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Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa

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Abstract

This article is the tenth series of the Fungal Diversity Notes, where 114 taxa distributed in three phyla, ten classes, 30 orders and 53 families are described and illustrated. Taxa described in the present study include one new family (viz. Pseudoberkleasmiaceae in Dothideomycetes), five new genera (*Caatingomyces*, *Cryptoschizotrema*, *Neoaccladium*, *Paramassaria* and *Trochilisporea*) and 71 new species, (viz. *Acrogenospora thailandica*, *Amniculicola aquatica*, *A. guttulata*, *Angustimassarina sylvatica*, *Blackwellomyces lateris*, *Boubovia gelatinosa*, *Buellia viridula*, *Caatingomyces brasiliensis*, *Calophoma humuli*, *Camarosporidiella mori*, *Canalisporium dehongense*, *Cantharellus brunneopallidus*, *C. griseotinctus*, *Castanediella meliponae*, *Coprinopsis psammophila*, *Cordyceps succavus*, *Cortinarius minusculus*, *C. subscotoides*, *Diaporthe italiana*, *D. rumicicola*, *Diatrypella delonicis*, *Dictyocheirospora aquadulcis*, *D. taiwanense*, *Digitodesmium Chiangmaiense*, *Distoseptispora dehongensis*, *D. palmarum*, *Dothiorella styphnolobii*, *Ellisembia aurea*,

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Falciformispora aquatic, *Fomitiporia carpineae*, *F. lagerstroemiae*, *Grammothele aurantiaca*, *G. micropora*, *Hermatomyces bauhiniae*, *Jahnula queenslandica*, *Kamalomyces mangrovei*, *Lecidella yunnanensis*, *Micarea squamulosa*, *Muriphaeosphaeria angustifoliae*, *Neoacladium indicum*, *Neodidymelliopsis sambuci*, *Neosetophoma miscanthi*, *N. salicis*, *Nodulosphaeria aquilegiae*, *N. thalictri*, *Paramassaria samaneae*, *Penicillium circulare*, *P. geumsanense*, *P. mali-pumilae*, *P. psychrotrophicum*, *P. wandoense*, *Phaeoisaria siamensis*, *Phaeopoacea asparagicola*, *Phaeosphaeria penniseti*, *Plectocarpon galapagoense*, *Porina sorediata*, *Pseudoberkleasium chiangmaiense*, *Pyrenochaetopsis sinensis*, *Rhizophydium koreanum*, *Russula prasina*, *Sporoschisma chiangraiense*, *Stigmatomyces chamaemyiae*, *S. cocksii*, *S. papei*, *S. tschirnhausii*, *S. vikhrevii*, *Thysanorea uniseptata*, *Torula breviconidiophora*, *T. polyseptata*, *Trochilispora schefflerae* and *Vaginatispora palmae*). Further, twelve new combinations (viz. *Cryptoschizotrema cryptotrema*, *Prolixandromyces australi*, *P. elongatus*, *P. falcatus*, *P. longispinae*, *P. microveliae*, *P. neolardi*, *P. polhemorum*, *P. protuberans*, *P. pseudoveliae*, *P. tenuistipitis* and *P. umbonatus*), an epitype is chosen for *Cantharellus goossensiae*, a reference specimen for *Acrogenospora sphaerocephala* and new synonym *Prolixandromyces* are designated. Twenty-four new records on new hosts and new geographical distributions are also reported (i.e. *Acrostalagmus annulatus*, *Cantharellus goossensiae*, *Coprinospora villosa*, *Dothiorella plurivora*, *Dothiorella rhamni*, *Dothiorella symphoricarposicola*, *Dictyocheirospora rotunda*, *Fasciatispora arengae*, *Grammothele brasiliensis*, *Lasiodiplodia iraniensis*, *Lembosia xylicola*, *Morenoina palmicola*, *Murispora cicognanii*, *Neodidymelliopsis farokhinejadii*, *Neolinocarpon rachidis*, *Nothophoma quercina*, *Peroneutypa scoparia*, *Pestalotiopsis aggestorum*, *Pilidium concavum*, *Plagiostoma salicellum*, *Protopenestella ulmi*, *Sarocladium kiliense*, *Tetraploa nagasakiensis* and *Vaginatispora armatispora*).

Keywords 71 new taxa · Ascomycota · Basidiomycota · Dothideomycetes · Eurotiomycetes · Lecanoromycetes · Leotiomyces · Pezizomycetes · Phylogeny · Taxonomy

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Caliciaceae Chevall.

1106. *Buellia viridula* Ekanayaka, & K.D. Hyde, *sp. nov.* (contribution by Hasini Ekanayaka)

Lecanorales Nannf.

Lecanoraceae Körb.

1107. *Lecidella yunnanensis* Ekanayaka, & K.D. Hyde, *sp. nov.* (contribution by Hasini Ekanayaka)

Pilocarpaceae Zahlbr.

1108. *Micarea squamulosa* Aptroot, Lücking & M. Cáceres, *sp. nov.* (contribution by André Aptroot/Robert Lücking/Marcela E. S. Cáceres)

Ostropomycetidae V. Reeb, Lutzoni & Cl. Roux

Ostropales Nannf.

Porinaceae Rchb.

1109. *Porina sorediata* Aptroot, Lücking & M. Cáceres, *sp. nov.* (contribution by André Aptroot/Robert Lücking/Marcela E.S. Cáceres)

Graphidaceae Dumort.

1110. *Cryptoschizotrema* Aptroot, Lücking & M. Cáceres, *gen. nov.* (contribution by André Aptroot/Robert Lücking/Marcela E.S. Cáceres)

1111. *Cryptoschizotrema cryptotrema* (Nyl.) Aptroot, Lücking & M. Cáceres, *comb. nov.* (contribution by André Aptroot/Robert Lücking/Marcela E.S. Cáceres)

Leotiomyces O.E. Erikss. & Winka

Helotiales Nannf.

Chaetomellaceae Baral, P.R. Johnst. & Rossman

1112. *Pilidium concavum* (Desm.) Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 124: 148 (1915), *new geographical record* (contribution by Milan Samarakoon/Jian-Kui Liu)

Pezizomycetes O.E. Erikss. & Winka

Pezizales J. Schröt.

Ascodesmidaceae J. Schröt.

1113. *Boubovia gelatinosa* M. Zeng, Q. Zhao & K.D. Hyde, *sp. nov.* (contribution by Ming Zeng/Hasini Ekanayaka)

Sordariomycetes O.E. Erikss. & Winka

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde

Diaporthales Nannf.

Diaporthaceae Höhn. ex Wehm.

1114. *Diaporthe italiana* Chethana, Camporesi & K. D. Hyde, *sp. nov.* (contribution by Thilini Chethana/Chinthani Senanayaka)

1115. *Diaporthe rumicicola* Manawas., Camporesi & K.D. Hyde, *sp. nov.* (contribution by Ishara Manawasinghe/Chinthani Senanayaka)

Gnomoniaceae G. Winter

1116. *Plagiostoma salicellum* (Fr.) Sogonov, Stud. Mycol. 62: 73 (2008), *new geographical record* (contribution by Digvijayini Bundhun/Chinthani Senanayaka/Rajesh Jeewon)

Diaporthomycetidae, families incertae sedis

Distoseptisporaceae K.D. Hyde & McKenzie

1117. *Distoseptispora dehongensis* W. Dong, H. Zhang & K.D. Hyde, *sp. nov.* (contribution by Wei Dong/Mingwan Doilom)

1118. *Distoseptispora palmarum* S.N. Zhang, K.D. Hyde & J.K. Liu, *sp. nov.* (contribution by Shengnan Zhang/Jian-Kui Liu)

Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Plectosphaerellaceae W. Gams, Summerb. & Zare

1119. *Acrostalagmus annulatus* (Berk. & M.A. Curtis) Seifert, Stud. Mycol. 68: 186 (2011), *new geographical record* (contribution by Subhashini Chathumini/Hansika Perera/Ruvishika S. Jayawardena)

Hypocreales Lindau

Cordycipitaceae Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

1120. *Cordyceps succavus* Y.P. Xiao, T.C. Wen & K.D. Hyde, *sp. nov.* (contribution by Yuanpin xiao/Ting-Chi Wen/Sinang Hongsan)

1121. *Blackwellomyces lateris* Y.P. Xiao, T.C. Wen & K.D. Hyde, *sp. nov.* (contribution by Yuanpin xiao/Ting-Chi Wen/Sinang Hongsan)

Hypocreales genera incertae sedis

1122. *Sarocladium kiliense* (Grütz) Summerb., Stud. Mycol. 68: 158 (2011), *new record* (contribution by Deping Wei/Dhanushka Wanasinghe)

Pleurotheciales Réblová & Seifert

Pleurotheciaceae Réblová & Seifert

1123. *Phaeoisaria siamensis* Jayasiri & K.D. Hyde, *sp. nov.* (contribution by Subashini Chathumini)

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

Savoryellaceae Jaklitsch & Réblová

1124. *Canalisporium dehongense* W. Dong, H. Zhang & K.D. Hyde, *sp. nov.* (contribution by Wei Dong/Mingkwan Doilom)

Sordariomycetidae O.E. Erikss. & Winka

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

1125. *Sporoschisma chiangraiense* N.G. Liu & K.D. Hyde, *sp. nov.* (contribution by Ningguo Liu/Jian-Kui Liu)

1126. *Ellisembia aurea* Réblová & J. Fourn., *sp. nov.* (contribution by Réblová Martina/Jacques Fournier/Jana Nekvindová)

Linocarpaceae Konta & K.D. Hyde

1127. *Neolinocarpon rachidis* Konta & K.D. Hyde, *Mycosphere* 8: 1968 (2017), *new record* (contribution by Sirinapa Konta/Saranyaphat Boonmee)

Xylariomycetidae O.E. Erikss & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Amphisphaeriaceae G. Winter

1128. *Trochilisporea* V.P. Abreu, A.W.C. Rosado & O.L. Pereira, *gen. nov.* (contribution by Olinto Pereira/Abreu VP/Rosado AWC)

1129. *Trochilisporea schefflerae* V.P. Abreu, A.W.C. Rosado & O.L. Pereira, *sp. nov.* (contribution by Olinto Pereira/Abreu VP/Rosado A.W.C)

Sporocadaceae Corda.

1130. *Pestalotiopsis aggestorum* F. Liu & L. Cai, *Nature Scientific Reports* 7: 870 (2017), *new geographical record* (contribution by Nimali I. De silva/Sajeewa Maharachchikumbura)

Xylariales Nannf.

Castanediellaceae Hern.-Restr., Guarro & Crous

1131. *Castanediella meliponae* J.E. Felinto-Santos, R.N. Barbosa & N.T. Oliveira, *sp. nov.* (contribution by Renan do Nascimento Barbosa/José Ewerton Felinto dos Santos/Neiva Tinti de Oliveira)

Diatrypaceae Nitschke

1132. *Diatrypella delonicis* R.H. Perera & K.D. Hyde, *sp. nov.* (contribution by Hansika Perera/Monika Dayarathna)

1133. *Peroneutypa scoparia* Carmarán & A.I. Romero, *Fungal Divers.* 23: 84 (2006), *new record from mangrove habitat* (contribution by Vinith Kumar/Monika Dayarathna)

Xylariaceae Tul. & C. Tul.

1134. *Fasciatispora arengae* Konta & K. D. Hyde, *Mycosphere* 9: 725 (2018), *new record* (contribution by Sirinapa Konta/Saranyaphat Boonmee)

Basidiomycota R.T. Moore

Agaricomycetes Doweld

Agaricomycetidae Parmasto

Agaricales Underw.

Cortinariaceae R. Heim ex Pouzar (contribution by Tuula Niskanen/Kare Liimatainen)

1135. *Cortinarius minusculus* Liimat. & Niskanen, *sp. nov.*

1136. *Cortinarius subscotoides* Niskanen & Liimat., *sp. nov.*

Psathyrellaceae Vilgalys et al.

1137. *Coprinopsis psammophila* Mešić & Tkalčec, *sp. nov.* (contribution by Armin Mešić/Zdenko Tkalčec)

1138. *Coprinopsis villosa* L. Nagy, Desjardin, Vágvolgyi & Papp, *Mycologia* 105(1): 120 (2013), *new geographical record* (contribution by Armin Mešić/Zdenko Tkalčec)

Cantharellales Gäum.

Botryobasidiaceae Jülich (contribution by Sanjay K. Singh/Paras Nath Singh)

1139. *Neoaccladium* P.N. Singh & S.K. Singh, *gen. nov.*

1140. *Neoaccladium indicum* P.N. Singh & S.K. Singh, *sp. nov.*

Hydnaceae Chevall (contribution by Bart Buyck/E. Randrianjohany/V. Hofstetter)

1141. *Cantharellus goossensiae* (Beeli) Heinem., *Bull. Jard. Bot. Etat Brux.* 28: 406 (1958), *epitypification and new records*

1142. *Cantharellus brunneopallidus* Buyck, Randrianjohany & V. Hofst., *sp. nov.*

1143. *Cantharellus griseotinctus* Buyck, Randrianjohany & V. Hofst., *sp. nov.*

Hymenochaetales Oberw.

Hymenochaetaceae Donk (contribution by Yu-Cheng Dai/Xiao-Hong Ji/Xue-Mei Tian)

1144. *Fomitiporia carpinea* X.H. Ji, X.M. Tian & Y.C. Dai, *sp. nov.*

1145. *Fomitiporia lagerstroemiae* X.H. Ji, X.M. Tian & Y.C. Dai, *sp. nov.*

Polyporales Gäum.

Grammotheleaceae Jülich (contribution by Tatiana B. Gibertoni/A.M.S. Soares/Helio Longoni Plautz Jr/Helen Maria Pontes Sotão/William Kalhy Silva Xavier)

1146. *Grammothele aurantiaca* A.M.S. Soares, *sp. nov.*

1147. *Grammothele micropora* A.M.S. Soares & W.K.S. Xavier, *sp. nov.*

1148. *Grammothele brasiliensis* Ryvarden, Syn. Fung. 33: 38 (2015), *new record*

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David

Russulaceae Lotsy (contribution by Guo-Jie Li/Rui-Lin Zhao)

1149. *Russula prasina* G.J. Li & R.L. Zhao, *sp. nov.*

Chytridiomycota Arx

Rhizophyidiomycetes Tedersoo, Koljalg

Rhizophydiales Letcher

Rhizophydiaceae Werderm. (contribution by Hyang Burn Lee/Sun Jeong Jeon/Thuong T.T. Nguyen)

1150. *Rhizophydium koreanum* Hyang B. Lee, S.J. Jeon, T.T.T. Nguyen, *sp. nov.*

Introduction

Fungi play vital roles in all ecosystems, as decomposers, epiphytes, endophytes, other symbionts of plants, as well as animal and plant pathogens (de Silva et al. 2016; Liu et al. 2017; Hyde et al. 2018a). They are hyper-diverse and heterogeneous group of organisms that represent a large and diverse component of microbial diversity (Hawksworth 2001; Hernández-Restrepo et al. 2017). Fungi show a great variation in morphology, reproduction, life cycles and modes of dispersal (Promputtha et al. 2007; Lofgren et al. 2018). They exhibit different lifestyles, including being endophytes, biotrophs, hemi-biotrophs, necrotrophs and saprotrophs (de Silva et al. 2016). Fungal communities are a major component of soil biomass; they accelerate rock weathering and decay dead plant material (Kendrick 2000; Finlay 2008). They are an essential part of the ecosystem because they play an important role in the decomposition of organic materials (Soares et al. 2017; Asplund et al. 2018).

The diversity of fungi has been estimated to range between 2.2 to 3.8 million (Hawksworth and Lücking 2017) however, only 120,000 species are presently known. Hence, many species are still undescribed. One reason behind this is due to the fact that many common fungi are cosmopolitan, having a wider geographical distribution than plants and other organisms. The fungi of many continents besides Europe have been poorly studied and in many cases European names have been given to non-European taxa without in depth analysis. Fungal inventories in many countries and in their infancy. This was shown in a recent study on the fungi of northern Thailand where up to 96% of species in a genus of mushrooms were found to be new to science (Hyde et al. 2018b). Despite all challenges, researchers have established reliable ways to resolve fungal taxa at the ordinal, familial and generic, as

well as species levels (Hyde et al. 2013, 2017a, b, 2018b; Ariyawansa et al. 2015; Wanasinghe et al. 2018a; Phookamsak et al. 2019). Major results include 16 phyla being accepted in the kingdom fungi (Tedersoo et al. 2018; Wijayawardene et al. 2018a), an outline of the Ascomycota provided by Wijayawardene et al. (2018a) and an outline of the basal fungi by Wijayawardene et al. (2018b). In addition, *Fungal Diversity notes* (Ariyawansa et al. 2015; Hyde et al. 2016, 2018a; Wanasinghe et al. 2018a; Phookamsak et al. 2019), *Fungal Planet* (Crous et al. 2014) and *Mycosphere notes* series (Hyde et al. 2017b; Thambugala et al. 2017b; Jayawardena et al. 2018) have provided outlets for introducing the numerous new species of fungi.

More than 1000 entries in *Fungal Diversity notes* introducing new taxa, reference specimens, new data, and other taxonomic contributions have been published with phylogenetic analyses. This is the tenth in the series of *Fungal Diversity notes* with more than 100 entries mainly collected from China, Italy, Russia, Thailand, plus some other Asian and European countries. The outcome of the series provides a stable taxonomy and phylogeny that can provide definitive classifications for researchers who need to accurately identify fungi in their research work.

Materials and methods

Materials and methods follow the previous fungal diversity notes (Hyde et al. 2016; Tibpromma et al. 2017; Wanasinghe et al. 2018a; Phookamsak et al. 2019).

Ascomycota R.H. Whittaker

Notes: We follow the latest treatments and updated accounts of Ascomycota in Wijayawardene et al. (2017a, 2018a).

Class Arthoniomycetes O.E. Erikss. & Wink

Arthoniomycetidae P.M. Kirk, P. Cannon, Minter & Stalpers

Arthoniales Henssen ex D. Hawksw. & O.E. Erikss.

Notes: The order Arthoniales is one of the main lichenized groups of the Ascomycota and belongs to the class Arthoniomycetes O.E. Erikss. & Wink in the Pezizomycotina O.E. Erikss. & Wink. The order currently includes the families Andreiomycetaceae B.P. Hodk. & Lendemer, Arthoniaceae Rchb. ex Rchb., Chrysotrichaceae Zahlbr., Lecanographaceae Ertz et al., Opegraphaceae Körb. ex Stizenb., Roccellaceae Chevall. and Roccellographaceae, and about 1500 accepted species (Lücking et al. 2017). Most species of Arthoniales form lichen symbioses, mainly with trentepohlioid algae, but 285 species are obligately lichenicolous (non-lichenized) (Diederich et al. 2018) and a few are considered as being doubtfully or not lichenized.

Lecanographaceae Ertz et al.

Notes: The family Lecanographaceae was recognized in Ertz and Tehler (2011) and a formal description was given in Frisch et al. (2014) based on the type genus *Lecanographa* Egea & Torrente, along with *Alyxoria* Ach. ex Gray, *Phacographa* Hafellner, *Plectocarpon* Fée and *Zwackhia* Körb. Some *Opegrapha* species (viz. *O. brevis* and *O. celtidicola*) were placed in this family with molecular evidence but will have to be combined in another genus because the type of *Opegrapha* (*O. vulgata*) belongs to the Opegraphaceae.

Plectocarpon Fée

Notes: The genus *Plectocarpon* Fée was introduced in 1825 as a replacement for *Delisea* Fée, a later homonym of *Delisea* Lamouroux (Rhodophyta). *Plectocarpon* was first established for a lichen (now *Pseudocyphellaria glabra*) because Fée did not realized that the ascomata were those of a lichenicolous fungus. The lichenicolous habit was recognized 159 years later and the name *Plectocarpon* resurrected for a genus of lichenicolous fungi (Hawksworth and Galloway 1984; Galloway 2006). A world monograph of the genus accepted 32 species, 15 newly described (Ertz et al. 2005), while a few other species were added in recent years. The genus was placed in the Lecanographaceae with molecular evidence using *Plectocarpon lichenum* (Sommerf.) D. Hawksw. and *P. nephroleum* (Norman) R. Sant. (Frisch et al. 2014), but the generic type still needs to be sequenced.

Plectocarpon galapagoense Ertz & Bungartz, *sp. nov.*

Index Fungorum number: IF556360; **Facesoffungi number:** FoF05977; **Fig. 1**

Etymology: Referring to the occurrence in the Galapagos Islands.

Holotype: CDS 33415

Ascomata lichenicolous, infecting and developing inside the host ascomata and thallus of *Sarcographa tricola* sensu lato, at first immersed, later bursting through the host ascomata and thallus, black, epruinose, star-shaped becoming rounded, 1–2 mm diam., not gall-inducing, not constricted at the base, not producing necrotic areas; surface of lichenicolous ascomata plane to slightly convex, distinctly lirellate-labyrinthiform with slit-like hymenial disc, epruinose, typically delimited by remnants of lirellae and thallus cortex from the host, in particular along the ascomatal margins of the lichenicolous fungus. **Stroma** c. 90–130 µm thick; sterile stromatic hyphae dark brown to carbonized above, 15–40 µm thick, poorly developed between the loculi, absent below, K–. **Hymenium** hyaline, not interspersed with oil droplets, 65–100 µm high; hymenial gel I + directly reddish or I + blue turning reddish, K/I + blue; epihymenium hyaline to pale brown, K–, I + blue turning reddish with some parts remaining blue.

Subhymenium hyaline or pale brown, K–, I + blue with some parts turning reddish, 10–20 µm high. **Paraphysoids** sparingly branched in the hymenium, richly branched in the epihymenium, 1.5 µm thick, with broadened tips, 2.5–3 µm. **Asci** subcylindrical to narrowly clavate, with a narrow ocular chamber, with a tiny K/I + blue ring in mature asci, (4–)6(–8)-spored, 55–70 × 11–14 µm. **Ascospores** fusiform, (2–)3-septate, septation starts with one median septum, the second cell often slightly larger, hyaline, becoming dark brown granulose when overmature, (15–)16.5–20.0(–22) × (4.5–)4.5–5.5(–6) µm (n = 50), l/b ratio 3.5–4.0; perispore hyaline, 1–1.5(–2) µm thick. **Conidiomata** sphaerical, immersed between the lirellae: wall dark brown, K–, c. 4–10 µm thick; conidia bacilliform, 4–5 × 1 µm.

Material examined: ECUADOR, Galapagos Islands, Pinta Island, just below the highest point of the island, 0° 35' 2" N, 90° 45' 13" W, 615 m elev., forest of *Zanthoxylum fagara* with abundant ferns in the understory, lichenicolous on *Sarcographa tricola* sensu lato growing on twigs and branches of *Chiococca alba*, 26 February 2007, F. Bungartz 5759 A (CDS 33415, **holotype**); F. Bungartz 5755 A (CDS 33411, **paratype**); F. Bungartz 5760 A (CDS 33416, **paratype**).

Distribution and ecology: Described as new from Galapagos and probably endemic; this lichenicolous fungus seems to be weakly parasitic, as no necrotic areas are visible on the hosts ascomata and thallus of *Sarcographa tricola* sensu lato. However, as the lichenicolous fungus frequently occur on the ascomata of the host, it should incur a significant damage and deprive the host of some of its reproductive structures. The host lichen belongs to *S. trigosa* sensu lato (identification by Robert Lücking): excipulum very thin, c. 8–25 µm laterally; hymenium not interspersed, of c. 100–125 µm high; hypothecium hyaline, c. 12–25 µm; ascospores 5-septate, with thick septa, hyaline becoming greyish brown, c. 20–28 × 7–8 µm.

Notes: In the key to *Plectocarpon* provided by Ertz et al. (2005), the new species would key out close to *Plectocarpon macaronesiae* Diederich, Etayo & Sérusiaux, but that species is endemic to Macaronesia and differs from *P. galapagoense* by smaller ascomata (up to 1.1 mm diam.), with a shiny rough surface, K + green intensifying sterile stromatic hyphae and a different host genus (*Lobaria*). Among the recently described *Plectocarpon* species, *P. dirinariae* Ertz & van den Boom is the most similar to *P. galapagoense* but it differs by strongly convex and entirely non-carbonized ascomata and a different host genus (*Dirinaria*) (Ertz & van den Boom 2012). *Plectocarpon aequatoriale* Etayo, described from Ecuador, has notably strongly convex ascomata, longer ascospores and a different host genus (*Sticta*) (Etayo 2017). *Opegrapha plectocarpoidea* Diederich is lichenicolous on *Phaeographis* and

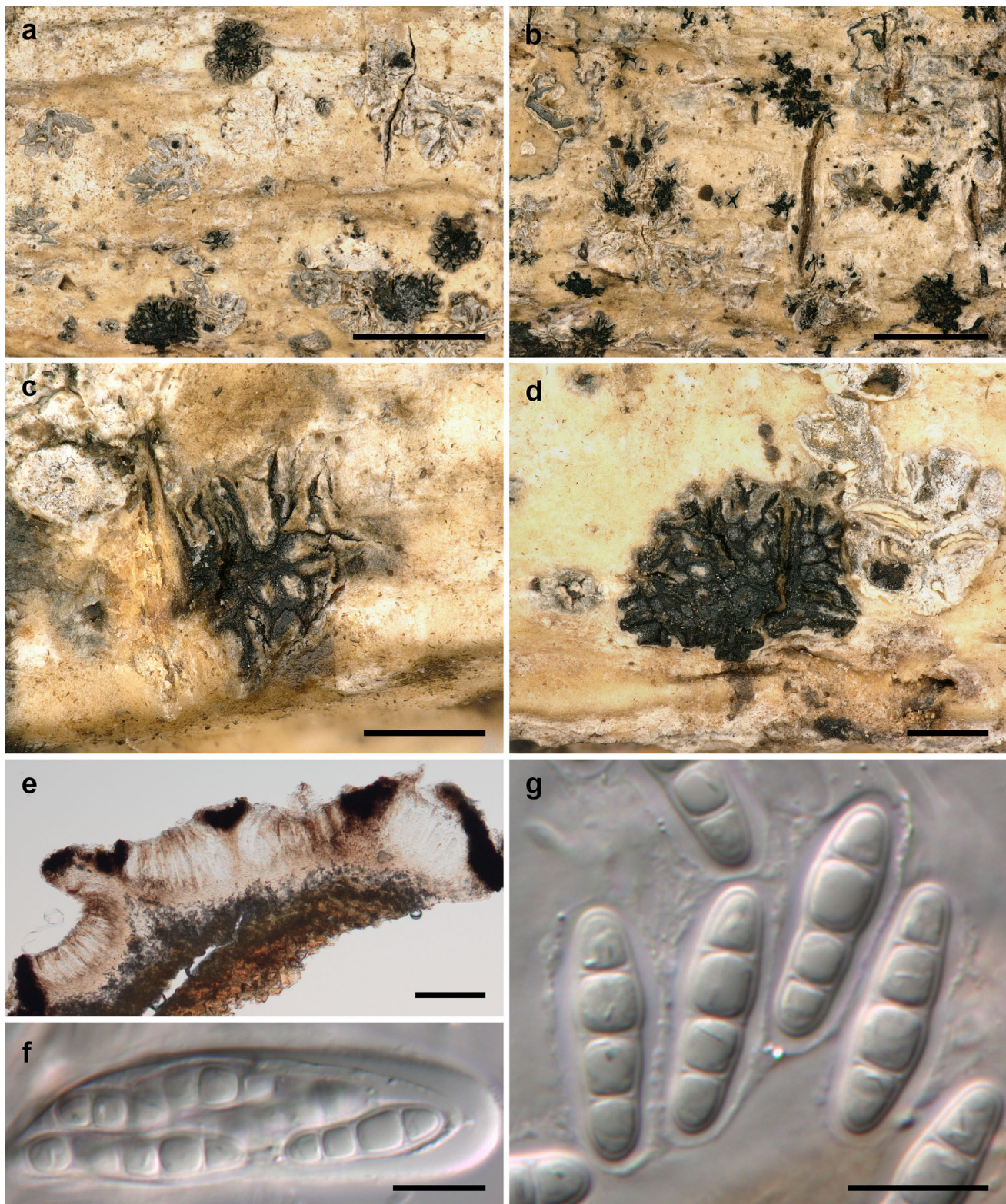


Fig. 1 *Plectocarpon galapagoense* (Bungartz 5759A, holotype). **a–d** Black ascomata emerging from the lirellate ascomata and the thallus of the host lichen (= *Sarcographa tricola* sensu lato, with paler, distinctly pruinose disc). **a, b** Overview of the infected host lichen. **c, d** Detail of lichenicolous ascomata. **c** The left part of the lichenicolous

ascoma has been removed for microscopical examination. **d** The lichenicolous ascoma can be seen on the left, the still intact part of an ascoma of the host on the right. **e** Section through an ascoma of *Plectocarpon*, in water. **f** Ascus in KOH. **g** Ascospores in KOH. Scale bars: **a, b** = 2.5 mm, **c, d** = 500 µm, **e** = 100 µm, **f, g** = 10 µm

reminds of a species of *Plectocarpon* (Aptroot et al. 1997). That species, known from high altitude in Papua New Guinea, differs from *Plectocarpon galapagoense* by indistinctly lirellate, almost rounded ascomata with 8-spored asci and a dark brown exciple that continues below the hymenium.

