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Article

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AJOM new records and collections of fungi: 101-150

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Abstract

This article is the second in the Asian Journal of Mycology Notes series, wherein we report 50 new fungal collections distributed in two phyla, six classes, 23 orders and 38 families. The present study provides descriptions and illustrations for three new species (*Acolium yunnanense*, *Muyocopron cinnamomi* and *Thyrostroma ulmeum*), 44 new host records and new geographical distributions and three new reference collections. All these introductions are supported by morphological data as well as the multi-gene phylogenetic analyses. This article provides a venue to publish fungal collections with new sequence data, which is important for future studies. An accurate and timely report of new fungus-host or fungus-county records are essential for diagnostics, identification and management of economically significant fungal groups, especially the phytopathogens.

Key words – 3 new taxa – 44 new records – Ascomycota – Basidomycota – Dothideomycetes – Molecular phylogeny – Sordariomycetes – Taxonomy

Table of contents

The taxa in this study are organized in accordance to the Outline of Ascomycota: 2017 (Wijayawardene et al. 2018), Outline of fungi and fungus-like taxa (Wijayawardene et al. 2020), 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. 2019).

Phylum Ascomycota
Class Dothideomycetes O.E. Erikss. & Winka
Subclass Pleosporomycetidae C.L. Schoch et al.
Pleosporales Luttrell ex M.E. Barr
Dictyosporiaceae Boonmee & K.D. Hyde

1. ***Dendryphiella vinosa*** (Berk. & M.A. Curtis) Reisinger, Bulletin de la Société Mycologique de France 84, 27 (1968) (contributed by Sun YR)

Didymosphaeriaceae Munk

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

Dothidotthiaceae Crous & A.J.L. Phillips

3. ***Thyrostroma ulmeum*** Senwanna, Bulgakov & K.D. Hyde, sp. nov. (contributed by Senwanna C)
4. ***Thyrostroma ulmicola*** Senwanna, Wanas., Bulgakov, Phookamsak & K.D. Hyde, Mycosphere 10, 729 (2019) (contributed by Senwanna C)

Hermatomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka

5. ***Hermatomyces thailandicus*** Doilom D.J. Bhat & K.D. Hyde, Fungal Diversity 82, 121 (2016) (contributed by Tang X)

Longipedicellataceae Phukhams., Bhat & K.D. Hyde

6. ***Pseudoxylomyces elegans*** (Goh, W.H. Ho, K.D. Hyde & C.K.M. Tsui) Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 126 (2015) (contributed by Calabon MS)

Parabambusicolaceae Kaz. Tanaka & K. Hiray.

7. ***Aquastroma magniostiolatum*** Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 115 (2015) (contributed by Zhang JY)

Sporormiaceae Munk

8. ***Westerdykella purpurea*** (Cain) Arx, Kavaka 3, 33 (1976) (contributed by Calabon MS)

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

9. ***Phyllosticta capitalensis*** Henn., Hedwigia 48: 13 (1908) (contributed by Ma XY)

Muyocopronales Mapook, Boonmee & K.D. Hyde
Muyocopronaceae K.D. Hyde

10. ***Muyocopron cinnamomi*** Marasinghe, C.H. Kuo & K.D Hyde sp. nov. (contributed by Marasinghe DS)
11. ***Muyocopron dipterocarpi*** Mapook, Doilom, Boonmee & K.D. Hyde, Phytotaxa 265, 232 (2016) (contributed by Tennakoon DS)

Stigmatodiscales Voglmayr & Jaklitsch
Stigmatodiscaceae Voglmayr & Jaklitsch

12. ***Stigmatodiscus enigmaticus*** Voglmayr & Jaklitsch, Fungal Diversity 80: 278 (2016) (contributed by de Silva NI)

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde
Sympoventuriaceae Y. Zhang ter, C.L. Schoch & K.D. Hyde

13. ***Yunnanomyces pandanicola*** Tibpromma & K.D. Hyde, Fungal Diversity 93, 75 (2018) (contributed by Tennakoon DS)

Class Lecanoromycetes O.E. Erikss. & Winka
Subclass Lecanoromycetidae P.M. Kirk et al.
Caliciales Bessey
Caliciaceae Chevall.

14. ***Acolium yunnanense*** Thiyagaraja & Hyde, sp. nov. (contributed by Thiyagaraja V)

Class Leotiomycetes O.E. Erikss. & Winka
Subclass Leotiomycetidae P.M. Kirk, P. Cannon, Minter & Stalpers
Erysiphales Warm.
Erysiphaceae Tul. & C. Tul.

15. ***Erysiphe heraclei*** DC., Flore Françoise 6: 107 (1815) (contributed by Rathnayaka AR)

Class Pezizomycetes O.E. Erikss. & Winka
Subclass Pezizomycetidae Locq.
Pezizales J. Schröt.
Sarcoscyphaceae Le Gal ex Eckblad

16. ***Kompsoscypha chudei*** (Pat. ex Le Gal) Pfister, Memoirs of the New York Botanical Garden 49, 341 (1989) (contributed by Zeng M)
17. ***Cookeina indica*** Pfister & R. Kaushal, Mycotaxon 20, 117 (1984) (contributed by Zeng M)

Class Sordariomycetes O.E. Erikss. & Winka
Subclass Diaporthomycetidae Senan., Maharachch. & K.D. Hyde
Coniochaetales Huhndorf, A.N. Mill. & F.A. Fernández

Coniochaetaceae Malloch & Cain

18. ***Coniochaeta acaciae*** Samarakoon, Gafforov & K.D. Hyde, Phytotaxa 336, 49 (2018) (contributed by Pem D)
19. ***Coniochaeta taeniospora*** (Sacc.) Friebes, Jaklitsch & Voglmayr, Sydowia 68, 91 (2016) (contributed by Samarakoon MC)

Diaporthales Nannf.
Cytosporaceae Fr.

20. ***Cytospora cedri*** Syd., P. Syd. & E.J. Butler, Annales Mycologici 14, 193 (1916) (contributed by Norphanphoun C)

Diaporthaceae Höhn. ex Wehm.

21. ***Diaporthe asheicola*** L. Lombard & Crous, Phytopathologia Mediterranea 53, 93 (2014) (contributed by Dissanayake AJ)
22. ***Diaporthe eucalyptorum*** Crous & R.G. Shivas, Persoonia 28, 153 (2012) (contributed by Niranjan M)
23. ***Diaporthe salsuginosa*** Vrijmoed, K.D. Hyde & E.B.G. Jones, Mycological Research 98, 699 (1994) (contributed by Devadatha B)

Lamproconiaceae Norph., T.C. Wen & K.D. Hyde

24. ***Lamproconium desmazieri*** (Berk. & Broome) Grove, British Stem and Leaf Fungi (Coelomycetes) 2, 321 (1937) (contributed by Karunarathna A)

Melanconidaceae G. Winter

25. ***Melanconis italica*** Senan., Camporesi & K.D. Hyde, Studies in Mycology 86, 273 (2017) (contributed by de Silva NI)

Schizoparmaceae Rossman

26. ***Coniella vitis*** Chethana, J.Y. Yan, X.H. Li & K.D. Hyde, Plant Disease 101, 2129 (2017) (contributed by Chethana KWT)

Magnaporthales Thongk., Vijaykr. & K.D. Hyde
Ophioceraceae Klaubauf, E.G. LeBrun & Crous

27. ***Ophioceras commune*** Shearer, J.L. Crane & W. Chen, Mycologia 91, 146 (1999) (contributed by Luo ZL)

Pseudohalonectriaceae Hongsanan & K.D. Hyde

28. ***Pseudohalonectria lutea*** Shearer, Canadian Journal of Botany 67, 1950 (1989) (contributed by Bao DF)

Tirisporellales Suetrong, E.B.G. Jones & K.L. Pang
Tirisporellaceae Suetrong, E.B.G. Jones & K.L. Pang

29. ***Tirisporella beccariana*** (Ces.) E.B.G. Jones, K.D. Hyde & Alias, Canadian Journal of Botany 74, 1490 (1996) (contributed by Zhang SN)

Subclass Hypocreomycetidae O.E. Erikss. & Winka
Hypocreales Lindau
Bionectriaceae Samuels & Rossman

30. ***Clonostachys byssicola*** Schroers, Studies in Mycology 46, 80 (2001) (contributed by Perera RH)
31. ***Clonostachys rosea*** (Link) Schroers, Samuels, Seifert & W. Gams, Mycologia 91, 369 (1999) (contributed by Perera RH)

Hypocreaceae De Not.

32. ***Trichoderma erinaceum*** Bissett, C.P. Kubicek & Szakács, Canadian Journal of Botany 81, 583 (2003) (contributed by Niranjan M)

Jobellisiales M.J. D'souza & K.D. Hyde
Jobellisiaceae Réblová

33. ***Jobellisia guangdongensis*** F. Liu & L. Cai, Mycologia 104, 1181 (2012) (contributed by Dong W)

Subclass Lulworthiomycetidae Dayar., E.B.G. Jones & K.D. Hyde
Lulworthiales Kohlm., Spatafora & Volkm. -Kohlm.
Lulworthiaceae Kohlm., Spatafora & Volkm. -Kohlm.

34. ***Sammeyersia grandispora*** (Meyers) S.Y. Guo, E.B.G. Jones & K.L. Pang, Botanica Marina 60, 483 (2017) (contributed by Dayarathne MC)

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

35. ***Phaeoisaria clematidis*** (Fuckel) S. Hughes, Canadian Journal of Botany 36, 794 (1958) (contributed by Dong W)

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

36. ***Canalisporium pulchrum*** (Hol.-Jech. & Mercado) Nawawi & Kuthub., Mycotaxon 34, 481 (1989) (contributed by Dong W)

Subclass Sordariomycetidae O.E. Erikss & Winka
Meliolales Gäum. ex D. Hawksw. & O.E. Erikss.
Meliolaceae G.W. Martin ex Hansf.

37. ***Meliola telosmae*** Rehm, Philippines Journal of Science 8, 392 (1913) (contributed by Zeng XY)

Sordariales Chad. ex D. Hawksw. & O.E. Erikss.
Chaetomiaceae G. Winter

38. ***Chaetomium globosum*** Kunze, Mykologische Hefte (Leipzig) 1, 16 (1817) (contributed by Jayawardena RS and Huanraluek N)
39. ***Dichotomopilus ramosissimus*** (X. Wei Wang & L. Cai) X. Wei Wang & Samson, Studies in Mycology 84, 217 (2016) (contributed by Niranjan M)

Subclass Xylariomycetidae O.E. Erikss & Winka
Order Amphisphaeriales D. Hawksw. & O.E. Erikss.
Sporocadaceae Corda

40. ***Neopestalotiopsis rhizophorae*** Norphanphoun, T.C. Wen & K.D. Hyde, Mycosphere 10, 545 (2020) (contributed by Norphanphoun C)
41. ***Pestalotiopsis verruculosa*** Maharachch. & K.D. Hyde, Fungal Diversity 56, 123 (2012) (contributed by Goonasekara ID)
42. ***Seiridium neocupressi*** G. Bonthond, M. Sand.-Den. & P.W. Crous, Persoonia 40, 110 (2017) (contributed by Goonasekara ID)

Xylariales Nannf.
Hypoxylaceae DC.

43. ***Daldinia eschscholtzii*** (Ehrenb.) Rehm., Annales mycologici 2, 175 (1904) (contributed by Niranjan M)
44. ***Hypomontagnella monticulosa*** (Mont.) Sir, L. Wendt & C. Lambert, Mycological Progress 18, 190 (2018) (contributed by Samarakoon MC)

Lopadostomataceae Daranag. & K.D. Hyde

45. ***Lopadostoma gastrinum*** (Fr.) Traverso, Flora Italica Cryptogama 1, 169 (1906) (contributed by Samarakoon MC)

Xylariaceae Tul. & Tul. (as 'xylariei')

46. ***Nemania bipapillata*** (Berk. & M.A. Curtis) Pouzar, Česká Mykologie 39, 24 (1985) (contributed by Niranjan M)

Zygosporiaceae Li et al.

47. ***Zygosporium masonii*** S. Hughes, Mycological Papers 44, 15 (1951) (contributed by Chaiwan N)

Sordariomycetes orders *incertae sedis*
Catabotryales K.D. Hyde & Senan.
Catabotrydaceae Petr. ex M.E. Barr

48. ***Catabotrys deciduum*** (Berk. & Broome) Seaver & Waterston, Mycologia 38, 184 (1946) (contributed by Zhang SN)

Phylum Basidiomycota
Class Agaricomycetes Doweld
Subclass Agaricomycetidae Locq.
Boletales E.-J. Gilbert
Boletaceae Chevall.

49. ***Phylloporus attenuatus*** Hosen, in Hosen & Li, Mycologia 109, 279 (2017) (contributed by Chuankid B)
50. ***Phylloporus gajari*** Hosen & Zhu L. Yang, Mycoscience 56, 585 (2015) (contributed by Chuankid B)

Introduction

Fungal communities influence ecosystem functioning as one of its main structural components (Schimann et al. 2017). They play a variety of roles on or associated with plants, such as being saprobes, epiphytes, endophytes, animal and plant pathogens, and other symbionts of plants. With their high species diversity, fungi exhibit immense variations in morphology, lifestyles and modes of dispersal (Hawksworth & Lücking 2017, Hyde et al. 2018, Chethana et al. 2020).

The diversity of the fungal kingdom is estimated to range between 2.2 to 3.8 million species, though Wu et al. (2019) estimated the diversity to be closer to 12 million based on culture dependent and culture independent techniques), with less than 10% being named and classified (Hawksworth & Lücking 2017, Hyde et al. 2020b). Therefore, many species are unknown to science and some are poorly described and lack molecular data (Hyde et al. 2020b). Classification of this kingdom is undergoing continuous revisions with the inclusion of DNA sequences in species delimitation. Identification of new taxa, recollection of already known taxa, establishment of reference specimens and epitypification or neotypification of the historic taxa with fresh material and cultures are all important as they provide strong evidence for stable taxonomy and phylogeny (Chethana et al. 2020). In the recent years, different mycological groups have published series of articles such as Fungal Diversity notes (Liu et al. 2015, Ariyawansa et al. 2015, Hyde et al. 2017, Wanasinghe et al. 2018, Hyde et al. 2019, Phookamsak et al. 2019), Fungal Planet (Crous et al. 2015, 2017a) and Mycosphere notes series (Thambugala et al. 2017, Hyde et al. 2018, Jayawardena et al. 2018) to provide an outlet for mycologists throughout the world to publish their new fungal collections. As a result, many new taxa, new geographical and host records were introduced with morphological and molecular data. Documenting the geographical range and host range of fungi, particularly pathogens and opportunistic pathogens is important for the diagnosis and monitoring of plant diseases (Dugan et al. 2009).

This is the second in the series of Asian Journal of Mycology notes with entries mainly collected from China, India, Italy, Russia, Taiwan, Thailand and Ukraine. Our aim is to provide new data including morphological, geographical and sequence data for a stable taxonomy and phylogeny, which is significantly important for accurate identification of fungi. In the current study, we provide detailed descriptions of collections, with listed herbarium material, sequence data and discussions on the genera. Future researchers can include this data in their studies of the genera and new species can be introduced or combined as a better understanding of the genera develops.

Materials and methods

Materials and methods follow the Asian Journal of Mycology Notes series (Hyde et al. 2020c). Fresh and dried specimens in this study were collected from China, India, Italy, Russia, Taiwan, Thailand and Ukraine (further details for each taxon studied are given in the taxonomy section). Phylogenetic analyses were performed based on Bayesian inference (BI), maximum likelihood (ML) and maximum parsimony (MP) with details as outlined by Dissanayake et al. (2020). Establishment of new species and species differences are based on recommendations outlined by (Jeewon & Hyde 2016).

Taxonomy

Phylum Ascomycota
Class Dothideomycetes

For Dothideomycetes, we follow the recent treatments of (Liu et al. 2017a, Wijayawardene et al. 2018, 2020, Hongsanan et al. 2020a, b).

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

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

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

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

Index Fungorum number: IF551574; Facesoffungi number: FoF01256

Dictyosporiaceae was introduced by Boonmee et al. (2016) to accommodate a holomorphic group of Dothideomycetes. Most species of Dictyosporiaceae were found on decaying wood and plant debris in terrestrial and freshwater habitats (Boonmee et al. 2016, Liu et al. 2017b, Hyde et al. 2018).

Dendryphiella Bubák & Ranoj., Annales Mycologici 12, 417 (1914)

Index Fungorum number: IF7951; Facesoffungi number: FoF08212

Dendryphiella is an asexual genus placed in the Dictyosporiaceae and was established by Ranojevic (1914). There are 16 species so far described in the genus and only five have sequence data (Liu et al. 2017b, Hyde et al. 2018, Iturrieta-González et al. 2018, Index Fungorum 2020). A new record of *Dendryphiella vinosa* is reported from *Dendrobium officinale* in Guangxi, China. An updated phylogeny for the genus is provided in Fig. 1.

Dendryphiella vinosa (Berk. & M.A. Curtis) Reisinger, Bulletin de la Société Mycologique de France 84, 27 (1968) Fig. 2

Index Fungorum number: IF329796; Facesoffungi number: FoF08673

Saprobic on the stem of *Dendrobium officinale*. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate clustered, superficial, effuse, brown to dark brown. *Conidiophores* 70–106 µm ($\bar{x}$ = 86 µm), n = 25) macronematous, mononematous, erect, straight or slightly flexuous, unbranched, dark brown at base, slightly paler towards the apex, smooth or delicately rough-walled, septate, wider at septa. *Conidiogenous cells* polytretic, terminal and intercalary, integrated, proliferating asymmetrically, brown, enlarged at vertex. *Conidia* 17–29 × 5–8 µm ($\bar{x}$ = 21.74 × 6.73 µm, n = 30), oblong with obtuse ends, rounded at apex, truncate at the base, forming simple or branched chains, pale brown when young, brown or dark brown, 3(4)-septate when mature, slightly constricted at septa, smooth or occasionally verruculose.

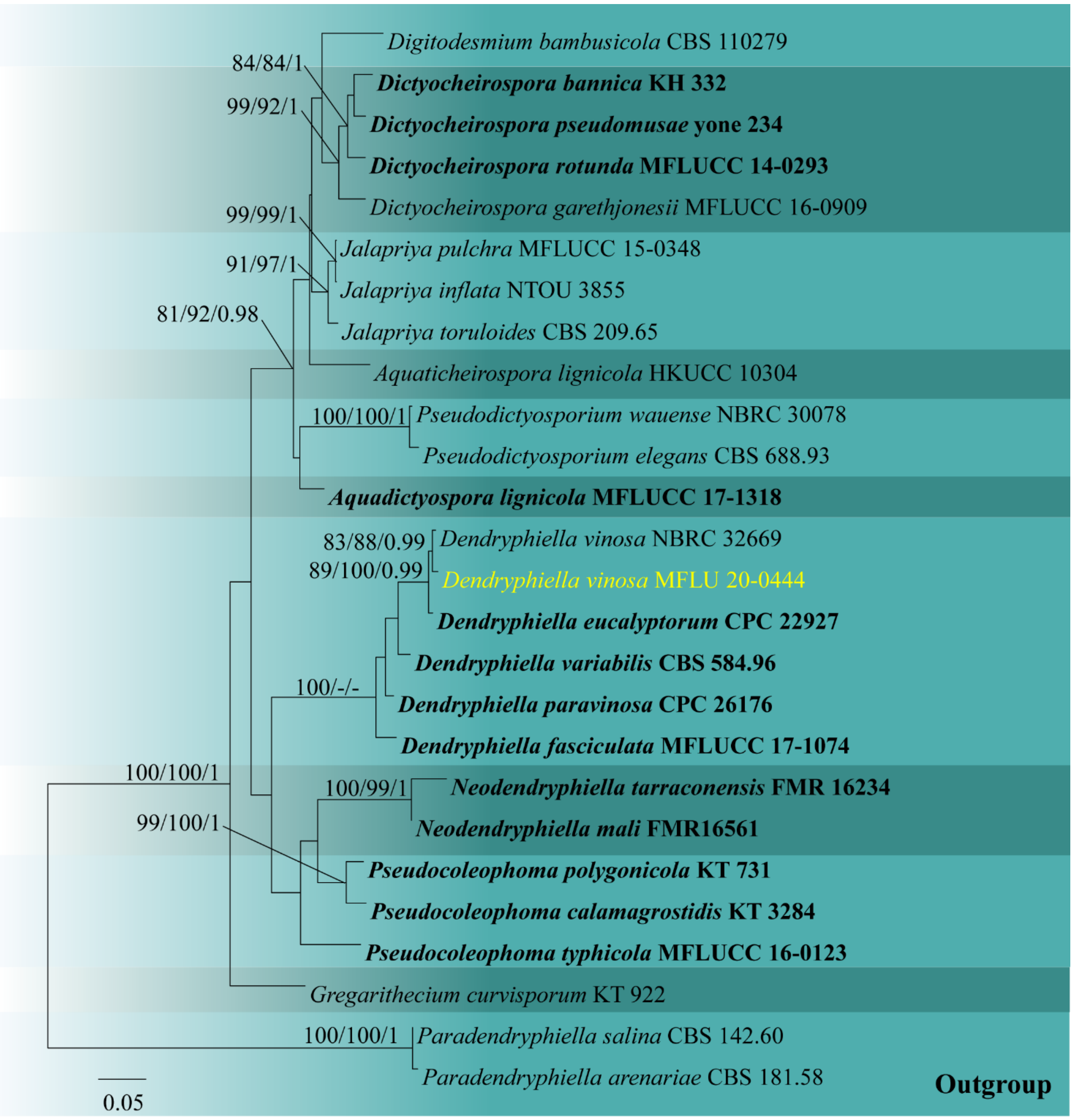

Fig. 1 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty-six strains are included in the combined analyses which comprised 1381 characters (774 characters for LSU, 607 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6956.854232 is presented. Estimated base frequencies were as follows: A = 0.236779, C = 0.235875, G = 0.280332, T = 0.247014; substitution rates AC = 1.437615, AG = 2.073326, AT = 2.469104, CG = 0.311068, CT = 5.886259, GT = 1.000000; gamma distribution shape parameter α = 0.158358. For both gene regions, GTR+G was applied as the evolutionary

model. Bootstrap support values for ML and MP greater than 80% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *P. salina* (CBS 142.60) and *P. arenariae* (CBS 181.58). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tubes produced from both ends. Colonies reached about 5 cm diameter after 2 weeks on PDA at 26°C. *Mycelia* are superficial, with entire edge, floccose at the center, white to light brown from above and light brown from below.

Material examined – China, Guangxi Province, Nanning City, on the stem of *Dendrobium officinale* (Orchidaceae), 14 September 2019, Yaru Sun G19 (MFLU 20-0444).

GenBank numbers – ITS: MT907477, LSU: MT907480.

Known distribution (based on molecular data) – Japan (Dela Cruz & Edison 2006) and China (this study).

Known hosts (based on molecular data) – decomposing leaf (Dela Cruz & Edison 2006) and *Dendrobium officinale* (this study).

Notes – Our collection only differs from the holotype of *Dendryphiella vinosa* in having shorter conidiophores (70−106 μm *vs* up to 400 μm). Detailed morphological study and molecular analysis of combined LSU and ITS sequence data indicated that our isolate clustered together with another strain of *D. vinosa*. Based on the morphology and phylogeny, we identified it as *D. vinosa*. This is the first report of *D. vinosa* on *Dendrobium officinale* in China.

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

Index Fungorum number: IF80702; Facesoffungi number: FoF00200

Munk (1953) introduced Didymosphaeriaceae using *Didymosphaeria* as the type genus. Ariyawansa et al. (2014) accepted 16 genera in Didymosphaeriaceae (i.e., *Alloconiothyrium, Barria, Bimuria, Kalmusia, Karstenula, Letendraea, Montagnula, Neokalmusia, Paraconiothyrium, Paraphaeosphaeria*, *Phaeodothis* and *Tremateia*). Wijayawardene et al. (2014a, b) added *Paracamarosporium* and *Pseudocamarosporium* to the family. Crous et al. (2015, 2017a) introduced two new genera (*Verrucoconiothyrium* and *Xenocamarosporium*) and Ariyawansa et al. (2015) further included *Austropleospora* and *Pseudopithomyces*. Tanaka et al. (2015) accommodated *Spegazzinia* (previously placed in *Apiosporaceae*) in Didymosphaeriaceae and Wanasinghe et al. (2016) introduced *Laburnicola* and *Paramassariosphaeria* as new genera. Wanasinghe et al. (2016) synonymized two species of *Munkovalsaria* under *Montagnula*. Thambugala et al. (2017) introduced *Kalmusibambusa* and recently, *Chromolaenicola* (Mapook et al. 2020), *Cylindroaseptospora* (Jayasiri et al. 2019), and *Vicosamyces* (Phookamsak et al. 2019) were introduced to Didymosphaeriaceae. Samarakoon et al. (2020a) accommodated *Dictyoarthrinium* (previously placed in Apiosporaceae) in Didymosphaeriaceae. An updated phylogeny for selected genera in this family is provided (Fig. 3).

Spegazzinia Sacc., Michelia 2, 37 (1880)

Index Fungorum number: IF9963; Facesoffungi number: FoF08241

Spegazzinia was established by Saccardo (1880) based on *S. ornata*. There are 17 taxa listed in Species Fungorum (2020). Based on morphology, the genus was placed in Apiosporaceae (Sordariomycetes) by Hyde et al. (1998). According to the phylogenetic analyses based on SSU, LSU, ITS and *TEF1-α* sequence data of *S. deightonii* and *S. tessarthra*, Tanaka et al. (2015) accommodated *Spegazzinia* in Didymosphaeriaceae (Dothideomycetes). This placement was supported by the phylogenetic analysis of Thambugala et al. (2017) that placed *Spegazzinia* in a basal clade in Didymosphaeriaceae. Hughes (1953) characterized *Spegazzinia* as a hypomycetous taxon with a unique basauxic conidiogenous cell development wherein conidiophore produces cupulate to doliiforn conidiophore-mother-cells. These conidiophore-mother-cells produce monoblastic conidiogenous cells. The conidia of *Spegazzinia* are brown to dark brown and imorphic in most species, with a disc-shaped form and a stellate form (Ellis 1971, Manoharachary& Kunwar 2010). However, very little molecular data for this genus is available in the GenBank. Therefore, more fresh collections with DNA sequences are needed. Recently, Thambugala et al. (2017), Jayasiri et al. (2019) and Samarakoon et al. (2020b) introduced novel taxa to *Spegazzinia* with morpho-molecular data which further support the taxonomic establishment of the genus in Didymosphaeriaceae.

Fig. 2 – *Dendryphiella vinosa* (MFLU 20-0444, a new geographical and host record). a Host. b Colonies on natural substrate. c, d Conidiophore with conidia. e Conidiogenous cell. f–l Conidia. Scale bars: c–d = 20 µm, e–l = 10 µm.

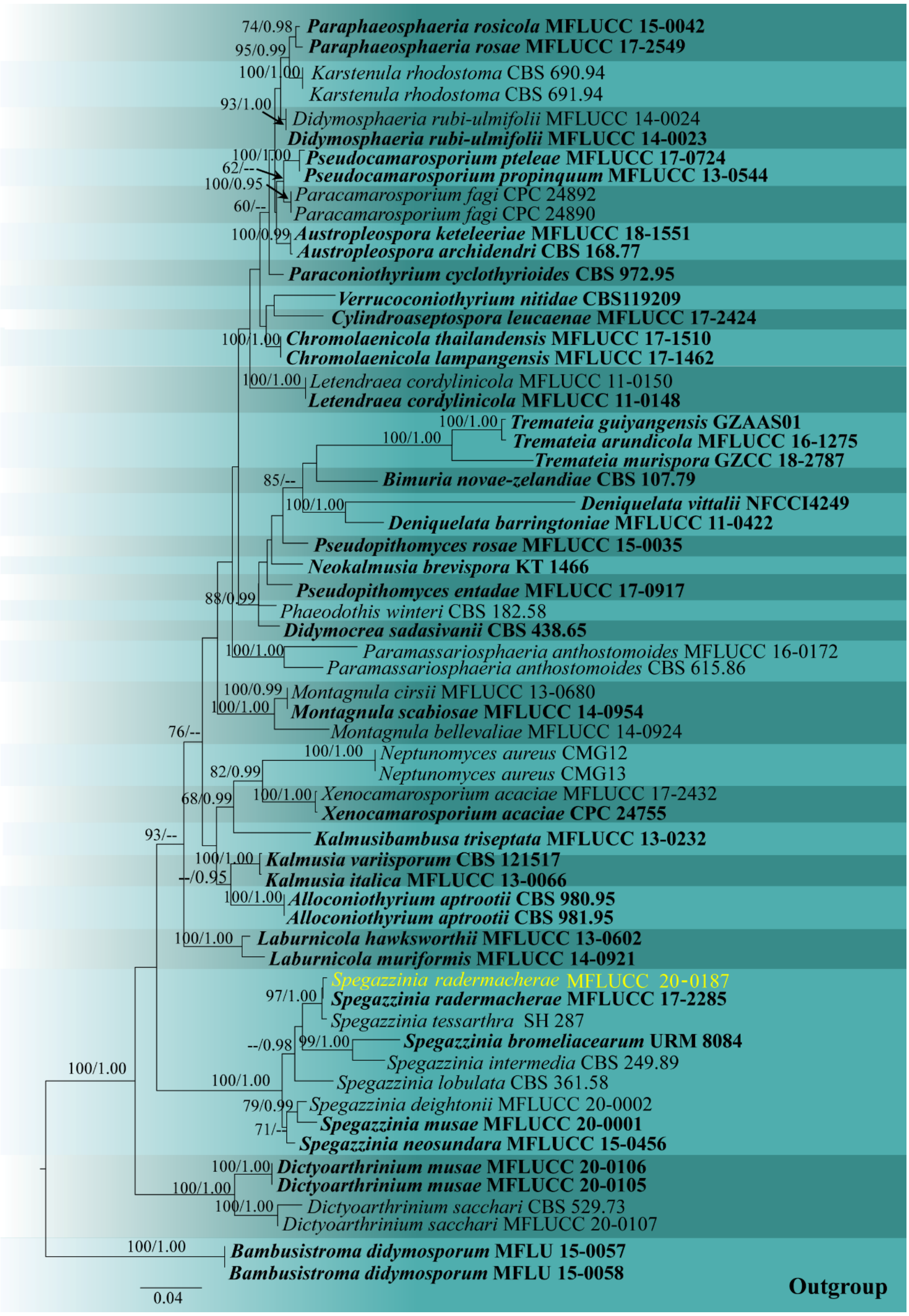

Fig. 3 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU and ITS sequence data of selected genera of Didymosphaeriaceae. Sixty-one strains are included in the combined analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12735.79is presented. Estimated base frequencies were as follows: A = 0.239117, C = 0.235992, G = 0.282602, T = 0.242289; substitution rates AC = 1.549464, AG = 2.256429, AT = 1.420163, CG = 1.078196, CT = 4.911225, GT = 1.000000; proportion of invariable sites I = 0.537571; gamma distribution shape parameter α = 0.429959. The matrix had 635 distinct alignment patterns, with 23.79% of undetermined characters or gaps. Bootstrap support values for ML greater than 60% and Bayesian

posterior probabilities greater than 0.95 are given near nodes, respectively. The tree was 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)

Fig. 4

Index Fungorum number: IF555547; Facesoffungi number: FoF05249

Saprobic on a dead leaf of *Musa* sp. Asexual morph: Hyphomycetous. *Sporodochia* dark, dense, dry, powdery, velvety. *Conidiophores* macronematous, mononematous, arising singly from subspherical, ampuliform, cupulate to doliiform, sub hyaline or light brown, sub spherical, smooth to verrrucose *condiophore mother cells* 2–3 × 3–4 µm ($\bar{x}$ = 2.6 × 3.4 µm, n = 10). *Conidiophores* usually have long ones and short ones that bear two kinds of conidia referred as α and β respectively. *Conidiophores* of α conidia 20–80 × 1.5–2.5 µm ($\bar{x}$ = 62 × 1.8 µm; n = 10), pale brown or dark golden brown, rough-walled, erect or slightly flexuous, narrow and long, unbranched. *Conidiophores* of β conidia 4–6 × 1.5–2 µm ($\bar{x}$ = 5.0 × 1.6 µm, n = 10), erect, unbranched, hyaline. *Conidiogenous cells* basauxic, integrated, forming a single, terminal holoblastic conidium at the apex. *Conidia* solitary, dry, two types. *α conidia* stellate, 15–25 × 12–22 µm ($\bar{x}$ = 20 × 17 µm; n = 30), 4–5-celled, each cell globose to subglobose, deeply constricted at the septa, conspicuously spinulate, 4–8 spines, each 2–8 µm long arise from surface of each cell; *β conidia* disc-shaped, 12–20 × 5–12 µm ($\bar{x}$ = 12.5 × 8.5 µm; n = 30), initially hyaline, dark brown to brown at maturity, 4-celled, each cell turbinate, crossed-septate, smooth-walled, deeply constricted at the septa, flat from side view, always attached to the conidiogenous cells. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12–15 h, germ tubes produced from one or several cells. Colonies growing on PDA, reaching a diam. of 10 mm after 7 d at 25°C, pinkish white, evenly raised, surface smooth, moderately dense, margin entire to crenulate; reverse white to pinkish white.

Material examined – Thailand, Chiang Rai Province, on a dead leaf of *Musa* sp. (Musaceae), 15 September 2018, B.C. Samarakoon BNS010 (MFLU 20-0469), living culture MFLUCC 20-0187.

GenBank numbers – ITS: MW084622, SSU: MW084351, LSU: MW084354.

Known distribution (based on molecular data) – Thailand, Chiang Rai Province (Jayasiri et al. 2019).

Known hosts (based on molecular data) – on a fallen pod of *Radermachera sinica* (Jayasiri et al. 2019).

Notes – *Spegazzinia radermacherae* (MFLU 20-0469) clustered with *S. radermacherae* (MFLUCC 17–2285) sister to *S. tessarthra* with a strong statistical support (Fig. 3). The nucleotide base comparison of SSU, LSU and ITS regions showed that our strain (MFLUCC 17–2285) differs from the other strain of *S. radermacherae* (MFLUCC 17–2285) by 1/830 bp (0.1%), 1/825 bp (0.1%) and 1/571 bp (0.1%), respectively. The holotype of *S. radermacherae* illustrated by Jayasiri et al. (2019) shares similar morphology to our strain such as dark brown, 4-celled, disked-shaped, conidia and four celled stellate conidia. *Spegazzinia radermacherae* differs from *S. tessarthra* by having two types of conidia whereas *S. tessarthra* only poses one type of conidia (Jayasiri et al. 2019). With morphological (Fig. 4) and multi-gene phylogenetic support (Fig. 3), we report *S. radermacherae* from *Musa* sp. as a saprobe for the first time from Thailand. *Spegazzinia radermacherae* was previously recorded on a fallen pod of a dicotyledon, *Radermachera sinica* (Bignoniaceae) in Thailand as a saprobe (Jayasiri et al. 2019). This is the first report of *S. radermacherae* from Musaceae and on a monocotyledon.

Dothidotthiaceae Crous & A.J.L. Phillips, Persoonia 21, 35 (2008)

Index Fungorum number: IF511706; Facesoffungi number: FoF09123

Dothidotthiaceae can be found as endophytes, pathogens and saprobes on various substrates worldwide (Marin-Felix et al. 2017, Pem 2019, Senwanna et al. 2019a, Hyde et al. 2019). This family was described by Phillips et al. (2008) with *Dothidotthia* as the generic type, and also includes *Belizeana*, *Mycocentrospora*, *Muellerites*, *Phaeomycocentrospora*, *Pleiochaeta*, *Thyrostroma* and *Wilsonomyces* (Hongsanan et al. 2020a). An updated phylogeny for the family is provided in Fig. 5.

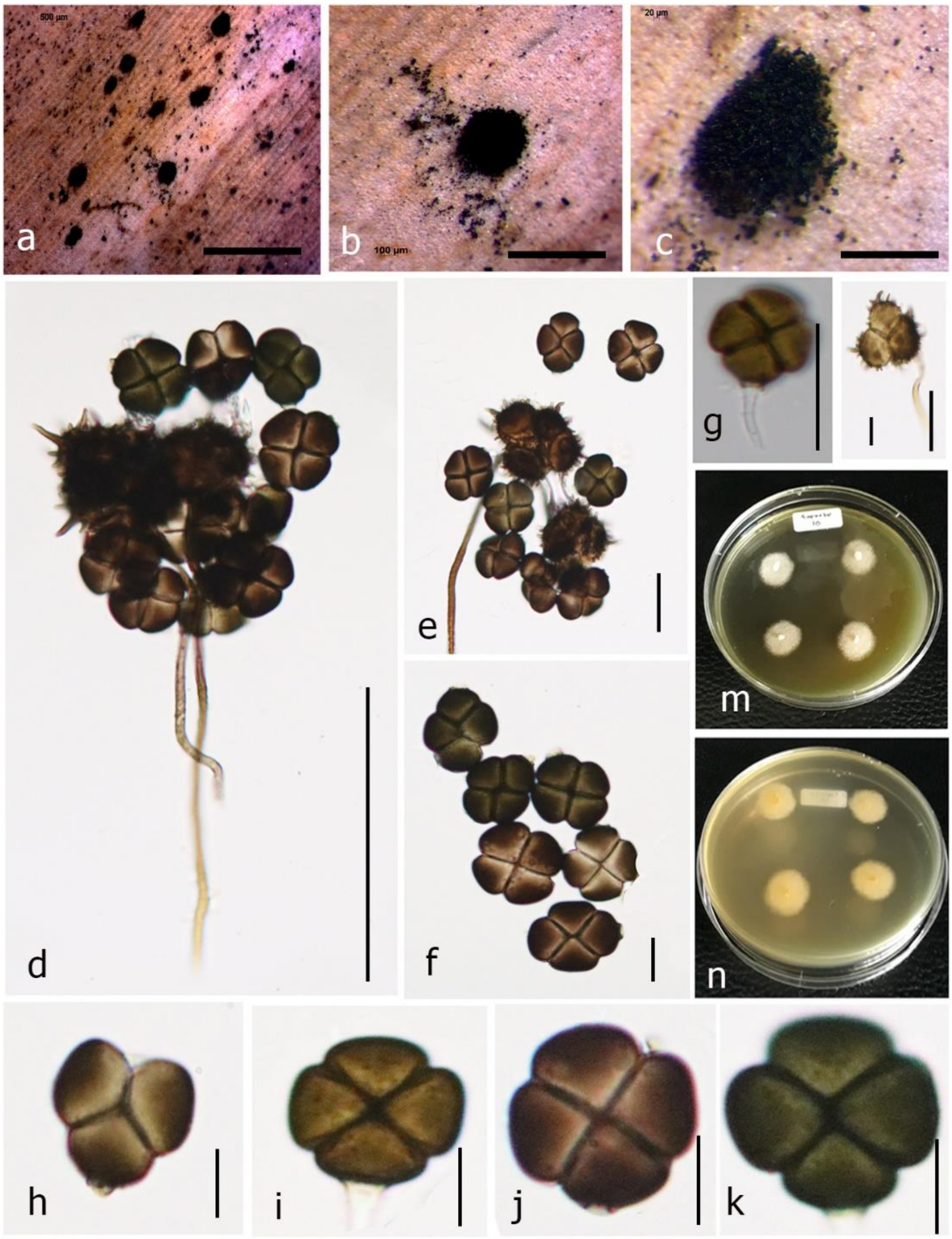

Fig. 4 – *Spegazzinia radermacherae* (MFLU 20-0469, a new host record). a–c Fungal colonies on host surface. d, e Conidia. f–k β Conidia with unbranched conidiophores. l α Conidium. m, n Colonies on PDA after 7 days. Scale Bars: a, b, c = 200 µm, d, e = 20 µm, f–k = 5 µm.

Thyrostroma Höhn., Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Math.-naturw. Klasse Abt. 1 120, 472 (1911)

Index Fungorum number: IF10224; Facesoffungi number: FoF07941

Thyrostroma was introduced by Höhnel (1911) and typified with *T. compactum*. This genus is characterized by immersed, globose to subglobose ascomata, clavate asci, fusiform to ellipsoidal, pale brown ascospores with 1 transverse septum; asexual morphs with immersed to erumpent sporodochium, clavate, ellipsoidal, obpyriform, subglobose, or oblong to subcylindric-clavate, phragmosporous to muriform, pale to dark brown conidia (Senwanna et al. 2019a). There are 33 *Thyrostroma* species listed in Index fungorum (2020), but only 13 species have been confirmed by molecular data. The most recent introduction to genus is *Thyrostroma alhagi* (Hyde et al. 2020c). In this study, we report a new species *Thyrostroma ulmeum* and *Ulmus minor* as a new host for *Thyrostroma ulmicola*.

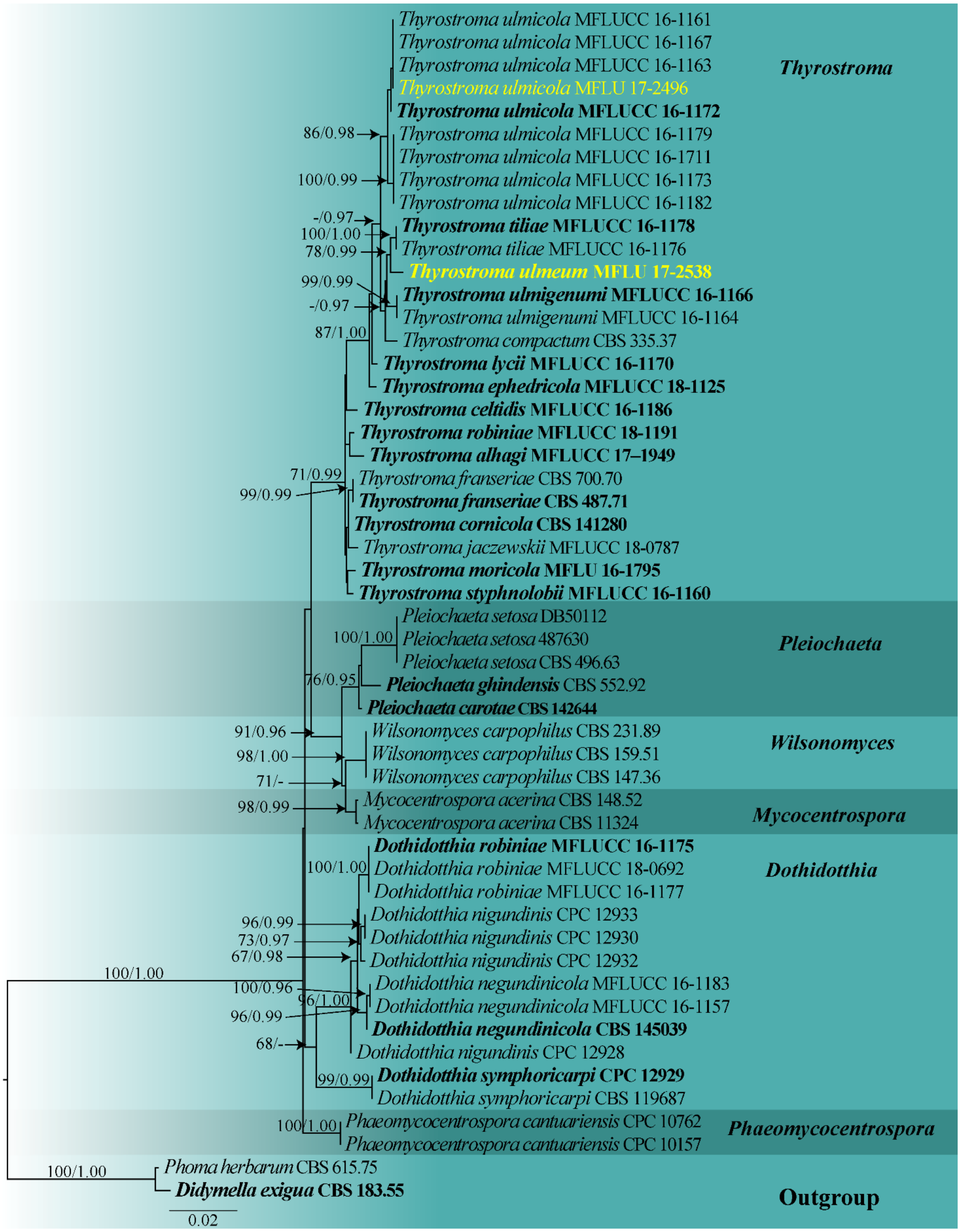

Fig. 5 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *TEF1-α* sequence data for Dothidotthiaceae. Fifty-one strains are included in the combined

analyses which comprised 3101 characters (806 characters for LSU, 923 characters for SSU, 507 characters for ITS, 865 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 -7031.098045 is presented. Estimated base frequencies were as follows: A = 0.243728, C = 0.237416, G = 0.270699, T = 0.248157; substitution rates AC = 2.019840, AG = 6.434457, AT = 3.692459, CG = 1.477652, CT = 17.673435, GT = 1.000000; gamma distribution shape parameter α = 0.587217. Bootstrap support values for ML and MP greater than 65% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Didymella exigua* (CBS 183.55) and *Phoma herbarum* (CBS 615.75). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Thyrostroma ulmeum Senwanna, Bulgakov & K.D. Hyde, sp. nov. Fig. 6

Index Fungorum number: IF557793; Facesoffungi number: FoF08711

Etymology – Named after the host genus on which it occurs, *Ulmus*.

Associated with canker on twigs of hybrid elm *Ulmus minor* × *Ulmus pumila*. Sexual morph: Undetermined. Asexual morph: *Colonies* effuse, partly immersed, stromatic, erumpent through host epidermis, pulvinate to applanate, black, velvety, with lenticular or irregularly dehiscent openings. *Sporodochia* up to 500 µm diam., with pseudoparenchymatous basal stroma. *Conidiophores* 40–56 × 9–11 µm ($\bar{x}$ = 51.5 × 10.6 µm, n = 16), macronematous, erect, compactly packed, septate, branched, hyaline to pale brown, smooth. *Conidiogenous cells* 22–34 µm long, enteroblastic, annellidic, with 1–2 annellations, integrated, terminal. *Conidia* 44–58 × 14–21 µm ($\bar{x}$ = 51.8 × 17.7 µm, n = 50), acrogenous, fusiform to obclavate or obpyriform, muriform, pale to dark brown, truncate at base, 3–6 µm diam., rounded at apex, 3–5-transverse septate, with longitudinally 0–1-septate, rough-walled, minutely echinulate.

Material examined – Ukraine, Donetsk region, Donetsk Botanical Garden, trees near pond, on dead twigs of hybrid elm *Ulmus minor* × *Ulmus pumila* (Ulmaceae), 20 May 2017, T.S. Bulgakov DNK117 (MFLU 17-2538, holotype).

GenBank submissions – ITS: MT627476, LSU: MT627478, *TEF1-α*: MT614250.

Known distribution (based on molecular data) – Ukraine (this study).

Known hosts (based on molecular data) – *Ulmus minor* × *Ulmus pumila* (this study).

Notes – *Thyrostroma ulmeum* is similar to *Dothidotthia* species and *Wilsonomyces* species in conidial shape (Marin-Felix et al. 2017, Senwanna et al. 2019a). However, *Thyrostroma* and *Dothidotthia* have holoblastic, monoblastic, or annellidic, percurrently proliferating conidiogenous cells, whereas *Wilsonomyces* has holoblastic, sympodially proliferating conidiogenous cells. In addition, *Thyrostroma ulmeum* differs from *Dothidothia* in having longer conidia and a different number of transverse and longitudinal septa. Based on the NCBI BLASTn search of LSU and ITS sequence data, closest matches for *Thyrostroma ulmeum* are *Dothidotthia negundinicola* (CBS 145039 98% similarity) and *Thyrostroma cornicola* (CPC 25427 96% similarity) respectively. Phylogenetic analyses based on a combined LSU, SSU, ITS and *TEF1-α* sequence data (Fig. 5) reveal that *Thyrostroma ulmeum* forms a sister lineage with *T. tiliae* and groups with *T. ulmigenum*. *Thyrostroma ulmeum* is easily distinguished from *T. tiliae* and *T. ulmigenum* by the conidial shape. The conidial shape of *Thyrostroma tiliae* is cylindrical to ellipsoidal, or subclavate to vermiform and *T. ulmigenum* is oblong to subcylindric-clavate, or clavate, phragmosporous to muriform, while conidial shape of *T. ulmeum* is fusiform to obclavate or obpyriform. Based on the comparison of LSU and ITS nucleotides, *Thyrostroma ulmeum* is not significantly different from *T. tiliae* and *T. ulmigenum* (0/804 bp of LSU, 7/480 (1.45%) bp of ITS). While, a comparison of *TEF1-α* nucleotides shows that *T. ulmeum* differs from *T. tiliae* and *T. ulmigenum* in 9/865 bp (1.04%) and 15/865 bp (1.73 %), respectively.

Thyrostroma ulmicola Senwanna, Wanas., Bulgakov, Phookamsak & K.D. Hyde, Mycosphere 10, 729 (2019) Fig. 7

Index Fungorum number: IF556533; Facesoffungi number: FoF09097

Associated with canker on twigs of *Ulmus minor*. Sexual morph: Undetermined. Asexual morph: *Colonies* effuse, stromatic, black, velvety. *Sporodochia* 300–750 µm diam., partly immersed, with pseudoparenchymatous basal stroma, erumpent through host epidermis, pulvinate to applanate. *Conidiophores* 28–57 × 6–8 µm (x̄ = 41.8 × 7.3 µm, n = 30), macronematous, erect, compactly packed, septate, branched, hyaline to pale brown, smooth. *Conidiogenous cells* 13–23 µm (x̄ = 18.3 µm, n = 40) long, holoblastic, monoblastic, annellidic, percurrently proliferating with 1–3 annellations, integrated, terminal. *Conidia* 24–30 × 12–16 µm (x̄ = 27.5 × 14.4 µm, n = 40), acrogenous, ellipsoidal to obovoid, subclavate, muriform, pale to dark brown, truncate at base, 3–6 µm diam., rounded at apex, mostly 3-transverse septate, with longitudinally 0–1-septate, constricted at the septa, rough-walled, minutely echinulate.

Material examined – Ukraine, Donetsk region, regional landscape park "Donetsky Kryazh" ("Donetsk Ridge", protected area), ravine forest, on dead twigs of *Ulmus minor* (Ulmaceae), 19 May 2017, T.S. Bulgakov DNK074 (MFLU 17-2496).

GenBank submissions – ITS: MT627475, LSU: MT627477.

Known distribution (based on molecular data) – Russia (Senwanna et al. 2019a), Ukraine (this study).

Known hosts (based on molecular data) – *Ulmus pumila* (Senwanna et al. 2019a), *Ulmus minor* (this study).

Notes – *Thyrostroma ulmicola* was introduced by Senwanna et al. (2019a) based on morphological comparisons and phylogenetic analysis. The new isolate (MFLU 17-2496) was collected from the twigs of *Ulmus minor* in Russia. The morphology of our isolate is similar to *T. ulmicola* described by Senwanna et al. (2019a), even though our isolate has longer conidiogenous cells and smaller conidia than in the original description (conidiogenous cells: 11–29 µm *vs.* 6–13 µm; conidia: 23–32 × 11–17 µm *vs.* 30–59 × 12–26 µm) (Senwanna et al. 2019a). Phylogenetic analyses of the combined LSU, SSU, ITS and *TEF1-α* sequence dataset show that our strain (MFLU 17-2496) groups with *T. ulmicola* with moderate support (88% ML and 0.99 BYPP). According to the NCBI BLASTn search of LSU and ITS sequences, our new isolate showed 99% and 98% similarities to *T. ulmicola* respectively. *Thyrostroma ulmicola* has been reported from *Ulmus pumila* in Russia (Senwanna et al. 2019a). Thus, we identify the new isolate as *T. ulmicola* and our new collection as a new host record from Russia.

Hermatomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka, Persoonia 39, 56 (2017)

Index Fungorum number: IF819238; Facesoffungi number: FoF08251

Hermatomycetaceae was introduced as a provisional name (Locquin 1984) and reintroduced and typified by *Hermatomyces* (Hashimoto et al. 2017). Only *Hermatomyces* is reported in this family (Wijayawardene et al. 2018).

Hermatomyces Speg., Anales del Museo Nacional de Historia Natural Buenos Aires ser. 3 13, 445 (1910)

Index Fungorum number: IF8517; Facesoffungi number: FoF08252

Hermatomyces was established and typified by *H. tucumanensis* (Spegazzini 1910). This genus was introduced based only on the asexual morph, and it has been treated as '*incertae sedis*' for a long time, within Ascomycota (Wijayawardene 2012). Subsequently, *Hermatomyces* was placed to Lophiotremataceae based on their phylogenetic analyses using SSU, LSU, *TEF1-α*, and *RPB2* gene regions (Tibpromma et al. 2016a, Doilom et al. 2017). Hashimoto et al. (2017) found that *Hermatomyces* is distantly related to Lophiotremataceae by using additional species of Lophiotremataceae, and *Hermatomyces* was placed in Hermatomycetaceae. *Hermatomyces* has a wide host range; most species of this genus occur on angiosperms and monocotyledons in general, and rarely from ferns (Ruiz & Heredia 2000) or gymnosperms (Mel'nik 2000). In this study, an updated phylogenetic tree for *Hermatomyces* species with new host records from angiosperms is presented (Fig. 8)

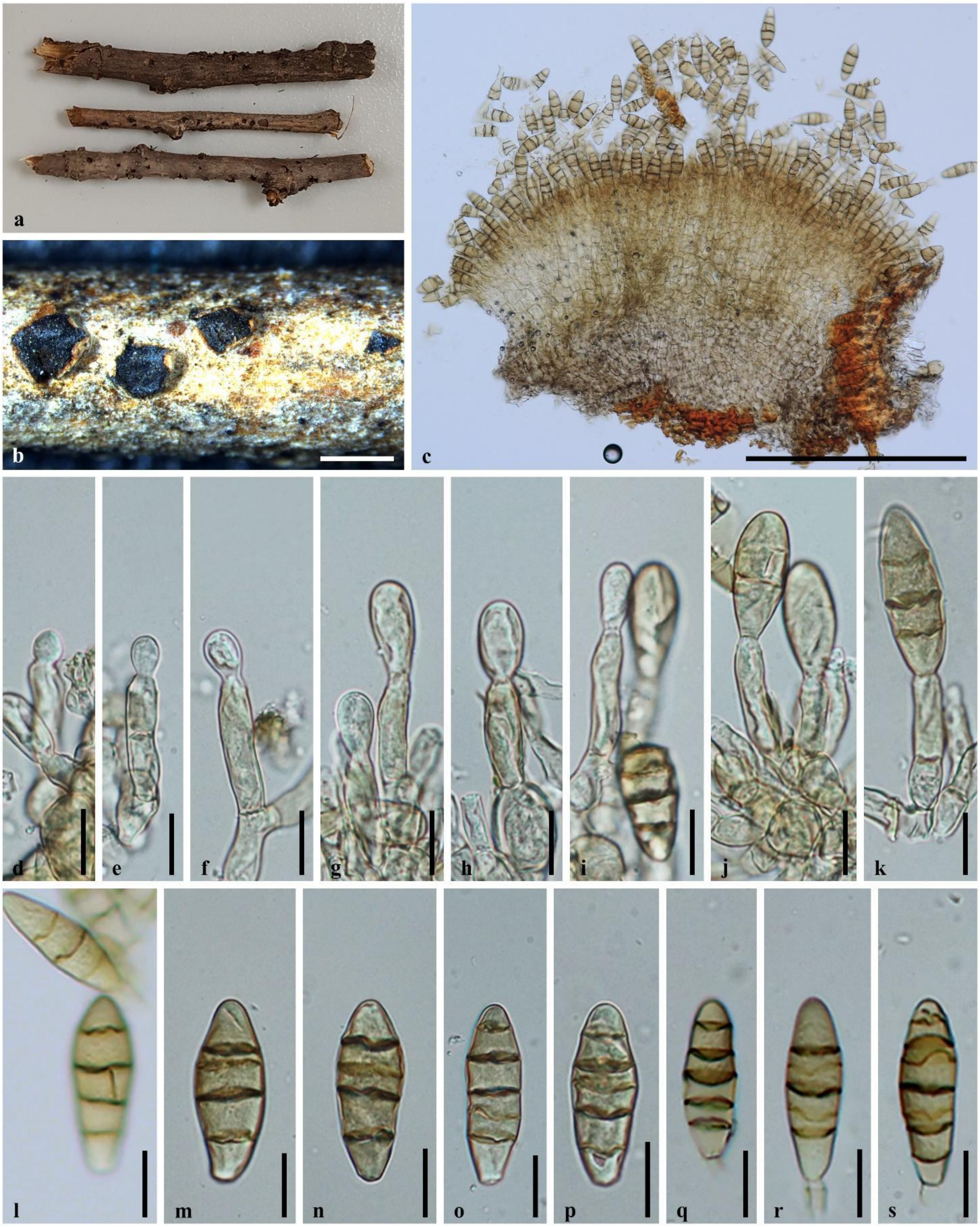

Fig. 6 – *Thyrostroma ulmeum* (MFLU 17-2538, holotype). a, b Sporodochia on host surface. c Vertical section of sporodochium. d–k Stages of developing conidia. l–q Conidia. Scale bars: b = 1000 µm, c = 300 µm, d–s = 20 µm.

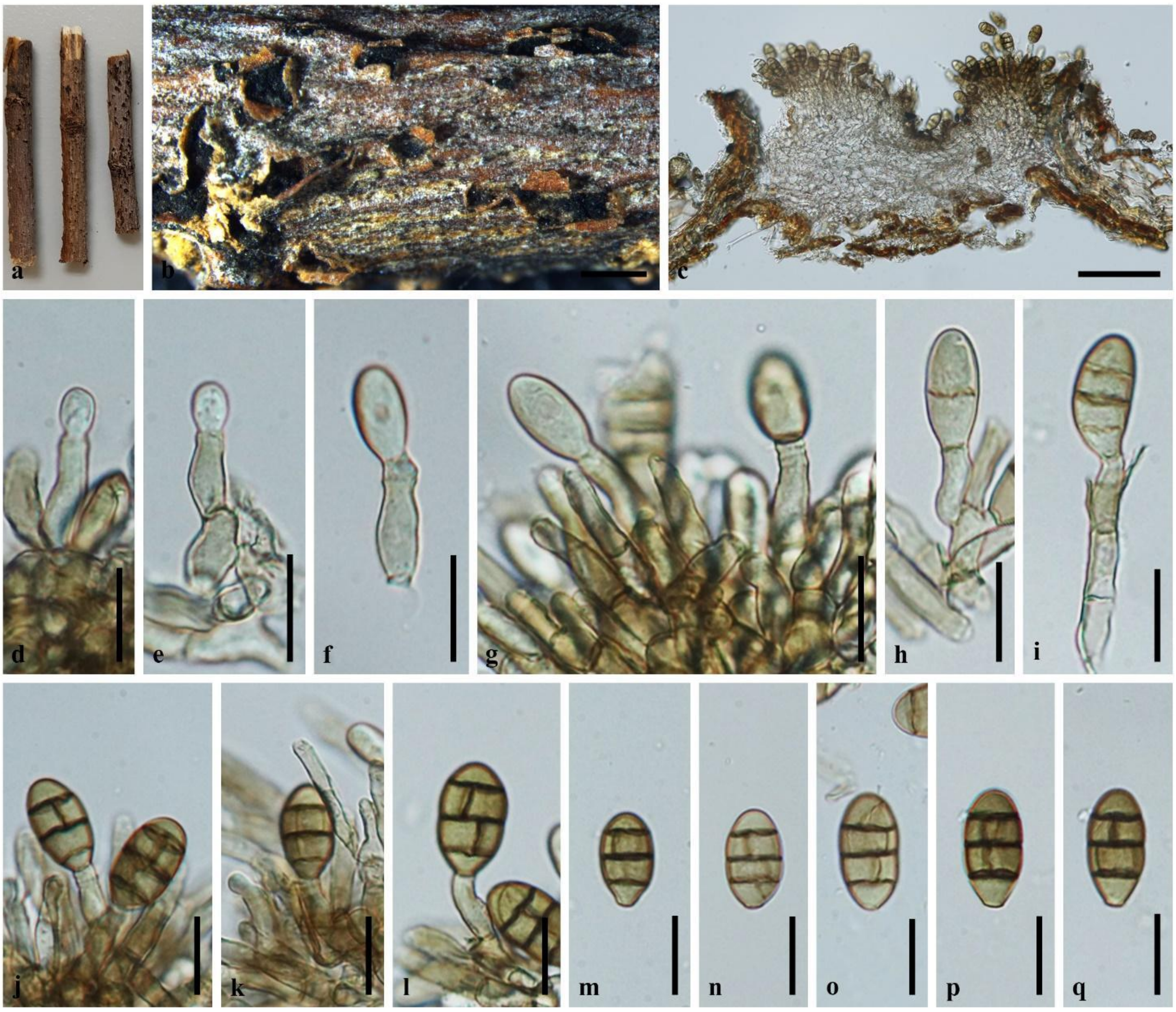

Fig. 7 – *Thyrostroma ulmicola* (MFLU 17-2496, a new host record). a–b Sporodochia on host surface. c Vertical section of sporodochium. d–l Stages of developing conidia. m–q Conidia. Scale bars: b = 1000 µm, c = 100 µm, d–q = 20 µm.

Hermatomyces thailandica Doilom D.J. Bhat & K.D. Hyde, Fungal Diversity 82, 121 (2016)

Fig. 9

Index Fungorum number: IF622304; Facesoffungi number: FoF01851

Saprobic on cankers of *Dipterocarpus* species. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate, superficial, gregarious, scattered, circular or oval, velvety, bird nest-like, brown to black. *Mycelium* 1.5–3 µm wide, hyaline to brown, superficial, septate, branched, anastomosing, composed of a compact network, geniculate, reddish-brown. *Conidiophores* 1.5–3 µm wide, micronematous to semi-macronematous, mononematous, straight or flexuous, cylindrical, septate, unbranched, slightly constricted at the septa, hyaline to brown, short, smooth corresponding to conidiogenous cells. *Conidiogenous cells* monoblastic, integrated, terminal, arising directly on the superficial mycelium and closely packed together at the fertile centre, cylindrical, hyaline to sub-hyaline, smooth. *Conidia* two types, dimorphic, lenticular and cylindrical. *Lenticular conidia* thick-walled, smooth, central cells mostly black or dark brown to blackish brown, with peripheral cells hyaline to subhyaline, forming a distinct ring on the outside up to 2–4 µm wide, with one column composed of 6–7 cells, slightly constricted at the septa, 28–34 × 19–26 µm thick in lateral views ($\bar{x}$ = 30.5 × 22.9 µm, n = 30). *Cylindrical conidia* 27–39 × 14–24 wide in broadest part of lower cells, ($\bar{x}$ =33.6 × 18.5 µm, n = 30), with 2 columns composed of 3 cells, with black peripheral cells, dark brown upper cells, usually with two cells hyaline in the lower cells, subglobose, swollen at the lower part, verrucose.

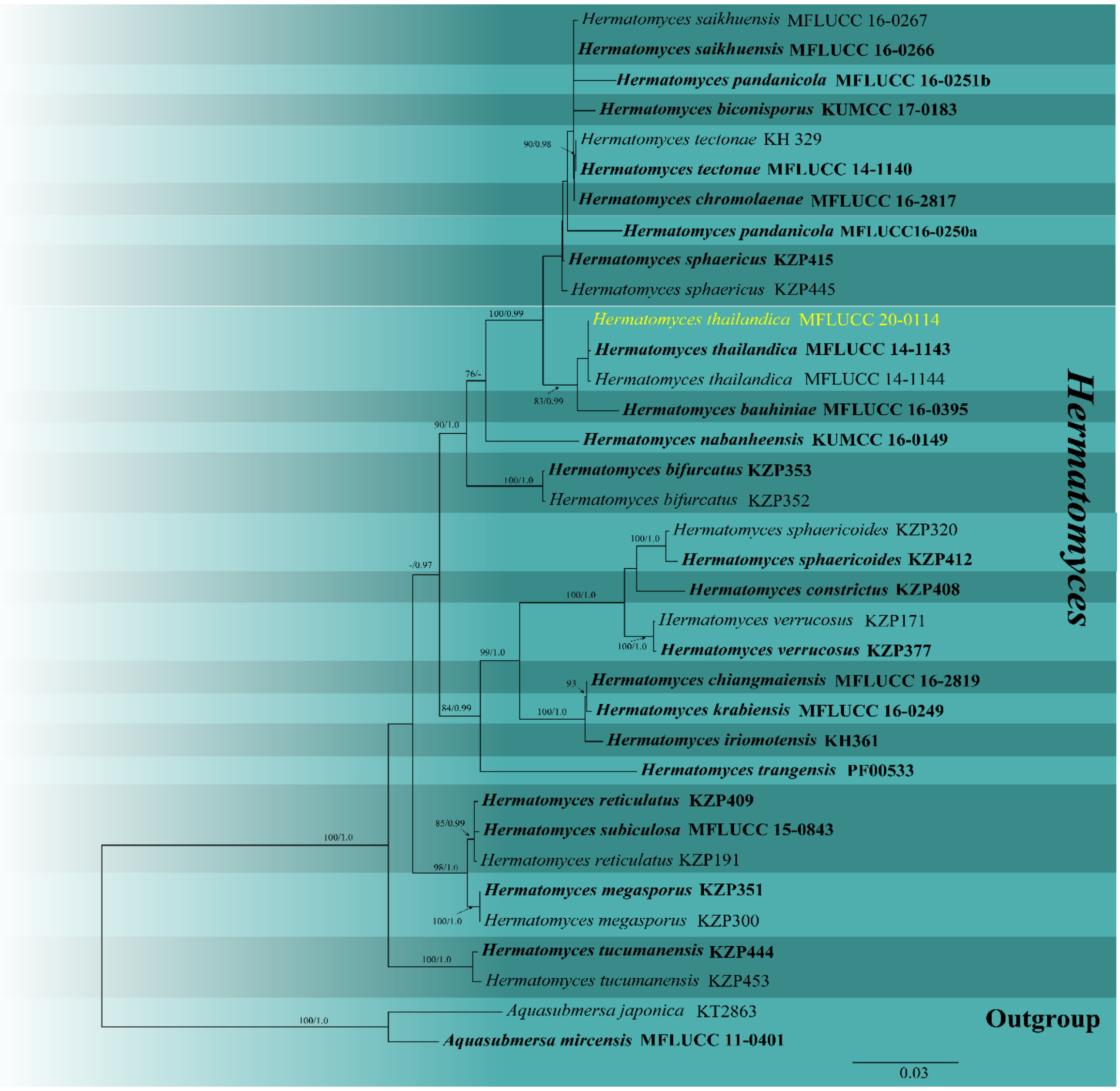

Fig. 8 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU *RPB2* and *TEF1-α* sequence data. Thirty-five strains are included in the combined analyses which comprised 1381 characters 3298 characters (551 characters for ITS, 817 characters for LSU, 1009 characters for *RPB2*, 921 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 -11086.573181 is presented. Estimated base frequencies were as follows: A = 0.2445500, C = 0.262230, G = 0.262433, T = 0.229837; substitution rates AC = 1.114857, AG = 4.503160, AT = 1.470167, CG = 0.813085, CT = 11.941093, GT = 1.000000; gamma distribution shape parameter α = 0.134388. The evolutionary model SYM+I+G applied to both ITS and *TEF1-α* sequence data, while GTR+I+G applied to both LSU and *RPB2* gene regions. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Aquasubmersa japonica* (KT2863) and *A. mircensis* (MFLUCC 11-0401). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes produced around conidia. Colonies reached about 7 cm diameter after 2 weeks on PDA at room temperature. *Colonies* are superficial with entire edge, flat or effuse at the convex with papillate surface at the center, gray to hyaline, dark at the center, fluffy, dense; grey at the center and yellowish grey at the edge from the reverse of culture.

Material examined – Thailand, Chiang Rai Province, Muang District, Mae Fah Luang University, Botanic Garden, on cankers of *Dipterocarpus* (Dipterocarpaceae), 10 March 2019, Xia Tang Dip03 (MFLU 20-0527), living culture MFLUCC 20-0114.

GenBank numbers – ITS: MT883355, LSU: MT883353, RPB2: MT890636.

Known distribution (based on molecular data) – Thailand (Doilom et al. 2017, this study).

Known hosts (based on molecular data) – dead moist twigs of *Tectona grandis* and cankers of *Dipterocarpus* (Dipterocarpaceae) (Doilom et al. 2017, this study).

Notes – *Hermatomyces thailandica* was described from dead moist twigs of *Tectona grandis* by Doilom et al. (2017). Subsequently, Koukol et al. (2018) reduced *Hermatomyces indicus* to a synonymy of *H. thailandica*, based on the morphological data. Compared to the holotype, our collection was in an acceptable range in morphology. Comparisons of ITS, LSU and *RPB2* sequence data between our collection and the holotype showed that they are 100% similar. Our collection is identified as *H. thailandica* following the guidelines for species delineation proposed by Jeewon & Hyde (2016). This is the first report of *H. thailandica* on *Dipterocarpus* in Thailand.

Longipedicellataceae Phukhams., Bhat & K.D. Hyde, Mycosphere 7, 1722 (2016)

Index Fungorum number: IF552532; Facesoffungi numbers: FoF02665

Longipedicellataceae was introduced by Phukhamsakda et al. (2016) to accommodate two saprobic genera, *Longipedicellata* and *Pseudoxylomyces* found on woody substrates in freshwater habitats. Longipedicellataceae is characterized by semi-immersed or erumpent, clypeate ascomata on the host tissues with black to brown ostioles, clavate asci with long pedicels, and 2-celled, hyaline ascospores. Chlamydospore formation is a significant character of this family (Phukhamsakda et al. 2016). The latest treatment and updated account of Longipedicellataceae followed recent papers of Hongsanan et al. (2020a) and Wijayawardene et al. (2020). An updated phylogeny for the family is provided in Fig. 10.

Pseudoxylomyces Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 126 (2015)

Index Fungorum number: IF811332; Facesoffungi number: FoF08272

Pseudoxylomyces was introduced by Tanaka et al. (2015) to accommodate *P. elegans* (≡*Xylomyces elegans*). *Xylomyces* (Aliquandostipitaceae, Jahnulales) is characterized by large, thick-walled, dark, multiseptate, intercalary, narrowly fusiform chlamydospores but lacks conidiophores and conidiogenous cells (Goos et al. 1977, Goh et al. 1997). In contrast, *Pseudoxylomyces* is distinct in producing broadly fusiform conidia holoblastically at the tip of their conidiophores (Tanaka et al. 2015). *Pseudoxylomyces* morphologically resembles *Pithomyces* (Astrosphaeriellaceae, Pleosporales) but the latter has obovate to oblong conidia with cells without distinct granular cytoplasm.

Pseudoxylomyces elegans (Goh, W.H. Ho, K.D. Hyde & C.K.M. Tsui) Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 126 (2015)

≡ *Xylomyces elegans* Goh, W.H. Ho, K.D. Hyde & K.M. Tsui, Mycological Research 101, 1324 (1997) Fig. 11

Index Fungorum number: IF811333; Facesoffungi number: FoF09259

Saprobic on submerged decaying wood in a freshwater stream. *Mycelium* immersed in agar, pale brown to reddish brown. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous. Conidiophores* macronematous, septate, flexuous, hyaline to subhyaline, smooth, up to 160 µm long. *Conidiogenesis* intercalary in the hyphae, gangliar-type. *Conidia* 50–86 × 22–34 µm ($\bar{x}$ = 66.7 × 26.3 µm), broadly fusiform, 4–7-septate, with central two cells widest, constricted at septa, dark brown, with paler end cells, smooth at young, warty when matured, cells with granular cytoplasm.

