jph.13181

Phillips AJL, Alves A, Pennycook SR, Johnston PR, et al. 2008 – Resolving the phylogenetic and taxonomic status of dark-spored teleomorph genera in the *Botryosphaeriaceae*. Persoonia: Molecular Phylogeny and Evolution of Fungi 21, 29–55.

Phillips AJL, Alves A, Abdollahzadeh J, Slippers B, et al. 2013 – The *Botryosphaeriaceae*: genera and species known from culture. Studies in Mycology 76, 51–167.

Phillips AJL, Hyde KD, Alves A, Liu JK (Jack). 2019 – Families in *Botryosphaeriales*: a phylogenetic, morphological and evolutionary perspective. Fungal Diversity 94, 1–22.

Phookamsak R, Boonmee S, Norphanphoun C, Wanasinghe D, et al. 2016 – *Schizothyriaceae*. Mycosphere 7, 154–189.

Photita W, Lumyong S, Lumyong P, Ho WH, McKenzie EH, Hyde KD. 2001 – Fungi on *Musa acuminata* in Hong Kong. Fungal Diversity 6, 99–106.

Phukhamsakda C, Jeewon R, McKenzie EH, Xu JC. 2019 – Morphology and phylogeny of *Phaeoseptum mali* sp. nov.(*Phaeoseptaceae*, *Pleosporales*) on bark of *Malus halliana*. Asian Journal of Mycology 2, 118–128.

Phukhamsakda C, Mckenzie E, Phillips A, Jones E, et al. 2020 – Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. Fungal diversity 120, 1–203.

Pipattanapuckdee A, Boonyakait D, Tiyayon C, Seehanam P, Ruangwong OU. 2019 – *Lasiodiplodia pseudotheobromae* causes postharvest fruit rot of longan in Thailand. Australasian Plant Disease Notes 14, 1–7.

Plantix. 2023 – Phomopsis blight. Accessed at: https://plantix.net/en/library/plant-diseases/100276/phomopsis-blight- on 16th May 2023.

Preuss CGT. 1851 – Übersicht untersuchter Pilze, besonders aus der Umgegend von Hoyerswerda. Linnaea 24, 99–153.

Prihastuti H, Cai L, Chan H, McKenzie EHC, Hyde KD. 2009 – Characterization of *Colletotrichum* species associated with coffee berries in northern Thailand. Fungal Diversity 39, 89–109.

Promputtha I, Lumyong S, Dhanasekaran V, McKenzie EH, et al. 2007 – A phylogenetic evaluation of whether endophytes become saprotrophs at host senescence. Microbial Ecology 53, 579–590.

Qiu C, Zhu W, Niu T, Liu Z. 2022 – *Nigrospora oryzae* causing Leaf Spot on Asiatic Dayflower in Chongqing, China. Plant disease 106, 763.

Quaedvlieg W, Binder M, Groenewald JZ, Summerell BA, et al. 2014 – Introducing the consolidated species concept to resolve species in the *Teratosphaeriaceae*. Persoonia: Molecular Phylogeny and Evolution of Fungi 33, 1–40.

Raja H, Schoch C, Hustad V, Shearer C, Miller A. 2011 – Testing the phylogenetic utility of MCM7 in the Ascomycota. MycoKeys 1, 63–94.