Class Dothideomycetes O.E. Erikss. & Winka

Notes: Dothideomycetes is the largest class of Ascomycota. Liu et al. (2017) provided an updated multi-locus phylogeny of the class Dothideomycetes with molecular dating evidence to unravel the evolutionary relationships and strengthen the ranking among taxa. In this study, we follow the classifications in the studies of Hyde et al. (2013), Wijayawardene et al. (2014) and Liu et al. (2017). The subclasses of Dothideomycetes and their families in each order are listed in alphabetical order.

Dothideomycetidae P.M. Kirk, P.F. Cannon, J.C. David & Stalpers

Notes: Dothideomycetidae was introduced by Kirk et al. (2001) and later validated by Schoch et al. (2006). According to the present status, Dothideomycetidae comprises the orders Capnodiales, Dothideales and Myriangiales which lack pseudoparaphyses and periphyses (Hyde et al. 2013).

Capnodiales Woron.

Notes: See Chomnunti et al. (2011) and Hyde et al. (2013) for details.

Teratosphaeriaceae Crous & U. Braun

Notes: The family Teratosphaeriaceae (Capnodiales, Dothideomycetes) represents complex cryptic taxa that are characterized by globular ascomata with brown walls of *textura angularis*, located in a stroma of pseudoparenchymatous cells (Crous et al. 2007). Teratosphaeriaceae comprises 59 quite diverse genera (Wijayawardene et al. 2018a), accommodating endophytic, saprobic, phytopathogenic, and opportunistic species (Crous et al. 2009; Quaedvlieg et al. 2014). We introduce a new genus *Caatingomyces* within Teratosphaeriaceae based on phylogenetic analyses of ITS and LSU rDNA sequence data, morphology and ecology. In this paper we introduce a new monotypic genus.

Caatingomyces T.G.L. Oliveira, C.M. Souza-Motta, O.M.C. Magalhães & J.D.P. Bezerra, *gen. nov.*

Mycobank number: MB827888; **Facesoffungi number:** FoF05818

Etymology: Named after its occurrence in the Brazilian tropical dry forest, Caatinga.

Endophytic in plants. **Sexual morph** Undetermined. **Asexual morph** *Mycelium* superficial or immersed, hyaline to medium brown, septate, branched, hyphae thin-walled,

broad and darker when adhered to the conidiomata. **Conidiomata** pycnidial, superficial or immersed, isolated or clustered, globose to subovoid, medium brown when young and dark at maturity, pseudoparenchymatous, glabrous, thin-walled. **Neck** absent or poorly developed, conidia released by irregular rupture. **Conidiogenous cells** phialidic, slightly tapered and truncated at the apex with robust base, sometimes branched, hyaline to medium brown, formed from the internal cells of the pycnidial wall. **Conidia** hyaline, aseptate, ellipsoid, obtuse apex with truncated base, smooth, thin-walled.

Type: *Caatingomyces brasiliensis* T.G.L. Oliveira, C.M. Souza-Motta, O.M.C. Magalhães & J.D.P. Bezerra.

Caatingomyces brasiliensis T.G.L. Oliveira, C.M. Souza-Motta, O.M.C. Magalhães & J.D.P. Bezerra, *sp. nov.*

Mycobank number: MB827889; **Facesoffungi number:** FoF05817; **Fig. 2**

Etymology: Named after its occurrence in Brazil.

Holotype: URM 91831

Endophyte of branches of *Poincianella pyramidalis*.

Sexual morph Undetermined. **Asexual morph** *Mycelium* superficial or immersed, hyaline to medium brown, septate, branched, hyphae thin-walled, broad and darker when linked to the conidiomata. **Conidiomata** pycnidial (28.6–) 31.2–52 (–67.6) × (23.4–) 26–31.2 (–52) µm, superficial or immersed in the culture medium, isolated or clustered, globose to subovoid, medium brown when young and dark at maturity, pseudoparenchymatous, glabrous, thin-walled. **Rostrate ostiole** absent or poorly developed, conidia released by irregular rupture. **Conidiogenous cells** (3–) 3.5–5 (–6.5) × (3–) 4–5.5 µm, phialidic, slightly tapered and truncated at apex with robust base, sometimes branched, hyaline to medium brown, arising from the internal cells of the pycnidial wall. **Conidia** (3.2–) 4.2–5.3 × 2.1 µm, hyaline, aseptate, ellipsoid, apex obtuse with truncated base, smooth and thin-walled.

Culture characteristics: Colonies reaching 3 to 3.5 cm in diameter after 15 days at 25 °C in the dark. On OA spreading, erumpent, aerial mycelium sparse with smooth margins; surface grey-olivaceous to white, reverse black. On PDA spreading, erumpent, aerial mycelium sparse with smooth and uneven margins; surface yellowish-brown to pale brown with presence of yellowish exudate, reverse pale brown centre to black at the extremities. On MEA spreading, initially creamy, erumpent, surface yellowish-whitish with smooth margins and presence of exudate, reverse beige.

Material examined: BRAZIL, Paraíba State, Santa Teresinha municipally, Tamanduá farm, 07°1.524S, 037°23.518 W, as endophyte from branches of *Poincianella pyramidalis* (Fabaceae), May 2013, J.D.P. Bezerra (URM 91831, **holotype**), ex-type living culture (URM 7916); as endophyte from branches of *Poincianella*

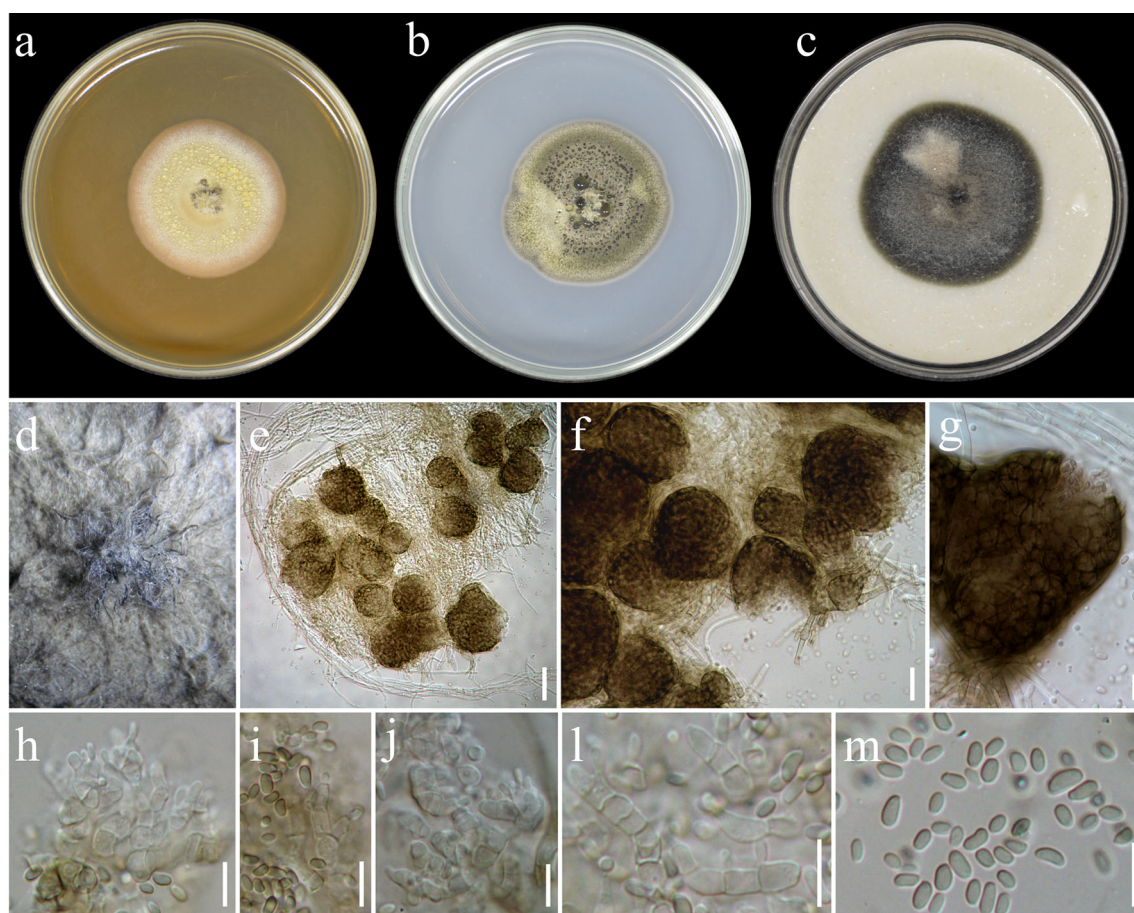


Fig. 2 *Caatingomyces brasiliensis* (URM 91831, **holotype**). **a** Colony on MEA after 7 days. **b** Colony on PDA after 7 days. **c** Colony on AO after 7 days. **d** Detail of colony on PDA after 7 days.

e Pycnidia. **f** Detail of pycnidia. **g** Detail of pycnidial wall. **h–l** Conidiogenous cells and conidia. **m** Conidia. Scale bars: **e** = 50 μ m, **f** = 25 μ m, **g–m** = 10 μ m

pyramidalis (Fabaceae), May 2013, J.D.P. Bezerra, living culture (URM 7917).

GenBank numbers: ITS: MH929437, MH929438, LSU: MH929439, MH929440, RPB2: MH929441, MH929442, TEF1- α : MH929443, MH929444.

Notes: Maximum likelihood analysis using the alignment of LSU rDNA sequences as presented by Quaedvlieg et al. (2014), demonstrated relationships of the new genus with *Readeriella* Syd. & P. Syd. in Teratosphaeriaceae (data not shown). In the phylogenetic analyses (Fig. 3) using combined LSU and ITS sequence data of Teratosphaeriaceae, the new genus *Caatingomyces* is related to *Readeriella* species, but was placed in a distinct clade with high support. The TEF1- α and RPB2 sequences of *C. brasiliensis* were not included in the combined analyses, but are available in GenBank for further verification of its relationships and placement in Teratosphaeriaceae and affiliated families.

Caatingomyces brasiliensis mainly differs from *Readeriella* species that have a thick conidiomata wall, the presence of single and circular ostiole, by the shape of the

conidiogenous cells producing three collarettes and deltoid, thick-walled and guttulate conidia with 3 lateral obtuse projections (Sutton 1980). Furthermore, *Caatingomyces* also differs from species of other genera in Teratosphaeriaceae, such as *Parapenidiella* Crous & Summerell which has conidia arranged in branched acropetal chains, pigmented ramoconidia, and erect and macrone-matous conidiophores (Crous et al. 2012); from *Eupenidiella* Quaedvl. & Crous by erect and solitary, terminally penicillate conidiophores and subcylindrical conidia arranged in branched chains and secondary conidia (Quaedvlieg et al. 2014).

Subclass Pleosporomycetidae C.L. Schoch et al.

Pleosporales Luttr. ex M.E. Barr

Notes: Pleosporales was established by Luttrell (1955) to accommodate members of Dothideomycetes having perithecioid ascomata with pseudoparaphyses amongst the asci (Zhang et al. 2009a). Pleosporales members are highly diverse and can be endophytes or epiphytes, parasitices, lichenicolous or saprobes in terrestrial or aquatic

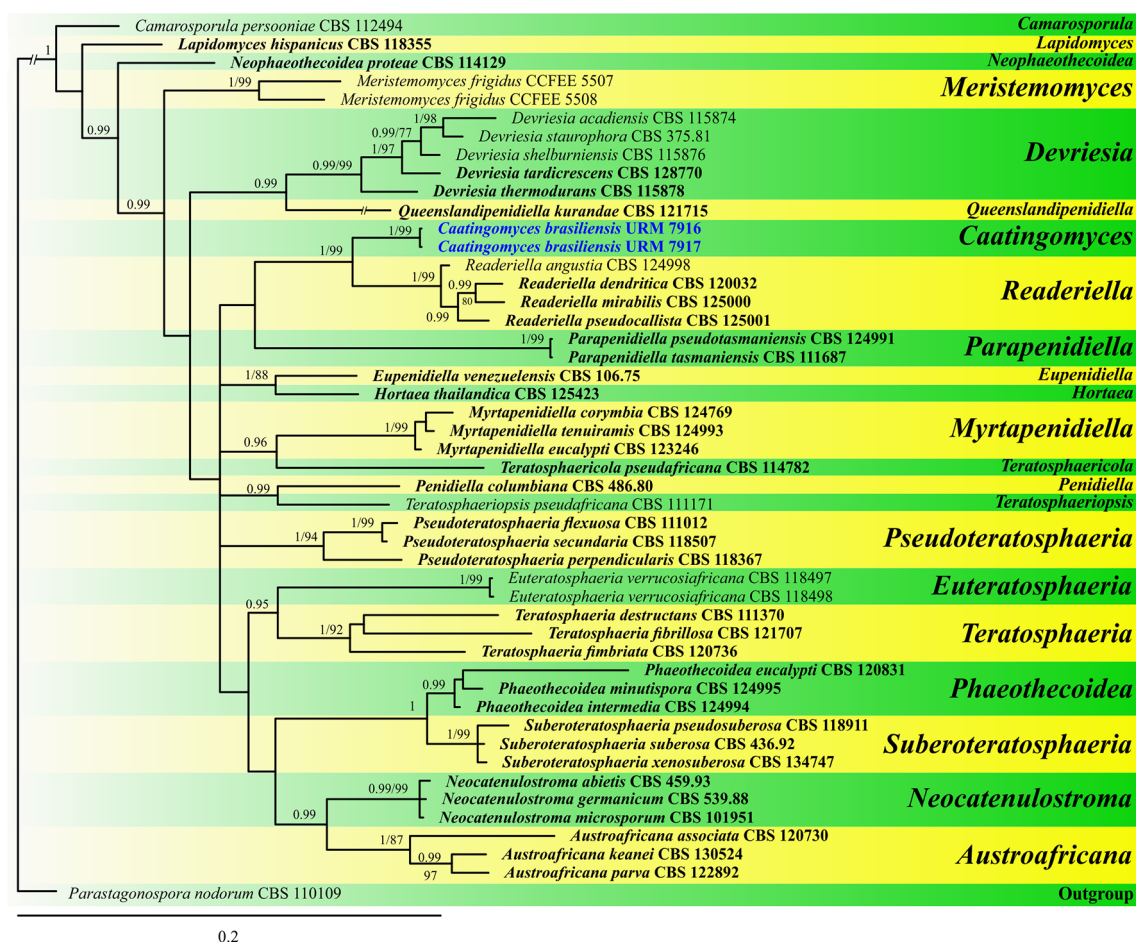


Fig. 3 Phylogram generated from Bayesian inference analysis based on combined LSU and ITS sequence data from 45 representative members of Teratosphaeriaceae. Related sequences are taken from Quaedvlieg et al. (2014). Forty-eight strains are included in the combined gene analyses comprising 1326 characters after alignment (708 characters for LSU, 618 characters for ITS). *Parastagonospora nodorum* (CBS 110109) (Phaeosphaeriaceae, Pleosporales) is used as the outgroup taxon. Analyses of each single gene were performed and the topology of each tree had clade stability. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. In the Bayesian inference analysis presented, the estimated base frequencies for the LSU region were as follows: A = 0.2445, C = 0.2356, G = 0.3014, T = 0.2186; substitution rates AC = 0.5614,

AG = 1.2118, AT = 0.8832, CG = 0.6931, CT = 5.0186, GT = 1.0000; range distribution parameter α = 0.6982. The estimated base frequencies for the ITS region were as follows: A = 0.1855, C = 0.3132, G = 0.2366, T = 0.2647; substitution rates AC = 2.1196, AG = 3.1193, AT = 2.6297, CG = 2.0375, CT = 5.3598, GT = 1.0000; range distribution parameter α = 0.4064. The best ranking RaxML tree with a final probability value was of -8679.44 . The matrix presented 1063 distinct alignment patterns, with 35.42% of characters or indeterminate intervals. Branches with later Bayesian probabilities (BYPP) equal to or greater than 0.95 and bootstrap support values for maximum likelihood (ML) analysis greater than 70 are placed above or below nodes. Ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

environments or even occur on animal dung (Zhang et al. 2009a). Among the orders of Dothideomycetes, Pleosporales is the largest and most diverse order containing more than 75 families (Wijayawardene et al. 2018a).

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

Notes: The family Amniculicolaceae was introduced by Zhang et al. (2009a) to describe various freshwater taxa from Europe and later accepted by Shearer et al. (2009) with a well-supported phylogeny. The family is characterized by “ascmata with a rough black surface, usually staining the woody substrate purple, narrow

pseudoparaphyses and short-pedicellate asci, bearing hyaline, reddish-brown or pale, 1- to multi-septate or muriform ascospores, generally with a hyaline gelatinous sheath” (Zhang et al. 2008).

Amniculicola Y. Zhang ter & K.D. Hyde

Notes: *Amniculicola* was introduced to accommodate *A. lignicola*, which was isolated from submerged wood in freshwater in France (Zhang et al. 2008). This genus is characterised by ascmata with slit-like ostioles, thin, branching and anastomosing pseudoparaphyses, cylindrical asci, and hyaline, 1–3-septate ascospores. Presently, four species, viz. *Amniculicola immersa*, *A. lignicola*, *A.*

longissima, *A. parva* are accepted in *Amniculicola* and all species were collected from freshwater habitats.

Amniculicola aquatica Z.L. Luo, K.D. Hyde & H.Y. Su, *sp. nov.*

Index Fungorum number: IF555506; *Facesoffungi* number: FoF05308; Fig. 4

Etymology: Referring to the aquatic habitat of this fungus.

Holotype: MFLU 18–1324

Saprobic on decaying wood submerged in freshwater.

Sexual morph *Ascomata* 260–330 µm high, 250–320 µm diam., solitary, scattered, or in small groups, superficial, coriaceous, with basal wall remaining immersed in host tissue, globose to subglobose, black, often laterally flattened, with a flattened base not easily removed from the substrate, mostly bearing remnants of wood fibres. *Peridium* 35–50 µm thick, 2-layered, outer layer composed of small, dark brown to black, heavily pigmented, thick-walled cells of *textura angularis*, cells at apex smaller and walls thicker, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Hamathecium* of dense, very long trabeculate pseudoparaphyses. *Asci* 110–130(–152) × 10–13 µm (\bar{x} = 120 × 11.5 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, twisted, bifurcate pedicel. *Ascospores* 24–32 × 6–8 µm (\bar{x} = 28 × 7 µm, n = 25), obliquely uniseriate and partially overlapping, fusiform, with narrowly rounded to acute ends, hyaline, uniseptate, deeply constricted at the septum, sometimes curved, smooth, with 4–6 prominent guttules, and a wide gelatinous sheath. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, saprobic on decaying wood submerged in Erhai Lake, March 2015, Z.L. Luo, S-318 (MFLU 18-1324, **holotype**; HKAS 92579, **isotype**), ex-type living culture (MFLUCC 16-1123); saprobic on decaying wood submerged in Erhai Lake, March 2015, H.Y. Su, S-467 (MFLU 18-1325, **paratype**; HKAS 92559), ex-paratype living culture (MFLUCC 16-0915).

GenBank numbers: LSU: MK106096, TEF1- α : MK109800 (MFLUCC 16-1123); LSU: MK106097, SSU: MK106108, TEF1- α : MK109801 (MFLUCC 16-0915).

Notes: *Amniculicola aquatica* mostly resembles *A. parva* in having superficial, coriaceous ascomata of similar size, cylindrical asci with a short, narrowed, twisted, bifurcate pedicel and fusiform, hyaline ascospores with a wide gelatinous sheath. However, *A. aquatica* differs from *A. parva* has a thicker peridium, and uniseptate, wider ascospores (6–8 vs. 4.5–6.5 µm) (Zhang et al. 2009b). Phylogenetic analysis based on LSU, SSU and TEF1- α sequence data showed that *A. aquatica* is a distinct taxon in the genus *Amniculicola* (Fig. 7).

Amniculicola guttulata Z.L. Luo, K.D. Hyde & H.Y. Su, *sp. nov.*

Index Fungorum number: IF555507; *Facesoffungi* number: FoF05309; Fig. 5

Etymology: Referring to the ascospores with large guttules.

Holotype: MFLU 18–1326

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph** *Ascomata* 290–320 µm high, 280–300 µm diam., solitary, scattered, or in small groups, superficial, coriaceous, with basal wall remaining immersed in host tissue, globose to subglobose, black, often laterally flattened, with a flattened base not easily removed from the substrate, mostly bearing remnants of wood fibres. *Peridium* 27–35 µm thick, 2-layered, outer layer composed of small, brown to dark brown, thick-walled cells of *textura angularis*, cells at apex smaller and walls thicker, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Hamathecium* of dense, very long trabeculate pseudoparaphyses. *Asci* 113–127 × 9–11 µm (\bar{x} = 120 × 10 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, twisted, bifurcate pedicel. *Ascospores* 23–27 × 5–7 µm (\bar{x} = 25 × 6 µm, n = 25), obliquely uniseriate and partially overlapping, fusiform, with narrowly rounded to acute ends, hyaline, uniseptate, deeply constricted at the septum, sometimes curved, smooth, with 4–6 prominent guttules, and gelatinous sheath. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, saprobic on decaying wood submerged in Dulong River, May 2015, Z.L. Luo, S-428 (MFLU 18-1326, **holotype**; HKAS 92685, **isotype**), ex-type living culture (MFLUCC 16-0907); saprobic on decaying wood submerged in Dulong River, May 2015, Z.L. Luo, S-516, living culture MFLUCC 16-1297; saprobic on decaying wood submerged in Nujiang River, May 2015, Z.L. Luo, S-538 (MFLU 18-1327, **paratype**), ex-paratype living culture (DLUCC 0538).

GenBank numbers: LSU: MK106098, TEF1- α : MK109802 (MFLUCC 16-0907); LSU: MK106099 (MFLUCC 16-1297); LSU: MK106100, SSU: MK106109, TEF1- α : MK109803 (DLUCC 0538).

Notes: The new species *Amniculicola guttulata* resembles *A. aquatica* in having superficial, coriaceous, globose to subglobose ascomata, cylindrical asci of similar size and with a short, narrowed, twisted, bifurcate pedicel, and fusiform, hyaline, uniseptate ascospores deeply constricted at the septum. However, *A. guttulata* differs from *A. aquatica* has a thinner peridium and smaller ascospores (23–27 × 5–7 vs. 24–32 × 6–8 µm). Phylogenetic analysis showed that isolates of *A. guttulata* formed a separate

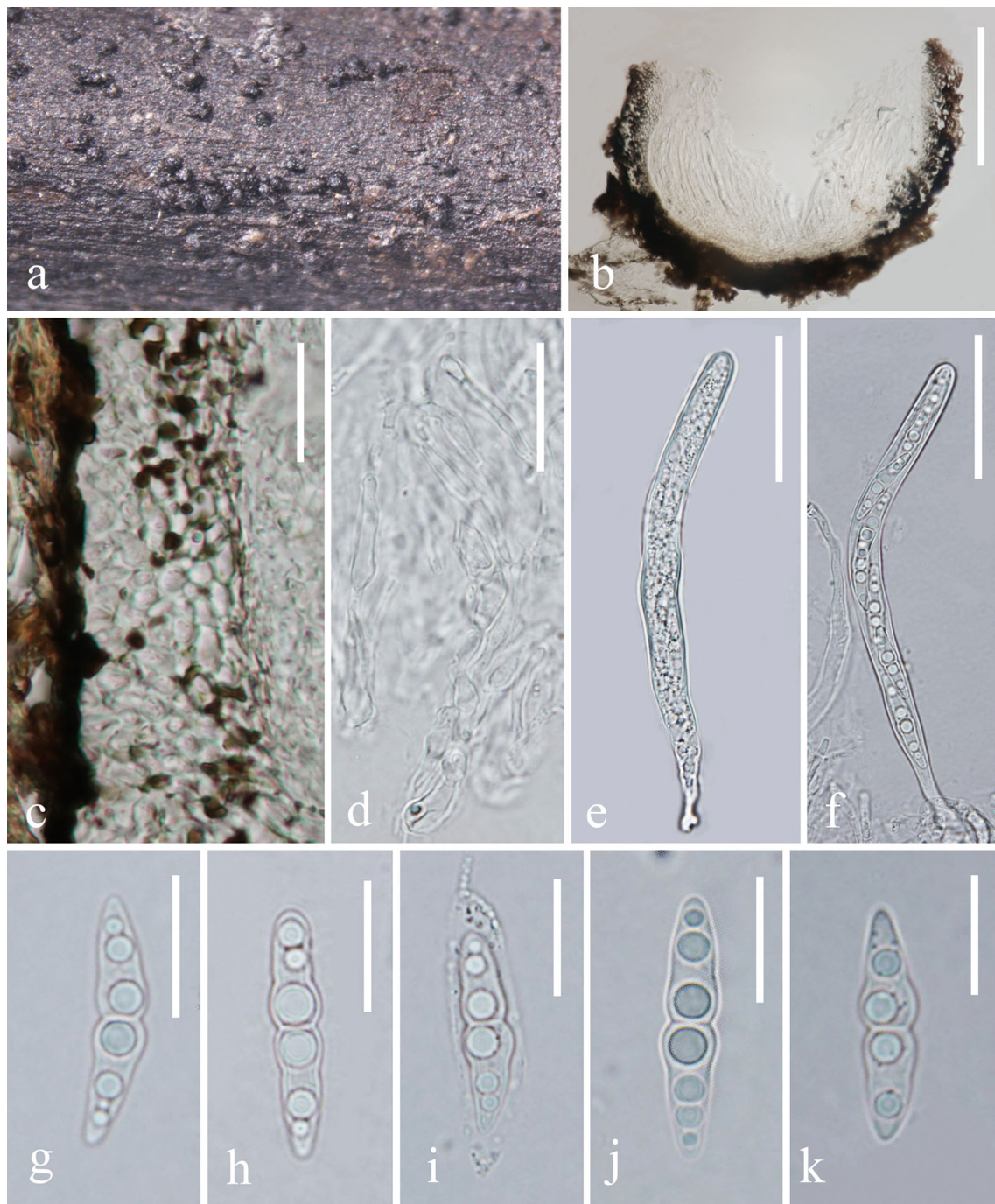


Fig. 4 *Amniculicola aquatica* (MFLU 18–1324, **holotype**). **a** Appearance of ascomata on host substrate. **b** Section through ascoma. **c** Structure of peridium. **d** Pseudoparaphyses. **e, f** Asci. **g–k** Ascospores. Scale bars: **b** = 150 μ m, **e, f** = 40 μ m, **c, d** = 20 μ m, **g–k** = 15 μ m

clade in this genus with high support (98 ML/0.99 Bayesian).