Culture characteristics – Conidia germinating on MEA within 24 h and germ tubes produce from anterior and basal part of conidia. Colonies on the MEA, 10–15 mm diam. after 15 days at 25°C, circular, fluffy, aerial, light gray mycelium with fimbriate margin, dark brown to reddish brown reverse.

Material examined – Thailand, Phuket Province, Thalang District, Mai Khao, stream, on submerged wood, 5 May 2019, Mark S. Calabon FWHY1 (MFLU 20-0554), culture MFLUCC 20-0186.

GenBank submissions – ITS: MT465322, LSU: MT447878

Known distribution (based on molecular data) – Australia (Goh et al. 1997), Brazil (Barbosa & Gusmão 2011), China (Tsui & Hyde 2004), India (Patil & Borse 2015), Japan (Tanaka et al. 2015), Seychelles (Goh et al. 1997), Thailand (Sivichai et al. 2000, Dong et al. 2020) and USA (Raja et al. 2007).

Known hosts (based on molecular data) – submerged wood of unknown hosts in a river (Tanaka et al. 2015) and a stream (Pratibha & Prabhugaonkar 2017, Dong et al. 2020).

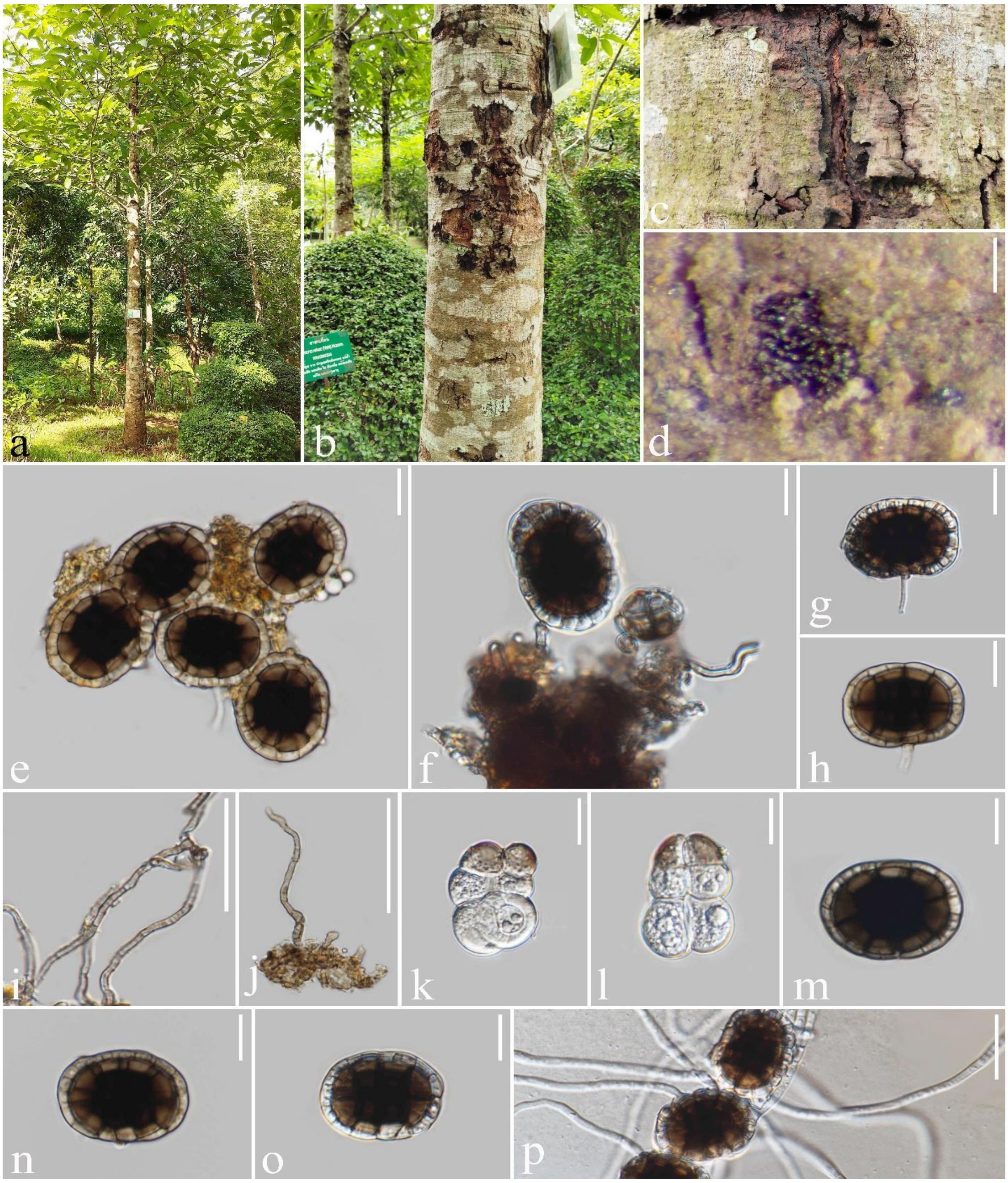

Fig. 9 – *Hermatomyces thailandica* (MFLUCC 20-0114, a new host record). a–c Host. d Colonies. e Conidia and conidiophores. f Conidia and conidiogenous cells. g, h Conidia bearing mycelia. i, j Mycelia. k–l Cylindrical conidia. m–o Lenticular conidia. p Germinated conidia. Scale bars: d = 200 µm, e–h, k–p = 20 µm, i, j = 50 µm.

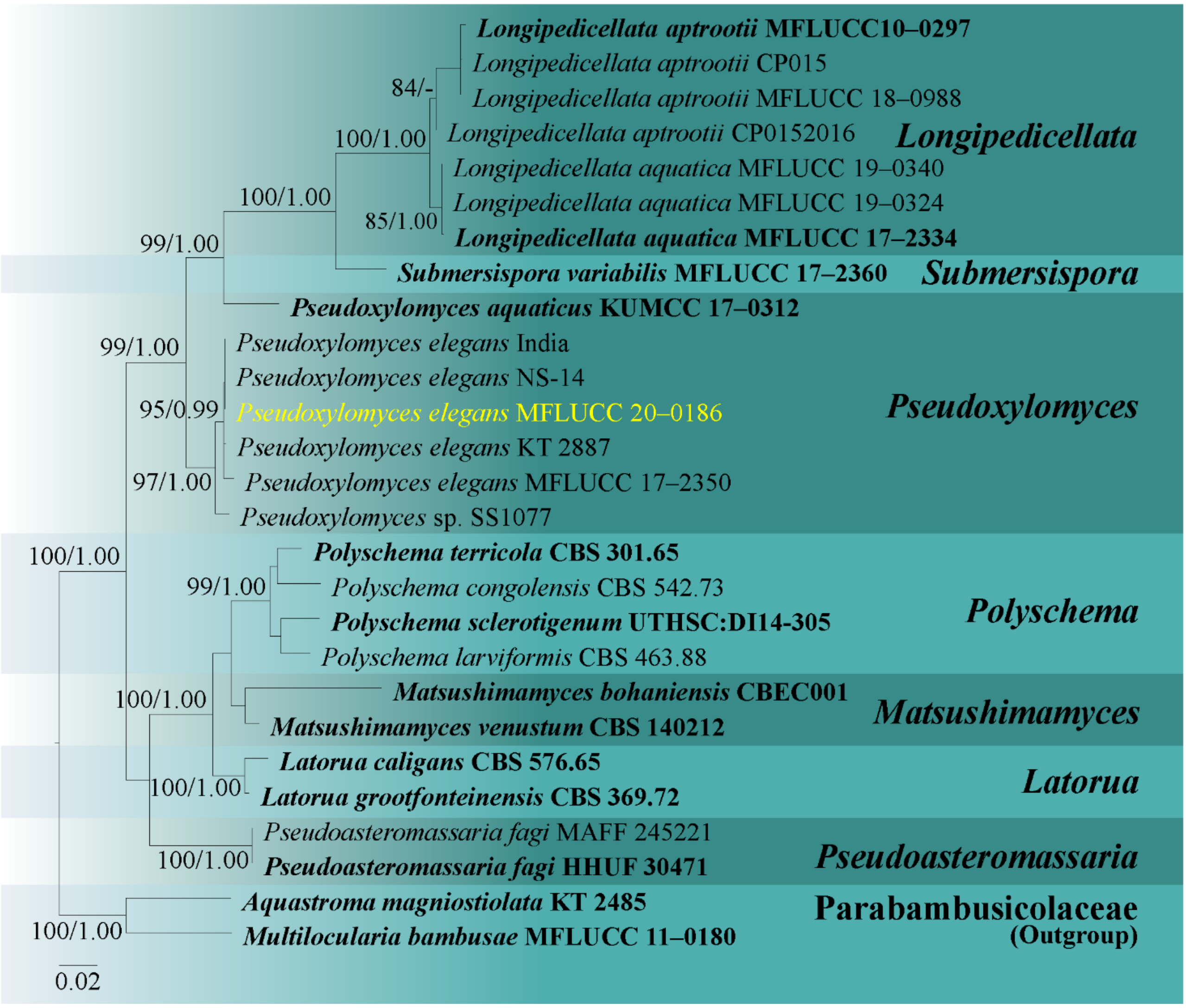

Fig. 10 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty-seven strains are included in the combined analyses which comprised 1886 characters (1339 characters for LSU, 547 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -7174.310436 is presented. Estimated base frequencies were as follows: A = 0.237417, C = 0.247156, G = 0.291555, T = 0.223872; substitution rates AC = 2.233365, AG = 2.340939, AT = 1.327491, CG = 1.608602, CT = 7.032238, GT = 1.000000; gamma distribution shape parameter a = 0.199782. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Aquastroma magniostiolata* (KT 285) and *Multilocularia bambusae* (MFLUCC 11-0180). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Notes – *Pseudoxylomyces elegans* is widely distributed in the freshwater habitats and has been recorded from different countries (see known distribution) but only Pratibha & Prabhugaonkar (2017) and Tanaka et al. (2015) provided the molecular data of the species. Our collection (MFLUCC 20-0186) resembles *P. elegans* in having similar morphology such as broadly fusiform, 4–7-septate, brown conidia, with paler end cells (Tanaka et al. 2015). Multi-gene phylogeny also indicates that our collection nested with *Pseudoxylomyces elegans* with high bootstrap support (92% ML, 0.99 BYPP). *Pseudoxylomyces elegans* was formerly collected from submerged baits of *Dipterocarpus alatus* and *Xylia dolabriformis* in Nakorn Ratchassima, Thailand by Sivichai et al. (2000) but the molecular data was not provided. Therefore, based on both morphology and phylogeny, we introduce a new geographical record (Phuket, Thailand) of *Pseudoxylomyces elegans*.

Fig. 11 – *Pseudoxylomyces elegans* (MFLU 20-0554, new geographical record). a Appearance of the host tissue. b, c Appearance of conidial structures on host. d–g Conidiophores and conidia. h–l Conidia. m Germinating conidia. n Obverse and reverse view of colony on MEA, 25 days at 25 °C. Scale bars: b, c = 1 mm, d = 100 µm, e–m = 100 µm.

Parabambusicolaceae Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 115 (2015)

Index Fungorum number: IF811324; Facesoffungi number: FoF06708

Parabambusicolaceae (Massarineae, Pleosporales) was established with *Parabambusicola* as the type (Tanaka et al. 2015). The family is characterized by pseudothecioid ascomata, clavate to fusiform, fissitunicate asci, and hyaline or brown phragmospores. The asexual morphs in Parabambusicolaceae are sporodochial or monodictys-like hyphomycetes or coelomycetes (Liu et al. 2015, Tanaka et al. 2015, Li et al. 2016, Wanasinghe et al. 2017, Phukhamsakda et al. 2018, Samarakoon et al. 2019a). Wijayawardene et al. (2020) accepted nine genera in Parabambusicolaceae. An updated phylogeny for the family is provided in Fig. 12.

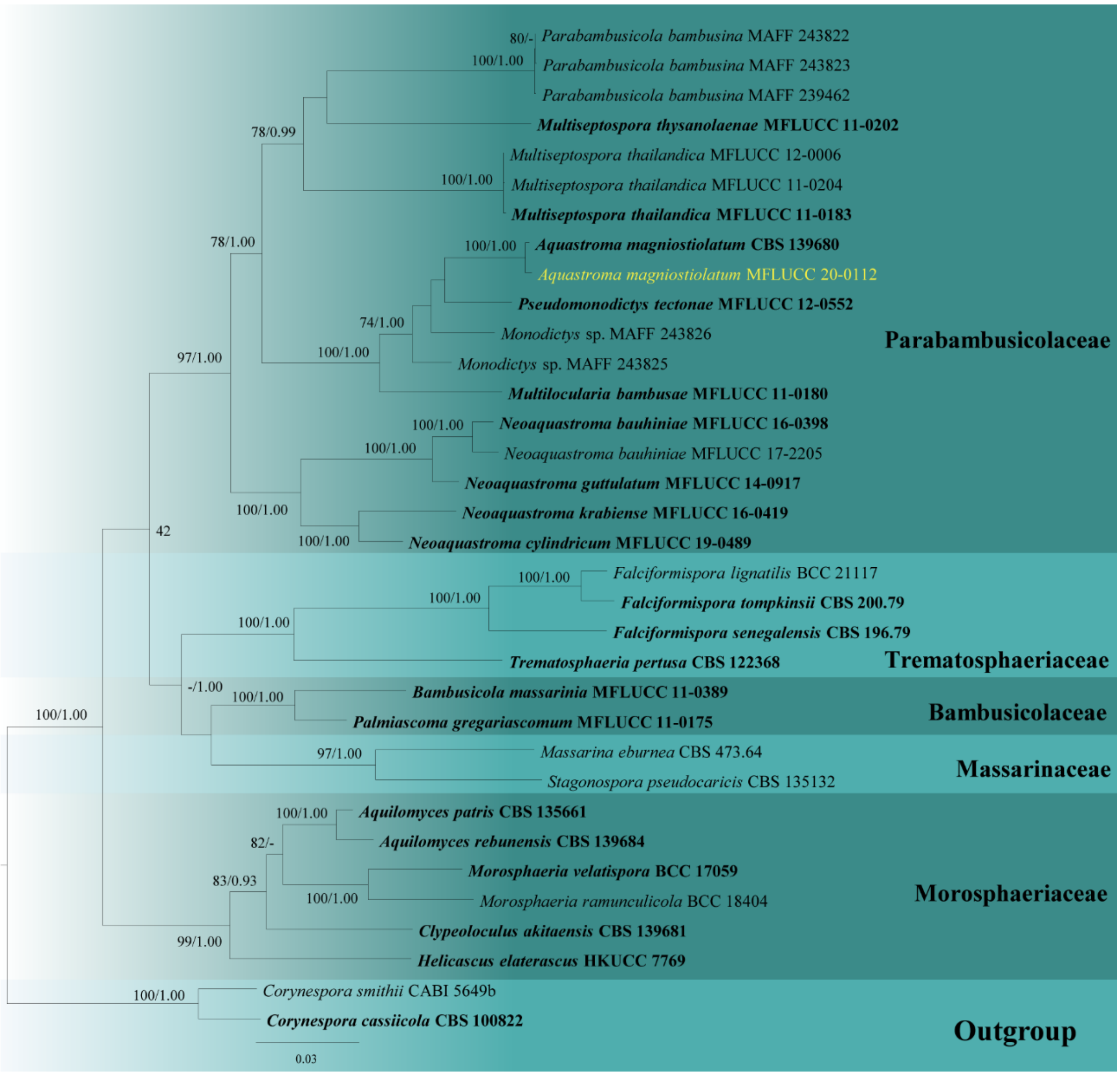

Fig. 12 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *TEF1-α* sequence data. Thirty-four strains are included in the combined analyses which comprised 3329 characters (909 characters for LSU, 1019 characters for SSU, 481 characters for ITS, 920 characters 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 -16400.001719 is presented. Estimated base frequencies were as follows: A =0.238160, C = 0.251390, 0.273492, T = 0.236959; substitution rates AC = 1.273333, AG = 2.948753, AT = 1.564711, CG = 1.244097, CT = 7.370215, GT = 1.000000. For all the gene regions GTR+I+G was applied as the evolutionary model. Bootstrap support values for ML and MP greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes respectively. The tree is rooted with *Corynespora cassiicola* (CBS 100822) and *C. smithii* (CABI 5649b). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Aquastroma Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 115 (2015)

Index Fungorum number: IF811325; Facesoffungi number: FoF08321

Aquastroma was introduced as a monotypic genus by Tanaka et al. (2015) with *A. magniostiolatum* as the type species. The genus is characterized by immersed to erumpent, globose in surface view, scattered to grouped compressed ascomata, with heavily melanised, subglobose cells, with a thick-walled ostiolar neck, fissitunicate, clavate, stipitate, 8-spored asci, hyaline, smooth-walled, multiseptate ascospores constricted at septa, surrounded by an entire sheath (Tanaka et al. 2015). *Aquastroma magniostiolata*, being the only species in the genus, was found from freshwater environment (Tanaka et al. 2015). In this study, a new geographical record of *A. magniostiolata* is described and illustrated (Fig. 13).

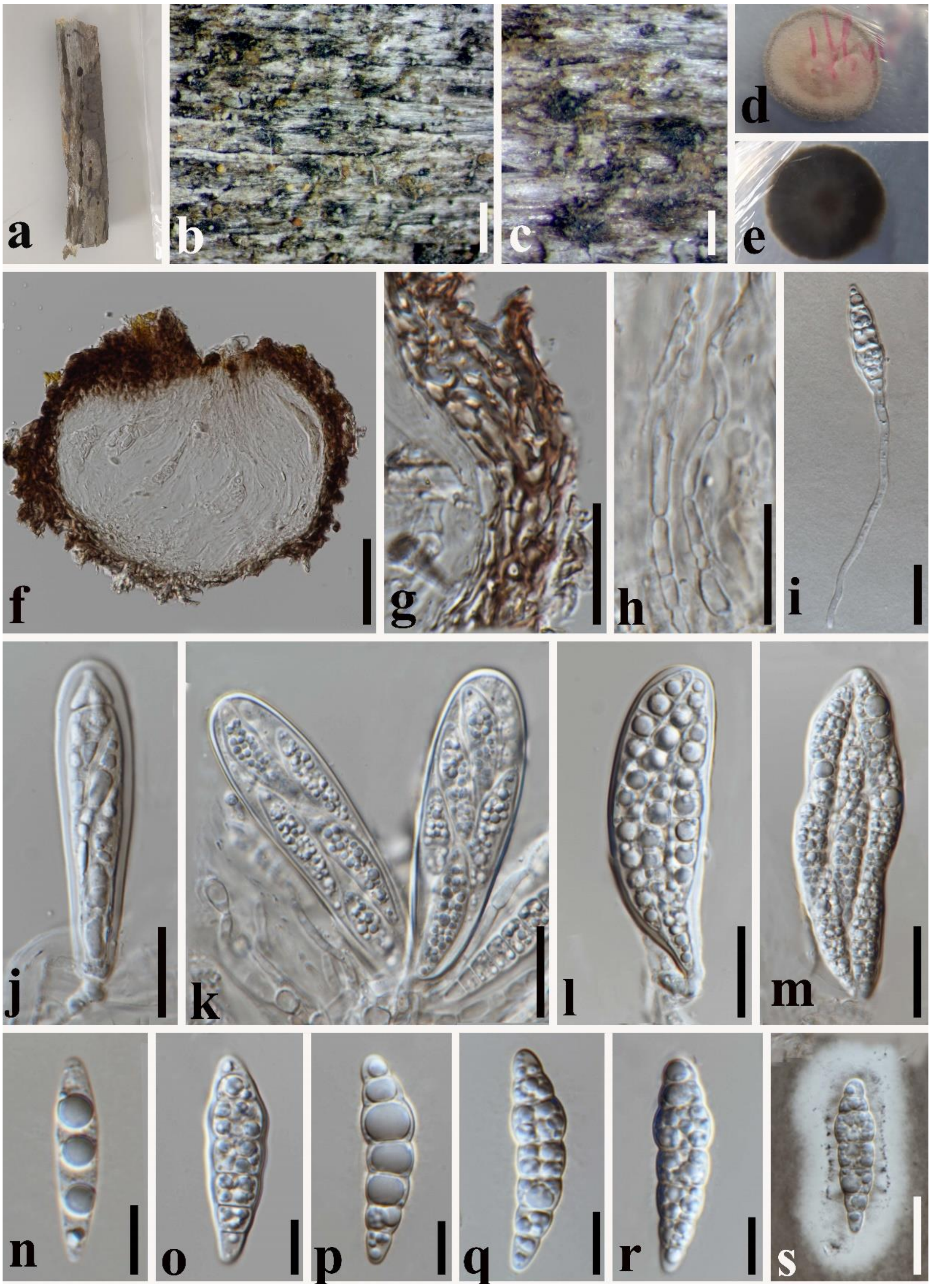

Fig. 13 – *Aquastroma magniostiolata* (MFLU 20-0484, new geographical record). a–c Appearance of ascoma on host surface. d–e Culture from above and below. f Vertical section of an ascoma. g Peridium. h Pseudoparaphyses. i Germinating ascospore. j–m Asci. n–r Ascospores. s Sheath surrounding the spore stained with Indian ink. Scale bars: b = 500 µm, c = 200 µm, f = 50 µm, g–m, s = 20 µm, n–r = 10 µm.

Aquastroma magniostiolatum Kaz. Tanaka & K. Hiray., Studies in Mycology 82, 115 (2015)

Fig. 13

Index Fungorum number: IF828557; Facesoffungi number: FoF08694

Saprobic on dead wood. Sexual morph: *Ascomata* 176–241 µm diam., 146–206 µm high, black domes visible on host cortex, solitary to gregarious, elliptical. *Peridium* thick-walled, pale brown cells of *textura angularis*. *Hamathecium* comprising numerous, 2–4 µm ($\bar{x}$ = 3 µm, n = 22), broad, septate, hyaline, smooth-walled, pseudoparaphyses. *Asci* 74–99 × 19–29 µm ($\bar{x}$ = 84 × 23 µm, n = 20), 8-spored, fissitunicate, pedicellate, clavate, bitunicate, short pedicellate, apically rounded with invisible ocular chamber, hyaline. *Ascospores* 34–42.6 × 6.8–9.7 µm ($\bar{x}$ = 38 × 8.5 µm, n = 30), crowded, clavate to fusiform, guttulate to granular, straight or slightly curved, multi-septate, constricted at septa, hyaline, smooth-walled, surrounded with mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 15 h at room temperature (25–28 ºC), reaching 3.2 cm in 22 days, entire edge, white in front, greenish grey to black at back, no pigment produced, flat or effuse, without aerial mycelium, smooth hyphae.

Material examined – Thailand, Chiang Rai Province, Mae Fah Luang University, on dead woody culm, 5 August 2019, Jing-Yi Zhang (MFLU 20-0484), living culture, MFLUCC 20-0112.

GenBank numbers – LSU: MT772011, ITS: MT772005, *TEF1-α*: MT777678.

Known distribution (based on molecular data) – Japan (Tanaka et al. 2015) and Thailand (this study).

Known hosts (based on molecular data) – Dead woody culms (Tanaka et al. 2015), this study).

Notes – *Aquastroma magniostiolatum* was introduced by Tanaka et al. (2015) based on a specimen collected from Japan. A new sample (MFLU 20-0484) was collected from Thailand for the first time in this study. Multi-gene phylogenetic analyses of the combined LSU, SSU, ITS and *TEF1-α* sequence data indicated that MFLU 20-0484 is conspecific with the ex-type of *A. magniostiolatum* (CBS 139680) (100% MLBP/1.00 BYPP/100% MP). MFLU 20-0484 is similar to CBS 139680 in morphology. Furthermore, MFLU 20-0484 has identical base pairs with CBS 139680 based on a comparison of LSU and ITS, while 6 base pair differences were observed out of 920 base pairs in *TEF1-α* sequences (Jeewon & Hyde 2016).

Sporormiaceae Munk, Dansk botanisk Arkiv 17, 450 (1957)

Index Fungorum number: IF81414; Facesoffungi number: FoF06565

Sporormiaceae typified by *Sporormia*, was established by Munk (1957). It includes nine genera: *Chaetopreussia*, *Forliomyces*, *Pleophragmia*, *Preussia*, *Sparticola*, *Sporormia*, *Sporormiella*, *Sporormurispora* and *Westerdykella* (Hongsanan et al. 2020a). Sporormiaceae species are saprobes on dung, plant debris, soil, wood and in some cases endophytic (Hausmann et al. 2002, Burney et al. 2003, van Geel et al. 2003, Kruys & Wedin 2009, Gonzalez-Menendez et al. 2017).

Westerdykella Stolk, Transactions of the British Mycological Society 38, 422 (1955)

Index Fungorum number: IF5772; Facesoffungi number: FoF06570

Westerdykella, typified with *W. ornata*, is characterized by cleistothecioid ascomata, small, short pedicellate asci encasing one-celled, verruculose ascospores, without germ slits (Kruys & Wedin 2009). The genus has a cosmopolitan distribution and have been isolated from various substrates such as dung, mud, plant material and soil (Clum 1955, Cain 1961, Malloch & Cain 1972, Ito & Nakagiri 1995). *Westerdykella* produce phoma-like asexual morphs in culture (Sue et al. 2014, Crous et al. 2017b). To date, 14 species have been described within *Westerdykella* (Index Fungorum 2020). Abdel-Aziz (2016) reported *Westerdykella* species in freshwater habitats. An updated phylogeny for the genus is provided in Fig. 14

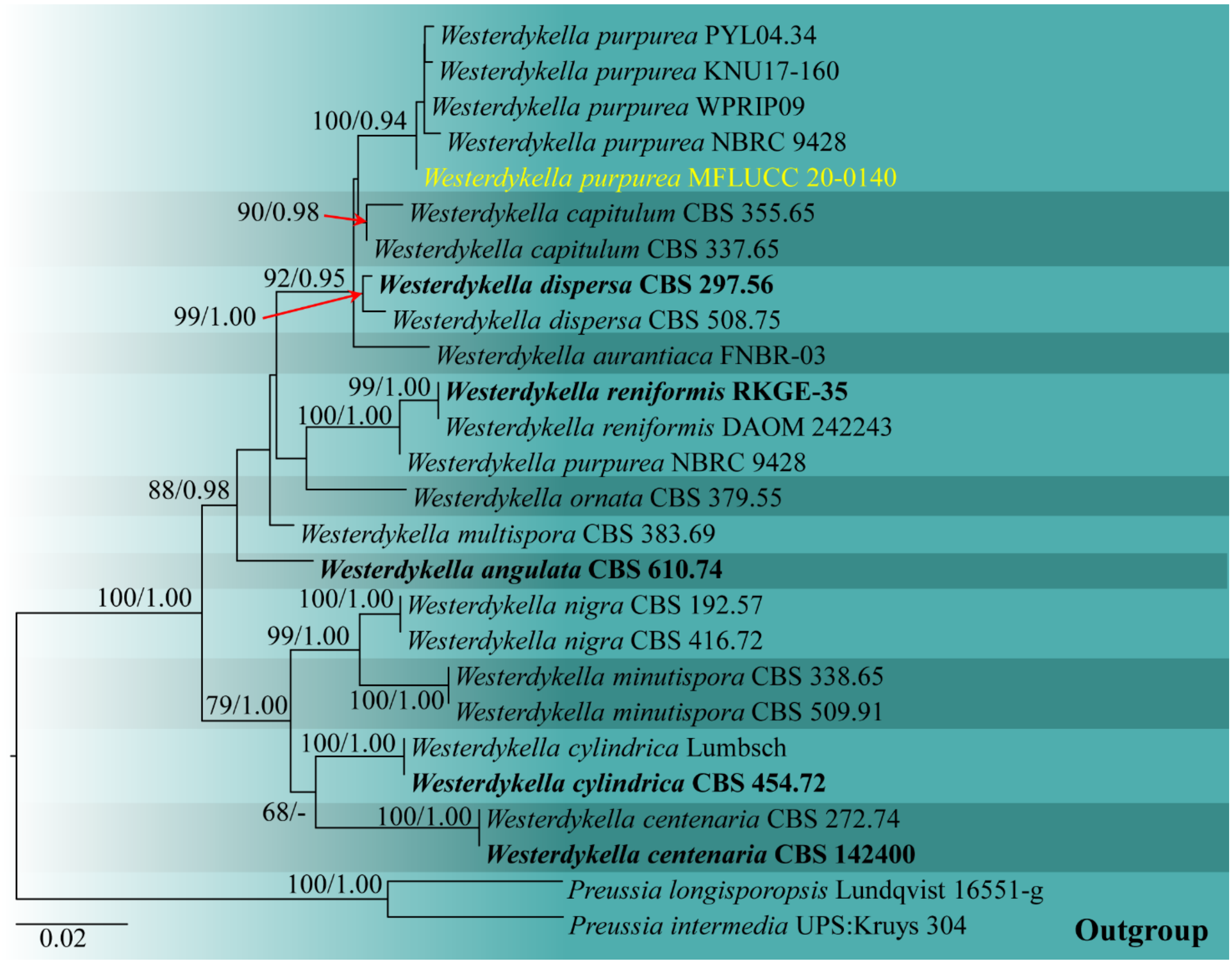

Fig. 14 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty-six strains are included in the combined analyses which comprised 1380 characters (877 characters for LSU, 503 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -4024.762813 is presented. Estimated base frequencies were as follows: A = 0.243185, C = 0.237776, G = 0.280053, T = 0.238986; substitution rates AC = 0.948333, AG = 1.449700, AT = 1.765595, CG = 0.630050, CT = 4.794304, GT = 1.000000; gamma distribution shape parameter α = 0.199782. Bootstrap support values for ML and MP greater than 65% and Bayesian posterior probabilities greater than 0.90 are given near nodes respectively. The tree is rooted with *Preussia longisporopsis* (Lundqvist 16551-g) and *P. intermedia* (UPS: Kruys 304). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Westerdykella purpurea (Cain) Arx, Kavaka 3, 33 (1976)

≡ *Preussia purpurea* Cain, Canadian Journal of Botany 39, 1647 Fig. 15

Index Fungorum number: IF325553; Facesoffungi number: FoF09408

Saprobic in submerged decaying wood in a freshwater habitat. Sexual morph: For illustrations and descriptions see Cain (1961). Asexual morph: *Conidiomata* 300–530 µm, pycnidial, globose to subglobose, black, shiny, smooth, superficial, without ostiole. *Conidiomatal wall* thin, membranaceous, semitransparent, with outer single layer of light olivaceous-brown, thin-walled, very distinct, composed of brown cells of *textura angularis* with inner thicker layer of hyaline, swollen cells. *Conidia* 2.5–6 × 1.5–4 µm ($\bar{x}$ = 4.71 × 2.61 µm), ellipsoid, light olivaceous-brown, smooth, with two prominent oil globules.

Culture characteristics – Conidia germinating on MEA within 24 h and germ tubes produce from the basal part of the ascospores. Colonies on the MEA, 20–25 mm diam. after 15 days at

25°C, circular, powdery, aerial, flat, initially white mycelium then becoming light yellow in old cultures, entire margin, yellowish orange reverse.

Material examined – Thailand, Phitsanulok Province, Wang Thong District, Kaeng Sopha waterfall stream, on submerged wood, 25 July 2019, S. Boonmee PSL/WT-05 (MFLU 20-0553), living culture MFLUCC 20-0140.

GenBank submissions – ITS: MT465323, LSU: MT447879

Known distribution (based on molecular data) – Africa (Ebead et al. 2012), China (Jie et al. 2015), Thailand (this study)

Known hosts (based on molecular data) – mangrove sediment (Jie et al. 2015), sandy soil (Ebead et al. 2012), unidentified decaying wood (this study)

Notes – *Preussia purpurea* was synonymized by Arx (1975) under *Westerdykella purpurea*. In the phylogenetic analysis, *W. purpurea* is closely related to *W. capitulum*. *Westerdykella purpurea* has a known sexual morph and this paper records its asexual morph. Sue et al. (2014) and Crous et al. (2017b) recorded a phoma-like asexual morphs in culture wherein conidia are clavate, ellipsoidal to pyriform, hyaline conidia while our collection has an ellipsoidal, light olivaceous brown, conidia. Multi-gene phylogeny indicates that our collection grouped with other strains of *W. purpurea* with good bootstrap support (100% ML, 0.94 BYPP). Based on morphology and phylogenetic analysis, we introduce a new geographical and habitat record of *W. purpurea*.

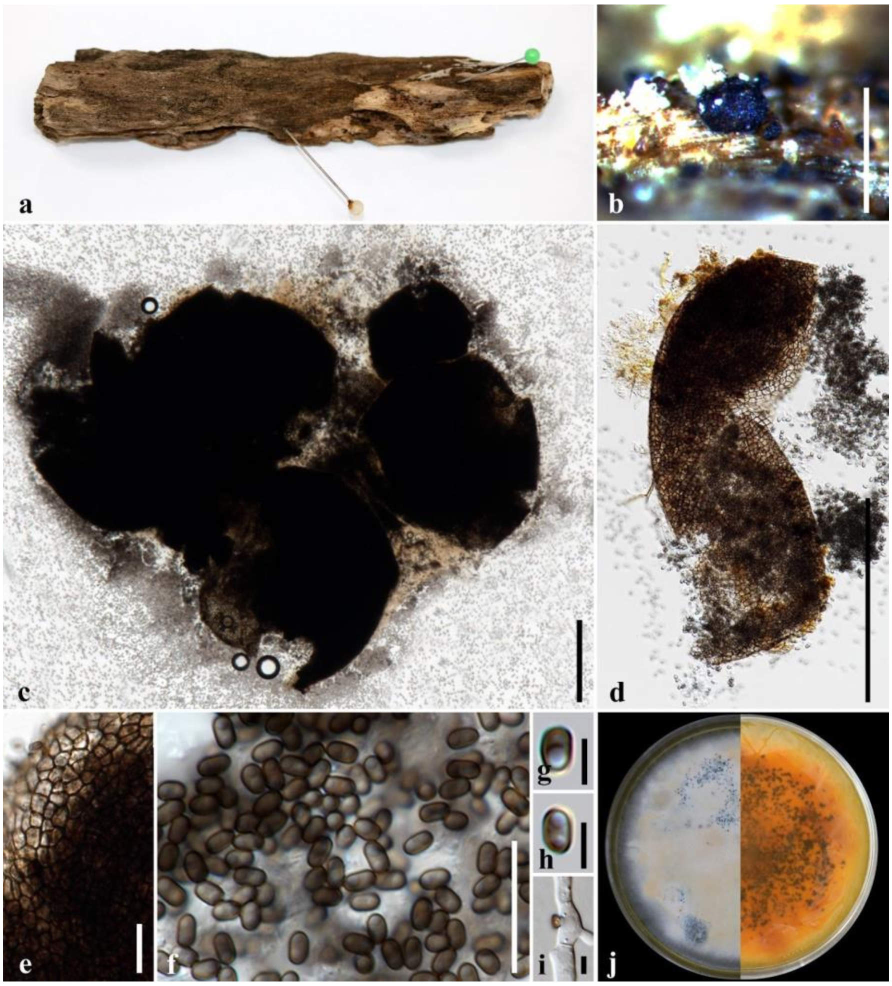

Fig. 15 – *Westerdykella purpurea* (MFLUCC 20-0140, new geographical and habitat record). a Appearance of the host tissue. b Appearance of conidiomata on host. c–d Squash mounts of conidiomata. e Conidiomatal wall. f–h Conidia. i Germinating conidia. j Obverse and reverse view of colony on MEA, 25 days at 25ºC. Scale bars: b = 500 µm, c–d = 200 µm, e–f = 20 µm, g–i = 5 µm.

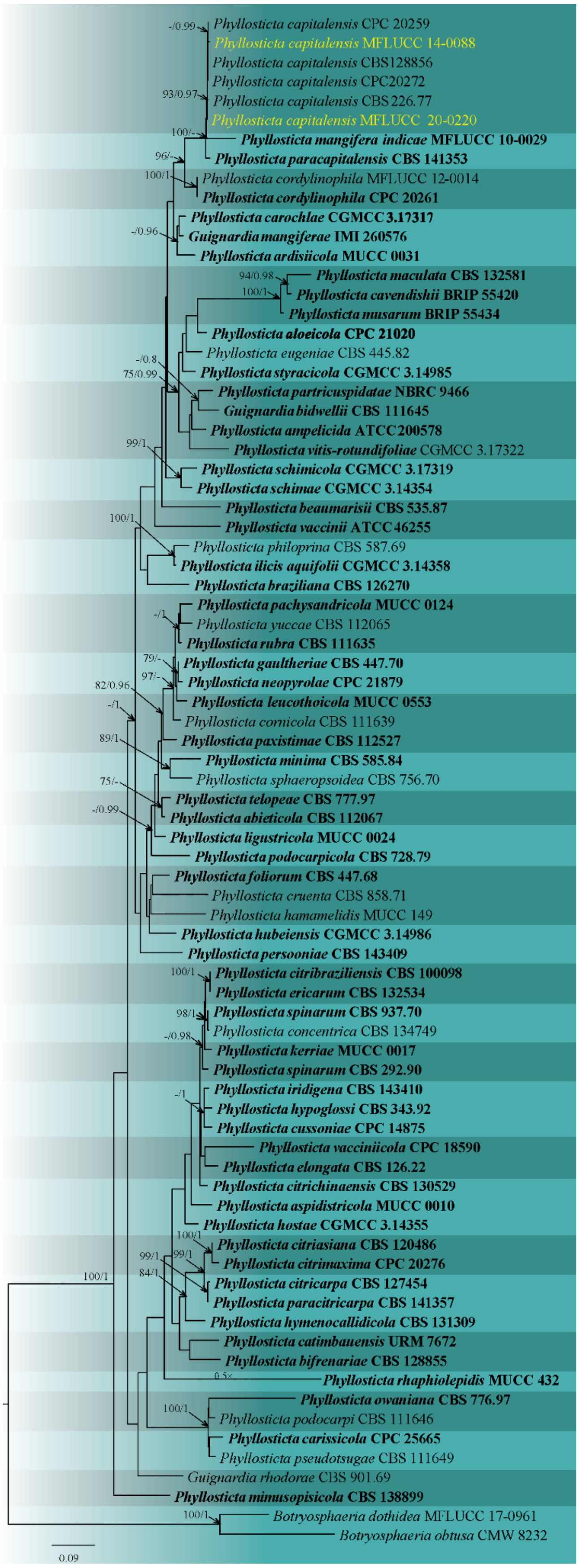

Fig. 16 – Phylogram generated from maximum likelihood analysis based on combined ITS, *ACT* and *TEF1-α* sequence data. Seventy-nine strains are included in the combined analyses which comprised 1076 characters (564 characters for ITS, 235 characters for *ACT*, 277 characters for *TEF1-α*) after alignment. Tree topology of the maximum likelihood analysis is similar to the

Bayesian analysis. The best RaxML tree with a final likelihood value of -6956.854232 is presented. The best RaxML tree with a final likelihood value of -14943.587215 is presented. Estimated base frequencies were as follows: A = 0.185925, C = 0.309856, G = 0.273842, T = 0.230377; substitution rates AC = 1.270161, AG = 3.369060, AT = 1.523062, CG = 1.329349, CT = 5.079430, GT = 1.000000; gamma distribution shape α = 0.5. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Botryosphaeria dothidea* (MFLUCC 17-0961) and *B. obtusa* (CMW 8232). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Dothideomycetes orders *incertae sedis*
Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98, 1050 (2007)
Phyllostictaceae Fr., Summa vegetabilium Scandinaviae 2, 420 (1849)

Index Fungorum number: IF81162; Facesoffungi number: FoF05823

Phyllostictaceae was introduced by Fries (1849), which was accepted by Hawksworth & David (1989). Wikee et al. (2013b) proposed Phyllostictaceae as a distinct family in Botryosphaeriales and Slippers et al. (2013) accepted.

Phyllosticta Pers., Traité sur les Champignons Comestibles 55, 147 (1818)

Index Fungorum number: IF9384; Facesoffungi number: FoF00155

Phyllosticta was introduced by Persoon (1818) to accommodate *P. convallariae* (nom. inval., No description). *Phyllosticta cruenta* is a synonym of *P. convallariae*, which was proposed as the type species (Sutton & van der Aa 1974). It was regarded as a genus in Botryosphaeriaceae by Schoch et al. (2006), and confirmed in Phillips et al. (2019). Liu et al. (2012a) found that *Phyllosticta* is distinct from other genera in the Botryosphaeriaceae and it was widely accepted as a single genus. Species of *Phyllosticta* have significant economic importance causing diseases on leaf and fruit, which was regarded as a quarantine pest in Europe and the USA (Baayen et al. 2002, Glienke et al. 2011, Wikee et al. 2013a). Some species are common fungal endophytes (Wikee et al. 2013a, Liu et al. 2017a). This genus is mainly characterized by hyaline and aseptate conidia that may be or not covered by a mucoid layer with a single apical appendage growing in pycnidia (asexual), and erumpent ascomata (globose to pyriform) (Wikee et al. 2013b). In this study, we record *Dendrobium chrysanthum* as a new host for *Phyllosticta capitalensis*. An updated phylogeny for the genus is provided in Fig. 16.

Phyllosticta capitalensis Henn., Hedwigia 48, 13 (1908) Figs 17, 18

Index Fungorum number: IF168326; Facesoffungi number: FoF06888

Endophytic in the leaves of *Dendrobium chrysanthum*. Sexual morph: (on WA of a slide culture) vegetative mycelia 1.7–4.4 µm diameter, brown, curved, septate, swollen at nodes. *Ascomata* protrude from the surface of media, clavate to cylindrical, black, independent. *Asci* 50–61 × 8–8.5 µm (x̄ = 54.8 × 8.1 µm, n = 12), unitunicate, mostly with 8 ascospores, cylindrical to clavate with obtusely rounded or slightly square at apex, hyaline, smooth-walled. *Ascospores* 8–9 × 4–4.5 µm (x̄ = 8.5 × 4.5 µm, n = 8), sub-globose to pyriform, two ends rounded or truncated, hyaline, widest in the middle or near the middle, guttulate, smooth-walled, listed interlaced. Asexual morph: (on PDA) vegetative hyphae 0.8–2.1 µm diameter, hyaline, septate, branched, smooth. *Conidiomata* scattered around colony surface, aggregate, globose to irregular, greenish black. *Conidiophores* 4–52.5 µm long, cylindrical, straight to flexuous, hyaline, septate. *Conidiogenous cells* holoblastic. *Conidia* 6.5–7 × 3.5–4 µm (x̄ = 6.6 × 3.6 µm, n = 20), ellipsoidal, hyaline, guttulate, sometimes slightly curved, solitary, smooth-walled.

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

Material examined – China, Guizhou Province, Xingyi City, orchid nursery, leaves of *Dendrobium chrysanthum* (Orchidaceae), 16 October 2016, Bao-Wen Chen, living culture

MFLUCC 20-0220; Thailand, Chiang Rai Province, Wat Phra That Doi Tung, leaves of *Dendrobium chrysanthum*, 19 December 2013, Sureeporn Nontachaiyapoom, Natdanai Aewsakul, Xiao-Ya Ma, living culture MFLUCC 14-0088.

GenBank submissions – ITS: MW084361 (MFLUCC 14-0088), MW084362 (MFLUCC 20-0220); *ACT*: MW092167 (MFLUCC 14-0088), MW092168 (MFLUCC 20-0220); *TEF1-α*: MW160396 (MFLUCC 14-0088), MW160397 (MFLUCC 20-0220).

Known distribution (based on molecular data) – Worldwide (Okane et al. 2003, Glienke et al. 2011, Wikee et al. 2013a, Lin et al. 2017).

Known hosts (based on molecular data) – 70 plant families (Okane et al. 2003, Glienke et al. 2011, Wikee et al. 2013a, Lin et al. 2017).

Notes – Isolates MFLUCC 14-0088 and MFLUCC 20-0220 have identical sequences, so we regard them as the same species. Both clustered with *Phyllosticta capitalensis* isolates with its ex-type strain CBS 128856. There are only three base pair differences between 564 base pairs of ITS sequences of *P. capitalensis* MFLUCC 14-0088 and CBS 128856. The asci of MFLUCC 14-0088 are bitunicate and smaller than that of other *P. capitalensis* strains, and ascospores are also smaller. The conidia are shorter and wider than that of *P. mangifera-indica* 9 × 5 µm. No mucilaginous sheath was found around conidia. Therefore, we conclude our isolate as a new host record of *Phyllosticta capitalensis.*

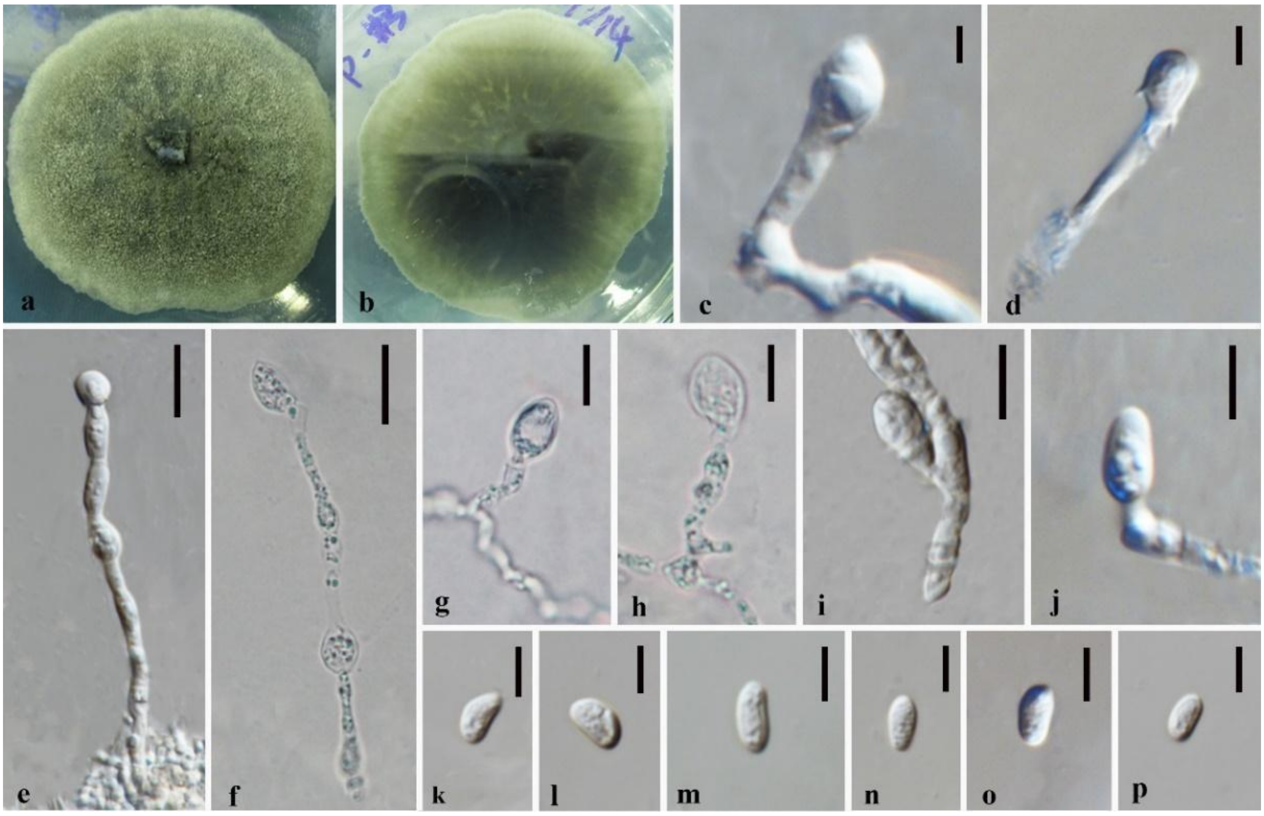

Fig. 17 – Asexual morph of *Phyllosticta capitalensis* (MFLUCC 14-0088, new host record). a–b Colony on PDA (a Surface, b Reverse). c–j Conidiophores with conidia. k–p Conidia. Scale bars: c–f = 10 µm, g–p = 5 µm.

Muyocopronales Mapook, Boonmee & K.D. Hyde, Phytotaxa 265, 230 (2016)

Muyocopronaceae K.D. Hyde, Fungal Diversity 63, 164 (2013)

Index Fungorum number: IF804506; Facesoffungi number: FoF08090

Muyocopronaceae was introduced by Luttrell (1951) in Hemisphaeriales to accommodate *Muyocopron* as the type (Spegazzini 1882). Hyde et al. (2013) reintroduced this as a distinct family (Dothideomycetes family, *incertae sedis*) with the monotypic genus *Muyocopron*. In this study, we followed the recent treatment of Mapook et al. (2020) for Muyocopronaceae. An updated phylogenetic tree based on available sequence data for Muyocopronaceae is provided in Fig. 19.

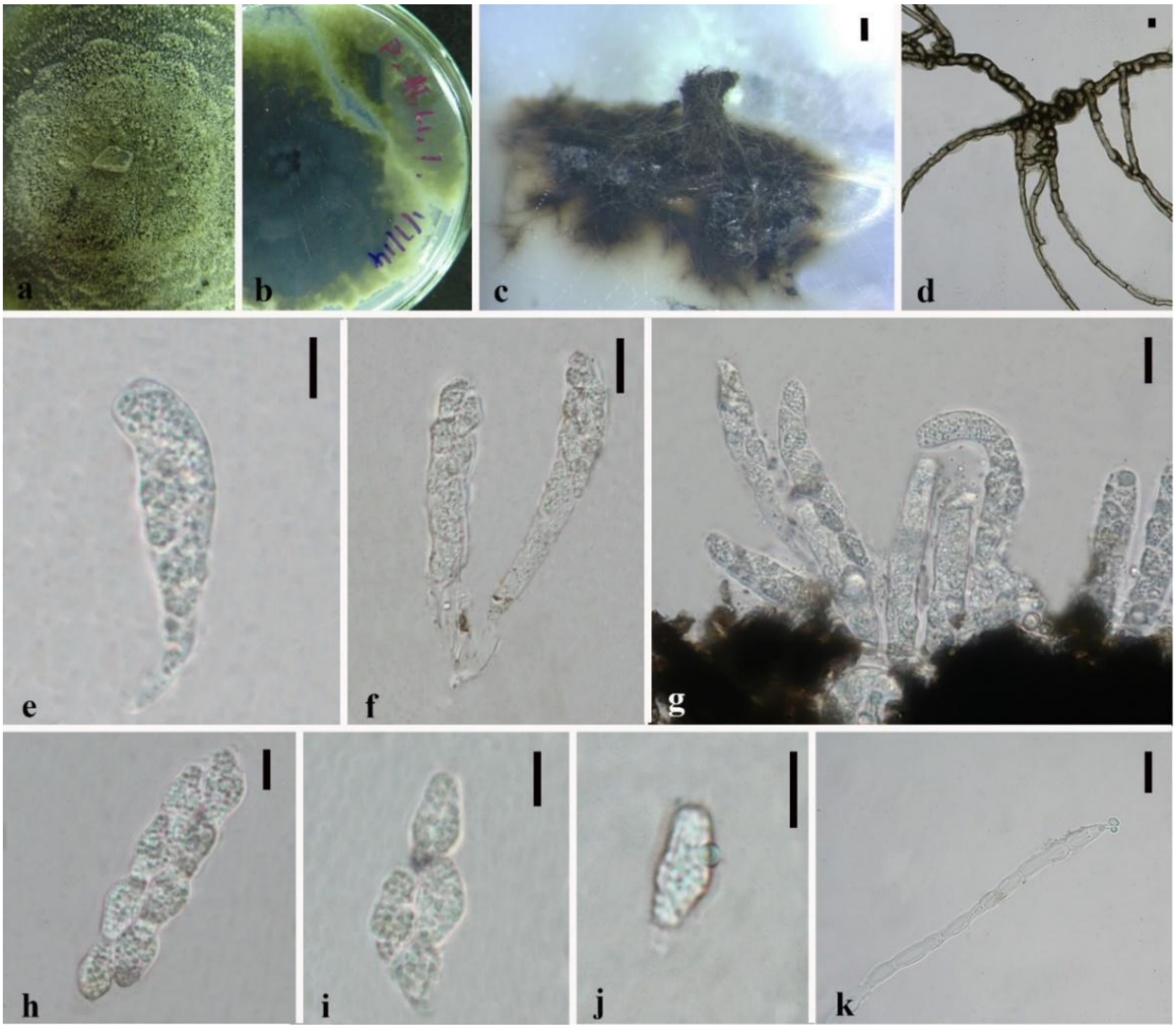

Fig. 18 – Sexual morph of *Phyllosticta capitalensis* (MFLUCC 14-0088, new host record). a–b Colony on PDA (a Surface, b Reverse). c Fruiting body on WA slide culture. d Mycelia on slide culture. e–i Asci. j Ascospore. k Mycelium with nucleates. Scale bars: c = 500 µm, d–g = 10 µm, h–j = 5 µm, k = 10 µm.

Muyocopron Speg., Anales de la Sociedad Científica Argentina 12, 113 (1881)

Index Fungorum number: IF3294; Facesoffungi number: FoF01887

Muyocopron was introduced by Spegazzini (1882) to accommodate *M. corrientinum* as the type species. The genus is characterized by small, superficial, black spots, without mycelium, dimidiate-scutate, subcarbonaceous ascomata with centrally ostiole, bitunicate, 8-spored asci, and ellipsoidal, hyaline ascospores (Spegazzini 1882, Mapook et al. 2016). *Muyocopron* species occur worldwide and are associated with a wide variety of plant substrates (Mapook et al. 2016, Tibpromma et al. 2016b, Senwanna et al. 2019b). There are 48 *Muyocopron* species listed in Species Fungorum (2020). In this study, we introduce a new species, *Muyocopron cinnamomi* from dead leaves of *Cinnamomum kotoense* (Lauraceae) and a new host record of *Muyocopron dipterocarpi* from *Celtis formosana* (Cannabaceae).

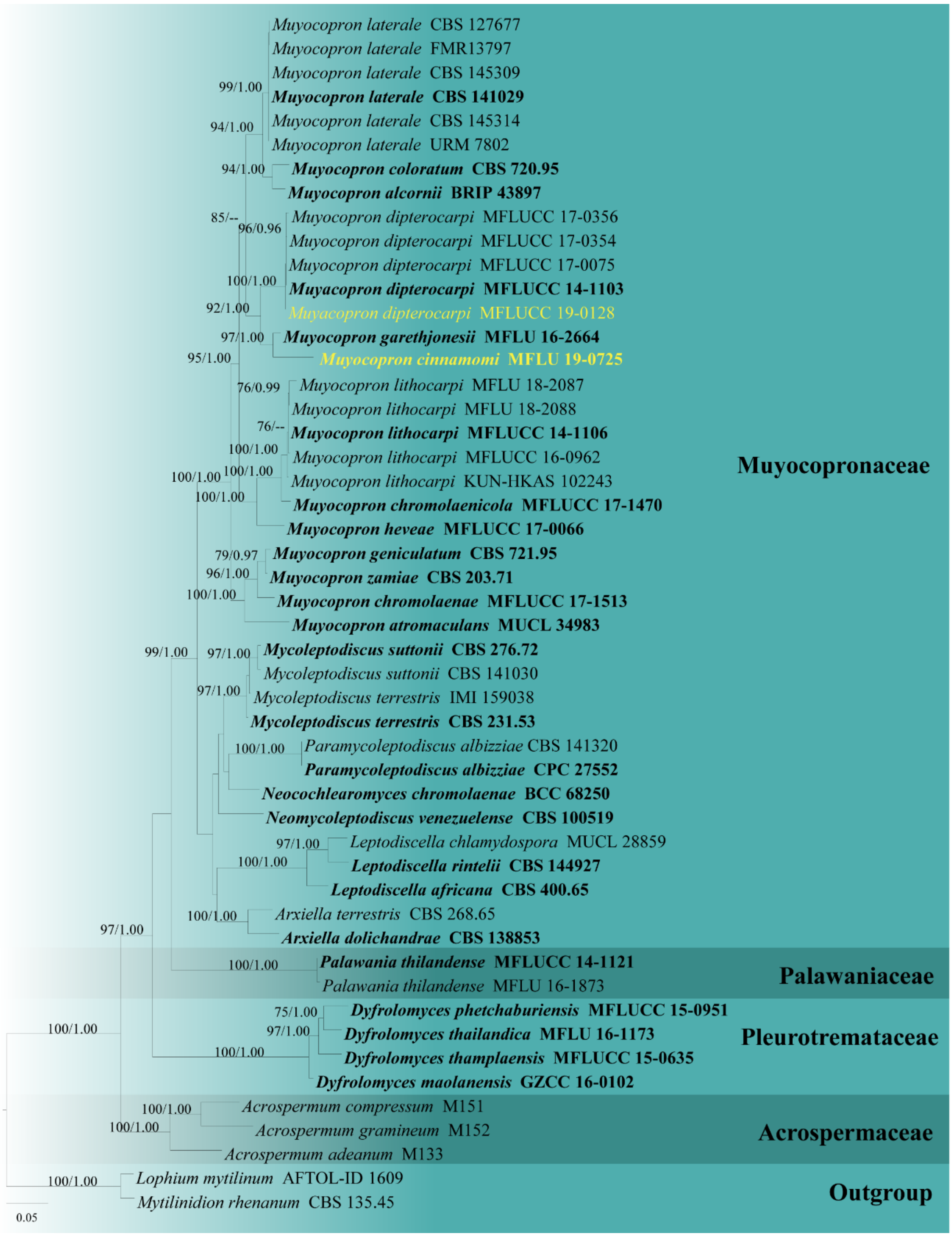

Fig. 19 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Fifty strains are included in the combined analyses which comprised 2745 characters (871 characters for LSU, 1109 characters for SSU, 765 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -15675.083415 is presented. Estimated base frequencies were as follows: A = 0.240159, C = 0.243562, G = 0.294893, T = 0.200000; substitution rates AC = 1.621279, AG = 2.691558, AT = 1.673290, CG = 1.290027, CT = 1.290027, GT = 1.000000; gamma distribution shape parameter α = 0.524676. The GTR+I+G was applied as the evolutionary model for all the gene regions. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Lophium mytilinum* (AFTOL-ID 1609) and *Mytilinidion rhenanum* (CBS 135.45). Ex-type strains are in **bold**. The newly generated sequences are in yellow.

Muyocopron cinnamomi Marasinghe, C.H. Kuo & K.D Hyde, sp. nov. Fig. 20

Index Fungorum number: IF551617; Facesoffungi number: FoF09449

Etymology – The specific epithet 'cinnamomi' was referred the host, where the fungus was collected.

Holotype – MFLU 19-0725

Saprobic on dead leaves of *Cinnamomum kotoense*. Sexual morph: Colonies on natural substrate dry, black, circular, dull, undulate, umbonate, rough. *Ascomata* 100–140 µm high × 350–500 µm diam. ($\bar{x}$ = 120 × 454 µm, n = 10), superficial, solitary or scattered, appearing as circular, flattened, dark brown to black spots, carbonaceous, with irregular margin, central ostiole. *Peridium* 30–65 µm wide, outer layer comprising dark brown to black, pseudoparenchymatous cells, inner layer comprising yellow-brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1.5–2.5 µm wide, cylindrical to filiform, aseptate, unbranched pseudoparaphyses. *Asci* 65–110 × 15–35 µm ($\bar{x}$ = 85 × 28 µm, n = 20), 4–8-spored, bitunicate, broadly cylindrical to ovoid, with short pedicle. *Ascospores* 20–25 × 10–14 µm ($\bar{x}$ = 22 × 12 µm, n = 20), overlapping 1–3-seriate, hyaline to pale yellowish, 1-celled, ellipsoid to obovoid, granular, with 1–2 oil guttules when immature stage. Asexual morph: Undetermined.

Material examined – Taiwan, Chiayi Province, Chiayi National University, on dead leaves of *Cinnamomum kotoense* (Lauraceae), 19 September 2019, Diana Sandamali DTUF01 (MFLU 19-0725, holotype).

GenBank submissions – LSU: MT909524, SSU: MT909523.

Known distribution (based on molecular data) – Taiwan (this study).

Known hosts (based on molecular data) – *Cinnamomum kotoense* (this study).

Notes – *Muyocopron cinnamomi* has a close phylogenetic affinity with *M. garethjonesii*, however, it differs in having a hamathecium with cylindrical to filiform, aseptate pseudoparaphyses. According to the phylogenetic analysis based on LSU and SSU sequence data, our strain clusters with *M. garethjonesii* (MFLU 16-2664) with relatively high bootstrap and Bayesian probabilities (97% ML, 1.00 BYPP respectively). ITS base pair difference is unable to do as lack of sequence data of ITS of *M. garethjonesii*. The LSU sequence comparison shows 7.5 % (832 bp, without including gaps) bp differences between *M. garethjonesii* and *M. cinnamomi* and no significant base pair difference in SSU.

Muyocopron dipterocarpi Mapook, Doilom, Boonmee & K.D. Hyde, Phytotaxa 265, 232 (2016) Fig. 21

Index Fungorum number: IF551617; Facesoffungi number: FoF01889

Saprobic on decaying twig of *Celtis formosana*. Sexual morph: *Ascomata* 80–120 µm high × 200–250 µm diam. ($\bar{x}$ = 108 × 230 µm, n = 10), superficial, coriaceous, solitary or scattered, appearing as circular, scattered, flattened, brown to dark brown spots, covering the host, without a subiculum, with a poorly developed basal layer and an irregular margin. *Ostiole* central. *Peridium* 22–25 µm wide, widest at the sides, outer layer comprising dark brown to black pseudoparenchymatous, occluded cells of *textura angularis*, inner layer comprising light brown cells of *textura angularis*. *Hamathecium* of 1–2 µm wide, cylindrical to filiform, septate, pseudoparaphyses. *Asci* 52–60 × 17–20 µm ($\bar{x}$ = 55 × 18.4 µm, n = 30), 8-spored, bitunicate, broadly cylindrical to subglobose, pedicellate, straight or slightly curved, with small ocular chamber. *Ascospores* 14–17 × 8–10 µm ($\bar{x}$ = 16.2 × 9 µm, n = 30), irregularly arranged, overlapping in the ascus, hyaline, oval to obovoid with obtuse ends, aseptate, with granular appearance. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA, 30–35 mm, diam. after 3 weeks, colonies medium dense, circular, raised, surface smooth, entire edge, colony from above, light brown to yellowish at margin, white to cream at centre; from below, light brown to yellowish at margin, dark brown to black at centre, no pigmentation produced in media.

Material examined – Taiwan, Chiayi, Fanlu Township area, Dahu forest (23°27.535'N 120°36.348'E), decaying twig of *Celtis formosana* (Cannabaceae), 18 July 2019, D.S. Tennakoon SV021 (MFLU 18-2584), living culture MFLUCC 19-0128.

GenBank submissions – ITS: MW872334, LSU: MW872338, SSU: MW872340.

Known distribution (based on molecular data) – Thailand (Mapook et al. 2016, Jayasiri et al. 2019, Senwanna et al. 2019b), Taiwan (this study).

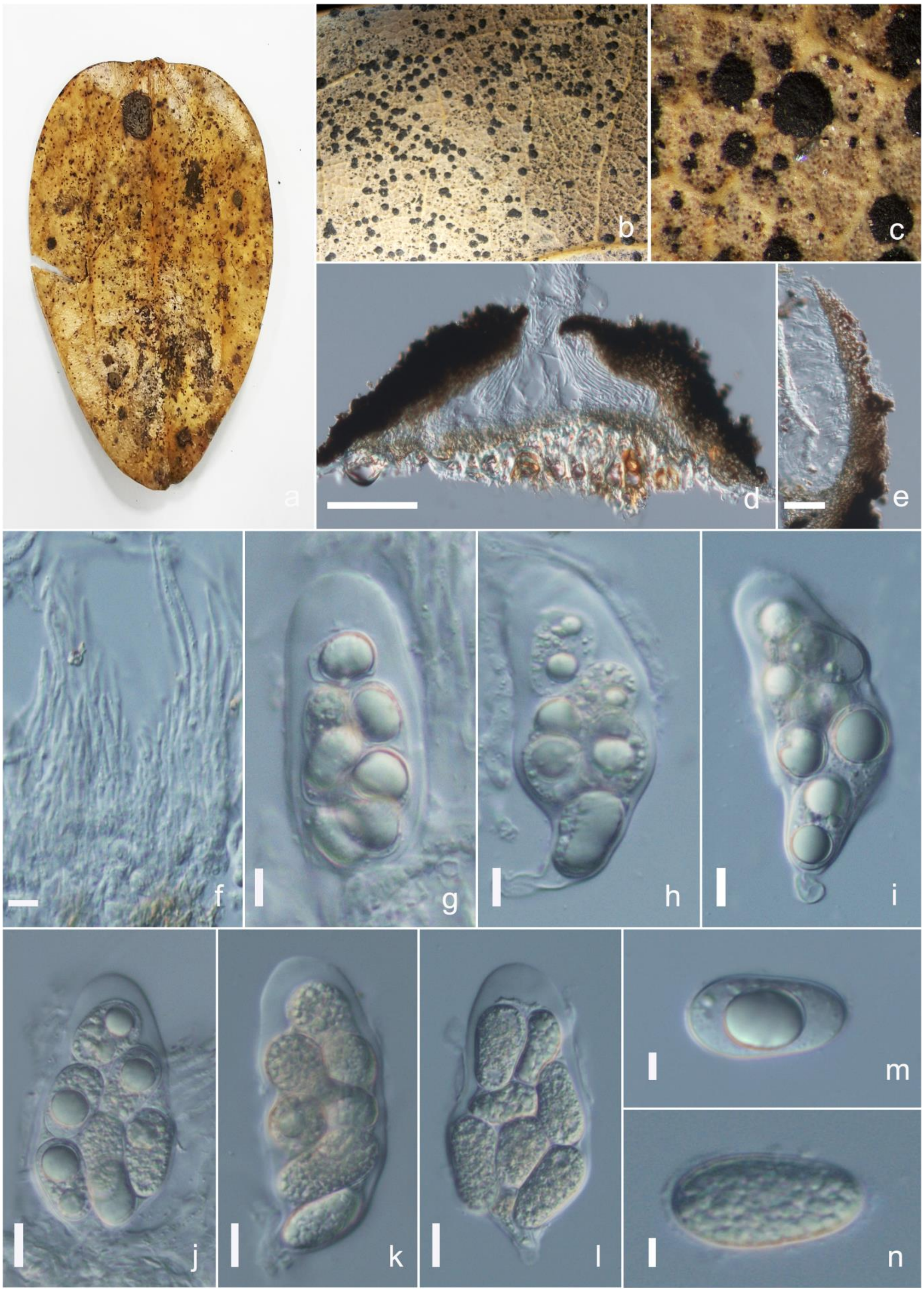

Fig. 20 – *Muyocopron cinnamomi* (MFLU 19-0725, holotype). a–c Superficial ascomata on substrate. d Section of an ascoma. e Peridium. f Pseudoparaphyses. g–l Asci. m–n Ascospores. Scale bars: d = 100 µm, e, g–l = 10 µm, f, m–n = 5 µm.

Known hosts (based on molecular data) – on dried twigs of *Dipterocarpus tuberculatus* (Mapook et al. 2016), on decaying pod septum of *Delonix regia* (Jayasiri et al. 2019), on dried twig of *Hevea brasiliensis* (Senwanna et al. 2019b), on decaying twig of *Celtis formosana* (this study).

Notes – As morphological characters examined largely overlap with those of *Muyocopron dipterocarpi*, we, report our collection as a new record of *M. dipterocarpi* from decaying twig of *Celtis formosana* in Taiwan. According to combined multi-gene (LSU, SSU and ITS) phylogenetic analyses, our collection nests with other *M. dipterocarpi* strains in a well-supported clade (100% ML, 1.00 BYPP). Our collection shares similar morphology with the type species (MFLUCC 14-1103) in having superficial, black ascomata, cylindrical to filiform, septate, pseudoparaphyses, broadly cylindrical to subglobose asci with short pedicels and oval to obovoid, hyaline, aseptate ascospores (Mapook et al. 2016). *Muyocopron dipterocarpi* species have been recorded from various host families (i. e. Dipterocarpaceae, Euphorbiaceae, Fabaceae) (Mapook et al. 2016, Jayasiri et al. 2019, Senwanna et al. 2019b). This is the first record of *Muyocopron dipterocarpi* collected from Cannabaceae.

Stigmatodiscales Voglmayr & Jaklitsch, Fungal Diversity 80, 275 (2016)

Stigmatodiscaceae Voglmayr & Jaklitsch, Fungal Diversity 80, 275 (2016)

Index Fungorum number: IF815326; Facesoffungi number: FoF08772

Voglmayr et al. (2016) introduced Stigmatodiscaceae in Stigmatodiscales with two genera, *Asterodiscus* and *Stigmatodiscus* based on phylogenetic analyses and morphological investigations. *Asterodiscus* (*A. tamaricis*) was synonymized with *Stigmatodiscus* and the new combination *S. tamaricis* was proposed by Voglmayr & Amengual (2018).

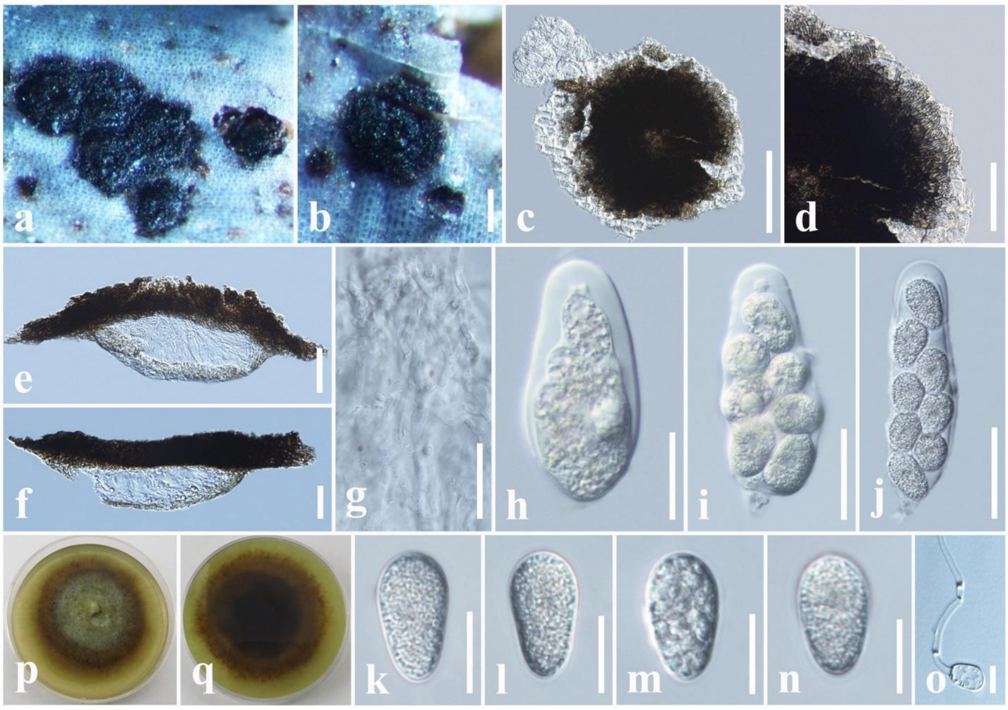

Fig. 21 – *Muyocopron dipterocarpi* (MFLU 18-2584, new host record) a Appearance of ascomata on host. b Close-up of an ascoma. c Squash mount showing ascoma. d Squash mount showing ascomata wall. e, f Sections through ascomata. g Pseudoparaphyses. h–j Asci. k–n Ascospores. o Germinated ascospore. p Colony from above. q Colony from below. Scale bars: b, c = 100 µm, d = 30 µm, e, f = 50 µm, g–j = 20 µm, k–o = 10 µm.

Stigmatodiscus Voglmayr & Jaklitsch, Fungal Diversity 80, 278 (2016)

Index Fungorum number: IF815327; Facesoffungi number: FoF01654

Voglmayr et al. (2016) introduced the genus with the type *Stigmatodiscus enigmaticus*.