Rashmi M, Kushveer J, Sarma V. 2019 – A worldwide list of endophytic fungi with notes on ecology and diversity. Mycosphere 10, 798–1079.
Raspé O, Vadthanarat S, De Kesel A, Degreef J, Hyde KD, Lumyong S. 2016 – *Pulveroboletus fragrans*, a new *Boletaceae* species from northern Thailand, with a remarkable aromatic odor. Mycological Progress 15, 38.
Rathnayaka AR, Chethana KWT, Phillips AJ, Liu JK, et al. 2021 – First report of *Botryosphaeriaceae* species on *Camellia sinensis* from Taiwan with a global checklist of *Botryosphaeriaceae* species on this host. Chiang Mai Journal of Sciences 48, 1199–1223.
Rathod DP, Dar MA, Gade AK, Rai MK, Baba G. 2014 – Griseofulvin producing endophytic *Nigrospora oryzae* from Indian *Emblica officinalis* Gaertn: a new report. Austin Journal of Biotechnology and Bioengineering 1, 1–5.
Raza M, Zhang ZF, Hyde KD, Diao YZ, Cai L. 2019 – Culturable plant pathogenic fungi associated with sugarcane in southern China. Fungal diversity 99, 1–104.
Rebriev YA, Rusanov VA, Bulgakov TS, Svetasheva TY, Zmitrovich IV, Popov ES. 2012 – Mycobiota of the arid territories of the South-West of Russia. Publishing House of Southern Federal University, Rostov-on-Don, 1–86 p. (in Russian)
Riedl H, von Ershad D. 1977 – Mykologische Ergebnisse einer Sammelreise in den Iran im Frühjahr 1974. – I. Sydowia 29(1–6), 155–169.
Rosado AW, Custodio FA, Pinho DB, Ferreira APS, Pereira OL. 2019 – *Cladosporium* species associated with disease symptoms on *Passifora edulis* and other crops in Brazil, with descriptions of two new species. Phytotaxa 409, 239–260.
Saccardo PA. 1877 – Fungi Italici autographice delineati a Prof. P.A. Saccardo. Michelia 1, 73–100.
Saccardo PA. 1880 – Conspectus generum fungorum Italiae inferorium. Michelia 2, 1–38.
Saccardo PA. 1882 – Sylloge Pyrenomycetum, Vol. II. Sylloge Fungorum 1, 1–768.
Saccardo PA. 1913 – Sylloge Fungorum (Saccardo PA & Trotter A eds.). Padova 22.
Salaemae N, Srilaong V, Pongprasert N, Boonyaritthongchai P, et al. 2022 – Alterations in morphological and biochemical properties in 'Namwa' banana associated with freckles caused by *Lasiodiplodia theobromae* in Thailand. Physiological and Molecular Plant Pathology 117, 101783.
Salazar SC, De García MC. 2005 – Aislamiento de hongos endofitos en rosa (*Rosa hybrida*) en Bogotá, Colombia. Revista Iberoamericana de Micología 22, 99–101.
Salunkhe VN, Gawande SP, Nagrale DT, Hiremani NS, et al. 2019 – First report of *Corynespora* leaf spot of cotton caused by *Corynespora cassiicola* in central India. Plant Disease 103, 1785.
Salvatore MM, Andolfi A, Nicoletti R. 2020 – The thin line between pathogenicity and endophytism: The case of *Lasiodiplodia theobromae*. Agriculture 10, 488.
Samarakoon MC, Gafforov Y, Liu N, Maharachchikumbura SS, et al. 2018 – Combined multi-gene backbone tree for the genus *Coniochaeta* with two new species from Uzbekistan. Phytotaxa 336, 43–58.
Sangchote S, Pongpisutta R. 1998 – Fruit rots of mangosteen and their control. In: Australian Centre for International Agricultural Research (ACIAR) Proceedings, Vol. 81, 81–86.
Schroers HJ. 2001 – A monograph of *Bionectria* (*Ascomycota*, *Hypocreales*, *Bionectriaceae*) and its *Clonostachys* anamorphs. Studies in Mycology 46, 1–211.
Scomparin A, Seguin M, Roeckel-Drevet P, Pujade-Renaud V. 2012 – First characterization of endophytic *Corynespora cassiicola* isolates with variant cassiicolin genes recovered from rubber. Fungal Diversity 54, 87–99.
Senanayake IC, Rathnayaka AR, Marasinghe DS, Calabon MS, et al. 2020 – Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere 11, 2678–2754.

Senwanna C, Phookamsak R, Doilom M, Hyde KD, Cheewangkoon R. 2017 – Novel taxa of *Diatrypaceae* from Para rubber (*Hevea brasiliensis*) in northern Thailand: introducing a novel genus *Allocryptovalsa*. Mycosphere 8, 1835–1855.

Senwanna C, Hongsanan S, Hyde KD, Cheewangkoon R, Konta S, Wang Y. 2020 – First report of the sexual morph of *Pseudofusicoccum adansoniae* on Para rubber. Cryptogamie, Mycologie 41, 133–146.