Murispora Y. Zhang bis, J. Fourn. & K.D. Hyde

Notes: The genus *Murispora* was introduced by Zhang et al. (2009a) to accommodate *Pleospora rubicunda* Niessl which is characterized by immersed, erumpent or nearly superficial, globose to subglobose, elongate, weakly

papillate ascomata that stain the woody substrate purple, filamentous, narrow, branched, septate, pseudoparaphyses, 8-spored, bitunicate, cylindro-clavate asci, and oval to ellipsoidal or fusiform, pale or reddish brown, asymmetrical, muriform ascospores, with one side flattened. Wanasinghe et al. (2015) introduced six species for this genus which were collected from Italy and the UK. In this

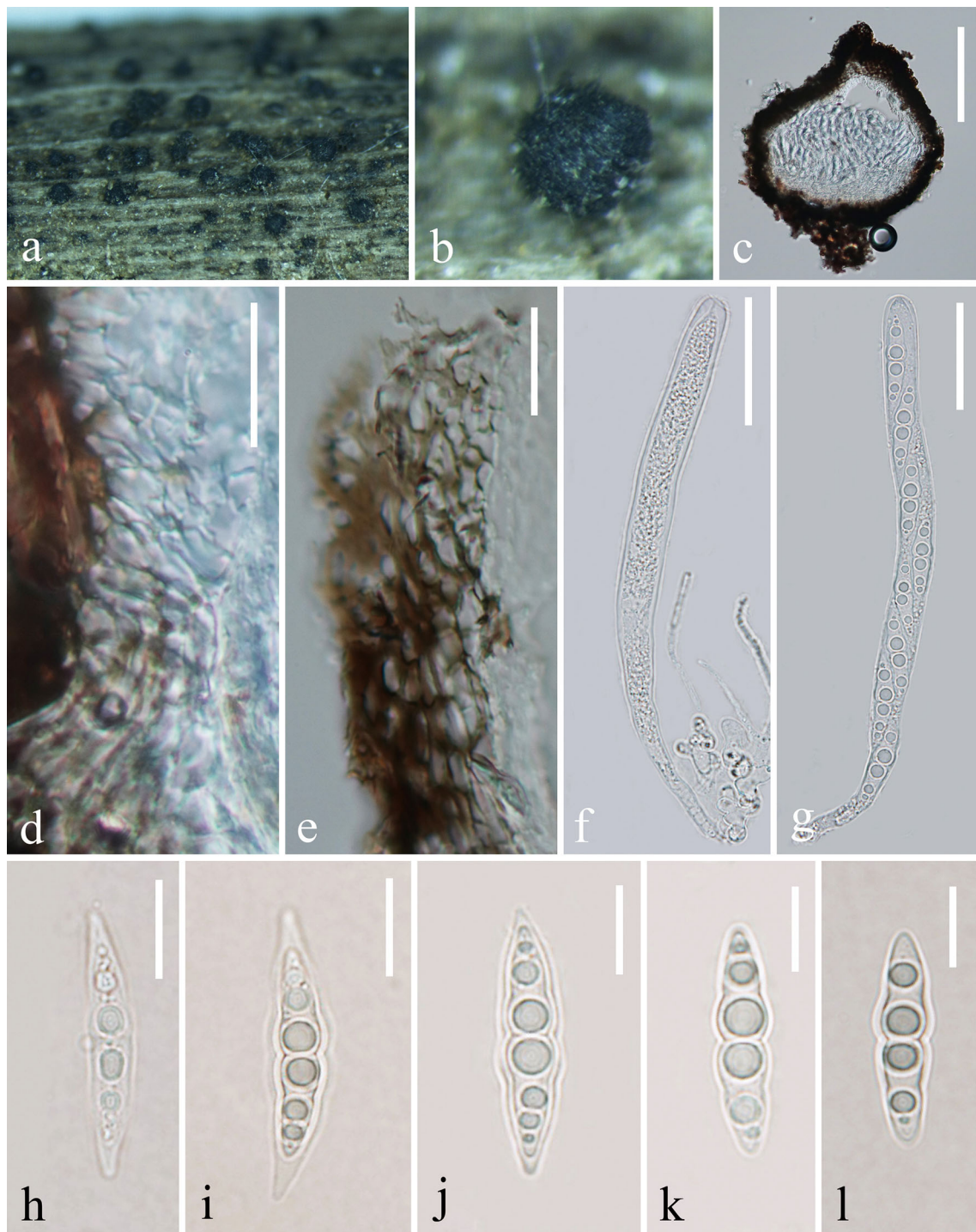


Fig. 5 *Amniculicola guttulata* (MFLU 18–1326, **holotype**). **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d, e** Structure of peridium. **f, g** Asci. **h–l** Ascospores. Scale bars: **c** = 150 μ m, **f, g** = 30 μ m, **d, e** = 20 μ m, **h–l** = 10 μ m

paper, we report on *Murispora cicognanii* as a new record for China.

Murispora cicognanii Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde, Cryptog. Mycol. 36: 437 (2015)

Facesoffungi number: FoF01108; Fig. 6

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph** *Ascomata* 200–260 μ m high, 160–250 μ m diam., solitary, globose to subglobose, dark brown to black, semi-immersed to immersed, substrate stained purple, fused to the host tissue. *Peridium* comprising 3–4 layers of brown to reddish brown cells of *textura angularis*,

with inner 1–2 layers of cells thin-walled and hyaline. *Hamathecium* comprising numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 120–150 × 20–25 µm (\bar{x} = 135 × 22.5 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, thick-walled at the apex. *Ascospores* 32–36 × 11–15 µm (\bar{x} = 34 × 13 µm, n = 20), overlapping uniseriate, golden yellow turning brown when mature, fusiform, asymmetrical with one side flattened, muriform with 5–9 transverse septa, and 1–2 longitudinal septa, slightly constricted at the middle septum, conical and narrowly rounded at the ends, surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, saprobic on decaying wood submerged in a freshwater stream in Cangshan Mountain, May 2016, F. Yang, S-757, living culture (MFLUCC 17–1682).

GenBank numbers: LSU: MK106101, SSU: MK106110, TEF1- α : MK109804.

Notes: *Murispora cicognanii* was introduced by Wanasinghe et al. (2015) based on a collection from Italy and is only known from the type locality. This species is characterized by globose to subglobose, immersed ascumata, cylindric-clavate, short pedicellate asci with a minute ocular chamber and golden yellow, fusiform, asymmetrical, muriform ascospores, turning brown when mature, with one side flattened and surrounded by a mucilaginous



Fig. 6 *Murispora cicognanii* (S-757, new record). **a** Appearance of ascomata on host substrate. **b** Section through ascoma. **c** Structure of peridium. **d** Pseudoparaphyses. **e** Asci. **f–i** Ascospores. **j, k** Colonies

on MEA from surface and reverse. Scale bars: **b** = 100 µm, **e** = 50 µm, **c, d** = 20 µm, **f–i** = 15 µm

sheath (Wanasinghe et al. 2015). The morphology of our new isolate fits well with *M. cicognanii*. Phylogenetic analysis of LSU, SSU and TEF1- α sequence data shows that our isolate clustered with *M. cicognanii* with good support (100 ML/1.00 BYPP) (Fig. 7). Based on morphology and phylogeny, we identify our isolate as *M. cicognanii*. This is first record for China and the first collection from freshwater.

Amorosiaceae Thambug. & K.D. Hyde

Notes: Thambugala et al. (2015) introduced Amorosiaceae to accommodate the genera *Amorosi* Mantle & D. Hawksw and *Angustimassarina* Thambuga., Kaz. Tanaka & K.D. Hyde. Amorosiaceae is characterized by immersed to semiimmersed ascomata with crest-like, papillate ostiole and hyaline, 1–3-septate ascospores with mucilaginous sheath and hyphomycetous asexual morph (Thambugala et al. 2015).

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

Notes: Thambugala et al. (2015) introduced *Angustimassarina* based on the type species *Angustimassarina populi* Thambug. & K.D. Hyde. Most *Angustimassarina* species are fungicolous and they may be parasitic on other fungi and appear to grow within other ascomata of other ascomycetes (Hyde et al. 2017b). Currently, 10 epithets are listed in Index Fungorum (2019). In this study, we introduce a new *Angustimassarina* species; *A. sylvatica* on *Fagus sylvatica* from Italy.

Angustimassarina sylvatica N.I. de Silva, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF556268; **Facesoffungi number:** FoF05992; Fig. 8

Etymology: The specific epithet reflects the host *Fagus sylvatica*.

Holotype: MFLU 15-2603

Saprobic on dead twigs of *Fagus sylvatica* **Sexual morph** Ascomata 180–260 μm high, 150–200 μm diam. (\bar{x} = 200 \times 180 μm , n = 5), uniloculate, scattered, immersed to semi-immersed in the plant host tissue, dark brown to black, globose to subglobose. **Ostiole** in the centre without a papilla. **Peridium** 8–12 μm wide, unequally thick, comprising brown cells of *textura angularis* of inner layer and 17–24 μm wide, unequally thick, comprising irregular dark brown cells of *textura prismatica*. **Hamathecium** comprising 1–1.5 μm septate, unbranched, cellular pseudoparaphyses, embedded in gelatinous matrix, between and above the asci. **Asci** 95–110 \times 8–12 μm (\bar{x} = 98 \times 10 μm , n = 15), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with short pedicel, rounded at the apex. **Ascospores** 21–25 \times 4–5 μm (\bar{x} = 23 \times 4 μm , n = 25), bi-seriate, hyaline, fusiform, 1–

septate with 2 pseudosepta, deeply constricted at the septum, widest at the centre and tapering toward the ends, straight, smooth-walled, guttulate, surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: ITALY, Province of Forlì-Cesena, Monte Fumaiolo - Verghereto, on dead land twigs of *Fagus sylvatica* (Fagaceae), 5 August 2015, Erio Camporesi, IT2574 (MFLU 15-2603, **holotype**), ex-type living culture (MFLUCC 18-0550).

Culture characteristics: Colonies growing on PDA at 25 °C reaching 2 cm in 1 week, irregular, white, fluffy appearance with undulate edge, reverse white.

GenBank numbers: ITS: MK307843, LSU: MK307844, SSU: MK314097, TEF1- α : MK360181.

Notes: In our phylogenetic analysis, *Angustimassarina sylvatica* groups as a distinct clade with *A. alni*, *A. premilcurensis* and *Exosporium stylobatum* (Fig. 9). *Angustimassarina sylvatica* has longer asci (95–110 μm) and longer ascospores (21–25 μm) than *A. alni* (asci 71–89 μm , ascospores 19–22 μm) and *A. premilcurensis* (asci 64–93 μm , ascospores 19–23 μm) (Tibpromma et al. 2017). Additional details of morphological differences are mentioned in Table 1. *Angustimassarina sylvatica* was isolated from *Fagus sylvatica* (Sapindaceae) in Italy, whereas *A. alni* was recorded from *Alnus glutinosa* (Betulaceae) in Germany and *A. premilcurensis* recorded on a dead branch of *Carpinus betulus* (Betulaceae) in Italy (Tibpromma et al. 2017). There are six base pair differences between *Angustimassarina sylvatica* and *A. alni* and four base pair differences between *A. sylvatica* and *A. premilcurensis* for 485 ITS nucleotide sequences. There is no TEF1- α sequence data available for *A. alni* and *A. premilcurensis*.

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

Notes: In an investigation of *camarosporium*-like taxa, Wanasinghe et al. (2017a) introduced Camarosporidiellaceae to accommodate the genus *Camarosporidiella* which was well-positioned within the suborder Pleosporineae and phylogenetically distinct from other families. Camarosporidiellaceae species are characterized by coelomycetous asexual morphs, comprising pycnidial conidiomata, with a single, papillate ostiole, enteroblastic, annellidic, integrated to discrete, doliiform, lageniform or cylindrical, hyaline conidiogenous cells and pale to dark brown conidia that are phragmosporous to muriform and mostly ellipsoidal. Their sexual morphs are gregarious to solitary, globose to subglobose ascomata having a papillate, central ostiole, a peridium containing cell layers of *textura angularis*, cylindrical, (2–)4–8-spored asci and uniseriate, ellipsoidal, brown, muriform ascospores. However, taxonomic classification of Camarosporidiellaceae

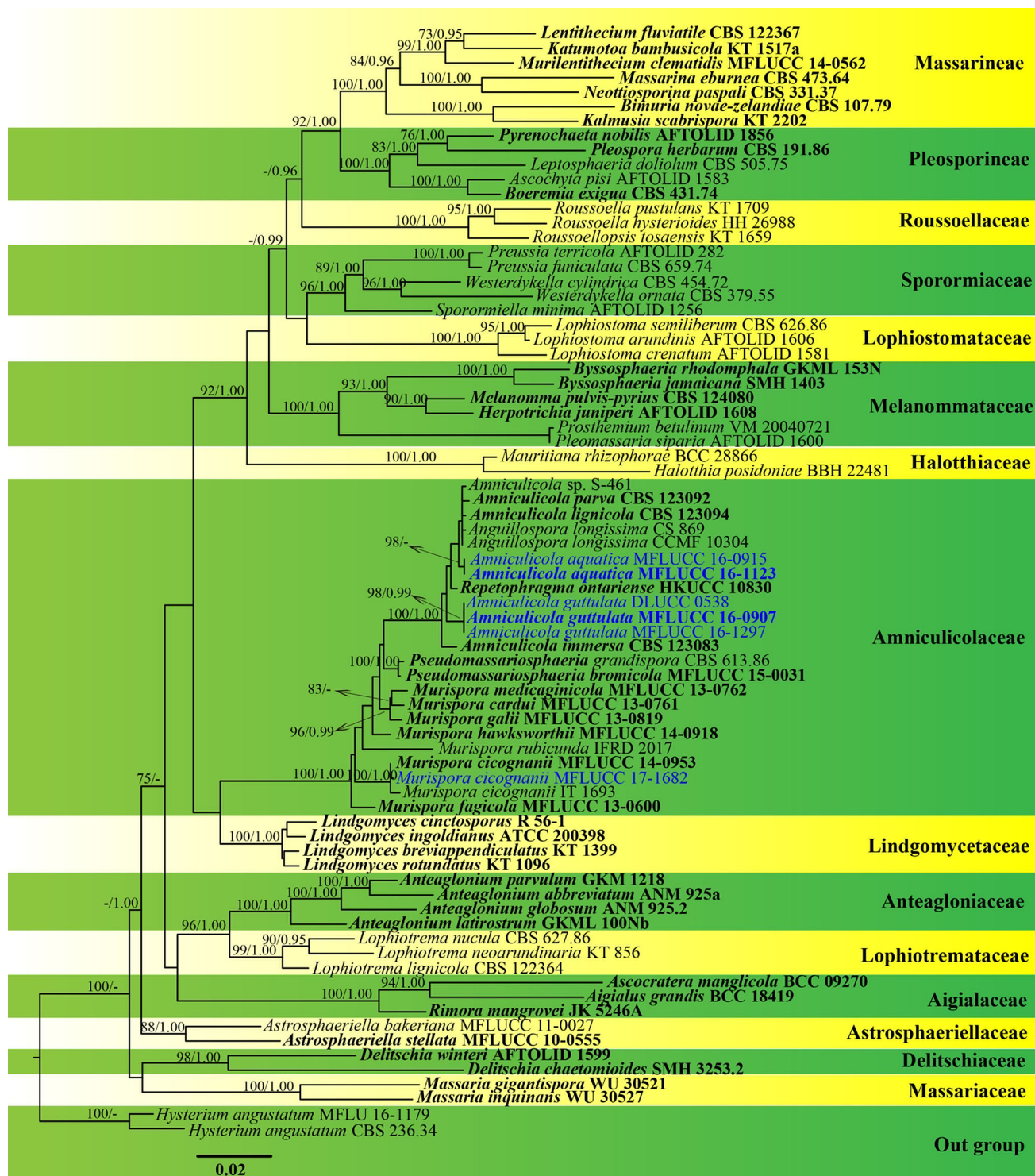


Fig. 7 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and TEF1- α sequence data. Seventy-six strains are included in the combined analyses which comprised 2640 characters (804 characters for LSU, 995 characters for SSU, 841 characters for TEF1- α) after alignment. *Hysterium angustatum* (CBS 236.34) and (MFLU 16-1179) (Hysteriaceae, Hysteriales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -19536.000988 is presented. Estimated base frequencies were as follows: A = 0.244757, C = 0.246173, G = 0.275709, T = 0.233360; substitution rates AC = 0.971666, AG = 3.423862, AT = 1.366124, CG = 1.101326, CT = 8.907769, 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 *H. angustatum* (MFLU 16-1179 and CBS 236.34). Ex-type strains are in bold and black. The newly generated sequences are indicated in blue

species based exclusively on morphological characteristics is insufficient for designating new species because of their inadequate phenotypic variability. Mostly taxa are saprobic and sometimes can be endophytic or pathogenic or potential opportunistic pathogens on leaves and woody materials. The current understanding of ecological and pathogenic aspects of this group is superficial and extensive sampling should be carried out in different regions and hosts. Pathogenetic virulence of this family also should be further investigated with more taxon sampling and DNA based sequence analyses.

Camarosporidiella Wanas., Wijayaw., K.D. Hyde

Notes: *Camarosporidiella* was established by Wanasinghe et al. (2017a) with *C. caraganicola* (Phukhams., Bulgakov & K.D. Hyde) Phukhams., Wanas. & K.D. Hyde as the type species. Wanasinghe et al. (2017a) placed 20 species in this genus based on morphological and multi-gene phylogenetic analyses. In a recent study, Hyde et al. (2018b) added *Camarosporidiella populina* as a novel species from Russia. Species of *Camarosporidiella* are morphologically less-diverse and distributed throughout a broad range of environments especially in the Northern Hemisphere. *Camarosporidiella* species are saprobes, endophytes or pathogens of a wide range of hosts (Wanasinghe et al. 2017a). Species identification based solely on morphology and plant host association is difficult since many species have overlapping characters. The genus is similar to other camarosporium-like genera and distinguishing these genera can be problematic (Wanasinghe et al. 2017a). LSU is useful for preliminary genus identification. It is recommended to use a combination of LSU, SSU, ITS and TEF1- α sequence data (Wanasinghe et al. 2017a). In this study, we introduce the 22nd species of this

genus, *Camarosporidiella mori*, which was collected on *Morus alba* in Russia.

Camarosporidiella mori Phutthacharoen, Bulgakov, Wanas. & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555709; **Facesoffungi number:** FoF0549; **Fig. 10**

Etymology: The specific epithet “mori” refers to the plant host genus *Morus*.

Holotype: MFLU 17–2147

Necrotrophic on branches of *Morus alba* L. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 370–520 \times 220–430 μm (\bar{x} = 428 \times 358 μm , n = 10), pycnidial, solitary or gregarious, scattered on wood, immersed to semi-erumpent, unilocular, dark brown, globose, black in centre with a papillate ostiole; *Pycnidial wall* 30–60 μm (\bar{x} = 38.5 μm , n = 10), composed of cells of *textura angularis*, multi-layered, with outer layer composed of 4–6 layers of heavily pigmented, light brown cells, inner layer composed of 3–4 layers, inwardly lighter. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, rough, enteroblastic, numerous, clavate, formed from the inner most layer of the pycnidial wall. *Conidia* 15.5–21 \times 6.5–9.5 μm (\bar{x} = 18 \times 8.5 μm , n = 20), hyaline when immature, brown when mature, oval, with 4-transverse septa and 1-longitudinal septum, smooth and thin-walled, blunt at both ends.

Material examined: RUSSIA, Rostov region, Shakhty City, trees near buildings, on dying branch of *Morus alba* L. (Moraceae), 9 April 2017, Timur S. Bulgakov (MFLU 17–2147, **holotype**).

GenBank numbers: ITS: MK590359, LSU: MK590358.

Notes: Three species have been found on *Morus alba*, viz. *Camarosporidiella celtidis*, *C. moricola* and *C. mori*. *Conidiomata* are similar in dimensions and shape. They are unilocular, globose and black, with papillate ostioles in the centre. The shape of conidiogenous cells are not significantly different. The conidia of *C. mori* are pale brown, while *C. moricola* has much darker conidia. *Camarosporidiella mori* conidia are comparatively larger than *C. moricola* (18 \times 8.5 μm vs 11 \times 5.5 μm). *Camarosporidiella moricola* and *C. mori* have conidia with longitudinal septa, while septa are lacking in *C. celtidis*. In the phylogenetic analyses, *C. mori* groups with *C. eufemiaea* and *C. premilcurensis* with high bootstrap support and is clearly distinct from *C. moricola* (Fig. 11). Comparison with the *C. eufemiaea* and *C. premilcurensis* asexual morph characters are currently impossible as they have introduced only as sexual morphs, while *C. mori* is known only from its asexual morph. Therefore, we introduce our novel collection as a new species.

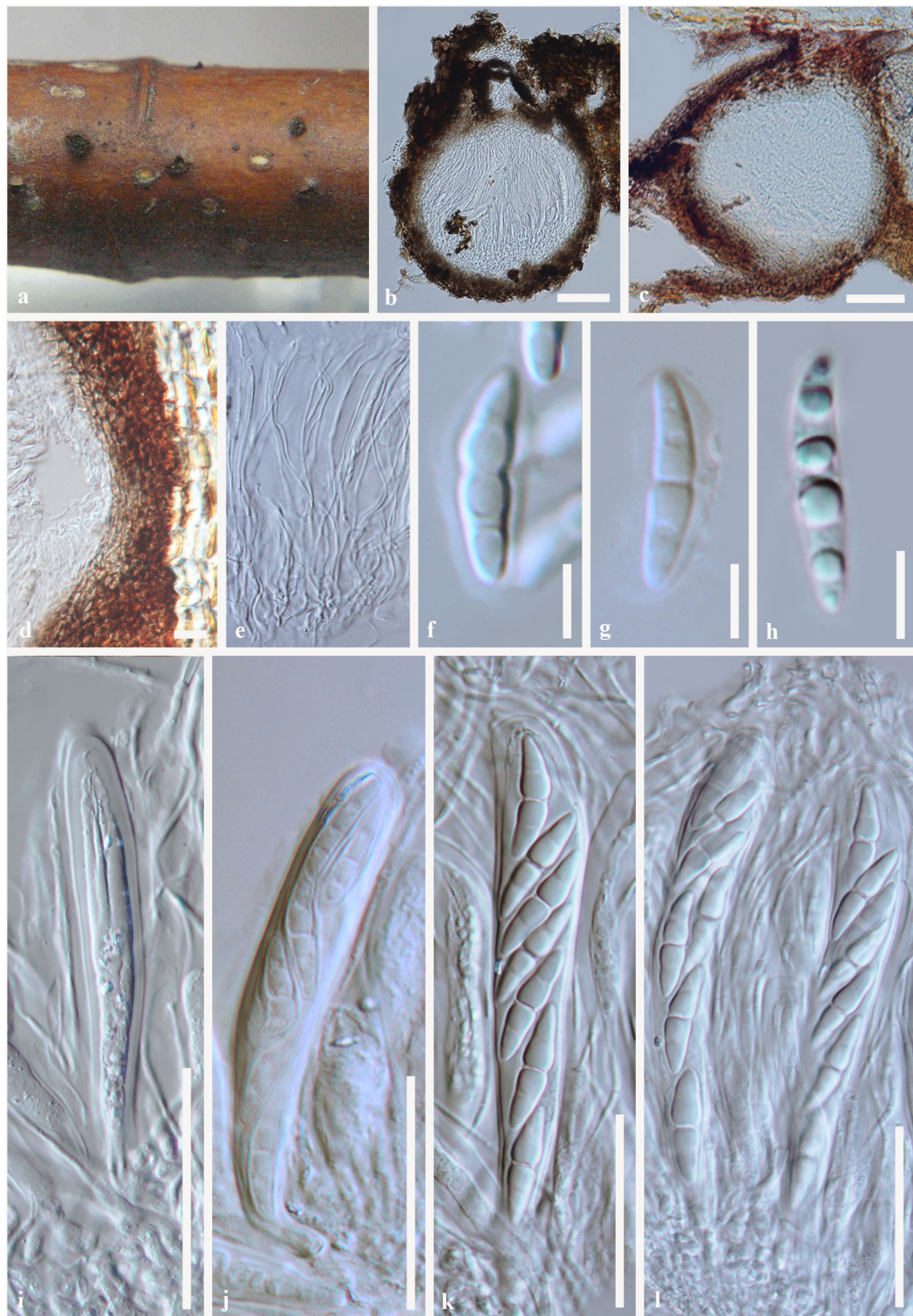


Fig. 8 *Angustimassarina sylvatica* (MFLU 15–2603, **holotype**). **a** Ascomata on the host material. **b, c** Sections through ascomata. **d** Peridium. **e** Pseudoparaphyses. **f–h** Ascospores. **i–l** Asci. Scale bars: **b, c** = 80 µm, **d, i–l** = 50 µm, **f–h** = 10 µm

Cucurbitariaceae G. Winter

Notes: The family Cucurbitariaceae, in the order Pleosporales, was established by Winter (1885) and *Cucurbitaria* Gray is the type genus (Doilom et al. 2013; Hyde et al. 2013; Wijayawardene et al. 2014; Li et al. 2016). Species belonging to this family have grouped, ostiolate ascomata located superficially on their hosts or on a pseudostromatic structure with cylindrical asci and phragmosporous or muriform ascospores (Hyde et al. 2013). They are either saprobes or necrotrophs on woody substrates (Hyde et al. 2013). While Index Fungorum (2019) lists numerous epithets belonging to Cucurbitariaceae, many of them are not linked to the latter and only a few species have molecular data in GenBank (Wanasinghe et al. 2017b; Jaklitsch et al. 2018). The family has been subjected to several generic additions and exclusions (Barr 1987; de Gruyter et al. 2010, 2013; Hyde et al. 2013; Doilom et al. 2013). Known asexual morphs of Cucurbitariaceae are pyrenochaeta- or phoma-like (Jaklitsch et al. 2018). For this reason, *Pyrenochaeta* De Not. was accommodated in the family (de Gruyter et al. 2010, 2013; Chen et al. 2015). *Pyrenochaeta quercina* Kabát & Bubák, *P. unguis-hominis* Punith. & M.P. English, *P. cava* (Schulzer) Gruyter, Aveskamp & Verkley, *P. hakeae* Crous and *P. keratinophila* Verkley, C. Ferrer & Gené (Wanasinghe et al. 2017b; Valenzuela-Lopez et al. 2018) were, however, recently transferred to the novel genus *Neocucurbitaria* Wanas., E.B.G. Jones & K.D. Hyde introduced by Wanasinghe et al. (2017b). Valenzuela-Lopez et al. (2018) introduced another genus, *Paracucurbitaria* Valenz.-Lopez, Stchigel, Guarro & Cano, which currently has two species, *Paracucurbitaria corni* (Bat. & A.F. Vital) Valenz.-Lopez, Stchigel, Guarro & Cano., formerly identified as *Pyrenochaeta corni* (Bat. & A.F. Vital) Boerema, Loer. & Hamers (Boerema et al. 1996) and a new species, *P. italica* Valenz.-Lopez, Crous, Stchigel, Guarro & Cano to the family. They established the new monotypic genus *Allocucurbitaria* Valenz.-Lopez, Stchigel, Guarro & Cano and the new families Pseudopyrenochaetaceae Valenz.-Lopez, Crous, Stchigel, Guarro & Cano and Neopyrenochaetaceae Valenz.-Lopez, Crous, Cano, Guarro & Stchigel to accommodate taxa previously belonging to the genus *Pyrenochaeta*, thereby, eliminating *Pyrenochaeta* sensu stricto from Cucurbitariaceae. Additionally, species of *Pyrenochaetopsis* Gruyter, Aveskamp & Verkley, also previously included in Cucurbitariaceae, have been transferred to the new family Pyrenochaetopsidaceae Valenz.-Lopez, Crous, Cano, Guarro & Stchigel (Valenzuela-Lopez et al. 2018). The latest generic additions to the family Cucurbitariaceae include *Astragalicola* Jaklitsch & Voglmayr, *Cucitella* Jaklitsch & Voglmayr, *Parafenestella* Jaklitsch & Voglmayr, *Protofenestella* Jaklitsch &

Voglmayr and *Seltsamia* Jaklitsch & Voglmayr (Jaklitsch et al. 2018).