Species of this genus are widely distributed in Central and Southern Europe (Voglmayr et al. 2016). These species are mainly saprobes that found on dead corticated twigs still attached to the trees (Voglmayr et al. 2016). There are six species accepted in the genus (Voglmayr & Amengual 2018). An updated phylogeny for the genus is provided in Fig. 22.

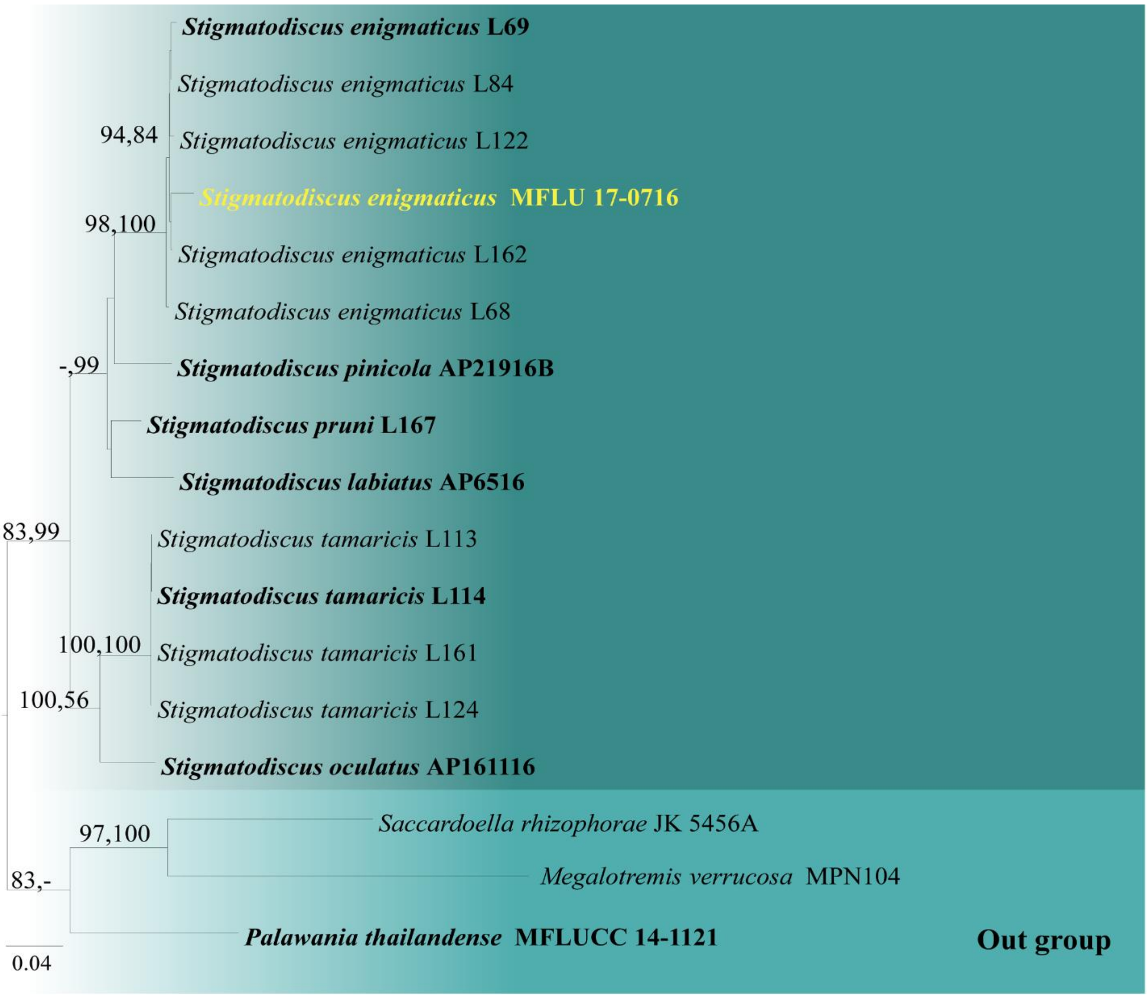

Fig. 22 – Phylogram generated from the maximum likelihood analysis based on combined ITS, SSU, *TEF1-α*, *RPB2* and *β-TUB* sequence data of genus *Stigmatodiscus*. Seventeen strains are included in the combined analyses which comprised 6745 characters (1625 characters for ITS, 1727 characters for SSU, 1163 characters for *TEF1-α*, 1384 characters for *RPB2*, 846 characters for *β-TUB*) after alignment. The best RaxML tree with a final likelihood values of -19048.074675 is presented. The matrix had 1070 distinct alignment patterns, with 47.59 % undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233721, C = 0.264938, G = 0.286269, T = 0.215072; substitution rates AC = 1.432191, AG = 2.914708, AT = 1.405249, CG = 1.332164, CT = 7.594185, GT = 1.000000; gamma distribution shape parameter α = 0.579606. For all the gene regions, GTR+G was applied as the evolutionary model. Bootstrap values for ML equal to or greater than 80% (first set) and MP equal to or greater than 55% (second set) are given above the nodes. The tree is rooted with *Saccardoella rhizophorae* (JK 5456A), *Megalotremis verrucosa* (MPN104) and *Palawania thailandense* (MFLUCC 14-1121). Ex-type strains are in **black**. Newly generated sequences are indicated in yellow.

Stigmatodiscus enigmaticus Voglmayr & Jaklitsch, Fungal Diversity 80, 278 (2016) Fig. 23

Index Fungorum number: IF815328; Facesoffungi number: FoF08773

Saprobic on twigs of *Acer monspessulanum*. Sexual morph: *Ascomata* 350–400 µm diam., dark brown to black, apothecioid, embedded in cortex of dead twigs, initially covered by bark, later becoming exposed through irregular cracks. *Subhymenium* thin, 14–16 µm height from base of ascomata and composed of tightly packed hyaline hyphae. *Pseudoparaphyses* 70–80 µm long, 1–2 µm wide. *Asci* 115–120 × 35–40 µm ($\bar{x}$ = 116 × 37 µm, n = 20), bitunicate, broadly fusiform to ellipsoid, almost sessile, with a distinct apical chamber, containing 8 irregularly bi- to triseriate ascospores. *Ascospores* 50–55 × 14–16 µm ($\bar{x}$ = 116 × 37 µm, n = 30), brown, asymmetric, at first 1-septate, developing 2 additional distosepta constricted at the septa, surrounded by gelatinous sheath, dark brown, the contents granular. Asexual morph: not observed.

Material examined – Italy, Province of Forlì-Cesena, Rocca delle Caminate - Predappio, on twigs of *Acer monspessulanum* (Sapindaceae), 1 March 2017, E. Camporesi IT425 (MFLU 17-0716).

GenBank numbers – ITS: MT965719

Known distribution (based on molecular data) – Austria, Croatia, Czech Republic, France, Greece, Italy, Morava and Spain (Voglmayr & Amengual 2018).

Known hosts (based on molecular data) – *Acer* sp., *Carpinus* sp., *Cistus* sp., *Globularia* sp., *Quercus* sp., *Olea* sp., *Pistacia* sp., *Pinus* sp., *Populus* sp. and *Tamarix* sp. (Voglmayr & Amengual 2018).

Notes – A fungal strain obtained from twigs of *Acer monspessulanum* was identified as *Stigmatodiscus enigmaticus*, with support from both morphology and phylogeny. The new strain clustered with the type of *S. enigmaticus* (L69), in the combined ITS, SSU, *TEF1-α*, *RPB2* and *β-TUB* phylogeny. *Stigmatodiscus enigmaticus* was recorded from *Acer monspessulanum* in the Czech Republic, France and Slovenia (Voglmayr et al. 2016). This is the first record of *S. enigmaticus* from *Acer monspessulanum* in Italy.

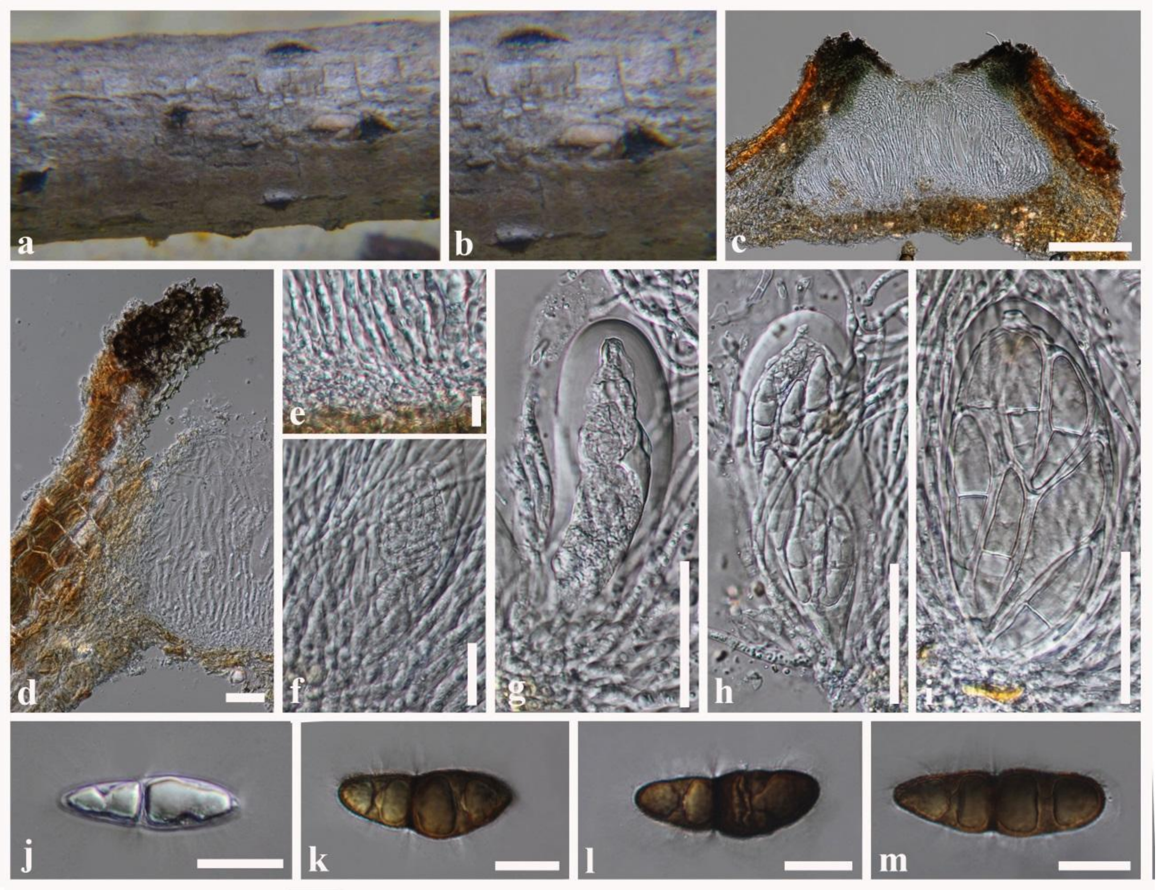

Fig. 23 – *Stigmatodiscus enigmaticus* (MFLU 17-0716, new host record). a, b Appearance of ascomata erumpent from bark. c Vertical section of apothecioid ascomata. d Peridium. e Subhymenium and base of pseudoparaphyses. f Pseudoparaphyses. g–i Asci. j–m Ascospores. Scale bars: c = 50 µm, d = 20 µm, e = 5 µm, f = 20 µm, e = 5 µm, g–i = 50 µm, j–m = 20 µm.

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde, Fungal Diversity 51, 251 (2011)
Sympoventuriaceae Y. Zhang ter, C.L. Schoch & K.D. Hyde, Fungal Diversity 51, 255 (2011)

Index Fungorum number: IF563117; Facesoffungi number: FoF06346

Sympoventuriaceae was introduced by Zhang et al. (2011) to accommodate *Sympoventuria* as the type. The species in this family are characterized by immersed, subglobose ascomata that are black, papillate and ostiolate, septate, anastomosing pseudoparaphyses, that are constricted at the septa and extending above the asci, 8-spored, bitunicate, fissitunicate, subcylindrical, pedicellate asci and hyaline, fusoid-ellipsoidal ascospores, constricted at the median septum (Zhang et al. 2011, Tibpromma et al. 2018). Most species in Sympoventuriaceae play vital roles as both saprobes and pathogens of plants, and animals and have been reported from different environments, such as soil, hot springs, industrial effluents, terrestrial and aquatic habitats (Samerpitak et al. 2014, Tibpromma et al. 2018, Zhang et al. 2019). Nine genera are accepted in Sympoventuriaceae (Wijewardene et al. 2020). An updated phylogenetic tree for Sympoventuriaceae is provided in Fig. 24.

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

Index Fungorum number: IF555334; Facesoffungi number: FoF04518

Yunnanomyces species are characterized by broadly oval, yellow-brown, muriform conidia. *Yunnanomyces* was introduced by Tibpromma et al. (2018) to include *Y. pandanicola* as the type species. Currently, only two species are accepted in Species Fungorum (2020), viz *Y. pandanicola* and *Y. phoenicis*. In this study, we record *Y. pandanicola* from a different host species, *Ananas comosus*.

Yunnanomyces pandanicola Tibpromma & K.D. Hyde, Fungal Diversity 93, 75 (2018) Fig. 25

Index Fungorum number: IF555335; Facesoffungi number: FoF04519

Saprobic on dead leaves of *Ananas comosus*. Sexual morph: Undetermined. Asexual morph: Hypomycetous. *Colonies* on natural substrate, in small groups, blackish brown, velvety, glistening, with conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* micronematous, mononematous, fasciculate, septate, hyaline, smooth, unbranched. *Conidiogenous cells* 2.8–4 × 2–3 µm ($\bar{x}$ = 3.4 × 2.6 µm, n = 20), holoblastic, monoblastic, hyaline, integrated, terminal or intercalary, determinate, cylindrical. *Conidia* 20–24 × 15–17 µm ($\bar{x}$ = 23.1 × 16 µm, n = 30), acrogenous, solitary, globose to broadly oval, flattened, thick-walled, muriform, consisting of 15–25 cells, yellow–brown.

Culture characteristics – Colonies on PDA, reaching 25–30 mm diam. after 3 weeks, colonies medium dense, cottony, circular, edge irregular, colony from above, dark brown; from below, dark brown to black, not pigmentation produced in media.

Material examined – Taiwan, Chiayi, Fanlu Township area, Dahu forest, dead leaves of *Ananas comosus* (Bromeliaceae), 20 July 2019, D.S. Tennakoon TAP025 (MFLU 18-2607), living cultures, MFLUCC 19-0068, NCYUCC 19-0128.

GenBank submissions – LSU: MW872339, SSU: MW872341.

Known distribution (based on molecular data) – China (Tibpromma et al. 2018), Thailand (Zhang et al. 2019), Taiwan (this study).

Known hosts (based on molecular data) – on dead leaves of *Pandanus amaryllifolius* (Tibpromma et al. 2018), on fallen rachides and leaves of *Phoenix paludosa* (Zhang et al. 2019), on dead leaves of *Ananas comosus* (this study).

Notes – Morphology of our collection (MFLU 18-2607) resembles *Yunnanomyces pandanicola* in having broadly oval, yellow-brown, muriform conidia (Tibpromma et al. 2018). In multi-gene phylogeny, our collection clustered with *Y. pandanicola* with high bootstrap support (100% ML, 1.00 BYPP). Based on both morphology and phylogenetic support, we introduce our collection as a new host record of *Y. pandanicola* from *Ananas comosus*.

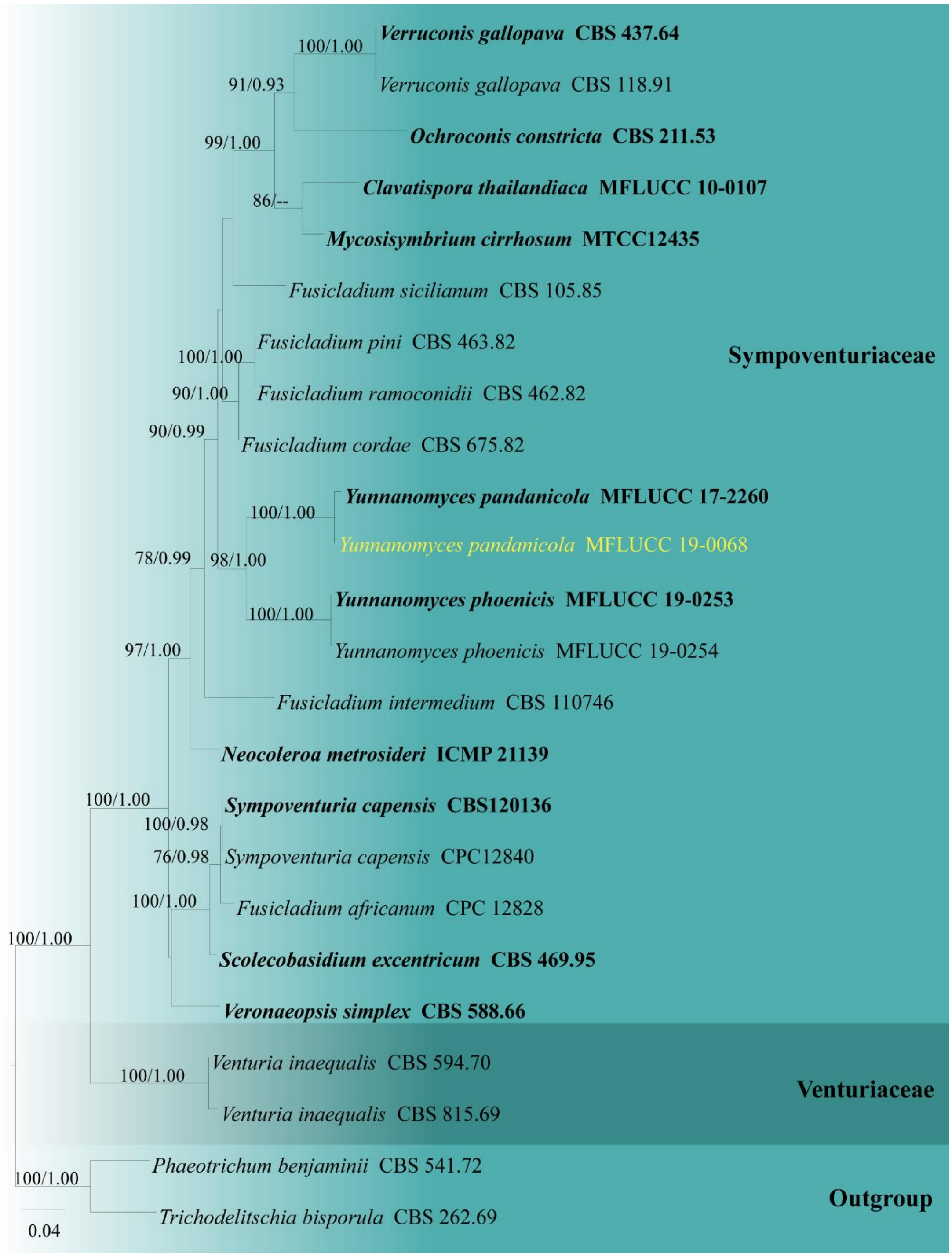

Fig. 24 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *RPB2* sequence data. Twenty-four strains are included in the combined analyses which comprised 2989 characters (868 characters for LSU, 1027 characters for SSU, 1094 characters for *RPB2*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12068.262814 is presented. Estimated base frequencies were as follows: A = 0.255633, C = 0.224040, G = 0.291498, T = 0.228829; substitution rates AC = 1.259733, AG = 3.035194, AT = 1.574956, CG = 1.189243, CT = 6.856152, GT = 1.000000; gamma distribution shape parameter α = 0.525657. The GTR+I+R was applied as the evolutionary model for all the gene regions. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Phaeotrichum benjaminii* (CBS 541.72) and *Trichodelitschia bisporula* (CBS 262.69). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

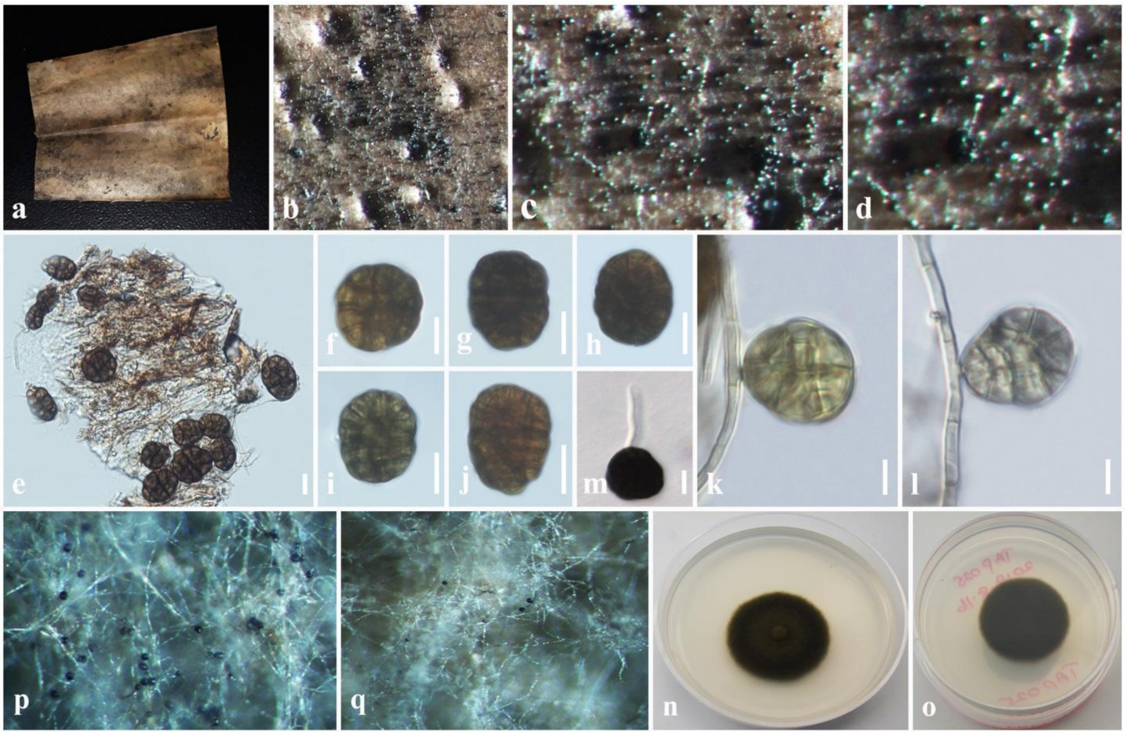

Fig. 25 – *Yunnanomyces pandanicola* (MFLU 18-2607, new host record). a Dead leaf of *Ananas comosus*. b–d Colonies on dead leaf. e–j Conidia. k, l Conidiogenous cells. m Germinated conidium. n Colony from above. o Colony from below. p, q Colonies on PDA. Scale bars: e = 15 µm, f–l = 10 µm.

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

For Lecanoromycetes, we follow the recent treatment (Wijayawardene et al. 2020).

Subclass Lecanoromycetidae P.M. Kirk et al., Mycological Research 111, 529 (2007)

Caliciales Bessey, University of Nebraska Studies 7, 299 (1907)

Caliciaceae Chevall., Flore Générale des Environs de Paris 1, 314. (1826)

Index Fungorum number: IF80543; Facesoffungi number: FoF09427

The lichenized family Caliciaceae was introduced by Chevallier (1826) to encompass both lichenized and lichenicolous species (Prieto & Wedin 2017). This family comprises 36 genera (Lücking et al. 2017, Wijayawardene et al. 2017, 2020). The taxa are characterized by prototunicate asci and mazaedium, which facilitates the dispersal of the ascospores (Wedin & Tibell 1997, Prieto & Wedin 2017). Gaya et al. (2012) proposed two subfamilies in Caliciaceae including, Calicioideae and Buellioideae. Nonetheless, this classification was rather unclear due to poor taxon sampling. Caliciaceae is a poorly studied group, and its taxonomy needs to resolve (Prieto & Wedin 2017). An updated tree for the family is given in Fig. 26.

Acolium (Ach.) Gray, A natural arrangement of British plants 1, 482 (1821)

Index Fungorum number: IF43; Facesoffungi number: FoF09428

Acolium was resurrected by Prieto & Wedin (2017), and comprises both lichenized and lichenicolous taxa. These species grow on wood or bark and are characterized by a dark excipulum, greyish-brown thallus (or are lichenicolous and do not form an independent thallus), sessile to somewhat immersed ascomata and sometimes grey pruina present on the rim of the excipulum. *Acolium* species were formally affiliated in *Cyphelium* and presently comprise seven species with the type *Acolium inquinans* (Species fungorum 2020). *Acolium sessile* and *A. marcianum* are lichenicolous on *Pertusaria sensu lato*, while *Acolium chloroconium*, *A. inquinans*, *A. karelicum* and *A. marcianum* are recorded as lichenized taxa (Prieto & Wedin 2017).

Acolium yunnanense Thiyagaraja & K.D. Hyde, sp. nov. Fig. 27

Index Fungorum number: IF557875; Facesoffungi number: FoF09217

Etymology – The specific epithet 'yunnanense' was given after the place, where the fungus was collected.

Holotype – MFLU 19-0725

Thallus crustose, corticolous, epiphloedal, corticated and well-developed, surface pale gray. *Prothallus* indistinct. *Photobiont* present. Asexual morph: Undetermined. Sexual morph: *Ascomata* apothecial, 450–850 µm diam., 110–190 µm high (x̄ = 650 × 150 µm, n = 10), stipitate, mazaedioid, disc black, short cylindrical with whitish pruina on the upper and outer surface of the edge of the exciple. *Exciple* blackish brown, 65–105 µm thick laterally and 110–120 µm thick at the basal, carbonized. *Hypothecium* 40–70 µm thick, pale brown. *Hymenium* 40–70 µm thick, hyaline, not inspersed. *Paraphyses* 1–2 µm wide, branched, easily separable, irregularly branched. *Asci* 40–55 × 6.5–7.5 µm (x̄ = 47.5 × 7 µm, n = 20), 8-spored, cylindrical, with uniseriately arranged ascospores. *Ascospores* 8–12 × 5–7 µm (x̄ = 10 × 6 µm, n = 40), ellipsoidal to broadly ellipsoid, greenish to dark brown, hyaline when immature, 1-septate, thick-walled, constricted at the middle, distinctive ornamentation of longitudinally arranged ridges and irregular cracks, one large guttule per cell and verrucose, sometimes appendages present in the both ends, ejected ascospore masses lying on the thallus surface.

Material examined – China, Yunnan Province, Shangri La (27°55'54.9" N, E099° 34'39.0'E', alt. 4045 m), on living bark of unidentified plant, 12 September 2018, Vinodhini Thiyagaraja (MFLU 19-0725, holotype).

Chemistry – Thallus, Ascomatal gel I-, K-, Asci I-, K-

GenBank submissions – ITS: MW018873, *β-TUB*: MW116835, LSU: MW018872.

Known distribution (based on molecular data) – China (this study).

Notes – *Acolium yunnanense* formed a distinct clade with the extant species of *Acolium* in the multi-gene phylogenetic analysis of combined LSU, ITS and *β-TUB* (Fig. 26). However only *A. karelicum* and *A. inquinans* have molecular data in this genus. The new species differs in the ascospore morphology and size of exciple in comparison to *A. inquinans*. Greenish ascospores sometimes have small appendages at both ends, guttulate in each locus, and a small exciple (65–105 µm thick laterally and 110–120 µm thick at the base) were observed in *A. yunnanense* in contrast to the dark brown ascospores without appendages and the absence of guttules and a larger exciple (125–160 µm thick laterally and, 290–380 µm thick at the base) in *A. inquinans* (Singh & Singh 2014). *Acolium yunnanense* reveals more than 2 % base pair differences in the ITS gene region in comparison to *A. karelicum* (MP56, 2001 Tibell UPS) and *A. inquinans* (O-L-186246, O-L-200169). Our new taxon also differs from *Acolium sessile* and *A. marcianum* in the lichenized lifestyle whereas *Acolium sessile* and *A. marcianum* show lichenicolous life style which they lack in molecular data (Prieto & Wedin 2017). Our new taxon also differs from *A. chloroconium* in larger apothecia and mazaedioid disk whereas *A. chloroconium* shows smaller apothecia (up to 600 µm) with yellow streak on the margin of the disk (Weber 1967).

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

For Leotiomycetes, we follow the recent treatment of Wijayawardene et al. (2020).

Subclass Leotiomycetidae O.E. Erikss. & Winka, Myconet 1, 7 (1997)

Erysiphales Warm., Haandbog i den systematiske Botanik ed. 2, 63 (1884)

Erysiphaceae Tul. & C. Tul., Selecta Fungorum Carpologia 1, 191 (1861)

Index Fungorum number: IF80754; Facesoffungi number: FoF05856

Tulasne & Tulasne (1861) introduced the name *Erysiphei*, with the detailed discussion and description, which was later, interpreted as Erysiphaceae and used in the taxonomic literature of powdery mildews (Braun & Cook 2012, Braun 2017). Erysiphaceae comprises 20 genera, *Arthrocladiella, Blumeria, Brasiliomyces, Bulbomicroidium, Caespitotheca, Cystotheca, Erysiphe,* *Golovinomyces*, *Leveillula*, *Microidium*, *Neoerysiphe*, *Parauncinula*, *Phyllactinia*, *Pleochaeta*, *Podosphaera*, *Pseudoidium*, *Queirozia*, *Sawadaea*, *Takamatsuella*, and *Typhulochaeta* (Wijayawardene et al. 2020).

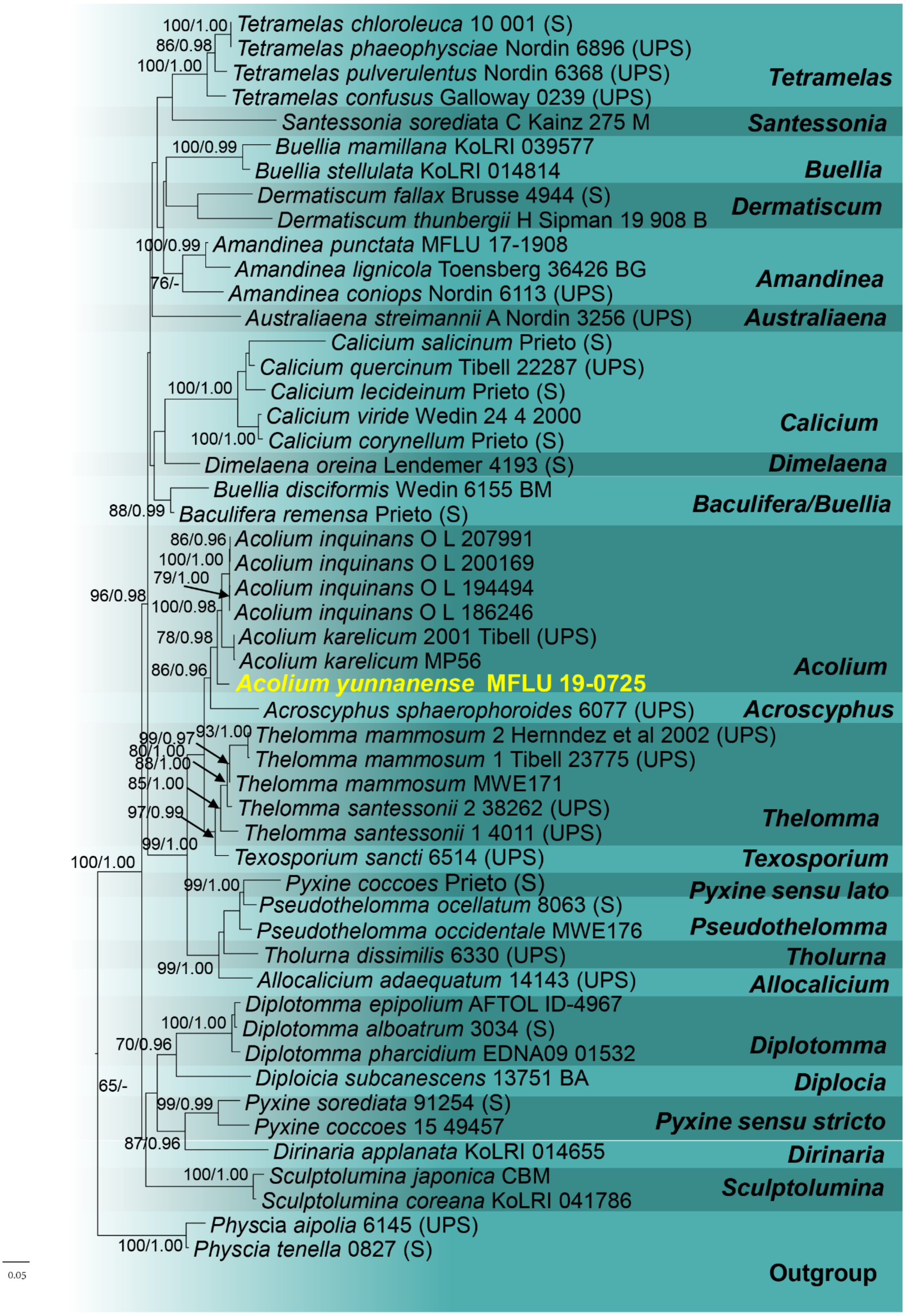

Fig. 26 – Phylogram generated using maximum likelihood analysis based on combined LSU, ITS and *β-TUB* sequence data. Fifty-two strains are included in the combined analyses which comprised 2124 characters (819 characters for LSU, 584 characters for ITS, 721 characters for *β-TUB*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best RaxML tree with a final likelihood value of -17812.590222 is presented. Estimated base frequencies were as follows: A = 0.229337, C = 0.261337, G = 0.276938, T = 0.232388; substitution rates AC = 1.720213, AG = 3.344718, AT = 1.750478, CG = 1.168734, CT = 8.621223, GT = 1.000000; gamma distribution shape parameter α = 0.478984. Bootstrap support values for ML greater than 65% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Physcia aipolia* (Wedin 6145 UPS and Odelvik & Hellstrm 0827 S). The newly generated sequences are indicated in yellow.

Erysiphe R. Hedw. ex DC., Flore française 2, 272 (1805)

Index Fungorum number: IF1898; Facesoffungi number: FoF09218

Erysiphe is typified with *E. polygoni*. *Erysiphe* is the largest genus in the Erysiphaceae and includes more than 50% of the family (Takamatsu et al. 2015). *Erysiphe* mainly consists of powdery mildew pathogens. *Erysiphe* species cause serious diseases on economically important plants such as cereals, crops, vegetables, flowers, fruit trees and ornamental plants (Braun & Cook 2012, Abasova et al. 2018b). An updated phylogenetic tree for Erysiphaceae species with new records is presented in Fig. 28

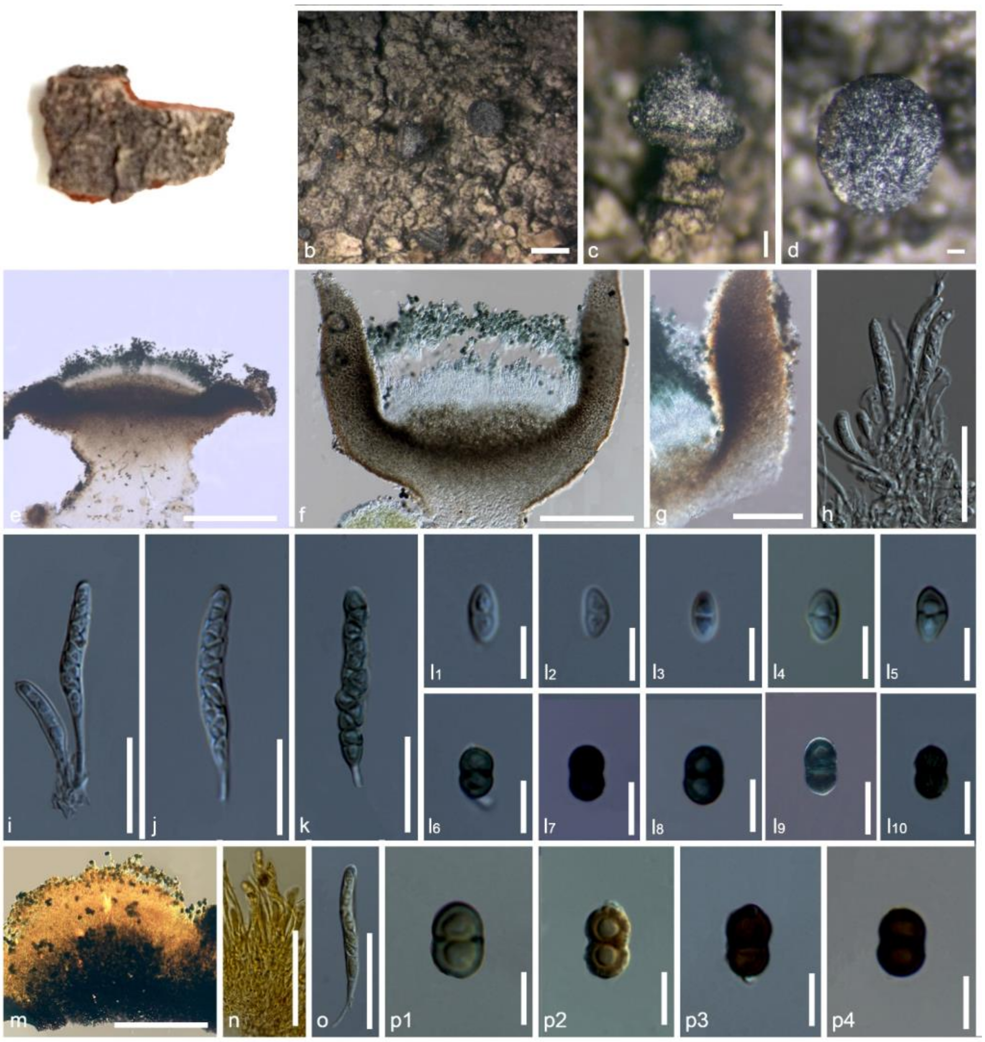

Fig. 27 – *Acolium yunnanense* (MFLU 19-0725, holotype). a–d, m Ascomata on substrate. e, f Vertical section through ascoma. g Vertical section through exciple. h, n Paraphyses. i–k, o Asci. l1–l10, p1–p4 Ascospores. m, n, o, p1–p4 Ascospores stained with lugol's solution. Scale bars: c = 200 µm, d = 100 µm, e–f = 200 µm, g–k, o = 20 µm, l1–l10, p1–p4 = 10 µm.

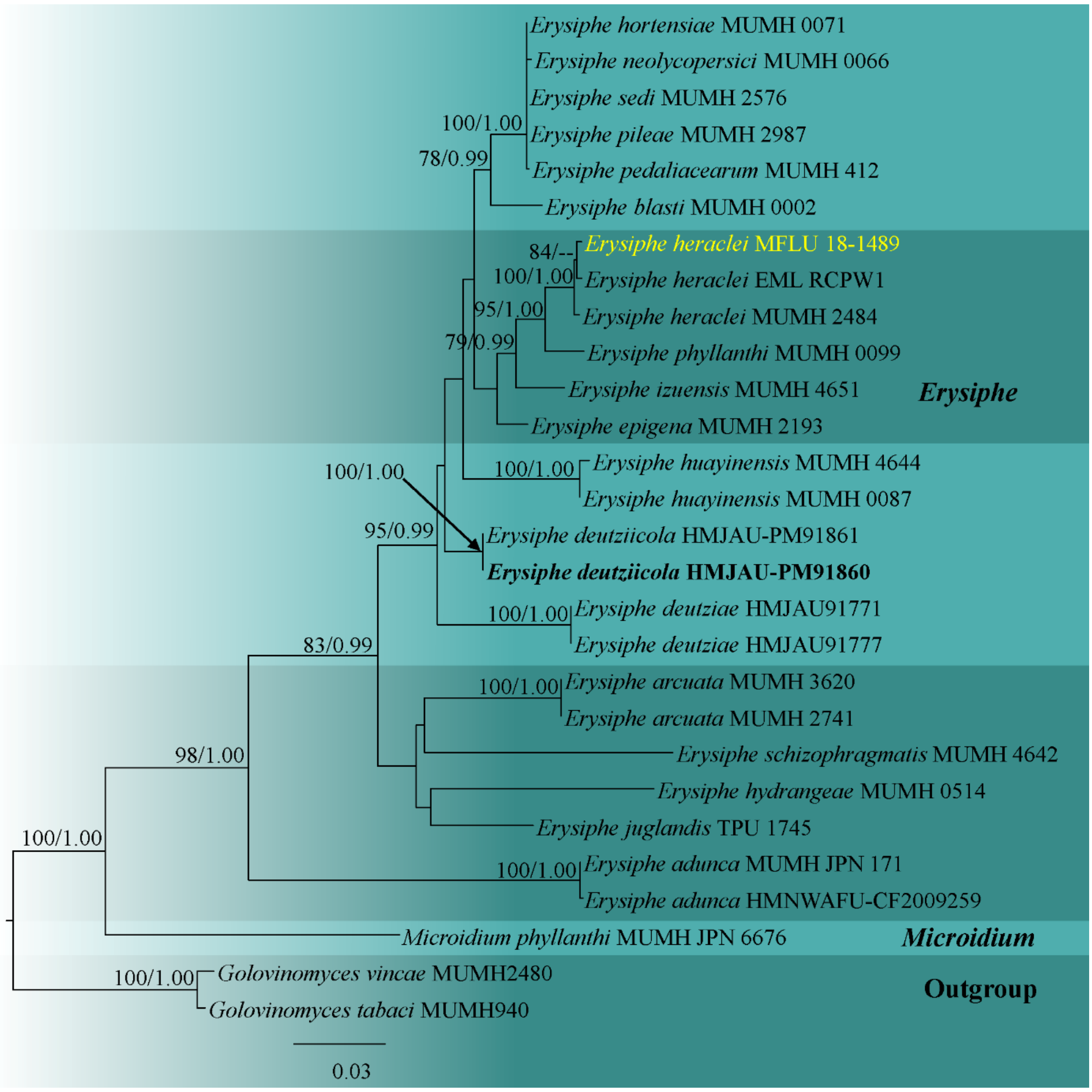

Fig. 28 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Twenty-nine strains are included in the combined analyses which comprised 1432 characters (806 characters for LSU, 622 characters for ITS). Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6405.264052 is presented. Estimated base frequencies were as follows: A = 0.237207, C = 0.237737, G = 0.292866, T = 0.232190; substitution rates AC = 1.004461, AG = 2.056312, AT = 1.198273, CG = 0.588661, CT = 4.363283, GT = 1.000000; gamma distribution shape parameter α = 0.177556. The evolutionary model GTR+I+G was used as the model for all the genes. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *G. vincae* (MFLU 16-1179 and CBS 236.34). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Erysiphe heraclei DC., Flore française 6, 107 (1815) Fig. 29

Index Fungorum number: IF120607; Facesoffungi number: FoF09219

Saprobic on living stem of *Torilis arvensis*. Sexual morph: *Ascomata* 70–80 × 85–90 µm (x̄ = 76 × 87 µm, n = 10), immersed to semi immersed, solitary to aggregate, sessile, globose, uniloculate. *Peridium* 20–28 µm (x̄ = 23 µm, n = 10), slightly wide at the sides, comprising of 3–4 cell layers, outermost layer comprising heavily pigmented, thick-walled, dark brown to pale brown cells of *textura angularis*, inner layer comprising pale brown to hyaline cells of *textura angularis*. *Hamathecium* comprising numerous, 2–4 µm wide (x̄ = 2.8 µm, n = 10), filamentous, aseptate, pseudoparaphyses. *Asci* 50–80 × 35–46 µm (x̄ = 58 × 39 µm, n = 10), 4-spored, bitunicate, saccate or broadly obpyriform, straight or slightly curved, apically rounded with indistinct ocular chamber, short pedicellate. *Ascospores* 14–21 × 11–15 µm (x̄ = 17 × 13 µm, n = 20), globose to subglobose, aseptate, with rounded ends, hyaline in both immature and mature stages, smooth-walled. Asexual morph: Undetermined.

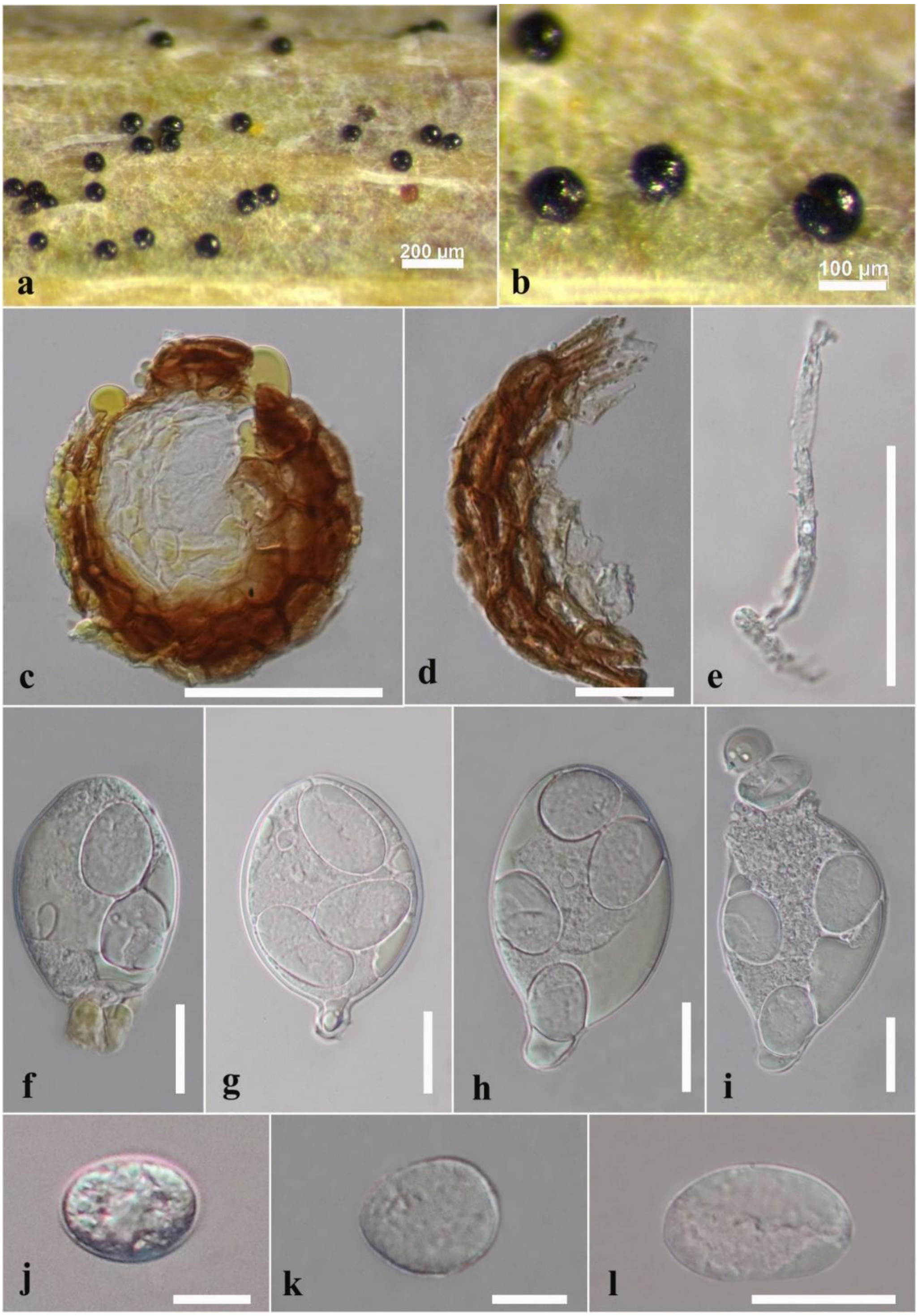

Fig. 29 – *Erysiphe heraclei* (MFLU 18-1489, new geographical record). a, b Appearance of ascomata on a living stem of *Torilis arvensis*. c Longitudinal section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–l Ascospores. Scale bars: a = 200 µm, b = 100 µm, c, e = 50 µm, d, f–i, l = 20 µm, j–k = 10 µm.

Material examined – Italy, Forlì-Cesena Province, living stem of *Torilis arvensis* (Apiaceae), 6 August 2018, Erio Camporesi IT3973 (MFLU 18-1489).

GenBank numbers – ITS: MT921775, LSU: MT921669.

Known distribution (based on molecular data) – Azerbaijan, Tengaltı Province (Abasova et al. 2018a), Italy, Forlì-Cesena Province (this study).

Known hosts (based on molecular data) – *Conium maculatum* (Qiu et al. 2019), *Torilis arvensis* (Abasova et al. 2018a, this study).

Notes – All powdery mildew species are exclusively obligate biotrophs of plants, i.e., they feed on living plants (Liyanage et al. 2017). Ascospores did not germinate in PDA and MEA media at different temperatures. Therefore, DNA was obtained directly from the fruiting bodies. *Erysiphe heraclei* is most common on Apiaceae hosts worldwide (Abasova et al. 2018a). In this study, we introduce the first geographical record of *E. heraclei* in Italy.

Class Pezizomycetes O.E. Erikss. & Winka, Myconet 1, 8 (1997)

For Pezizomycetes, we follow the recent treatment of Wijayawardene et al. (2020).

Subclass Pezizomycetidae Locq., De Taxia fungorum: I. Syllabus, 7 (1974)

Pezizales J. Schröt., Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1, 173 (1897)

Sarcoscyphaceae Le Gal ex Eckblad, Nytt Magasin for Botanik 15, 103 (1968)

Index Fungorum number: IF81256; Facesoffungi number: FoF04253

This family consists of mostly saprobic species (Ekanayaka et al. 2018). There are no documented hypogeous taxa (Pfister 2015). The family is characterized by vivid apothecia, pigmented paraphyses, suboperculate asci, and smooth or ornamented ascospores (Ekanayaka et al. 2018). These species abundantly occur in tropical areas (Pfister 2015). Fourteen genera are accepted by Ekanayaka et al. (2018), while the updated outline of fungi listed 12 genera in this family (Wijayawardene et al. 2020). An updated phylogeny is provided in Fig. 30.

Kompsoscypha Pfister, Memoirs of the New York Botanical Garden 49, 340 (1989)

Index Fungorum number: IF25317; Facesoffungi number: FoF09177

This genus was introduced by Pfister (1989) and typified by *K. chudei*. It is distinguished by orange to red apothecia of less than 10 mm, J- asci, ellipsoid ascospores with multi guttules (Zhuang et al. 2004, Ribes et al. 2015, Kaya & Uzun 2018). In addition to the type species, three others are accepted, *K. phyllogena*, *K. waterstonii* and *K. ziziphi* (Wijayawardene et al. 2017, 2020). *Kompsoscypha* species have a widespread distribution in tropical regions. Zhuang et al. (2004) introduced only *K. waterstonii* from China.

Kompsoscypha chudei (Pat. ex Le Gal) Pfister, Memoirs of the New York Botanical Garden 49, 341 (1989) Fig. 31

Index Fungorum number: IF136053; Facesoffungi number: FoF09178

Saprobic on dead wood. Sexual morph: *Apothecia* 0.5–1.5 mm high, 1–3 mm broad superficial, scattered to gregarious. *Disc* orange to reddish, discoid to convex. *Receptacle* yellowish to orange. *Stipe* 200–500 µm long, 200–500 µm broad, yellowish. *Medullary excipulum* 100–150 µm broad, have cells of *textura intricata*, composed of 4–6 µm broad, hyaline hyphae. *Ectal excipulum* 30–80 µm broad, composed of 10–14 × 6–7 µm, hyaline cells of *textura angularis*. *Stipitipellis* 30–70 µm, comprised of 11–15 × 7–9 µm hyaline cells of *textura angularis*. *Paraphyses* filiform, 1–2 µm broad in the middle, hyaline, septate. *Asci* 267–315 × 12–15 µm, 8-spored, operculate, subcylindrical, J-. *Ascospores* 19–21.5 × 11.5–13 µm, l:w = 1.4–2 ($\bar{x}$ = 1.65, n = 20), ellipsoid, equilateral uniseriate, inamyloid, guttulate, smooth-walled. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, Xishuangbanna (alt. 665 m), on an unidentified dead wood, 9 June 2018, M. Zeng Zeng011 (HKAS 107663).

GenBank numbers – ITS: MT907443, LSU: MT907444.

Known distribution (based on molecular data) – China (this study), France, Spain, Turkey (Romero et al. 2012)

Known hosts (based on molecular data) – dead wood or leaves (Romero et al. 2012, this study)

Notes – *Kompsoscypha chudei* is distinguished by orange to reddish apothecia, broad stipe, and ellipsoid, smooth ascospores with guttules. Ribes et al. (2015) discussed the differences between *Kompsoscypha* species. Except for *K. waterstonii* which is distinguished from the other species by its pinkish to white receptacle, the other three species are distinguished mainly by asci and ascospores size (Ribes et al. 2015). Asci of *K. ziziphi* do not exceed 200 µm in length, whereas ascospores of *K. phyllogena* always less than 20 µm in length (Pfister 1989, Ribes et al. 2015). Across the LSU sequences, there are 4 notable nucleotide differences among the 882 bp between *K. phyllogena* (DHP 10-690) and our species. Based on the morphology and phylogeny, we introduced a new record of *K. phyllogena* from China.

Cookeina Kuntze, Revisio generum plantarum 2, 849 (1891)

Index Fungorum number: IF1224; Facesoffungi number: FoF09179

This genus was introduced by Kuntze (1891) and is typified by *C. tricholoma*. There are 11 species in this genus (Wijayawardene et al. 2020). *Cookenia* is characterized by brightly coloured, cupulate apothecia with stipitate, J-, operculate asci, ellipsoid to fusiform ascospores with smooth-walled or longitudinal ribs (Ekanayaka et al. 2016).

Cookeina indica Pfister & R. Kaushal, Mycotaxon 20, 117 (1984) Fig. 32

Index Fungorum number: IF106712; Facesoffungi number: FoF02671

Saprobic on dead wood. Sexual morph: *Apothecia* superficial, scattered. *Disc* cupulate, yellowish, up to 1.5 cm high, 2 cm broad, nearly smooth. *Receptacle* concave, receptacle surface yellowish to orange, nearly smooth. *Stipe* up to 1.0 cm long, 0.2 cm broad, white to yellowish. *Medullary excipulum* 170–310 µm broad, of hyaline cells of *textura intricata*, composed of 3–6 µm broad hyphae. *Ectal excipulum* 50–100 µm broad, hyaline cells of *textura angularis* to *textura globulosa*, 17–22 × 12–15 µm, J^-. *Stipitipellis* 70–110 µm, hyaline, comprised of 18–23 × 13–16 µm cells of *textura angularis* to *textura globulosa*, J^-. *Paraphyses* filiform, 2–4 µm broad, hyaline, septate, branched, J^-. *Asci* 305–357 × 13–16 µm, 8-spored, operculate, subcylindrical to clavate, a short, pedicellate, J^-. *Ascospores* 27.5–32 × 8.4–10, l:w 2.94–4.09 ($\bar{x}$ = 3.39, n = 20), ellipsoid, uniseriate, inequilateral, inamyloid, 1–3-guttulate, ornamentation with striae arranged longitudinally. Asexual morph: Undetermined.

Material examined – Thailand, Ranong, on unidentified dead wood, 5 October 2017, M. Zeng ST02 (MFLU 20-0548).

GenBank numbers – ITS: MT941004, LSU: MT941005.

Known distribution (based on molecular data) – China, India, Thailand (Ekanayaka et al. 2016, Kropp 2017, this study)

Known hosts (based on molecular data) – dead wood (Ekanayaka et al. 2016, Kropp 2017, this study)

Notes – This species is characterized by cupulate apothecia, a nearly smooth hymenium and ellipsoid, inequilateral, guttulate ascospores with longitudinal striae. Morphologically similar *C. cremeirosea* is different from our species in pinkish apothecia, and smooth-walled ascospores (Ekanayaka et al. 2016, Kropp 2017). For phylogeny, our species clustered with other two *C. indica* species (MFLU 16-0610 & C ind 119) forming distinct sister clade of *C. cremeirosea*.

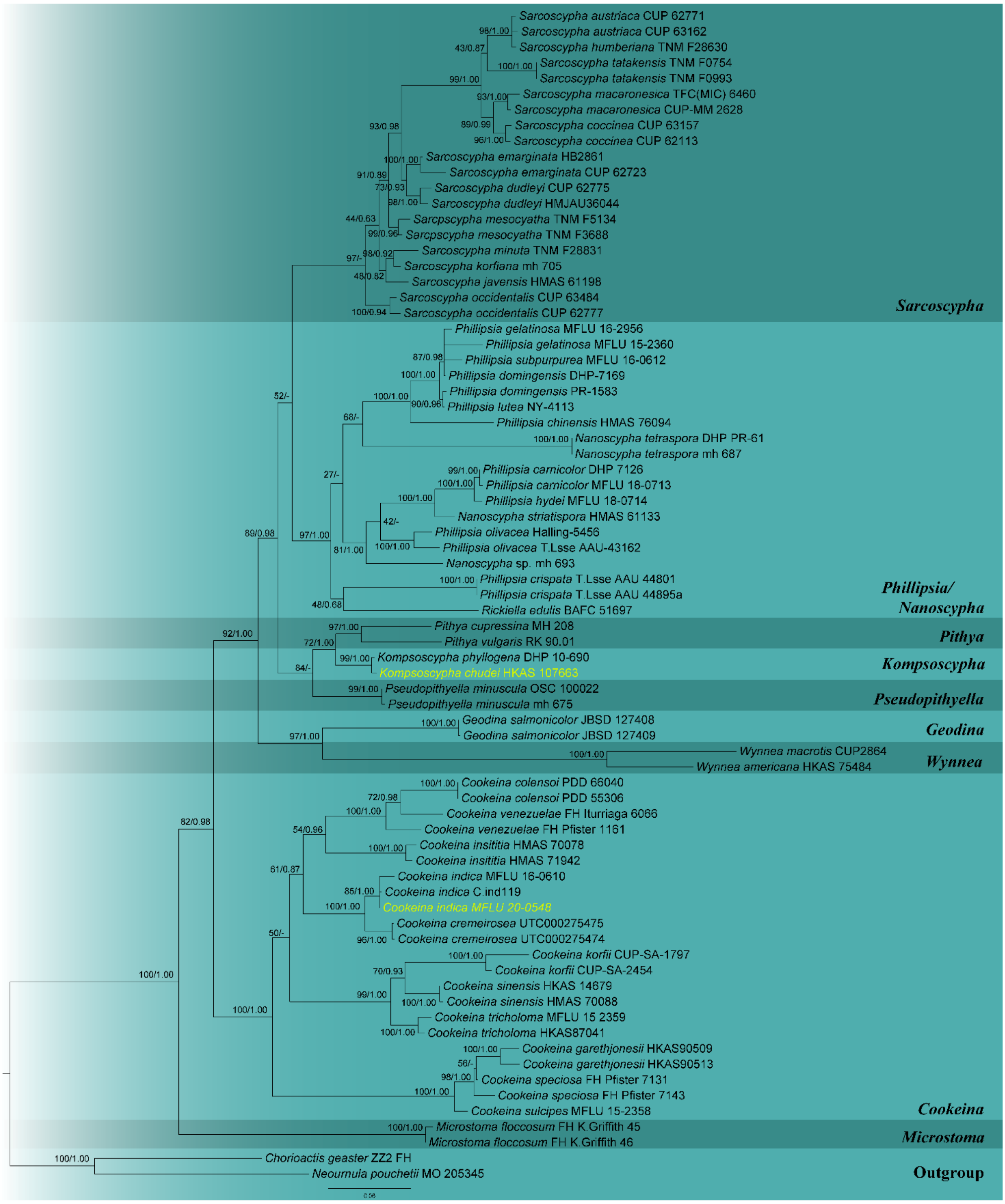

Fig. 30 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Seventy-five strains are included in the combined analyses which comprised 1479 characters (604 characters for ITS, 875 characters for LSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -14833.676115 is presented. Estimated base frequencies were as follows: A = 0.230206, C = 0.253698, G = 0.280642, T = 0.235454; substitution rates AC = 1.200880, AG = 2.035026, AT = 1.401259, CG = 1.177486, CT = 4.247817, GT = 1.000000; gamma distribution shape parameter α = 0.330664. The GTR+I+R was applied as the evolutionary model for all the gene regions. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with

Chorioactis geaster (ZZ2 FH) and *Neournula pouchetii* (MO 205345). The newly generated sequences are indicated in yellow.

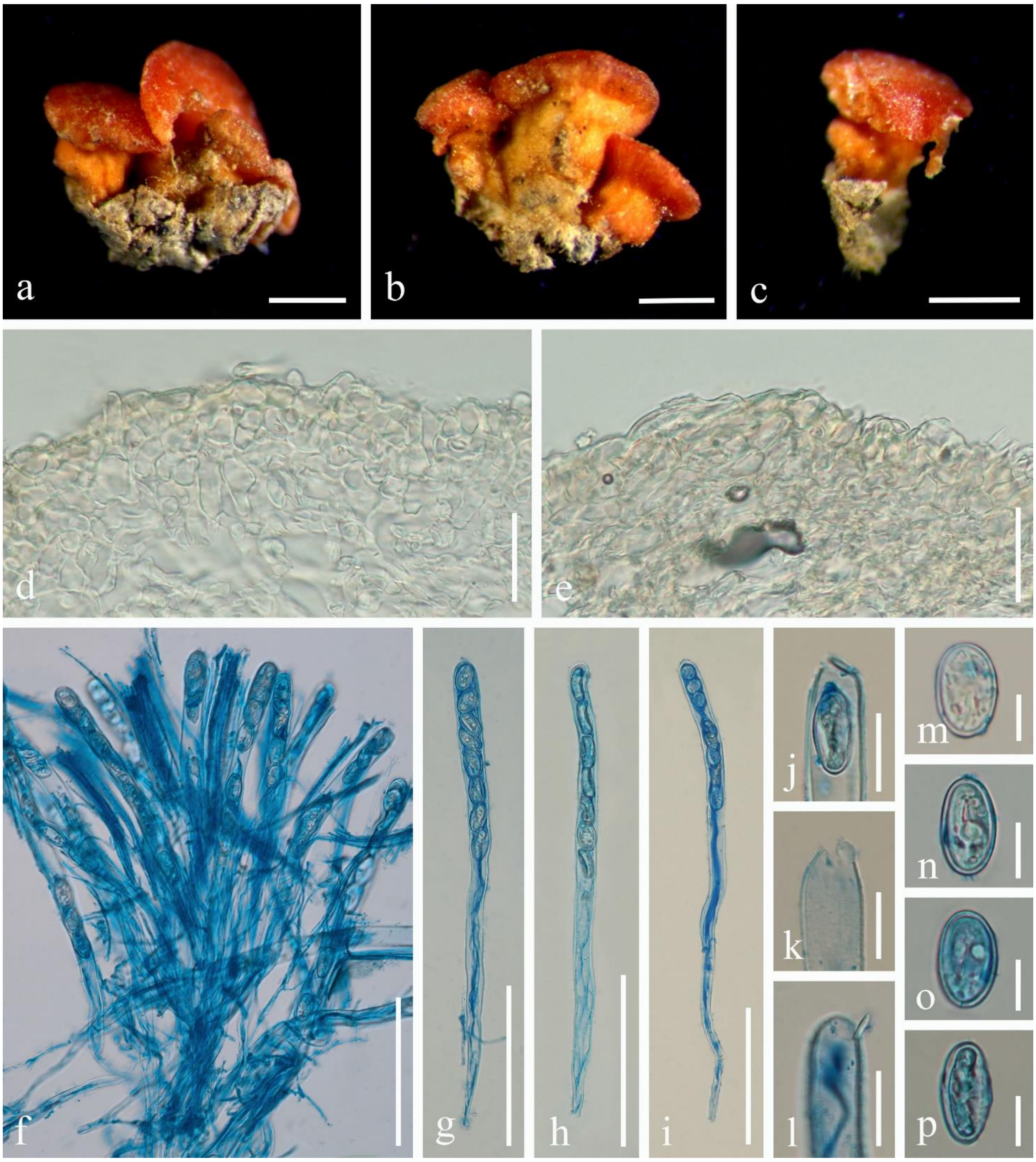

Fig. 31 – *Kompsoscypha chudei* (HKAS 107663, new geographical record). a–c Typical mature specimens. d Stipitipellis. e Receptacle surface of pileus. f Asci and paraphyses in Cotton blue. g–i Asci in Cotton blue. j–l Apices of asci in Cotton blue. m–p Ascospores in Cotton blue. Scale bars: a–c = 500 µm, d–e = 30 µm, f–i = 100 µm, j–l =20 µm, m–p =10 µm.

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

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

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

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

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

Index Fungorum number: IF80629; Facesoffungi number: FoF01332

Coniochaetaceae was established by Malloch & Cain (1971) and comprises two genera, *Coniochaeta* and *Coniochaetidium*. The family is accommodated in Coniochaetales (Huhndorf et al. 2004). Maharachchikumbura et al. (2016) studied the herbarium specimens of the family and provided a key for Coniochaetaceae. Species of Coniochaetaceae are usually saprobic or pathogenic on plants and animals (Samarakoon et al. 2018).

Coniochaeta (Sacc.) Cooke, Grevillea 16, 16 (1887)

Index Fungorum number: IF1209; Facesoffungi number: FoF01333

Coniochaeta is the type genus of Coniochaetaceae, Coniochaetales. The genus consists of 98 species (Species Fungorum 2020). The type species is *C. ligniaria*. Members of *Coniochaeta* are characterized by dark brown to black, pyriform to globose ascomata with or without ostioles, a membranaceous to pseudoparenchymatous peridium, presence or absence of paraphysate hamathecium, unitunicate thin-walled asci with a small J- apical ring and one-celled ascospores. The asexual morph is hyphomycetous (Weber et al. 2002, Khan et al. 2013). An updated phylogeny for the genus is provided in Fig. 33.

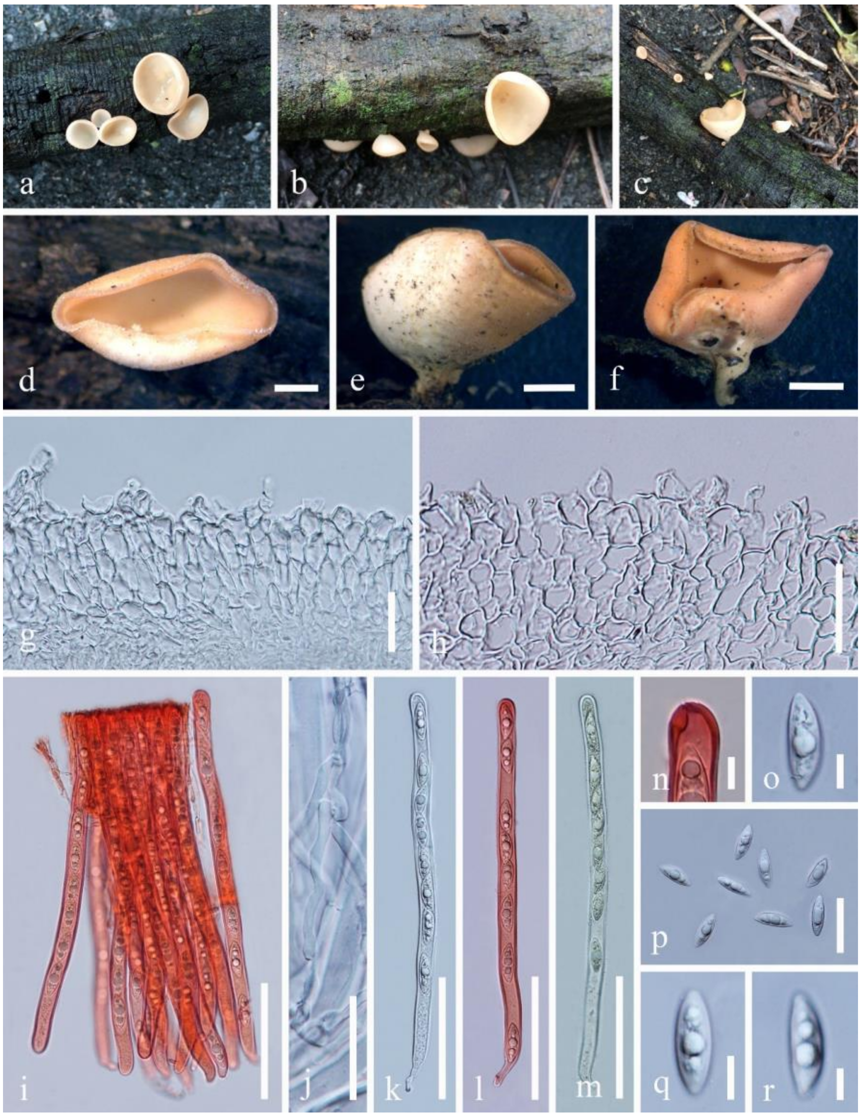

Fig. 32 – *Cookeina indica* (MFLU 20-0548, new geographical record). a–f Typic mature specimens. g Stipitipellis. h Receptacle surface of pileus. i Asci and paraphyses. j Paraphyses. k–m Asci (l Asci in Congo Red, m Asci in Melzer’s reagent). n Apex of asci in Congo Red. o–r Ascospores. Scale bars: d = 1000 µm, e, f = 2000 µm, g, h, j = 30 µm, i, k–m = 100 µm, n, o, q, r = 10 µm, p = 40 µm.