Sharma G, Shenoy BD. 2014 – *Colletotrichum fructicola* and *C. siamense* are involved in chilli anthracnose in India. Archives of Phytopathology and Plant Protection 47, 1179–1194.

Sharma M, Kulshrestha S. 2015 – *Colletotrichum gloeosporioides*: an anthracnose causing pathogen of fruits and vegetables. Biosciences Biotechnology Research Asia 12, 1233–1246.

Sharma R, Rajak RC, Pandey AK. 2007 – New Indian record of a rare fungus: *Asterophora lycoperdoides*. Biodiversity 8, 21–26.

Sharma P, Meena PD, Chauhan JS. 2013 – First report of *Nigrospora oryzae* (Berk. & Broome) Petch causing Stem Blight on *Brassica juncea* in India. Journal of Phytopathology 161, 439–441.

Shoemaker RA, Babcock CE, Irwin JAG. 1991 – *Massarina walkeri* nov. sp., the teleomorph of *Acrocalymma medicaginis* from *Medicago sativa* contrasted with *Leptosphaeria pratensis, L. weimeri* n. sp., and *L. viridella*. Canadian Journal of Botany 69, 569–573.

Si HL, Su YM, Zheng XX, Ding MY, et al. 2021 – Phylogenetic and morphological analyses of *Coniochaeta* isolates recovered from Inner Mongolia and Yunnan revealed three new endolichenic fungal species. MycoKeys 83, 105–121.

Simmons EG. 2007 – *Alternaria. An identification manual. CBS Biodiversity Series 6*. CBS Fungal Biodiversity Centre, Utrecht, The Netherlands.

Sinadsky YV. 1973 – Birch. its pests and diseases. Science, Moscow, 1–215. (in Russian)

Sivanesan A. 1996 – *Corynesporasca caryotae* gen. et sp. nov. with a *Corynespora* anamorph and the family *Corynesporascaceae*. Mycological Research 100, 783–788.

Slippers B, Crous PW, Denman S, Coutinho TA, et al. 2004 – Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria dothidea*. Mycologia 96, 83–101.

Slippers B, Smit WA, Crous PW, Coutinho TA, et al. 2007 – Taxonomy, phylogeny and identification of *Botryosphaeriaceae* associated with pome and stone fruit trees in South Africa and other regions of the world. Plant Pathology 56, 128–139.

Slippers B, Boissin E, Phillips AJL, Groenewald JZ, et al. 2013 – Phylogenetic lineages in the *Botryosphaeriales*: A systematic and evolutionary framework. Studies in Mycology 76, 31–49.

Sogonov MV, Castlebury LA, Rossman AY, Mejia LC, White JF. 2008 – Leaf-inhabiting genera of the *Gnomoniaceae, Diaporthales*. Studies in Mycology 62, 1–79.

Species Fungorum 2023 – Available from https://wwwspeciesfungorumorg/Names/Namesasp (Accessed on August 1, 2022).

Stauber L, Prospero S, Croll D. 2020 – Comparative genomics analyses of lifestyle transitions at the origin of an invasive fungal pathogen in the genus *Cryphonectria*. Msphere 5, e00737-20.

Sun X, Guo LD, Hyde KD. 2011 – Community composition of endophytic fungi in *Acer truncatum* and their role in decomposition. Fungal Diversity 47, 85–95.

Sun XD, Cai XL, Pang QQ, et al. 2020 – First record of leaf spot disease on *Costus speciosus* caused by *Nigrospora oryzae* in Hainan, China. Plant disease 105, 506.

Sun YR, Liu NG, Samarakoon MC, Jayawardena RS, et al. 2021 – Morphology and phylogeny reveal *Vamsapriyaceae* fam. nov. (*Xylariales, Sordariomycetes*) with two novel *Vamsapriya* species. Journal of Fungi 7, 891.

Sung GH, Hywel-Jones NL, Sung JM, Luangsa-Ard JJ et al. 2007 – Phylogenetic classification of *Cordyceps* and the clavicipitaceous fungi. Studies in mycology 57, 5–9.

Sutton BC. 1980 – The coelomycetes. Fungi imperfecti with pycnidia, acervuli and stromata. Commonwealth Mycological Institute, Kew, UK, pp 496.