Protofenestella Jaklitsch & Voglmayr

Notes: *Protofenestella* (Cucurbitariaceae, Pleosporales) was established and defined as the primitive form of the genus *Fenestella* Tul. & C. Tul. (Jaklitsch et al. 2018), by virtue of non-clustered, ill-defined ascomata on host materials, as well as distant phylogenetic placement. The genus currently accommodates the single species *Protofenestella ulmi* Jaklitsch & Voglmayr, whose sexual morph was reported on *Ulmus* sp. from Europe (Jaklitsch et al. 2018). Its asexual morph was described from culture (Jaklitsch et al. 2018). In this study, we introduce the asexual morph of *P. ulmi* from its host with evidence from morphology and concatenated phylogenetic analysis based on ITS, LSU and TEF1- α sequence data.

Protofenestella ulmi Jaklitsch & Voglmayr

Facesoffungi number: FoF05078; Fig. 12

Saprobic on dead twigs and branches of *Ulmus pumila* L. **Sexual morph** See Jaklitsch et al. (2018) for description and illustrations. **Asexual morph** Coelomycetous, phoma-like. *Conidiomata* 78–131 μ m high, 71–135 μ m diam. (\bar{x} = 96 \times 96.4 μ m, n = 6), globose to depressed subglobose, erumpent through host periderm, solitary or loosely aggregated in ill-defined groups. *Peridium* 9–12.8 μ m wide at the top, 5.8–8.9 μ m wide at the sides, consisting of 4–6 layers, outer layer comprising olivaceous brown, relatively thin-walled cells of *textura angularis*, inner layer becoming paler and comprising pale brown, thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9–27 \times 0.9–2.8 μ m (\bar{x} = 14.3 \times 1.66 μ m, n = 32) hyaline, enteroblastic, phialidic, lageniform, doliiform to cylindrical, straight to faintly curved, discrete or integrated. *Conidia* 2.5–5.4 \times 0.9–2.4 μ m (\bar{x} = 3.9 \times 1.4 μ m, n = 76), hyaline, aseptate, cylindrical or oblong to allantoid, mostly containing 2 small guttules, smooth-walled.

Culture characteristics: Colonies on MEA reaching 1.5 cm diam. after 21 days at 25 °C, circular, colony initially greyish olive, eventually turning unevenly brown after 4 weeks, with limited aerial mycelium, reverse olivaceous dull green to grey, odour indistinct.

Material examined: RUSSIA, Rostov region, Shakhty City, Cotton fabric microdistrict, artificial grove (47.72195° N, 40.25177° E), on dead twigs of *Ulmus pumila* L. (Ulmaceae), 26 May 2017, Timur S. Bulgakov (MFLU 17-2047, HKAS 104976), living culture (MFLUCC 18-0376).

GenBank numbers: ITS: MK418793, LSU: MK418783, TEF1- α : MK424969.

Notes: The asexual morph of *Protofenestella ulmi* has so far only been reported from culture (Jaklitsch et al. 2018).

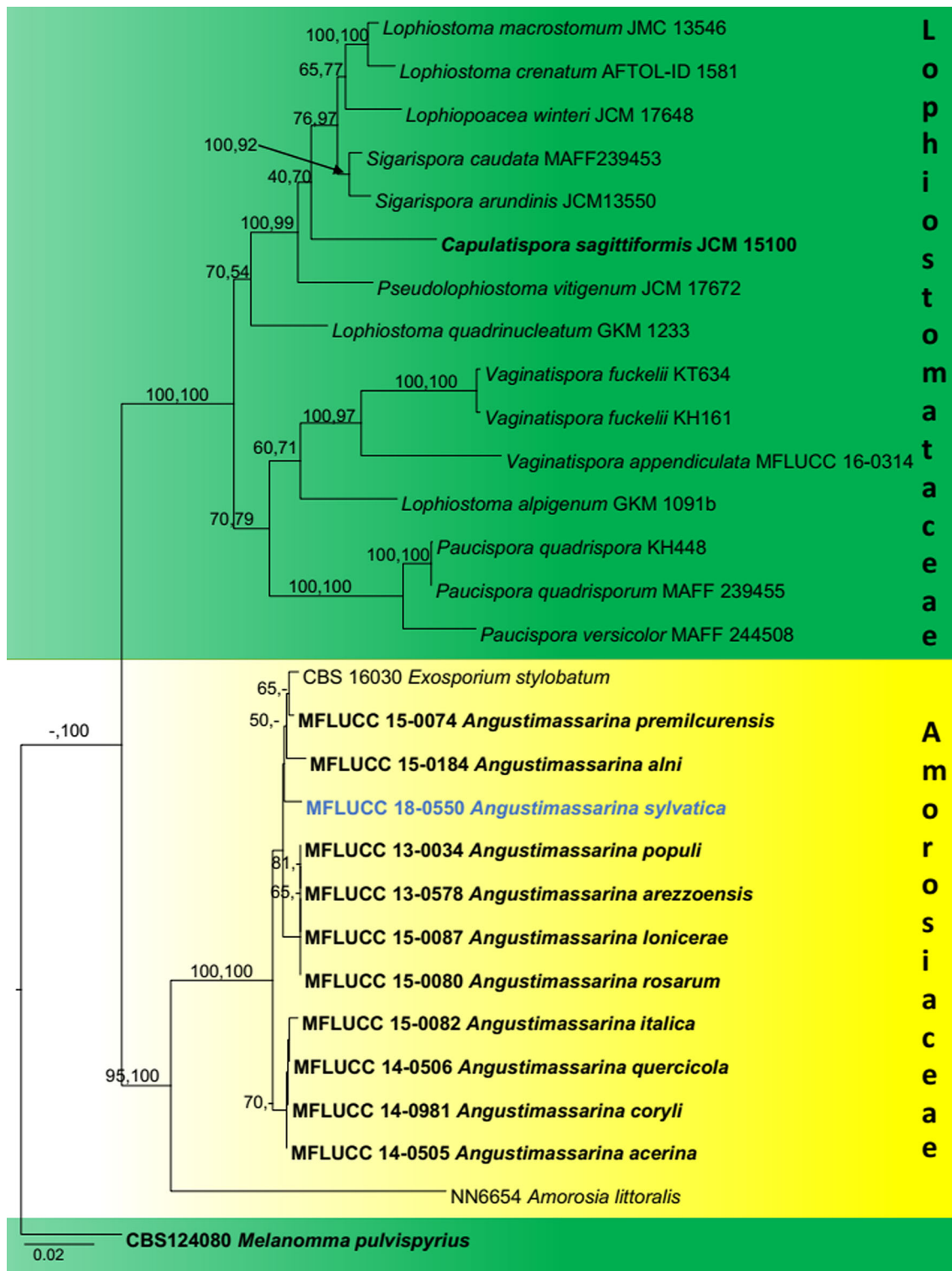


Fig. 9 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF1- α sequence data. Related sequences are obtained from GenBank. *Melanomma pulvispyrius* (CBS 124080) is used as the outgroup taxon. Twenty-nine strains are included in the combined analyses which comprise 3297 characters (525 characters for ITS, 847 characters for LSU, 984 characters for SSU, 941 characters for TEF1- α) after alignment. Single gene analyses were carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis. The best RaxML tree with a final likelihood value of -12251.741088 is presented. The matrix had 784 distinct alignment patterns, with 18.70% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244380, C = 0.247658, G = 0.268826, T = 0.239136; substitution rates AC = 1.50180, AG = 2.768806, AT = 1.335846, CG = 1.292688, CT = 6.996209, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.137453$. Maximum parsimony analysis of 2585 constant characters and 485 informative characters resulted in two equally most parsimonious tree of 1370 steps (CI = 0.688, RI = 0.838, RC = 0.577, HI = 0.312). Bootstrap support values for ML (first set) and MP equal to or greater than 50% are given above the nodes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

In the present study, the asexual morph of the species is illustrated from natural substrate, *Ulmus pumila*. The strain obtained from this study clusters with the type strain of *P. ulmi* with high bootstrap support (100% ML, 100 BYPP) in Fig. 13. The conidia of *P. ulmi* observed in our study are similar in size to those obtained from the ex-holotype culture [$2.5\text{--}5.4 \times 0.9\text{--}2.4 \mu\text{m}$ (this study) vs $2.9\text{--}5.4 \times 1.3\text{--}2.2 \mu\text{m}$ (Jaklitsch et al. 2018)]; slight differences may be accounted for by the fact that the asexual morph of *P. ulmi* in this study was observed from natural substrate while that reported by Jaklitsch et al. (2018) was obtained from culture.

Dictyosporiaceae Boonmee & K.D. Hyde

Notes: The family Dictyosporiaceae was erected by Boonmee et al. (2016) with *Dictyosporium* Corda. as the type genus with morphological data and multi-gene

analysis. The asexual morphs are cheirosporous hyphomycetes (Boonmee et al. 2016) and the sexual morphs are characterized by immersed to erumpent or superficial, globose to subglobose, dark brown to black ascomata, bitunicate asci and septate, hyaline, sheathed ascospores. Currently, there are twelve genera in this family (Wijayawardene et al. 2018a).

Dictyocheiropora D'souza et al.

Notes: *Dictyocheiropora* was introduced by Boonmee et al. (2016) with *D. rotunda* D'souza, Bhat & K.D. Hyde as the type species. *Dictyocheiropora* species are characterized by dark sporodochial colonies with aeroaquatic cheiroid dictyospores and all are saprobes (Boonmee et al. 2016). Currently, there are 19 epithets in Index Fungorum (2019).

Dictyocheiropora aquadulcis Sorvongxay, S. Boonmee & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF556308; **Facesoffungi number:** FoF05963; Fig. 14

Etymology: From the Latin *aquadulcis* (*aqua* = water and *dulcis* = sweet, in reference to its freshwater habitat.

Holotype: MFLU 18-1088

Saprobic on decaying, submerged wood in freshwater.

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. **Colonies** on natural substrate, superficial, scattered. **Mycelium** immersed, branched, septate, pale brown, smooth-walled. **Conidiomata** 117–412 μm diam., slightly, pulvinate, dark brown. **Conidiophores** microne-matous, undifferentiated from vegetative hyphae. **Conid-iogenous cells**, holoblastic, integrated, terminal, pale brown. **Conidia** 60–80 $\mu\text{m} \times 17\text{--}29 \mu\text{m}$ ($\bar{x} = 70 \times 24 \mu\text{m}$, $n = 20$), solitary, cheiroid, ellipsoid to cylindrical, rounded at the apex, consisting of 7 rows of cells, with each row composed of 11–14 cells, with rows digitate, cylindrical, inwardly curved at apex, arising from

Table 1 Synopsis of *Angustimassarina* species

Species name	Asci (μm)	Ascospores (μm)	Plant host	Locality	Reference
<i>A. acerina</i>	92–105	21–23	<i>Acer platanoides</i>	Germany	Thambugala et al. (2015)
<i>A. alni</i>	71–89	19–22	<i>Alnus glutinosa</i>	Germany	Tibpromma et al. (2017)
<i>A. arezzoensis</i>	67–95	19–21	<i>Salvia</i> sp.	Italy	Tibpromma et al. (2017)
<i>A. coryli</i>	70–100	20–25	<i>Corylus avellane</i>	Italy	Hyde et al. (2016)
<i>A. italica</i>	78–103	15–22	<i>Ilex aquifolium</i>	Italy	Tibpromma et al. (2017)
<i>A. lonicerae</i>	55–81	19–25	<i>Lonicera</i> sp.	Italy	Tibpromma et al. (2017)
<i>A. populi</i>	80–95	19–22	<i>Populus</i> sp.	Italy	Thambugala et al. (2015)
<i>A. premilcurensis</i>	64–93	19–23	<i>Carpinus betulus</i>	Italy	Tibpromma et al. (2017)
<i>A. quercicola</i>	60–94	17–21	<i>Quercus robur</i>	Germany	Thambugala et al. (2015)
<i>A. rosarum</i>	40–102	16–22	<i>Rosa canina</i>	Italy	Wanasinghe et al. (2018a)
<i>A. sylvatica</i>	95–110	21–25	<i>Fagus sylvatica</i>	Italy	This study

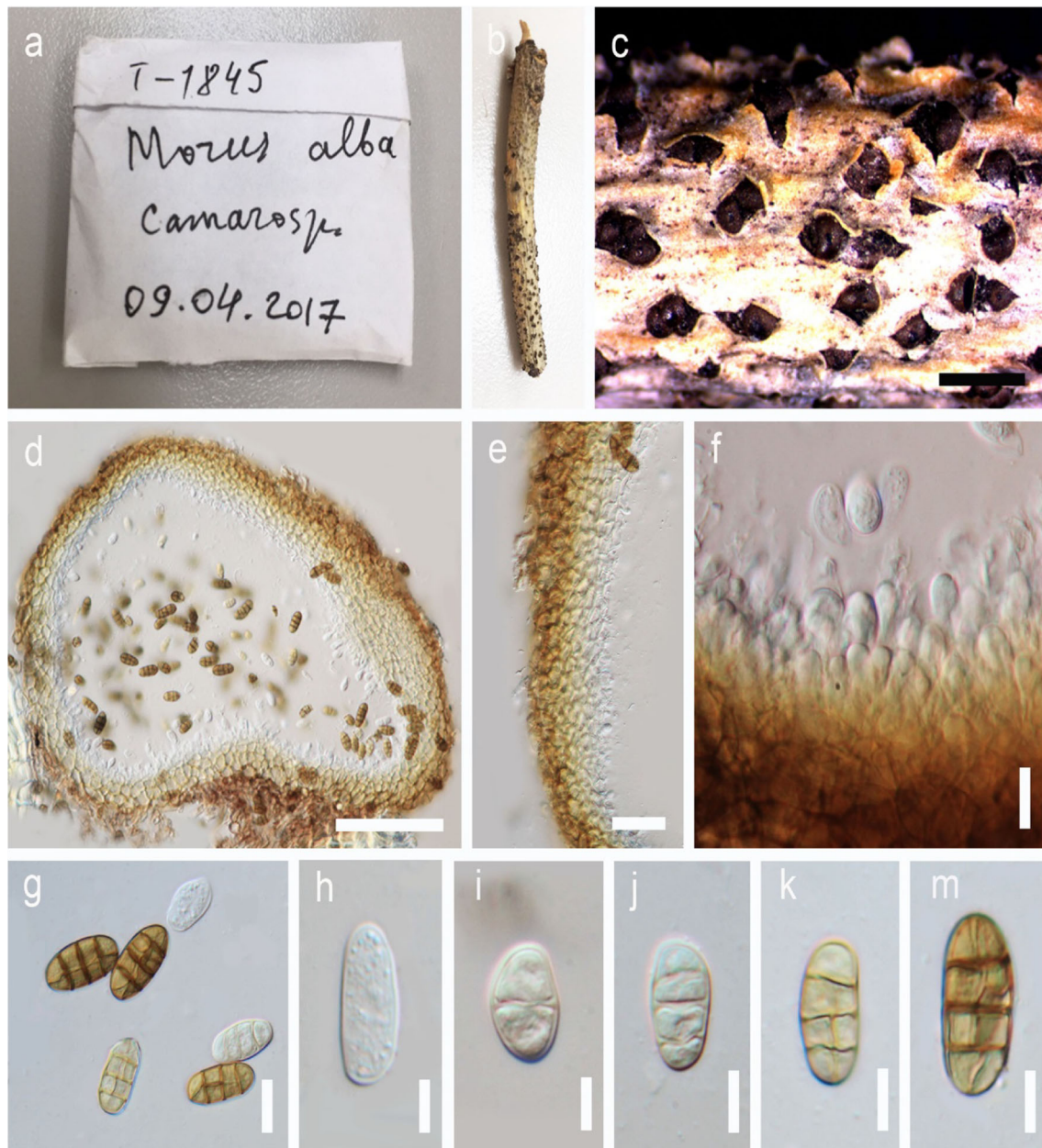


Fig. 10 *Camarosporidiella mori* (MFLU 17-2147, **holotype**). **a** Herbarium package. **b** Conidiomata on *Morus alba*. **c** Close up of conidiomata. **d** Cross section of conidioma. **e** Section through

conidioma wall. **f** Conidiogenous cells. **g–m** Conidia. Scale bars: **c** = 1000 µm, **d** = 100 µm, **e** = 30 µm, **f**, **g** = 10 µm, **h–m** = 5 µm

a basal cell, euseptate, slightly constricted at septa, brown, smooth-walled.

Culture characteristics: Conidia germinated on WA within 24 h. Colonies on MEA reaching 0.2–0.5 cm diam., in 5 days at 25 °C, with wavy margins, initial white and later becoming gray.

Material examined: THAILAND, Pha Yao Province, on decaying wood, in flowing freshwater stream, 11 September 2017, Saranyaphat Boonmee (PK12), (MFLU 18-1088, **holotype**), ex-type living culture (MFLUCC 17-2571).

GenBank numbers: ITS: MK634542, LSU: MK634545.

Notes: *Dictyocheirospora aquadulcis* is similar to *D. heptaspora* in having the same conidial shape and size. However, it differs in having elongate conidia with 11–14 septa, whereas *D. heptaspora* has ellipsoidal conidia with 10–11 septa. Phylogenetically, *D. aquadulcis* clustered with *D. heptaspora* with moderate bootstrap support (Fig. 18). We therefore, introduce *D. aquadulcis* as a new species in this study based on its morphological distinctness.

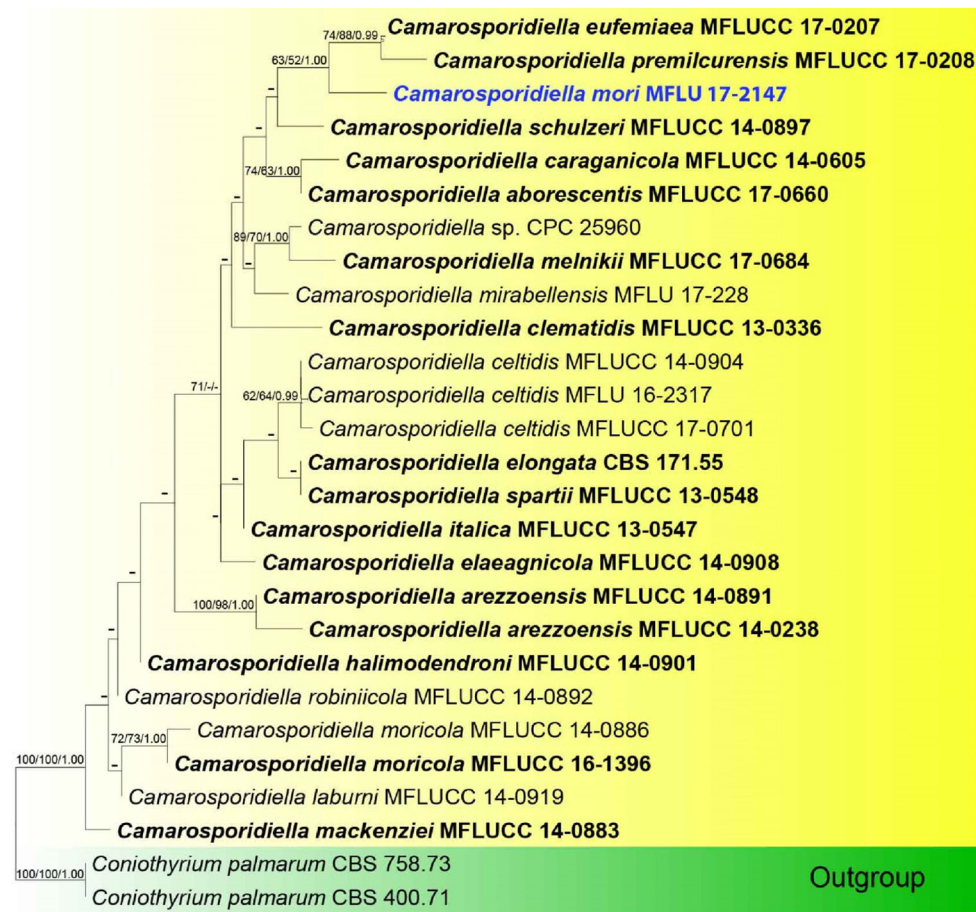


Fig. 11 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data for *Camarosporidiella* species and several closely related genera in Camarosporidiellaceae. Twenty-seven strains are included in the combined analyses which comprise 2376 characters (including gaps) (548 characters for ITS, 850 characters for LSU, 974 characters for SSU) after alignment. *Coniothyrium palmarum* (CBS 758.73 and CBS 400.71) (Coniothyriaceae, Pleosporales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis was similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -4091.750594 is presented. The matrix had 130 distinct

alignment patterns, with 5.97% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252474, C = 0.213418, G = 0.274008, T = 0.260100; substitution rates AC = 3.818489, AG = 8.876577, AT = 3.746626, CG = 0.477392, CT = 7.229081, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.020000$. Maximum parsimony analysis of 2313 constant characters and 47 informative characters (CI = 0.607, RI = 0.756, RC = 0.459, HI = 0.393). Bootstrap values for maximum likelihood and maximum parsimony equal to or greater than 50 and Bayesian posterior probabilities equal to or greater than 0.95 are placed above the branches respectively. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Dictyocheirosora rotunda M.J. D'souza, Bhat & K.D. Hyde

Facesoffungi number: FoF05063; Fig. 15

Saprobic on dead wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata* punctiform, sporodochial, velvety, brown to dark brown. *Mycelium* superficial, with brown, smooth, septate, branched hyphae. *Conidiophores* micronematous, pale brown. *Conidiogenous cells* $5\text{--}8 \times 6\text{--}9 \mu\text{m}$ ($\bar{x} = 6.5 \times 7 \mu\text{m}$, $n = 20$), holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* $16\text{--}29 \times 47\text{--}62 \mu\text{m}$ ($\bar{x} = 22 \times 55 \mu\text{m}$, $n = 50$), solitary, monoblastic, acrogenous, cheiroid, pale brown to brown, consisting of 6–8

rows of cells, rows digitate, cylindrical, inwardly curved at the tip, arising from a basal cell, each arm composed of 7–9-septated, constricted at septa.

Culture characteristics: Ascospores germinating on PDA (potato dextrose agar) within 1 week at 23 °C. Sporulation after 30 days, colony 1.5 cm diam. Initially, orange from above and reverse, becoming brown, with concentric zonation, with irregular form of margin, filamentous mycelium, with rough surface and raised elevation.

Material examined: CHINA, Yunnan Province, Kunming, Songhuaba Lake, on dead wood, 3 September 2017,

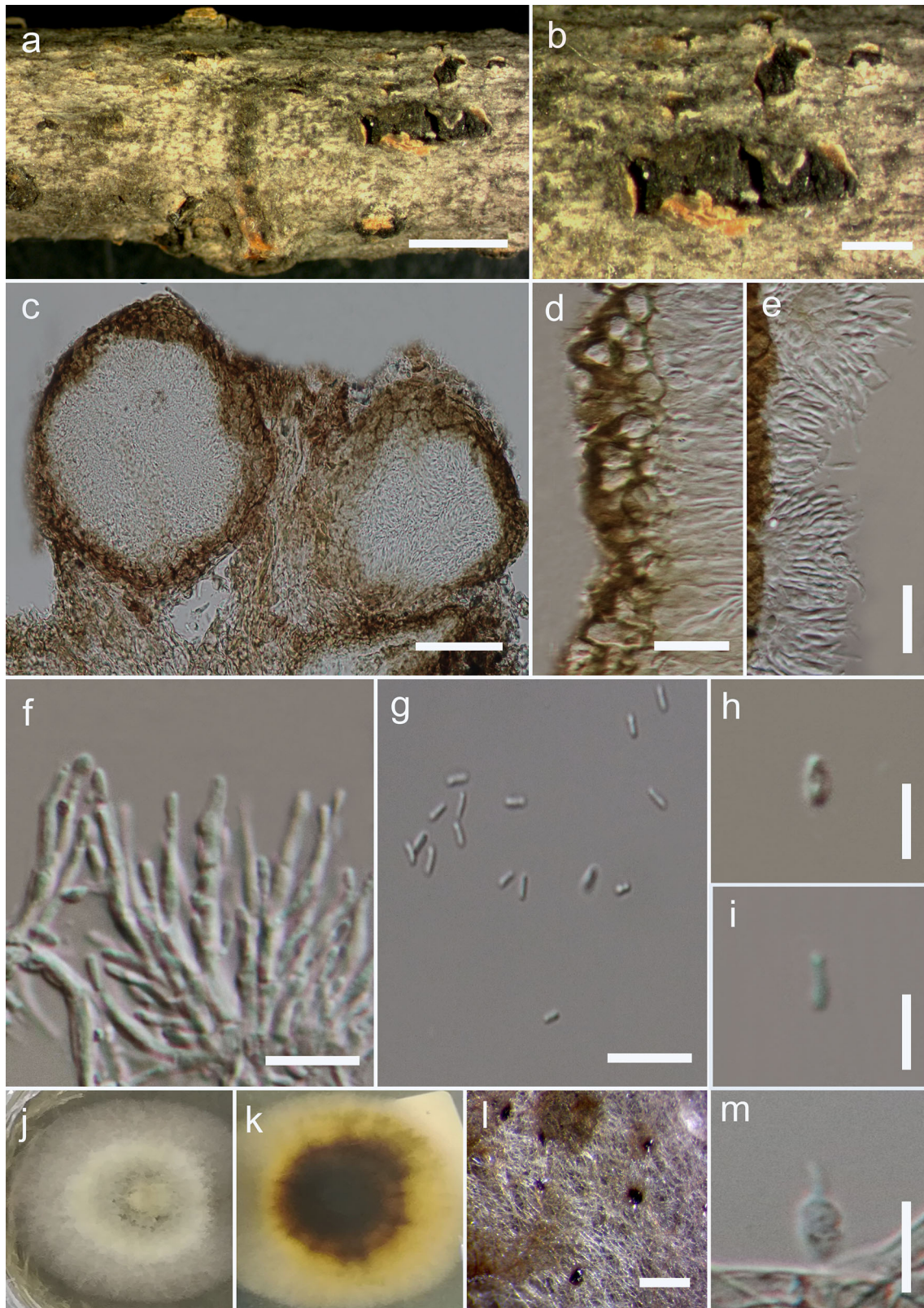


Fig. 12 *Protofenestella ulmi* (MFLU 17-2047, new record). **a, b** Appearance of conidiomata on host substrate. **c** Vertical section through conidioma. **d** Peridium. **e** Conidiogenous cells. **f** Mature and immature conidia attached to conidiogenous cells. **g–i** Conidia. **j, k**

Colony on MEA (**j** from above view, **k** from below view). **l** Conidiomata on colony. **m** Conidia attached to conidiogenous cell in culture. Scale bars: **a** = 1000 μ m, **b, l** = 100 μ m, **c** = 50 μ m, **d, e** = 20 μ m, **f** = 10 μ m, **m** = 7 μ m, **g–i** = 3 μ m

S.K. Huang (KUN-HKAS 99571), living culture (KUMCC 18-0014).