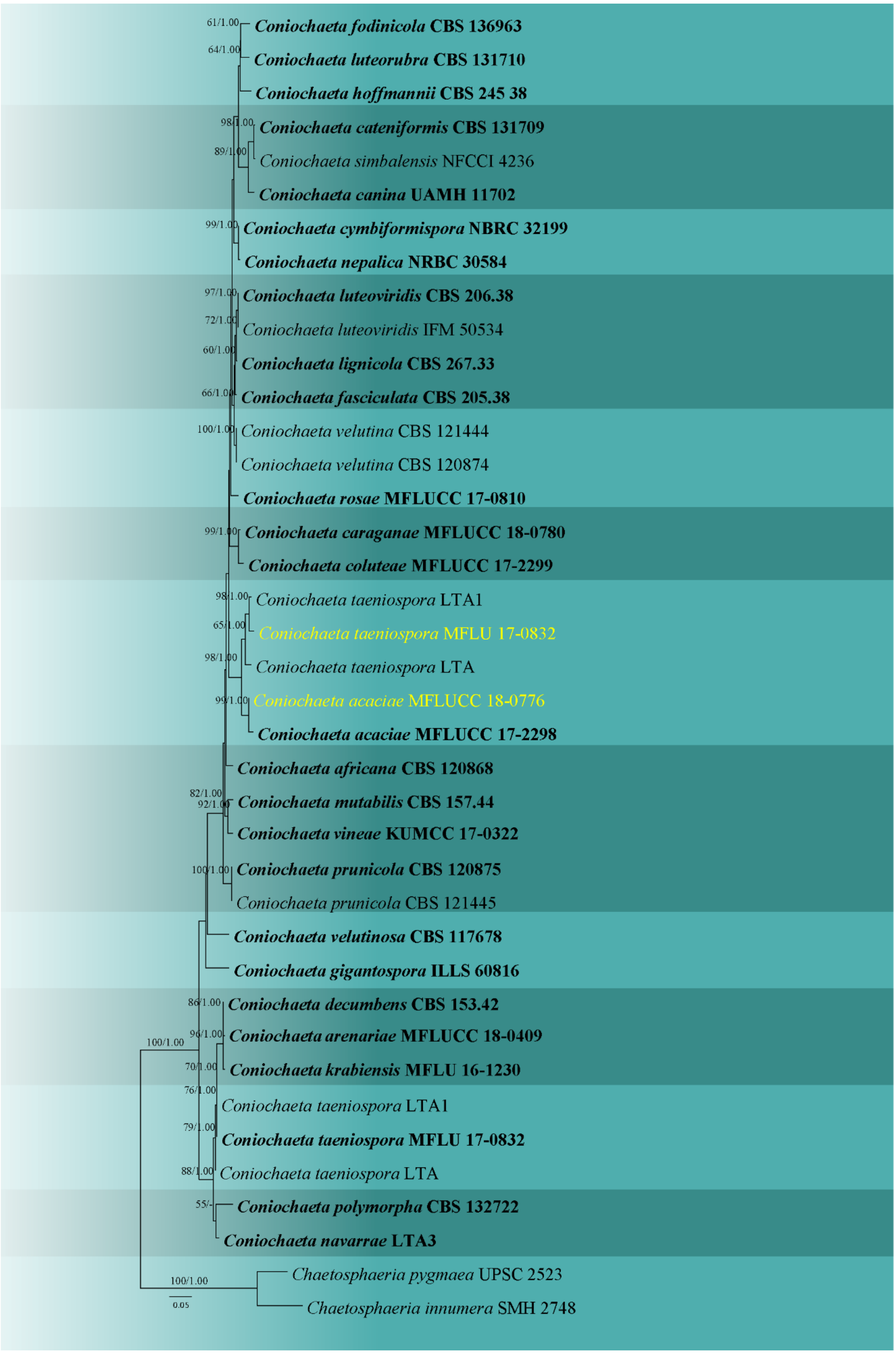

Fig. 33 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Thirty-five strains are included in the combined analyses which comprised 1544 characters (900 characters for LSU and 643 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6640.737819 is presented. Estimated base frequencies were as follows: A

= 0.246596, C = 0.243886, G = 0.288026, T = 0.221492; substitution rates AC = 1.659443, AG = 2.091549, AT = 1.486255, CG = 1.791599, CT = 7.712593, GT = 1.000000; gamma distribution shape parameter α = 0.559163. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.90 are given near nodes respectively. The tree is rooted with *Chaetosphaeria pygmaea* (UPSC 2523) and *C. innumera* (SMH 2748). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Coniochaeta acaciae Samarakoon, Gafforov & K.D. Hyde, Phytotaxa 336, 49 (2018) Fig. 34

Index Fungorum number: IF553912; Facesoffungi number: FoF03782

Saprobic on dead trunk and branches of *Betula pendula*. Asexual morph: See Samarakoon et al. (2018). Sexual morph: *Ascomata* 250–300 µm wide, 260–350 µm high, solitary to gregarious, semi-immersed to superficial, globose to ovoid, carbonaceous, papillate. *Peridium* 25–35 µm, two-layered, inner layer comprising of hyaline to subhyaline cells of *textura prismatica*, outer layer comprising of closely packed, thick-walled, brown cells of *textura intricata*. *Ostiolar necks* 10–11 × 15–16 µm ($\bar{x}$ = 10.1 × 15.2 µm, n = 10), papillate to cylindrical, filled with hyaline periphyses. *Paraphyses* 2.2 – 3.2 µm wide (n = 10), filiform, septate, hyaline. *Asci* 90–110 × 8–10 µm ($\bar{x}$ = 87.7 × 9.2 µm, n = 10), 8-spored, unitunicate, cylindrical, with small J- apical ring, pedicellate. *Ascospores* 14–16 × 7–8 µm ($\bar{x}$ = 14.5 × 7.6 µm, n = 10), uniseriate, slightly laterally compressed, ellipsoid to ovoid, dark brown, with straight germ slit across the entire length, smooth-walled, multi-guttulate, without sheath or appendages

Culture characteristics – Colonies on MEA, reaching 20–30 mm diam. after 4 weeks at 25°C, circular, surface rough, entire edge, in the middle orange, on the edge yellowish red, diffuse margin with light orange mycelium, reverse yellowish edges, grayish orange at the center, radiating, effuse and azonate.

Material examined – Ukraine, Donetsk region, Donetsk City, Donetsk Botanical garden, steppe community, on dead twigs and branches of *Betula pendula* (Betulaceae), 18 May 2017, T. Bulgakov (MFLU 17-2473), living culture MFLUCC 18-0776.

GenBank numbers – LSU: MT501618, ITS: MT498810, SSU: MT498798, *TEF1-α*: MT503199.

Known distribution (based on molecular data) – Uzbekistan (Samarakoon et al. 2018), Ukraine (this study).

Known hosts (based on molecular data) – *Acacia* sp. (Samarakoon et al. 2018), *Betula pendula* (this study).

Notes – Our new isolate MFLUCC 18-0776 is morphologically similar and phylogenetically related to *Coniochaeta acaciae* (MFLUCC 17-2298), but collected from a different host and geographical location. *Coniochaeta acaciae* was reported from Uzbekistan on branches of *Acacia* sp. (Fabaceae) (Samarakoon et al. 2018), while our collection is from Ukraine on *Betula pendula* (Betulaceae). The phylogenetic placement of our strain (MFLUCC 18-0776) is shown in Fig 33.

Coniochaeta taeniospora (Sacc.) Friebes, Jaklitsch & Voglmayr, Sydowia 68, 91 (2016) Fig. 35

Index Fungorum number: IF815856; Facesoffungi number: FoF06779

Saprobic on dead land branch of *Quercus* sp. Asexual morph: Undetermined. Sexual morph: *Ascostromata* forming inconspicuous groups in cracks of bark or erumpent through the bark, more rarely growing solitarily. *Perithecia* 350–550 × 450–620 µm ($\bar{x}$ = 465 × 542 µm), perithecial semi-immersed or erumpent, subglobose to ellipsoid, sometimes pyriform or lageniform, black, rough surface, covered with black exudate, ostiole visible in light brown covered with light black surrounding, neck around ostiole brown to black, rarely with unbranched, smooth, gradually tapering to round tip, short setae. *Ostiolar neck* papillate, hyaline, aseptate periphyses. *Peridium* 20–40 µm ($\bar{x}$ = 29.2 µm, n = 15) thick at base, 50–90 µm ($\bar{x}$ = 69 µm, n = 15) near the ostiole, brittle when dry, soft when rehydrated, two-layered, inner layer 7.5–12.5 × 2–4 µm ($\bar{x}$ = 9.8 × 2.9

µm, n = 25), consisting of *textura prismatica*, hyaline to subhyaline, with strongly compressed cells; outer layer 5–10 × 2–4 µm (x̅ = 7.8 × 2.9 µm, n = 25) consisting of densely packed, moderately thick-walled, brown cells of *textura angularis*, darker towards outside, turning green in 5% KOH. *Paraphyses* of 2–4 µm wide (x̅ = 2.8 µm, n = 20), filiform, septate. *Asci* 150–190 × 7–15 µm (x̅ = 170.6 × 9.5 µm, n = 30), 4–8-spored, cylindrical with short pedicel, with small, J- apical ring, more clearly visible in Congo Red. *Ascospores* 15–20 × 7–11 µm (x̅ = 15.5 × 9 µm, n = 30), l/w 1.7, uniseriate, dark brown, darker in 5% KOH, slightly laterally compressed, ellipsoid to ovoid, with straight germ slit across the entire length, smooth, multi-guttulate, without sheath or appendages.

Fig. 34 – *Coniochaeta acaciae* (MFLU 17-2473, new host and geographical record). a, b Appearance of ascomata on host surface. c Vertical section through an ascoma. d Peridium. e Hamathecium. f–h Asci. i–n Ascospores. o Germinated ascospore. p, q Culture characteristics on MEA (p: above view; q: reverse view). Scale bars: a = 2000 µm, b = 1000 µm, c = 100 µm, f–h = 20 µm, d, e, i–n = 10 µm, o = 30 µm.

Material examined – Italy, Province of Forlì-Cesena [FC], Camposonaldo - Santa Sofia, on fallen dead branch of *Quercus* sp. (Fagaceae), 13 March 2017, Erio Camporesi IT3275 (MFLU 17-0832, HKAS 102311).

GenBank numbers – ITS: MN337230, LSU: MN336234, *β-TUB*: MN509784.

Known distribution (based on molecular data) – Iran (unpublished), Italy (Friebes et al. 2016), this study).

Known hosts (based on molecular data) – *Quercus petraea*, *Q. robur* (Friebes et al. 2016), *Quercus* sp. (this study).

Notes – Our strain MFLU 17-0832 is similar to the type of *Coniochaeta taeniospora* epitypified by Friebes et al. (2016), in having 20–40 µm thick perithecial wall at base, 4–8-spored, cylindrical with short pedicel asci (150–190 × 7–15 *vs* 169–184 × 9–14 µm) and dark brown, slightly laterally compressed, ellipsoid to ovoid ascospores (15–20 × 7–11 vs 15.5–19.2 × 9.5–12.3 µm; 1.7 *vs* 1.4–1.8 l/w) with straight germ slit. However, perithecia of MFLU 17-0832 are larger than GZU000313629 (350–550 × 450–620 µm *vs* 200–410 × 200–450 µm). In addition, the LSU and ITS sequences are identical to each and in phylogeny formed a highly supported *Coniochaeta taeniospora* clade.

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

Cytosporaceae Fr., Systema Orbis Vegetabilis 1, 118 (1825)

Index Fungorum number: IF82042; Facesoffungi number: FoF06870

Cytosporaceae, introduced by Fries (1825), comprises phytopathogens and saprobes (Wehmeyer 1975, Barr 1978, Eriksson 2001, Castlebury et al. 2002, Senanayake et al. 2018). During the recent treatment, Senanayake et al. (2017) excluded seven genera and accepted only five genera in this family. In the outline of Ascomycota, Wijayawardene et al. (2018) accepted six genera in Cytosporaceae. In the same year, Senanayake et al. (2018) re-examined and added two genera to the family. Among the new inclusions, *Hypophloeda* was re-positioned in Diaporthales genera *incertae sedis* as it is atypical of Cytosporaceae (Hyde et al. 2020a).

Cytospora Ehrenb., Sylvae Mycologicae Berolinenses: 28 (1818)

Index Fungorum number: IF7904; Facesoffungi number: FoF01378

Cytospora has a broad host range and causes canker and dieback diseases on plants (Adams et al. 2005, 2006, Norphanphoun et al. 2018, Hyde et al. 2016, 2020a). The genus was established by Ehrenberg (1818), with the characters of hyaline, allantoid conidia and single or labyrinthine of pycnidial locules. There are 663 species listed in Index Fungorum (2020) and Kirk et al. (2008) estimated approximately 110 *Cytospora* species. However, most of *Cytospora* lack material, cultures, and DNA sequence data. An updated phylogeny for this genus is provided in Fig. 36.

Cytospora cedri Syd., P. Syd. & E.J. Butler, Annales Mycologici 14, 193 (1916) Fig. 37

Index Fungorum number: IF184521; Facesoffungi number: FoF06871

Associated with branches of *Rubus* sp. Sexual morph: Undetermined. Asexual morph: *Pycnidial* stromata immersed in the bark, scattered, producing black area on the bark, circular to ovoid, with multiple locules, occasionally slightly erumpent through the surface, ostiolate. *Ostiole* in the centre of the disc, black, conspicuous. *Locules* 150–500 µm, numerous, subdivided frequently by invaginations with common walls. *Conidiophores* hyaline, septate, branched at base, middle, thin-walled, occasionally septate, embedded in a gelatinous layer. *Conidiogenous cells* 4–7(–8) × 0.8–1.5 µm ($\bar{x}$ = 7 × 1.4), enteroblastic, phialidic, sub-cylindrical. *Conidia* (3–)4.5–5 × 0.5–1 µm ($\bar{x}$ = 5 × 0.8), hyaline, allantoid, aseptate, smooth-walled.

Material examined – Italy, on branches of *Rubus* sp., Erio Camporesi IT3288 (MFLU 17-0835).

GenBank numbers – ITS: MN871816, LSU: MN873004, *RPB2*: MN871989.

Known distribution (based on molecular data) – Canada, France, Italy, Portugal, Spain, Switzerland, USA (López-Moral et al. 2020, Shang et al. 2020).

Known hosts (based on molecular data) – *Abies alba*, *Acer saccharum*, *Castanea sativa*, *Cedrus deodara*, *Chamaecyparis*, *Cupressus sempervirens*, *Lonicera* sp., *Ostrya carpinifolia*, *Quercus ilex*, *Rubus* sp., *Thuja* sp. (López-Moral et al. 2020, Shang et al. 2020).

Notes – *Cytospora cedri* was introduced by Sydow et al. (1916) from *Cedrus libani* in India. Our strain was identified as *C. cedri* based on morphological characteristics and phylogenetic analyses (Fig. 36). The conidiophore and conidial characters of the type species differ slightly with our isolate by having allantoid conidia of 4–6 × 0.5–1.2 µm and 10–12 × 1–1.3 µm conidiophores (Sydow et al. 1916).

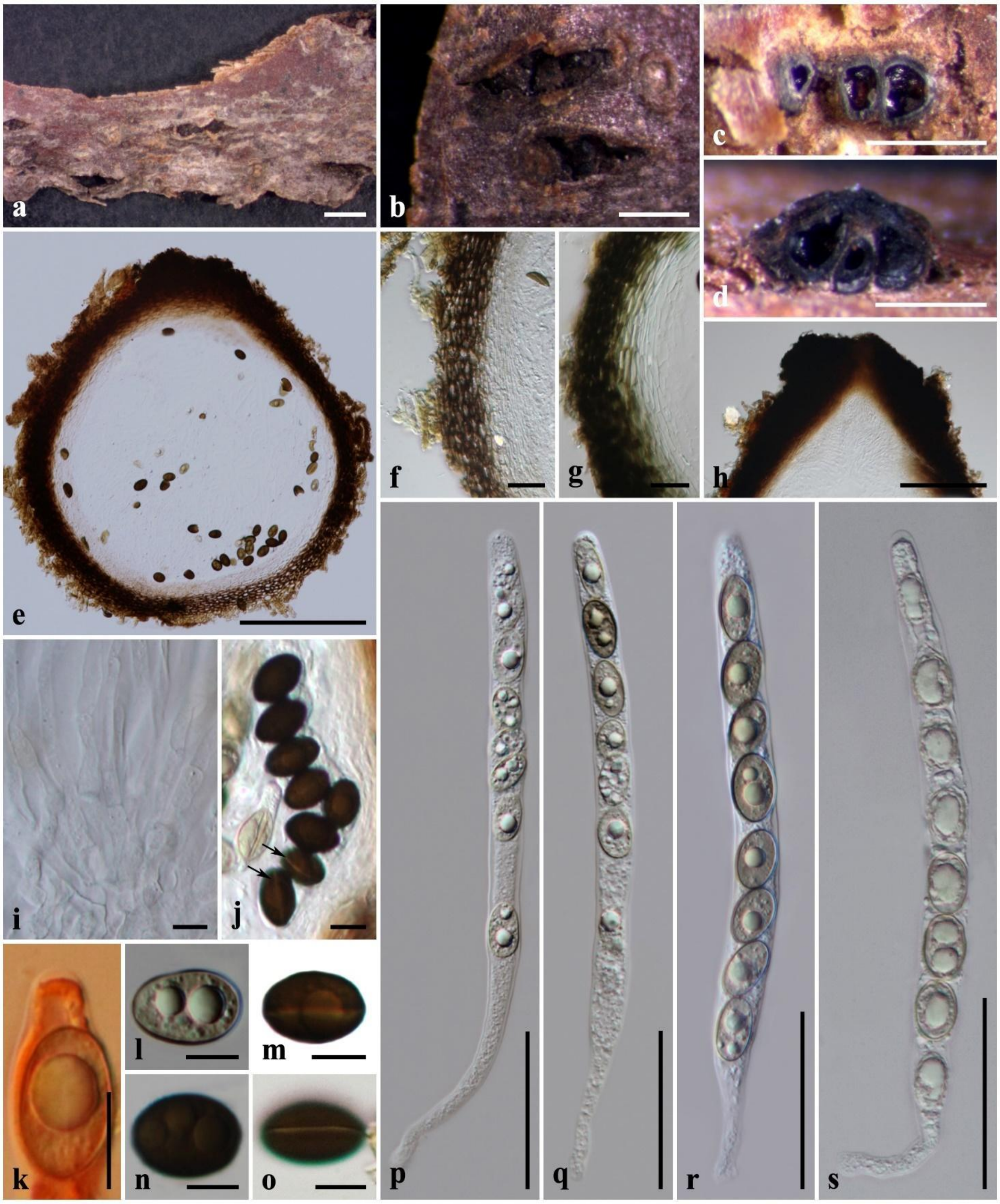

Fig. 35 – *Coniochaeta taeniospora* (MFLU 17-0832, additional collection). a–d Stroma on the host. e Cross section of an ascoma. f, g Peridium (g in 5% KOH). h Ostiole in section. i Paraphyses. j, l-o Ascospores (black arrow heads show germ slits). k Ascus apex in Congo Red. p-s Asci. Scale bars: a = 1 mm, b–d = 500 µm, e = 200 µm, h = 100 µm, p–s = 50 µm, f, g = 20 µm, j–o = 10 µm, i = 5 µm.

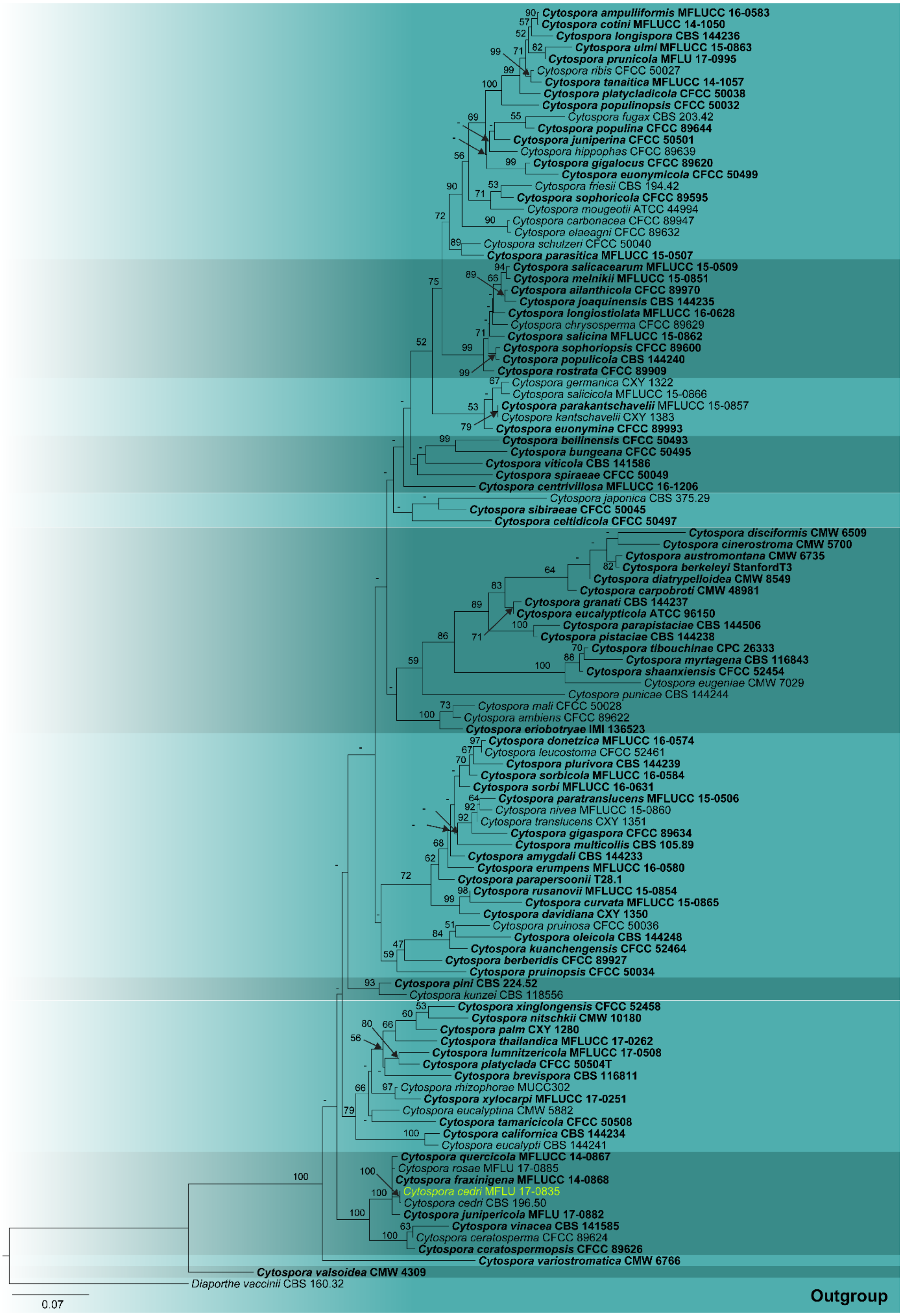

Fig. 36 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *ACT* and *RPB2* sequence data. One hundred and eleven strains are included in the combined analyses which comprised 2217 characters (629 characters for ITS, 524 characters for LSU, 337 characters for *ACT*, 727 characters for *RPB2*). Tree topology of the maximum likelihood analysis is

similar to the Bayesian analysis. The best ML tree with a final likelihood value of -20342.689825 is presented. Bootstrap support values for ML greater than 50%. The tree is rooted with *Diaporthe vaccinii* (CBS 160.32). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

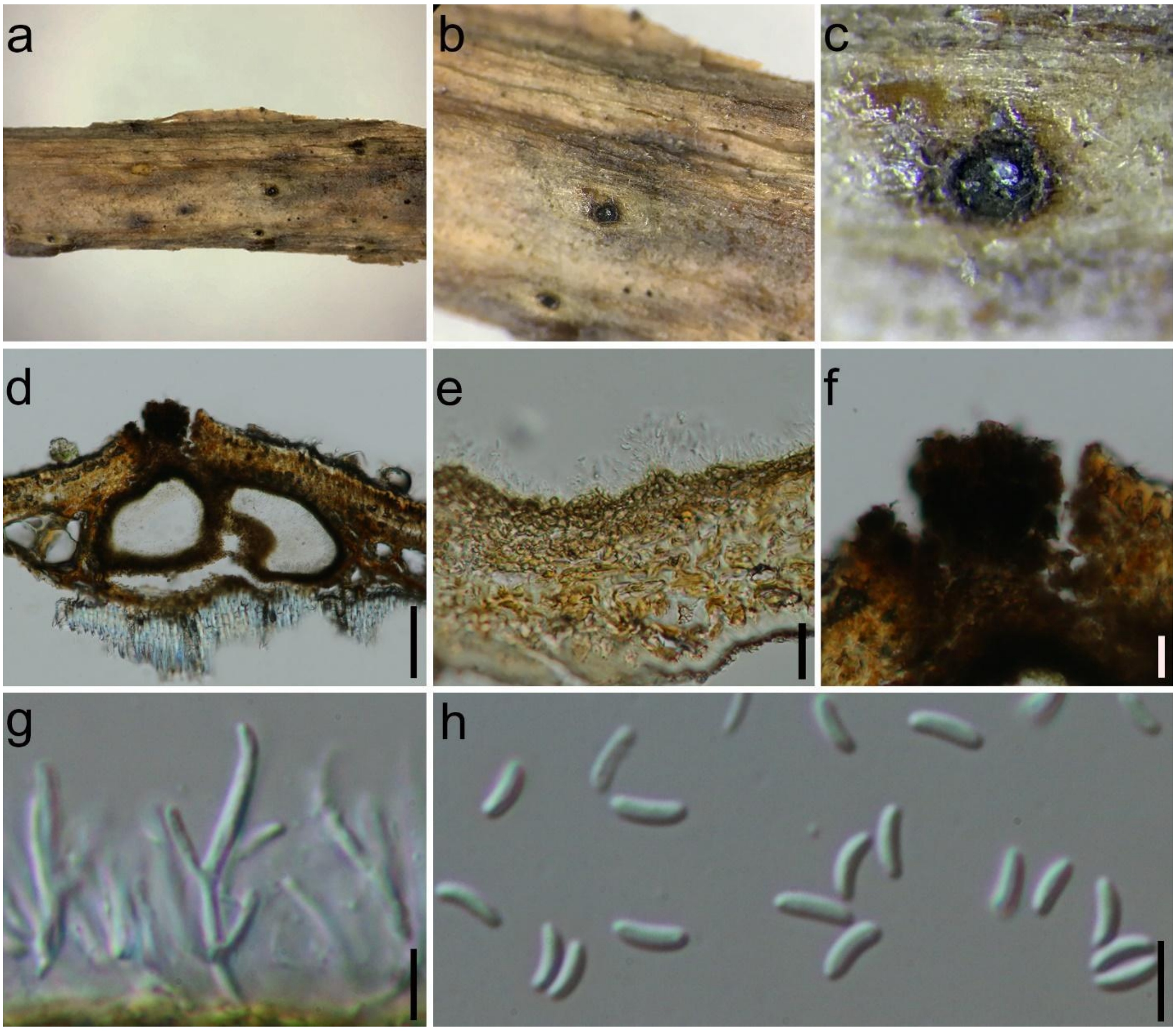

Fig. **37** – *Cytospora cedri* (MFLU 17-0835, new host record). a Stromatal habit in wood. b Fruiting bodies on host surface. c Surface of fruiting bodies showing the black ostioles. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g, h Conidiogenous cell containing conidia. i Conidia. Scale bars: d = 100 µm, e, f = 20 µm, g, h = 5 µm.

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

Index Fungorum number: IF80691; Facesoffungi number: FoF01383

Diaporthaceae, introduced by von Höhnel (1917), comprises many endophytic and phytopathogenic fungal species (Udayanga et al. 2012, Hyde et al. 2020a). This family has been subjected to critical revisions over the years (Maharachchikumbura et al. 2015, 2016, Senanayake et al. 2017, Hyde et al. 2020a). In recent treatments, 15 genera are accepted in Diaporthaceae (Hyde et al. 2020a, Wijayawardene et al. 2020).

Diaporthe Nitschke, Pyrenomycetes Germanici 2, 240 (1870)

Index Fungorum number: IF1497; Facesoffungi number: FoF00146

Nitschke (1867) established *Diaporthe* to accommodate taxa with stromata in the Sphaeriales. The genus comprised of saprobes, pathogens and endophytes and has a cosmopolitan distribution (Wijayawardene et al. 2020). There are 1067 epithets listed in Index Fungorum (2020), but only

261 have molecular data (Hyde et al. 2020a). The phylogenetic tree (Fig. 38) shows the relationships between the taxa introduced in this study.

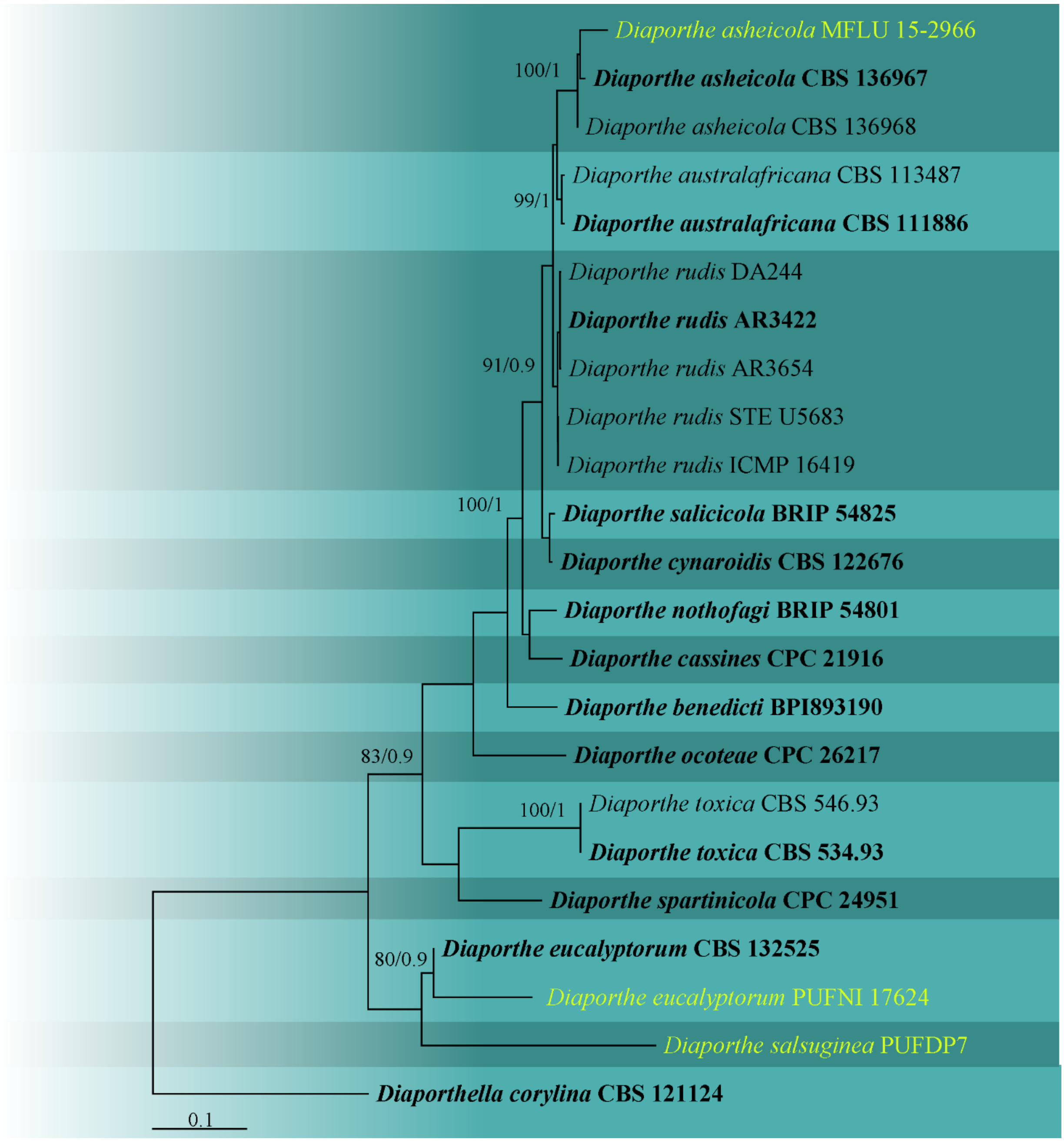

Fig. 38 – Phylogram generated from maximum likelihood analysis based on combined ITS, *TEF1-α*, *β-TUB* and *CAL* sequence data. Twenty-three strains are included in the combined analyses which comprised 1898 characters (573 characters for ITS, 335 characters for *TEF1-α*, 505 characters for *β-TUB*, 485 characters for *CAL*) 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 -8536.482989 is presented. Estimated base frequencies were as follows: A = 0.223206, C = 0.299928, G = 0.240952, T = 0.235914; substitution rates AC = 0.994418, AG = 2.320262, AT = 0.876368, CG = 0.702354, CT = 3.910746, GT = 1.000000; gamma distribution shape parameter α = 0.541230. The evolutionary model GTR+I+G was applied to all the gene regions. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.90 are given near nodes respectively. The tree is rooted with *Diaporthella corylina* (CBS 121124). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Diaporthe asheicola L. Lombard & Crous, Phytopathologia Mediterranea 53, 93 (2014)

Fig. 39

Index Fungorum number: IF807598; Facesoffungi number: FoF03396

Saprobic on *Fraxinus pennsylvanica*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* up to 530 µm wide and 290–420 µm length, (x̅ = 345 µm, n = 10), pycnidial, eustromatic, subepidermal, immersed to erumpent, globose, flask-like to conical, brown to black, scattered or aggregated, unilocular, smooth at outer surface, 1-ostiolate, including necks. *Pycnidial* wall consisting two regions of *textura angularis*; the outer region 8–15 µm wide, black, 4–5 cells thick, inner region 7–12 µm wide, brown, 3–4 cells thick, with the outside cells compressed. *Conidial mass* white, pale-yellow to yellow, predominantly pale-yellow, globose or in cirrhi. *Alpha conidiophores* 8–35 × 2–3 µm (x̅ = 27 × 2 µm, n = 20), cylindrical, filiform, aseptate and rarely branched. *Alpha conidiogenous cells* 3–15 × 1–2 µm (x̅ = 10 × 1.5 µm, n = 20), tapering towards the apex, subcylindrical, phialidic, collarettes and periclinal thickening present. *Alpha conidia* 6–9 × 2–3 µm (x̅ = 8 × 2 µm, n = 20), commonly found, fusoid to ellipsoidal, obtuse to subtruncate at base, acutely rounded at apex, multi-guttulate with guttules grouped at the polar ends, rarely biguttulate. *Beta conidiophores* 10–27 × 1–2 µm (x̅ = 16 × 1.5 µm, n = 20), ampulliform to subcylindrical, rarely branched. *Beta conidiogenous cells* 7–14 × 1–2 µm (x̅ = 11–1.5 µm, n = 20), subcylindrical, tapering towards the apex, phialidic, collarette and periclinal thickening present. *Beta conidia* 20–25 × 1–2 µm (x̅ = 23–1 µm, n = 20), less common than alpha conidia, straight, curved or hamate. *Gamma conidia* not observed.

Material examined – Russia, Rostov region, Rostov-on-Don City Botanical Garden of Southern Federal University, on stem of *Fraxinus pennsylvanica* (Oleaceae), 30 May 2015, T.S. Bulgakov T823 (MFLU 15-2966).

GenBank numbers – ITS: MF443248, *β-TUB*: MF443249, *CAL*: MF443250.

Known distribution (based on molecular data) – Chile (Lombard et al. 2014).

Known hosts (based on molecular data) – *Vaccinium ashei* (Lombard et al. 2014).

Notes – Lombard et al. (2014) introduced *D. asheicola*, but this species did not sporulate on any of the media used in their study, nor on sterilised *Vaccinium myrtillus* tissue placed on water agar. This species lacks any data related to morphological characters due to the age or repeated sub-culturing. In our study, a Russian specimen of *Diaporthe* revealed molecular similarity to *D. asheicola* in a combined gene phylogenetic analysis (Fig. 38). Since the original description of *D. asheicola* by Lombard et al. (2014) lacks morphological characters, we suggest this specimen be considered as the morphological description of *D. asheicola*. We could not obtain a culture from a single spore and DNA was extracted directly from the fruiting bodies.

Diaporthe eucalyptorum Crous & R.G. Shivas, Persoonia 28, 153 (2012) Fig. 40

Index Fungorum number: IF800374; Facesoffungi number: FoF09077

Saprobic on an unidentified twig. Sexual morph: *Stromata* immersed, ascomata covered with a blackened zone. *Ascomata* 432–560 × 422–467 µm (x̅ = 512 × 448), perithecial, globose to subglobose, solitary to gregarious, immersed, lignicolous, coriaceous, immersed, with long necks, periphysate. *Necks* 1–1.5 cm long, 88–133 µm wide, soft at base, apically carbonaceous, straight, sometimes laterally emerging through host surface, wall consists of *textura prismatica*. *Peridium* pale brown to hyaline consisting of *textura angularis* cell layers. *Paraphyses* filamentous, sparsely present, septate, unbranched, basally broad, narrowing towards apices, granulate. *Asci* 38–47 × 7–10 µm (x̅ = 42.4 × 8.3, n = 25), unitunicate, 8-spored, obclavate, apically flat-ended, with a cylindrical J- apical ring in Lougal's reagent, apedicellate. *Ascospores* 9–11 × 2.7–4.5 µm (x̅ = 9.9 × 3.5, n = 28), hyaline, uniseriate at apical end and overlapping tri-seriate at the centre and below, obpyriform to obclavate, smooth-walled, obtuse ends, with 2–3 pseudo-septa, constricted at the pseudosepta. Asexual morph: Undetermined.

Culture characteristics – Colonies on malt extract agar reached 42 mm diam. in one week at 28°C, cottony, initially white, becoming brown at maturity, circular, centrally brown.

GenBank numbers – ITS: MK990278, LSU: MK981540, SSU: MK981536.

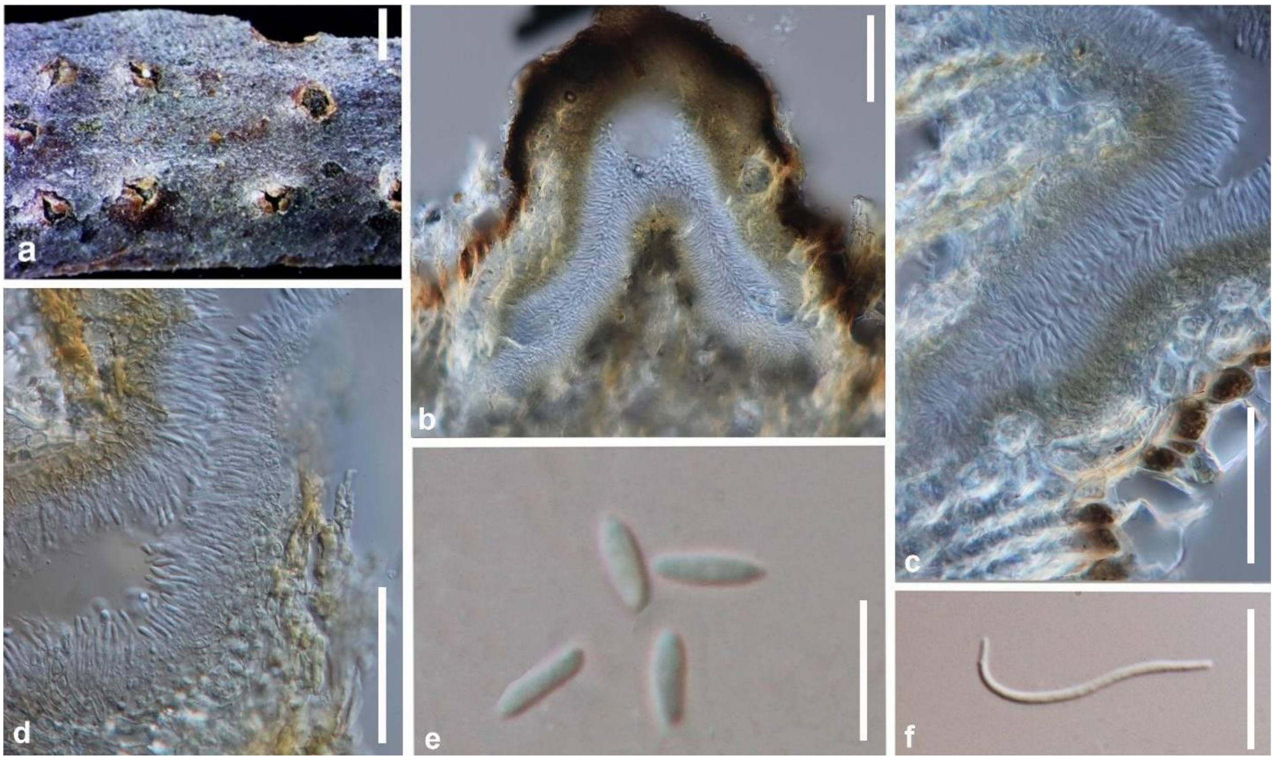

Fig. **39** – *Diaporthe asheicola* (MFLU 15-2966, new host record). a Conidiomata on host surface. b Cross section of conidioma. c Peridium. d Alpha conidium attached to conidiogenous cells. e Alpha conidia. f Beta conidium. Scale bars: a = 0.5 mm, b–d = 200 µm, e, f = 10 µm.

Material examined – India, Andaman and Nicobar Islands, South Andaman, Manjery (11˚52'68.2.0" N, 92˚64'74.9" E), isolated from an unidentified twig, 17 May 2018, M. Niranjan & V.V. Sarma (PUFNI 17624), living culture NFCC-4374.

Known distribution (based on molecular data) – Australia, Brazil, China, India, Republic of Korea, Thailand, Turkey and Vietnam (Schoch et al. 2014, Dissanayake et al. 2017, Kaliane et al. 2018, Deepthi & Ray 2018, Rajamani et al. 2018, Zhou et al. 2018, Manawasinghe et al. 2019, Gao et al. 2020, Zhao et al. 2020).

Known hosts (based on molecular data) – *Acampe praemorsa*, *Acanthus ilicifolius Bruguiera cylindrical*, *Bruguiera gymnorhiza*, *Bruguiera sexangula*, *Cerops tagal*, *Cocos nucifera*, *Epidendrum radicans*, *Eucalyptus* sp., *Camellia taliensis*, *Hevea brasiliensis*, *Ilex cornuta*, *Lumnitzera racemosa*, *Mangifera indica*, *Melia azedarach*, *Morinda officinalis*, *Rhizophora mucronata*, *Rhizophora stylosa*, *Rhyncostylis retusa*, *Scyphiphora hydrophyllacea*, *Sonneratia alba*, *Vellozia gigantean* and *Xylocarpus granatum* (Schoch et al. 2014, Dissanayake et al. 2017, Kaliane et al. 2018, Deepthi & Ray 2018, Rajamani et al. 2018, Zhou et al. 2018, Manawasinghe et al. 2019, Gao et al. 2020, Zhao et al. 2020).

Notes – The blast search results of ITS, LSU and SSU of our taxon reveals that it is closely related to *Diaporthe* species including *Diaporthe foeniculina*, *D. amygdali*, *D. eucalyptorum*, *D. musigena*, *D. foeniculina*, *D. velata* and *D. phaseoli*. However, our taxon has larger ascomata, smaller asci and ascospores as compared to *D. foeniculina*. *Diaporthe phaseoli* has smaller ascomata and asci, and larger ascospores (Niranjan et al. 2018). *Diaporthe velata* (Udayanga et al. 2014) has larger ascomata, asci and ascospores when compared to our taxon. *Diaporthe amygdali*, *D. eucalyptorum* and *D. musigena* have only asexual morph (Dissanayake et al. 2017). In the phylogenetic analysis, *D. eucalyptorum* (PUFNI 17624) clustered with *D. eucalyptorum* (KACC48653) showing high bootstrap support (ML 96%, BYPP 0.99) and the base pair difference between the two isolates is 1% (7/648 bp). Therefore, this taxon is considered as the sexual morph of *Diaporthe eucalyptorum*.

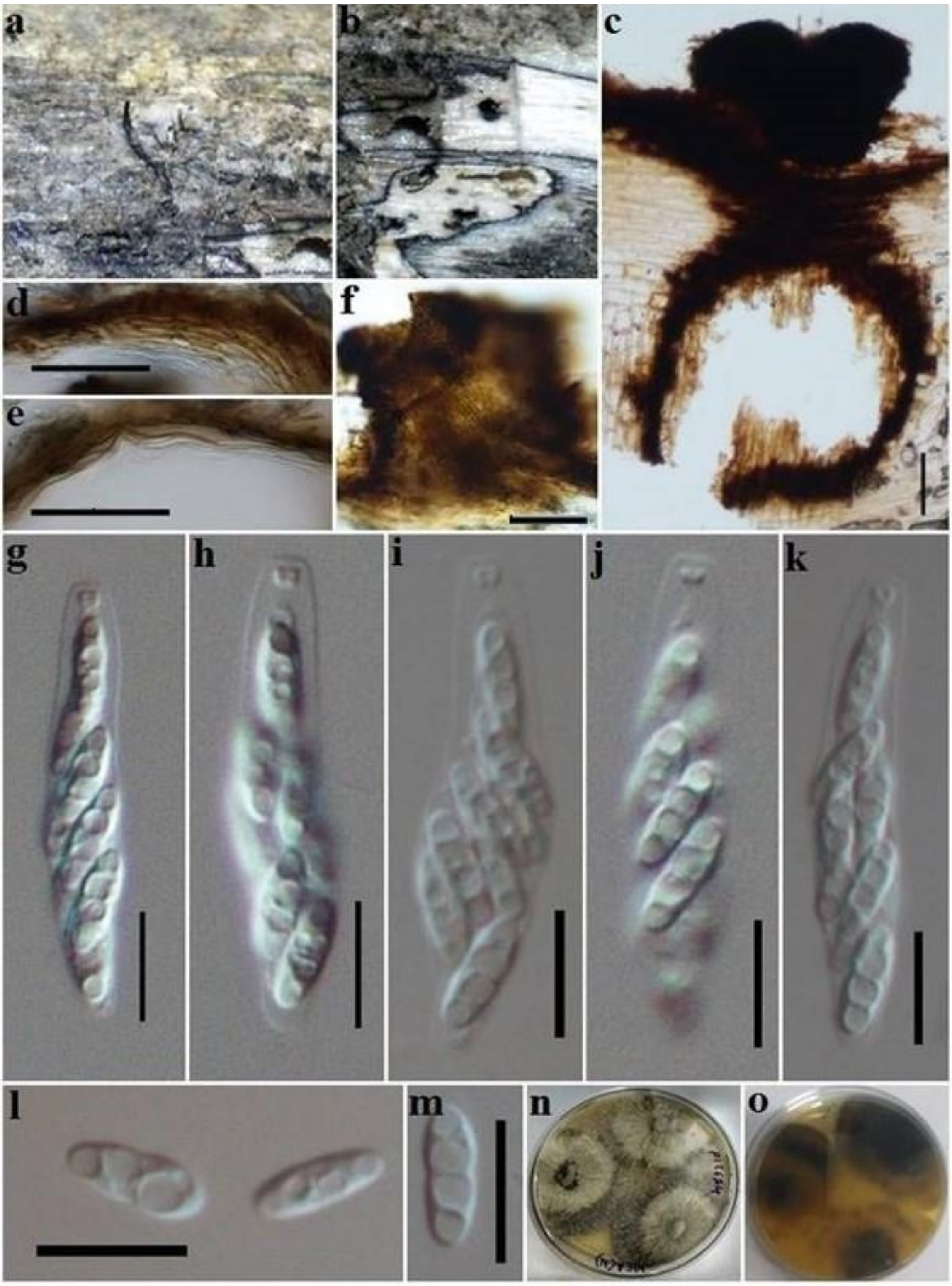

Fig. 40 – *Diaporthe eucalyptorum* (NFCC-4374, a new host record). a, b Ascomata. c Vertical section of ascoma. g–k Asci. l–n Ascospores. n, o Culture on malt extract agar. Scale bars: c–f = 10 µm, g–m = 10 µm.

Diaporthe salsuginosa Vrijmoed, K.D. Hyde & E.B.G. Jones, Mycological Research 98, 699 (1994) Fig. 41

Index Fungorum number: IF362640; Facesoffungi number: FoF06280

Saprobic on decaying wood of *Avicennia marina*. Sexual morph: *Ascomata* solitary or clustered, enclosed within a wide spreading blackened zone in the wood, both above the ascomata (dorsal zone) and below (ventral zone). *Stromata* appears as fine black lines when the substrate is cut at right angles to the surface; ascomata up to 160–300 µm high, 200–285 µm diameter (x̅ = 224 × 248 µm, n = 10), brown or black, immersed, coriaceous, commonly in small groups, in crater-like, darkened depressions (discs) on the wood surface. Blackened stromatic development around the area of clustered ascomata, which is variable and is composed of host cells filled with irregular brown fungal hyphae, with short ostioles piercing the host surface singly. *Ostiole* 40–100 µm high, 25–60 µm diameter (x̅ = 68 × 50 µm, n = 5), mostly immersed with short portion projecting above host surface, brown with periphyses. *Peridium* 20–40 µm (x̅ = 25 µm, n = 20), wide, composed of pallid elongate cells inwardly and brown thin-walled cells of *textura angularis* at the outside. The basal cells are hyaline. *Paraphyses* hypha-like, 2–4 µm wide at the base, filiform, tapering distally, septate. *Asci* 37–70 × 4–10 µm (x̅ = 52 × 7 µm, n = 20), 8-spored, unitunicate, thin-walled, cylindrical, short pedicellate, apically flattened with an iodine negative subapical ring, developing in the hymenium at the base of the ascomata. *Ascospores* 8–15 × 2.5–5 µm (x̅ = 10 × 3 µm, n = 30), hyaline, guttulate, 1–2-seriate, fusoid, 2-celled, smooth-walled, with or without constriction at the septum, with a small mucilaginous pad at each end which swells in water and attaches the spore to the glass slide. Asexual morph: *Conidiomata* 420–630 × 275–470 µm (x̅ = 470 × 376 µm, n = 5) in diam., pycnidial, superficial, aggregated in groups on MEA, stromatic, ostiolate, multilocular, globose, dark brown to black. *Peridium* 50–110 µm (x̅ = 74 µm, n = 5), thick, composed of thick-walled cells of *textura angularis*. *Conidiophores* 25–40 × 1–2 µm (x̅ = 31 × 1.5 µm, n = 10), branched, filiform, aseptate, densely aggregated. *Conidiogenous cells* subcylindrical, straight to curved, hyaline, tapering towards the apex. *Alpha conidia* 6–9 × 1.5–2.5 µm (x̅ = 7.5 × 2 µm, n = 5), hyaline fusiform or oval with obtuse ends rarely found. *Beta conidia* 25–40 × 1.5–2 µm (x̅ = 27 × 1.8 µm, n = 10), filiform, hamate, eguttulate, aseptate tapering towards both ends.

Culture characteristics – Ascospores germinating on 50% sea water agar within 24 h, with germ tubes developed from both ends of the cell and lateral sides of ascospores. Colonies on MEA, reaching 45–55 mm diam., after 7 days of incubation at 25°C, flat with an entire edge, surface hyaline to creamy initially, reaching pale yellow to dark brown at maturity, reverse hyaline to pale yellow, filamentous, cottony texture, circular, raised.

Material examined – India, Tamil Nadu, Parangipettai mangroves (11.59°N 79.5°E), on decaying wood of *Avicennia marina* (Acanthaceae), 23 April 2018, B. Devadatha (AMH-10013), living culture NFCCI-4385.

GenBank numbers – ITS: MN061372, LSU: MN061362, SSU: MN173346, *RPB2*: MN546859, *TEF1-α:* MN184789.

Known distribution (based on molecular data) – India, Tamil Nadu, Parangipettai (Vrijmoed et al. 1994, Jones et al. 2015)

Known hosts (based on molecular data) – *Avicennia marina, Kandelia candel* (Vrijmoed et al. 1994, Jones et al. 2015)

Notes – *Diaporthe salsuginosa* was described from decaying mangrove wood by Vrijmoed et al. (1994) based on morphological characteristics. We provide multi-gene sequence data for this species. *Diaporthe salsuginosa* is distinct from other *Diaporthe* species in having unique 1-septate ascospores with bipolar mucilaginous pads which swell in water. Our collection of *D. salsuginosa* (AMH-10013) is similar to the protologue of *D. salsuginosa,* but distinct in having constrictions at the septum and they have an asexual stage. In the phylogenetic analysis of combined ITS and *β-TUB* genes, *D. salsuginosa* clusters with *D. eucalyptorum* with significant support (ML 96%, 0.9 BYPP). *Diaporthe salsuginosa* can be distinguished from *D. eucalyptorum* (sexual morph) in having smaller stromatic ascomata, longer ascospores with guttules and a small mucilaginous pad at each end, and an asexual stage with larger pycnidia and containing both alpha and beta conidia. *Diaporthe eucalyptorum* was reported as an asexual morph from leaves of *Eucalyptus* (Crous et al. 2012). In the present study, we connect *D. salsuginosa* to the sexual morph.

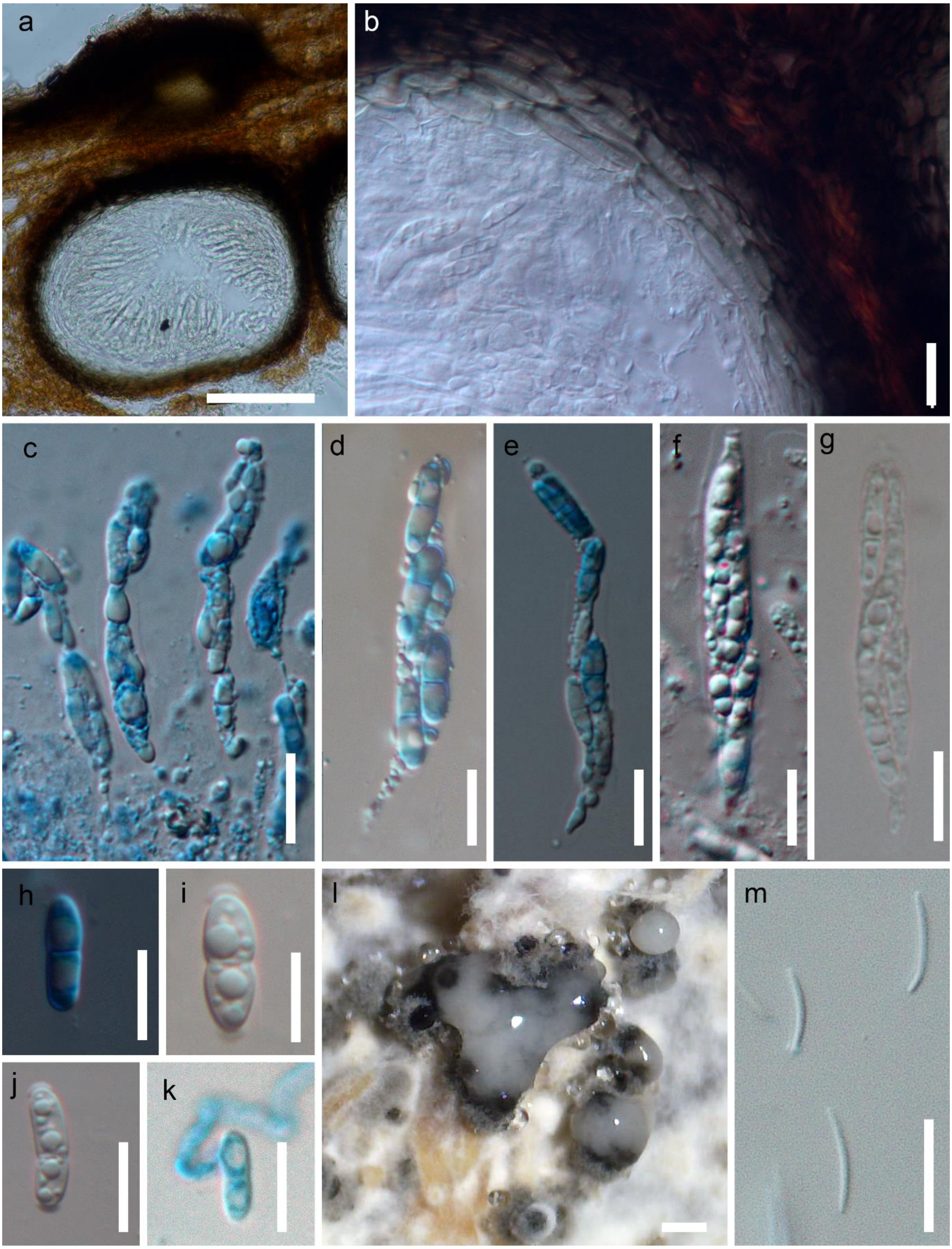

Fig. **41** – *Diaporthe salsuginosa* (AMH-10013). a Section of ascomata. b Peridium. c–g Immature and mature asci. h–j Ascospores with polar appendages. k Germinating ascospore. l Pycnidia developed on culture. m Alpha conidia. Scale bars: a = 100 μm, b–k, m = 10 μm, l = 200 μm.

Lamproconiaceae Norph., T.C. Wen & K.D. Hyde, Phytotaxa 270, 94 (2016)

Index Fungorum number: IF552187; Facesoffungi number: FoF02248

Lamproconiaceae was introduced by Norphanphoun et al. (2016) with *Lamproconium* and *Hercospora*. The family was typified with *Lamproconium*. The introduction of the family is based on the morphology, and ITS and LSU phylogeny (Norphanphoun et al. 2016). An updated tree for Lamproconiaceae is provided in Fig. 42.

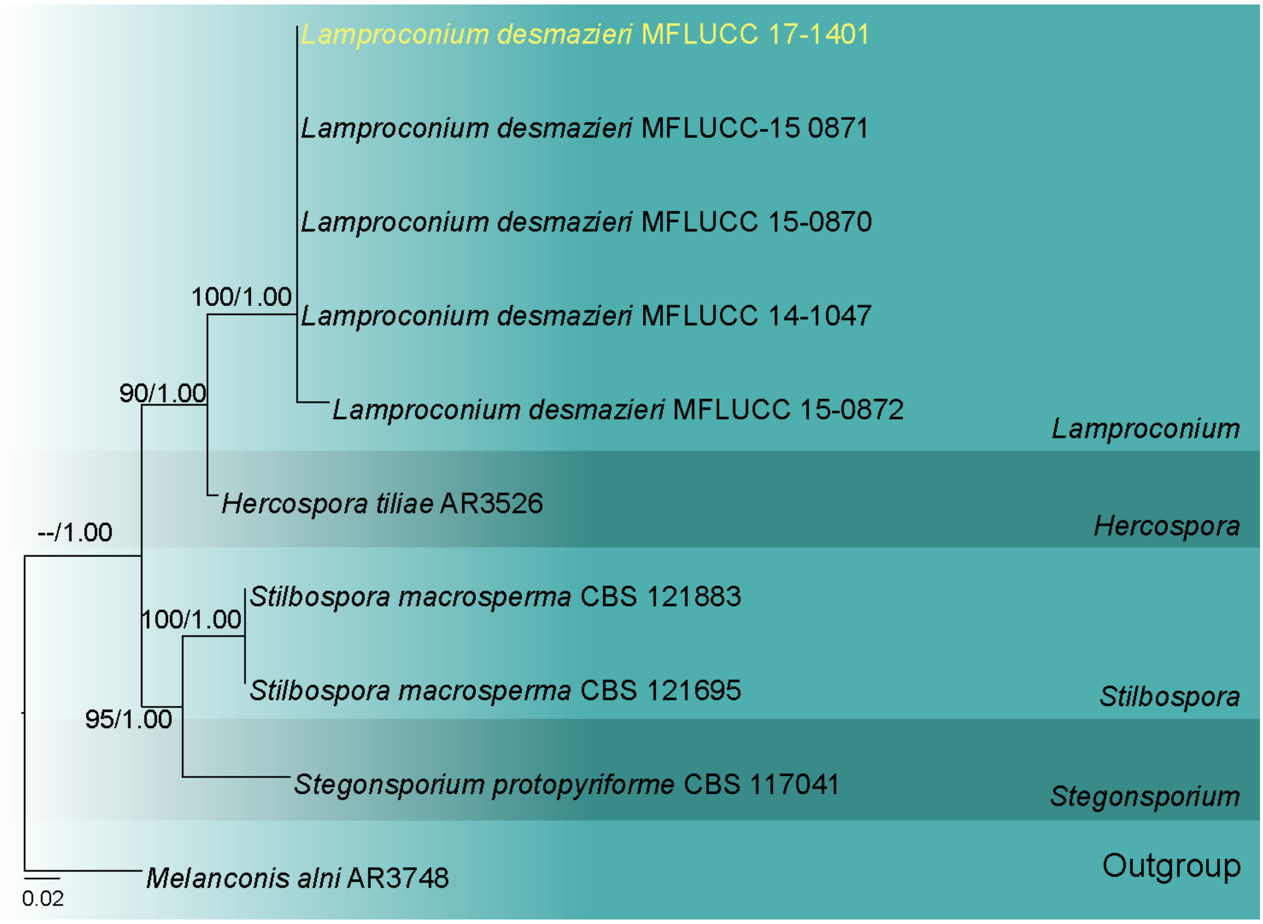

Fig. 42 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Ten strains are included in the combined analyses which comprised 1481 characters (888 characters for LSU, 588 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -3757.205650 is presented. Estimated base frequencies were as follows: A = 0.241207, C = 0.254436, G = 0.292063, T = 0.212294; substitution rates AC = 1.348299, AG = 1.144904, AT = 1.519494, CG = 1.207099, CT = 4.339344, GT = 1.000000; gamma distribution shape parameter α = 5.434534. Bootstrap support values for ML greater than 90% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Melanconis alni* (AR3748). The newly generated sequences are indicated in yellow.

Lamproconium (Grove) Grove, British Stem- and Leaf-Fungi (Coelomycetes) (Cambridge) 2, 321 (1937)

Index Fungorum number: IF8703; Facesoffungi number: FoF03491

Melanconium desmazieri was reported as the asexual morph of *Melanconis desmazieri*. Grove (1937) reported that *Melanconium desmazieri* differs from the type species of *Melanconium* with bluish to glistering bluish conidia. Hence, Grove (1937) erected *Lamproconium* as a separate genus (Sutton 1980). Cannon & Minter (2014) placed *Lamproconium* under Diaporthales *genera incertae sedis*. Norphanphoun et al. (2016) placed the *Lamproconium* under Lamproconiaceae.

Lamproconium desmazieri (Berk. & Broome) Grove, British Stem- and Leaf-Fungi (Coelomycetes) (Cambridge) 2, 321 (1937) Fig. 43

Index Fungorum number: IF251819; Facesoffungi number: FoF02249

Saprobic on dead branch of *Tilia* sp. Asexual morph: *Conidiomata* 750–1000 × 500–550 µm diam., pycnidial, solitary, partly immersed in host tissue, uniloculate, dark blue, with a raised centre. *Pycnidium* 50–70 µm, with multi-layered wall, thin at inner layer, hyaline, comprising wall cells of *textura angularis*. *Paraphyses* interspersed with conidiophores. *Conidiophores* 50–115 µm, arising from the innermost wall layer at the base of pycnidium, filiform or cylindrical, pale bluish to hyaline, septate, branched, smooth-walled. *Conidiogenous cells* cylindrical to subcylindrical, annellidic, percurrently proliferating up to 3–4 times, with flared periclinal thickenings in the collarette zone, colourless to olivaceous, smooth-walled. *Conidia* 22–28.5 × 8–10 µm ($\bar{x}$ = 25.25 × 9 µm, n = 30), fusiform, ellipsoid, infrequently slightly curved, 1-3 septate, initially hyaline, bluish to glistening dark blue at maturity, narrowly rounded at ends, smooth-walled. Sexual morph: Undetermined.

Material examined – Italy, on a dead branch of *Tilia* sp., Erio Camporesi IT3069 (MFLU 16-2481), living culture MFLUCC 17-1401.

GenBank numbers – ITS: MW159906, LSU: MW160135.

Known distribution (based on molecular data) – Russia (Norphanphoun et al. 2016).

Known hosts (based on molecular data) – *Telia* species (Norphanphoun et al. 2016).

Notes – Our strain MFLUCC 17-1401 clustered together with other *Lamproconium desmazieri* strains. *Lamproconium desmazieri* forms aseptate conidia (Norphanphoun et al. 2016) while conidia in our isolate are 1–3-septate.

Melanconidaceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze - Ascomyceten 1, 764 (1886)

Index Fungorum number: IF80988; Facesoffungi number: FoF01395

Melanconidaceae was introduced by Winter (1886). Species of this family are plant pathogens causing diseases of crops and as well as saprobes in terrestrial and aquatic habitats (Maharachchikumbura et al. 2016, Senanayake et al. 2017). Maharachchikumbura et al. (2016) listed 24 genera in this family. Senanayake et al. (2017) and Wijewardena et al. (2020) revised the family as monogeneric with *Melanconis* based morphology and available sequence data.

Melanconis Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei - Valsei - Sphaeriei 2, 115 (1863)

Index Fungorum number: IF3060; Facesoffungi number: FoF02119

Melanconis was introduced by Tulasne & Tulasne (1863) with the type *Melanconis stilbostoma*. The asexual morph of *Melanconis* is placed in *Melanconium*, and both of these genera have been linked (Maharachchikumbura et al. 2016). Species in both *Melanconis* and *Melanconium* cause diseases such as cankers and shoot blights on plants (Maharachchikumbura et al. 2016). There are 113 species epithets listed in Index Fungorum (2020). However, sequence data is available for osteoblastoma *Melanconis alni, M. betulae, M. italica, M. itoana, M. marginalis*, and *M. stilbostoma* in the GenBank. Placement of our isolates in the genus is provided in Fig. 44.

Melanconis italica Senan., Camporesi & K.D. Hyde, Studies in Mycology 86, 273 (2017) Fig. 45

Index Fungorum number: IF821560; Facesoffungi number: FoF03494

Saprobic on dead branch of *Alnus cordata*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 100–150 µm high, 400–450 µm diam., brown, scattered, solitary, immersed beneath the host epidermis, becoming raised, erumpent through host tissue. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 14–16 × 1–2 µm, phialidic, hyaline. *Conidia* 8–9 × 2–3 µm ($\bar{x}$ = 8.4 × 2.6 µm, n = 30), hyaline to pale brown, aseptate, fusiform with small guttules.

Material examined – Italy, Province of Forlì-Cesena, Passo della Braccina - Premilcuore, on twigs of *Alnus cordata* (Betulaceae), 1 May 2013, Nello Camporesi IT1209 (MFLU 16-1308).

GenBank numbers – ITS: MT955723, LSU: MT965724.

Known distribution (based on molecular data) – Italy (Senanayake et al. 2017).

Known hosts (based on molecular data) – *Alnus cordata* (Senanayake et al. 2017).

Notes – *Melanconis italica* was introduced by Senanayake et al. (2017) on the dead branch of *Alnus cordata* in Italy. The sexual morph of *Melanconis italica* was found on the natural substrate and asexual morph was observed on MEA media by Senanayake et al. (2017). The new strain MFLU 16-1308 is phylogenetically closely related to the type MFLU 17-0879 with strong statistical support (100% ML, Fig 43). Base pair similarity between the ITS and LSU sequences of our strain with other *Melanconis* strains are high, therefore, the new strain is considered herein as the first record of asexual morph of *Melanconis italica* from the natural substrate of same host plant.

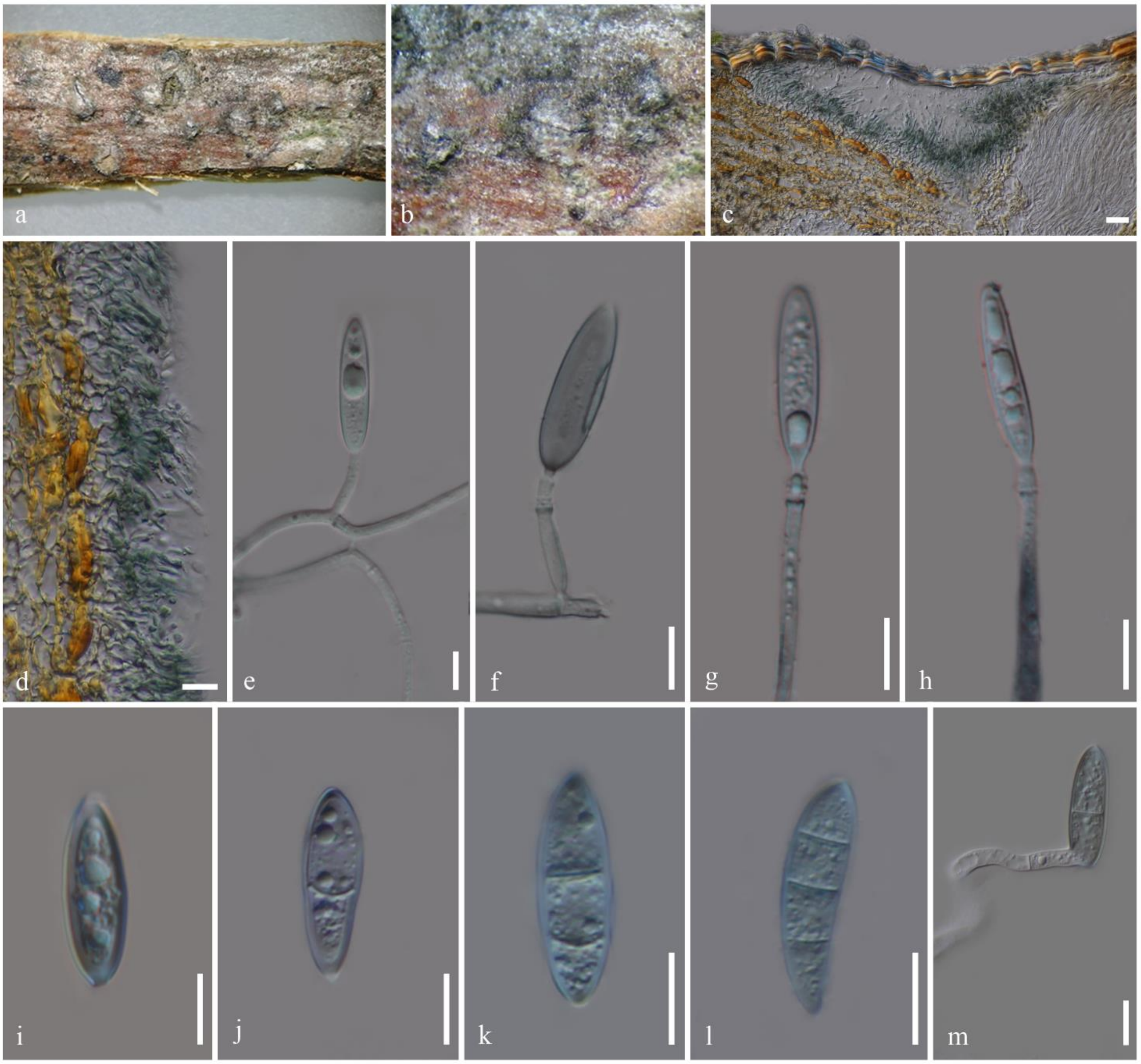

Fig. 43 – *Lamproconium desmazieresi* (MFLU 16-2481, a new geographic and host record). a–b Conidiomata on host. c Cross section of a conidioma. d Conidiomata wall and raised host tissue. e–h Conidiogenous cells with attached conidia (note: annellations at the tip of the conidiogenous cell). i–l Mature conidia. m Germinating conidium. Scale bars: c = 50 µm, d = 5 µm, e–m = 10 µm.

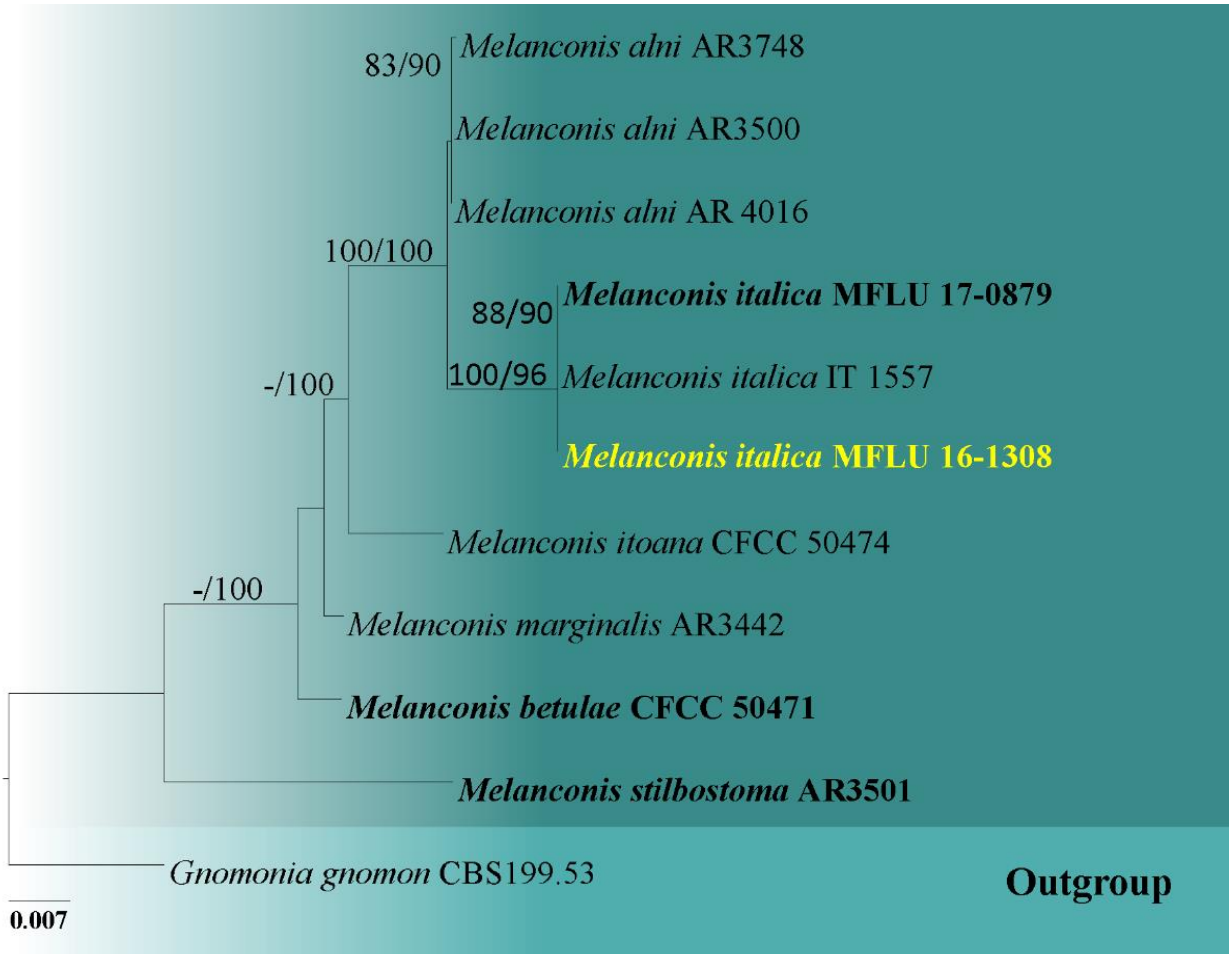

Fig. 44 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data of family Melanconidaceae. Eleven strains are included in the combined analyses which comprised 1720 characters (1200 characters for LSU, 520 characters for ITS) after alignment. The best RaxML tree with a final likelihood values of -3642.633452 is presented. The matrix had 162 distinct alignment patterns with 21.56% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.264876, C = 0.220455, G = 0.264749, T = 0.249920; substitution rates AC = 1.372772, AG = 2.103672, AT = 2.536727, CG = 0.502533, CT = 4.660794, GT = 1.000000; gamma distribution shape parameter α = 0.810266. For both genes, GTR+G was applied as the evolutionary model. Bootstrap values for ML equal to or greater than 75% (first set) and MP equal to or greater than 75% (second set) are given above the nodes. The tree is rooted with *Gnomonia gnomon* (CBS 119.53). Ex-type strains are in **bold.** The newly generated sequences are indicated in yellow.