Suwannarach N, Khuna S, Kumla J, Tanruean K, Lumyong S. 2020 – First report of *Lasiodiplodia theobromae* causing fruit rot on melon (*Cucumis melo*) in Thailand. Plant Disease 104, 280.
Svrček M. 1992 – New or less known Discomycetes. XXIII. Česká Mykologie 46, 149–162.
Sysouphanthong P, Bouamanivong S, Salichanh T. 2017 – Some mushrooms found in Houayang Preserves. Biotechnology and Ecology Institute, Vientiane, Laos. 87 pp.
Sysouphanthong P, Thongklang N, Suwannapoom S, Nuangmek W, Hyde KD. 2020 – *Lepiota* Section *Stenosporae* (*Agaricaceae*): Two new records to Lao People's Democratic Republic. Chiang Mai Journal of Science 47, 49–56.
Talhinhas P, Baroncelli R. 2021 – *Colletotrichum* species and complexes: Geographic distribution, host range and conservation status. Fungal Diversity 110, 109–198.
Tanaka K, Endo M, Hirayama K, Okane I, et al. 2011 – Phylogeny of *Discosia* and *Seimatosporium*, and introduction of *Adisciso* and *Immersidiscosia* genera nova. Persoonia 26, 85–98.
Tao YQ, Jia GG, Aung SLL, Wu QL et al. 2019 – Multigene phylogeny and morphology of *Alternaria* reveal a novel species and a new record in China. Phytotaxa 397, 169–176.
Tang JR, Liu YL, Yin XG, Lu JN. 2021 – First report on *Colletotrichum siamense* causing anthracnose of castor bean in Zhanjiang, China. Plant Disease 105, 3293.
Tennakoon DS, Kuo CH, Maharachchikumbura SS, Thambugala KM, et al. 2021a – Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*, *F. septica*, *Macaranga tanarius* and *Morus australis* leaf litter inhabiting microfungi. Fungal Diversity 108, 1–215.
Tennakoon DS, Jeewon R, Thambugala KM, Gentekaki E, et al. 2021b – Biphasic taxonomic approaches for generic relatedness and phylogenetic relationships of *Teichosporaceae*. Fungal Diversity 110, 199–241.
Than PP, Prihastuti H, Phoulivong S, Taylor PW, Hyde KD. 2008 – Chilli anthracnose disease caused by *Colletotrichum* species. Journal of Zhejiang University: Science B 10, 764–778.
Thanabalasingam D, Savitri Kumar N, Jayasinghe L, Fujimoto Y. 2015 – Endophytic fungus *Nigrospora oryzae* from a medicinal plant *Coccinia grandis*, a high yielding new source of Phenazine-1-carboxamide. Natural Product Communications 10, 1934578X1501001008.
Thambugala KM, Hyde KD, Tanaka K, Tian Q, et al. 2015 – Towards a natural classification and backbone tree for *Lophiostomataceae*, *Floricolaceae*, and *Amorosiaceae* fam. nov. Fungal Diversity 74, 199–266.
Theissen F, Sydow H. 1915 – Die Dothideales. Kritisch-systematische Originaluntersuchungen. Annales mycologici 13, 147–746.
Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN, et al. 2017 – Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 83, 1–261.
Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ, et al. 2018 – Fungal diversity notes 840–928: micro-fungi associated with Pandanaceae. Fungal Diversity 93, 1–160.
Timonin MI. 1940 – The interaction of higher plants and soil micro-organisms- I. Microbial population of rhizosphere of seedlings of certain cultivated plants. Canadian Journal of Research: section C 18, 307–317.
Trakunyingcharoen T, Cheewangkoon R, To-anun C. 2013 – Phylogeny and pathogenicity of fungal species in the family *Botryosphaeriaceae* associated with mango (*Mangifera indica*) in Thailand. International Journal of Agricultural Technology 9, 1535–1543.
Trakunyingcharoen T, Lombard L, Groenewald JZ, Cheewangkoon R, et al. 2014 – Mycoparasitic species of *Sphaerellopsis*, and allied lichenicolous and other genera. IMA fungus 18, 391–414.
Trakunyingcharoen T, Lombard L, Groenewald JZ, Cheewangkoon R, et al. 2015 – Caulicolous *Botryosphaeriales* from Thailand. Persoonia-Molecular Phylogeny and Evolution of Fungi 34, 87–99.