GenBank numbers: ITS: MK050008, LSU: MK050010, SSU: MK050009.

Notes: *Dictyocheiropora rotunda* has been previously reported from Thailand and northwestern Yunnan Province, China (Boonmee et al. 2016; Wang et al. 2016). In phylogenetic analysis of combined ITS and LSU sequence data of Dictyosporiaceae strains, our strain clusters with the ex-type strain of *Dictyocheiropora rotunda* (MFLUCC 14-0293) with relatively high-support (Fig. 18). Pairwise comparison of DNA sequences of ITS and LSU regions between KUMCC 18-0014 and MFLUCC 14-0293 reveals they are slightly different. Boonmee et al. (2016) introduced *D. rotunda* as having $5\text{--}7 \times 6\text{--}7 \mu\text{m}$, pale brown conidiogenous cells and $42\text{--}58 \times 19\text{--}38 \mu\text{m}$, cylindrical conidia. The morphological similarities reveal they are the same species. Thus, a record of *D. rotunda* from Kunming, Yunnan Province is reported.

Dictyocheiropora taiwanense Tennakoon, C.H. Kuo & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF556309; **Facesoffungi number:** FoF05964; Fig. 16

Etymology: Named after Taiwan, where this fungus was collected.

Holotype: MFLU 18-0070

Saprobic on decaying wood of *Macaranga tanarius* (L.) Müll.Arg. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. **Conidiomata** punctiform, sporodochial, $110\text{--}230 \mu\text{m}$ diam., velvety, dark brown to black. **Conidiophores** micronematous, pale brown, smooth, thin-walled. **Conidiogenous cells** holoblastic, cylindrical. **Conidia** $(72\text{--})74\text{--}84\text{--}(86) \times 16\text{--}20\text{--}(24) \mu\text{m}$ ($\bar{x} = 77.5 \times 18 \mu\text{m}$, $n = 30$), solitary, brown, ellipsoid to cylindrical, rounded at the apex, cheiroid, not complanate, consisting of 5 rows of cells, rows cylindrical, arising from a basal cell, each composed of 10–13 cells, constricted at septa, without appendages.

Culture characteristics: Conidia germinating on water agar within 24 h, germ tubes appearing from the basal cells of the conidium. Colonies on PDA covering 3 cm diam., in 3 weeks at 27 °C, at first white, colony from above: light orange to yellowish at the margin, yellowish to white at the centre; reverse, orange to yellowish at the margin, orange at the centre; mycelium yellowish to white with tufting; not producing pigments in PDA.

Material examined: TAIWAN, Chiayi, Shihong Forest Area, decaying wood of *Macaranga tanarius* (L.) Müll.Arg. (Euphobiaceae), 25 June 2017, D.S. Tennakoon, DTW013 (MFLU 18-0070, **holotype**), ex-type living culture (MFLUCC 17-2654).

GenBank numbers: ITS: MK495821, LSU: MK495820.

Notes: *Dictyocheiropora taiwanense* is typical of *Dictyocheiropora* in having aeroaquatic cheiroid dictyospores (Boonmee et al. 2016). Phylogenetically, *D. taiwanense* nests independently closely to *D. garethjonesii* (MFLUCC 16-0909), *D. aquatica* (KUMCC 15-0305), *D. cheiropora* (KUMCC 17-0035) and *D. rotunda* (MFLUCC 14-0293a, HKAS 99571) with moderate support (Fig. 18). However, *D. taiwanense* differs from *D. aquatica* and *D. garethjonesii* in having larger conidia ($74\text{--}84 \times 16\text{--}20 \mu\text{m}$) with a higher number of cells (10–13) in each conidial row, whereas the conidia of *D. aquatica* ($34\text{--}42 \times 12.5\text{--}19.5 \mu\text{m}$) and *D. garethjonesii* ($45.5\text{--}54.5 \times 15.5\text{--}24.5 \mu\text{m}$) are comparatively smaller and comprise 6–8, 7–10 cells in each conidial row (Wang et al. 2016). In addition, *D. pseudomusae* and *D. vinaya* are also show distinct morphological differences viz. mostly *D. taiwanense* conidia has 5 rows (10–13 cells in each row), whereas *D. pseudomusae* has 6–7 rows (13–15 cells in each row) and *D. vinaya* (6–7 rows, 9–13 cells in each row) (Tanaka et al. 2015; Boonmee et al. 2016).

Digitodesmium Corda, Weitenweber's Beitr.

Notes: *Digitodesmium* was established by Kirk (1981) with type species *Digitodesmium elegans* P.M. Kirk. The asexual morph of the *Digitodesmium* species is characterized by punctiform, sporodochial conidiomata and acrogenous, euseptate, cheiroid, digitate conidia, with apical gelatinous caps. There are six records in Index Fungorum (2019), however, these are lacking the molecular data with the exception of *D. bambusicola*.

Digitodesmium chiangmaiense Q.J. Shang & K.D. Hyde *sp. nov.*

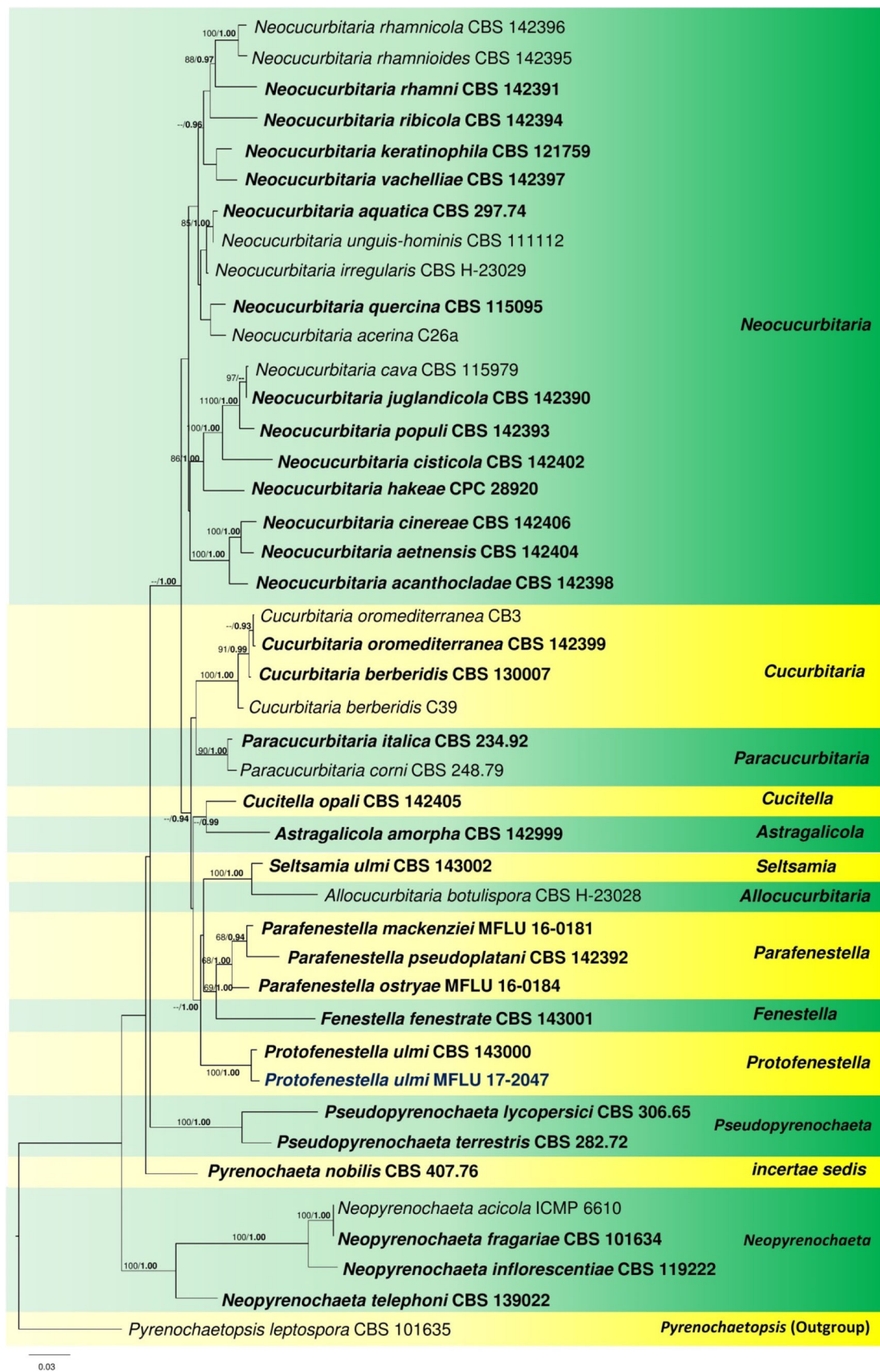
Indexfungorum number: IF556220; **Facesoffungi number:** FoF05098; Fig. 17

Etymology: Names reflects the province in Thailand, from where the holotype was collected.

Holotype KUN-HKAS 102163

Saprobic on decaying wood submerged in stream.

Sexual morph Undetermined. **Asexual morph** Hyphomycetous. Colonies punctiform, sporodochial, scattered, dark brown to black, glistening. **Conidiophores** micronematous, hyaline to pale brown, unbranched, thin-walled, smooth. **Conidiogenous cells** monoblastic, integrated, terminal, determinate, hyaline to pale brown, smooth. **Conidia** acrogenous, solitary, cheiroid, smooth-walled, complanate, brown to dark brown, consisting of three arms closely compact with side arms higher than middle arms, $(24\text{--})33\text{--}42\text{--}(44) \times (13\text{--})15\text{--}18\text{--}(21) \mu\text{m}$ ($\bar{x} = 38 \times 17 \mu\text{m}$, $n = 45$), 5–7-euseptate in each arm, without appendages attached at the two outer arms, arms $(20\text{--})27\text{--}37\text{--}(38) \times (4\text{--})4\text{--}7\text{--}(8) \mu\text{m}$ ($\bar{x} = 32 \times 5 \mu\text{m}$, $n = 30$), not discrete, unbranched, cylindrical.



◀**Fig. 13** Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and TEF1- α sequence data for *Protopenestella* species and several closely related genera in Cucurbitariaceae. Related sequences are taken from Wanasinghe et al. (2017b) and Jaklitsch et al. (2018). Forty-three strains are included in the combined analyses which comprise 2749 characters (601 characters for ITS, 914 characters for LSU and 1234 characters for TEF1- α) after alignment. *Pyrenochaetopsis leptospora* (CBS 101635) (Pyrenochaetopsidaceae, Pleosporales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree has clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -13415.377769 is presented. The matrix had 741 distinct alignment patterns, with 25.51% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234883, C = 0.253189, G = 0.270793, T = 0.241136; substitution rates AC = 1.125763, AG = 3.623108, AT = 2.100279, CG = 1.168787, CT = 6.351079, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.142500$. Bootstrap values for maximum likelihood equal to or greater than 60 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities equal to or greater than 0.90 are in bold. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Culture characteristics: Conidia germinating on PDA within 24 h. Germ tubes produced from the basal cell. Colonies on PDA reaching 3–5 mm diam. after 7 days at room temperature, colonies circular, with fluffy, dense, white mycelium in the middle and sparse mycelium in the outer ring on the surface with irregular brown margin; in reverse, brown in the middle and pale yellow to brown at the margin.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on dead wood, 27 January 2017, Qiuju Shang, M7P4-17 (KUN-HKAS 102163, **holotype**), ex-type living culture (MFLUCC, ICMP).

GenBank numbers: LSU: MK571766, SSU: MK571775.

Notes: Based on analysis of combined ITS and LSU sequence data (Fig. 18), *Digitodesmium chiangmaiense* (M7P4-17) groups with *D. bambusicola* (CBS 110279) with moderate support (57% ML, 52% MP and 0.92 BYPP). *Digitodesmium chiangmaiense* differs from *D. bambusicola* in lacking appendages on the outer of the arms and having longer conidia (Table 2). In addition, *D. chiangmaiense* differs from other *Digitodesmium* species in the dimension and number of arms (Table 2).

Didymellaceae Gruyter, Aveskamp & Verkley

Notes: The family Didymellaceae was established to accommodate *Didymella*, *Phoma* and phoma-like genera and is one of the most species rich families in the fungal kingdom (Chen et al. 2015, 2017), with 31 genera based on morphology and phylogeny (Chen et al. 2015; Jayasiri et al. 2017; Thambugala et al. 2017a; Wanasinghe et al. 2018b). Species of this family are distributed in a broad

range of environments. Most members are economically important plant pathogens causing leaf and stem spots and many are mentioned in quarantine regulations (Thambugala et al. 2017b, 2018; Knight et al. 2018; Valenzuela-Lopez et al. 2018). Limited studies have been carried out on the sexual morphs (Chen et al. 2015; Thambugala et al. 2017a, 2018; Wanasinghe et al. 2018b). The taxonomic placements of this family were treated based on phylogenetic and morphological analyses (Chen et al. 2015; Jayasiri et al. 2017; Thambugala et al. 2017a; Wanasinghe et al. 2018b).

Calophoma Qian Chen & L. Cai

Notes: The genus *Calophoma*, introduced by Chen et al. (2015), and is typified by *C. clematidina*. (Thum.) Q. Chen & L. Cai and accommodates *C. aquilegiicola*, *C. clematidina*, *C. clematidis-rectae*, *C. complanata*, *C. glaucii* and an insufficiently known species (CBS 186.55) (Chen et al. 2015). The sexual morph has been reported for *C. petasitis* (Tibpromma et al. 2017). The asexual morph has been reported with its unique characteristics such as subglobose, subcylindrical, ellipsoidal, somewhat obclavate-fusiform conidia with 0–1 septa and chlamydospores are produced in one species (Chen et al. 2015, 2017; Tibpromma et al. 2017). Currently there are eight species included in this genus (Tibpromma et al. 2017). We introduce a novel species to this genus with support from combined LSU, ITS, TUB2 and RPB2 sequence data.

Calophoma humuli Thiyagaraja., Bulgakov & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555424; *Facesoffungi* number: FoF05077; Fig. 19

Etymology: The specific epithet “*humuli*” refers to the host plant genus *Humulus*.

Holotype: MFLU 17-2205

Saprobic on dead stems of *Humulus lupulus* L. (Cannabaceae). **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. **Conidiomata** 190–220 μm high \times 210–230 μm diam. (\bar{x} = 205 \times 220 μm , n = 5), pycnidial, sub-immersed, solitary, globose, black. **Pycnidial wall** multi-layered, 10–25 μm wide at the base, 10–20 μm wide in sides, thick, comprising two layers, outer layer heavily pigmented, thick walled, comprising brown cells of *texura angularis*, cells towards the inside lighter, inner layer composed of hyaline *texura angularis*. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** phialidic, hyaline, smooth walled, formed from inner layer of the pycnidium wall. **Conidia** 3–10 \times 3–6 μm (\bar{x} = 6.5 \times 3.8 μm , n = 50), oblong, straight, rounded at the ends, sometimes narrowly rounded at the ends, smooth and thick-walled, aseptate when immature and becoming 1-septate when mature, initially hyaline, becoming pale brown at maturity.



Fig. 14 *Dictyocheirospora aquadulcis* (MFLU 18–1088, **holotype**). **a, b** Colonies on host surface. **c** Colony of conidia. **d–m** Conidium arms. **n** Germinating conidium. **o, p** Culture on MEA at 3 weeks. **q, r**

Culture on MEA at 7 months. Scale bars: **a, b** = 200 μ m, **c** = 100 μ m, **e–m** = 50 μ m, **d, n** = 20 μ m

Culture characteristics: Colonies on PDA reaching 40–45 mm diam. after 2 weeks at 20–25 °C, dense, circular, slightly raised, surface smooth with even edge, cottony, colony from above: white at the margin, grayish at the centre; from below: white at the margin, brownish

yellow at the centre; not producing pigmentation on PDA media.

Material examined: RUSSIA, Rostov region, Krasnosulinsky District, Gornensky protected landscape, edge of ravine forest (47.86602° N, 40.22959° E), on dead stems of

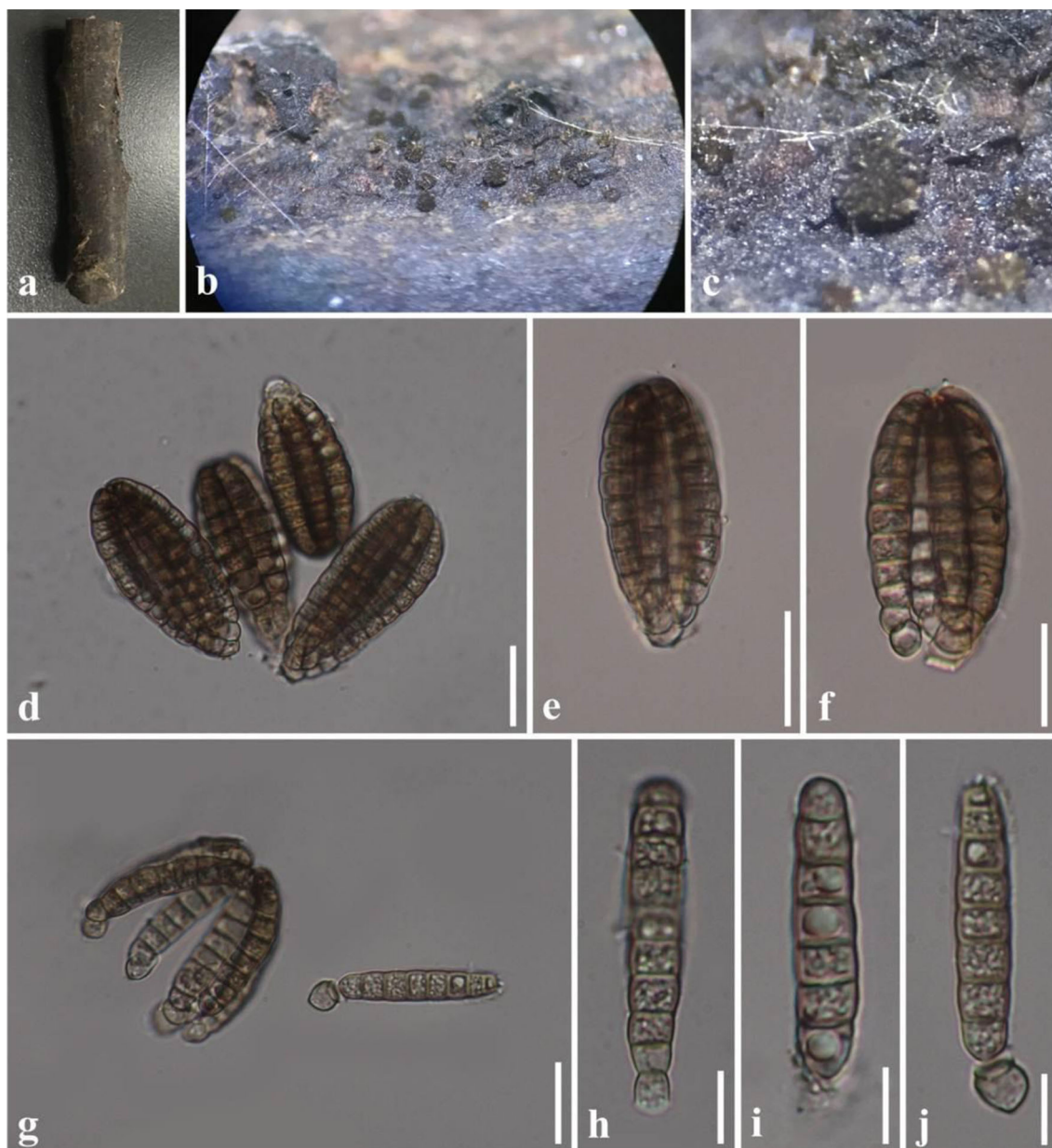


Fig. 15 *Dictyocheirospora rotunda* (HKAS 99571, new geographical record). **a** Material. **b** Appearance of conidiomata on host. **c** Conidioma. **d–f** Conidia. **g** Squashed conidium. **h–j** Arms of conidia. Scale bars: **d–g** = 20 µm, **h–j** = 10 µm

Humulus lupulus L. (Cannabaceae), 6 July 2017, Timur S. Bulgakov (MFLU 17-2205, **holotype**), ex-type living culture (MFLUCC 18-0101).

GenBank numbers: ITS: MK446317, LSU: MK446318, RPB2: MK492667, TUB2: MK492666.

Notes: In our multi-gene analyses, *Calophoma humuli* forms a monophyletic clade with *C. petasitis* with strong support. *Calophoma petasitis* is reported as the sexual morph in the genus *Calophoma* with the characteristics of subglobose ascomata and smooth-walled, guttulate, hyaline ascospores. A comparison of LSU, ITS and RPB2 with these two strains reveals 3/820 (0.36%), 9/441 (2.05%) and

75/797 (9.4%) base pair differences. Even though their LSU and ITS sequences are quite similar, the RPB2 region reveals they should be two different species following the guidelines of Jeewon and Hyde (2016). Therefore, we introduce our isolate as a new species in *Calophoma*.

Neodidymelliopsis Qian Chen & L. Cai

Notes: *Neodidymelliopsis* was introduced by Chen et al. (2015), with *Neodidymelliopsis cannabidis* (G. Winter) Q. Chen & L. Cai as the type species (Chen et al. 2015; Hyde et al. 2016).

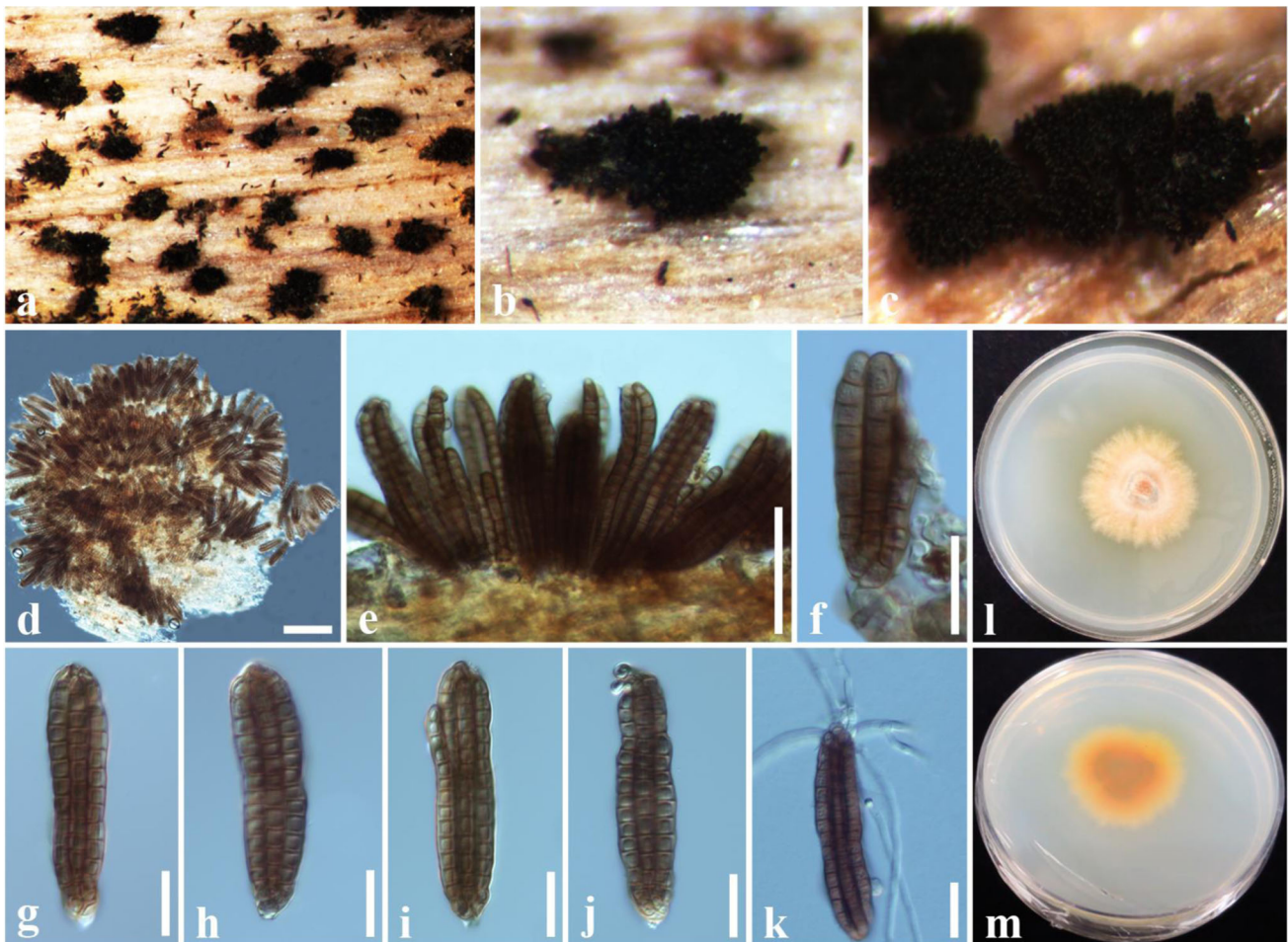


Fig. 16 *Dictyocheirospora taiwanense* (MFLU 18–0070, **holotype**). **a** Conidiomata on the substrate. **b, c** Close-up of conidiomata. **d** Squash mount of conidia. **e, f** Squash mount of conidioma with

conidiogenous cells. **g–j** Conidia. **k** Germinating conidium. Scale bars: **d** = 100 μ m, **e** = 50 μ m, **f–k** = 20 μ m

Neodidymelliopsis farokhinejadii S.A. Ahmadpour & M. Mehrabi-Koushki, Sydowia 69: 175 (2017)

Facesoffungi number: FoF04975; Fig. 20

Saprobic or *necrotrophic* on dead arial stem of *Cirsium* sp. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* on host 75–105 μ m diam. (\bar{x} = 74 μ m, n = 10), pycnidial, solitary, scattered, globose to subglobose, black, semi-immersed to immersed; pycnidial wall pseudoparenchymatous, *textura angularis* dark brown to hyaline cells. *Chlamydospores* not observed. *Conidiophores* not observed. *Conidiogenous cells* not observed. *Conidia* on host 4.5–7.2 \times 2.3–3.6 μ m diam. (\bar{x} = 6 \times 3.2 μ m, n = 40), oblong to ellipsoid, hyaline, aseptate, smooth-walled; in culture, 4.6–7.5 \times 2.4–3.9 μ m diam. (\bar{x} = 6 \times 3.4 μ m, n = 40), ellipsoidal to cylindrical, sometimes allantoid, hyaline, smooth- and thin-walled, aseptate, with small polar guttules.

Culture characteristics: Colonies on PDA reach 25–30 mm diam. after 7 days at 25 $^{\circ}$ C, with white aerial

mycelium, surface floccose to wooly, margin regular, pale greenish olivaceous; reverse dull green.

Material examined: ITALY, Forlì-Cesena Province, near Castrocaro Terme, on dead aerial stem of *Cirsium* sp. (Asteraceae), 25 February 2018, Erio Camporesi, living culture (MFLUCC 18-1569).

Genbank numbers: ITS: MK084580, LSU: MK084581.

Notes: *Neodidymelliopsis farokhinejadii* was first reported on dead branches of *Eucalyptus* sp. and was subsequently found on *Citrus limon*, *Conocarpus erectus*, *Ziziphus* sp., *Juglans regia* and *Cupressus* sp. (Ahmadpour et al. 2017) Our new isolate of *N. farokhinejadii* was collected from Forlì-Cesena Province in Italy. This is the first report of *N. farokhinejadii* on *Cirsium* species (Farr and Rossman 2019). Morphological observations such as spore characteristics support the inclusion of our taxa into *Neodidymelliopsis* (Chen et al. 2015). DNA sequence analyses from the LSU, ITS, TUB2 and RPB2 genes confirms that our taxon clades together with *N. farokhinejadii* (Fig. 21).