Schizoparmaceae Rossman, D.F. Farr & Castl., Mycoscience 48, 137 (2007)

Index Fungorum number: IF82150; Facesoffungi number: FoF01405

Rossman et al. (2007) introduced Schizoparmaceae to accommodate *Coniella*, *Pilidiella* and *Schizoparme* (Rossman et al. 2007, Alvarez et al. 2016). Species of Schizoparmaceae are common in both tropical and temperate regions, worldwide (Rossman et al. 2007). After several taxonomic revisions (Van Niekerk et al. 2004, Rossman et al. 2007, Alvarez et al. 2016), the family currently comprises a single genus, *Coniella*.

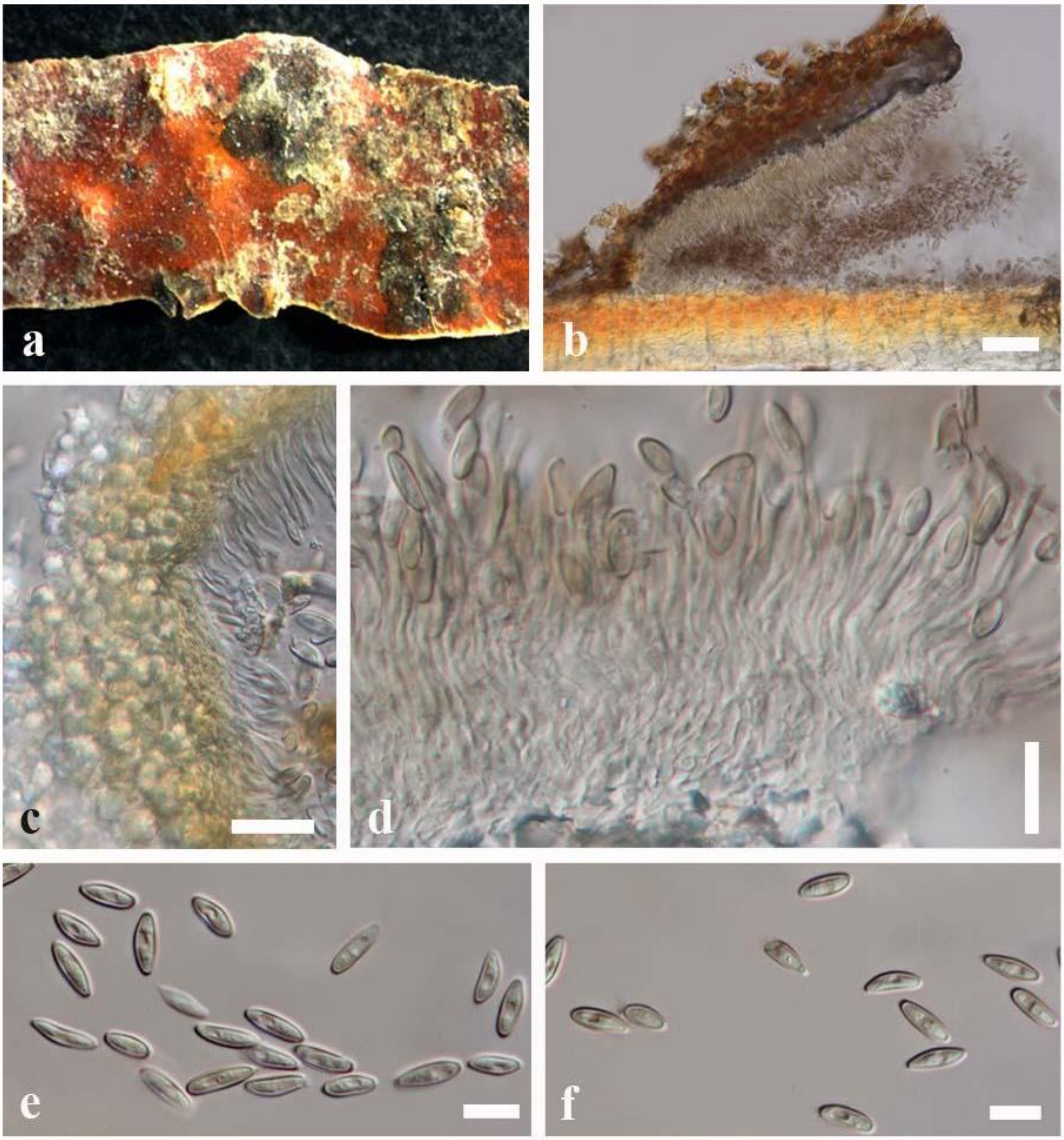

Fig. 45 – *Melanconis italica* (MFLU 16-1308, new host record). a Appearance of conidiomata on dead branch. b Vertical sections conidioma. c Conidiomatal wall. d Conidiophores. e, f Conidiospores. Scale bars: b = 80 µm, c = 20 µm, d = 20 µm, e, f = 10 µm.

Coniella Höhn., Berichte der Deutschen Botanischen Gesellschaft 36, 316 (1918)

Index Fungorum number: IF7753; Facesoffungi number: FoF04309

Coniella was introduced by Höhnel (1918) with *Coniella pulchella* (= *Coniella fragariae*) as the type species. *Coniella* comprises of many plant pathogens (Van Niekerk et al. 2004, Mirabolfathy et al. 2012, Chethana et al. 2017), saprobes, and endophytes (Samuels et al. 1993, Ferreira et al. 1997, Alvarez et al. 2016). This genus has been subjected to many revisions. Alvarez et al. (2016) synonymized both *Pilidiella* and *Schizoparme* under *Coniella*. An updated phylogeny for the genus is provided in Fig. 46.

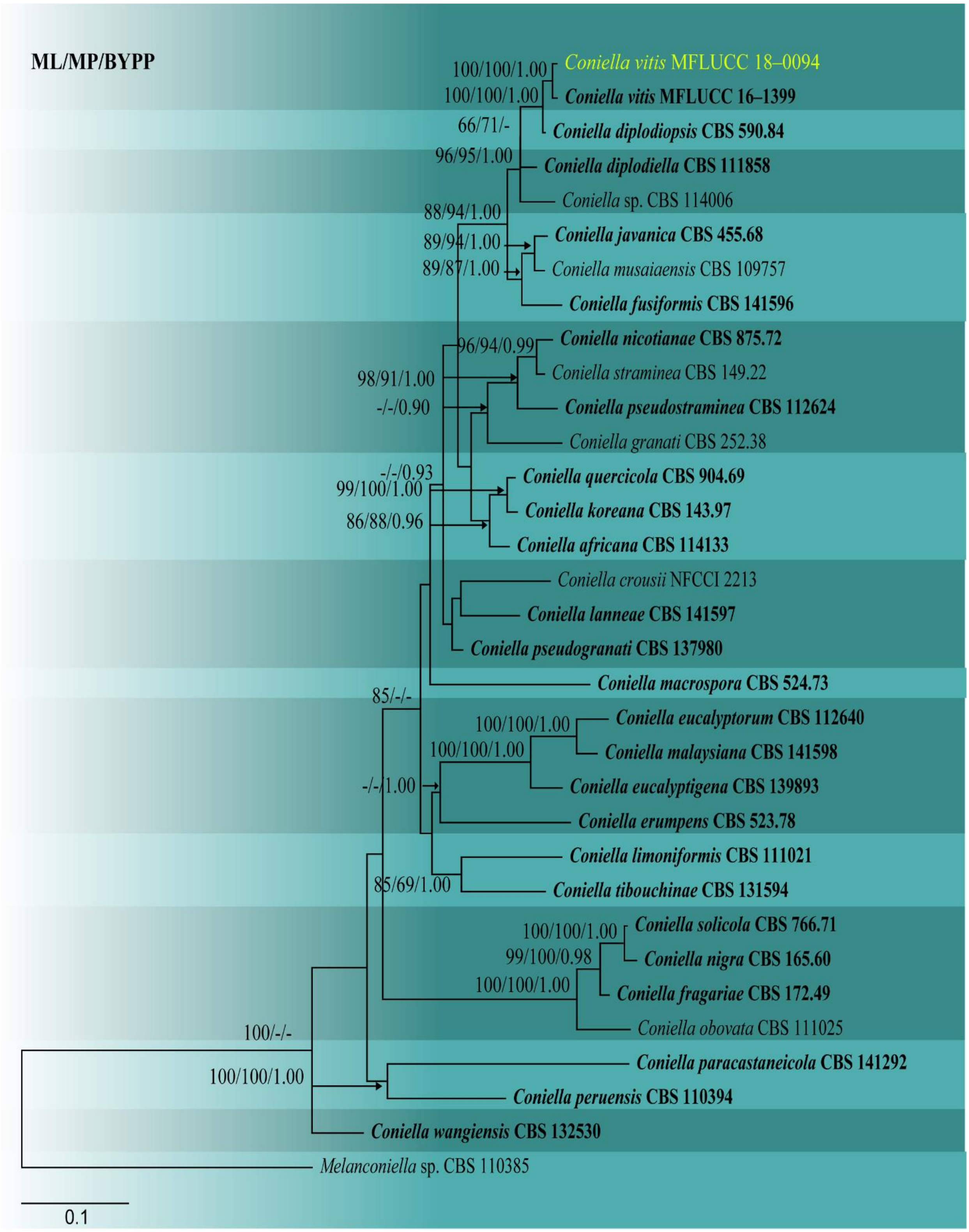

Fig. 46 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *histone* and *TEF1-α* sequence data. Thirty-three strains are included in the combined analyses which comprised 2876 characters including gaps. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony and Bayesian analyses. The best scoring RAxML tree with a final likelihood value of -15134.164466 is presented. The matrix had 807 distinct alignment patterns with 23.87% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.249426, C = 0.245786, G = 0.256290, T = 0.248498; substitution rates AC = 0.996078, AG = 2.077237, AT = 1.158367, CG = 0.708887, CT = 4.169021, GT = 1.000000;

gamma distribution shape parameter α = 0.145978. RAxML and maximum parsimony bootstrap support values greater than or equal to 60% and Bayesian posterior probabilities greater than or equal to 0.90 are shown respectively near the nodes. The tree is rooted with *Melanconiella* sp. (CBS 110385). The ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Coniella vitis Chethana, J.Y. Yan, X.H. Li & K.D. Hyde, Plant Disease 101, 2129 (2017)

Fig. 47

Index Fungorum number: IF819365; Facesoffungi number: FoF02722

Saprobic on *Salix alba*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 283–637 µm (x̄ = 452.7 µm, n = 20) diam., pycnidial, solitary, submerged in PDA, globose to slightly depressed globose, with verruculose wall, initially hyaline becoming dark brown to black at maturity, with a central ostiole. *Conidiophores* formed on a dense, cushion-like aggregation of hyaline cells, hyaline, mostly reduced to conidiogenous cells. *Conidiogenous* cells 8–10.5 × 2.5–3.5 µm (x̄ =9.4 × 3 µm, n = 10), phialidic, hyaline, simple, slender, smooth with a prominent periclinal thickening. *Conidia* 9.5–13.5 × 4.3–8.6 µm (x̄ = 11.1 × 6.3 µm, n = 40), l:w ratio 1.8, inequilateral, hyaline when immature becoming pale brown, aseptate, straight to slightly curved, narrowly ellipsoidal, often somewhat flattened on one side, both sides gradually tapering towards the subobtusely rounded apex, subtruncate at base, smooth-walled, and multi-guttulate with one or two prominent guttules.

Culture characteristics – Colonies fast growing up to 8 cm diam. after 5 days at 28°C on PDA, flat, mostly immersed mycelium, aerial mycelium mostly sparse, crenulated edges with concentric rings, white coloured on surface and buff in reverse. Conidia in mass, hyaline.

Material examined – Russia, Rostov Region, Shakhty City, on dead and dying branch of *Salix alba* L. (Salicaceae), 5 March 2016, T.S. Bulgakov T1278 (MFLU 16-1572), living culture MFLUCC 18-0094.

GenBank numbers – ITS: MH356592, LSU: MH356593, *histone*: MH366484, *TEF1-α*: MH366485.

Known distribution (based on molecular data) – China (Chethana et al. 2017), Russia (Phookamsak et al. 2019, this study).

Known hosts (based on molecular data) – *Prunus armeniaca* (Phookamsak et al. 2019), *Vitis vinifera* (Chethana et al. 2017).

Notes – *Coniella vitis*, the causative agent of grape white rot, was introduced from *Vitis vinifera* in China (Chethana et al. 2017). Based on our phylogenetic analysis of combined ITS, LSU, *histone*, and *tef1* sequence data of *Coniella* species (Fig. 45), our strain (MFLUCC 18-0094) clustered together with the ex-type strain of *Coniella vitis* (MFLUCC 16-1399) with relatively high bootstrap and Bayesian probabilities (100 BS, 1.00 PP). When comparing our strain with the type specimen of *C. vitis* (MFLUCC 16-2677), they are similar in morphology. However, our strain has slightly larger pycnidia, and larger conidia compared to the type strain of *C. vitis*.

Magnaporthales Thongk., Vijaykr. & K.D. Hyde, Fungal Diversity 34, 168 (2009)

Ophioceraceae Klaubauf, E.G. LeBrun & Crous, Studies in Mycology 79, 103 (2014)

Index Fungorum number: IF810201; Facesoffungi number: FoF01254

Ophioceraceae was established with *Ophioceras* as the type in Magnaporthales (Klaubauf et al. 2014). This family includes saprobic taxa that play important roles in nutrient and carbon cycling, biological diversity and ecosystem functioning (Palmer et al. 1997, Wong et al. 1998).

Ophioceras Sacc., Sylloge Fungorum 2, 358 (1883)

Index Fungorum number: IF3595; Facesoffungi number: FoF01255

Ophioceras was introduced by Saccardo (1883) with *O. dolichostomum* as the type species. The genus contains mostly saprobic species in freshwater habitats worldwide (Shearer et al. 1999, Tsui et al. 2001, Thongkantha et al. 2009, Hu et al. 2012). For an updated phylogeny for this genus, please see Hyde et al. (2020a). In this entry, a new host record of *Ophioceras commune* is described and illustrated (Fig. 48).

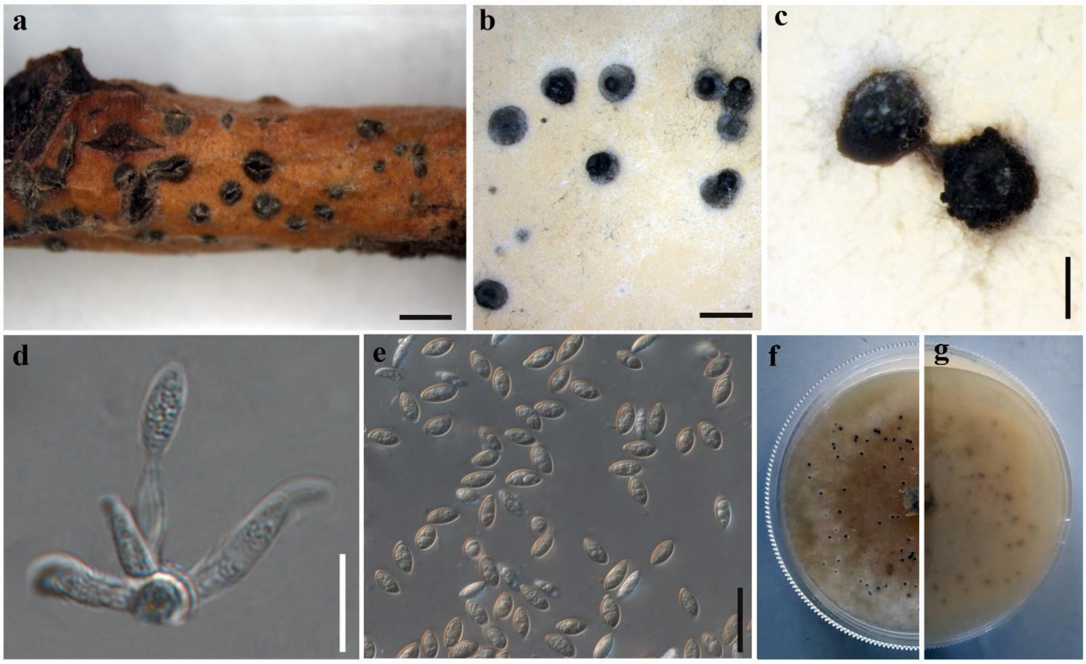

Fig. **47** – *Coniella vitis* (MFLU 16-1572, new host record). a Host tissue. b Submerged pycnidia on PDA. c Close view of the pycnidia and the spore mass. d Conidiogenous cells. e Hyaline to brown conidia. f, g Upper view (f) and the reverse view (g) of the colony on the PDA. Scale bars: a, b = 1 mm, c = 500 µm, d = 5 µm, e = 20 µm.

Ophioceras commune Shearer, J.L. Crane & W. Chen, Mycologia 91, 146 (1999) Fig. 48

Index Fungorum number: IF450197; Facesoffungi number: FoF04926

Saprobic on submerged wood in freshwater habitats. Sexual morph: *Ascomata* 180–330 × 270–390 µm, immersed to superficial, scattered to clustered, black, globose to elongated globose, with a long neck. *Peridium* about 35 µm thick, two-three layers, inner layer of hyaline, small pseudoparenchyma cells, outer layer brown to dark brown. *Paraphyses* septate, broad at base, tapering to a point, longer than asci. *Asci* 90–104 × 5.5–11.5 µm ($\bar{x}$ = 97 × 8.5 µm, n = 20), 8-spored, basal and peripheral, cylindrical, sigmoidal. *Ascospores* 83–91 × 2.5–3.5 µm ($\bar{x}$ = 87 × 3 µm, n = 20), fasciculate, hyaline, filiform, arcuate, septate, uniform width throughout or one end more broadly rounded than the other, ascospores frequently released by deliquescence of basal half of ascus. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, saprobic on decaying wood submerged in Erhai Lake, March 2015, X.Y. Liu S-578 (HKAS 92587); *ibid.*, March 2015, H.Y. Su S-536 (HKAS 92569); *ibid.*, June 2015, S.M. Tang S-338 (HKAS 92640).

GenBank numbers – ITS: MH795813 (HKAS 92640), MH795814 (HKAS 92587), MH795815 (HKAS 92569), MH795816 (S-132); LSU: MH795818 (HKAS 92640), MH795819 (HKAS 92587), MH795820 (HKAS 92569), MH795821 (S-132); *TEF1-α:* MH801192 (HKAS 92640), MH801193 (HKAS 92587), MH801194 (HKAS 92569).

Known distribution (based on molecular data) – Canada (Chen et al. 1999), China (Tsui et al. 2000, Cai et al. 2002, Luo et al. 2004, Tsui & Hyde 2004), Egypt (Abdel-Aziz 2016), Japan (Tsui et al. 2003), Panama (Chen et al. 1999, Shearer et al. 1999), USA (Shearer et al. 1999)

Known hosts (based on molecular data) – on submerged wood in freshwater habitats, herbaceous debris (Chen et al. 1999, Shearer et al. 1999).

Notes – *Ophioceras commune* was introduced by Shearer et al. (1999) based on the collections of submerged wood in freshwater habitats in the USA. Several studies have reported

Ophioceras commune from freshwater habitats in China (Tsui et al. 2000, Cai et al. 2002, Luo et al. 2004, Tsui & Hyde 2004). However, no descriptions and illustrations have been provided in those studies. In this study, four specimens were collected from submerged wood in Erhai Lake, Yunnan Province, China. The morphology of our fungus fits well with the original descriptions of *Ophioceras commune* (Shearer et al. 1999). Phylogenetic analysis based on combined ITS, LSU and *tef1* sequence data also showed that our fungus clustered with *Ophioceras commune* with strong support (see Hyde et al. 2020a). Therefore, we identified our species as *Ophioceras commune* and this is the first time to provide the descriptions and illustrations for this species from China.

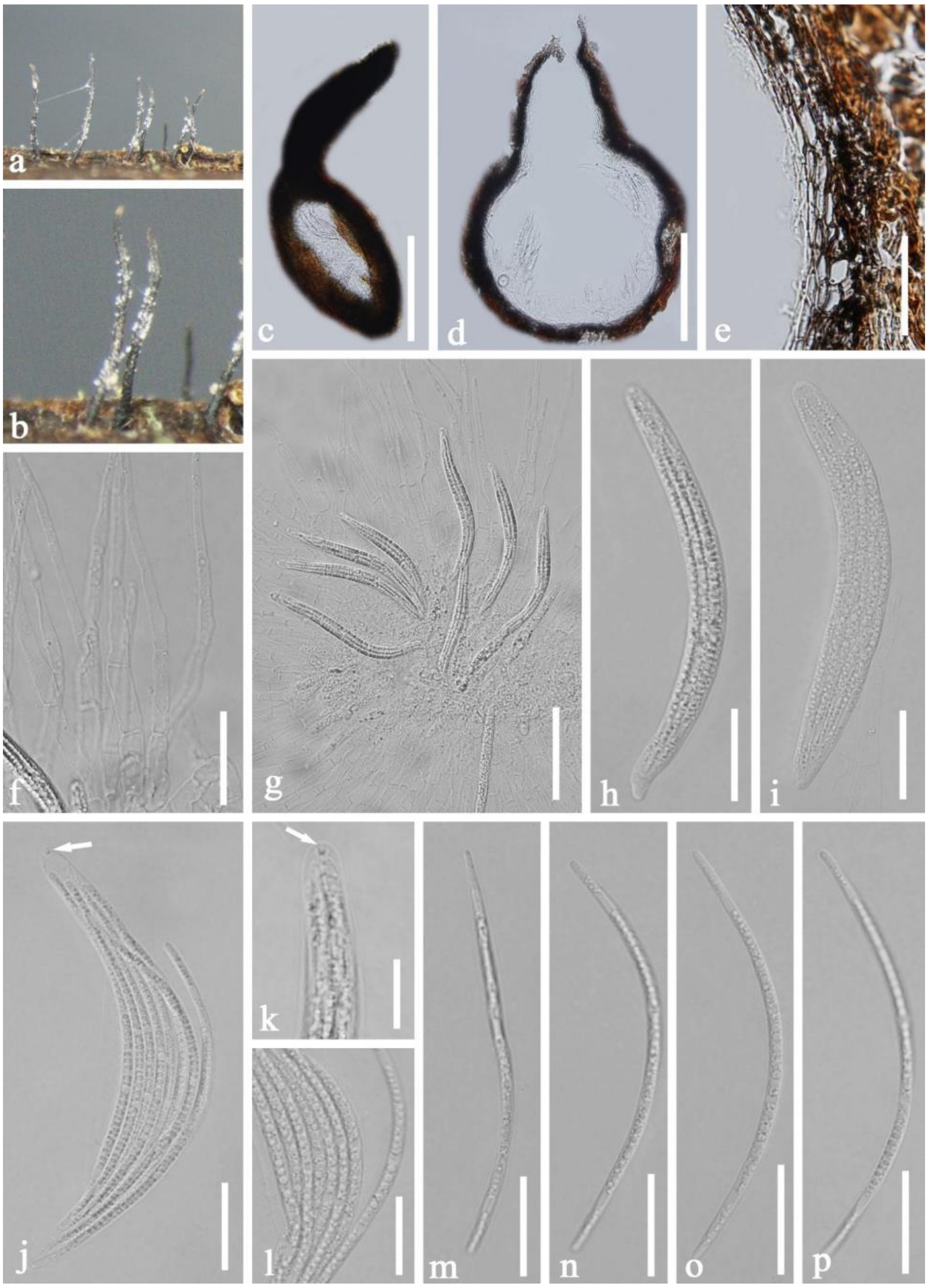

Fig. 48 – *Ophioceras commune* (HKAS 92569, new geographical record). a, b Neck. c, d Longitudinal sections through ascomata. e Longitudinal section of peridium. f Paraphyses. g-k Asci. l-p Ascospores. Scale bars: c = 170 µm, d = 120 µm, e, f = 30 µm, g = 55 µm, h–j, m–p = 20 µm, k, l = 15 µm.

Pseudohalonectriaceae Hongsanan & K.D. Hyde, Fungal Diversity 84, 33 (2017)

Index Fungorum number: IF553215; Facesoffungi number: FoF03355

Pseudohalonectriaceae was introduced by Hongsanan et al. (2017) to accommodate *Pseudohalonectria*. The placement of *Pseudohalonectria* was discussed by Chen et al. (1999), Shearer et al. (1999), Klaubauf et al. (2014) and Maharachchikumbura et al. (2015, 2016). Finally, Hongsanan et al. (2017) placed this genus in Magnaporthales and introduced a new family, Pseudohalonectriaceae for this genus. This was followed by the consequent studies (Hongsanan et al. 2017, Hyde et al. 2020a). An updated phylogeny for the Pseudohalonectriaceae is provided in the Fig. 49.

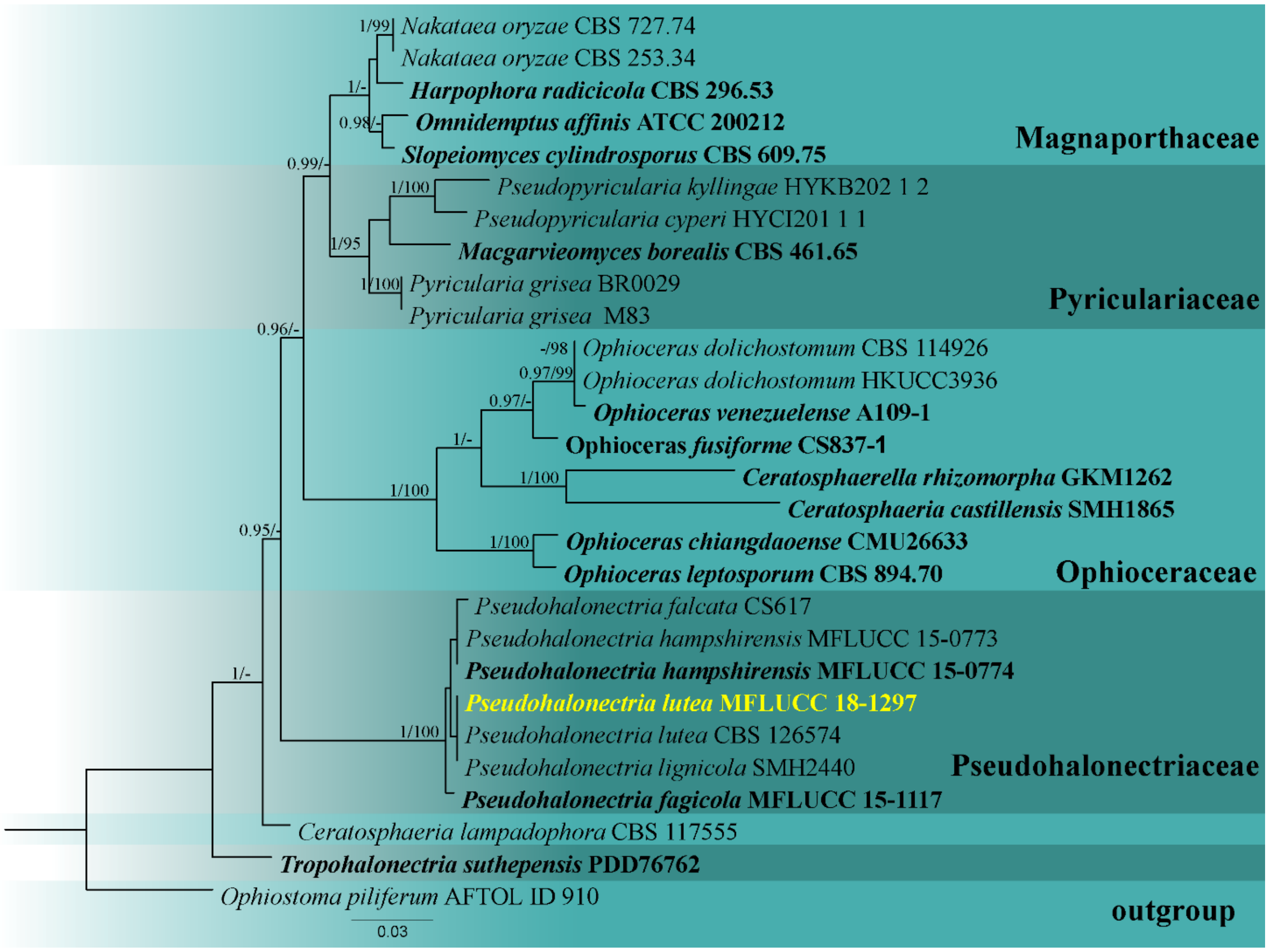

Fig. 49 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and *TEF1-α* sequence data for some selected families within the Dothideomycetes. Twenty-eight strains are included in the combined analyses which comprised 2521 characters (765 characters for LSU, 872 characters for SSU, 884 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 -9112.213419 is presented. The matrix had 485 distinct alignment patterns with 38.97% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244964, C =0.249484, G = 0.287318, T = 0.218234; substitution rates AC = 0.938310, AG = 2.052303, AT = 0.949976, CG = 1.371675, CT = 6.258074, GT = 1.000000; gamma distribution shape parameter α = 0.197446. For all the gene regions, GTR+I+G evolutionary model was applied. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Ophiostoma piliferum* (AFTOL ID 910). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Pseudohalonectria Minoura & T. Muroi, Transactions of the Mycological Society of Japan 19, 132 (1978)

Index Fungorum number: IF4437; Facesoffungi number: FoF06274

Pseudohalonectria was introduced by Minoura & Muroi (1978) with only *P. lignicola*. Afterwards, several species were introduced to *Pseudohalonectria* (Shearer 1989, Hyde et al. 1999, Ono & Kobayashi 2001, Cai et al. 2002, Kohlmeyer et al. 2005). There are 16 species listed for this genus in Index Fungorum (2020). Hongsanan et al. (2017) placed this genus in Pseudohalonectriaceae, Magnaporthales based on phylogenetic analyses. The genus is characterized by bright yellow to brown ascomata with long cylindrical, periphysate necks; unitunicate, cylindrical to clavate, J- asci with thimble-shaped, refractive apical rings; paraphysate and cylindrical, hyaline to slightly pigmented and usually septate ascospores (Shearer 1989). *Pseudohalonectria* species were reported from freshwater, marine and terrestrial habitats (Perera et al. 2016, Luo et al. 2019).

Pseudohalonectria lutea Shearer, Canadian Journal of Botany 67, 1950 (1989) Fig. 50

Index Fungorum number: IF136213; Facesoffungi number: FoF04911

Saprobic on decaying wood submerged in a river. Sexual morph: *Ascomata* 300–550 × 300–600 µm, solitary to less commonly aggregated, immersed, globose to depressed globose, with a long neck, greenish yellow-brown, gradually becoming dark near the base, rostrate. *Neck* cylindrical to conical, composed of parallel hyphae, greenish yellow above, dark brown to black at the base, periphysate. *Peridium* membranous, comprising 5–10 layers, inner layers composed of pale yellow cells of *textura angularis*, outer layer composed of darkened yellow compressed cells of *textura angularis*. *Paraphyses* 4–6 µm wide, numerous, septate, hyaline, smooth-walled. *Asci* 125–188 × 16–24 µm ($\bar{x}$ = 151 × 20.2 µm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, with thimble-shaped subapical ring, separating from ascogenous hyphae. *Ascospores* 46–60 × 6.5–9 µm ($\bar{x}$ = 54 × 7.5 µm, n = 20), long ellipsoidal, end cells less pigmented than inner cells, hyaline to pale orange in mass, 5-septate, smooth-walled, guttulate, slightly constricted at septa. Asexual morph: Undetermined.

Material examined – China, Tibet Autonomous Region, on submerged decaying wood, 28 April 2015, Z.L. Luo XZ A 2–2–1, S-1048 (MFLU 18-1463), living culture MFLUCC 18-1297.

GenBank numbers – LSU: MK063809, SSU: MK063810, *TEF1-α:* MK099812.

Known distribution (based on molecular data) – China, France (Perera et al. 2016).

Known hosts (based on molecular data) – Submerged wood (Perera et al. 2016).

Notes – *Pseudohalonectria lutea* was introduced by Shearer (1989). Morphological features of our new isolate fit well with the original description of *P. lutea*. The phylogenetic analysis showed that our new isolate (MFLUCC 18-1297) clustered together with *P. lutea* (CBS 126574) and *P. lignicola* isolates. However, *Pseudohalonectria lutea* differs from *P. lignicola* in having longer and wider asci (125–188 × 16–24 *vs* 90–132 × 11–17.5 µm). Moreover, ascospores of *P. lutea* are ellipsoidal and 5-septate, while they are cylindrical and 5–11-septate in *P. lignicola* (Shearer 1989). Perera et al. (2016) discussed the taxonomic circumscriptions of *P. lutea* and *P. lignicola*. It seems that *P. lignicola* sequences available in the GenBank are falsely identified. Our new collection is morphologically similar to *P. lutea*, therefore, we identified our isolate as a new host record of *P. lutea.*

Tirisporellales Suetrong, E.B.G. Jones & K.L. Pang, Fungal Diversity 73, 42 (2015)

Tirisporellaceae Suetrong, E.B.G. Jones & K.L. Pang, Cryptogamie Mycologie 36, 323 (2015)

Index Fungorum number: IF812184; Facesoffungi number: FoF01413

Tirisporellaceae (Suetrong et al. 2015) accommodates three monotypic genera, *Bacusphaeria* (Abdel-Wahab et al. 2017), *Thailandiomyces* (Pinruan et al. 2008) and *Tirisporella* (Jones et al. 1996). The family is characterized by large, black perithecial, ostiolate ascomata, a thick-walled peridium, cylindrical asci, 1–7-septate, fusoid ascospores with or without appendages and *Craspedodidymum* and *Phialophora*-like asexual morphs (Jones et al. 2015, Suetrong et al. 2015, Maharachchikumbura et al. 2016, Hyde et al. 2020a). An updated phylogeny for Tirisporellales is provided in Fig. 51.

Fig. 50 – *Pseudohalonectria lutea* (MFLU 18–1463, a new host record). a An ascomatal neck on decaying wood. b, c Section of an ascoma. d Ostiole. e Section of peridium. f Paraphyses. G Acal apical ring inside view, g Ascal apical ring in side view. h–l Asci. m–p Ascospores. q, r Culture on MEA. Scale bars: b = 50 µm, c, d= 100 µm, e, h–l = 30 µm, f, m–p = 20 µm, g = 10 µm.

Tirisporella E.B.G. Jones, K.D. Hyde & Alias, Canadian Journal of Botany 74, 1489 (1996)

Index Fungorum number: IF27659; Facesoffungi number: FoF02139

Tirisporella is a monotypic genus based on *T. beccariana*, for which we provide the description and illustration in this study. The genus resembles *Bacusphaeria* but they are distinct in phylogeny and morphology (Abdel-Wahab et al. 2017, Hyde et al. 2020a). Familial placement of *Tirisporella* was uncertain (Jones et al. 2009) until it was confirmed by Suetrong et al. (2015).

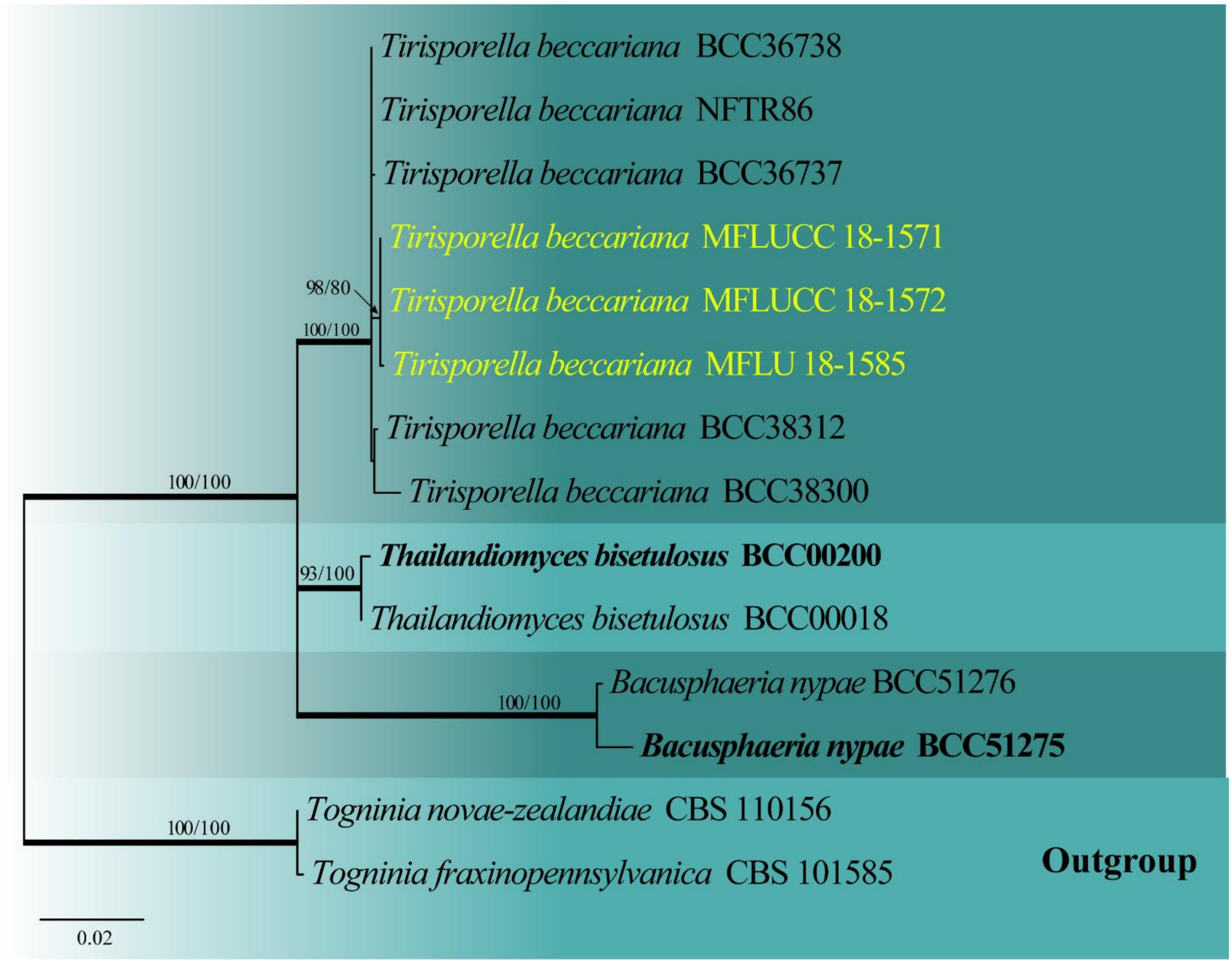

Fig. 51 – Phylogram generated from maximum likelihood analysis based on combined LSU and SSU sequence data of taxa in Tirisporellales. Fourteen strains are included in the combined analyses which comprised 1861 characters (845 characters for LSU, 1016 characters for SSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -4201.831746 is presented. Estimated base frequencies were as follows: A = 0.243036, C = 0.242271, G = 0.307289, T = 0.207404; substitution rates AC = 0.625317, AG = 1.610478, AT = 0.601945, CG = 0.831636, CT = 4.876660, GT = 1.000000; gamma distribution shape parameter α = 1.078289. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated in bold branches. The tree is rooted with *Togninia novae-zealandiae* (CBS 110156) and *T. fraxinopennsylvanica* (CBS 101585). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Tirisporella beccariana (Ces.) E.B.G. Jones, K.D. Hyde & Alias, Canadian Journal of Botany 74, 1490 (1996) Fig. 52

Index Fungorum number: IF415898; Facesoffungi number: FoF04323

Saprobic on submerged petiole of *Nypa fruticans*. Sexual morph: *Ascomata* 590–740 µm in diameter, 840–1020 µm high ($\bar{x}$ = 660 × 864 µm, n = 10), black, solitary or gregarious, globose to subglobose, uniloculate, coriaceous to carbonaceous, superficial, with a short neck and central ostiole, periphysate. *Peridium* 95–125 µm wide, reddish brown to dark brown, comprising outer thick layers of *textura angularis*, and inner layers of prosenchymatous or elongate cells. *Paraphyses* 4.5–9 µm wide, hyaline, unbranched, septate, constricted at the septa and tapering. *Asci* 125–220 × 15–21 µm ($\bar{x}$ = 175.5 × 18.3 µm, n = 20), 8-spored, short pedicellate, apex flattened, with a J-, subapical ring. *Ascospores* 28–45 × 6–11 µm (x̅ = 37.6 × 7.6 µm, n = 30), biseriate, brown, falcate to lunate, or ellipsoid, 4-septate, verrucose, apical cell appendaged, basal cell pointed and hyaline. Asexual morph: Hyphomycetous. Cultures grow well on PDA and MEA, forming greenish to dark brown colonies. *Mycelium* composed of branched, septate, hyaline to brown hyphae. *Conidiophores* macronematous, mononematous, erect, pale brown to brown, pale toward the apex, straight or flexuous, smooth. *Conidiogenous cells* 5.5–12 × 2–4 µm (x̅ = 8.6 × 3.1 µm, n = 32), enteroblastic, monophialidic, integrated on hyphae, terminal, sometimes erect on hyphae, pale brown, subcylindrical, ampulliform. *Conidia* 3–5.5 × 1.5–3.5 µm (x̅ = 4 × 2.6 µm, n = 80), unicellular, hyaline, fusoid-ellipsoid, obovoid or ellipsoid, obtuse or broadly rounded at apex, tapering to a truncate base, smooth-walled.

Material examined – Thailand, Ranong, Ngao (Ranong) Mangrove Forest Research Center, on intertidal petiole of *Nypa fruticans* (Arecaceae), 7 December 2016, S.N. Zhang SNT82 (MFLU 18-1582, HKAS 97482), living culture MFLUCC 18-1572; Thailand, Prachuap Khiri Khan, Pak Nam Pran, on intertidal petiole of *Nypa fruticans*, 2 December 2016, S.N. Zhang SNT102 (MFLU 18-1584), living culture MFLUCC 18-1571; Thailand, Krabi, Pali, on intertidal petiole of *Nypa fruticans*, 30 August, 2017, S.N. Zhang SNT203 (MFLU 18-1585, HKAS 97483).

GenBank numbers – LSU: MK078627 (MFLUCC 18-1572), MK078628 (MFLUCC 18-1571), MK078629 (MFLU 18-1585); SSU: MK078631 (MFLUCC 18-1572), MK078632 (MFLUCC 18-1571), MK078633 (MFLU 18-1585); *TEF1-α*: MK087664 (MFLUCC 18-1572), MK087665 (MFLUCC 18-1571), MK087666 (MFLU 18-1585).

Known distribution (based on molecular data) – Thailand (Jones et al. 1996, Suetrong et al. 2015, this study).

Known hosts (based on molecular data) – *Nypa fruticans* (Jones et al. 1996, Suetrong et al. 2015, this study).

Notes – The phylogenetic analysis indicates that the three new isolates of the current study clustered together with five strains of *T. beccariana* with strong support (Fig. 51). The sequences of these new isolates and previous *T. beccariana* isolates are similar, with only 5 gaps across the 1768 nucleotides of the LSU sequence. Additionally, the morphological characters in both asexual and sexual morphs are consistent with the previous studies (Jones et al. 1996, Suetrong et al. 2015). Thus, we consider the new isolates conspecific to *T. beccariana*.

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

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

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

Index Fungorum number: IF82088; Facesoffungi number: FoF01367

Bionectriaceae was introduced by Rossman et al. (1999) to accommodate 26 genera, including five cleistothecial genera. Rossman et al. (2001) established that Bionectriaceae as a monophyletic family within Hypocreales. The family has been subjected to many revisions over the years (Maharachchikumbura et al. 2015, 2016). In the most recent revision, Wijayawardene et al. (2018) accepted 39 genera in the family. Few sequence data are available for the family except for the LSU gene region and well-studied genera such as *Geosmithia* and *Clonostachys* (Voglmayr & Jaklitsch 2019). Among this family, few species are identified as plant pathogens, and some are being used as biocontrol agents (Auer & Ludwig-Müller 2014, Hyde et al. 2020a).

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

Index Fungorum number: IF7701; Facesoffungi number: FoF02102

Rossman et al. (2013) linked *Bionectria* with *Clonostachys*. Being the older and most common name, *Clonostachys* was prioritized over the other. We provide the updated phylogeny for selected taxa in *Clonostachys* in Fig. 53.

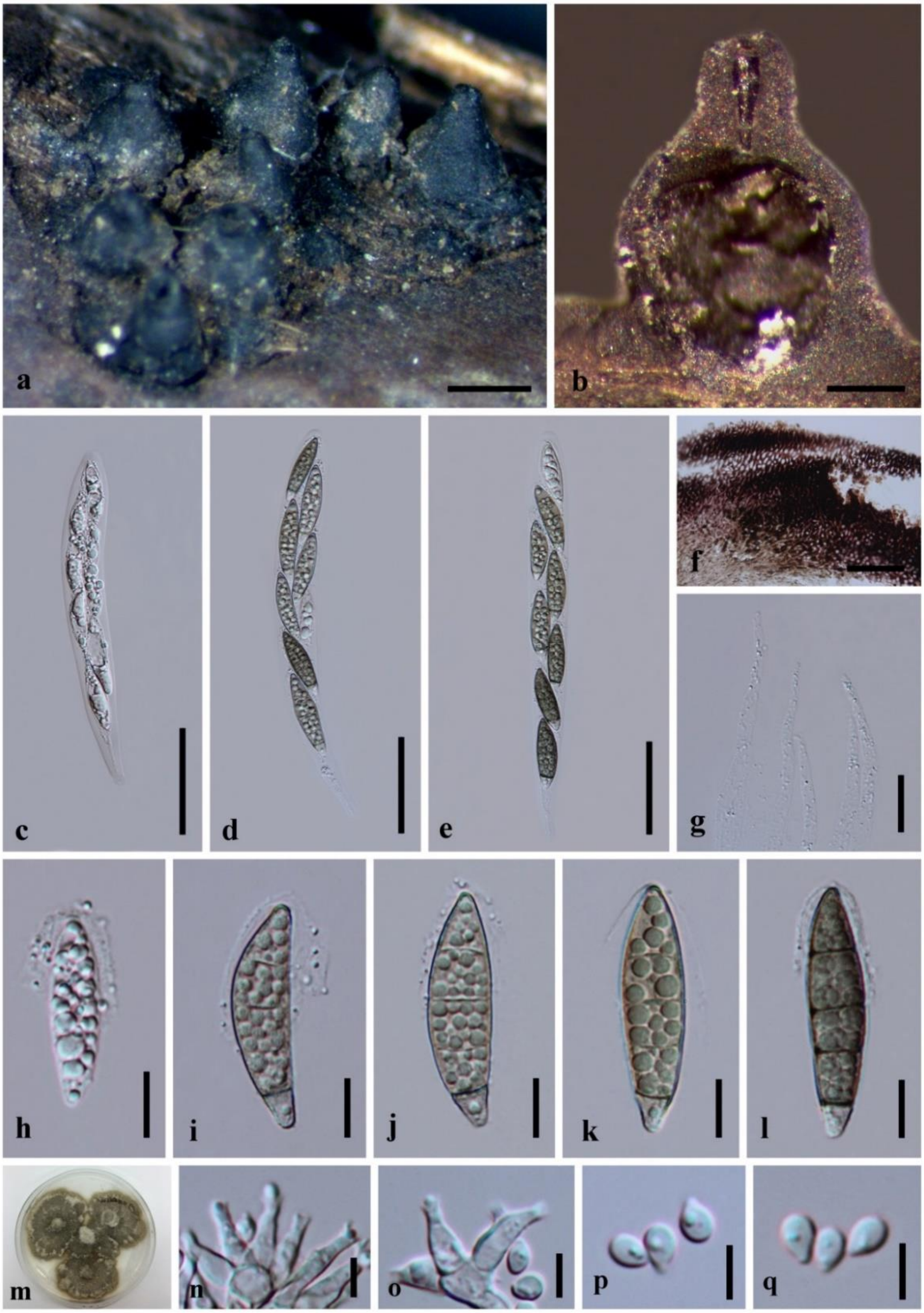

Fig. **52** – *Tirisporella beccariana* (MFLU 18-1582, MFLU 18-1585, Additional collections). a Appearance of ascomata on host surface with ostioles. b Vertical section through the ascoma. c–e Asci. f Peridium. g Paraphyses. h–l Ascospores. m Colony on PDA. n–q Sporulation in culture. Scale bars: a = 500 µm, b = 200 µm, c–f = 50 µm, g = 20 µm, h–l = 10 µm, n–o = 5 µm.

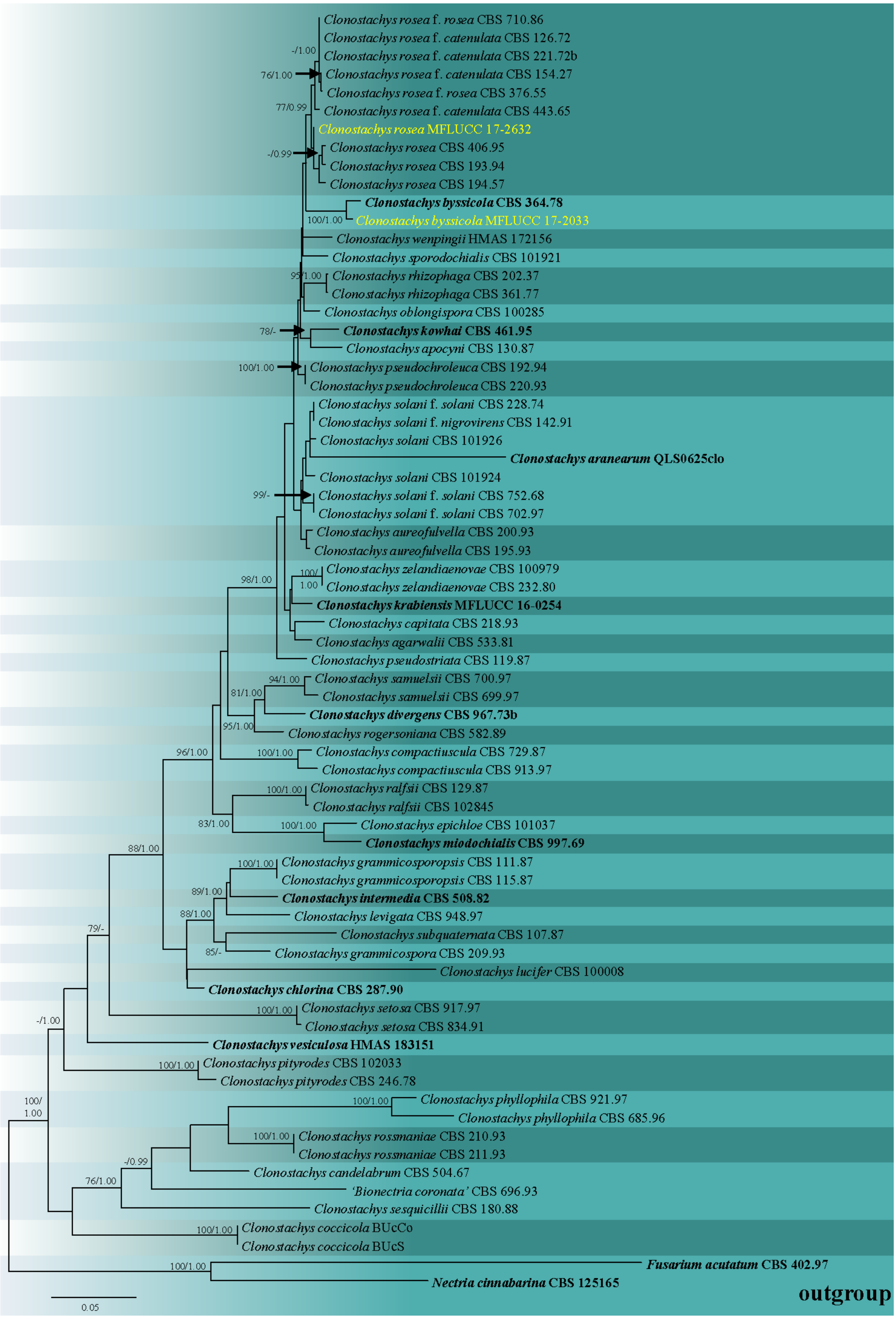

Fig. 53 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *β-TUB* sequence data. Seventy strains are included in the combined analyses which comprised 1913 characters (494 characters for ITS, 826 characters for LSU, 593 characters for *β-TUB)* after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best RAxML tree with a final likelihood value of -14769.468086 is presented. Estimated base frequencies were as follows: A = 0.221888, C = 0.265899, G = 0.263656, T = 0.248558; substitution rates AC = 1.146223, AG = 2.770669, AT = 1.186738, CG = 0.735209, CT = 4.296741, GT = 1.000000; gamma distribution shape parameter α = 0.623634. For all the gene regions GTR+I+G was applied as the evolutionary model. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.99 are given near nodes respectively. The tree is rooted with *Fusarium acutatum* (CBS 402.97) and *Nectria cinnabarina* (CBS 125165). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Clonostachys byssicola Schroers, Studies in Mycology 46, 80 (2001) Fig. 54

Index Fungorum number: IF485119; Facesoffungi number: FoF06865

Associated on a dead stem of *Chromolaena odorata*. Sexual morph: see Schroers (2002). Asexual morph: Sporodochial. *Sporodochia* pale yellow or pale orange, appearing as dome-shaped masses on the host. *Conidiophores* dimorphic. *Primary conidiophores* 3–5.2 µm wide at base, septate, verticillately branched, rare, forming towards the margin, main stipe short, hyaline, smooth-walled. *Phialides* 15.3–38 µm ($\bar{x}$ = 28.2 µm, n = 6) long, 1.8–3.3 µm ($\bar{x}$ = 2.2 µm, n = 8) wide at base, in whorls of 2–4, straight, cylindrical, slightly tapering towards the tip, with periclinal thickening at their apex, collarette lacking or minute. *Secondary conidiophores* bi- to quinquies-verticillate, densely aggregated, formed in sporodochia on the host surface, septate, stipes short. Phialides in loose whorls of 3–5, straight to slightly curved, narrowly flask-shaped or cylindrical, tapering in the upper part, with a periclinal thickening at the apex, without a visible collarette, 8–15.6 ($\bar{x}$ = 14.1 µm, n = 15) µm long, 1.5–3.1 µm ($\bar{x}$ = 2.2 µm, n = 15) wide at base, intercalary phialides absent. *Conidia* 3.2–6 × 2–3.7 µm ($\bar{x}$ = 4.9 – 3 µm, n = 35), ovoidal to subglobose, minutely curved, broadly rounded distally, with a laterally displaced hilum, hyaline, smooth-walled.

Material examined – Thailand, Chiang Mai Province, on a dead stem of *Chromolaena odorata* (Asteraceae), 2 February 2017, R.H. Perera BN4 (MFLU 18-2729), living culture MFLUCC 17-2033.

GenBank numbers – ITS: MN597463, LSU: MT940528, *β-TUB*: MN599047, *TEF1-α:* MN599044.

Known distribution (based on molecular data) – China, New Zealand, Venezuela (Taylor & Hyde 2003), Thailand (this study)

Known hosts (based on molecular data) – *Archontophoenix* species, *Castanopsis carlesii*, *Rhopalostylis* sp. (Taylor & Hyde 2003), *Chromolaena odorata* (this study)

Notes – The new isolate MFLUCC 17-2033 grouped with the ex-isotype of *Clonostachys byssicola* (CBS 364.78) with high statistical support (100% MLBT, 1.00 MBPP) (Fig. 52). Our collection resembles *C. byssicola* in having similar conidiomatal morphology and conidiophore and conidia dimensions (Schroers 2002). Hence, we identify our collection as *C. byssicola.*

Clonostachys rosea (Link) Schroers, Samuels, Seifert & W. Gams, Mycologia 91, 369 (1999)
Fig. 55

Index Fungorum number: IF461067; Facesoffungi number: FoF06012

Associated with a dicotyledonous plant. Sexual morph: *Stromata* well-developed, erumpent. *Ascomata* 170–215 × 160–218 µm ($\bar{x}$ = 183 × 185 µm, n=10), perithecial, densely crowded in groups, globose to subglobose to oval, not collapsing or sometimes slightly laterally pinched when dry, light orange to yellowish orange, KOH-, not papillate, surface smooth to slightly roughened, but not distinctly warted. *Ostiole* periphysate. *Peridium* 25–40 µm wide, wider around the ostiole, two strata: outer region 20–30 µm wide, comprising brownish yellow cells of *textura angularis* to *textura globosa*, most cells containing a vacuole; inner region 8–15 wide, composed of flat, hyaline cells of *textura angularis*. *Apical paraphyses* present. *Asci* 50–65 × 6–7.2 µm ($\bar{x}$ = 54.2 × 6.7 µm, n=15), 8-spored, unitunicate, narrowly clavate, apex flat with somewhat rounded edges, short pedicellate, apical ring J-. *Ascospores* 9–12 × 3–3.4 µm ($\bar{x}$ = 10.6 × 3.1 µm, n=20), overlapping uniseriate, hyaline, 1-septate, not constricted at the septum or slightly constricted in mature ascospores, ellipsoidal to oblong ellipsoidal, 4-guttulate, spinulose, without a mucilaginous sheath. Asexual morph: See Schroers et al. (1999).

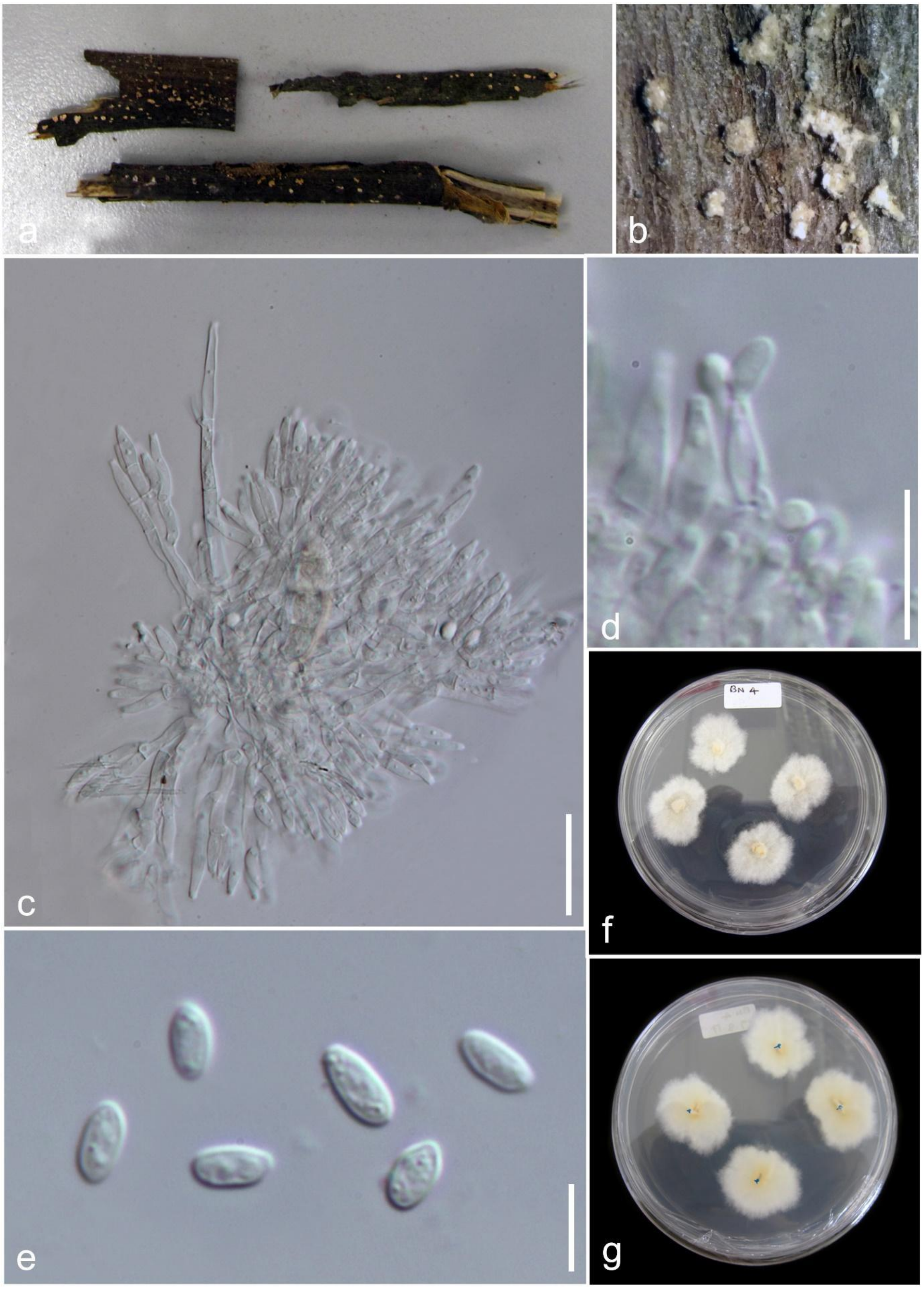

Fig. 54 – *Clonostachys byssicola* (MFLU 18-2729, a new host record) a Herbarium material. b Sporodochia on the host. c Primary and secondary conidiophores. d Phialides with conidia. e Conidia. f, g Colony on PDA. Scale bars: c = 20 µm, d = 10 µm, e = 5 µm.

Culture characteristics – Colonies growing on PDA reached 25 mm in 14 days at 28°C, surface effused, smooth, margin entire to undulate, aerial mycelium rare, white, reverse yellowish with pale orange center.

Material examined – Thailand, Phayao Province, Chiang Kham District, on twigs of a dicotyledonous plant, 11 September 2017, R.H. Perera Bion 17 (MFLU 19-0960), living culture MFLUCC 17-2632.

GenBank numbers – ITS: MN597465, LSU: MN597462.

Known distribution (based on molecular data) – Brazil, United States of America (Moreira et al. 2016), Thailand (this study).

Known hosts (based on molecular data) – *Fragaria* sp., *Lilium auratum* (Moreira et al. 2016).

Notes – The new isolate MFLUCC 17-2632 grouped with *Clonostachys rosea* isolates (Fig. 52). A comparison of nucleotides showed one nucleotide difference in the ITS locus of *C. rosea* isolates CBS 194.57 and CBS 193.94. Our collection resembles *C. rosea* by having similar ascomatal morphology and asci and ascospore dimensions (Rossman et al. 1999, Schroers 2002).

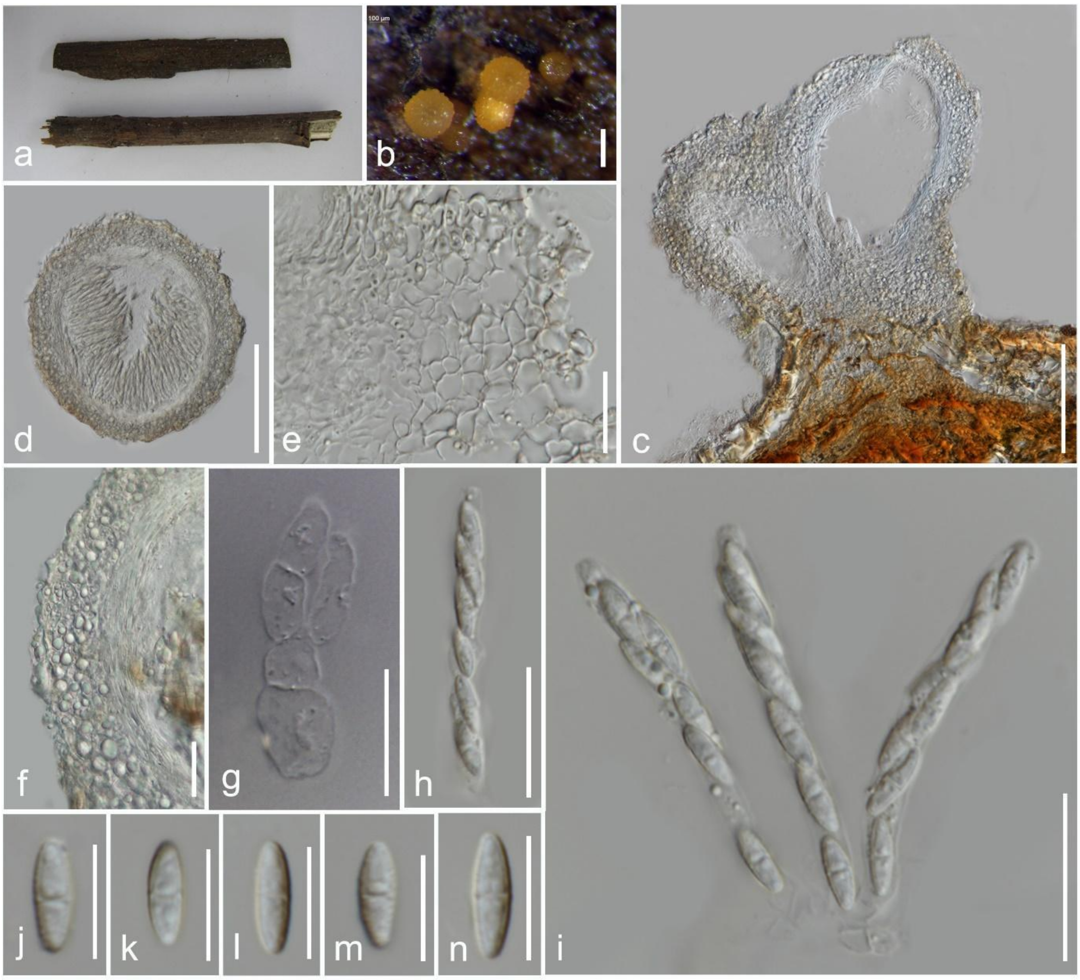

Fig. 55 – *Clonostachys rosea* (MFLU 19-0960, new host record). a Herbarium material. b Ascomata on host. c, d Sections of ascomata. e Section of stroma. f Section of peridium. g Apical paraphyses. h, i Asci. j–n Ascospores. Scale bars: b = 200 µm, c, d = 100 µm, e–i = 20 µm, j–n = 10 µm.

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

Index Fungorum number: IF80892; Facesoffungi number: FoF01904

Members of the Hypocreaceae have bright-coloured, fleshiest stroma found in nature. They are found as biotrophic, hemibiotrophic, saprobic or hypersaprobic and fungicolus forms (Chaverri & Samuels 2003, Jaklitsch 2009, 2011, Rossman et al. 2013, Talavera-Ortiz et al. 2020). The family consists of 606 species distributed among 17 genera (Hyde et al. 2020a, Wijayawardene et al. 2020). This family is characterized by superficial and brightly coloured ascostromata; immersed, single to bundled perithecia; cylindrical, 8-spored, rarely polyspored asci; single-celled to partially split, hyaline, yellowish-pink to greenish-brown ascospores with various surface morphologies. The phylogenetic tree showed that it has a close relationship with Bionectriaceae and Nectriaceae. Phylogeny of selected taxa in Hypocreaceae is shown in Fig. 56.

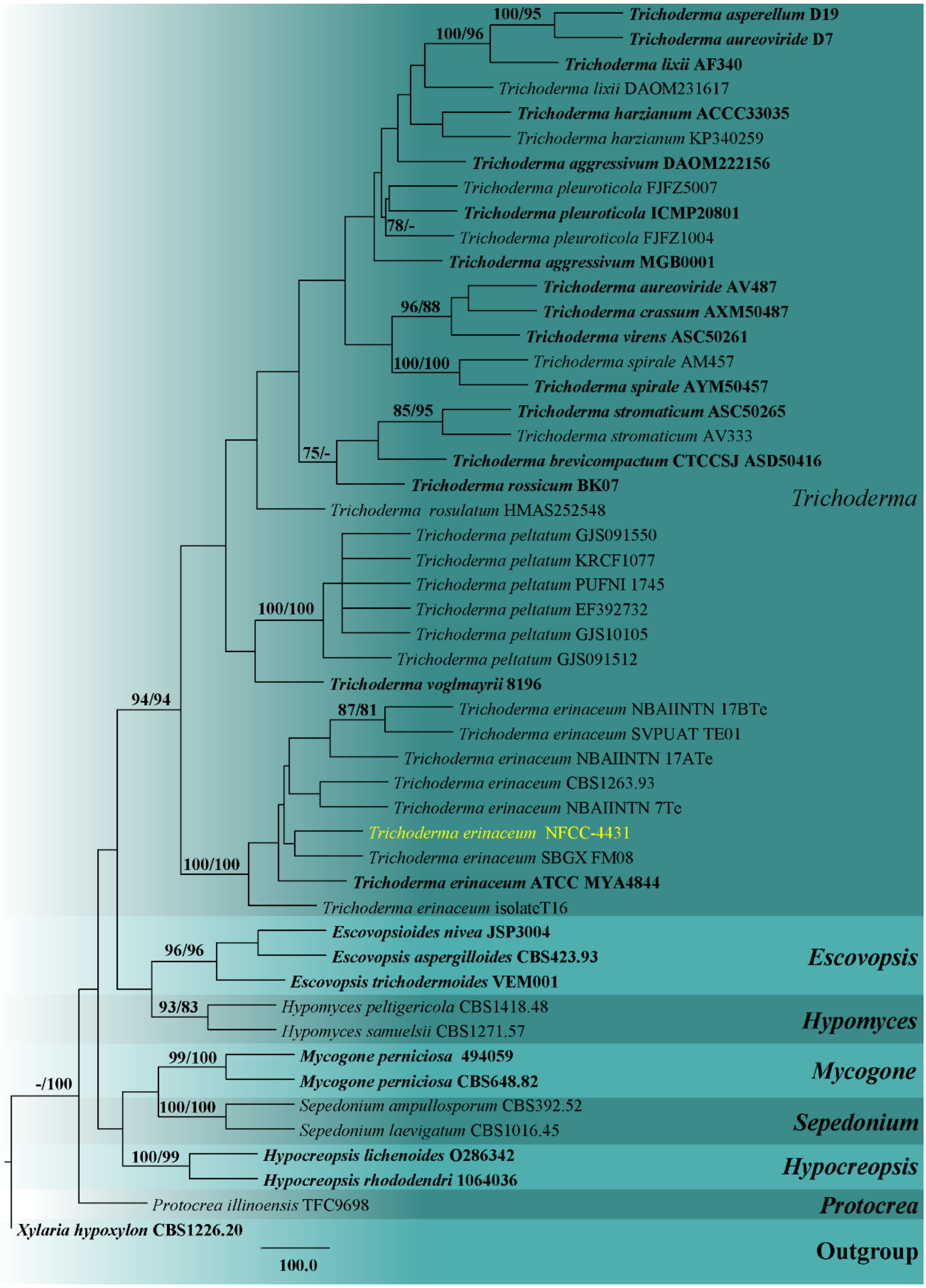

Fig. 56 – Phylogram generated from maximum parsimony analysis based on ITS sequence data. Fifty

strains are included in the analyses which comprised 581 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 -5591.621626 is presented. The matrix had 363 distinct alignment patterns with 6.96% of indeterminate characters or gaps. Estimated base frequencies were as follows: A = 0.223613, C = 0.308526, G = 0.263639, T = 0.204222; substitution rates AC = 1.152229, AG = 1.233710, AT = 1.491694, CG = 0.731040, CT = 2.057046, GT = 1.000000; Proportion of invariable sites I = 0.000100; gamma distribution shape parameter α = 0.475501. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Xylaria hypoxylon* CBS 1226.20. Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Trichoderma Pers., Neues Magazin für die Botanik 1, 92 (1794)

Index Fungorum number: IF10282; Facesoffungi number: FoF02075

Trichoderma is the type of Hypocreaceae and the family consists of 378 known species (Hyde et al. 2020a). *Trichoderma* species were the most wide spread in ubiquitous environments such as rotting plant materials, animals and microbes (Jaklitsch & Voglmayr 2015, Talavera-Ortiz et al. 2020). The phylogenetic analyses showed that many species form a hypocrea-shared sister relationship with *Trichoderma* and, therefore, were synonymized and validated the *Trichoderma* (Chaverri & Samuels 2003, Jaklitsch & Voglmayr 2015).