Trouillas FP, Pitt WM, Sosnowski MR, Huang R, et al. 2011 – Taxonomy and DNA phylogeny of Diatrypaceae associated with *Vitis vinifera* and other woody plants in Australia. Fungal Diversity 49, 203–223.

Tulasne LR. 1856 – Note sur l`appareil reproducteur multiple des Hypoxylées (DC.) ou Pyrénomycètes (Fr.). Annales des Sciences Naturelles, Botanique, sér. 4, 5, 107–118.

Udayanga D, Liu X, McKenzie EH, Chukeatirote E et al. 2011 – The genus *Phomopsis*: biology, applications, species concepts and names of common phytopathogens. Fungal diversity 50, 189–225.

Udayanga D, Manamgoda DS, Liu X, Chukeatirote E, Hyde KD. 2013 – What are the common anthracnose pathogens of tropical fruits?. Fungal Diversity 61, 165–179.

Udayanga D, Castlebury LA, Rossman AY, Hyde KD. 2014 – Species limits in *Diaporthe*: molecular re-assessment of *D. citri*, *D. cytosporella*, *D. foeniculina* and *D. rudis*. Persoonia: Molecular Phylogeny and Evolution of Fungi 32, 83–101.

Uzun Y, Demirel K, Kaya A, Gucin F. 2010 – Two new genus records for Turkish mycota. Mycotaxon 111, 477–480.

Van Vooren N, Mourgues Y. 2009 – Notes sur nouvelles récoltes françaises d'une espèce éconnue, *Tatraea dumbirensis* (Velen.) Svrček (*Ascomycotina*, *Helotiales*). Bulletin de la Fédération des Associations Mycologiques Méditerranéennes 36, 39–42.

Vasco-Palacios AM, Franco-Molano AE. 2013 – Diversity of Colombian macrofungi (*Ascomycota* and *Basidiomycota*). Mycotaxon 121, 100–158.

Vellinga EC. 2001 – *Agaricaceae*. In: Noordeloos ME, Kuyper TW, Vellinga EC, eds. Flora Agaricina Neerlandica 5. Rotterdam: A.A. Balkema Publishers 76–151.

Vellinga EC. 2003 – Phylogeny of *Lepiota* (*Agaricaceae*) – evidence from nrITS and nrLSU sequences. Mycological Progress 2, 305–322.

Vig R, Bhadra F, Gupta SK, et al. 2022 – Neuroprotective effects of quercetin produced by an endophytic fungus *Nigrospora oryzae* isolated from *Tinospora cordifolia*. Journal of Applied Microbiology 132, 365–380.

Vijayalakshmi A, Soundharajan R, Srinivasan H. 2022 – Engineered green nanoparticles interact with *Nigrospora oryzae* isolated from infected leaves of *Arachis hypogaea*. Journal of Basic Microbiology 62, 1393–1401.

Voglmayr H, Jaklitsch WM. 2017 – *Corynespora*, *Exosporium* and *Helminthosporium* revisited-new species and generic reclassification. Studies in Mycology 87, 43–76.

Voglmayr H, Rossman AY, Castlebury LA, Jaklitsch WM. 2012 – Multigene phylogeny and taxonomy of the genus *Melanconiella* (*Diaporthales*). Fungal Diversity 57, 1–44.

Vries GA de. 1952 – Contribution to the knowledge of the genus *Cladosporium* Link ex Fr.

Walker C, Muniz MF, Rolim JM, Martins RR, et al. 2016 – Morphological and molecular characterization of *Cladosporium cladosporioides* species complex causing pecan tree leaf spot. Genetics and Molecular Research 15, 1.

Wanasinghe DN, Hyde KD, Konta S, To-Anun C, Jones EG. 2017 – Saprobic *Dothideomycetes* in Thailand: *Neoaquastroma* gen. nov. (*Parabambusicolaceae*) introduced based on morphological and molecular data. Phytotaxa 302, 133–144.