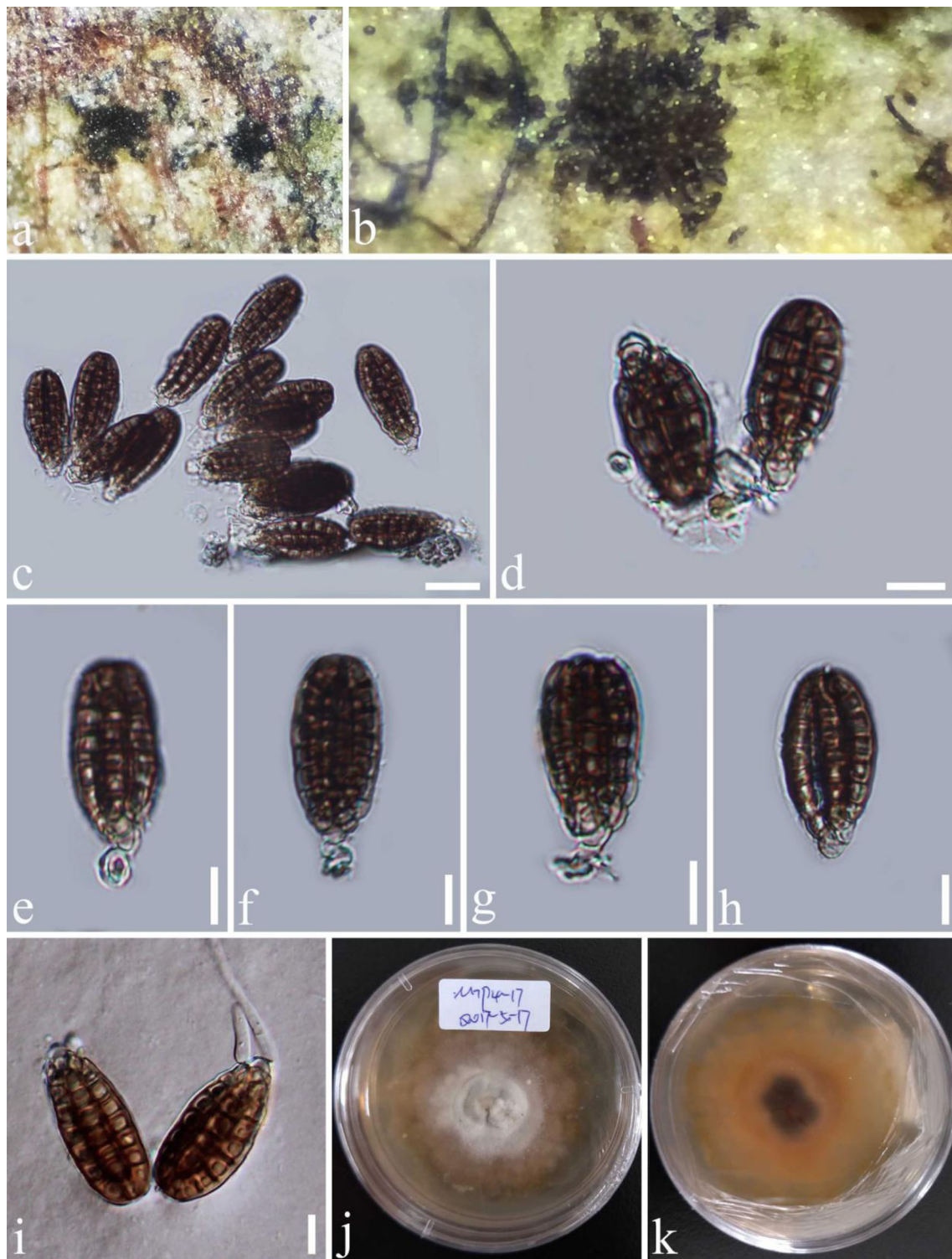


Fig. 17 *Digitodesmium chiangmaiense* (KUN-HKAS 102163, **holotype**). **a, b** Colonies on submerged wood. **c** Squash mount of a sporodochium. **d–g** Conidia with conidiophores. **h** Conidium.

i Germinated conidia. **j, k** Culture characteristics on PDA (**j** from above view, **k** from below view) Scale bars: **c** = 20 μ m, **d–i** = 10 μ m

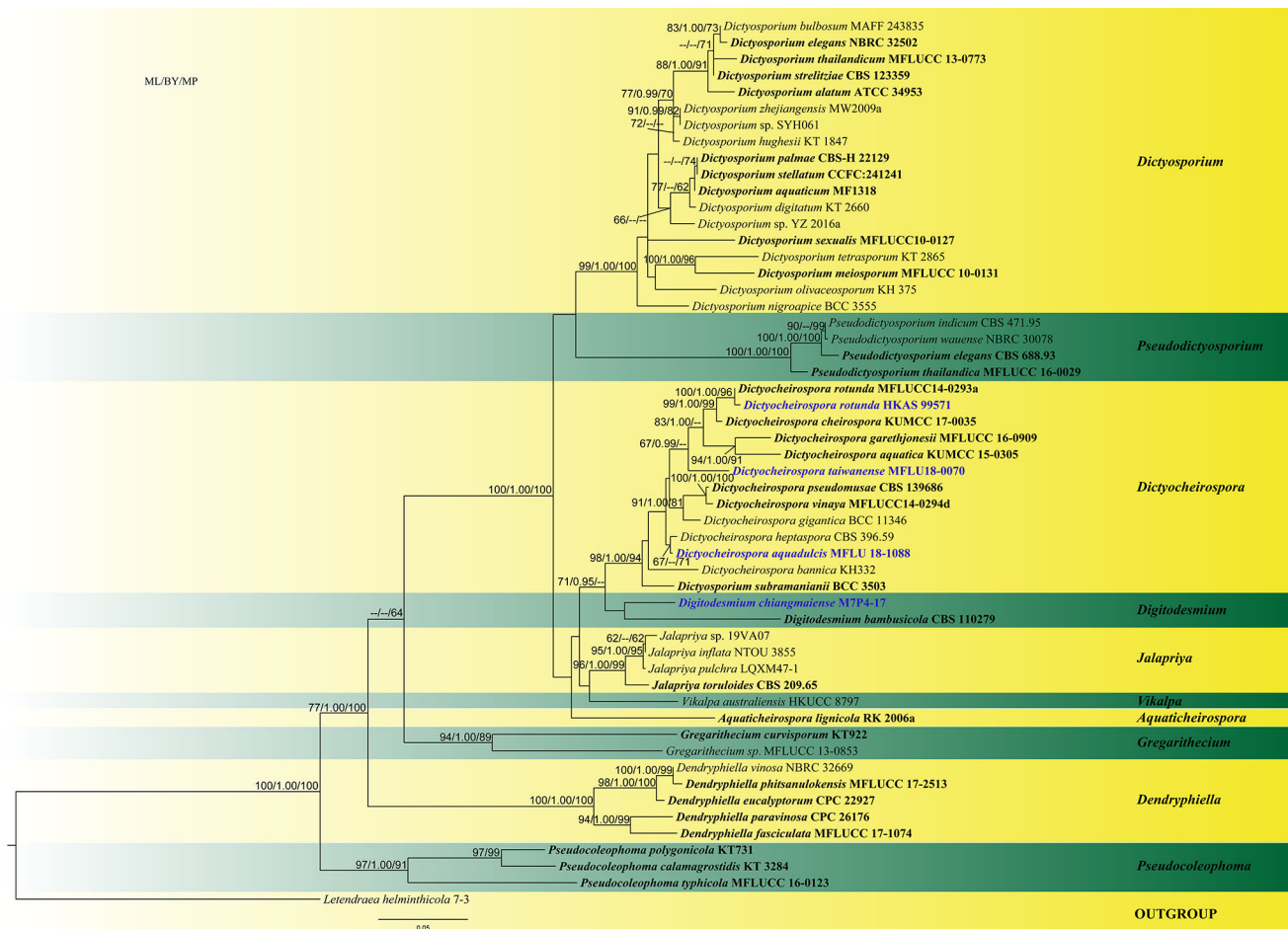


Fig. 18 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequences data in Dictyosporiaceae. Related sequences are taken from Boonmee et al. (2016) and Wang et al. (2016). Fifty-three strains are included in the combined analyses which comprise 1405 characters (553 characters for ITS, 852 characters for LSU) after alignment. *Letendreaa helminthicola* 7-3 (Montagnulaceae, Pleosporales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis and the maximum parsimony analysis. The best RAxML tree with a final likelihood value of -8736.227244 is presented. The matrix had 523 distinct alignment patterns, with 18.97% undetermined characters or gaps. Estimated base frequencies

were as follows: A = 0.241508, C = 0.237486, G = 0.270256, T = 0.250751; substitution rates AC = 2.173342, AG = 3.473225, AT = 3.246966, CG = 0.531302, CT = 36.318285, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.567927$. Maximum parsimony analysis of 981 constant characters and 292 informative characters resulted in two equally most parsimonious trees of 1392 steps (CI = 0.486, RI = 0.744, RC = 0.361, HI = 0.514). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 60 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

Neodidymelliopsis sambuci Manawasinghe, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555378; *Facesoffungi* number: FoF04939; Fig. 22

Etymology: Name reflects the host genus.

Holotype: MFLU 18-0177

Saprobic or *necrotrophic* on dead and dying twigs and branches of *Sambucus nigra*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* on host 37–82 μm diam. (\bar{x} = 58 μm , n = 10), pycnidial, solitary, scattered, globose, black, semi-immersed to immersed. *Conidiophores* not observed. *Conidiogenous*

cells not observed. *Conidia* on host 4–7 \times 2–3.5 μm diam. (\bar{x} = 6 \times 2 μm , n = 40), oblong to ellipsoid, hyaline, aseptate, smooth-walled; in culture, 5–8 \times 1–3.5 μm diam. (\bar{x} = 6 \times 2.7 μm , n = 40). Conidial exudates not observed. *Culture characteristics*: Colonies on PDA reach 65 mm diam. after 7 days at 25 °C, with circular, entire edge, raised grey olivaceous aerial mycelium, surface floccose to woolly.

Material examined: ITALY, Province of Ravenna, Santa Lucia, Faenza, on living branch of *Sambucus nigra* L. (Adoxaceae), 5 January 2018, Erio Camporesi (MFLU

Table 2 Conidia of *Digitodesmium* species discussed in this study

Taxa	<i>D. bambusicola</i>	<i>D. Chiangmaiense</i>	<i>D. elegans</i>	<i>D. heptasporum</i>	<i>D. intermedium</i>	<i>D. macrosporum</i>	<i>D. recurvum</i>
Colour	Pale brown	Brown to dark brown	–	Pale brown	Brown to dark brown	Brown to dark brown	Pale brown
Dimension (µm)	24–32.5 × 12.5–23	(25–)30–45(–44) × (13–)12–21(–21)	45–60 × 12–21	50–75 × 32.5–70	39–76 × 25–35	130–145 × 19–26	30–45 × 12.5–23
Appendages	Yes	No	No	No	No	No	No
Wall	Smooth	Smooth	Smooth	Smooth	Smooth	Smooth	Smooth
Septal pores	Conspicuous	Conspicuous	Inconspicuous	Conspicuous	Conspicuous	Conspicuous	Conspicuous
Number of arms	3	3	(2–)3–4(–6)	6–7	3–11	5–8	(2–)4–6(–7)
Number of septa in each of arm	4–7	5–7	9–12	11–17	7–13	17–19	6–10
Country	Philippines	Thailand	UK	China	Spain	Spain	China
Reference	Cai et al. (2002)	This study	Kirk. (1981)	Cai et al. (2003)	Silvera-Simón et al. (2010)	Silvera-Simón et al. (2010)	Ho et al. (1999)

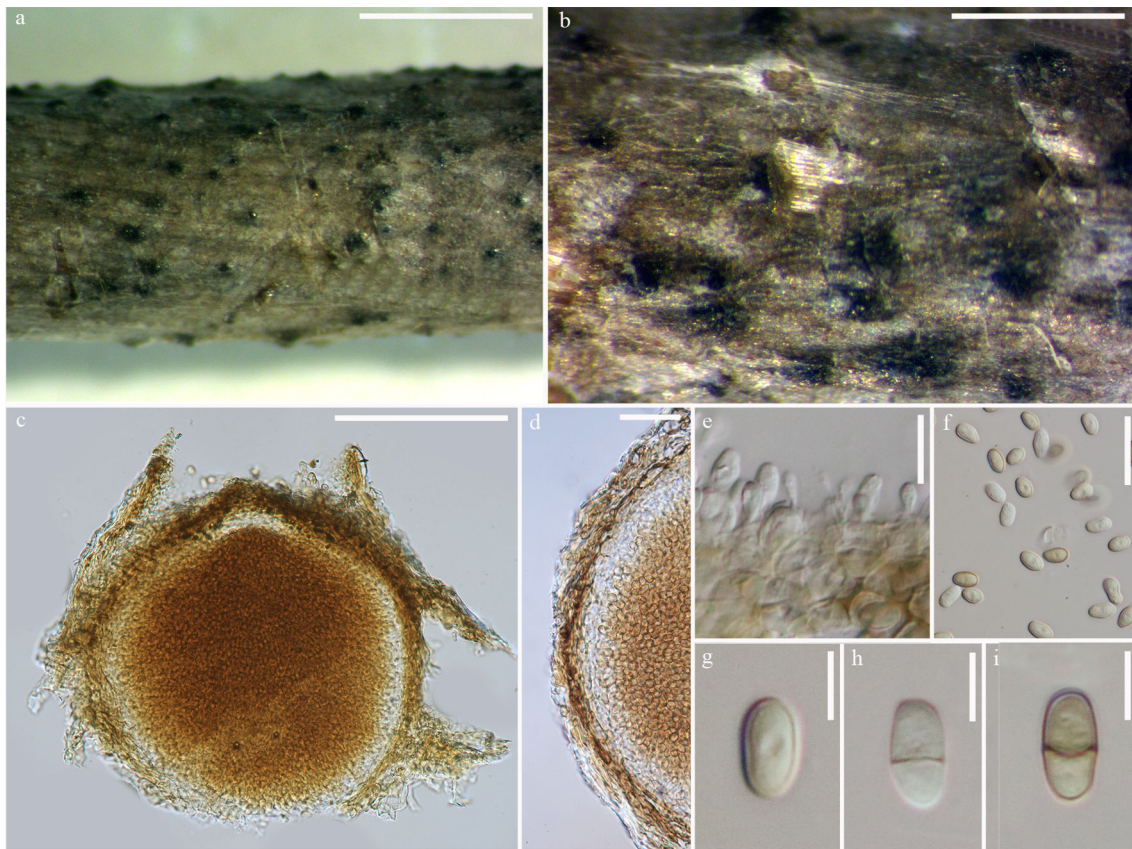
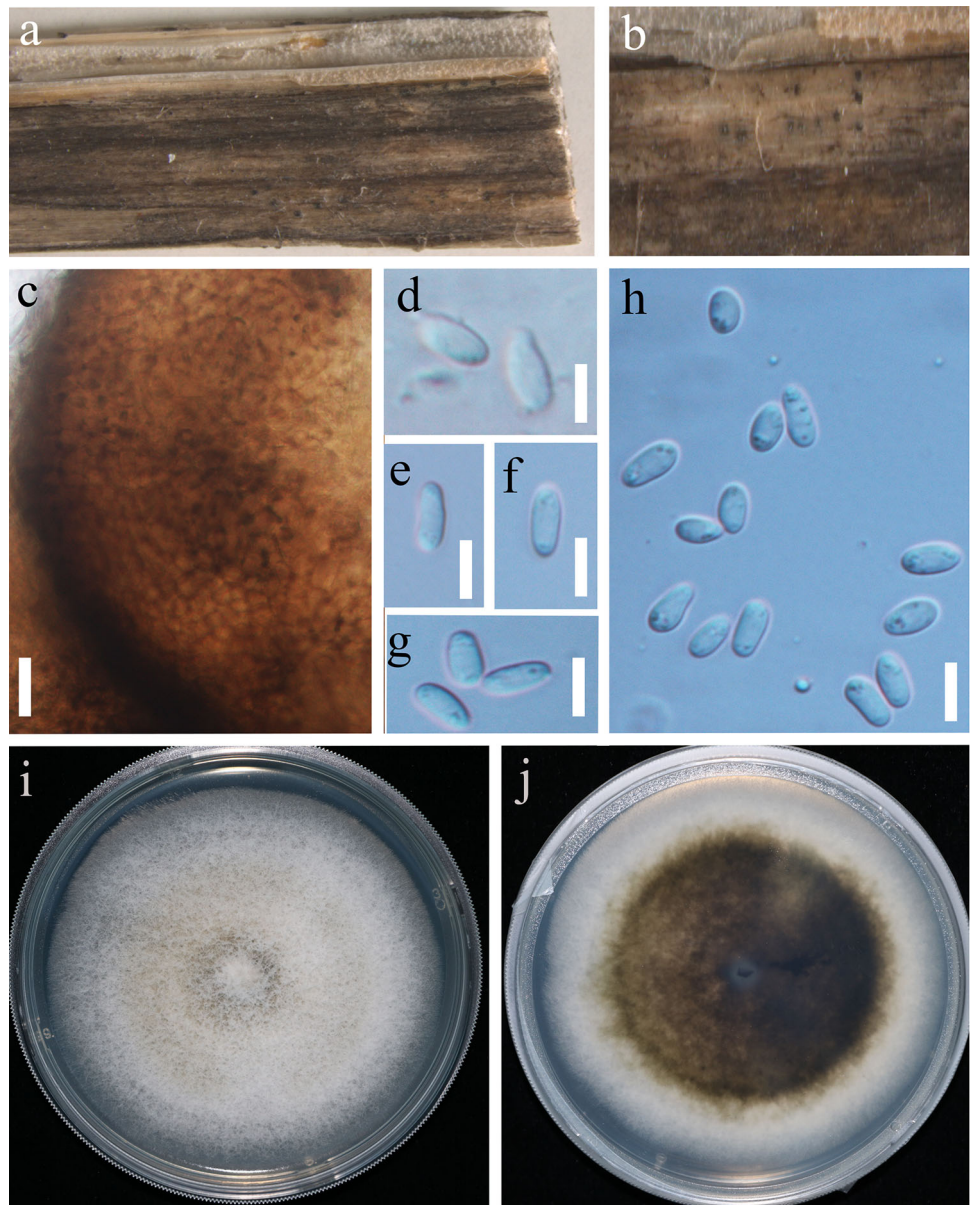
**Fig. 19** *Calophoma humuli* (MFLU 17–2205, holotype). **a, b** Conidiomata on host. **c** Section through conidioma. **d** Section through conidioma wall. **e** Conidiogenous cells. **f–i** Conidia. Scale bars: **a, b** = 500 µm, **c** = 100 µm, **d** = 20 µm, **e** = 10 µm, **f–i** = 5 µm

Fig. 20 *Neodidymelliopsis farokhinejadii* (JZB–H380023, new host record). **a, b** Conidiomata on the host tissue. **c** Section of the pycnidial wall. **d–h** Conidia. **i** Upper view of 7-day old culture. **j** Reverse view of 7-day old culture. Scale bar: **c–h** = 10 μ m



18-0177, **holotype**), ex-type living culture (MFLUCC 18-1565).

GenBank numbers: ITS: MH84232, LSU: MH84231, TUB2: MK049556.

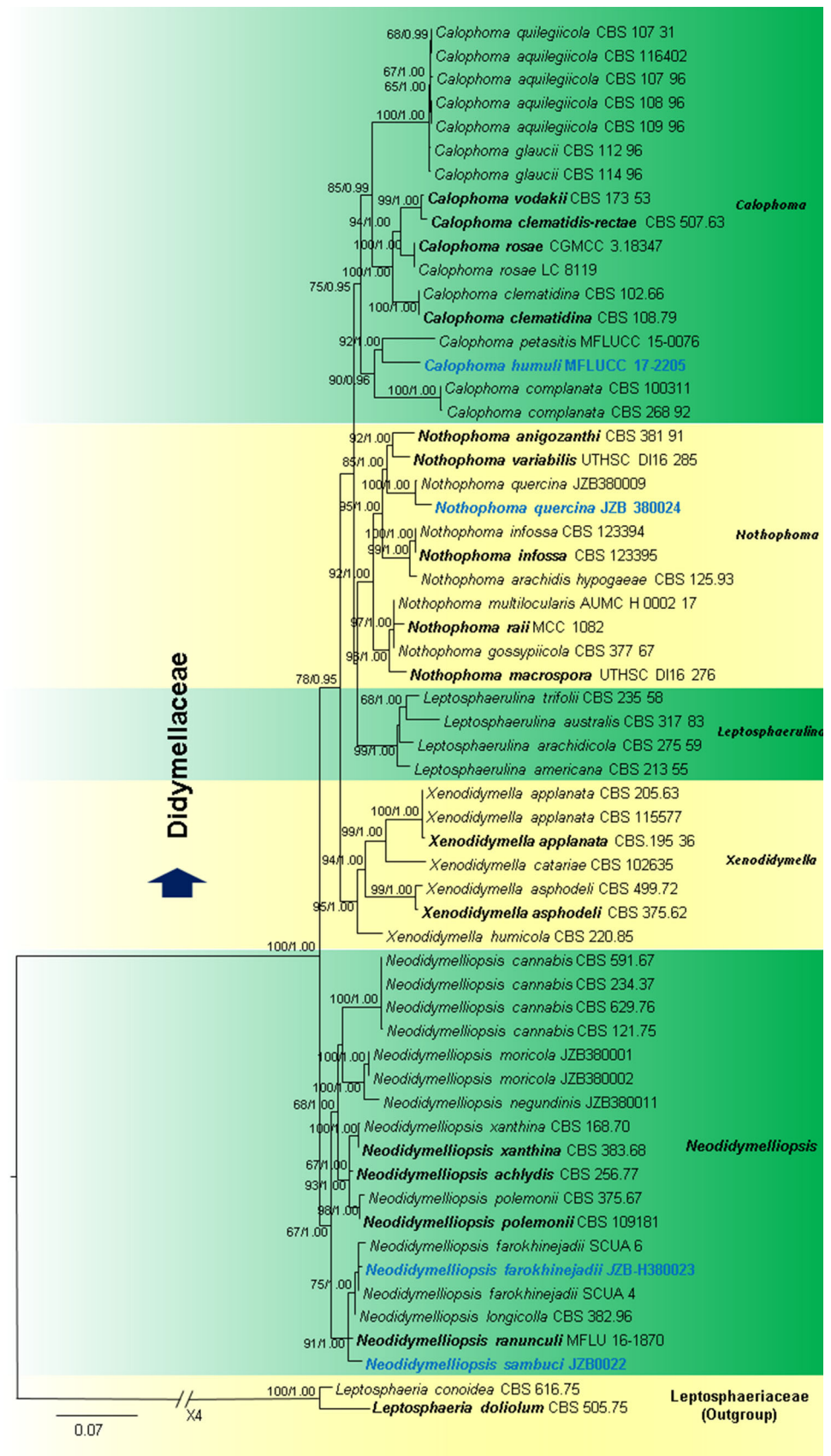
Notes: Morphological characters such as conidial size and shape (Fig. 22) fit well within the concept of *Neodidymelliopsis* (Chen et al. 2015). The combined gene sequence analyses of LSU, ITS, RPB2 and TUB2 genes confirm that present taxon belongs in genus *Neodidymelliopsis* in a strongly supported monophyletic lineage (Fig. 21) within family Didymellaceae. In phylogenetic analysis *Neodidymelliopsis sambuci* is in a sister clade with *N. longicolla*. Morphologically, *N. sambuci* can be distinguished from *N. longicolla* by its smaller conidia ($12\text{--}15 \times 4\text{--}7 \mu\text{m}$ in *N. longicolla*). This is the first report

of *Neodidymelliopsis* reported on *Sambucus* species (Farr and Rossman 2019).