Trichoderma erinaceum Bissett, C.P. Kubicek & Szakács, Canadian Journal of Botany 81, 583 (2003) Fig. 57

Index Fungorum number: IF488348; Facesoffungi number: FoF09083

Saprobic on *Baccaurea ramiflora*. Sexual morph: *Stromata* scattered or aggregated in small numbers; pulvinate with circular or oblong outline when fresh, pale brown, ostiolar dots distinct, 0.2 mm high × 0.5–1 mm wide, narrowly attached, margin free, flat or convex, dark brown, surface smooth to slightly tubercular, white when young, pale brown with a reddish tinge or brown with a thin whitish to greyish covering, appearing grey-brown at maturity, often covered by white powdery spore mass; lower side white, papyraceous, not changing colour in 10% KOH, cortical layer 15–22.5 µm thick, comprising a light (yellow-) to brown, *textura angularis* of thin-walled cells. *Subcortical tissue* a loose *textura intricata* of hyaline, thin-walled hyphae. *Sub-perithecial tissue* consists of a mixture of *textura angularis* and *textura epidermoidea* cells, hyaline, partly pale brownish, thin-walled cells denser toward the base, often collapsing and entirely hyphal, periphysate, ostiolate. *Perithecia* 100–110 × 113–141 µm wide, crowded, globose to subglobose. *Peridium* 12.5 µm wide with few layers of *textura angularis* cells, yellow. *Asci* 58–66 × 3–5 µm ($\bar{x}$ = 63 × 4 µm, n = 25), 8-spored, cylindrical. *Ascospores* 1–2 × 1–1.5 µm ($\bar{x}$ = 1.5 × 1.2 µm, n = 25), uniseriate, splitting into part spores, cells dimorphic, globose, oblong with 1–3 guttules, hyaline. Asexual morph: Undetermined.

Culture characteristics – White colonies on malt extract agar, filamentous, sterile mycelium, reverse white, reaching 46 mm diam. in a week at 28°C

Material examined – India, Andaman and Nicobar Islands, North Andaman, Diglipur, Nabagram (13˚13'18.1"N 92˚55'59.3"E), on decaying twig of *Baccaurea ramiflora* (Phyllanthaceae), 17 May 2018, M. Niranjan & V.V. Sarma (PUFNI 18730, AMH-10060), living culture NFCC-4431.

GenBank accession numbers – ITS: MK990281, LSU: MK981537.

Known distribution (based on molecular data) – Bangladesh, Brazil, China, Colombia, India, Mexico, Nigeria, Papua New Guinea, Singapore, Taiwan, Thailand, South Korea, Sri Lanka, Pakistan, Peru, USA, Venezuela & Vietnam (da Silva et al. 2019).

Known hosts (based on molecular data) – *Acanthaster planci*, *Atractylodes macrocephala*, *Baccaurea ramiflora*, *Cassia tora*, *Caulerpa scalpelliformis*, *Curcuma longa*, *Lygus lineolaris*, *Pterocarpus dalbergioides*, *Theobroma cacao*, Rhizosphere of Pomegranate, Coastal soil & Rhizosphere of chickpea (da Silva et al. 2019).

Notes – *Trichoderma* is one of the most common genera in Ascomycota and consists of 100 species (Wijayawardene et al. 2018), and is characterized by superficial stromata, flat on the substrate, unitunicate asci, and eight ascospores that become partial spores when mature. Many new species have been introduced into this genus (Jaklitsch 2009, 2011, Qin & Zhuang 2016). The blastn search of sequences at NCBI showed that our isolate closely related to *T. erinaceum, T. dingleyae, T. caribbaeum* var. *caribbaeum,* and *T. koningii* with over 99% similarity. These species have slight differences among them; *T. koningii* has larger ascostromata and smaller ascospores than *T. erinaceum*. *Trichoderma dingleyae* has the largest ascostromata and perithecia.

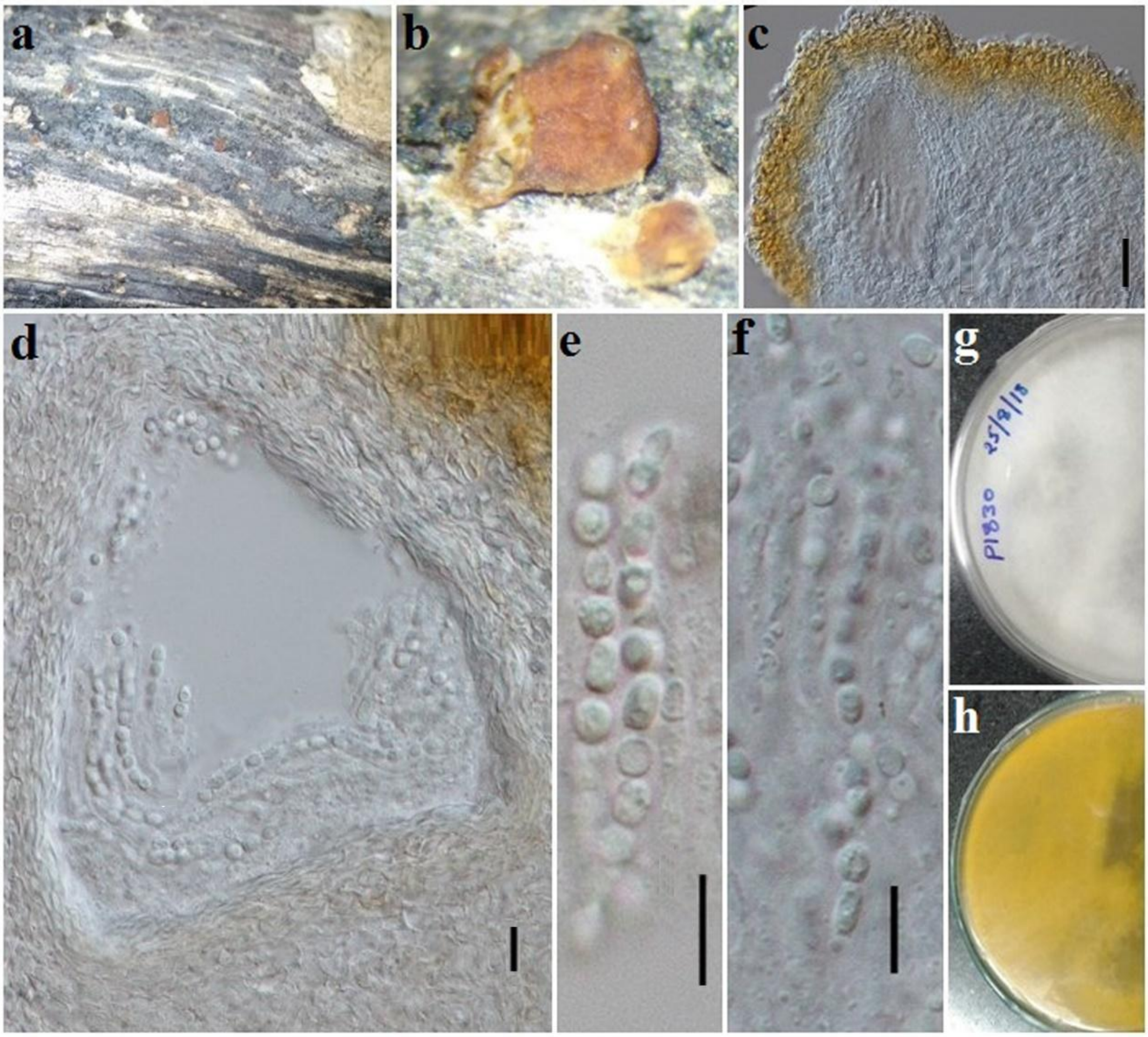

Fig. **57** – *Trichoderma erinaceum* (NFCC-4431, new host record). a, b Stroma on host. c Vertical section of the stroma. d Section through a perithecial ascoma. e, f Asci. g, h Culture on MEA. Scale bars: c = 50 µm, d = 20 µm, e–f = 10 µm.

Jobellisiales M.J. D'souza & K.D. Hyde, Fungal Diversity 72, 219 (2015)
Jobellisiaceae Réblová, Mycologia 100, 899 (2008)

Index Fungorum number: IF508692; Facesoffungi number: FoF01906

Jobellisiaceae was established by Réblová (2008) to accommodate *Jobellisia*. The placement of Jobellisiaceae is unstable and, therefore, was placed in Calosphaeriales based on divergence time estimates (Hongsanan et al. 2017). Hyde et al. (2020a) placed Jobellisiaceae in an independent order, Jobellisiales and related to Calosphaeriales and Diaporthales. This treatment is followed in this study.

Jobellisia M.E. Barr, Mycotaxon 46, 60 (1993)

Index Fungorum number: IF26310; Facesoffungi number: FoF05182

Jobellisia comprises nine species in Index Fungorum (2020), and only three have sequence data in GenBank, viz., *Jobellisia fraterna*, *J. guangdongensis* and *J. luteola* (type species). *Jobellisia* is characterized by superficial ascomata with light reddish apex, reddish-brown peridium, cylindrical asci with a refractive apical ring and ellipsoidal ascospores (Barr 1993). The asexual morph of *Jobellisia* is still unknown. Placement of the *Jobellisia* species in a phylogenetic analysis is presented in Fig. 58.

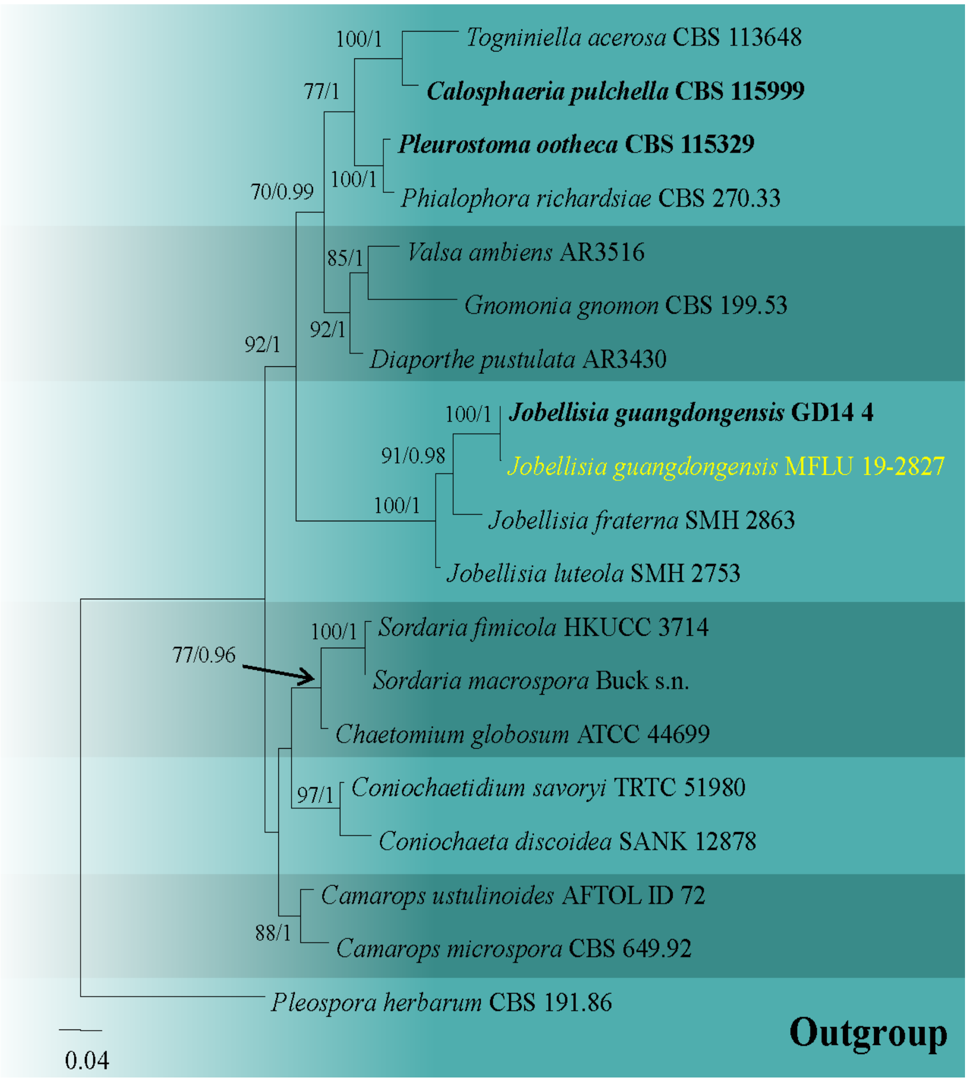

Fig. 58 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Nineteen strains are included in the combined analyses which comprised 1395 characters (860 characters for LSU, 535 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -5328.282817 is presented. Estimated base frequencies were as follows: A = 0.241807, C = 0.240515, G = 0.317101, T = 0.200577; substitution rates AC = 0.824389, AG = 2.607842, AT = 1.742277, CG = 1.207733, CT = 7.488055, GT = 1.000000; gamma distribution shape parameter a = 0.296714. For both LSU and ITS gene regions GTR+I+G was applied as the evolutionary model. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near the nodes respectively. The tree is rooted with *Pleospora herbarum* (CBS 191.86). Ex-type strains are in **bold**. The newly generated sequence is indicated in yellow.

Jobellisia guangdongensis F. Liu & L. Cai, Mycologia 104, 1181 (2012) Fig. 59

Index Fungorum number: IF564385; Facesoffungi number: FoF06965

Saprobic on submerged wood. Sexual morph: *Ascomata* globose to subglobose, superficial, dark brown to black, gregarious, carbonaceous, easily cracked, prominently papillate, ostiolate. *Peridium* 55–75 µm wide, three-layered, composed of pale brown to brown, thick-walled, irregular shaped cells. *Paraphyses* 3.5–4.5 µm wide, numerous, filamentous, septate, constricted at the septa, not embedded in a gelatinous matrix. *Asci* 90–105 × 5–6 µm ($\bar{x}$ = 97 × 6 µm, n = 10), 8-spored, unitunicate, cylindrical, short pedicellate with a refractive, large 4–4.5 µm diam. apical ring. *Ascospores* 8–10 × 3.2–4 µm ($\bar{x}$ = 9.2 × 3.5 µm, n = 30), uniseriate, fusoid to fusiform with acute ends, 1-septate, slightly constricted and thick-walled at the septum, greenish-brown, sometimes guttulate. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, on submerged wood in a stream, 25 August 2019, G.N. Wang DQ09 (MFLU 19-2827).

GenBank numbers – ITS: MN733257; LSU: MN733255.

Known distribution (based on molecular data) – China (Liu et al. 2012b, this study)

Known hosts (based on molecular data) – Undetermined wood (Liu et al. 2012b, this study)

Notes – Our collection MFLU 19-2827 clusters with *Jobellisia guangdongensis* with high bootstrap support (Fig. 58). *Jobellisia guangdongensis* was initially collected from submerged wood in Guangdong Province, China (Liu et al. 2012b). Our new collection from Yunnan Province, China, has identical morphological characteristics with the holotype of *J. guangdongensis* (MFLU 19-2827). The isolate MFLU 19-2827 is identified as *J. guangdongensis* based on identical sequence data and similar morphology. *Jobellisia guangdongensis* exclusively occurs in freshwater habitats. We sequenced from the fruiting body as ascospores did not germinate in culture.

Lulworthiales Kohlm., Spatafora & Volkm. -Kohlm., Mycologia 92, 456 (2000)

Lulworthiaceae Kohlm., Spatafora & Volkm.-Kohlm., Mycologia 92, 456 (2000)

Index Fungorum number: IF82091; Facesoffungi number: FoF01295

Lulworthiaceae was introduced to accommodate several species belonging to *Lulworthia* and *Lindra* with filamentous ascospores (Kohlmeyer et al. 2000). This family comprises the genera, *Halazoon*, *Haloguignardia*, *Hydea*, *Kohlmeyeriella*, *Lindra*, *Lulwoidea*, *Lulworthia*, *Matsusporium*, *Moleospora*, *Moromyces*, *Orbimyces*, *Spathulospora* and *Sammeyersia* (Jones et al. 2015, Maharachchikumbura et al. 2016, Abdel-Wahab et al. 2017, Hyde et al. 2020a). However, the placements of *Haloguignardia* and *Spathulospora* in Lulworthiales is still doubtful (Inderbitzin et al. 2004, Campbell et al. 2005, Jones et al. 2009, Hyde et al. 2020a). An updated phylogeny for the genus is presented in Fig. 60.

Sammeyersia S.Y. Guo, E.B.G. Jones & K.L. Pang, Botanica Marina 60, 483 (2017)

Index Fungorum number: IF820458; Facesoffungi number: FoF06955

Sammeyersia is a monotypic genus introduced by Abdel-Wahab et al. (2017) to accommodate *Sammeyersia grandispora* (= *Lulworthia grandispora*).

Sammeyersia grandispora (Meyers) S.Y. Guo, E.B.G. Jones & K.L. Pang, Botanica Marina 60, 483 (2017) Fig. 61

Index Fungorum number: IF820461; Facesoffungi number: FoF06423

Saprobic on submerged mangrove wood. Sexual morph: *Ascomata* 100–350 × 135–300 µm, globose or subglobose to pyriform, immersed or superficial, ostiolate, with a long neck, brown to black, solitary or gregarious. *Necks* upto 700–800 long, cylindrical, straight or curved, sometimes two on one ascoma. *Peridium* 20–35 µm wide, two-layered, composed of an outer layer of *textura angularis* and an inner layer of elongated cells with large lumina; inner layer thickened at the base of the neck, composed of cells with thickened and highly melanized wall. *Asci* 312–450 µm ($\bar{x}$ = 420, n = 10), 8-spored, elongate-fusiform or cylindrical, unitunicate, thin-walled, early deliquescing. *Ascospores* 312–450 × 2–4 µm ($\bar{x}$ = 370 × 3.8 µm, n = 10), filamentous, curved, hyaline, multi-guttulate, tapering at each end into an elongate, conical process or apical chamber, acute or rounded, filled with mucus that is released through an apical pore. Asexual morph: Undetermined.

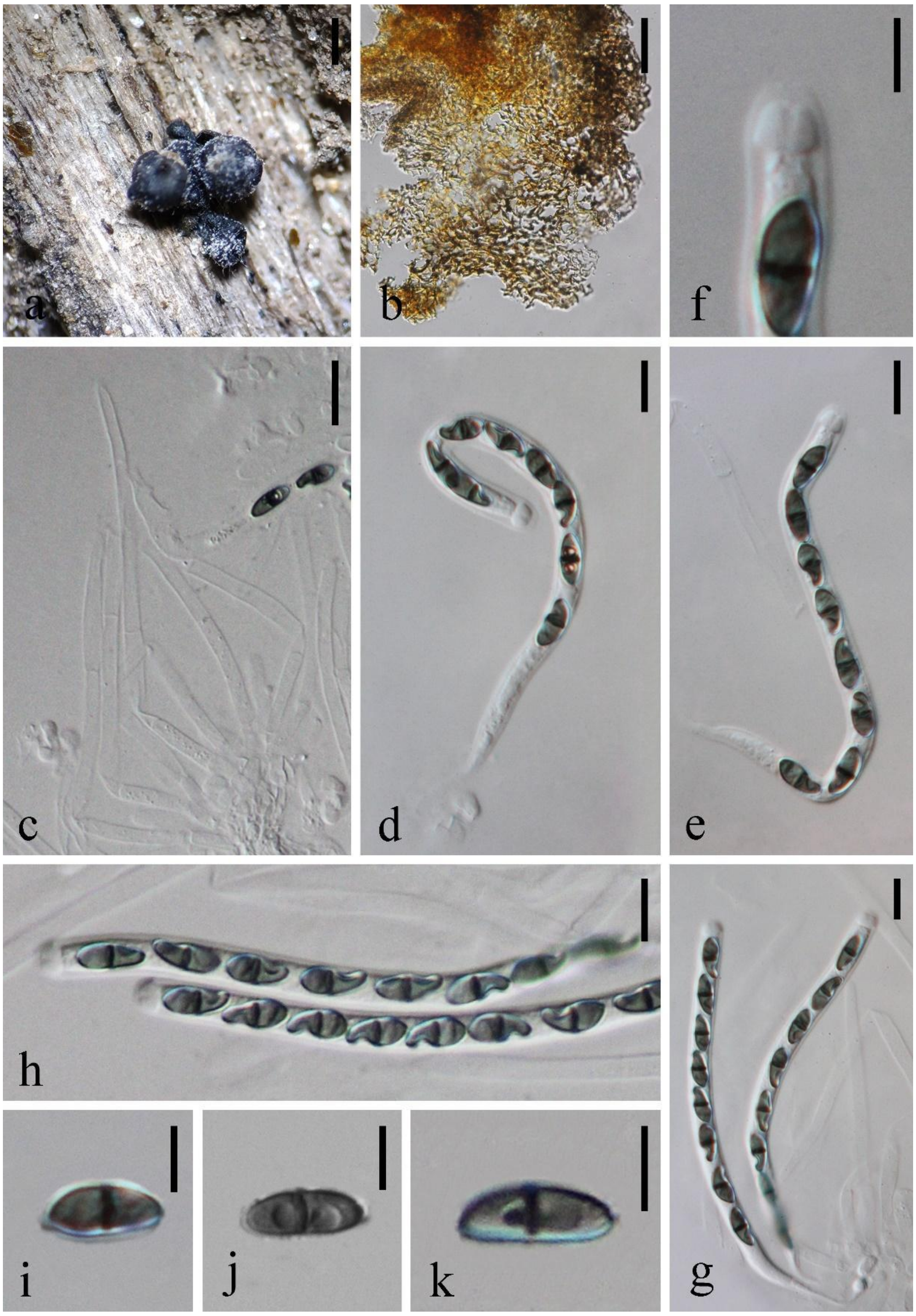

Fig. 59 – *Jobellisia guangdongensis* (MFLU 19-2827, new collection). a Appearance of black ascomata on host. b Peridium. c Paraphyses. d–h Asci. i–k Ascospores. Scale bars: a = 200 µm, b = 20 µm, c–e, g, h = 10 µm, f, i–k = 5 µm.

Material examined – Thailand, Phetchaburi Province, Hat Chao Samran (47° 72506' E, 40° 25038' N), on intertidal decayed wood of *Rhizopora* sp. (Rhizophoraceae) at a mangrove stand, 28 August 2015, M. Dayarathne CHAM005 (MFLU 16-1172).

GenBank numbers – LSU: MN592678, SSU: MN592679.

Known distribution (based on molecular data) – Belize, India, Malaysia, Taiwan (Schoch et al. 2009, Abdel-Wahab et al. 2018), Thailand (this study)

Known hosts (based on molecular data) – *Avicennia marina*, mangrove wood, *Rhizophora apiculata*, *R. mucronata*, *Rhizophora* sp., *Sonneratia acida*, *S. apetala* (Schoch et al. 2009, Jones & Pang 2012, Abdel-Wahab et al. 2018, this study)

Notes – *Lulworthia grandispora* is a mangrove inhabiting species, often found in tropical and subtropical countries (Jones & Pang 2012). This was synonymized to *Sammeyersia grandispora* and identified by the length of its ascospores, which is over 400 µm (Abdel-Wahab et al. 2017). Our new isolate (MFLU 16-1172) groups with the *S. grandispora* isolates deposited in the GenBank (Fig. 60). Therefore, depending on both morphological and phylogenetic data, we identified our new isolate as *S. grandispora*.

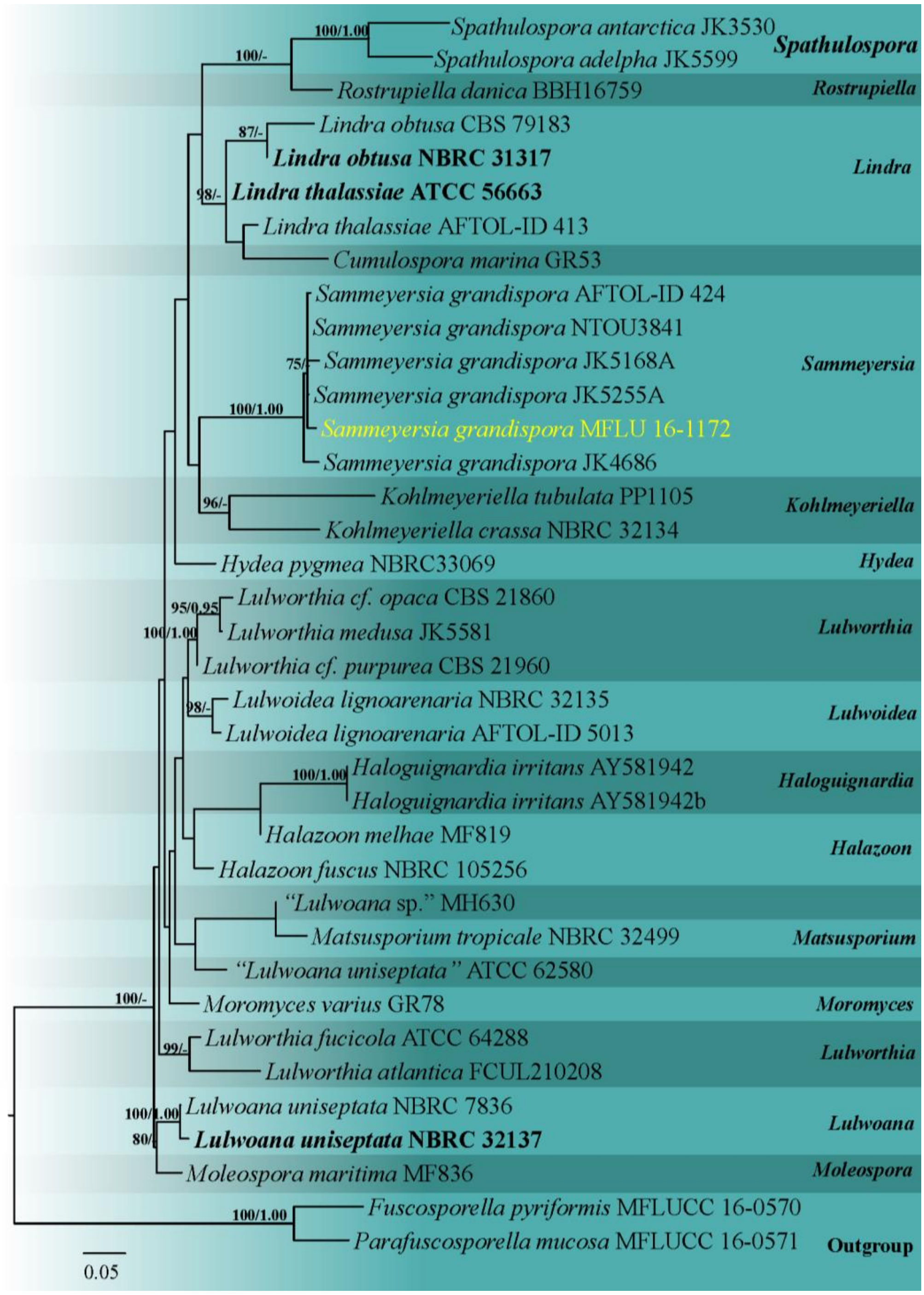

Fig. 60 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Thirty-seven strains are included in the combined analyses which comprised 2770 characters (930 characters for LSU, 1057 characters for SSU, 783 characters for

ITS) after alignment. The best RaxML tree with a final likelihood value of -17530.495296 is presented. Estimated base frequencies were as follows: A = 0.249147, C = 0.237452, G = 0.292161, T = 0.221241; substitution rates AC = 0.972203, AG = 2.135907, AT = 1.056736, CG = 1.215059, CT = 6.333743, GT = 1.000000; gamma distribution shape parameter α = 0.341853. The GTR+I+G evolutionary model was applied. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Fuscosporella pyriformis* (MFLUCC 16-0570) and *Parafuscosporella mucosa* (MFLUCC 16-0571). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Fig. **61** – *Sammeyersia grandispora* (MFLU 16-1172, new host record). a Ascomata on wood surface. b Section through ascoma in wood. c Peridium composed of thick-walled angular cells. d, f Asci. g Filamentous ascospore. h Polar end chamber of ascospore. Scale bars: a = 500 µm, b, d–f, g = 100 µm, c = 10 µm.

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

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

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

Index Fungorum number: IF813229; Facesoffungi number: FoF05316

The family comprises 11 genera (Wijayawardene et al. 2020) and the latest treatment was carried out by Luo et al. (2019).

Phaeoisaria Höhn., Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Math. - naturw. Klasse Abt. I 118, 330 (1909)

Index Fungorum number: IF9305; Facesoffungi number: FoF05521

Phaeoisaria, typified by *P. bambusae*, comprises 30 epithets in Index Fungorum (2020). *Phaeoisaria* is characterized by dark brown to black synnemata, polyblastic conidiogenous cells and ellipsoidal to obovoidal conidia (Luo et al. 2019). *Phaeoisaria* species form a well-supported clade in Pleurotheciaceae (Luo et al. 2019), but the sequences of the type species *P. bambusae* are still unavailable. An updated phylogeny for the genus is provided in Fig. 62.

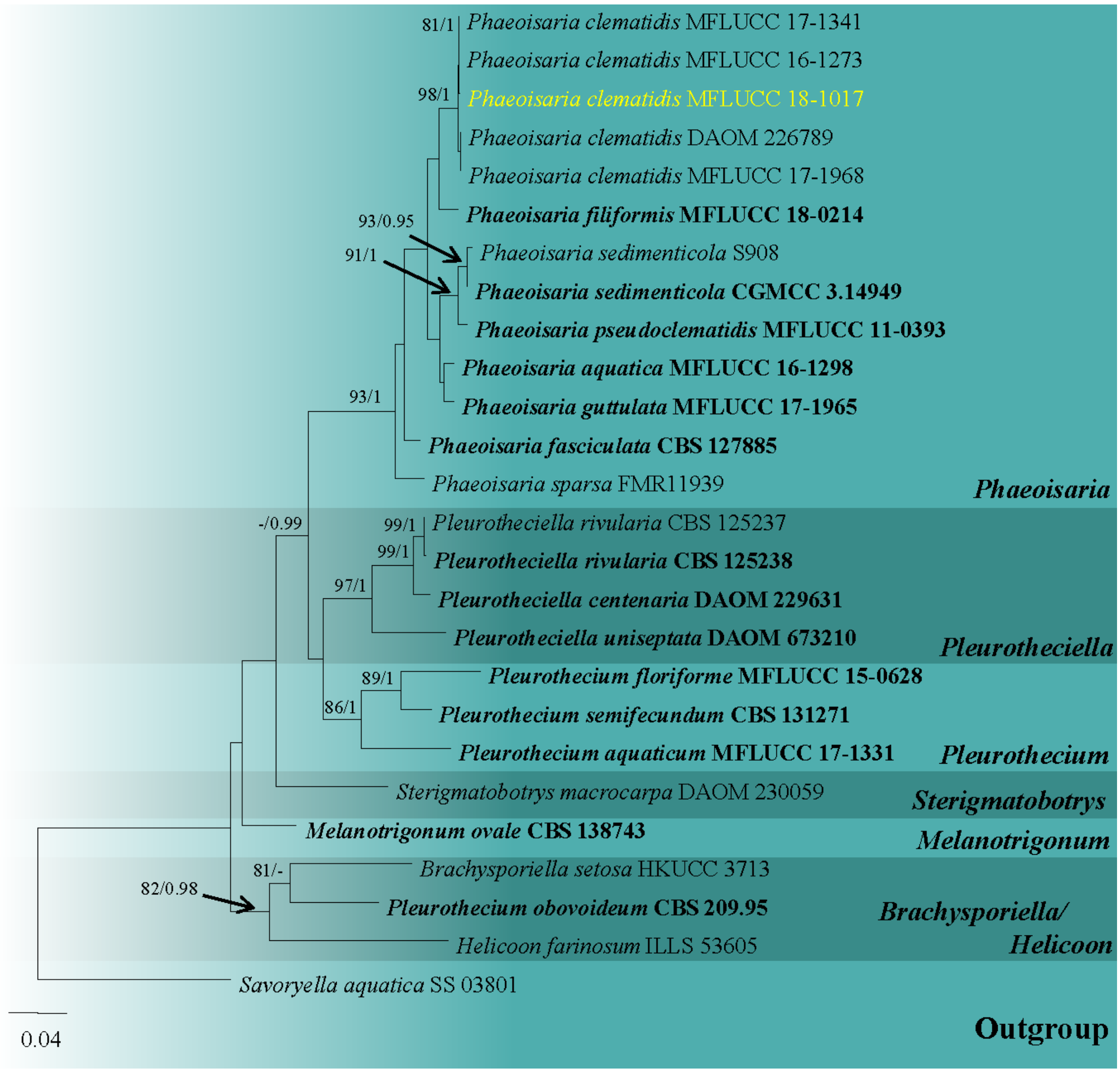

Fig. 62 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Twenty-six strains are included in the combined analyses which comprised of 2343 characters (843 characters for LSU, 871 characters for SSU, 629 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best RaxML tree with a final likelihood value of -9202.581935 is presented. Estimated base frequencies were as follows: A = 0.234130, C = 0.255242, G = 0.295085, T = 0.215543; substitution rates AC = 2.002438, AG = 2.838660, AT = 2.153563, CG = 0.815836, CT = 8.189358, GT = 1.000000; gamma distribution shape parameter α = 0.167151. For all the gene regions, GTR+I+G was applied as the evolutionary model. Bootstrap support values for ML greater than 80% and Bayesian posterior probabilities greater than 0.95 are given near the nodes respectively. The tree is rooted with *Savoryella aquatica* (SS 03801). Ex-type strains are in **bold**. The newly generated sequence is indicated in yellow.

Phaeoisaria clematidis (Fuckel) S. Hughes, Canadian Journal of Botany 36, 794 (1958) Fig. 63

Index Fungorum number: IF302703; Facesoffungi number: FoF00452

Saprobic on submerged wood. Sexual morph: Undetermined. Asexual morph: Hypomycetous. *Colonies* effuse, scattered to gregarious, hairy, brown, covered with bright white conidia. *Mycelium* partly immersed, partly superficial. *Conidiophores* 870–900 × 23–28 μm ($\bar{x}$ = 885 × 25 μm, n = 5), macronematous, synnematous, septate, branched, dark brown to black, paler towards apex, straight or slightly bent, flared at the apex, smooth. *Conidiogenous cells* holoblastic, polyblastic, integrated, terminal, sympodial, subcylindrical, denticulate, each with several conidiogenous loci, subhyaline. *Conidia* 6.3–8.7 × 3–4.3 μm ($\bar{x}$ = 7.8 × 3.5 μm, n = 20), narrowly ellipsoidal, obovoid, rounded at the apex, hyaline, aseptate, straight, smooth-walled.

Culture characteristics – on PDA, colony circular, reaching 7 mm diam. in 20 days at 25°C, grey from above, pale grey from below, surface rough, dry, with dense mycelium, raised, undulated edge.

Material examined – China, Yunnan Province, Pingbian, on submerged wood, 20 September 2017, W. Dong WF-17A-1 (MFLU 18-1176), living culture MFLUCC 18-1017; *ibid*., WF-17A-2 (HKAS 101709), living culture KUMCC 18-0058.

GenBank numbers – ITS: MW131990, LSU: MW132065, SSU: MW132063 (MFLUCC 18-1017).

Known distribution (based on molecular data) – Australia (Réblová et al. 2012), China (Luo et al. 2018, this study)

Known hosts (based on molecular data) – *Protea* sp. (Réblová et al. 2012)

Notes – Our isolate from freshwater (MFLUCC 18-1017) clusters with four strains of *Phaeoisaria clematidis* with high bootstrap support (Fig. 62). *Phaeoisaria clematidis* was initially published in 1958 (Index Fungorum 2020). Réblová et al. (2012) first sequenced *P. clematidis* isolate collected from the bark of *Protea* in Australia. Luo et al. (2018) added another two freshwater collections from Lancang River, China, with illustrations and detailed descriptions. Our isolate (MFLUCC 18-1017) has nearly identical morphological characters with the collection of Luo et al. (2018), except for the longer conidiophores (870–900 μm *vs* 312–568 μm) of isolate MFLUCC 18-1017. Based on morphological and molecular evidence, we identify MFLUCC 18-1017 as *P. clematidis*.

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

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

Index Fungorum number: IF551026; Facesoffungi number: FoF01283

Savoryellaceae was erected by Jaklitsch in 2015 and followed by Maharachchikumbura et al. (2016), Hyde et al. (2016) and (2020a). Four genera are accommodated in Savoryellaceae, i.e., *Ascotaiwania*, *Canalisporium*, *Rhexoacrodictys* and *Savoryella*.

Canalisporium Nawawi & Kuthubutheen, Mycotaxon 34, 477 (1989)

Index Fungorum number: IF11041; Facesoffungi number: FoF05485

Canalisporium is the largest genus in Savoryellaceae comprising 16 species (Index Fungorum 2020). The latest treatment of *Canalisporium* was carried out by Hyde et al. (2020a) and this is followed in this study (Fig. 64).

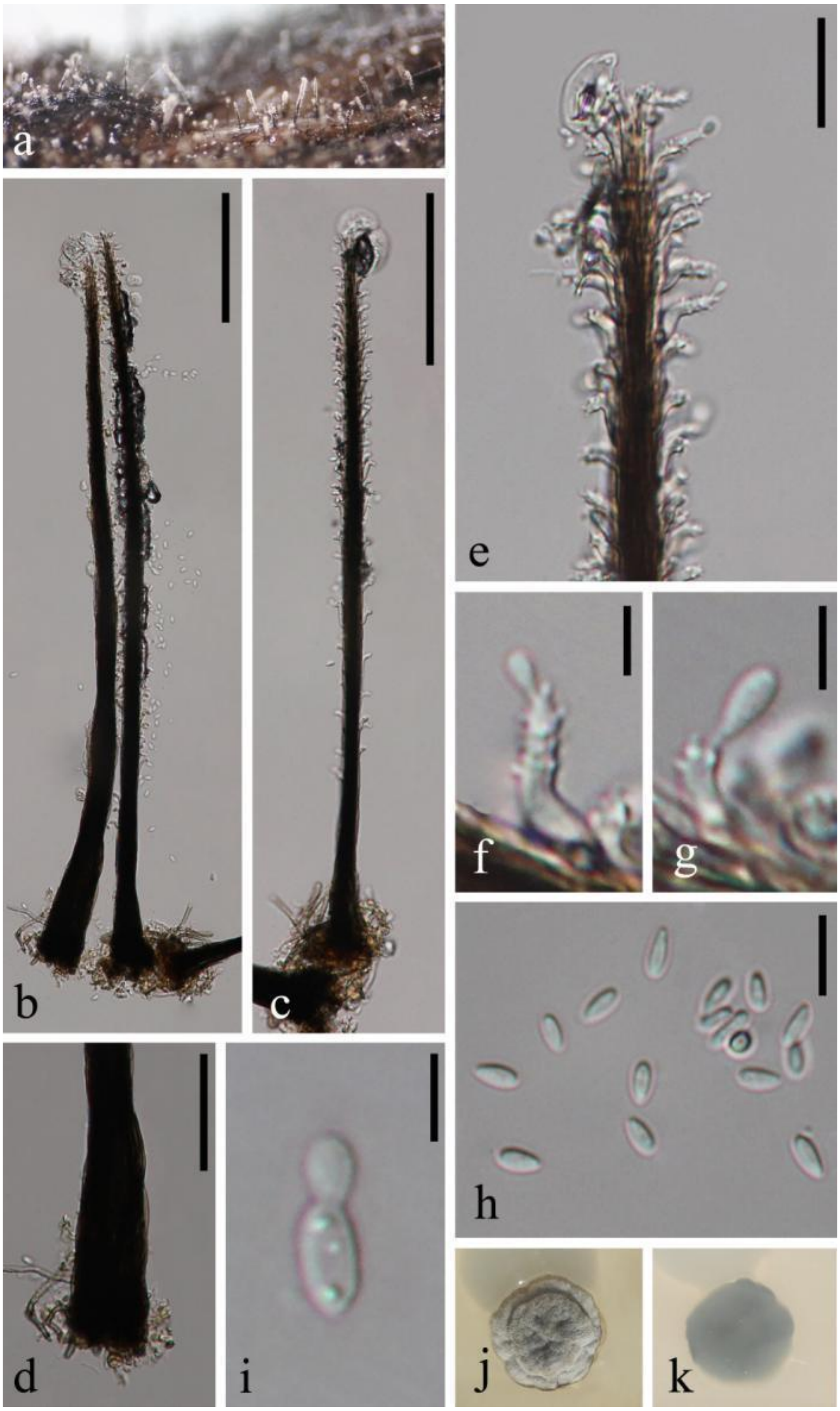

Fig. 63 – *Phaeoisaria clematidis* (MFLU 18-1176, new collection). a Colonies on submerged wood. b–c, e Conidiophores with attached conidia. d The base of conidiophore. f, g Conidiogenous cells with conidia. h Conidia. i Germinated conidium. j, k Colony on PDA (left-front, right-reverse). Scale bars: b, c = 100 µm, d = 50 µm, e = 20 µm, f, g, i = 5 µm, h = 10 µm.

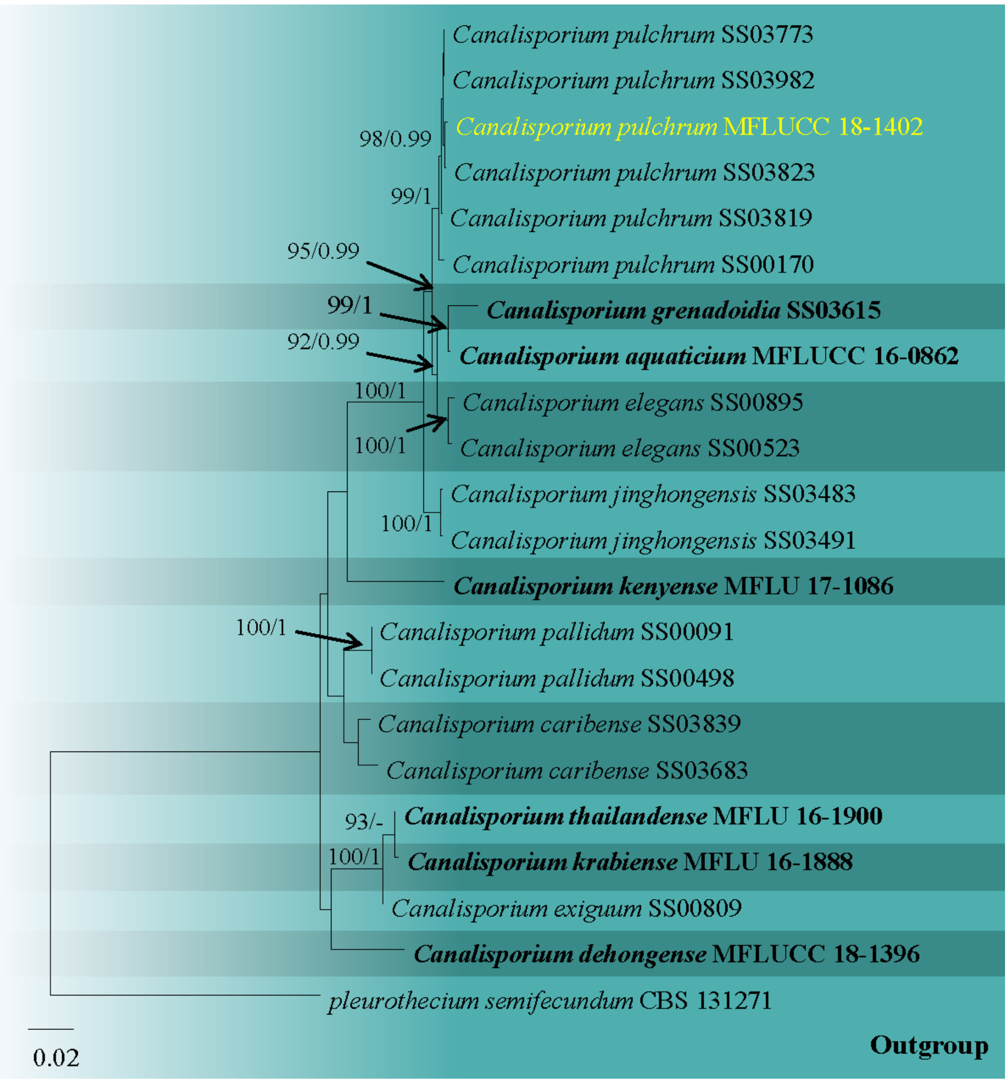

Fig. 64 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data. Twenty-two strains are included in the combined analyses which comprised 2756 characters (741 characters for ITS, 846 characters for LSU, 1169 characters for SSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -7912.691553 is presented. Estimated base frequencies were as follows: A = 0.225339, C = 0.258163, G = 0.306839, T = 0.209659; substitution rates AC = 1.225977, AG = 3.213328, AT = 1.956116, CG = 0.495328, CT = 6.284499, GT = 1.000000; gamma distribution shape parameter α = 0.162166. For all the gene regions, GTR+I+G was applied as the evolutionary model. Bootstrap support values for ML greater than 80% and Bayesian posterior probabilities greater than 0.95 are given near the nodes respectively. The tree is rooted with *pleurothecium semifecundum* (CBS 131271). Ex-type strains are in **bold**. The newly generated sequence is indicated in yellow.

Canalisporium pulchrum (Hol.-Jech. & Mercado) Nawawi & Kuthub., Mycotaxon 34, 481 (1989)
Fig. 65

Index Fungorum number: IF125433; Facesoffungi number: FoF09421

Saprobic on submerged wood. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Sporodochia* scattered, punctiform, pulvinate, granular, black, shining. *Mycelium* mostly immersed, consisted of branched, thin-walled, hyaline to pale brown hyphae. *Conidiophores* up to 75 µm long, micronematous, mononematous, septate, unbranched, constricted at septa. *Conidiogenous cells* 4–6.5 × 4–4.5 µm ($\bar{x}$ = 5.5 × 4.4 µm, n = 10), holoblastic, monoblastic, terminal, determinate, subcylindrical, hyaline, smooth, thin-walled. *Conidia* 32–46 × 15–22 µm ($\bar{x}$

= 43 × 19 µm, n = 20), solitary, acrogenous, ellipsoidal to obovoid, narrowly to broadly subcylindrical, muriform, smooth, brown to dark brown, with two straight columns of vertical septa and 5–6 rows of transverse septa, constricted at the septa, darkened and thickly banded at the septa, cuneiform, pale brown to subhyaline, with single basal cell.

Culture characteristics – on PDA, colony irregular, 8 mm in 55 days at 25°C, dark grey from above, black from below, surface rough, raised, felty wooly, fairly dense

Material examined – Thailand, Songkhla Province, Hat Yai District, Chestnut Hill, on submerged wood, 10 May 2018, W. Dong hat463-1 (MFLU 18-1563), living culture MFLUCC 18-1402; *ibid*., hat463-2 (HKAS 105047), living culture KUMCC 19-0066.

GenBank numbers – ITS: MW131989, LSU: MW132064 (MFLUCC 18-1402).

Known distribution (based on molecular data) – Thailand (Sri-indrasutdhi et al. 2010, this study).

Known hosts (based on molecular data) – *Alstonia scholaris* (Sri-indrasutdhi et al. 2010).

Notes – Our freshwater collection (MFLUCC 18-1402) clusters with five Thai strains of *Canalisporium pulchrum* with high bootstrap support (Fig. 64). The isolate MFLUCC 18-1402 resembles the holotype of *C. pulchrum* (PRM 831528) in all aspects, such as conidial shape, size and septation (Holubová-Jechová & Mercado Sierra 1984). *Canalisporium pulchrum* occurs on submerged or rotten wood in many countries and shows a wide range in conidial dimensions (Goh et al. 1998). However, the real identities of those collections have not been supported by molecular data. We provide sequence data and description for an additional Thai specimen MFLUCC 18-1402 collected from freshwater.

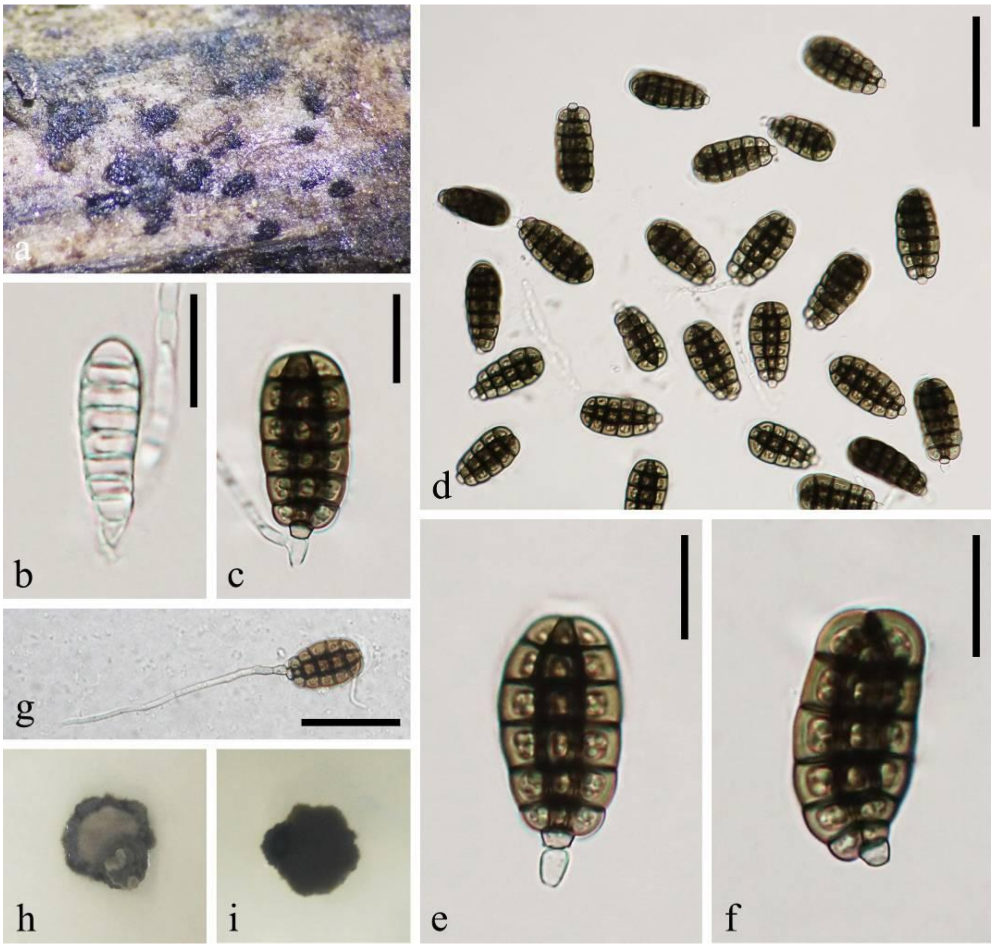

Fig. 65 – *Canalisporium pulchrum* (MFLU 18-1563, new collection). a Colonies on submerged wood. b Immature conidium with conidiophore. c Matured conidium with conidiophore. d–f Conidia. g Germinated conidium. h, i Colony on PDA (left-front, right-reverse). Scale bars: b = 15 µm, c, e, f = 20 µm, d, g = 50 µm.

Subclass Sordariomycetidae O.E. Erikss & Winka, Myconet 1, 10 (1997)
Meliolales Gäum. ex D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5, 180 (1986)
Meliolaceae G.W. Martin ex Hansf., Mycological Papers 15, 23 (1946)

Index Fungorum number: IF80993; Facesoffungi number: FoF00741

Meliolaceae is the largest group of epifoliar fungi characterized by larviform ascospores and dark brown hyphae with phialides and 2-celled appressoria (Zeng et al. 2017, 2020). Members of this family are unculturable, and host information is the primary criterion for their identification. The phylogenetic relationship of several genera in Meliolaceae are shown in Fig. 66.

Meliola Fr., Systema Orbis Vegetabilis 1, 111 (1825)

Index Fungorum number: IF3100; Facesoffungi number: FoF00740

Meliola is the largest genus of Meliolaceae characterized by globose ascomata and the presence of hyphal setae (Zeng et al. 2017, 2020).

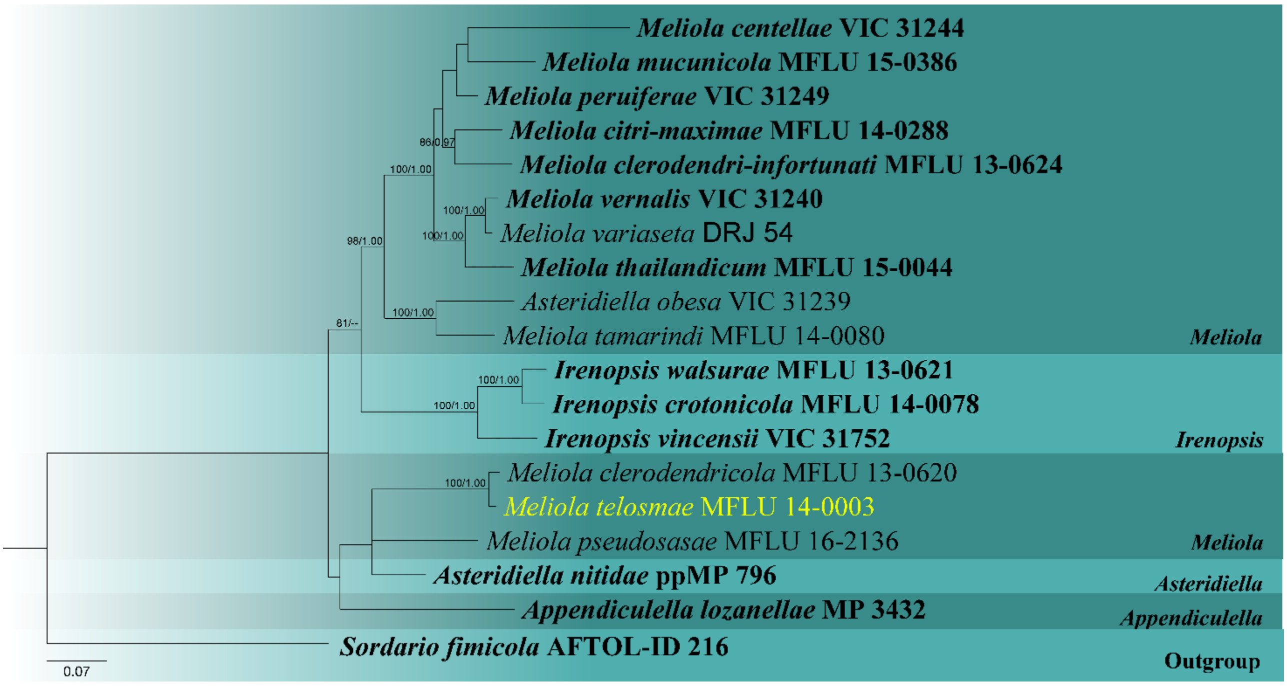

Fig. 66 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Nineteen strains are included in the combined analyses which comprised 2547 characters (834 characters for LSU, 1020 characters for SSU, 693 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12296.492874 is presented. Estimated base frequencies were as follows: A = 0.251820, C = 0.221366, G = 0.284447, T = 0.242367; substitution rates AC = 0.925122, AG = 3.316599, AT = 1.863343, CG = 0.262623, CT = 6.798329, GT = 1.000000; gamma distribution shape parameter α = 0.530371. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Sordaria fimicola* (AFTOL-ID 216). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Meliola telosmae Rehm, Philippines Journal of Sciences 8, 392 (1913) Fig. 67

Index Fungorum number: IF237666; Facesoffungi number: FoF05218

Parasitic on living leaves of *Telosma cordata*. *Colonies* epiphyllous, scattered. *Hyphae* superficial, substraight to crooked, branching opposite at acute to wide angles, reticulate. *Hyphal setae* straight, up to 200 µm, tapering at the apex. *Appressoria* alternate to unilateral, straight to curved, antrorse, 2-celled, clavate to spathulate, 14–22 × 7–10 µm ($\bar{x}$ = 17 × 8 µm, n = 20). Sexual morph: *Ascomata* up to 150 µm in diam., superficial, globose to subglobose, dense, grouped, dark brown, composed of hyaline inner cell and dark brown outer wall with *textura angularis*, with a central ostiole and dark brown setae around the base. *Asci* 2–4-spored, unitunicate, ellipsoid to ovoid, ascus wall becomes thinner and asci without a certain shape at mature state. *Ascospores* 30–36 × 12–15 µm (x̅ = 33 × 13 µm, n = 10), 2–4-seriate, hyaline when young, brown or olive-brown when mature, cylindrical to ellipsoid, 4-septate, slightly constricted at septa, middle cell larger than others, with a sheath. Asexual morph: *Phialides* 13–18 × 5–7 µm (x̅ = 15 × 6 µm, n = 10), opposite to alternate, with few mixed with appressoria, ampulliform.

Material examined – Thailand, Nang Lae, Chaing Rai, on the living leaves of *Telosma cordata* (Apocynaceae), 4 January 2014, Saranyaphat Boonmee (MFLU 14-0003), **reference specimen designated here**.

GenBank numbers – ITS-LSU: MK103389, SSU: MK103390.

Known distribution (based on molecular data) – China (Zhuang 2001), Thailand (this study)

Known hosts (based on molecular data) – Asclepiadaceae species, *Dischidanthus urceolatus* (Zhuang 2001), *Telosma cordata* (this study)

Notes – The only species of Meliolaceae found on the *Telosma* hosts is *Meliola telosmae*. The new collection matches all the morphological features given in the description of the reported species, except for the ascospore size. However, there are no sequence data from previous collections of *Meliola telosmae* in GenBank. In the phylogenetic analysis, our new collection clusters with *M. clerodendricola* with 100%/1.00 bootstrap support (Fig. 66). There is 90% (547/607 nucleotide, 33/607 gaps) similarity in the ITS region between our isolate and *M. clerodendricola*. Morphologically, *Meliola telosmae* differs from *M. clerodendricola* in having dense colonies, longer setae (up to 200 µm vs up to 170 µm), and thinner ascospores (12–15 µm *vs* 10–13 µm). Therefore, we assign this new collection as a reference specimen of *M. telosmae* with sequence data.

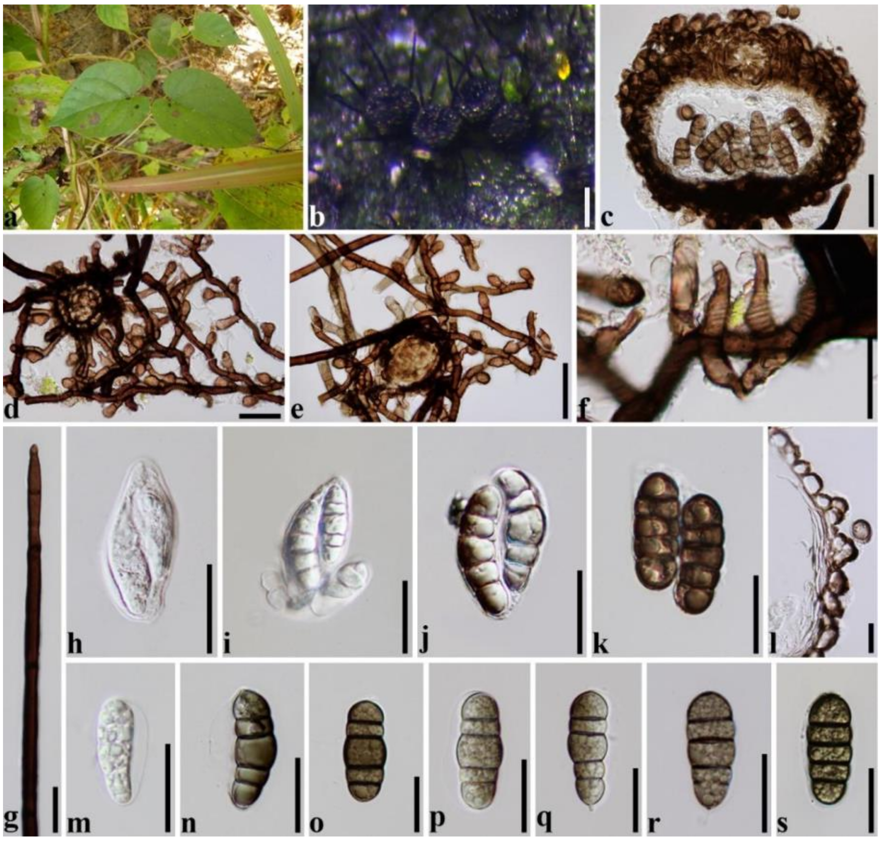

Fig. 67 – *Meliola telosmae* (MFLU 14-0003, reference specimen). a The host plant. b Ascomata on leaf surface. c Cross section of an ascoma. d, e Hyphae with appressoria. f Phialides. g Setae. h–k Asci from young to mature state. l Peridium. m–s Ascospores. Scale bars: b = 100 µm, c–e = 50 µm, f–s = 20 µm.

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5, 182 (1986)

Chaetomiaceae G. Winter, Rabenh. Kryptogamen-Flora Ed 2 1, 153 (1885)

Index Fungorum number: IF80582; Facesoffungi number: FoF01842

Chaetomiaceae was introduced by Winter (1885) and is typified by *Chaetomium* (Grunow et al. 1887). This family is composed of 36 genera. Chaetomiaceae is characterized by species producing humicola-like, thick-walled spores (Wang et al. 2019a). An updated phylogenetic tree for *Chaetomium* and *Dichotomopilus* is presented in Fig. 68.

Chaetomium Kunze, Mykologische Hefte (Leipzig) 1, 15 (1817)

Index Fungorum number: IF953; Facesoffungi number: FoF01843

Chaetomium is a cosmopolitan genus with more than 400 species (Index Fungorum 2021). Special characteristics of *Chaetomium* are ascomata covered with hairs or setae, clavate or fusiform or sometimes cylindrical thin-walled asci, lack of paraphyses before ascomata mature and 1-celled, brown or grey-brown ascospores with germ pores (Zhang et al. 2017, Jayawardena et al. 2018).

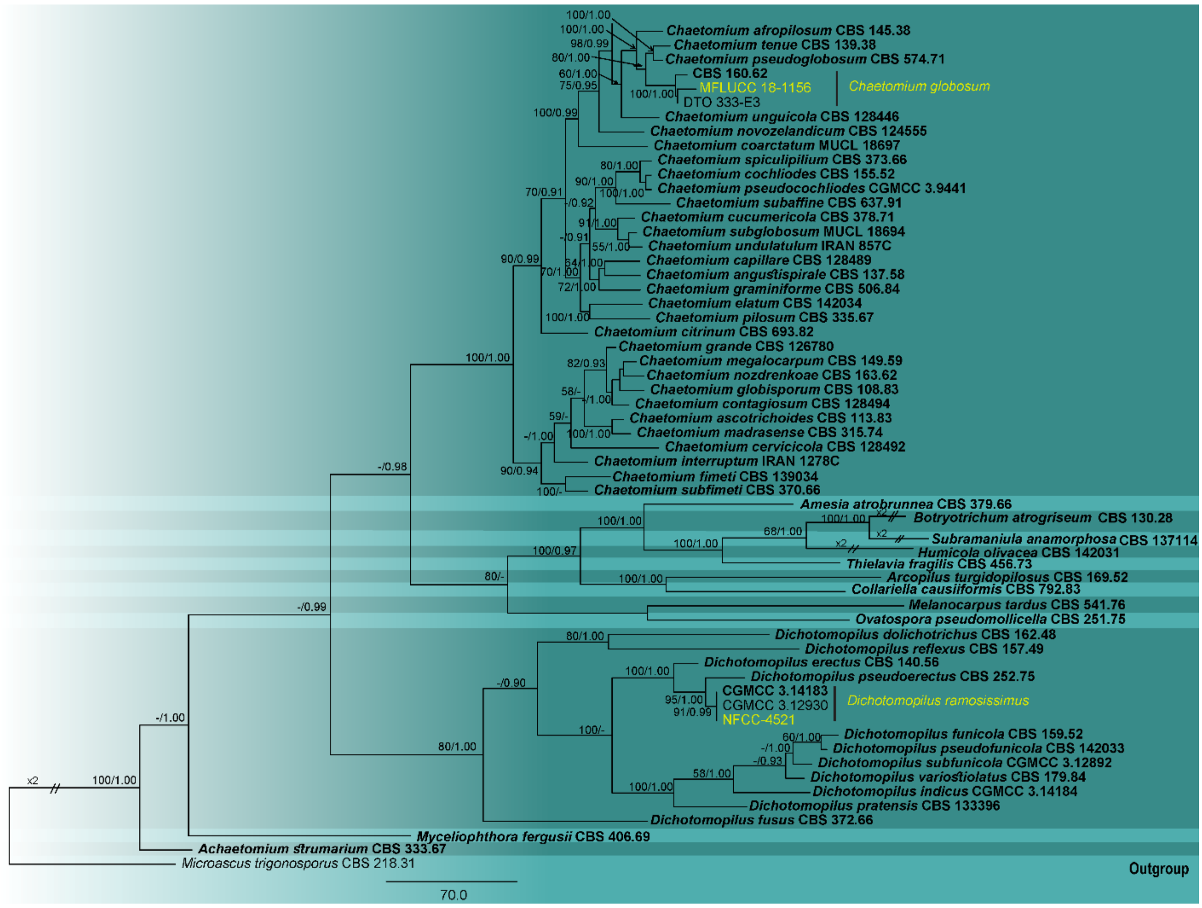

Fig. 68 – Phylogram generated from maximum parsimony analysis based on combined sequences of ITS, LSU and *β-TUB* sequence data. Sixty strains are included in the combined analyses, which comprise 2319 characters including gaps, of which 1421 characters are constant, 310 characters are parsimony-uninformative and 588 characters parsimony-informative. Tree topology of the maximum parsimony analysis is similar to the Bayesian analysis. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 3496 steps (CI = 0.446, RI=0.626, RC = 0.279, HI = 0.554) in the first tree. Evolutionary model GTR+I+G was applied to both ITS and LSU gene regions and HYK+I+G was applied to *β-TUB* sequence data. The tree was rooted with *Microascus trigonosporus* (CBS 218.31). MP bootstrap support value greater than or equal to 50% and BYPP greater than or equal to 0.9 are shown respectively near the nodes. Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Chaetomium globosum Kunze, in Kunze & Schmidt, Mykologische Hefte (Leipzig) 1, 16 (1817) Fig. 69

Index Fungorum number: IF172545; Facesoffungi number: FoF02196

Saprotrophic on dead flower of *Rosa* sp. Asexual morph: Undetermined. see Maharachchikumbura et al. (2016) for description. Sexual morph: *Ascomata* 160–300 × 130–220 µm (x̅ = 243 × 178), superficial, globose, ellipsoid, ovate or obovate, greenish olivaceous or slightly dark olivaceous buff to grey in reflected light owing to ascomatal hairs, ostiolate. *Peridium* brown, composed of hypha-like or amorphous cells, *textura intricata* in surface view. *Terminal hairs* abundant, finely verrucose, brown, tapering and fading towards the tips, 3–5 µm diam. near the base, flexuous, undulate to loosely coiled with erect or flexuous lower part, usually unbranched. *Lateral hairs* brown, flexuous, fading and tapering towards the apices. *Asci* 28–40 × 10–15 µm (x̅ = 34 × 12), fasciculate, fusiform or clavate, spore-bearing part, stalks 18–25 µm long, with eight biseriate ascospores, evanescent. *Ascospores* 8–11 × 6–7 µm (x̅ = 9 × 6), olivaceous brown when mature, limoniform, usually biapiculate, bilaterally flattened, with an apical germ pore.

Culture characteristics – Colonies on PDA reaching 50 mm in 7 days at 25°C, brown or orange or white, woolly, even margin, reverse buff-coloured to brown, aerial mycelium cottony or felty, with funiculose setae and hyphae. Mycelium abundant, intramatrical and aerial, composed of hyaline or dark brown, septate, hyphae.

Material examined – Thailand, Chiang Rai, on dead flower of *Rosa* sp. (Rosaceae), 15 May 2018, Ruvishika S. Jaywardena RKB1 (MFLU 18-1833), living culture MFLUCC 18-1156.

GenBank numbers – ITS: MN788674, LSU: MN788679

Known distribution (based on molecular data) – Canada, Thailand (Esmaeili et al. 2017, Tibpromma et al. 2018)

Known hosts (based on molecular data) – *Pandadus* sp., *Pisum sativum*, *Vitis* sp., (Esmaeili Taheri et al. 2017, Jayawardena et al. 2018, Tibpromma et al. 2018), *Rosa* sp. (this study)

Notes – *Chaetomium* is a cosmopolitan genus with more than 150 species (Zhang et al. 2012). *Chaetomium globosum* is widely known for its biological control properties (Wang et al. 2012). This study provides the first report of *C. globosum* as a saprotroph associated with *Rosa* sp. in Thailand.

Dichotomopilus X. Wei Wang, Samson & Crous, Studies in Mycology 84, 185 (2016)

Index Fungorum number: IF818840; Facesoffungi number: FoF08466

Dichotomopilus established by Wang is based on the type species, *D. indicus*. The fruiting bodies of this genus have unique characters; they consist of dichotomically branched terminal hairs and are saprobic in nature. Many *Chaetomium* species were transferred and two new species, *D. pseudofunicla* and *D. pseudoerectus* were introduced to this genus (Wang et al. 2016). *Dichotomopilus* species are widely distributed in Asia, Europe, North America and moderately in Australia (New Guinea) (Zhang et al. 2017, Hyde et al. 2020a). Most of them were found in interiors, outdoors and on decomposing twigs (Wang et al. 2016, Hyde et al. 2020a), Phukhamsakda et al. 2020). Twelve species were known so far (Index Fungorum 2020). In phylogenetic analysis (Fig. 68), *Dichotomopilus* nested separately from *Chaetomium*, revealing both morphological and molecular divergence.