Wanasinghe DN, Wijayawardene NN, Xu J, Cheewangkoon R, Mortimer PE. 2020 – Taxonomic novelties in *Magnolia*-associated pleosporalean fungi in the Kunming Botanical Gardens (Yunnan, China). PLoS ONE 15, e0235855.

Wang JD, Zhao J, Zhang J, Hou RT, Yin HX, Yang ZR. 2004 – Preliminary study on sporocarp formation and the characteristics of *Asterophora lycoperdoides*. Journal Sichuan University Natura Science Edition 41, 198–202.

Wang M, Liu F, Crous PW, Cai L. 2017 – Phylogenetic reassessment of *Nigrospora*: ubiquitous endophytes, plant and human pathogens. Persoonia - Molecular phylogeny and evolution of Fungi 39, 118–142.

Wang X, Zhang X, Li M, Ji X, et al. 2020 – First report of *Ficus carica* bot rot caused by *Botryosphaeria dothidea* in China. Plant Disease 104, 1869.

Wang D, Li Y, Sun G, Ai Y, Wang F, Wang X. 2022 – First report of leaf spot disease caused by *Nigrospora oryzae* on *Nicotiana tabacum* in China. Plant disease 106, 2526.
Wang F, Wang K, Cai L, Zhao M, et al. 2023 – Fungal names: a comprehensive nomenclatural repository and knowledge base for fungal taxonomy. Nucleic Acids Research 51, D708–D716.
Widmer T, Kirk A, Kirk G, Guermache F. 2007 – Foliar and cane rot of *Arundo donax* caused by *Nigrospora oryzae* in Europe. Plant disease 90, 1107–1107.
Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, et al. 2022 – Outline of *Fungi* and fungi-like taxa-2021. Mycosphere 13, 53–453.
Wolseley PA, Aguirre-hudson B, McCarthy PM. 2002 – Catalogue of the lichens of Thailand. Bulletin of the Natural History Museum Botany Series 32, 13–59.
Woudenberg JHC, Groenewald JZ, Binder M, Crous PW. 2013 – *Alternaria* redefined. Studies in Mycology 75, 171–212.
Wright JE, Wright E. 2005 – Checklist of the mycobiota of Iguazu National Park (Misiones, Argentina). Boletín de la Sociedad Argentina de Botánica 40, 23–44.
Wright JE, Lechner BE, Popoff OF. 2008 – Hongos. Atlas pictórico del Parque Nacional Iguazú. L.O.L.A., Buenos Aires. 227p.
Wu JB, Zhang CL, Mao PP, Qian YS, Wang HZ. 2014 – First report of leaf spot caused by *Nigrospora oryzae* on *Dendrobium candidum* in China. Plant disease 98, 996.
Wu N, Dissanayake AJ, Manawasinghe IS, Rathnayaka AR, et al. 2021 – https://botryosphaeriales.org/, an up-to-date classification and account of taxa of *Botryosphaeriales*. Database 2021, 1–9.
Xu G, Yang T, Tian F, Wang T. 2023 – Leaf spot disease on *Euonymus japonicus* caused by *Nigrospora oryzae* in China. Plant disease. https://doi.org/10.1094/pdis-05-22-1188-pdn
Yamagishi N, Nishikawa J, Oshima Y, Eguchi N. 2009 – Black spot disease of Alstroemeria caused by *Alternaria alstroemeriae* in Japan. Journal of General Plant Pathology 75, 401–403.
Yang HL, Du CM, Liang LY, Qin QY, et al. 2022 – First report of *Davidia involucrata* leaf blight caused by *Nigrospora oryzae* in Sichuan, China. Plant disease 106, 2520.
Yu Z, Jiang X, Zheng H, Zhang H, Qiao M. 2022 – Fourteen new species of foliar *Colletotrichum* associated with the invasive plant *Ageratina adenophora* and surrounding crops. Journal of Fungi 8, 185 (1–34).
Zakaria L, Aziz WNW. 2018 – Molecular identification of endophytic fungi from banana leaves (*Musa* spp.). Tropical Life Sciences Research 29, 201.
Zare R, Gams W, Evans HC. 2001 – A revision of *Verticillium* section *Prostrata*. V. The genus *Pochonia*, with notes on *Rotiferophthora*. Nova Hedwigia, 51–86.
Zelski SE, Balto JA, Do C, Raja HA, et al. 2014 – Phylogeny and morphology of dematiaceous freshwater microfungi from Perú. IMA Fungus 5, 425–438.
Zeng NK, Liang ZQ, Tang LP, Li YC, Yang ZL. 2017 – The genus *Pulveroboletus* (*Boletaceae*, *Boletales*) in China. Mycologia 109, 422–442.
Zeng XY, Hongsanan S, Hyde KD, Putarak C, et al. 2018 – *Translucidithyrium thailandicum* gen. et sp. nov.: a new genus in *Phaeothecoidiellaceae*. Mycological Progress 17, 1087–1096.
Zhai FY, Lu HJ, Xie XY, Li CQ, Zeng LG. 2019 – *Nigrospora oryzae* causing leaf spot of *Centranthera cochinchinensis* (Swamp Foxglove) in China. Plant disease 103, 3286.
Zhai LF, Liu J, Zhang MX, Hong N, Wang GP, Wang LP. 2013 – The first report of leaf spots in *Aloe vera* caused by *Nigrospora oryzae* in China. Plant disease 97, 1256.
Zhang LX, Li SS, Tan GJ, Shen JT, He T. 2012 – First report of *Nigrospora oryzae* causing leaf spot of Cotton in China. Plant disease 96, 1379.
Zhang Y, Fournier J, Phookamsak R, Bahkali AH, Hyde KD. 2013 – *Halotthiaceae* fam. nov. (*Pleosporales*) accommodates the new genus *Phaeoseptum* and several other aquatic genera. Mycologia 105, 603–609.