Nothophoma Qian Chen & L. Cai

Notes: The genus *Nothophoma* was introduced by Chen et al. (2015) with the type species *Nothophoma infossa* (Ellis & Everh.) Q. Chen & L. Cai. (syn. *Phoma infossa*) and five other species transferred from *Phoma*, namely *N. anigozanthi* (syn. *P. anigozanthi*), *N. arachidis-hypogaeae* (syn. *P. arachidis-hypogaeae*), *N. quercina* (syn. *P. fungicola*), and *N. gossypicola* (syn. *P. gossypicola*) (Chen et al. 2015). There are nine species in this genus with the recently introduced *N. variabilis* (Valenzuela-Lopez et al. 2018). Ovoid, oblong to ellipsoidal aseptate conidia are a characteristic of the genus *Nothophoma*. This genus

Fig. 21 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, TUB2 and RPB2 sequence data for Didymellaceae. Related sequences are taken from Chen et al. (2015), Jayasiri et al. (2017), Thambugala et al. (2017a) and Wanasinghe et al. (2018b). Fifty-nine strains are included in the combined genes sequence analyses which comprise total 2683 characters (960 characters for LSU, 547 characters for ITS, 360 characters for TUB2, 816 characters for RPB2) after alignment. *Leptosphaeria conidia* (CBS 616.75) and *L. doliolum* (CBS 505.75) (*Leptosphaeriaceae*, Pleosporales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best sorting RaxML tree with a final likelihood value of -16885.291744 is presented. The matrix had 945 distinct alignment patterns, with 21.62% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241571, C = 0.241856, G = 0.271818, T = 0.244754; substitution rates AC = 1.630628, AG = 4.058235, AT = 1.775626, CG = 0.954941, CT = 9.716323, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.414994$. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue



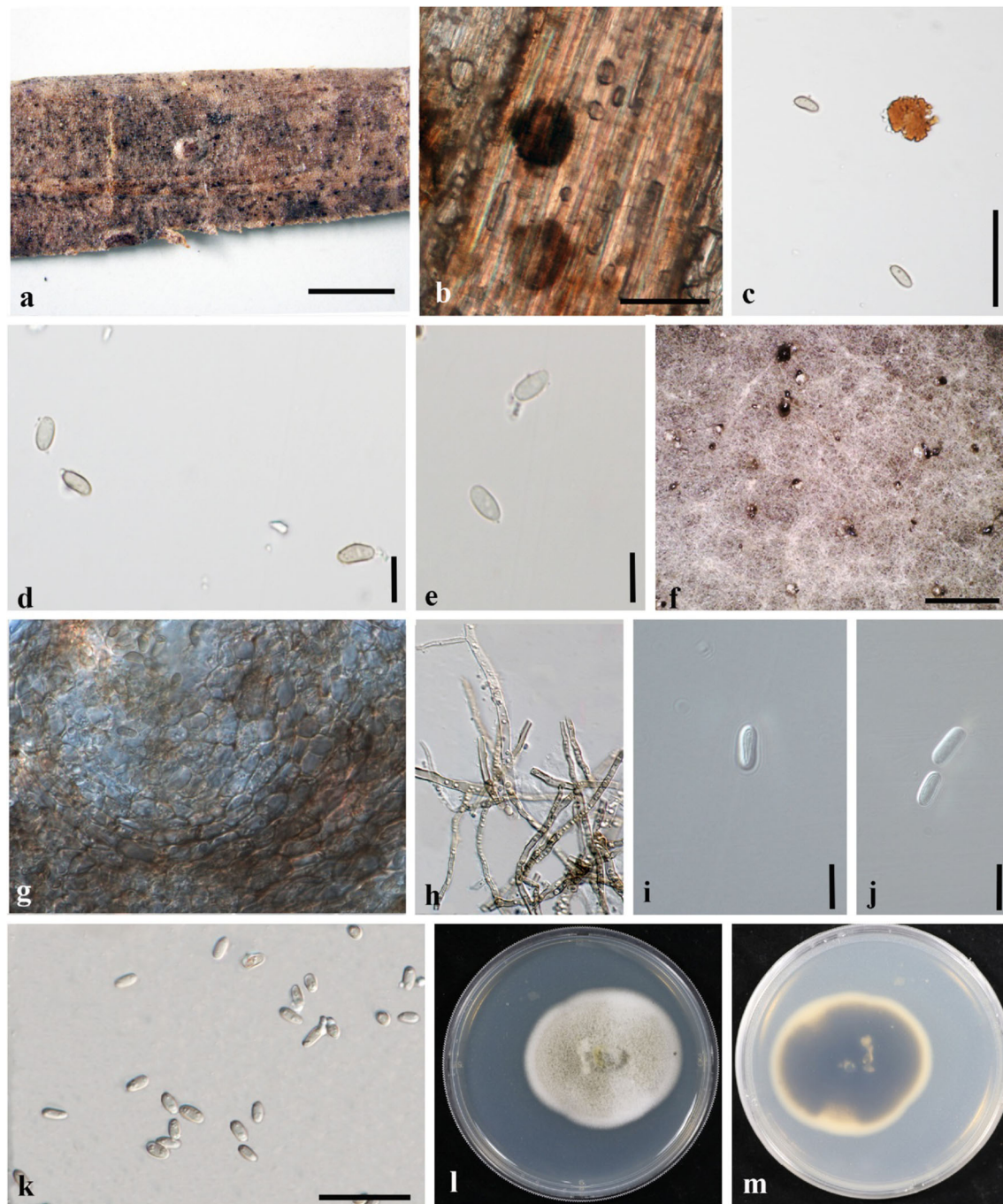


Fig. 22 *Neodidymelliopsis sambuci* (MFLU 18-0177, **holotype**). **a** Appearance of pycnidia on dead branch of *Sambucus nigra*. **b** Appearance of pycnidia under the light microscope. submerged conidiomata on the host surface. **c–e** Conidia on host. **f** Pycnidia on

agar. **g** pycnidial wall. **h** Developing hyphae. **i–k** Conidia on PDA. **l** Upper view of 7 days old culture on PDA. **m** Reverse view of 7 days old culture on PDA. Scale bars: **a** = 1000 µm, **b**, **f** = 100 µm, **c**, **k** = 20 µm, **d**, **e**, **i**, **j** = 10 µm

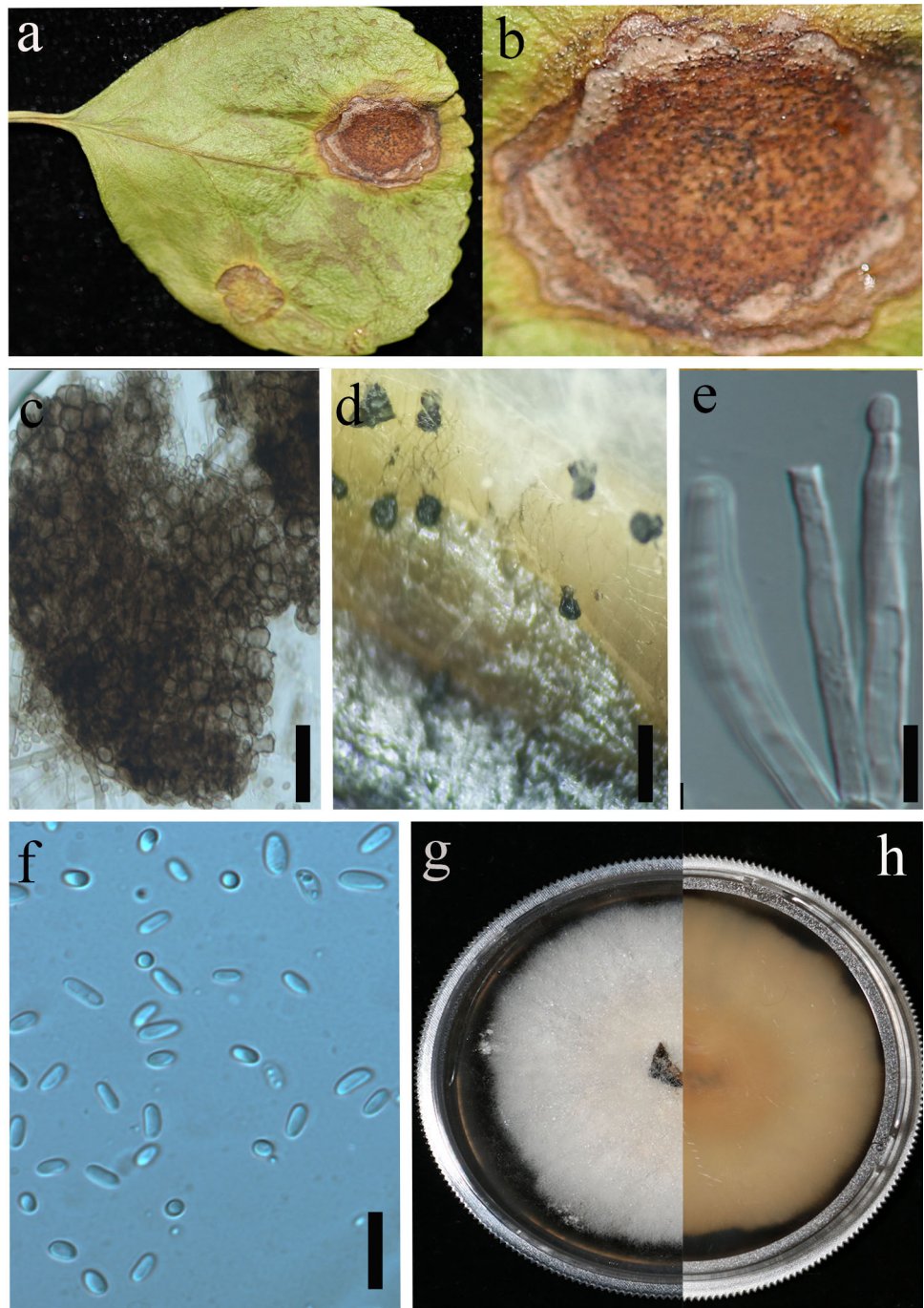
contains ubiquitous fungal species, of which many are plant pathogens, some of which are of quarantine concern (Chen et al. 2015).

Nothophoma quercina (Syd. & P. Syd.) Q. Chen & L. Cai, Stud. Mycol. 82: 213. 2015.

Facesoffungi number: FoF04974; Fig. 23

Pathogenic on leaves of *Buxus megistophylla* H.Lév. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* produced on the PDA surface, 0.19–0.47 mm (\bar{x} = 0.25 mm, n = 10) diam., pycnidial, solitary, scattered, globose to irregularly shaped, black, ostiolate. *Pycnidial wall* multi-layered, composed of pale brown,

Fig. 23 *Nothophoma quercina* (JZB380024, new host record). **a, b** Conidiomata on the host tissue. **c** Section of the pycnidial wall. **d** Pycnidia on PDA. **e** Conidiogenous cells on culture. **f** Conidia on culture. **g** Upper view on colonies on PDA. **h** Lower view on colonies on PDA. Scale bar: **c** = 1 mm, **d–f** = 20 μ m



pseudoparenchymatous cells. *Conidiogenous cells* phialidic, hyaline, simple, doliiform to ampulliform, variable in size. *Conidia* $4\text{--}5.6 \times 1.4\text{--}3.3 \mu\text{m}$ ($\bar{x} = 5.2 \times 2.3 \mu\text{m}$, $n = 40$), variable in size and shape, subglobose to oval or obtuse, initially hyaline, but brown at maturity, aseptate, smooth-walled. Conidial exudates not recorded.

Culture characteristics: Colonies on PDA reach 80 mm diam. after 7 days at 28 °C, with regular margin, dull white aerial mycelium surface floccose to wooly, greenish

olivaceous to olivaceous near the centre and reverse dark ochreous in the centre and white in the margin.

Material examined: CHINA, Haidian District, Beijing, on leaves of *Buxus megistophylla* (Buxaceae), November 2017, D. Harishchandra, living culture (JZB380024, MFLUCC 18-1568).

GenBank numbers: ITS: MK070136, LSU: MK070139.

Notes: *Nothophoma quercina* has been reported as a pathogen on *Pistacia vera* (Chen et al. 2013), *Chaenomeles sinensis* (Yun and Oh 2016), *Olea europaea* (Moral et al.

2017) and was reported as a saprobe on *Quercus* sp. in Ukraine (Chen et al. 2015). This is the first record of *N. quercina* on *Buxus* sp. Phylogenetic analysis with the combined sequence data of ITS, TEF1- α , TUB2 and RPB2 of our strain (MFLUCC 18-1568) clusters together with the ex-type strain of *Nothophoma quercina* (CBS 633.92) with relatively high bootstrap and Bayesian probabilities (99% MP/1.00 PP).

Hermatomycetaceae Locq.

Notes: Hashimoto et al. (2017) introduced Hermatomycetaceae for a separate lineage of *Hermatomyces* species in Pleosporales, with *Hermatomyces* Speg. as the generic type. Hermatomycetaceae was introduced by Locquin (1984) based on their distinctive characteristics, recently, the family placement had been formalised with a robust phylogenetic information (Doilom et al. 2017; Hashimoto et al. 2017). Several taxa have been introduced in the family, interestingly, no sexual morph has been discovered (Koukol et al. 2018; Tibpromma et al. 2016, 2018). In this study, we introduce a novel *Hermatomyces* species based on the distinctive morphology and supportive phylogenetic relationships (Fig. 24).

Hermatomyces Speg.

Notes: *Hermatomyces* was introduced by Spegazzini (1911) with *H. tucumanensis* Speg. as a type species. The genus is commonly present as sporodochial conidiomata and muriform, lenticular, hyaline or dematiaceous conidia of one or two types (Chang 1995; Tibpromma et al. 2016; Hashimoto et al. 2017). Koukol et al. (2018) synonymized several species of *Hermatomyces* based on morphological similarity and possible artefacts in the phylogenetic analysis. Tibpromma et al. (2018) confirm that the species homogeneity needs sufficient evidence from characters and TUB2 gene sequence data are still required (Jeewon and Hyde 2016). Therefore in this study, we follow Tibpromma et al. (2018) and introducing a novel species of *Hermatomyces*, *H. bauhiniae* based on its morphological and phylogenetically distinct from other *Hermatomyces* species (Fig. 24).

Hermatomyces bauhiniae Phukhams., D.J. Bhat & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555500; **Facesoffungi number:** FoF04827; Fig. 25

Etymology: Name refers to the host plant, *Bauhinia variegata* from which this fungus was isolated.

Holotype: MFLU 18-1381

Saprobic on dead branch of *Bauhinia variegata* L.

Sexual morph Undetermined. **Asexual morph** Colonies on natural substrate forming sporodochial conidiomata, superficial, scattered, circular or oval, blackish brown, velvety, glistening, consisting of an orbicular, abundantly

sporulation, conidia readily liberated when agitated, 160–180 μm wide. *Mycelium* mostly superficial, composed of a loose or compact network of repent, branched, septate, rough-walled, thick-walled, reddish brown to brown hyphae, 2–4 μm wide; subicular hyphae short, irregularly geniculate or flexuous, densely packed. *Conidiophores* 4–10 \times 2–5 μm , micronematous or semimacronematous, mononematous, cylindrical, erect, smooth or finely verruculose, aseptate, unbranched, often corresponding to conidiogenous cells, hyaline. *Conidiogenous cells* 3–8 \times 4–9 μm , holoblastic, monoblastic, integrated, terminal, determinate, cylindrical or slightly subulate, subsphaerical or ampulliform, hyaline. *Conidia dimorphic*, solitary, smooth-walled: *lenticular conidia*: 25–36 \times 15–20 μm (\bar{x} = 30 \times 18 μm , n = 70), muriform, smooth, broadly ellipsoidal to oval in front view, brown to dark brown, slightly constricted at the septa, in side view composed of one column of 4–6 cells, end cells subhyaline to pale brown, often carrying remnant of conidiogenous cell at base; *cylindrical conidia*: 20–28 \times 8–11 μm (\bar{x} = 24 \times 9 μm , n = 30), straight or flexuous, septate, constricted at the septa, consisting of one column, 2–3-septate, doliiform, cylindrical or subcylindrical, apical cells clavate or doliiform, verrucose, apex rounded, basal cells globose or subglobose, smooth, hyaline.

Culture characteristics: Colonies on MEA at room temperature (25 °C) reaching 7 cm in 2 weeks, circular with entire margin, with white–grey mycelium, white at the margin, smooth at the surface and raised, mycelium strongly radiating into agar; reverse beige, no sporulation in cultures.

Material examined: THAILAND, Phrae Province, on dried branch of *Bauhinia variegata* (Fabaceae), 25 July 2015, C. Phukhamsakda, S1_02 (MFLU 18-1381, **holotype**), ex-type living culture (MFLUCC 16-0395, ICMP 21948).

GenBank numbers: ITS: MK443382, LSU: MK443378, RPB2: MK443386, SSU: MK443380, TEF1- α : MK443384.

Notes: *Hermatomyces bauhiniae* is introduced as a new species based on its distinct morphology and support from phylogenetic analysis. *Hermatomyces bauhiniae* has distinct characteristics as compared to the other species. The lenticular conidia are not round or flat in one plane, and have well visible conidiogenous cells attached at the bottom of the conidia. In the phylogenetic analysis, *H. bauhiniae* formed a clade with *H. indicus* with good support (MLBS = 82; BYPP = 0.99). Both species were recorded from angiosperms plants. Nonetheless, *H. bauhiniae* can be distinguished from *H. indicus* by having straight conidia with only one column, hyaline, and cylindrical conidia, where as in *H. indicus* conidia are turbinate, grey-brown at the apex, and become hyaline towards the base with two

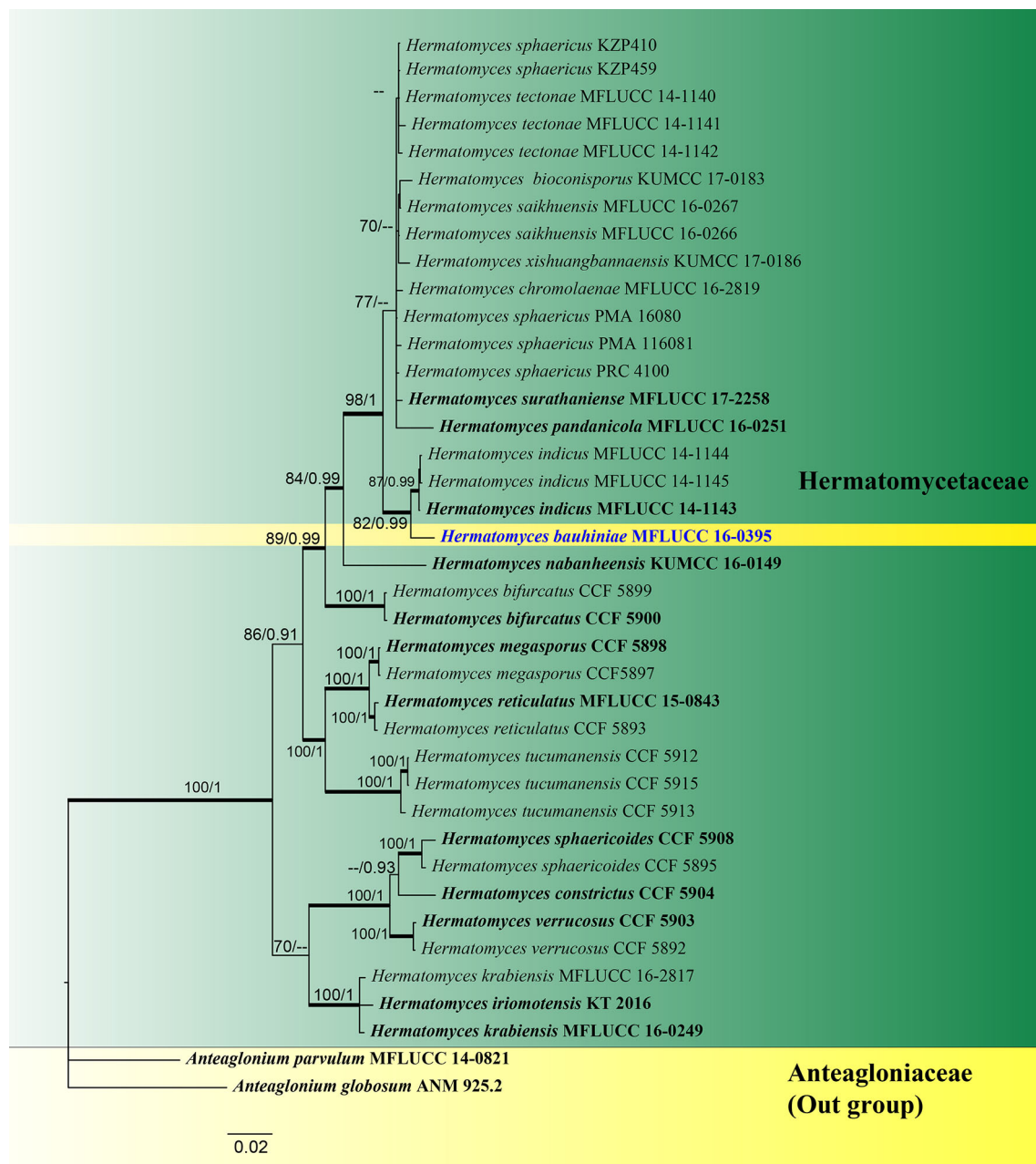


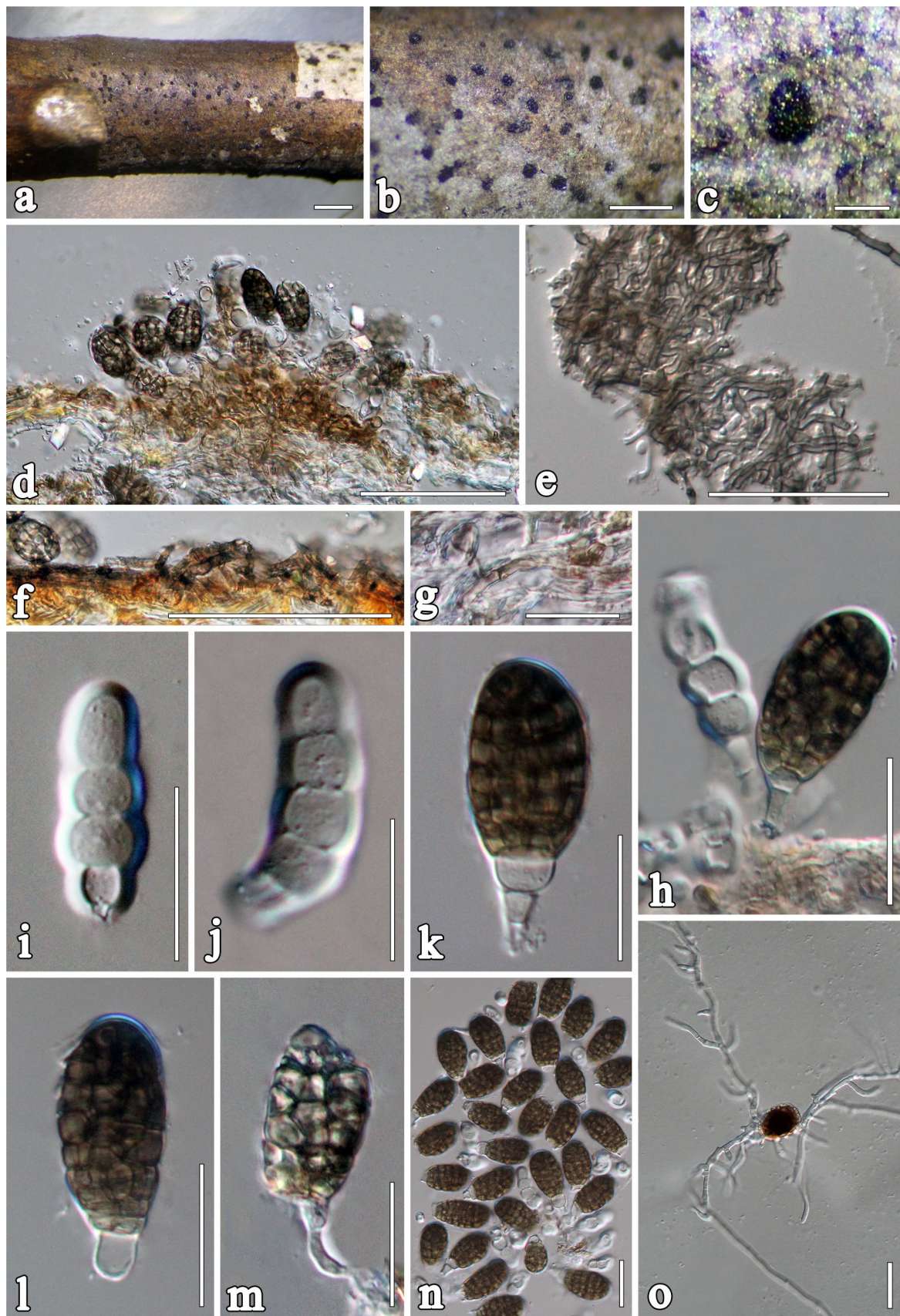
Fig. 24 Phylogram of 50% majority rule consensus tree from the Bayesian-inference analysis based on combined dataset of LSU, ITS, TEF1- α , and RPB2 sequence data representing Hermatomycetaceae. Related sequences are taken from Doilom et al. (2017), Hashimoto et al. (2017), Koukol et al. (2018) and Tibpromma et al. (2018). Thirty-nine strains are included in the combined analyses which comprise 3301 characters (826 characters for LSU, 514 characters for ITS, 941 characters for TEF1- α , 1020 characters for RPB2) after alignment. The tree is rooted with *Anteaaglioniaceae globosum* (ANM 925.2) and *A. parvulum* (MFLUCC 14-0821) in Anteaaglioniaceae (Pleosporales). Single gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree

topology of the maximum likelihood analysis is similar to the Bayesian analysis. Bootstrap support values for maximum likelihood analysis greater than 70% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian-inference analysis labeled on the nodes. The matrix has 710 distinct alignment patterns, with 20.65% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244863, C = 0.263683, G = 0.262259, T = 0.229195; substitution rates AC = 1.191383, AG = 5.252837, AT = 1.421242, CG = 1.059773, CT = 14.708510, GT = 1.000000; gamma distribution shape parameter α = 0.766883. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

columns. *Hermatomyces indicus* has larger cylindrical conidia but smaller lenticular conidia (Prasher and Sushma 2014; Doilom et al. 2017).

Lophiostomataceae Sacc.

Notes: The family was introduced as “Lophiostomeae” by Nitschke (1869) and recorded as “Lophiostomaceae” in



◀**Fig. 25** *Hermatomyces bauhiniae* (MFLU 18-1381, **holotype**). **a–c** Sporodochia on natural substrate. **d** Vertical section through sporodochia. **e–g** Subicular hyphae. **h** Cylindrical conidia and lenticular conidia on host substrate. **i, j** Cylindrical conidia. **k–m** Mature lenticular conidia. **n** Conidia. **o** Germinated conidium. Scale bars: **a** = 1 cm, **b** = 500 μ m, **c, d, f** = 100 μ m, **o** = 50 μ m, **h–m** = 20 μ m, **e, g** = 10 μ m

Saccardo (1883), but was accepted as Lophiostomataceae in Mugambi and Huhndorf (2009). Members of this family are saprobes and are found in terrestrial, aquatic and marine habitats (Tanaka and Harada 2003; Zhang et al. 2009c; Hirayama and Tanaka 2011; Hyde et al. 2013; Thambugala et al. 2015; Jones et al. 2015; Tennakoon et al. 2018). A generic re-evaluation of Lophiostomataceae by Thambugala et al. (2015) based on multi-locus phylogenies using LSU, SSU, ITS and TEF1- α sequence data, integrated 16 genera into this family, and resolved the phylogenetic and morphological boundaries of Lophiostomataceae. Hashimoto et al. (2018) revised the taxonomical classification of *Lophiostoma bipolare* (K.D. Hyde) E.C.Y. Liew, Aptroot & K.D. Hyde, and proposed a novel genus *Lentistoma* A. Hashim., K. Hiray. & Kaz. Tanaka to accommodate *Lophiostoma* sensu stricto. Four additional new genera and two new genera combinations were recognized from the other lineages of the *L. bipolare* complex. Therefore, there are currently 23 genera in Lophiostomataceae.

Vaginatispora K.D. Hyde

Notes: *Vaginatispora* was introduced by Hyde (1995b) with *V. aquatica* K.D. Hyde as the type species. *Vaginatispora aquatica* was initially placed in Massarinaceae, but Zhang et al. (2014a) revealed its phylogenetic affinity with Lophiostomataceae. Subsequently, Thambugala et al. (2015) considered *Vaginatispora* as a separate genus within Lophiostomataceae based on multi-gene phylogeny and morphology, of which *V. aquatica* and *V. fucklii* were included. Thereafter, *V. appendiculata* (Wanasinghe et al. 2016), *V. armatispora* (\equiv *Massarina armatispora* K.D. Hyde, Vrijmoed, Chinnarij & E.B.G. Jones) (Hyde et al. 1992; Liew et al. 2002; Wanasinghe et al. 2016), *V. microarmatispora* (Devadatha et al. 2017), *V. amygdali* and *V. scabrispora* (Hashimoto et al. 2018) were introduced based on morphology and phylogeny. However, *V. fucklii* was transferred to a new genus *Neovaginatispora* (Hashimoto et al. 2018) based on phylogenetic distinction and its typical characters of erumpent ascomatal and a thinner peridium. During observations of microfungi from marine (mangrove) and freshwater habitats, *Vaginatispora palmae* sp. nov. and *V. armatispora* were reported and illustrated herein. An updated phylogenetic tree is

provided, which includes all *Vaginatispora* taxa and closely related genera in Lophiostomataceae.

Vaginatispora palmae S.N. Zhang, J.K. Liu & K.D. Hyde, **sp. nov.**

Index Fungorum number: IF556316; **Facesoffungi number:** FoF05089; **Fig. 26**

Etymology: The epithet reflects the family of host plant.

Holotype: MFLU 18-1586

Saprobic on immersed rachis of *Nypa fruticans*. **Sexual morph** **Ascomata** in vertical section 250–340 μ m high, 215–385 μ m diam. (\bar{x} = 310 \times 326 μ m, n = 10), dark brown to black, scattered, semi-immersed, erumpent, subglobose to elongated, base flattened, coriaceous to carbonaceous. **Ostiole** crest-like, variable in shape, central papillate. **Peridium** 15–38 μ m wide, wider at the apex and thinner at the base, composed of several pale brown to brown cells of *textura angularis*, cells towards the inside lighter, at the outside darker, somewhat flattened, fusing and with the host tissues. **Pseudoparaphyses** 1–2.5 μ m wide, hypha-like, numerous, septate, rarely branched and anastomosed, tapering towards the apex. **Asci** 89–115 \times 12–20 μ m (\bar{x} = 100.5 \times 16.0 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a short bulbous pedicel, rounded at the apex, with an ocular chamber. **Ascospores** 23–45 \times 6–9 μ m, (\bar{x} = 35.3 \times 7.5 μ m, n = 30), hyaline, uniseriate or overlapping to biseriate, 1-septate, occasionally producing pseudosepta, slightly constricted at the central septum, cell above central septum swollen, guttulate, smooth-walled, surrounded by a narrow mucilaginous sheath and drawn out towards each end to form tapering appendages, 6–8 μ m long. **Asexual morph** Undetermined.

Culture characteristics: **Ascospores** germinating on PDA within 24 h. Colonies growing on PDA reaching 2 cm diam. after 21 days at 25 $^{\circ}$ C, the off-white hyphae in first week, then becoming grayish blue and dark bluish, composed of brown to dark brown, septate, smooth or verrucose hyphae.