Dichotomopilus ramosissimus (X. Wei Wang & L. Cai) X. Wei Wang & Samson, Studies in Mycology 84, 217 (2016) Fig. 70

= *Chaetomium ramosissimum* X. Wei Wang & L. Cai, Mycological Progress 13, 725 (2014)

Index Fungorum number: IF818869; Facesoffungi number: FoF07245

Saprobic on *Dolichandrone spathacea*. Sexual morph: *Ascomata* 860 × 540 µm diam., superficial, subglobose or ovate, greenish, olivaceous to olivaceous grey in reflected light, ostiolate. *Peridium* composed of brown, angular or elongate hypha-like cells. Terminal hairs dark brown, irregular in length, 3–6.5 µm diam. near the base, dichotomously branched at wide to acute angles starting near the bases, verrucose. Thinner hairs similar to the terminal ones but longer or seta-like, aseptate, 350 µm length. Lateral hairs are shorter spines. *Asci* early deliquescent. *Ascospores* 5–7 × 3–5 µm ($\bar{x}$ = 6.0 × 4.0, n = 25), brown, ovate to broad ovate, smooth-walled. Asexual morph: Undetermined.

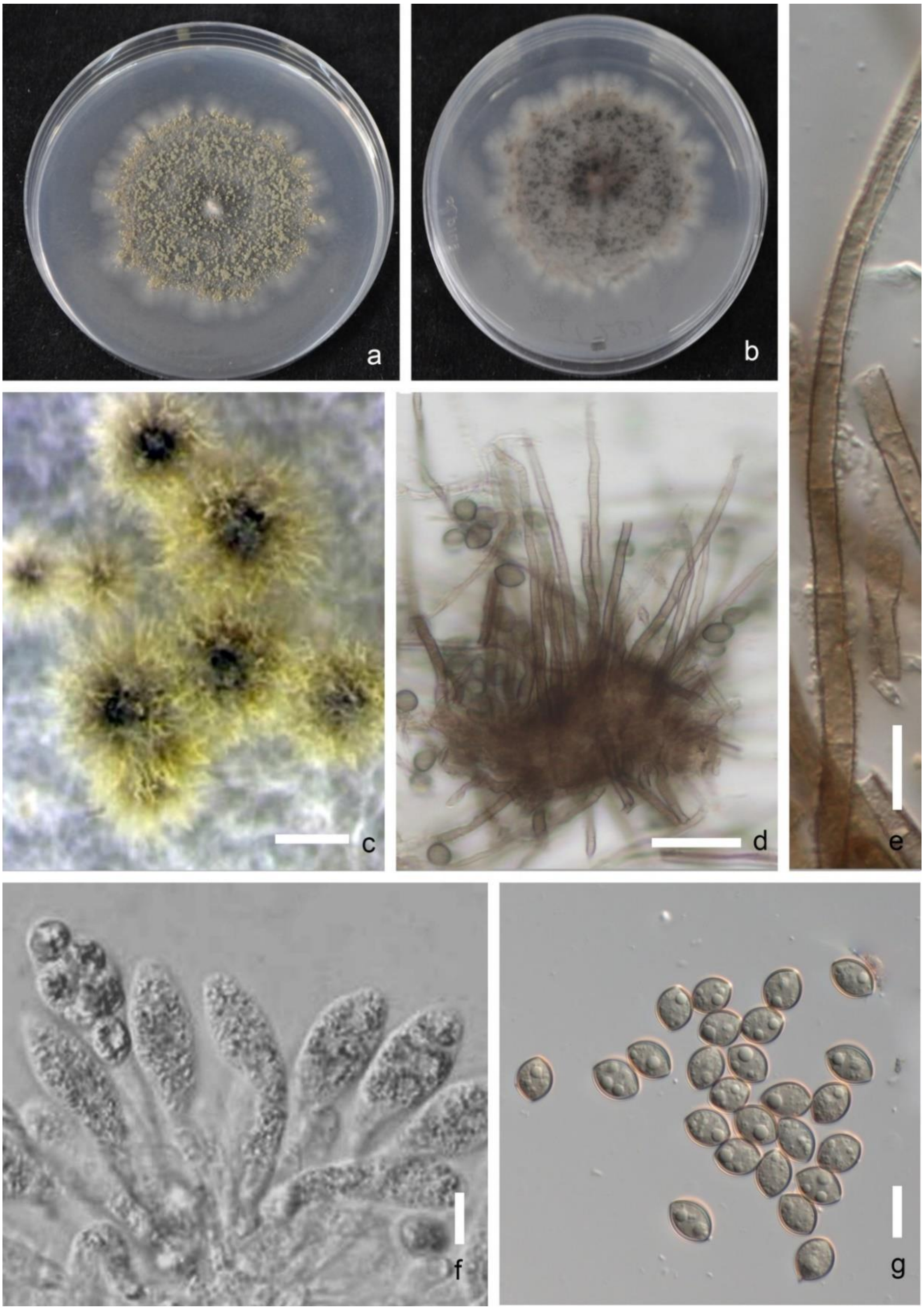

Fig. 69 – *Chaetomium globosum* (MFLU 18-1833, a new host record). a Upper view of 7-days old culture on PDA. b Reverse view of 7-days old culture on PDA. c Ascomata and ascospore masses on PDA. d Ascoma. e Terminal ascomatal hair. f Asci. g Ascospores. Scale bars: c = 500 µm, d = 100 µm, e–g = 5 µm.

Culture characteristics – Colonies on malt extract agar olivaceous with entire edge, about 53 mm diam. after 4 days of incubation at 28°C, pale yellow to pale luteus, sparse and floccose aerial hyphae, without coloured exudates; reverse honey colored.

Material examined – India, Andaman and Nicobar Islands, North Andaman, Diglipur, Near Sita Nagar (13˚11'14.2" N 92˚53'11" E), isolated on decaying twig of *Dolichandrone spathacea* (Bignoniaceae), 17 May 2018, M. Niranjan & V.V. Sarma PUFNI 18725 (AMH-10059), living culture NFCC-4521.

GenBank numbers – ITS: MK990280, LSU: MK981539.

Known distribution (based on molecular data) – India, China, UK (Wang et al. 2016)

Known hosts (based on molecular data) – *Clematis vitalba*, *Dolichandrone spathacea*, *Panax notoginseng* (Wang et al. 2016).

Notes – *Chaetomium ramosissimum* was introduced by Wang et al. (2014) and later transferred to *Dichotomopilus* as *D. ramosissimus* (Wang et al. 2016). *Dichotomopilus ramosissimus* is characterised by its superficial, sphaerical or ovate ascomata and peridial wall consisting of *textura intricata* or *epidermoidea* cell layers. Our collection shows similar morphology for ascomata to the type and also forms a yellow colony on malt extract agar. The ascospores are brown and ovate to limoniform. However, ascospores of our collection are slightly smaller (5.1–6.9 × 3–4.7 µm *vs* 5–7.5 × 4.5–5.5 × 3–4 µm) compared to the type (Wang et al. 2014).

Subclass Xylariomycetidae O.E. Erikss & Winka, Myconet 1, 12 (1997)
Order Amphisphaeriales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5, 177 (1986)
Sporocadaceae Corda, Icones fungorum hucusque cognitorum 5, 34 (1842)

Index Fungorum number: IF81408; Facesoffungi number: FoF06111

Sporocadaceae species occur on a wide range of hosts as saprobes, endophytes or pathogens (Nag Raj 1993, Liu et al. 2019, Hyde et al. 2020a). This genus consists of genera with acervular conidiomata that produce hyaline, pale or dark brown, septate, appendaged conidia (Nag Raj 1993, Jaklitsch et al. 2016, Maharachchikumbura et al. 2016, Liu et al. 2019). Liu et al. (2019) revised this family using morphology and multi-gene phylogeny to confirm the placement of 23 existing genera while establishing seven new genera. In Hyde et al. (2020a), *Annellolacinia* and *Doliomyces* were tentatively placed in Sporocadaceae based on morphological evidence, however, further studies using molecular data are required to confirm this placement. The placement of selected genera in Sporocadaceae is presented in Fig. 71.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, Studies in Mycology 79, 135 (2014)

Index Fungorum number: IF809759; Facesoffungi number: FoF06097

Maharachchikumbura et al. (2014) established *Neopestalotiopsis* based on conidial pigmentation, conidiophores and molecular phylogeny. These species occur as saprobes or pathogens or endophytes on various host plants (Guba 1961, Barr 1975, Nag Raj 1993, Maharachchikumbura et al. 2014, Norphanphoun et al. 2019). Fourty-three *Neopestalotiopsis* species are reported with morphology and sequences data (Hyde et al. 2020a).

Neopestalotiopsis rhizophorae Norphanphoun, T.C. Wen & K.D. Hyde, Mycosphere 10, 545 (2020) Fig. 72

Index Fungorum number: IF556437; Facesoffungi number: FoF05773

Isolated from leaf spots of *Rhizophora mucronata*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA releasing black conidia in a slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth and thin-walled, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (19–)19.5–25(–26.5) × (5.6–)6–8(–9) µm ($\bar{x}$ ± SD = 22.2 ± 1.9 × 7.2 ± 1.1 µm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)4–5(–5.7) µm long ($\bar{x}$ ± SD =

4 ± 0.8 µm); three median cells (12.4–)13–15(–16.1) µm long (x̅ ± SD = 15 ± 1.1 µm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (3.3–)4–5(–6) µm long (x̅ ± SD = 4.7 ± 0.7 µm); third cell brown, (3.3–)4–5(–6) µm long (x̅ ± SD = 4.8 ± 0.7 µm); fourth cell brown, (3.7–)4.5–5(–5.6) µm long (x̅ ± SD = 4.8 ± 0.6 µm); apical cell (2.8–)3–4(–5.2) µm long (x̅ ± SD = 4 ± 0.6 µm), hyaline, conic to acute; with 2–4 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (8.5–)11–29(–30) µm long (x̅ ± SD = 20 ± 6.9 µm); single basal appendage, tubular, unbranched, centric, (2.4–)3–11.5(–12) µm long (x̅ ± SD = 6.1 ± 2.8 µm).

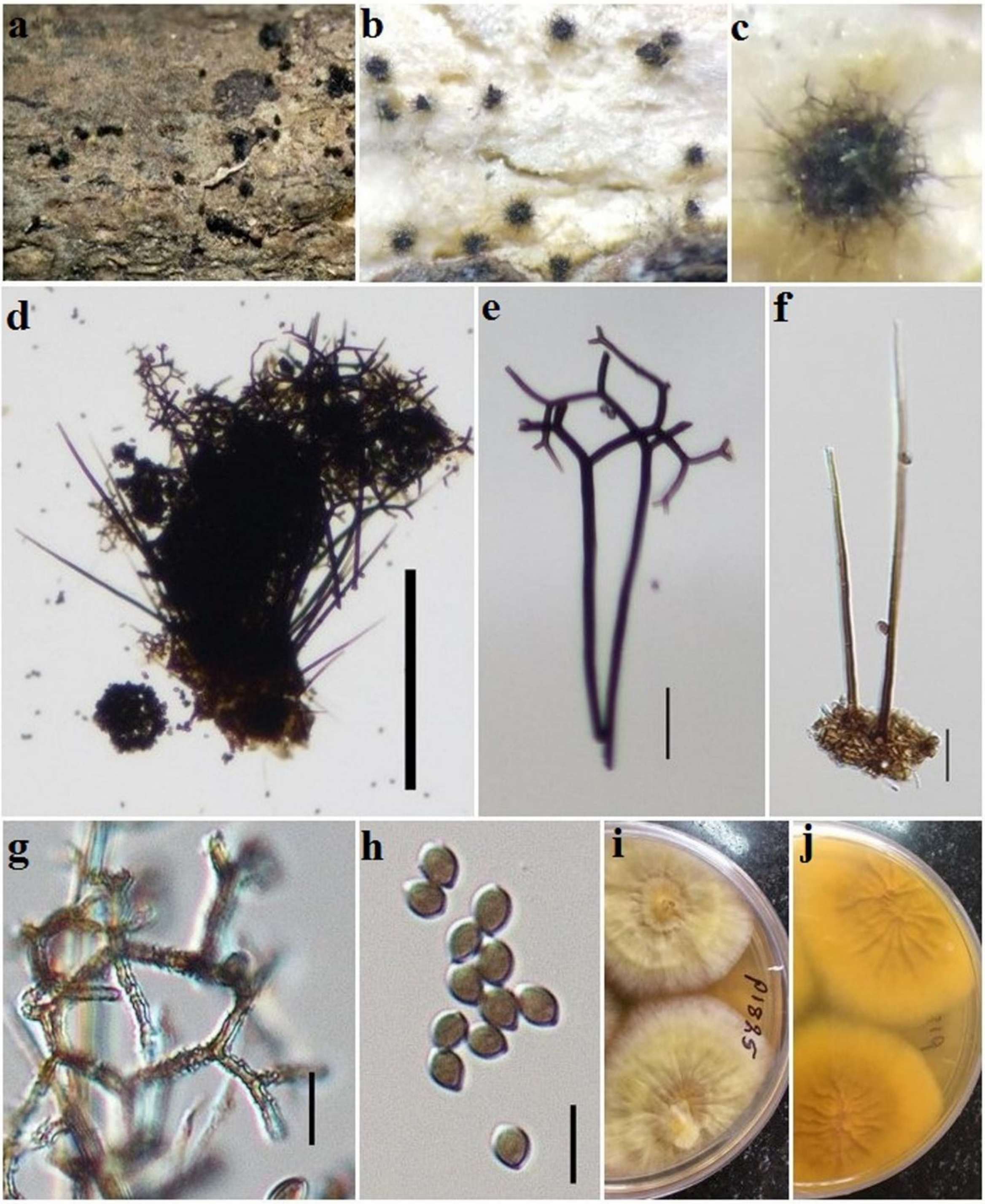

Fig. **70** – *Dichotomopilus ramosissimus* (AMH-10059, new host record). a–c Ascomata on host. d, e Mature ascomata on lacatophenol mount. f, g Terminal ascomatal hairs. h Ascospores. Scale bars: d = 200 µm, e = 100 µm, e, f = 20 µm, g, h = 10 µm.

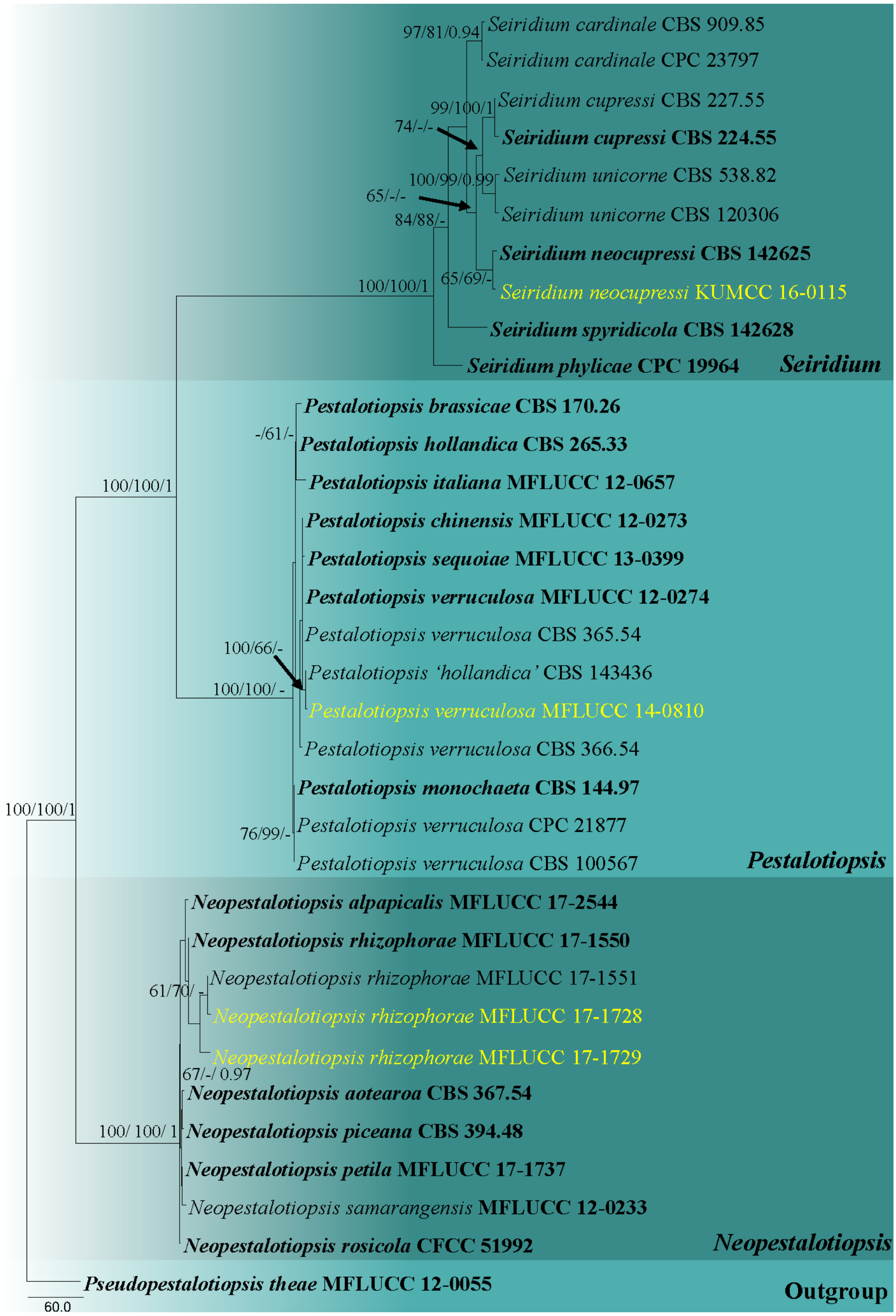

Fig. 71 – Phylogram generated from maximum parsimony (MP) analysis based on combined LSU, ITS, *β-TUB* and *TEF1-α* sequence data of taxa representing *Neopestalotiopsis*, *Pestalotiopsis* and *Seiridium* in Sporocadaceae. Thirty-four strains are included in the combined analyses which comprised 2960 characters (902 characters for LSU, 621 characters for ITS, 880 characters for *β-TUB*, 542 characters for *TEF1-α*) after alignment. The combined dataset contained 2222 constant, 146 parsimony uninformative and 592 parsimony informative characters. The tree topology of the maximum likelihood (ML) analysis and Bayesian analysis did not differ significantly from the maximum parsimony analysis. The best RaxML tree selected had a final likelihood value of -

9228.684058. Estimated statistics generated from MP analysis are as follows: TL = 1038, CI = 0.876, RI = 0.974, RC = 0.853, HI = 0.124. Evolutionary models HKY+I and GTR+G were applied to LSU and ITS gene regions respectively, while HKY+G model was applied to both *β-TUB* and *TEF1-α* genes. Bootstrap values for MP and ML analyses equal to or greater than 60 % and Bayesian posterior probabilities greater than 0.9 are given near the nodes, respectively. The tree is rooted with *Pseudopestalotiopsis theae* (MFLUCC 12-0055). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Culture characteristics – Colonies on PDA reaching 0.5-2 cm diameter after 7 days at room temperature (±25°C), colonies filamentous to circular, medium dense, aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy to fairy fluffy, white from above and below; fruiting bodies black; reverse similar in color.

Material examined – Thailand, Kor Chang, Trat Province, leaf spots of *Rhizophora mucronata* (Malpighiales), 27 April 2017, Norphanphoun C. KC23-1 (MFLU, dried culture), living culture, MFLUCC 17-1728; *ibid*. KC23-2 (MFLU, dried culture), living culture, MFLUCC 17-1729.

GenBank numbers – ITS: MN871770 (MFLUCC 17-1728), MN871771 (MFLUCC 17-1729); LSU: MN873006 (MFLUCC 17-1728), MN873007 (MFLUCC 17-1729); SSU: MN877440 (MFLUCC 17-1728), MN877441 (MFLUCC 17-1729); *TEF1-α*: MN871990 (MFLUCC 17-1728), MN871991 (MFLUCC 17-1729); *β-TUB*: MN871992 (MFLUCC 17-1728), MN871993 (MFLUCC 17-1729).

Known distribution (based on molecular data) – Thailand (Norphanphoun et al. 2019).

Known hosts (based on molecular data) – *Rhizophora mucronata* (Norphanphoun et al. 2019).

Notes – Based on multi-gene analyses and morphological characters, our isolate was identified as *Neopestalotiopsis rhizophorae* from leaf spots of *Rhizophora mucronata* in Thailand (Norphanphoun et al. 2019). Thus, these collections were considered as fresh collection of *N. rhizophorae*.

Pestalotiopsis Steyaert, Bulletin du Jardin Botanique de l'État à Bruxelles 19, 300 (1949)

Index Fungorum number: IF9272; Facesoffungi number: FoF00154

Pestalotiopsis is widely distributed, often occurring as pathogens, saprobes and endophytes (Maharachchikumbura et al. 2014, 2016, Wijayawardene et al. 2017). They have been reported from various terrestrial habitats, especially on crop plants, mangroves and as potential pathogens of humans (Maharachchikumbura et al. 2012, Norphanphoun et al. 2019, Farr & Rossman 2019). The genus established by Steyaert (1949) has over 350 species epithets listed in Index Fungorum (2020). The diversity, host distribution, morphology, and phylogenetic relationships of *Pestalotiopsis* species based on ITS, *β-TUB* and *TEF1-α* molecular data is well studied (Jeewon et al. 2002, Maharachchikumbura et al. 2011, 2012, 2013, 2014, Liu et al. 2019, Hyde et al. 2020a).

Pestalotiopsis verruculosa Maharachch. & K.D. Hyde, Fungal Diversity 56, 123 (2012)

Fig. 73

Index Fungorum number: IF800527, Facesoffungi number: FoF06983

Saprobic on dead cone of *Picea abies* appearing as rounded to elongated, slightly raised black lesions erupting through irregular slits on host surface tissue. Sexual morph: Undetermined. Asexual morph: *Conidiomata* semi-immersed to erumpent or partially erumpent, exuding brown to black conidial masses, acervulus, mostly oval to elongate, 175–250 µm in diam., solitary, black. *Conidiomata wall* indistinct, composed of light brown cells fusing with host tissue. *Conidiophores* not observed. *Conidiogenous cells* holoblastic, discrete or integrated, hyaline, smooth-walled, cylindrical to lageniform. *Conidia* broad fusiform, mostly straight, verruculose, occasionally slightly curved, 4-septate, slightly constricted at septa, 25.5–32 × 8.7–9.5 µm, ($\bar{x}$ = 30.5 × 9.2 µm, n = 40), basal cell obconic with a truncate base, colourless, smooth-walled, 4.5–5.5 µm long; three median cells 16–20 µm long, subcylindrical or doliiform, concolourous, brown to dark brown, second cell from base sometimes lighter, septa darker than the rest of the cell (second cell from base 6–8 µm long; third cell 6–8 µm long; third cell 6–8 µm); apical cell conic, hyaline, thin-walled, smooth, 3.6–4.5 µm long; with 4 or occasionally 3, tubular, unbranched, flexuous, apical appendages arising from the apical tip, 10–25.5 µm long, not knobbed; basal appendage single, unbranched, filiform, centric, up to 5.5–9.5 µm long.

Culture characteristics – Colonies on PDA reaching approximately 7 cm in diam. after 7 days at 16–18°C, greyish-white, round colony, with entire margins and reverse dark brown at the center becoming pale yellow towards the margins.

Material examined – Italy, Forlì-Cesena Province, Camposonaldo - Santa Sofia, on dead cone of *Picea abies* (Pinaceae), 6 May 2012, Erio Camporesi IT 309 (MFLU 15-0777), living culture MFLUCC 14-0810.

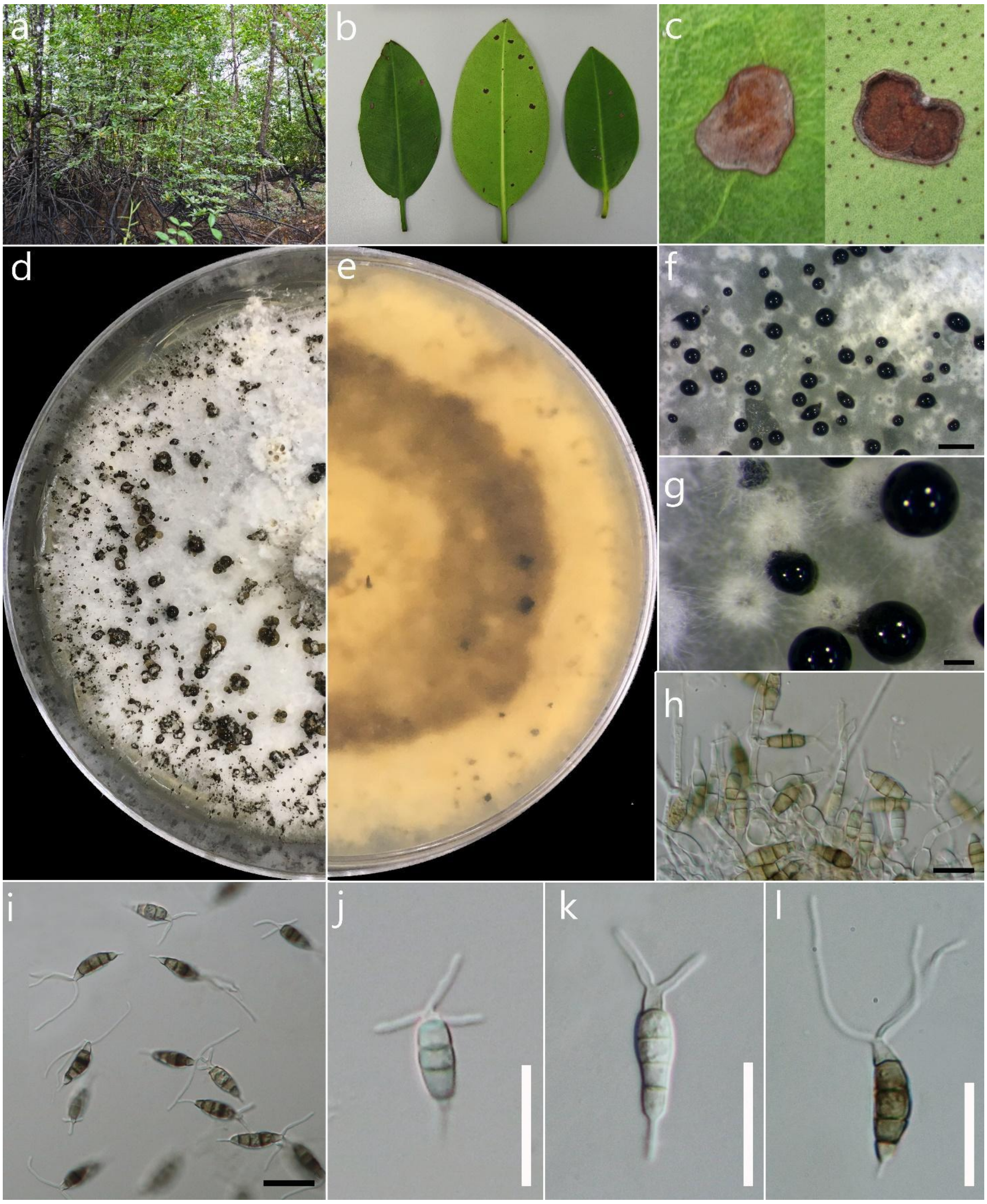

Fig. 72 – *Neopestalotiopsis rhizophorae* (MFLUCC 17-1728, MFLUCC 17-1729). a Collecting place. b, c Leaf spots of *Rhizophora mucronata*. d, e Culture on PDA (d-above, e-below). f–h

Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f = 200 µm, g = 1000 µm, h = 500 µm, i–p = 20 µm.

GenBank submissions – ITS: MN733174.

Known distribution (based on molecular data) – China (Maharachchikumbura et al. 2012), Italy (this study).

Known hosts (based on molecular data) – *Picea abies* (this study), *Rhododendron* sp. (Maharachchikumbura et al. 2012).

Notes – *Pestalotiopsis verruculosa* was introduced as an endophyte by Maharachchikumbura et al. (2012) from living leaves of *Rhododendron* species. It was distinguished from other related taxa in having larger conidia (28–35 × 9–11 µm) and 3–4, but longer apical appendages (25–40 µm). Our strain had similar conidial dimensions (25.5–32 × 8.7–9.5 µm), but shorter appendages (10–25.5 µm). *Pestalotiopsis verruculosa* also shares similar morphological characters with *P. hollandica* in having 25.5–33 × 8.5–10 µm (Maharachchikumbura et al. 2014) sized conidia bearing 1–4 appendages. In their recent study of Sporocadaceae and phylogenetic analysis of *Pestalotiopsis*, Liu et al. (2019) suggested the species *P. brassicae*, *P. hollandica*, *P. italiana*, *P. monochaeta*, *P. sequoiae* and *P. verruculosa* may be synonymous, however, additional genes are necessary to resolve this. Our phylogenetic analysis presents results similar to Liu et al. (2019). Based on the morphological comparisons and that our isolate grouped with the type strain of *P. verruculosa* (MFLUCC 12-0274), we identified our strain as *P. verruculosa*.

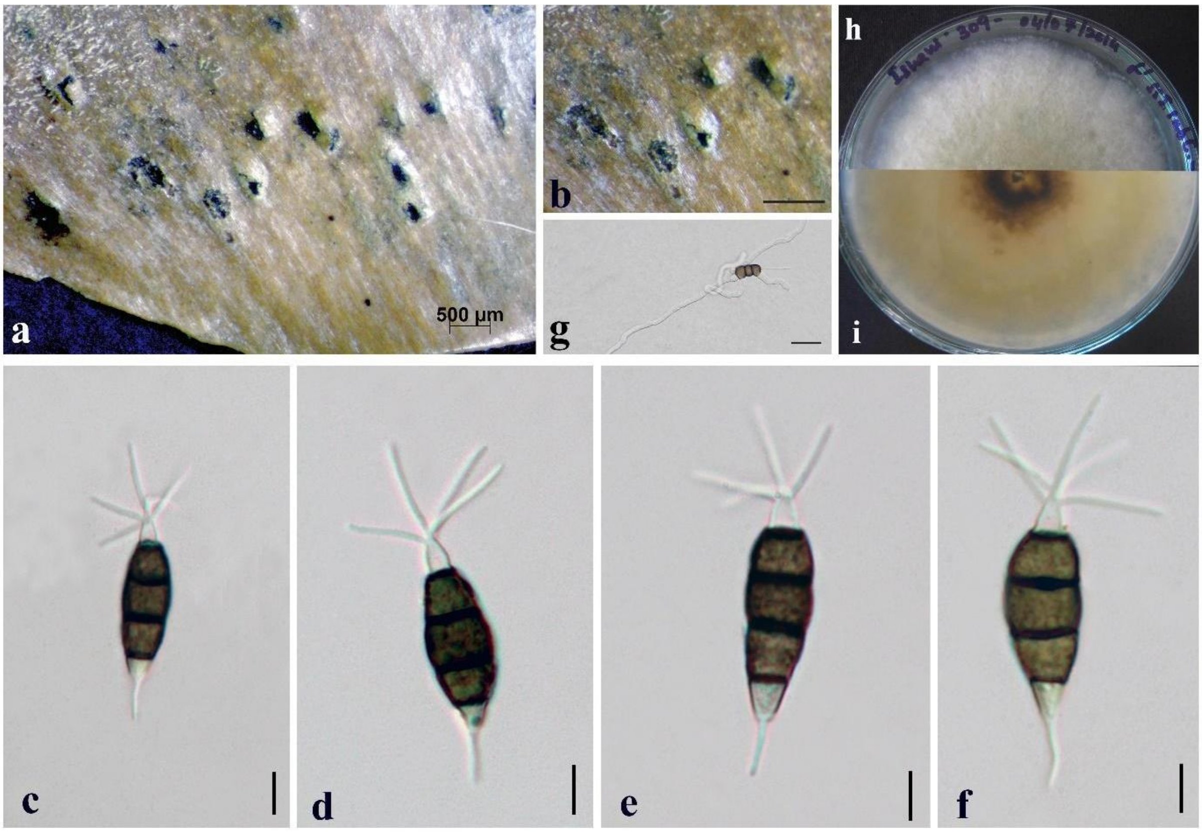

Fig. 73 – *Pestalotiopsis verruculosa* (MFLU 15-0777, a new host and geographical record). a, b Appearance of conidiomata on the host. c–f Conidia. g A germinating conidium. h, i Culture on PDA (h: from the above, i: reverse view). Scale bars: a, b = 500 µm, c–f = 10 µm, g = 50 µm.

Seiridium Nees, System der Pilze und Schwämme, 22 (1817)

Index Fungorum number: IF9868; Facesoffungi number: FoF01696

Seiridium, introduced by Nees (1817) is a widespread genus occurring on various terrestrial hosts as saprobes or pathogens (Tsopelas et al. 2007). The coelomycetous asexual morph produces

6-celled conidia (Jeewon 2003, Maharachchikumbura et al. 2014), while the sexual morphs have been identified as *Blogiascospora* and *Lepteutypa* (Nag Raj & Kendrick 1985, Senanayake et al. 2015). *Blogiascospora marginata* was confirmed to be the sexual morph of the type species *Seiridium marginatum* based on molecular data (Jaklitsch et al. 2016).

Seiridium neocupressi G. Bonthond, M. Sand.-Den. & P.W. Crous, Persoonia 40, 110 (2017)

Fig. 74

Index Fungorum number: IF823299; Facesoffungi number: FoF09147

Saprobic on dead land cone of *Picea abies*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* acervulus, pycnidial to sporodochial, 100–275 µm wide, mostly solitary, immersed, unilocular, conic or subglobose with flattened base, dark brown to black. *Conidiomata wall* comprising 3–5 layers of thin-walled cells of *textura angularis*, sometimes fusing at the base into the host tissue. *Conidiophores* septate, cylindrical, 10–70 µm long, occasionally branched, hyaline or pale brown, thin-walled. *Conidiogenous cells* annellidic, discrete, hyaline, cylindrical, smooth- and thin-walled, proliferating percurrently, with visible collarettes and minute periclinal thickenings. *Conidia* 22–28 × 7–9 µm ($\bar{x}$ = 26 × 8 µm), lunate to falcate, curved, 5-septate, rarely 4- or 6-septate, not striate, occasionally a short apical appendage present, euseptate with no visible pores, basal cell obconic with a truncate base, hyaline, walls smooth, 3.5–4 µm; four median cells, smooth, cylindrical to doliiform, brown to dark brown, and septa darker than the rest of the cells, second cell from base 5–6 µm long, third cell 5–6 µm long, fourth cell 5–6 µm long, fifth cell 4.5–5.5 µm long, apical cell conical, hyaline, smooth, 3.5–4 µm long.

Culture characteristics – Colonies on PDA reaching approximately 5 cm in diam. after 7 days at 16–18°C, circular, raised, with a filamentous margin, greyish-white at the center, then dark grey, white at the edge, reverse, greyish-white.

Material examined – Italy, Forli-Cesena Province, near Camposonaldo - Santa Sofia, on dead and land cone of *Picea abies* (Pinaceae), 15 April 2015, Erio Camporesi IT2444 (MFLU 15-0813), living culture KUMCC 16-0115.

GenBank numbers – ITS: MN848165, LSU: MN848234, SSU: MN848240.

Known distribution (based on molecular data) – Australia, Italy, New Zealand (Bonthond et al. 2018).

Known hosts (based on molecular data) – *Cupressus leylandii*, *C. macrocarpa*, *C. sempervirens* (Bonthond et al. 2018), *Picea abies* (this study).

Notes – In the phylogenetic analysis, our isolate KUMCC 16-0115 clustered with the type strain of *Seiridium neocupressi* CBS 142625. *Seiridium neocupressi* was introduced as a species phylogenetically and morphologically distinct from *S. cupressi* (Bonthond et al. 2018). The species described (from culture) by Bonthond et al. (2018) has larger conidia (26.5–31 × 8.5–10 µm) compared to our specimen illustrated here (22–28 × 7–9 µm). The morphological features of the conidiophores, conidiogenous cells, conidial septation and shape are similar in both collections. However, we did not observe any basal appendages attached to the conidia in our collection. *Seiridium neocupressi* is mostly recorded from *Cupressus* sp. while our collection from Italy is on *Picea abies*. This is the first record of a *Seiridium* species from this host.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis 8, 66 (1932)

Hypoxylaceae DC., Flore française 2, 280 (1805)

Index Fungorum number: IF81885; Facesoffungi number: FoF02979

Hypoxylaceae was validated by Wendt et al. (2018) in Xylariales based on multi-locus phylogeny, morphology and chemotaxonomy studies. Hyde et al. (2020a) accepted 18 genera in Hypoxylaceae. Hypoxylaceae is a diverse family which mainly consists of saprobes and endophytes. Moreover, this family is subjected to many investigations on secondary metabolites among all other families in the Xylariomycetidae. Recently, Wibberg et al. (2020) provided the first genome-based comparisons using 13 representatives of this family. An updated phylogeny for *Daldinia* and *Hypomontagnella* are provided in Fig. 75.

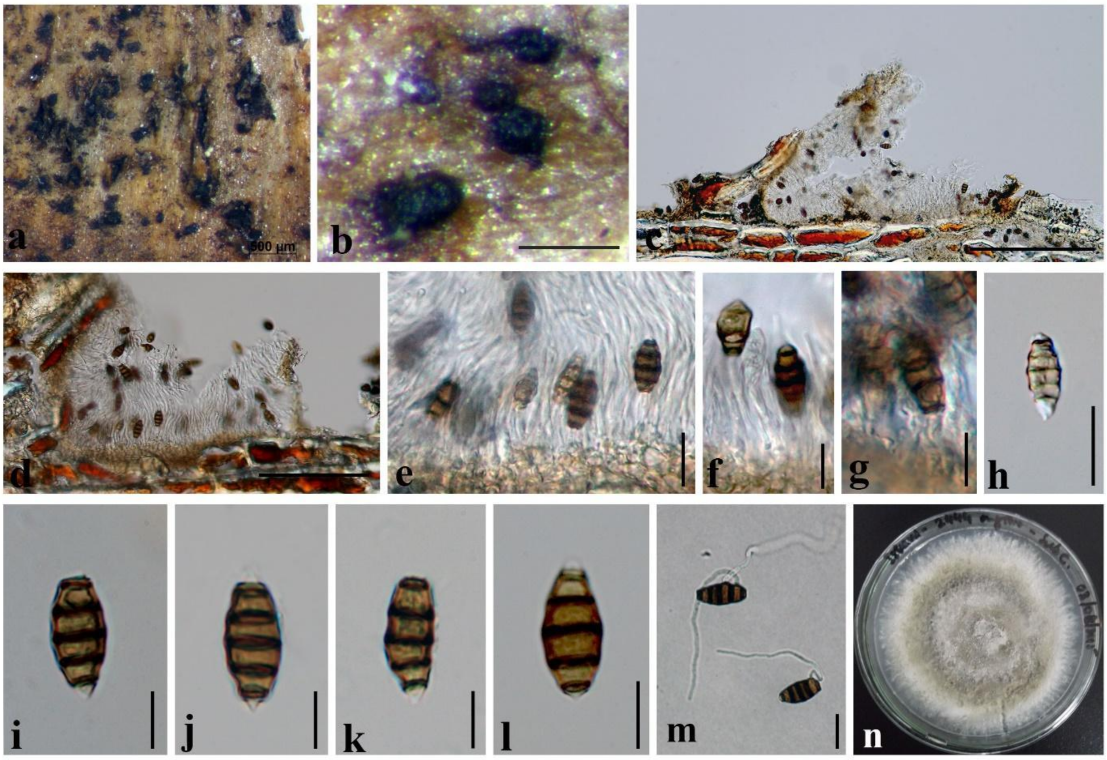

Fig. **74** – *Seiridium neocupressi* (MFLU 15-0813, new host record). a Conidiomata on host. b Close up of conidiomata. c, d Section of conidioma. e–g Conidiophores with conidia. h–l Conidia. m Germinating conidia. n Culture on PDA. Scale bars: b = 200 µm, c, d = 150 µm, e, m = 50 µm, f–h = 20 µm, i–l = 15 µm.

Daldinia Ces. & De Not., Commentario della Società Crittogamologica Italiana 1, 197 (1863)

Index Fungorum number: IF1408; Facesoffungi number: FoF02988

Daldinia described by Cesati & De Notaris (1863), is known for its most common macro ascomycetous fungi. They are found as saprobes and endophytes and distributed in various hosts including marine sponge (Stadler et al. 2014, Liao et al. 2019, Wang et al. 2019b, Sibero et al. 2020). Stadler et al. (2014) introduced many new species and accepted *Daldinia* as a member of Xylariaceae. Later, this was transferred to Hypoxylaceae due to its similarities with *Hypoxylon*. Most *Daldinia* species are characterized by their well-defined concentric zones in the stromata interior (Stadler et al. 2014). In the subsequent studies, several new species and combinations such as *Daldinia korfii*, *Daldinia subvernicosa* and *Daldinia kretzschmarioides* were added to this genus (Sir et al. 2016a, Wongkanoun et al. 2019). Fifty species are accepted for *Daldinia* (Wijayawardene et al. 2017, Samarakoon et al. 2019b). Multi-gene phylogeny studies revealed that the *Daldinia* comprises two well-supported clades within the family (Daranagama et al. 2018, Wendt et al. 2018, Samarakoon et al. 2020c). The present paper includes the description, photo plate and phylogeny of *Daldinia eschscholtzii* on *Tamarindus indica* as a new host record (Figs. 75, 76, 77).

Daldinia eschscholtzii (Ehrenb.) Rehm, Annales mycologici 2, 175 (1904) Figs. 76, 77

Index Fungorum number: IF544992; Facesoffungi number: FoF02990

Saprobic on *Tamarindus indica*. Sexual morph: *Ascostromata* 4 cm wide superficial, placentiform, superficial extracts give purple pigments in 10% KOH, interperithecial brown spongy tissue, column, ostiolated neck, narrow towards down. *Peridium wall* 13.8 µm wide, with brown to hyaline, *textura epidermoidea* and *angularis* cell layers. *Paraphyses* 3.4 µm wide, septate, branched, long, sparely present. *Asci* 139–176 × 7.5–12 µm ($\bar{x}$ = 161.9× 9.7 µm, n = 25), 8–spored, unitunicate, cylindrical, tapering below towards pedicel with a J+ apical ring, smooth-walled, long pedicellate, persistent. *Ascospores* 11–13 × 6–8 µm ($\bar{x}$ = 12 × 7.2 µm, n = 25), hyaline to brown and dirty brown at maturity, ovoid, straight germslit, obtuse ends, bilateral asymmetry, with a single guttule, and dehiscing perispore, smooth-walled. Asexual morph: Colonies on MEA, *Conidiogenous cells* 13–19 × 3 µm (x̄ = 15.3 µm, n = 25), polyblastic, cylindrical, narrow apex. *Conidia* 5.2–7.4 × 2.5–3.8 µm (x̄ = 6 × 3.1 µm, n = 25), hyaline, obovoid, blunt ended, smooth-walled.

Culture characteristics – Colonies on MEA, brown, laterally white edged, raised at centre, filamentous, reverse black at the centre, white towards edges, producing conidia.

Material examined – India, Andaman and Nicobar Islands, South Andaman, Manjery, Near Amber Sunset Point (11˚51'68.6"N 92˚65'38.8"E), on *Tamarindus indica* (Leguminosae), 10 December 2017, M. Niranjan PUFNI 1761 (AMH-10066), living culture NFCC 4365.

GenBank numbers – ITS: MK990277, LSU: MK981541.

Known distribution (based on molecular data) – Brazil, France, Germany, India, Indonesia, Mexico, Papua New Guinea, South Africa, Thailand, USA, Western Samoa (Samarakoon et al. 2019).

Known hosts (based on molecular data) – *Ficus* sp., *Musa* sp., *Tamarindus indica*, *Bucida palustris*, *Sizygium jambos*, *Eucalyptus alba*, *Sizygium jambos*, *Bucida palustris*, *Citrus* sp. *Jambosa vulgaris*, *Mangifera indica*, *Neohypodiscus cerebrinus*, *Cordia sebastina*, *Pogostemon cablin*, *Brguiera sexangula*, *Cocos nucifera*, *Excoecaria agallocha*, *Dendrobium officinale*, *Gliricidia sepium* and also found on *Xestospongia* sponge species (Samarakoon et al. 2019).

Notes – *Daldinia eschscholtzii* is a saprobic and endophytic with a wide range of agricultural and native plants. Stromata can be found on both angiosperm and gymnosperm wooden logs, but mostly on dicotyledonous wood (Yuyama et al. 2013, Stadler et al. 2014). *Daldinia eschscholtzii* of our collection has smaller stromata, and smaller asci and ascospores (Fig. 76), when compared to the type (Stadler et al. 2014). The nodulisporium-like anamorph also has been found in culture (Fig. 77). The present collection is a new record to Andaman and Nicobar Islands.

Hypomontagnella Sir, L. Wendt & C. Lambert, Mycological Progress 18, 190 (2018)

Index Fungorum number: IF827251; Facesoffungi number: FoF06136

Lambert et al. (2019) recently erected this genus typified by *Hypomontagnella monticulosa* to accommodate several species previously belonging to *Hypoxylon*. *Hypomontagnella* differs from *Annulohypoxylon* and *Jackrogersella* by having smooth perispores or with transversally striate ornamentations, and it differs from *Hypoxylon* by having woody to carbonaceous stromata lacking colored granules, papillate ostioles usually with a black annulate disc, and without apparent KOH-extractable pigments in mature stromata (Lambert et al. 2019).

Hypomontagnella monticulosa (Mont.) Sir, L. Wendt & C. Lambert, Mycological Progress 18, 190 (2018) Fig. 78

Index Fungorum number: IF827252; Facesoffungi number: FoF06781

Saprobic on dead branch of *Leucaena leucocephala*. Sexual morph: *Stromata* effused-pulvinate, with conspicuous to inconspicuous perithecial mounds, surface blackish, woody to carbonaceous tissue immediately beneath surface and between perithecia surface and perithecia, have KOH-extractable light purple pigments. *Perithecia* sphaerical to obovoid, ostioles higher than the stromatal surface. *Asci* 85–110 × 4.5–6.5 µm (x̄ = 97.5 × 5.4 µm, n = 25), 8-spored, cylindrical, with J+, discoid apical ring. *Ascospores* 7.5–9.3 × 3–4.5 µm (x̄ = 8.3 × 3.7 µm, n = 30), light brown to brown, unicellular, ellipsoid-inequilateral, with broadly to less frequently narrowly rounded ends, with straight germ slit spore-length on convex side; perispore eventually dehiscent in 10% KOH, epispore smooth. Asexual morph: hyphomycetous. *Conidiophores* in culture, mononematous, hyaline to olivaceous green or pale brown, roughened, usually with virgariella-like branching patterns. *Conidiogenous cells* 16.5–24 × 1.4–2.2 µm (x̄ = 20.1 × 1.8 µm, n = 20), polyblastic, sympodial, terminal, later becoming intercalary, finely denticulate, hyaline, smooth to finely roughened. *Conidia* 3–4.7 × 2–3 µm (x̄ = 3.9 × 2.5 µm, n = 25), ellipsoid, hyaline, smooth to finely roughened.

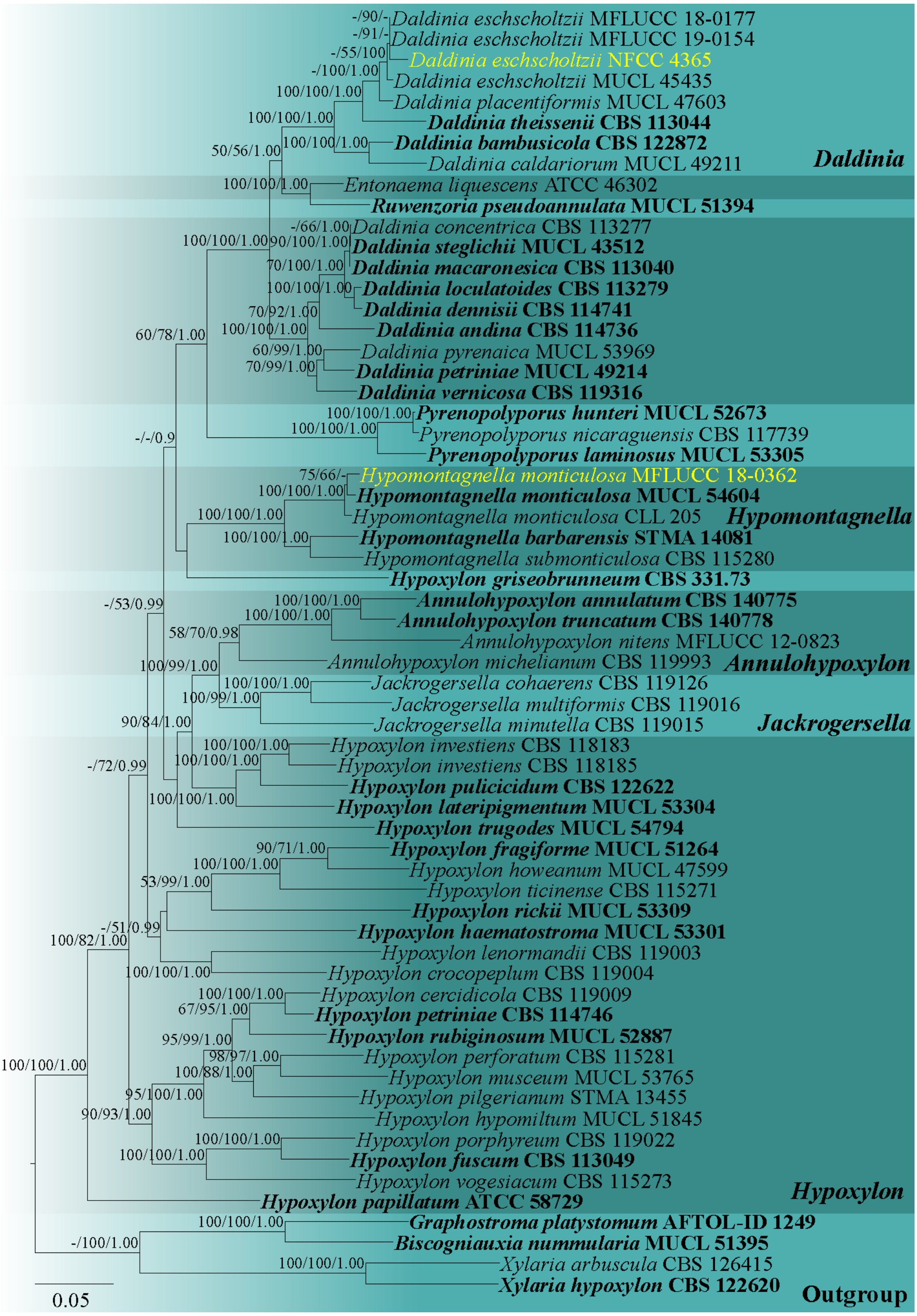

Fig. 75 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *RPB2* and *β-TUB* sequence data. Sixty-two strains are included in the combined analyses which comprised 3308 characters (774 characters for LSU, 636 characters for ITS, 809 characters for *RPB2*, 1089 characters for *β-TUB*) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian and maximum parsimony analyses. The best RaxML tree with a final likelihood value of -44932.107407 is presented. Estimated base frequencies were as follows: A = 0.234916, C = 0.260346, G = 0.264151, T = 0.240587; substitution rates AC = 1.374545, AG = 4.732739, AT = 1.502310, CG = 1.084367, CT = 7.435616, GT = 1.000000; gamma distribution shape parameter α = 0.822675. The

GTR+G+I evolutionary model was used for all the gene regions. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Xylaria arbuscula* (CBS 126415) and *X. hypoxylon* (CBS 122620). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

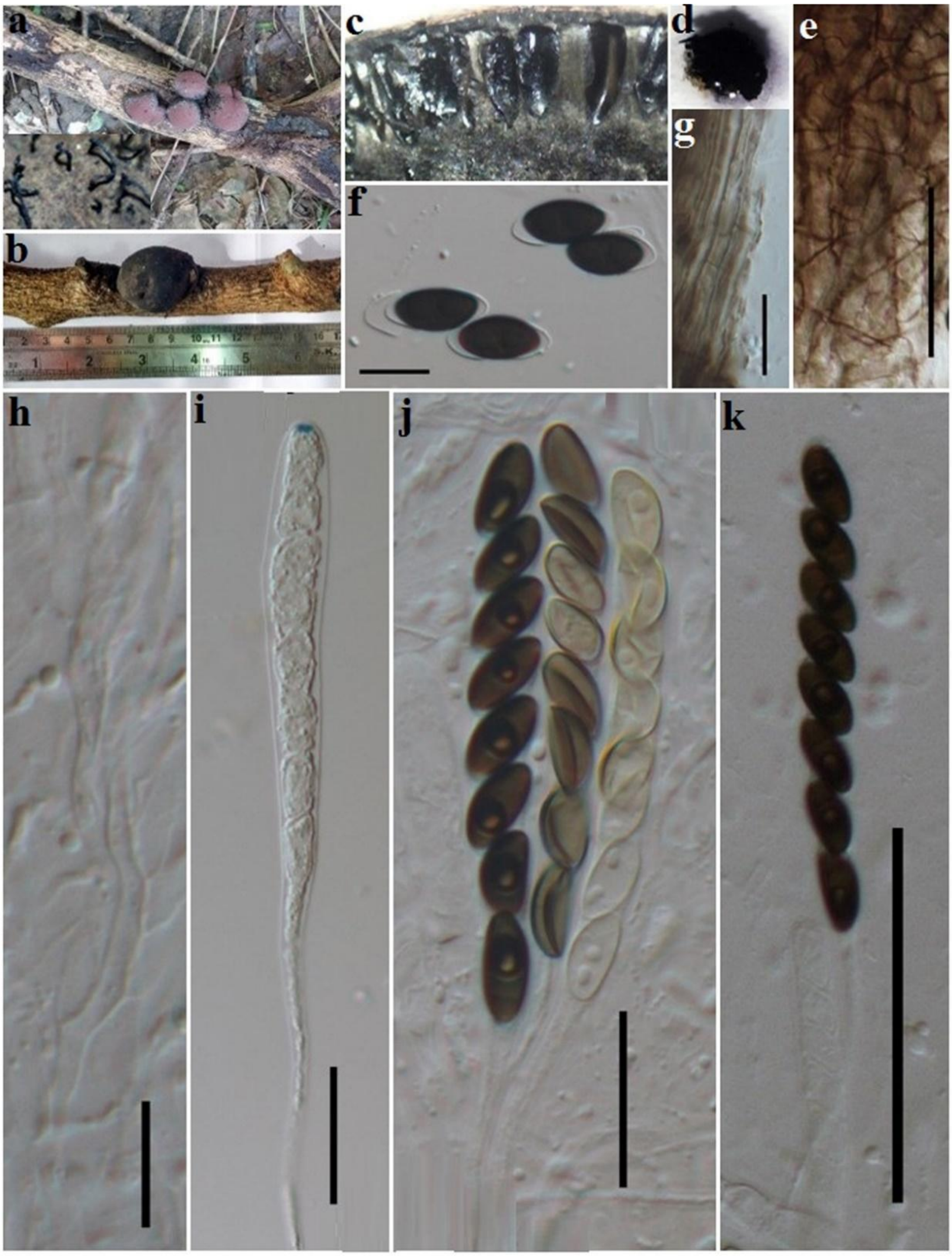

Fig. **76** – Sexual morph of *Daldinia eschscholtzii* (NFCC 4365, a new host and geographical record). a, b Stromata on decaying host. c Vertical section of stroma. f Ascospores. d Purple pigments in 10% KOH. e *Textura angularis* cells. g *Textura oblita* cells. h Paraphyses. i–k Asci. Scale bars: e, k = 50 µm, g–j = 20 µm. f, g = 10 µm.

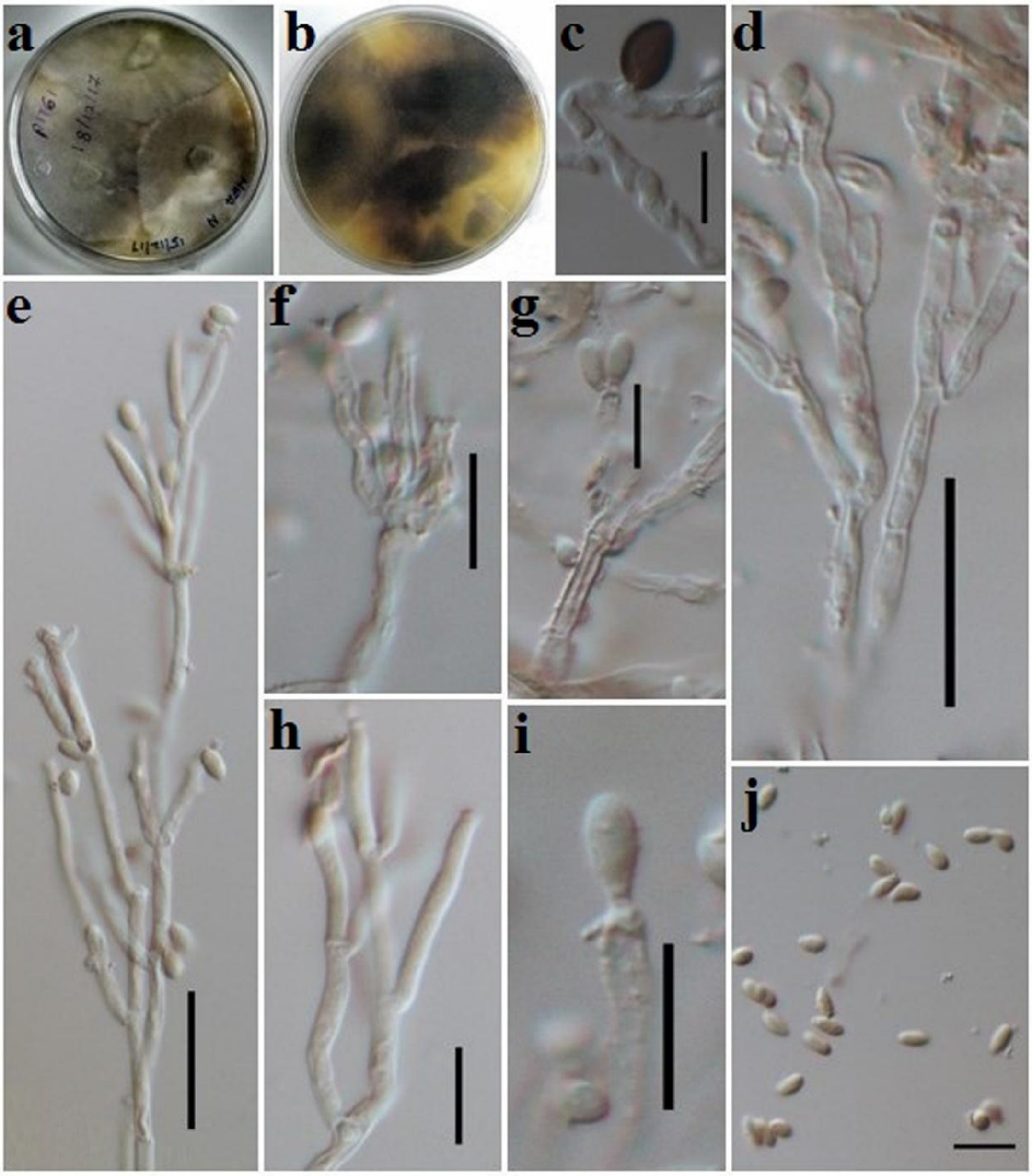

Fig. **77** – Asexual morph of *Daldinia eschscholtzii* (NFCC 4365, a new host and geographical record). a, b Culture in MEA plate. c Germinating spore. d–i Conidiophores. j Conidia. Scale bars: d–e = 20 µm. c, f–j = 10 µm.

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

Material examined – Thailand, Naan, dead branch of *Leucaena leucocephala* (Fabaceae), 4 August 2017, MC. Samarakoon SAMC007 (MFLU 18–0822, HKAS 102355), living culture MFLUCC 18–0362.

GenBank number – ITS: MN337231, LSU: MN336235, *RPB2*: MN366246, *β-TUB*: MN509783.

Known distribution (based on molecular data) – Argentina (Sir et al. 2016b), Brazil, French Guiana (Wendt et al. 2018), French Polynesia (Lambert et al. 2019), Indonesia, Malaysia (Zainee et al. 2018), South Korea, Thailand (Okane et al. 2008, Daranagama et al. 2015, this study), USA (Stadler et al. 2008, U'Ren et al. 2016).

Known hosts (based on molecular data) – *Cladonia leporina* (U'Ren et al. 2016), *Euterpe precatoria*, *Leucaena leucocephala* (this study). Lichen, Sargassum seaweed (Zainee et al. 2018), *Zingiber griffithii*.

Notes – This species has a circumtropical distribution and is frequently encountered in the rainforests of Africa, Asia and Latin America. Our specimen shares the characteristic features of stromata with conical papillate ostioles, encircled by superficial black discs that are typical of the genus and the microscopic features are in agreement with *Hypomontagnella monticulosa*. The comparisons of the base pairs of ITS show 0.7 % differences (4/555 bp) and both *RPB*2 and *β-TUB* are also highly similar. In our ITS, LSU, *RPB2* and *β-TUB* based combined analyses reveal that our strain clusters with *H. monticulosa* (MUCL 54604) with high statistical support (100% ML). Surup et al. (2014) described *H. monticulosa* from Thailand and this is the first known record of the occurrence of *H. monticulosa* on *Leucaena leucocephala*.

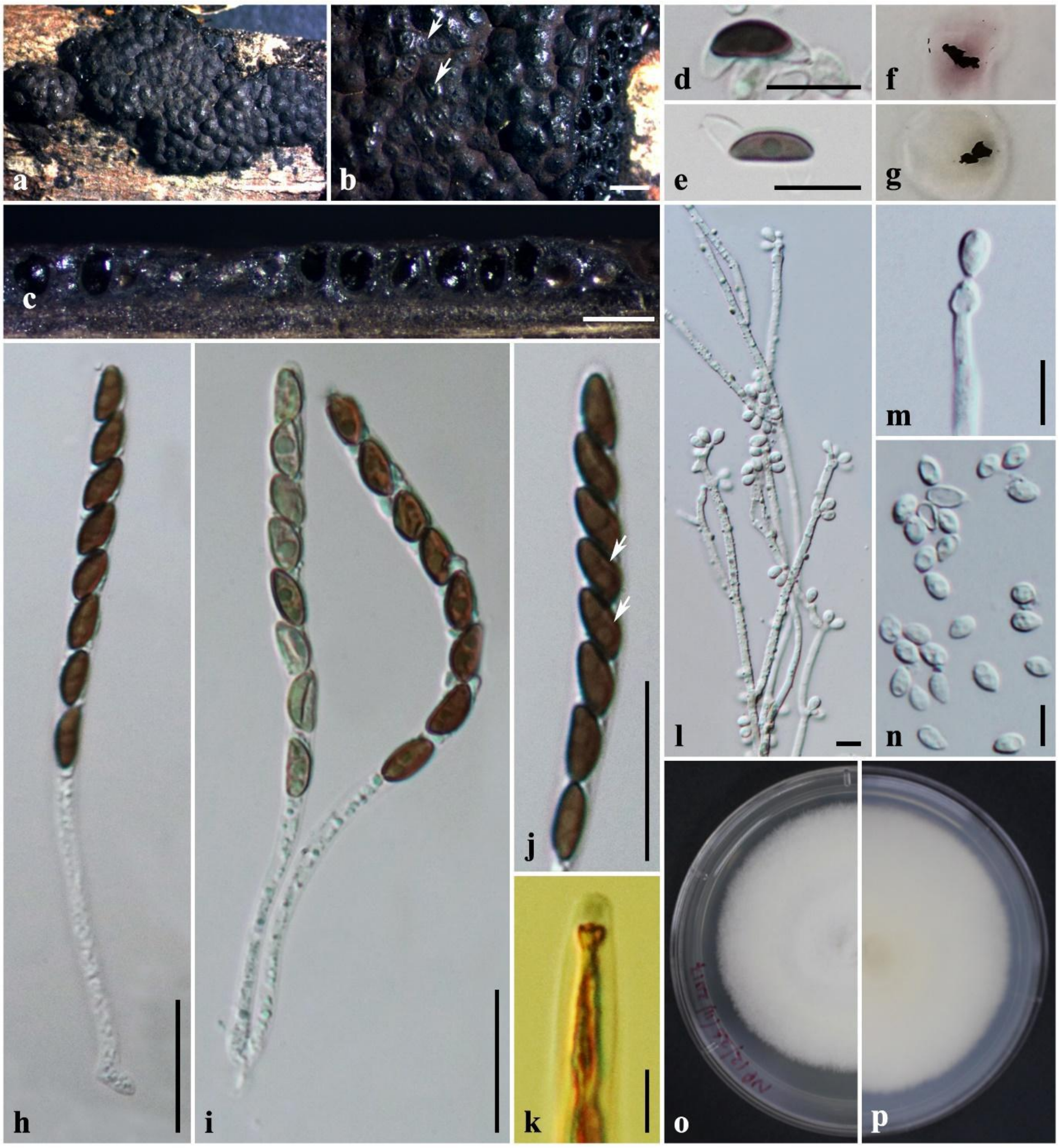

Fig. 78 – *Hypomontagnella monticulosa* (MFLU 18-0822, new host record). a Mature stroma on bark. b Stromatal surface showing papillate and ostiolar discs (indicated by white arrows). c Stromata in vertical section. d, e Perispores. f, g KOH-extractable pigments. h, i Asci. j Ascospores (sigmoid germ slits indicated by white arrows). k Ascus tip in Lugol's reagent. l–n Conidiophores

and conidia. o Surface of colony p Reverse of colony. Scale bars: a = 2 mm, b, c = 500 µm, h–j = 20 µm, d, e = 10 µm, l–n = 5 µm.

Lopadostomataceae Daranag. & K.D. Hyde, Fungal Diversity 73, 129 (2015)

Index Fungorum number: IF91005; Facesoffungi number: FoF00071

Lopadostomataceae was introduced by Senanayake et al. (2015) in Xylariales to accommodate *Creosphaeria* and *Lopadostoma*. In earlier considerations, *Creosphaeria* and *Lopadostoma* had coelomycetous, representatives of libertella-like asexual morphs and were treated as basal clade to Xylariaceae (Tang et al. 2009). At present, the family consists of *Creosphaeria*, *Jumillera*, *Lopadostoma* and *Whalleya* (Hyde et al. 2020).

Lopadostoma (Nitschke) Traverso, Flora Italica Cryptogama. Pars 1: Fungi. Pyrenomycetae. Xylariaceae, Valsaceae, Ceratostomataceae 1, 169 (1906)

Index Fungorum number: IF2925; Facesoffungi number: FoF00706

Lopadostoma is typified by *Lopadostoma turgidum* and consists of 12 accepted species from Europe (Jaklitsch et al. 2014). *Lopadostoma* species are saprobes which produce pseudostromatic sexual morphs and libertella-like asexual morphs. The species delimitation of *Lopadostoma* is provided in low resolution using ITS and LSU, however, incorporating protein-coding regions in the phylogeny together with secondary metabolites are important (Jaklitsch et al. 2014, Daranagama et al. 2016). An updated phylogeny for the genus is provided in Fig. 79.

Lopadostoma gastrinum (Fr.) Traverso, Flora Italica Cryptogama. Pars 1: Fungi. Pyrenomycetae. Xylariaceae, Valsaceae, Ceratostomataceae 1, 169 (1906) Fig. 80

Index Fungorum number: IF241129; Facesoffungi number: FoF06782

Saprobic on dead land branch of *Quercus* sp. Sexual morph: *Stromata* 0.7–2.2 × 0.3–1.1 mm, effuse-pulvinate, immersed in the host and erumpent from bark, bluntly conical, surrounded by a narrow, black, carbonized encasement, appearing as a black line, ectostromatic disc visible as a clypeus and surrounded by reddish brown bark surface, convex, raised, dark grey, entostroma dark, usually black, multi-peritheciate. *Ostiole* papillate with inconspicuous ostiolar openings, necks white or pale brown. *Perithecia* 0.3–1.1 mm diam., clustered in valsoid groups, monodistichous, subglobose to flask-shaped, at the periphery inclined toward the center, tissue between perithecia loosely arranged, composed of white fungal tissue, mixed with light coloured bark cells, tissue beneath the perithecia compact, black, with short convergent ostiolar necks. *Paraphyses* of two types, 1.4–2.4 µm ($\bar{x}$ = 1.9 µm, n = 20) wide, long, numerous, cylindrical, aseptate, smooth, guttulate and 1.9–3.9 µm ($\bar{x}$ = 3 µm, n = 20) wide, septate, constricted at septum, rarely branched, smooth. *Asci* 82.8–116.5 × 5.1–7.2 µm ($\bar{x}$ = 101.1 × 6.1 µm, n = 25), unitunicate, 8-spored, cylindrical, pedicellate, ellipsoidal-discoid, with a J+, apical ring. *Ascospores* 9.3–12.9 × 4.4–5.7 µm ($\bar{x}$ = 11.2 × 4.8 µm, n = 30), L/W 2.3, uniseriate, at first hyaline, turning pale brown and dark brown at maturity, oblong to narrowly ellipsoid, symmetrical to slightly inequilateral, unicellular, smooth-walled, with a straight germ slit across the entire spore length present, when immature with 2 large guttules. Asexual morph: Undetermined.

Material examined – Italy, Province of Forlì-Cesena [FC], Monte Mirabello - Predappio, on dead fallen branch of *Quercus* sp. (Fagaceae), 12 April 2017, Erio Camporesi IT3269C (MFLU 17-0941, HKAS 102310).

GenBank numbers – ITS: MN337229, LSU: MN336233, *RPB2*: MN366245.

Known distribution (based on molecular data) – Austria, France, Greece, Poland, Spain, Italy (Jaklitsch et al. 2014, this study).

Known hosts (based on molecular data) – *Acer campestre*, *Carpinus betulus*, *Prunus padus*, *Quercus* sp., *Ulmus glabra* and *U. minor* (Jaklitsch et al. 2014, this study).

Notes – Jaklitsch et al. (2014) revised the genus *Lopadostoma* with a neotype for *L. gastrinum*. In the identification key provided by Jaklitsch et al. (2014), *L. gastrinum* on *Ulmus* and other hosts were emphasized, but not on *Fagus* or *Quercus*. However, in this study, we found *L.*

gastrinum on a dead fallen branch of *Quercus* sp. from Italy. The type species described in Jaklitsch et al. (2014) is similar in morphology and phylogeny to the specimen described in this study. Size and shape of asci and ascospores of MFLU 17-0941 (asci 101.1 × 6.1 µm, ascospores 11.2 × 4.8 µm, L/W 2.3) overlap in the range of WU 32046 (neotype) (asci 88–110 × 6.5–8 µm, ascospores 10.5–12.8 × 4.5–5.5 µm, L/W 2–2.7). These morphological comparisons are more important for *Lopadostoma* species identification (Jaklitsch et al. 2014). Also, the BLASTn for ITS data of MFLU 17-0941 is 100% similar with *L. gastrinum* (WU 32046) and cluster with the same species in combined multi-gene analyses with high bootstrap support (Fig. 79). Thus, *L. gastrinum* (MFLU 17-0941) collected on *Quercus* sp. is herein reported as a new host record.