Zhang H, Hyde KD, Zhao YC, McKenzie EHC. 2014 – Freshwater ascomycetes: *Lophiostoma vaginatispora* comb. nov. (*Dothideomycetes*, *Pleosporales*, *Lophiostomaceae*) based on morphological and molecular data. Phytotaxa 176, 184–191.

Zhang QH, Huang LL, Liu YJ, Ai Y, Peng DH. 2018 – First report of leaf spot of lotus (*Nelumbo nucifera*) caused by *Nigrospora oryzae* in China. Plant disease 102, 1038.

Zhang LQ, Jiang S, Meng JJ, An HS, Zhang XY. 2019 – First report of leaf spot caused by *Nigrospora oryzae* on Blueberry in Shanghai, China. Plant disease 103, 2473.

Zhang JF, Liu JK, Thambugala KM, Yang J, et al. 2020 – Two new species and a new record of *Nigrograna* (*Nigrograna*ceae, *Pleosporales*) from China and Thailand. Mycological Progress 19, 1365–1375.

Zhang M, Sun W, Huang H, Li Q, et al. 2022a – *Philodendron bipinnatifidum* anthracnose caused by *Colletotrichum karsti* and *C. endophytica* in Guangxi, China. Plant Disease, DOI: 10.1094/PDIS-10-21-2236-PDN.

Zhang H, Kong N, Ji S, Liu B, et al. 2022b – First report of leaf blight caused by *Nigrospora oryzae* on Poplar in China. Plant disease 106, 1063.

Zheng L, Shi F, Kelly D, Hsiang T. 2012 – First report of leaf spot of Kentucky Bluegrass (*Poa pratensis*) caused by *Nigrospora oryzae* in Ontario. Plant disease 96, 909.

Zhu HY, Pan M, Wijayawardene NN, Jiang N, et al. 2021 – The hidden diversity of Diatrypaceous fungi in China. Frontiers in Microbiology 12, 646262.

Zhuang WY. 2005 – Fungi of northwestern China. Ithaca, NewYork.

Zhuang WY, Yu ZH, Wu WP, Langue C, Fouret N. 2000 – Preliminary notes on phylogenetic relationships in the *Encoelioideae* inferred from 18S rDNA sequences. Mycosystema 19, 478–484.

Zimmerman A. 1902 – Ueber einige an tropischen Kulturpflanzen beobachtete Pilze III. Zentralblatt Für Bakteriol Parasitenkd 8, 216–221.