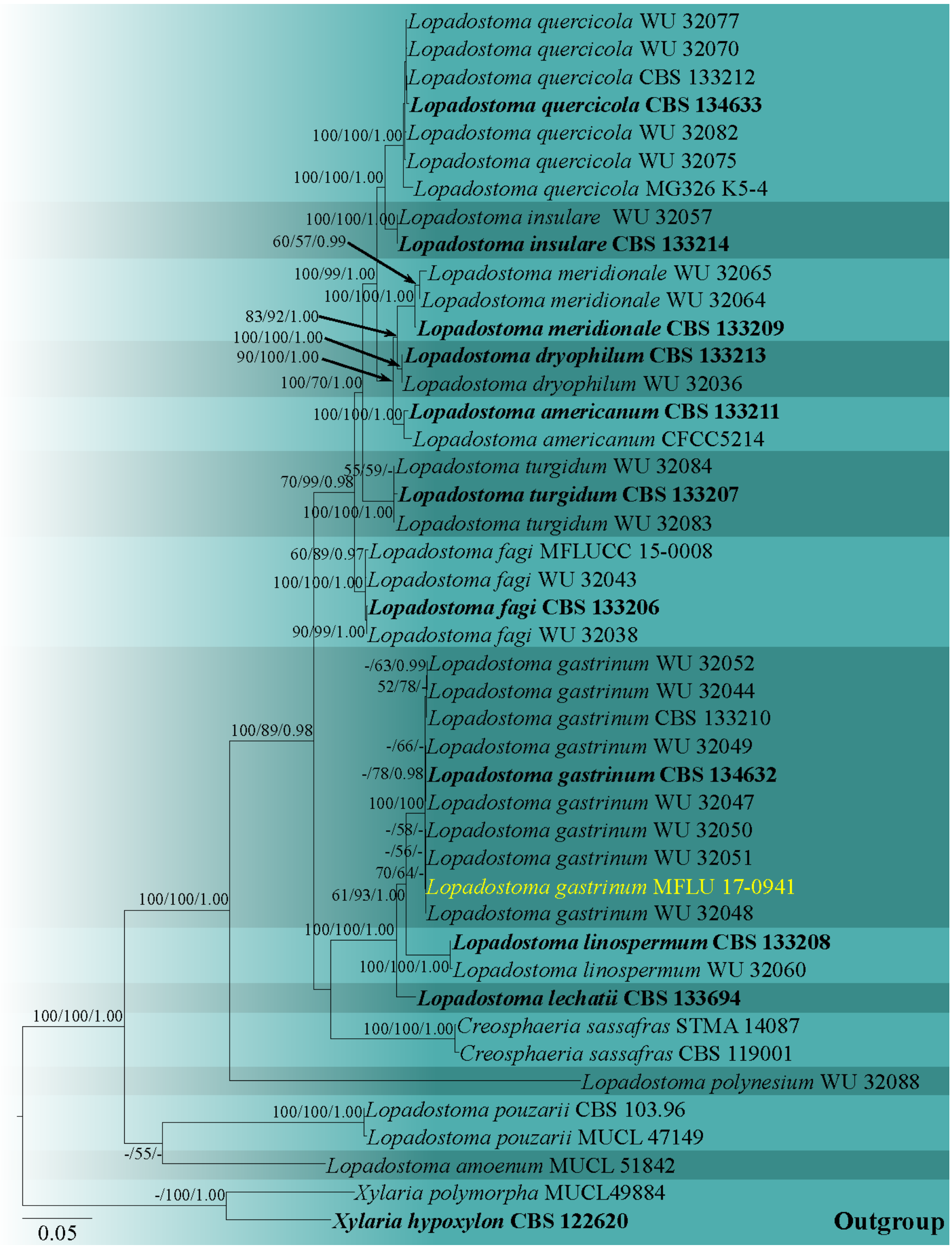

Fig. 79 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *RPB2* sequence data. Forty four strains are included in the combined analyses which comprised of 2680 characters (673 characters for ITS, 847 characters for LSU, 1160 characters for *rpb2*) after alignment.

Tree topology of the maximum likelihood analysis is similar to the Bayesian and maximum parsimony analyses. The best RaxML tree with a final likelihood value of -13068.839950 is presented. Estimated base frequencies were as follows: A = 0.252657, C = 0.247278, G = 0.267172, T = 0.23289; substitution rates AC = 1.514605, AG = 3.481258, AT = 1.196874, CG = 0.965675, CT = 6.380742, GT = 1.000000; gamma distribution shape parameter α = 0.622728. The GTR+G+I evolutionary model was used for all the gene regions. Bootstrap support values for ML and MP greater than 50% and Bayesian posterior probabilities greater than 0.9 are given near nodes respectively. The tree is rooted with *Xylaria hypoxylon* (CBS 122620) and *X. polymorpha* (MUCL 49884). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

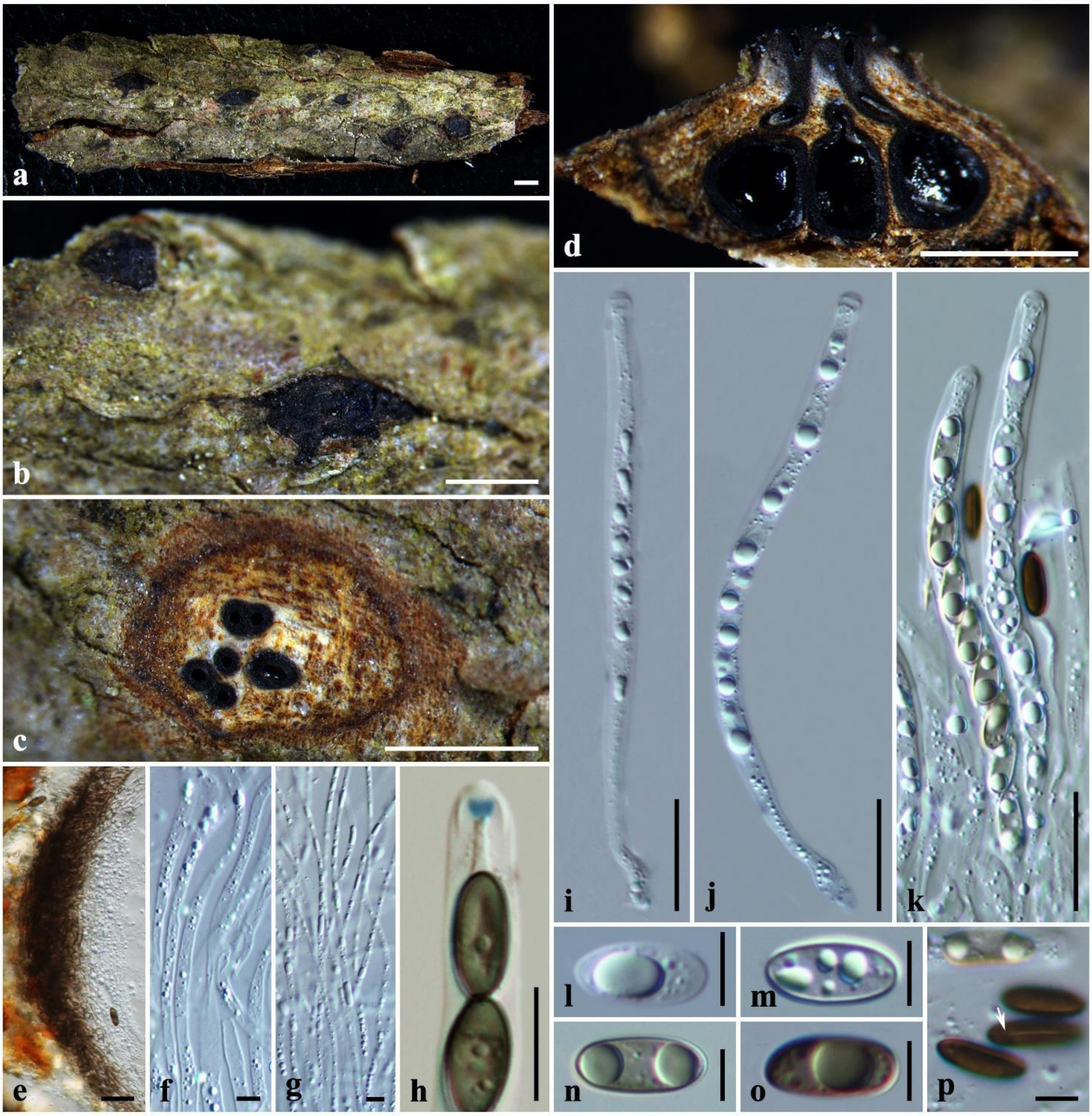

Fig. 80 – *Lopadostoma gastrinum* (MFLU 17-0941, new host record). a–c Stromata on the host. d Cross section of stroma. e Peridium. f, g Paraphyses. h J+, apical ring in Melzer's reagent. i–k Asci. l–p Ascospores (p white arrow shows germ slit). Scale bars: a–d = 1000 µm, e, i–k = 20 µm, h = 10 µm, f, g, l–p = 5 µm.

Xylariaceae Tul. & Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei - Valsei - Sphaeriei 2, 3 (1863)

Index Fungorum number: IF81528; Facesoffungi number: FoF00070

Xylariaceae is one of the largest families in Sordariomycetes established in 1863, comprising plant pathogens of economically important plants and saprobes of many decaying plant materials (Chang et al. 2018, Helaly et al. 2018). This family has been subjected to many revisions (Jaklitsch et al. 2016, Hongsanan et al. 2017, Hyde et al 2020a), and the recent studies divided the family into two subfamilies, Xylaroideae and Hypoxyloideae (Maharachchikumbura et al. 2016). Xylariaceae consists of 37 genera (Daranagama et al. 2018), of which only few genera such as *Gigantospora*, *Nipicola*, *Sabalicola*, *Spirodecospora*, *Striatodecospora* and *Xylotumulus* are excluded due to lack of molecular support. At present, 32 genera are accepted in Xylariaceae (Konta et al. 2020). Most Xylariaceae species consist of carbonaceous ascostromata for protection and produce many bioactive compounds. Therefore, in addition to the morpho- and molecular taxonomy, chemotaxonomy is another factor to consider when resolving the species variations in Xylariaceae (Stadler & Hellwig 2005, Song et al. 2014, Helaly et al. 2018). An updated phylogenetic tree for several genera in this family is provided in Fig. 81.

Nemania Gray, A natural arrangement of British plants 1, 516 (1821)

Index Fungorum number: IF3437; Facesoffungi number: FoF03055

Nemania is a well-known genus in Xylariaceae. Fifty-five species are accepted in this genus (Dayarathne et al. 2020). They are characterized by ascostromata on decaying branches and cracked areas in logs with papillary ostioles, J+ or J- apical rings in asci, and brown ascospores similar to *Kretzschmaria* and *Xylaria* (Smith & Hyde 2001, Fournier et al. 2018, Daranagama et al. 2018, Wendt et al. 2018). In the phylogenetic analysis (Dayarathne et al. 2020), *Nemania* species cluster sister to *Rosellinia*.

Nemania bipapillata (Berk. & M.A. Curtis) Pouzar, Ceská Mykologie 39, 24 (1985) Fig. 82

Index Fungorum number: IF106291; Facesoffungi number: FoF09082

Saprobic on a decaying twig. Sexual morph: *Stromata* superficial, aggregated, brown crustose on wood, laterally and apically very thick except for the ostiolar region. *Ascomata* perithecial, immersed in stroma, subglobose, carbonaceous, raised in central region with ostioles, flat apex with central brown papilla. *Peridium* black to brown cells of *textura angularis*, inner hyaline, *textura angularis* cell layers. *Paraphyses* filamentous, septate, unbranched, within the ascomatal content. *Asci* 120–176 × 6.8–8.4 µm ($\bar{x}$ = 150 × 7.4, n = 25), unitunicate, 8-spored, cylindrical, apically rounded with J+ apical ring, cylindrical 2–2.6 × 1.8 – 2 µm ($\bar{x}$ = 2.3 × 2, n = 25) long pedicellate. *Ascospores* 11.5–15.5 × 5.5–7.6 µm ($\bar{x}$ = 12.5 × 6.3, n = 25), aseptate, overlapping uniseriate, broad, ovoid, hyaline when young, becoming brown to dark brown when mature, slightly curved germslit, apically slightly wider than basal ends, obtuse apices, smooth-walled with a single guttule. Asexual morph: Undetermined.

Material examined – India, Andaman and Nicobar Islands, South Andaman, Mount Harriet, Gun Point (11˚72'23"N 92˚73'80"E), decaying twig, 7 December 2017, M. Niranjan & V.V. Sarma (AMH-10074, Ajrekar Mycological Herbarium, India), living culture PUFNI 17612.

GenBank number – LSU: MK994102.

Known distribution (based on molecular data) – Brazil, Cameroon, China, Ecuador, Germany, India, Malaysia, Mauritius, Philippines, Reunion, Thailand, Taiwan, USA (Smith & Hyde 2010).

Known hosts (based on molecular data) – *Acalypha diversifolia, Asparagopsis taxiformis, Camellia sinensis, Cinnamomum* sp., *Dendrobium heterocarpum, Dendrobium longicornu, Diospyros crassiflora, Faramea aff. Oblongifolia, Vaccinium dunalianum, Vanilla planifolia, Jatropha* sp., *Usnea* sp., Lichen Usnea (Ju & Rogers 2002).

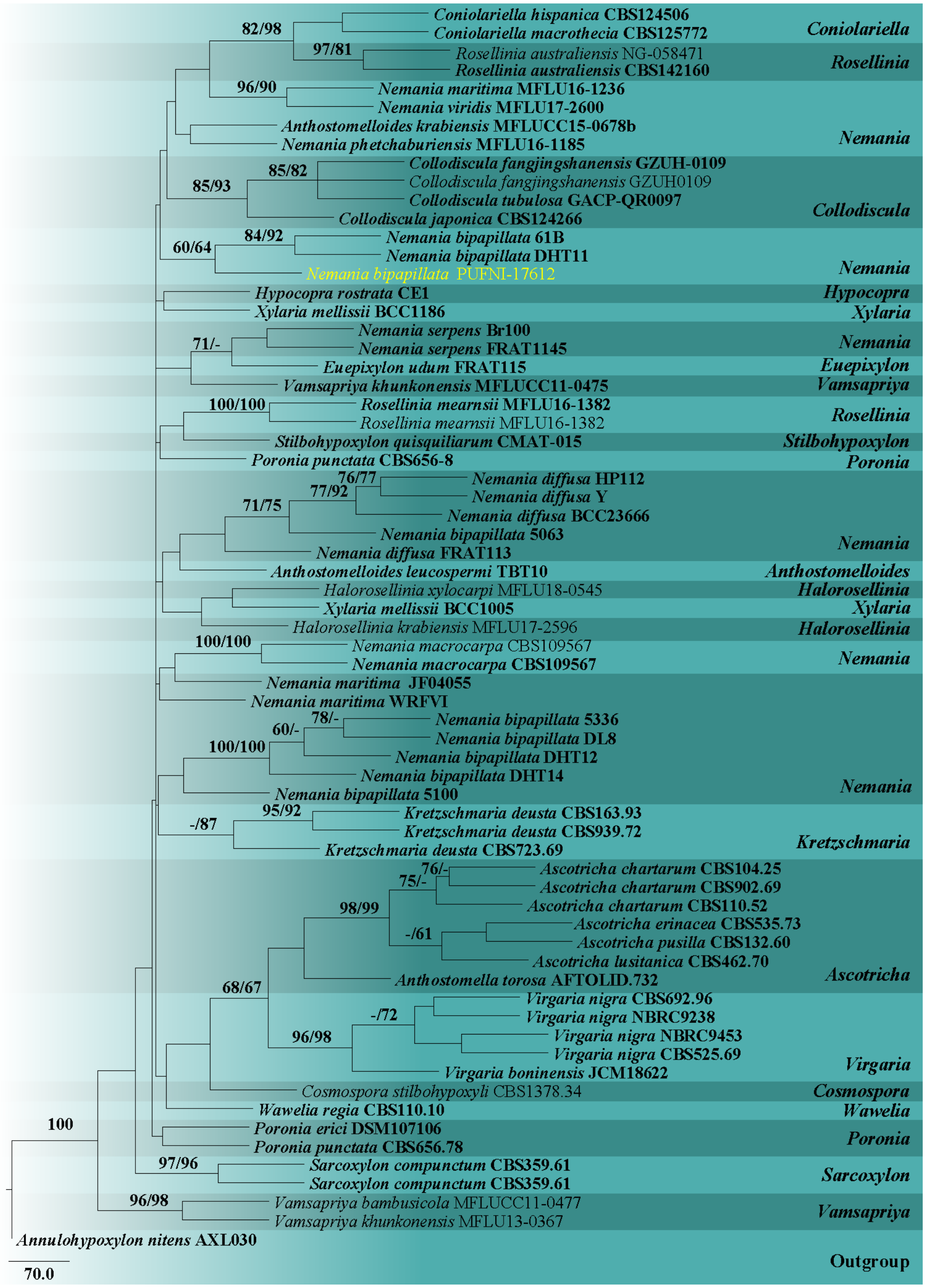

Fig. 81 – Phylogram generated from maximum parsimony analysis based on LSU sequence data. Sixty-seven strains are included in the analyses which comprised of 849 characters after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -3431.976159 is presented. The matrix had 481 distinct alignment patterns with 11.12% of indeterminate characters or gaps. Estimated base frequencies were as follows: A = 0.249644, C = 0.217974, G = 0.303477, T = 0.228905; substitution rates AC = 0.812086,

AG = 2.031374, AT = 0.996138, CG = 0.898665, CT = 8.561276, GT = 1.000000; Proportion of invariable sites I = 0.172639; gamma distribution shape parameter α = 0.443207. 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 *Annulohypoxylon nitens* AXL030. Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

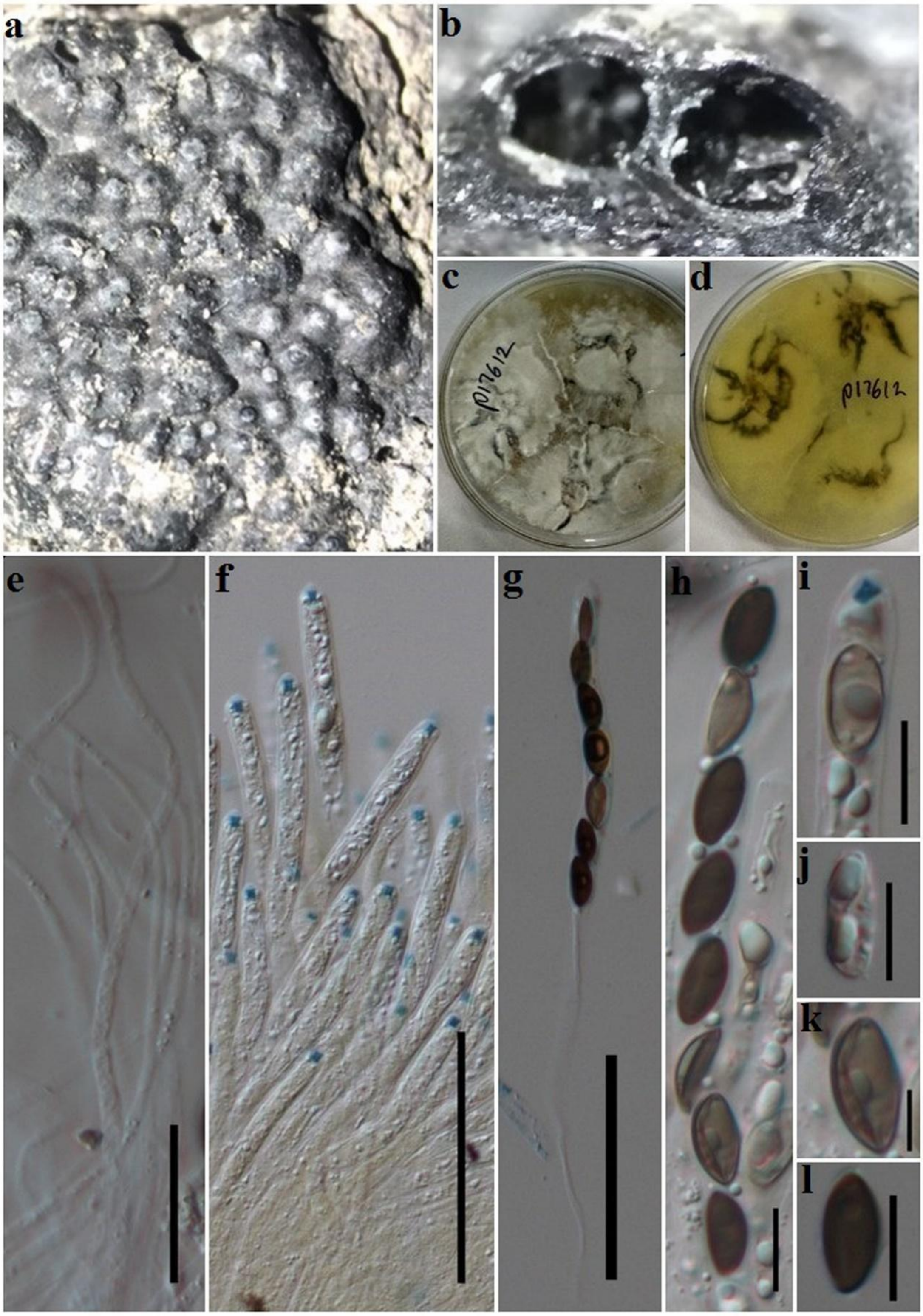

Fig. **82** – *Nemania bipapillata* (PUFNI 17612, a new host record). a Stromata on host. b Stromata vertical section. c, d Culture on MEA plates. e Paraphyses. f–h Asci. i J+ apical ring. j–l Ascospores. Scale bars: f, g = 50 µm e = 20 µm, h–l = 10 µm.

Notes – Morphological characters and sequence analyses results show that our taxon is *Nemania bipapillata* and its morphological description and a key to the species of *Nemania* is provided by Smith & Hyde (2001). Our collection has similar morphological features such as erumpent stromata that are hemispherical, dark brown, have one to many ascomata. The asci of our specimen are longer (120–176 × 7–9 vs. 70–90 × 6–8 µm) and slightly wider, and ascospores are wider than the type (11–16 × 5–8 vs. 10–15 × 5–6.5 µm) (Smith & Hyde 2001). The recent collection of *Nemania bipapillata* from French West Indies (Fournier et al. 2018) has ellipsoid to elongated stromata comprising outer carbonaceous and inner white loosely arranged fibrous tissue at margins, whereas in our collection these differences were not found. Further, the ascospores of our taxon are slightly larger than the ones reported from the French West Indies (Fournier et al. 2017). However, the subglobose to depressed-spherical perithecia are similar to our collection. In the phylogenetic analysis *N. bipapillata* (17612) showed 2.1 % base pair differences in the LSU region (18/848 bp) with *N. bipapillata* (DHT11).

Zygosporiaceae J.F. Li, Phookamsak & K.D. Hyde, Mycosphere 8, 1860 (2017)

Index Fungorum number: IF553846; Facesoffungi number: FoF03760

Zygosporiaceae was formally introduced by Li et al. (2017) to accommodate a single genus *Zygosporium*. Based on the phylogenetic analysis of LSU and ITS sequences, Zygosporiaceae is separated from other taxa in Xylariales. Species of Zygosporiaceae are saprobes on plant litter, especially on monocotyledons such as palms and Pandanaceae (Li et al. 2017). Phylogenetic placement of Zygosporiaceae species are presented in Fig. 83.

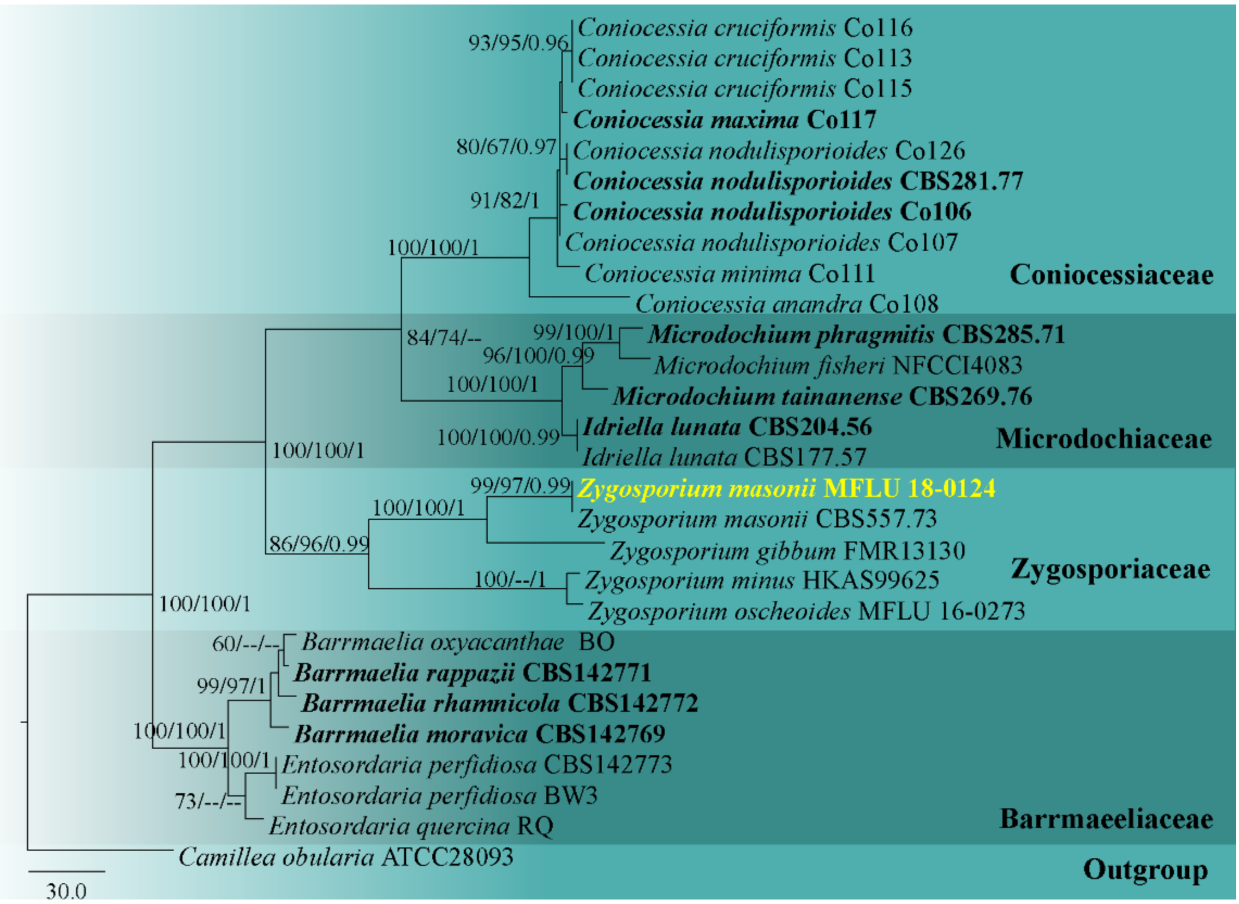

Fig. 83 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Twenty-eight strains are included in the combined analyses which comprised 1692 characters (886 characters for LSU, 806 characters for ITS) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6124.325108 is presented. Estimated base frequencies were as follows: A

= 0.251365, C = 0.225264, G = 0.263340, T = 0.260032; substitution rates AC = 1.698973, AG = 1.810312, AT = 1.340678, CG = 1.032354, CT = 5.136988, GT = 1.000000; gamma distribution shape parameter α = 0.478984. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Camillea obularia* ATCC28093. Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Zygosporium Mont., Annales des Sciences Naturelles Botanique 17, 120 (1842)

Index Fungorum number: IF10473; Facesoffungi number: FoF03761

Montagne (1842) introduced *Zygosporium*, with the type species *Z. oscheoides*. *Zygosporium* species are hyphomycetous (asexual morphs) and characterized by incurved vesicular cells, globose or ellipsoid and smooth or variously ornamented conidia (Mason 1941, Hughes 1951). Members in this family are usually saprobes in temperate to tropical regions (Photita et al. 2001, Whitton et al. 2003, Manoharachary et al. 2006, McKenzie et al. 2007, Abbas et al. 2011, Taheriyan et al. 2014). Sequence data are available for eight species (*Z. chartarum*, *Z. echinosporum*, *Z. gibbum*, *Z. masonii*, *Z. minus*, *Z. mycophilum*, *Z. oscheoides* and *Z. pseudogibbum*. Twenty-seven species are listed in the Index Fungorum (2020) for *Zygosporium*.

Zygosporium masonii S. Hughes, Annales des Sciences Naturelles Botanique 44, 15 (1951)

Fig. 84

Index Fungorum number: IF308038; Facesoffungi number: FoF06496;

Saprobic on leaves of *Dracaena* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse to compact, forming a thin layer, spreading on the substrate surface, numerous, conspicuous, black with flossy mycelium. *Mycelium* mostly superficial, consisting of cylindrical, light-brown to brown, smooth, septate, branched hyphae with slightly thick-walls. *Conidiophores* setiform portion 50–90 × 2–5 µm (x̄ = 66 × 3.5 µm, n = 20), macronematous, mononematous, scattered, up to 7 µm wide near the base, 2–4-septate, erect, straight or slightly flexuous, unbranched, brown at the base with connected conidiophores, subhyaline to light brown and narrowing towards the apex; swollen vesicles on short stalk arising from the side of the first cell of the conidiophores, cylindrical, brown, curved and smooth-walled. *Conidiogenous cells* 15–30 × 3–7 µm (x̄ = 21 × 5.5µm, n = 10), phialidic, 2–3 per vesicle, ellipsoidal to ampulliform, upwardly curved, smooth, brown to black, apex obtuse, thin-walled, borne in pairs, arising directly from the vesicular cell. *Conidia* 4–8 × 4–10 µm (x̄ = 6.9 × 6.7 µm, n = 20), solitary, globose to subglobose, aseptate, verruculose, subhyaline to pale brown, granules, thick and rough-walled.

Material examined – Thailand, Songkhla Province, on dead leaves of *Dracaena* sp., 5 May 2018, Napalai Chaiwan NSW5 (MFLU 18-0124).

GenBank numbers – ITS: MN480499, LSU: MN480500.

Known distribution (based on molecular data) – Australia (Paulus et al. 2007), Cuba (Delgado-Rodriguez et al. 2002), Florida (Delgado 2008), West Indies (Minter 2001), Italy (Lunghini et al. 2013), Japan (Kobayashi 2007), Myanmar (Thaung 2008), Nicaragua (Delgado 2011), Thailand (this study)

Known hosts (based on molecular data) – *Artabotrys burmanicus* (Thaung 2008), *Cecropia peltata* (Minter 2001), *Cyathea* sp. (Delgado-Rodriguez et al. 2002), *Daphniphyllum macropodum* (Kobayashi 2007), *Dracaena* (this study), *Ficus pleurocarpa* (Paulus et al. 2007), *Phillyrea angustifolia* (Lunghini et al. 2013), *Roystonea* sp. (Delgado 2011), *Tillandsia* sp. (Delgado 2008).

Notes – Based on the multi-gene analyses, our isolate clustered with *Zygosporium masonii* with high boostrap support (Fig. 82). *Zygosporium masonii* differs from our isolate in having ovoid, hyaline conidia (Whitton et al. 2012), while our isolate has subglobose, subhyaline to pale brown conidia. The Blastn search results showed that ITS and LSU sequences of our isolate are 100% identical to *Z. masonii* isolates (CBS 557.73 and CBS 138.71). This is the first report of *Z. masonii* from *Dracaena* sp. in Thailand.

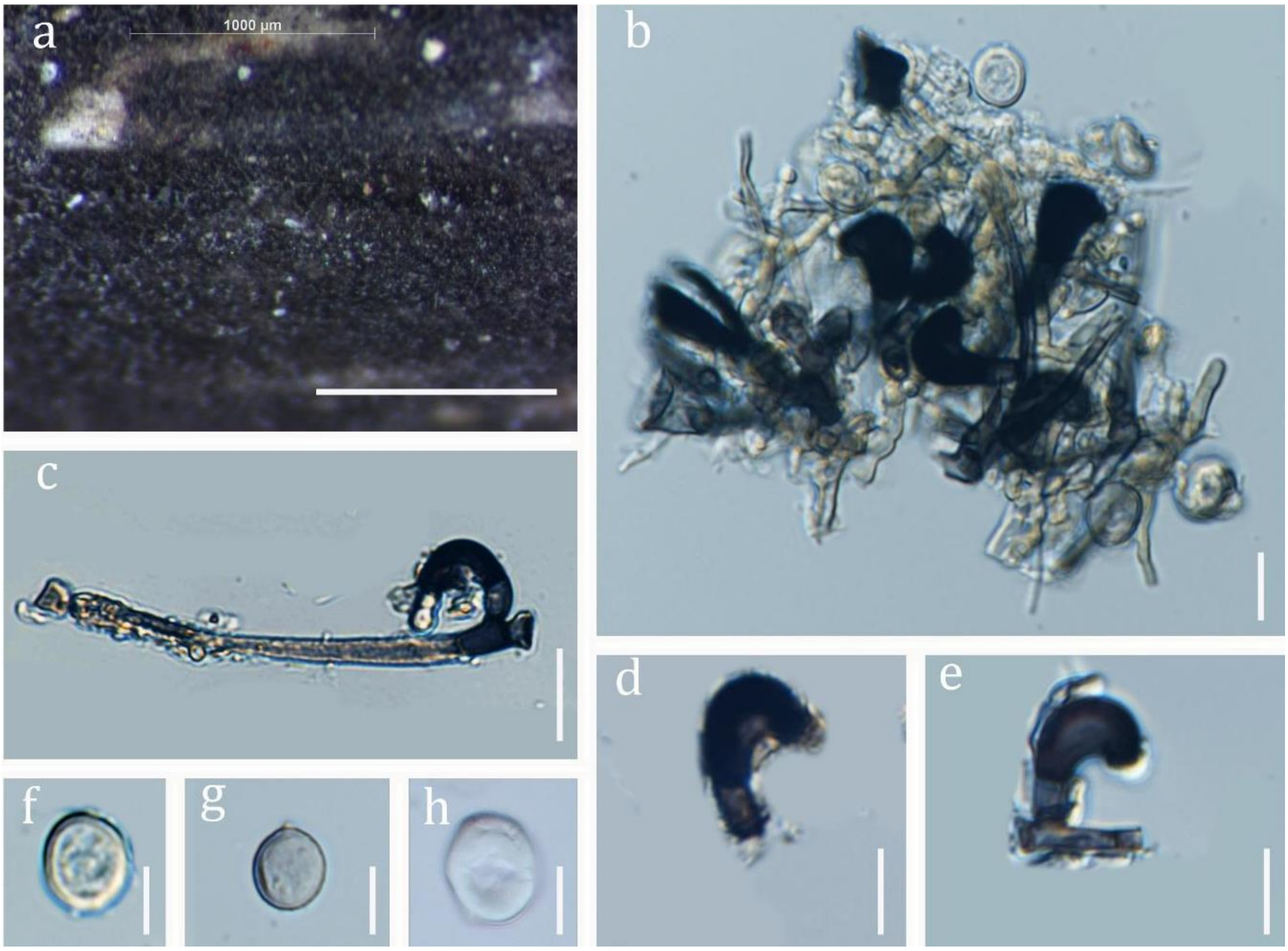

Fig. **84** – *Zygosporium masonii* (MFLU 18–0124, new geographical and host record). a Appearance on host surface. b–e Vesicle, conidiophores and conidiogenous cell. f–h conidia. Scale bars: a = 1000 µm; b, c = 50 µm; e, d, e = 20 µm; f, g, h = 5 µm.

Sordariomycetes orders *incertae sedis*
Catabotryales K.D. Hyde & Senan., Mycosphere 11, 374 (2020)
Catabotrydaceae Petr. ex M.E. Barr, Mycotaxon 39, 83 (1990)

Index Fungorum number: IF90924; Facesoffungi number: FoF01372

Catabotrydaceae (Petrak 1954, Barr 1990) accommodates only *Catabotrys* (Theissen & Sydow 1915) which comprise of two species *C. chandrapurensis* and the type species *C. deciduum*. The family is characterized by pulvinate, superficial stromata on substrates, long ostiolar ascomata embedded in stromatic columns, and hyaline, 1-celled, ellipsoidal ascospores (Seaver & Waterston 1946, Barr 1990). The taxonomic and phylogenetic placement of this family was detailed in Maharachchikumbura et al. (2015, 2016) and Hyde et al. (2020a), which is followed in this study. An updated phylogeny for the Catabotryales is provided in Fig. 85.

Catabotrys Theiss. & Syd., Annales Mycologici 13, 297 (1915)

Index Fungorum number: IF834; Facesoffungi number: FoF05087

Catabotrys species are generally saprobes on plant leaves or petioles, and they are also reported as endophytes in China (Wu et al. 2014a). There are two species listed in Index Fungorum (2021), and a new collection of *C. deciduum* is described and illustrated here.

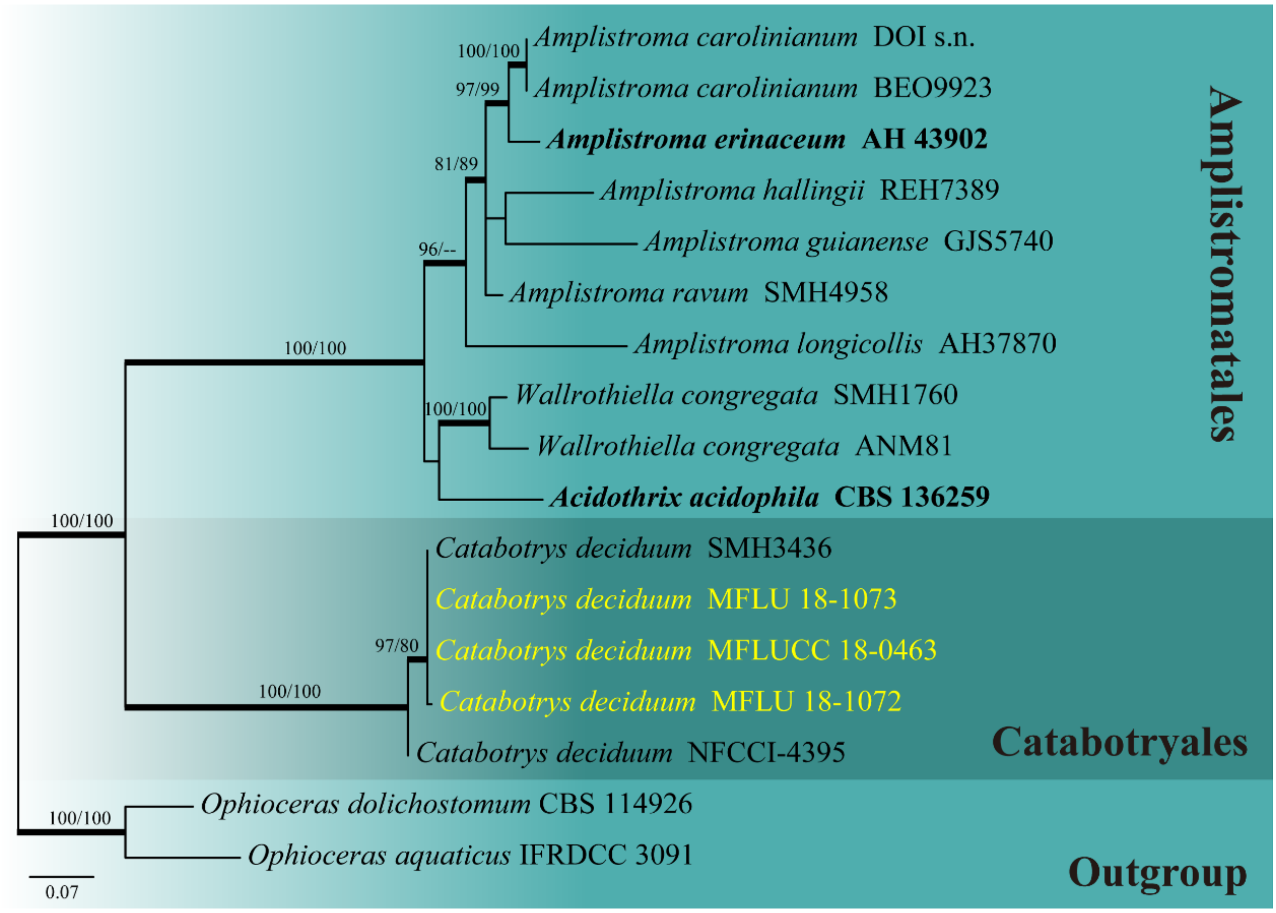

Fig. 85 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of taxa in Amplistromatales and Catabotryales. Seventeen strains are included in the combined analyses which comprised 1629 characters (715 characters for ITS, 914 characters for SSU) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -6794.539143. Estimated base frequencies were as follows: A = 0.222750, C = 0.268651, G = 0.321058, T = 0.187541; substitution rates AC = 0.917760, AG = 2.004735, AT = 1.911301, CG = 0.821570, CT = 8.716668, GT = 1.000000; gamma distribution shape parameter α = 0.485675. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated in bold branches. The tree is rooted with *Ophioceras aquaticus* (IFRDCC 3091) and *O. dolichostomum* (CBS 114926). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Catabotrys deciduum (Berk. & Broome) Seaver & Waterston, Mycologia 38, 184 (1946) Fig. 86

Index Fungorum number: IF626984; Facesoffungi number: FoF05088,

Saprobic on petioles and rachides of palms. Sexual morph: *Stromata* solitary or irregularly scattered, conspicuous, multi-loculate, superficial, with base slightly penetrating the epidermis at regular intervals, discoid to pulvinate, reddish brown to black, surface scurfy, flat or slightly convex. *Ascomata* deeply imbedded in stromatic columns, globose, with a long, periphysate, ostiolar neck. *Peridium* composed of several reddish-brown outer layer cells of *textura globosa* and *textura epidermoidea*, with pale brown to hyaline internal cells of *textura angularis*. *Paraphyses* 5–6.5 µm wide, hypha-like, numerous, tapering towards the apex, not embedded in a gelatinous matrix. *Asci* 56.5–66 × 7.3–9.5 µm ($\bar{x}$ = 60.4 × 8.8 µm, n = 20), 8-spored, unitunicate, broad cylindrical, short pedicellate, apically rounded or truncate, with a J-, discoid, refractive, apical ring. *Ascospores* 7.5–9.7 × 3–4.5 µm ($\bar{x}$ = 8.6 × 3.8 µm, n = 30), biseriate, hyaline, 1-celled, ellipsoidal to cylindrical, smooth-walled. Asexual morph: Hyphomycetous. *Vegetative hyphae* hyaline, septate, smooth-walled. *Conidiophores* micronematous. *Conidiogenous cells* holoblastic, terminal and intercalary. *Conidia* 3.5–7 × 3–7 µm ($\bar{x}$ = 5.3 × 4.7 µm, n = 80), globose or obovoid, hyaline, 1-celled and smooth-walled, often with denticles from conidiogenous cells.

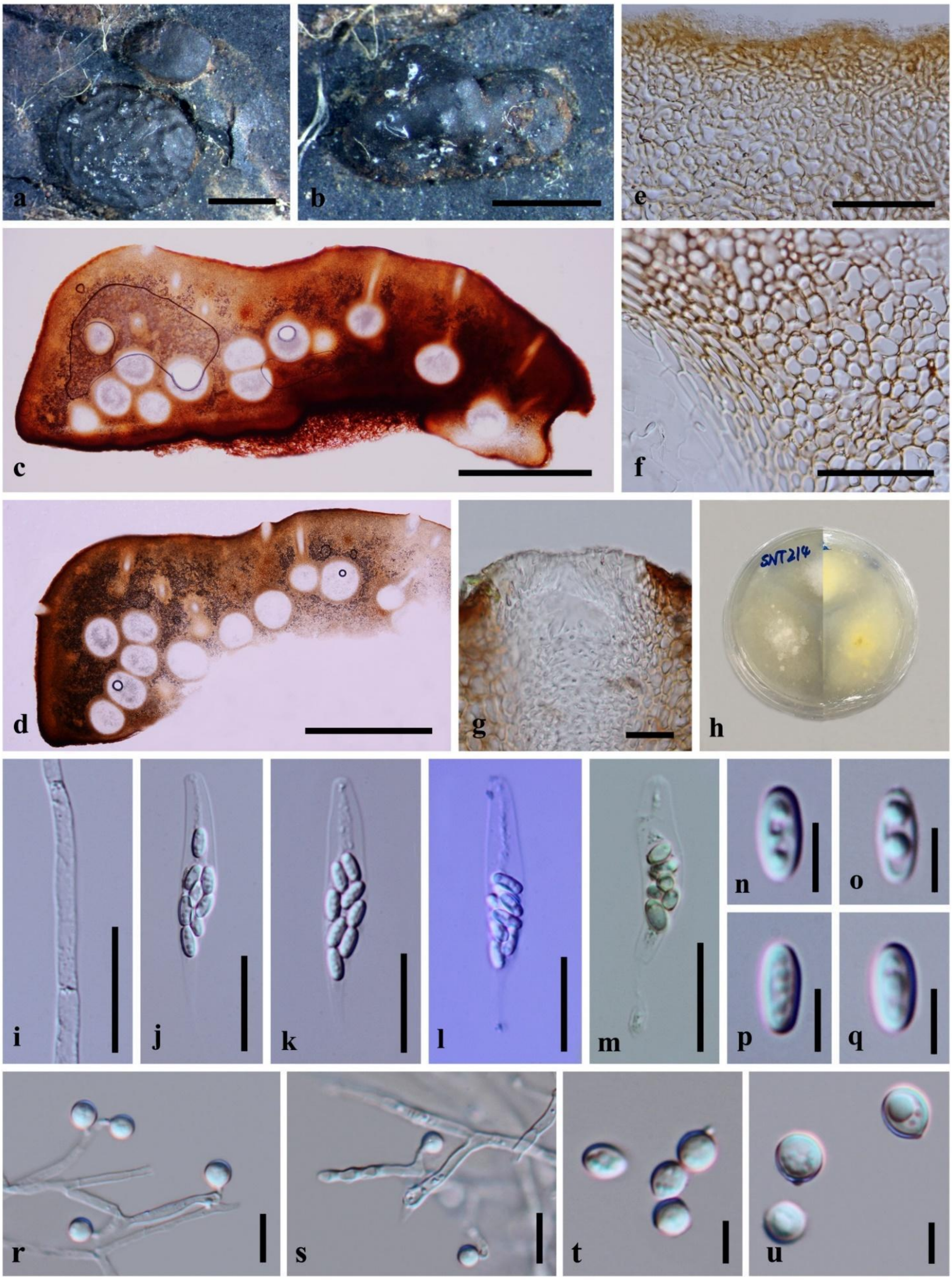

Fig. **86** – *Catabotrys deciduum* (MFLU 18-1073, new geographical record). a, b Appearance of stromata on host surface. c, d Vertical sections through the stromata. e, f Structure of peridium. g Ostiole with periphyses. h Colonies on PDA. i Paraphyses. j–m Asci. l Ascus in Cotton blue. m Ascus apex in Mealzer's reagent, J- subapical ring. n–q Ascospores. r–u Sporulation in culture. t, u Conidia in culture. Scale bars: a, b = 2 mm, c, d = 1000 µm, e, f = 50 µm, g–m = 20 µm, r, s = 10 µm, r, n–q, t, u = 5 µm.

Material examined – Thailand, Chumphon, Amphoe Pathio, on rachis of *Salacca* sp. (Arecaceae), 1 December, 2016, S.N. Zhang SNT33B (MFLU 18-1072); Thailand, Ranong, Amphoe Mueang Ranong, on decaying petiole of *Elaeis guineensis* (Arecaceae), 29 August 2017, S.N. Zhang SNT214 (MFLU 18-1073, HKAS 97484), living culture MFLUCC 18-0463.

GenBank numbers – LSU: MK078621 (MFLUCC 18-0463), MK078623 (MFLU 18-1072); ITS: MK078619 (MFLUCC 18-0463); SSU: MK078624 (MFLUCC 18-0463), MK078626 (MFLU 18-1072), MK078625 (MFLU 18-1073); *TEF1-α*: MK087661 (MFLUCC 18-0463), MK087663 (MFLU 18-1072), MK087662 (MFLU 18-1073); *RPB2*: MK087671 (MFLUCC 18-0463).

Known distribution (based on molecular data) – India (Hyde et al. 2020c), Panama (Huhndorf et al. 2004), Thailand (This study).

Known hosts (based on molecular data) – *Salacca* sp., *Elaeis guineensis* (This study), *Rhizophora mucronata* (Hyde et al. 2020c).

Notes – *Catabotrys deciduum* has been recorded from many localities and mostly found from palms (Theissen & Sydow 1915, Seaver & Waterston 1946). Huhndorf et al. (2004) provided the first sequence data for *C. deciduum*, which was obtained from a Panama specimen that preserved in the Field Museum of Natural History, Chicago, Illinois. Herein, we provide two fresh collections of *C. deciduum* from two kinds of palms in Thailand with morphological and molecular data.

Phylum Basidiomycota

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

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

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

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

Index Fungorum number: IF80523; Facesoffungi number: FoF09165

Boletaceae was described by Chevallier (1826) as a distinct family from Agaricaceae. Following the introduction, the family has been subjected to extensive research with many changes brought to the taxonomy based on molecular phylogenetic analyses (Binder & Hibbett 2006, Nuhn et al. 2013, Wu et al. 2014b, 2016). Boletaceae comprises about 92 genera (He et al. 2019, Wijayawardene et al. 2020).

Phylloporus Quél., Flore mycologique de la France et des pays limitrophes, 409 (1888).

Index Fungorum number: IF18275; Facesoffungi number: FoF09166

Phylloporus is characterised by having a gilled to somewhat poroid hymenophore and bacillate basidiospore ornamentation with few exceptions (Neves & Halling 2010, Neves et al. 2012, Chuankid et al. 2019). The type species, *P. pelletieri* was described from Europe and approximately 90 species have been described from all over the world (He et al. 2019, Index Fungorum 2020). *Phylloporus* species have been reported from tropical to subtropical as well as from temperate areas (Corner 1970). In Asia, they are found mostly in forests dominated by Fagaceae or Dipterocarpaceae trees (Chuankid et al. 2019). An updated three-gene phylogenetic tree for *Phylloporus* species with new records for Thailand is presented in Fig. 87.

Phylloporus attenuatus Hosen, Mycologia 109, 279 (2017) Figs 88, 89

Index Fungorum number: IF803939; Facesoffungi number: FoF09167

Basidiomata gregarious to caespitose, small to medium-sized. *Pileus* 11–62 mm in diam., convex to plano-convex, with age becoming slightly applanate to slightly depressed at center; margin inflexed, uplifted in age; surface dry, even, becoming cracked with age, brown (7E7-8) or brownish orange (7C7–8) to brick red or burnt Sienna (7D7–8) when young, fading with age; context 7–24 mm thick at center, pale yellow (1A3), turning slightly blue when cut. *Hymenophore* lamellate, subdecurrent to deeply decurrent. *Lamellae* 11–36 × 3–5 mm, intervenose, sometimes forked, ventricose, subdistant; surface transvenose, smooth, yellow (2A6), rapidly and intensely staining blue when injured, then turning red with time; edge entire, concolorous; lamellulae common, in 1–3 tiers. *Stipe* 24–44 × 3–10 mm, central, straight or sometimes curved, tapering downwards, sometimes slightly radicant; surface dry, with yellow pruina at the top, then with fine reddish dots mostly down to the lower third, lower part off-white to light greyish yellow (2A4); context solid, pale yellow (1A3), staining slightly blue at upper part when cut or injured, lower part remaining unchanged. *Basal mycelium* little developed, tomentose, yellow. *Odor and taste* not distinctive.

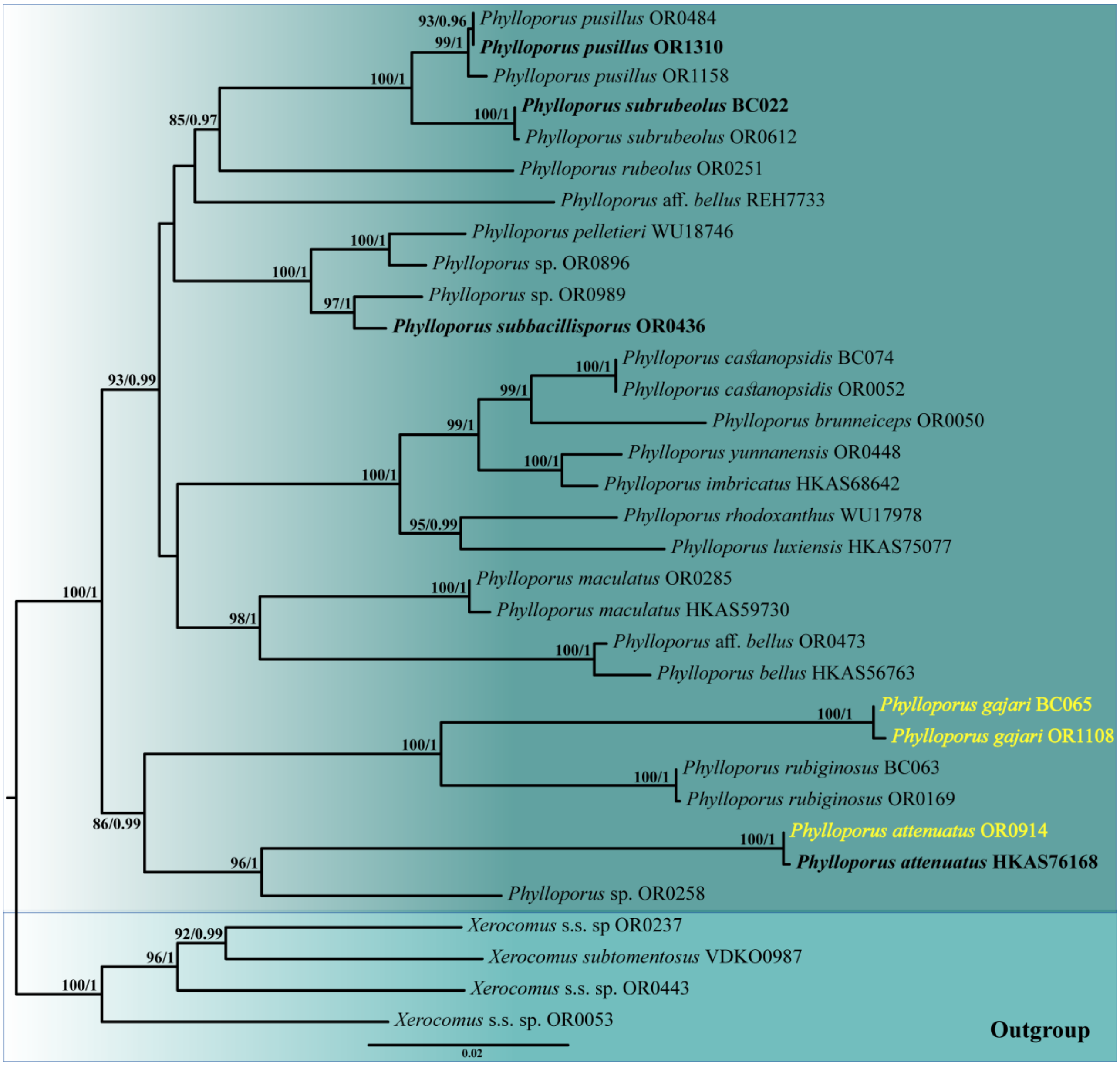

Fig. 87 – Phylogram generated from maximum likelihood analysis based on combined *ATP6*, *RPB2* and *TEF1-α* sequence data for selected *Phylloporus* species. Twenty-six strains are included in the combined analyses which comprised 1381 characters (774 characters for LSU, 607 characters for ITS) after alignment. The 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 -11227 is presented. The matrix has 766 distinct alignment patterns and 9.6% undetermined characters or gaps. For each gene, estimated base frequencies, substitution rates (relative to GT=1), and gamma distribution shape parameter α were as follows. *atp6*: A = 0.32, C = 0.12, G = 0.11, T = 0.45; AC = 0.64, AG = 1.36, AT = 1.12, CG = 0.24, CT = 1.23; α = 0.098; *ef1-α exons*: A = 0.23, C = 0.27, G = 0.25, T = 0.24; AC = 0.81, AG = 7.01, AT = 1.29, CG = 0.87, CT = 11.2; α = 0.206; *rpb2 exons*: A = 0.28, C = 0.23, G = 0.25, T = 0.24; AC = 1.37, AG = 9.93, AT = 0.97, CG = 0.51,

CT = 16.0; α = 0.187; *ef1-α and rpb2 introns*: A = 0.25, C = 0.18, G = 0.23, T = 0.34; AC = 1.94, AG = 8.12, AT = 1.03, CG = 1.24, CT = 8.37; α = 0.677. Bootstrap frequencies greater than or equal to 70% and posterior probabilities greater than or equal to 0.95 are shown above supported branches. The tree is rooted with four *Xerocomus* species. Holotypes are in **bold**. The newly generated sequences are indicated in yellow.

Fig. 88 – Basidiomata of *Phylloporus attenuatus* in the field. a *Phylloporus attenuatus* (OR0914). b *Phylloporus attenuatus* (OR0382). c *Phylloporus attenuatus* (OR0536). Scale bars: a–c = 2 cm.

Basidiospores [150/3/3] (6.5–)6.6–*7.6*–8.9(–9.7) × (4–)4–*4.4*–4.8(–4.9) µm, Q = (1.45–)1.58–*1.74*–2.19(–2.39), ovoid to ellipsoid, greyish yellow (1B2–4) when observed in H_2O and 5% KOH, smooth under light microscope. *Basidia* 23–36 × 7–10 µm, 4-spored, with sterigmata 3–6 µm long, narrowly clavate to clavate, hyaline to greyish yellow (1B3) in H_2O and 5% KOH. *Hymenophoral trama* 50–110 µm wide, bilateral, composed of cylindrical, hyaline hyphae 8–12 µm diam. *Cheilo- and pleurocystidia* 43–69 × 13–21 µm, narrowly clavate to clavate, sometime fusoid to narrowly fusoid, hyaline to greyish yellow (1B3) in H_2O and 5% KOH. *Pileipellis* a trichodermium, composed of cylindrical cells, more or less vertically arranged, slightly interwoven, hyaline to greyish yellow (1B3) in H_2O and KOH; terminal cells 19–47 × 7–17 µm, cylindrical, subclavate, sometimes attenuated toward the apex. *Pileal trama* made up of hyaline hyphae 6–14 diam. *Stipitipellis* an interrupted hymeniderm to trichoderm, hyphae 6–10 µm diam.; caulocystidia 28–54 × 11–19 µm, scattered, clavate, hyaline to greyish yellow (1B3), clay (5D5). *Stipe trama* composed of cylindrical, hyaline hyphae 6–13 µm diam. *Clamp connections* not seen in any tissue.

Material examined – Thailand. Chiang Mai Province, Mae On District (N18°51'55"–E99°17'23"), 4 July 2012, O. Raspé & K. Wisitrassameewong OR0382 (MFLU 12-0234); *ibid.*, Muang District (N18°48'-E 98°56'), 6 June 2013, O. Raspé & S. Vadthanarat OR0536 (CMU-SDBR); *ibid.*, Mae On District (N18°52'11"-E99°18'23"), 29 June 2014, O. Raspé & B. Thongbai OR0769 (MFLU14-0471); *ibid.*, (N18°51'57"-E99°17'23"), 1 June 2015, O. Raspé & S. Vadthanarat OR0914 (CMU-SDBR).

GenBank numbers – *ATP6*: MT861150 (OR0382), MT861151 (OR0536), MT861152 (OR0914); *RPB2*: MT861158 (OR0382), MT861159 (OR0536), MT861160 (OR0914); *TEF1-α*: MT861164 (OR0382), MT861165 (OR0536), MT861166 (OR0914).

Known distribution (based on molecular data) – Bangladesh (Hosen et al. 2017), Thailand (this study).

Known habitat (based on molecular data) – soil in forests dominated by *Shorea robusta* (Hosen et al. 2017), dry dipterocarp forest.

Notes – *Phylloporus attenuatus* can be recognized by its brownish-red pileus, somewhat forking, strongly decurrent and intensely and quickly bluing lamellae, and tapering stipe. Macro- and micro-morphology of *P. attenuatus* specimens from Thailand are identical to the previous description of the specimens from Bangladesh (Hosen et al. 2017). In the multi-gene tree, *P. attenuatus* from Thailand also groups with *P. attenuatus* (holotype, HKAS 76168) from Bangladesh with high support (BS=100% and PP=1). Both morphological and phylogenetic evidence indicate that the Thai specimens studied and the *P. attenuatus* specimens studied by Hosen et al. (2017) are conspecific.

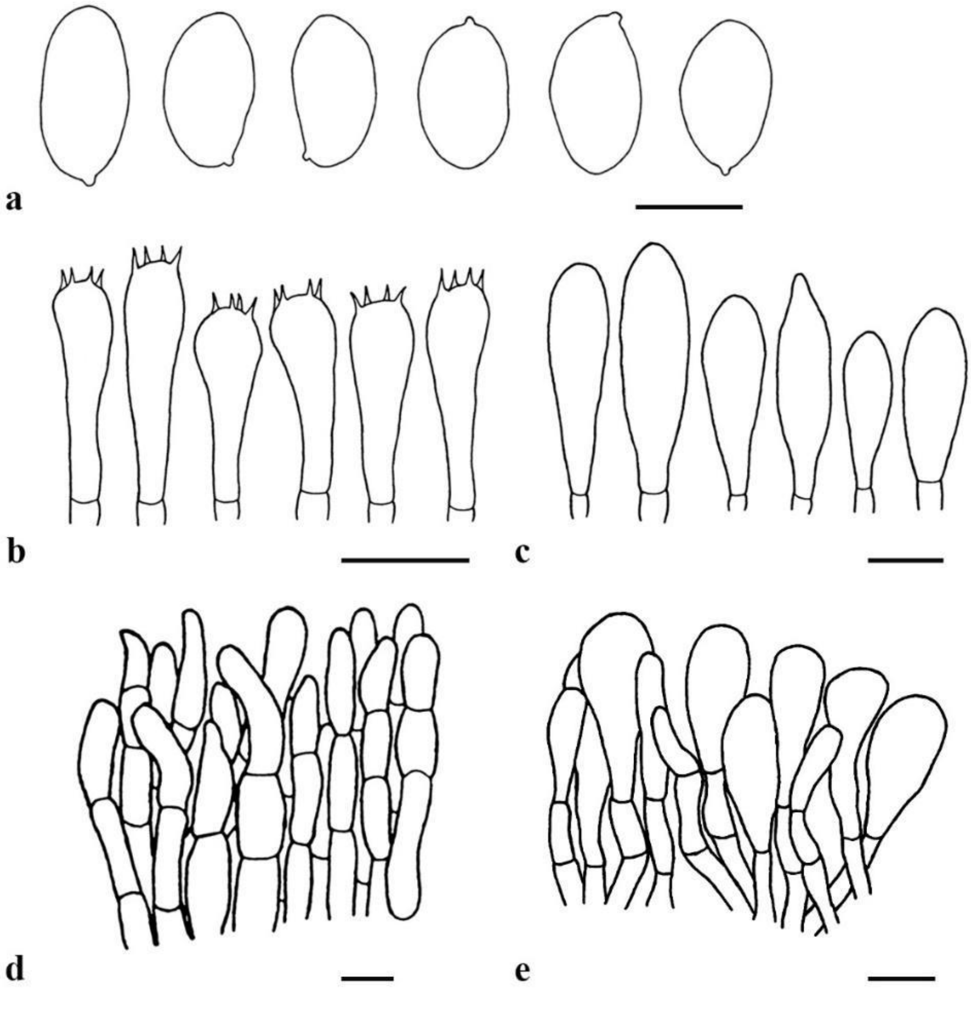

Fig. 89 – Microscopic characters of *Phylloporus attenuatus* (OR0914). a Basidiospores. b Basidia. c Cheilo- and pleurocystidia. d Pileipellis. e Stipitipellis. Scale bars: a = 5 µm, b–e = 20 µm.

Phylloporus gajari Hosen & Zhu L. Yang, Mycoscience 56, 585 (2015) Figs 90, 91

Index Fungorum number: IF803941; Facesoffungi number: FoF09168

Basidiomata solitary or rarely caespitose, small to medium-sized. *Pileus* 21–47 mm in diam., plano-convex when young, becoming applanate in age, slightly depressed to depressed at center;

surface dry, smooth when young, then becoming rough, finely areolate with age, mostly fox to English red (8D7–8), Sahara to caramel (6C5–6) around the edge when young, becoming yellowish brown or golden brown (5D7–8) to chamois (4C5–6) with age; margin straight to deflexed, usually uplifted when mature; context 4–8 mm thick at center, light yellow (1A4), slightly bluing when injured or cut. *Hymenophore* lamellate, deeply decurrent. *Lamellae* 15–26 × 2–8 mm, strongly intervenose to anastomosing, ventricose, subdistant, flexible; surface strongly transvenose, smooth, yellow (2A7) to pastel yellow (3A4), turning blue when injured; lamellulae common, in 1–2 tiers. *Stipe* 28–33 × 2–5 mm, central, straight to slightly curved, cylindrical; surface dry, fine yellow squamulose, fox to English red (8D7–8) when young, brownish orange (5C5–6) to brown (6E8); context solid, light yellow (1A4), slightly bluing then reddening with time in the upper part when cut or injured, but usually unchanging in the lower part. *Basal mycelium* well developed, tomentose, white. *Odor and taste* not distinctive.

Basidiospores [250/5/5] (9.2–)9.4–*11.6*–14.5(–14.9) × (4.4–)4.6–*5.1*–5.6(–5.8) µm, (1.76–)1.88–*2.25*–2.63(–2.9), ellipsoid to fusoid or subfusoid, light yellow (1A4) to greyish yellow (1B4) when observed in H_2O and 5% KOH, smooth under light microscope. *Basidia* 26–39 × 8–11 µm, 4-spored, with sterigmata 3–5 µm long, clavate, hyaline and light yellow (1A4) in H_2O and 5% KOH. *Hymenophoral trama* 100–140 µm wide, bilateral, composed of hyaline hyphae 5–10 µm wide, cylindrical. *Cheilo- and pleurocystidia* 42–72 × 10–17 µm, narrowly clavate to clavate, hyaline to light yellow (1A4) in H_2O and 5% KOH. *Pileipellis* a slightly interwoven trichoderm, composed of short chains of 4–5 cells, terminal cells 28–52 × 12–22 µm, cylindrical to somewhat slightly inflated, smooth, hyaline to yellowish white (1A2) in 5% H_2O and KOH. *Pileal trama* made up of hyaline hyphae 6–12 diam. *Stipitipellis* an interrupted hymeniderm, hyphae 6–13 µm diam; caulocystidia 22–46 × 13–21 µm, mostly clavate, sometimes mucronate, smooth, hyaline. *Stipe trama* composed of hyphae 8–11 µm wide, hyaline. *Clamp connections* not seen in any tissue.

Culture characteristics – uncultured.

Material examined – Thailand. Chiang Rai Province, Tha Sai District, Baan Hua Doi, 23 July 2016, B. Chuankid BC065 (MFLU16-2270); Chiang Mai Province, Muang District (N18°46'-E98°54'), 15 October 2015, O. Raspé & S. Vadthanarat OR1184 (CMU-SDBR); Ubon Ratchathani Province, Muang District (N15°18'-E104°48'), 03 August 2015, O. Raspé & S. Vadthanarat OR1104 and OR1110 (CMU-SDBR); *ibid.,* (N15°19'-E104°48'), 03 August 2015, O. Raspé & S. Vadthanarat OR1108 (CMU-SDBR).

GenBank numbers – *ATP6*: MT861154 (OR1104), MT861153 (BC065), MT861155 (OR1108), MT861157 (OR1184), MT861156 (OR1110); ITS: MT880254 (OR1104); *TEF1-α*: MT861168 (OR1104), MT861167 (BC065), MT861169 (OR1108), MT861170 (OR1110); MT861171 (OR1184); *RPB2*: MT861161 (BC065), MT861162 (OR1108), MT861163 (OR1184).

Known distribution (based on molecular data) – Bangladesh (Hosen et al. 2015), Thailand (this study).

Known habitat (based on molecular data) – Soil in forests with monodominant stands of *Shorea robusta* (Hosen et al. 2015), dry dipterocarp forests (this study).

Notes – *Phylloporus gajari* is one of the most frequently collected species in forests dominated by *Shorea robusta* in Bangladesh. The pileus surface is pale red or reddish brown to yellowish brown or golden brown. The hymenophore quickly stains blue when injured. The stipe is cylindrical, pale red to brownish orange or brown with white basal mycelium. Because sequences of the genes we used in our phylogenetic analyses were not available for the holotype of *P. gajari*, we did not include it in the phylogeny. However, the ITS sequence of the Thai specimen (OR1104) showed 100% identity to the sequence of *P. gajari* holotype (Hosen et al. 2015), which, together with the morphological evidence, indicates that the studied specimens from Thailand belong in *P. gajari*. In the multi-gene phylogeny, the sequences from the Thai specimens clustered together with BS = 100%, PP = 1.0 and were clearly distinct from other *Phylloporus* species included in the analyses.

Fig. 90 – Basidiomata of *Phylloporus gajari* in the field. a, b *Phylloporus gajari* (BC065). c *Phylloporus gajari* (OR1184). d, e *Phylloporus gajari* (OR1108). f Close up of the hymenophore. Scale bars: a–e = 2 cm, f = 1 cm.

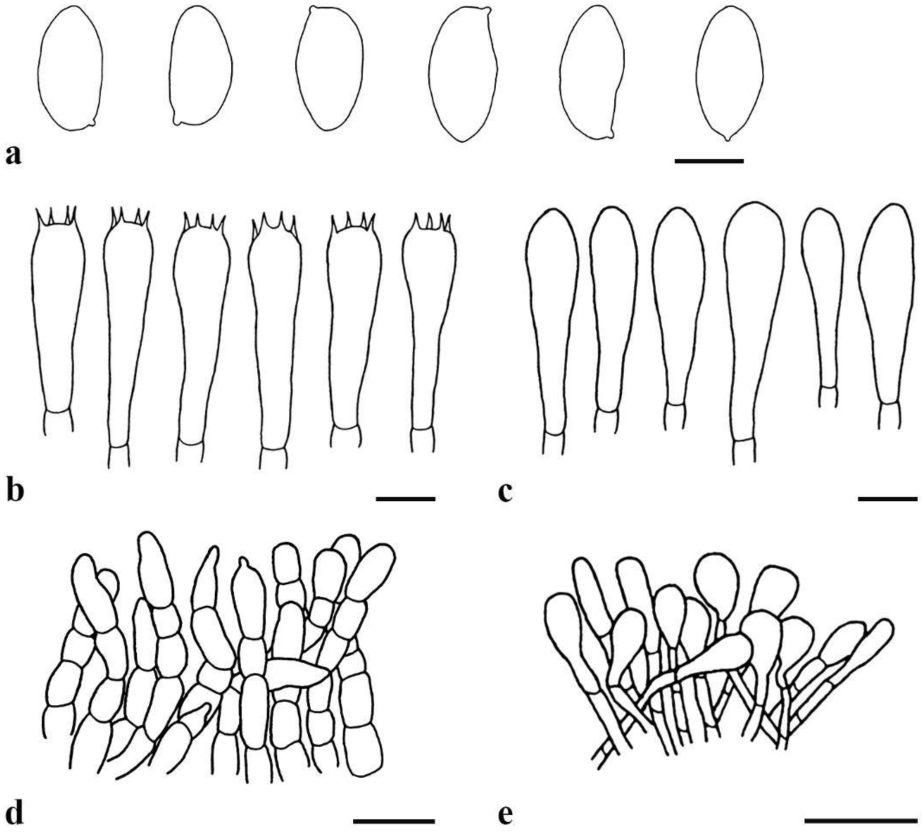

Fig. 91 – Microscopic characters of *Phylloporus gajari* (BC065). a Basidiospores. b Basidia. c Cheilo- and pleurocystidia. d Pileipellis. e Stipitipellis. Scale bars: a = 5 µm, b = 10 µm, c =20 µm, d–e = 50 µm.

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