Material examined: THAILAND, Ranong Province, on immersed rachis of *Nypa fruticans* Wurmb (Arecaceae), 3 December 2016, S.N. Zhang, SNT92 (MFLU 18-1586, **holotype**), ex-type living culture (MFLUCC 18-1526); *ibid.* (HKAS 102207, **isotype**).

GenBank numbers: ITS: MK085055, LSU: MK085059, SSU: MK085057, TEF1- α : MK087657.

Notes: Most species of *Vaginatispora* are found in tropical regions and commonly occur in freshwater and marine environments, but only one species *V. nypae* Jayasiri, E.B.G. Jones & K.D. Hyde (Jayasiri et al. 2019) has recently been recorded from a *Nypa fruticans*. Almost all *Vaginatispora* species have 1-septate ascospores with terminal appendages or sheaths (Hashimoto et al. 2018).

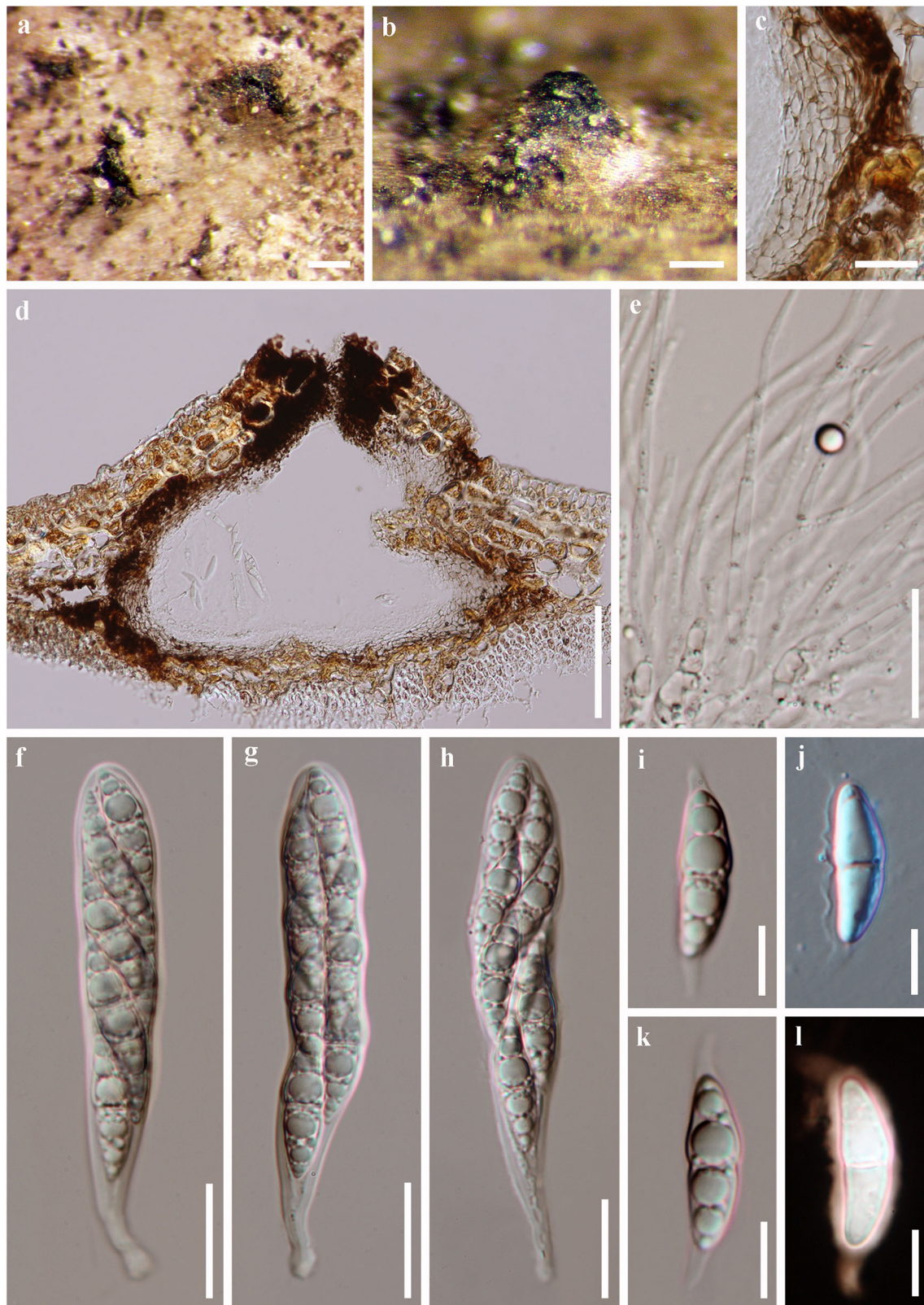


Fig. 26 *Vaginatispora palmae* (MFLU 18-1586, holotype). **a, b** Appearance of stromata on host surface. **c** Structure of peridium. **d** Vertical section through the stromata with ascomata. **e** Pseudoparaphyses. **f–h** Ascus. **i–k** Ascospores. **l** Ascospore in India Ink, with

clear terminal appendages and narrow sheath. Scale bars: **b** = 500 μ m, **a** = 200 μ m, **d** = 100 μ m, **c**, **e**, **f–h** = 20 μ m, **i–l** = 10 μ m

Detailed characters of ascospores are useful for distinguishing taxa at the species level, and molecular sequence data is key for identification of taxa in this group. The multi-gene analysis includes all species in this genus and the new isolate *Vaginatispora palmae* clustered with *V. amygdali* (Fig. 28). *Vaginatispora palmae* differs from *V. amygdali* because the latter species has a lateral pad-like structure within the sheath and an internal chamber at both ends of the ascospores, while *V. palmae* lacks those structures. They also differ in peridium width (15–38 μm vs. 37.5–62.5 μm), ascus (mean: $100.5 \times 16 \mu\text{m}$ vs. $115 \times 18.5 \mu\text{m}$) and ascospores size (mean: $35.3 \times 7.5 \mu\text{m}$ vs. $30.6 \times 8.8 \mu\text{m}$). In addition, polymorphic nucleotide comparison shows that these two strains differ in eight positions in the ITS1 and ITS2 regions including two gaps, and differ in eight positions in the TEF1- α region. The difference in molecular sequence data also distinguish *V. palmae* from *V. amygdali*, therefore, we introduce a new species *V. palmae*.

Vaginatispora armatispora (K.D. Hyde, Vrijmoed, Chin-naraj & E.B.G. Jones) Wanas., E.B.G. Jones & K.D. Hyde

Facesoffungi number: FoF05060; Fig. 27

Saprobic on decaying wood, submerged wood in freshwater and marine habitats. **Sexual morph** *Ascomata* 325–370 μm diam. 300–340 μm high, ($\bar{x} = 350 \times 317 \mu\text{m}$, $n = 10$), scattered, usually immersed or semi-immersed, globose to subglobose, black. *Ostiole* black, crest-like, central, filled with brown cells. *Peridium* 20–32 μm wide, 2–3 layers, composed of dark brown to hyaline, thick-walled cells of *textura porrecta* at side and *textura angularis* at the base. *Hamathecium* comprising 2–3 μm wide, septate, hyaline, pseudoparaphyses composing situated between and above the asci, embedded in a gelatinous matrix. *Asci* 94–118 \times 15–17 μm ($\bar{x} = 106 \times 16 \mu\text{m}$, $n = 20$), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short pedicellate, apically rounded with an ocular chamber, hyaline to subhyaline. *Ascospores* 29–34 \times 7–9 μm ($\bar{x} = 32 \times 8 \mu\text{m}$, $n = 30$), fusiform, hyaline to pale brown, smooth-walled, 1-septate, constricted at the septum, tapering to pointed apices, distinct large guttules in each cells, with distinct hyaline appendages, surrounded by a narrow mucilaginous sheath or not. **Asexual morph** undetermined.

Culture characteristics: *Ascospores* germinating on PDA within 24 h. Colonies on MEA at room temperature reaching 3 cm diam. in three weeks, mycelium pale brown at first, grayish brown after 3 weeks, composed pale brown to brown, septate, smooth hyphae.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on submerged decaying wood, August 2017, V. Kumar,

site1–4–1, (MFLU 18-1229), living culture (MFLUCC 18-0247).

GenBank numbers: ITS: MK085056, LSU: MK085060, RPB2: MK087669, SSU: MK085058, TEF1- α : MK087658.

Notes: The strain MFLUCC 18-0247 that was isolated and described in this study, phylogenetically clustered together with *Vaginatispora armatispora* (HKUCC 1562) (Wanasinghe et al. 2016) with high support (Fig. 28). On the other hand, these two *V. armatispora* strains (MFLUCC 18-0247 and HKUCC 1562) have only one base pair difference in the ITS1 region. These two isolates are quite similar, but isolate MFLUCC 18-0247 has a thicker peridium than that of HKUCC 1562. Based on such insignificant differences in morphology and molecular data, we consider the isolate (MFLUCC 18-0247) and *V. armatispora* are conspecific. *Vaginatispora armatispora* can be distinguished from other members in *Vaginatispora* because it has pale brown ascospores.

Massariaceae Nitschke

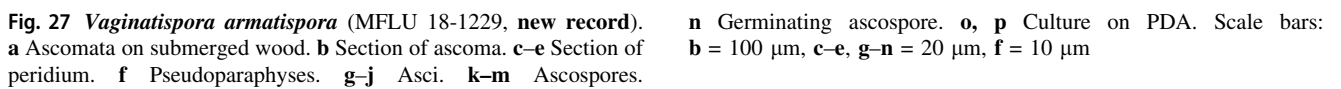
Notes: The family Massariaceae was introduced by Nitschke (1869) to accommodate the genus *Massaria* De Not. with *M. inquinans* (Tode) De Not. as the type species. The family is characterized by immersed, globose, subglobose to pyriform, ascomata, with a thin-walled peridium comprising cells of *textura angularis*, oblong to cylindrical asci with a wide ocular chamber and refractive ring, and large, oblong to ellipsoidal ascospores surrounded by a gelatinous sheath (Voglmayr and Jaklitsch 2011; Hyde et al. 2013, 2016). Based on combined LSU, SSU and TEF1- α sequence data, Hyde et al. (2016) introduced the genus *Neomassaria* Mapook, Camporesi & K.D. Hyde in Massariaceae but Ariyawansa et al. (2018) introduced Neomassariaceae Ariyawansa, Jaklitsch & Voglmayr to accommodate this genus. Based on morphology and LSU phylogeny, Huanraluek et al. (2018) described the genus *Massarioramusculicola* Huanraluek., Thambugala & K.D. Hyde. At present, the family comprises 31 *Massaria* species and a single *Massarioramusculicola* species. In this study, we introduced a new genus *Paramassaria* typified with *Paramassaria samaneae*.

Paramassaria Samarak., & K.D. Hyde, *gen. nov.*

Index Fungorum number: IF555521; *Facesoffungi* number: FoF05213

Etymology: Named because of its morphological similarity to *Massaria*.

Saprobic on branches. **Sexual morph** *Ascomata* immersed or semi-immersed in the yellow stained host, solitary, scattered, coriaceous, globose to subglobose, brown to dark brown. *Ostiole* central, raised, flattened around the dome-shaped ostiole, surrounded by blackish stromatic zone on the host, minutely papillate. *Peridium*



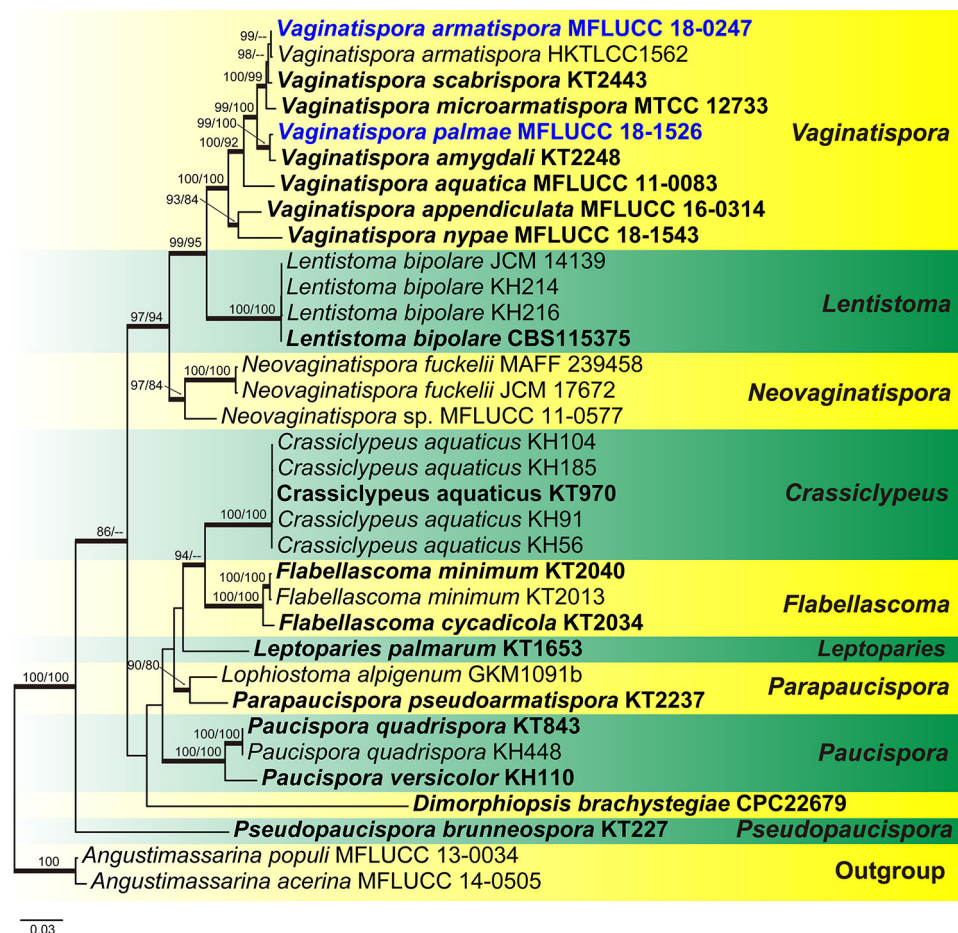
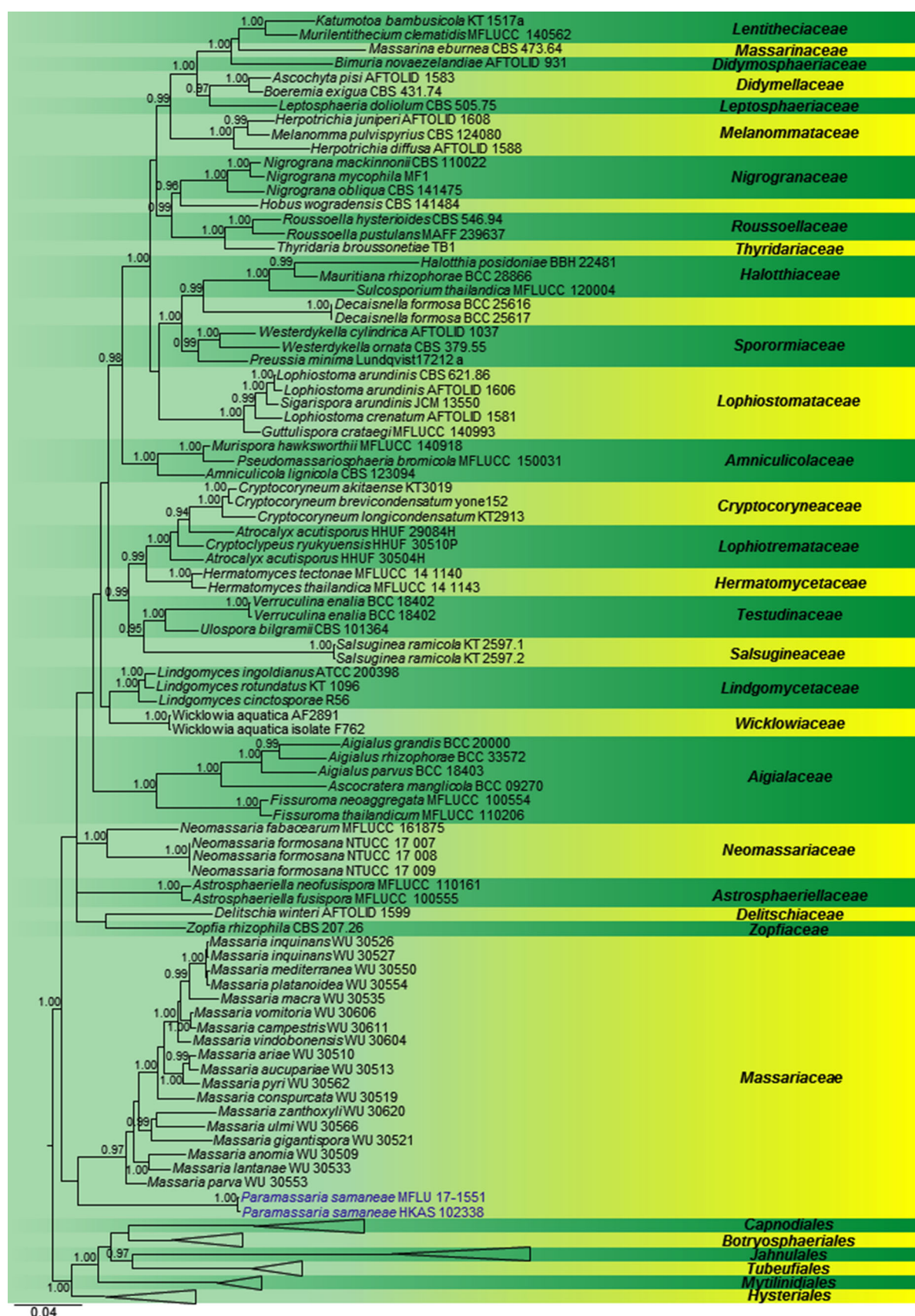


Fig. 28 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, TEF1- α and RPB2 sequence data for *Vaginatispora* species and several closely related genera in Lophiostomataceae. Related sequences are taken from Thambugala et al. (2015), Wanasinghe et al. (2016), Devadatha et al. (2017) and Hashimoto et al. (2018). Thirty-four strains are included in the combined analyses which comprise 4243 characters (605 characters for ITS, 832 characters for LSU, 895 characters for SSU, 894 characters for TEF1- α , 1017 characters for RPB2) after alignment. *Angustimassarina populi* (MFLUCC 13-0034) and *A. acerina* (MFLUCC 14-0505) (Amorosiaceae, Pleosporales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood

value of -17911.101212 is presented. The matrix had 1059 distinct alignment patterns, with 20.20% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248793, C = 0.250421, G = 0.268979, T = 0.231807; substitution rates AC = 1.458334, AG = 3.325243, AT = 1.282598, CG = 1.395939, CT = 8.065988, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.592418$. Maximum parsimony analysis of 3144 constant characters and 854 informative characters resulted in two equally most parsimonious tree with a tree length as 2508 (CI = 0.622, RI = 0.822, RC = 0.511, HI = 0.378). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

wide around the ostiole, outer layer; thick-walled, reddish to dark brown cells of *textura angularis*, inner layer; thin-walled hyaline cells of *textura angularis*. *Hamathecium* comprising wide, hyaline, cylindrical to filiform, septate, branched pseudoparaphyses. *Asci* 8-spored, bitunicate, oblong to cylindrical, absence of prominent ocular chamber, shortly pedicellate. *Ascospores* overlapping 1–2-seriate, ellipsoid to broadly fusiform, initially hyaline, 1-septate becoming brown and 3-septate, constricted at the septum, surrounded by a hyaline gelatinous sheath at maturity. **Asexual morph** Undetermined.

Notes: *Paramassaria samaneae* was collected on a dead branch of *Samanea saman* from Thailand. This taxon is similar to *Massaria* in its ascomata, asci and ascospore characters. The wide ostiole and absence of an ocular chamber in the asci distinguishes our taxon from *Massaria*. However, the combined phylogenetic analyses (Fig. 29) separate our taxon as a basal clade to *Massaria*. The closest BLAST search with the LSU and TEF1- α sequences of MFLU 17-1551 were GQ221892 (with 93% identity) *Rhytidhysterion opuntiae* and FJ161103 (with 93% identity) *Glioniopsis praelonga* belonging to Hysteriaceae. Only ITS,



◀**Fig. 29** Phylogram generated from Bayesian analysis based on combined LSU, SSU and TEF1- α sequence data for Massariaceae and several closely related families in Pleosporales. Related sequences are taken from Voglmayr and Jaklitsch (2011), Hyde et al. (2016) and Ariyawansa et al. (2018). One-hundred and one strains are included in the combined analyses which comprise 2519 characters (806 characters from LSU, 840 characters for SSU, 873 characters for TEF1- α) after alignment. Bayesian posterior probabilities (BYPP) equal to or greater than 0.9 are on branches. The newly generated sequences are indicated in bold and blue

LSU and SSU sequences are available for *Massariomusculicola* and resulted in inconsistent topologies with the absence sequence data. In addition, we observed that our strains have probabilities to cluster in Aigialaceae as a basal clade. However, *Massariomusculicola* differs from *Massaria* and *Paramassaria* by having a peridium with two strata with dark brown to hyaline cells of *textura angularis*, rarely branched, septate and trabeculate pseudoparaphyses and 3-septate hyaline ascospores. Including parallel morphology to *Massaria*, we prefer to place our strains into a new genus in Massariaceae. Voglmayr and Jaklitsch (2011) suggested that the ascospore and pseudothecia characters are important for the identification of phylogenetically distinct *Massaria* species. The strong host-specificity among *Massaria* species makes it complex for accurate identification (Voglmayr and Jaklitsch 2011). It might also not be a surprise if future discoveries of more species within Massariaceae converge the clade and there is a need to aggregate them into one genus, but it is unwise to do this at this stage.

Type species: *Paramassaria samaneae* Samarak., & K.D. Hyde

Paramassaria samaneae Samarak & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555522; *Facesoffungi* number: FoF05214; Fig. 30

Etymology: Name based on the host *Samanea*, from which it was collected.

Holotype: MFLU 17-1551

Saprobic on a dead branch of *Samanea saman*. **Sexual morph** *Ascomata* 520–580 μm high (\bar{x} = 540 μm , n = 15), 410–560 μm diam. (\bar{x} = 490 μm , n = 15), immersed or semi-immersed in the yellow stained host, solitary, scattered, coriaceous, globose to subglobose, brown to dark brown. *Ostiole* central, flattened on the top, surrounded by blackish stromatic zone on the host, ostiolar canal with hyaline paraphyses. *Peridium* 20–43 μm wide (\bar{x} = 33.5 μm , n = 25), inner cell layer hyaline, thin and outer cell layer comprising dark brown *textura angularis* cells. *Hamathecium* comprising 4.2–10 μm wide (\bar{x} = 6.6 μm , n = 25), hyaline, cylindrical to filiform, septate, branched pseudoparaphyses. *Asci* 190–215 \times 45.5–56 μm (\bar{x} = 212.5 \times 50.5 μm , n = 20), 8-spored,

bitunicate, oblong to cylindrical, short pedicellate. *Ascospores* 52.5–71.5 \times 13.5–18.5 μm (\bar{x} = 61.5 \times 16 μm , n = 50), l/w 3.9, overlapping 1–2-seriate, brown, ellipsoid to broadly fusiform, 3-septate, constricted at the septa, with 4 guttules, surrounded by hyaline gelatinous sheath observed clearly when mounted in Indian ink. **Asexual morph** Undetermined.

Material examined: THAILAND, Chiang Rai Province, Muang District, Mae Fah Luang University, on a dead branch of *Samanea saman* (Fabaceae), 2 August 2017, MC. Samarakoon, SAMC002 (MFLU 17-1551, **holotype**; HKAS 102338, **isotype**).

GenBank numbers: LSU: MK108190, MK108191, SSU: MK108187, MK108188, TEF1- α : MK105747, MK105747.

Phaeosphaeriaceae M.E. Barr

Notes: Phaeosphaeriaceae is the largest family in Pleosporales and was introduced by Barr (1979). It is typified with *Phaeosphaeria* with the type species *Phaeosphaeria oryzae* (Phookamsak et al. 2014). Phaeosphaeriaceae comprises 52 genera (Wijayawardene et al. 2018a). Phaeosphaeriaceae is a heterogenous family of saprobes, pathogens and endophytes on plants (Tennakoon et al. 2016a; Phookamsak et al. 2017; Tibpromma et al. 2018). The family is characterized by bitunicate asci with hyaline, yellow or brown spores that are aseptate or septate and holoblastic or enteroblastic conidiogenesis. Seven new species belonging to *Muriphaeosphaeria* (*M. angustifoliae*), *Neosetophoma* (*N. miscanthi*, *N. salicis*), *Phaeopoacea* (*P. asparagicola*), *Phaeosphaeria* (*P. penniseti*) and *Nodulosphaeria* (*N. thalictri*, *N. aquilegiae*) are introduced.

Muriphaeosphaeria Phukhamsakda et al.

Notes: The genus *Muriphaeosphaeria* was introduced by Phukhamsakda et al. (2015) based on the type species *Muriphaeosphaeria galatellae* found on dead and drying stems of *Galatella villosa* (L.) Rchb.f. (Asteraceae) in Russia. The morphological characters of the genus comprise superficial ascomata with a peridium containing thin-walled brown cells of *textura angularis*, cellular pseudoparaphyses and muriform ascospores. The asexual morph is coelomycetous and is characterized by conidiomata with a thick, hyaline, inner wall layer and cylindrical to subclavate, 1–3-transversely septate, brown conidia (Phukhamsakda et al. 2015). *Muriphaeosphaeria* contains three species (Index Fungorum 2019). Cultures and sequences are available.

Muriphaeosphaeria angustifoliae D. Pem, Gafforov & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555432; *Facesoffungi* number: FoF05109; Fig. 31



◀**Fig. 30** *Paramassaria samaneae* (MFLU 17-1551, **holotype**). **a, b** Ascumata on the substrate. **c** Horizontal section of ascumata. **d** Vertical section of ascumata. **e** Ostiole section. **f** Peridium (in water). **g** Pseudoparaphyses. **h–j** Asci. **k–s** Ascospores (s-in Indian ink). Scale bars: **a** = 1000 μm , **b–d** = 200 μm , **e** = 100 μm , **h–j** = 50 μm , **f, g, k–s** = 20 μm

Etymology: Name reflects the host from which the fungus was isolated.

Holotype: TASM 6138

Saprobic on dead branches of *Perovskia angustifolia*.

Sexual morph *Ascumata* 200–600 μm high \times 200–500 μm diam. (\bar{x} = 228.2 \times 226.5 μm , n = 10), scattered or sometimes clustered, or solitary, semi-immersed to superficial, globose to subglobose, brown to dark brown, with papillate central ostiole. *Ostiole* 17–18 μm high \times 28–33 μm wide, slightly raised, centrally located, lacking periphyses. *Peridium* 70–90 μm thick, smooth-walled comprising 2–3 layers of brown to dark brown, pseudoparenchymatous cells of *textura angularis*. *Hamathecium* comprising numerous, dense, 1–1.5 μm wide, filiform, broadly cellular pseudoparaphyses, branched and anastomosing, embedded in gelatinous matrix. *Asci* 125–175 \times 13–15 μm (\bar{x} = 148 \times 14.5 μm , n = 10), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate or sessile, apically rounded with an ocular chamber. *Ascospores* 21–28 \times 9–11 μm (\bar{x} = 25.9 \times 10.1 μm , n = 10), overlapping uniseriate, initially hyaline, becoming yellowish brown at maturity, broadly fusiform, multiseptate, constricted at the middle septa, narrowly rounded at both ends, smooth-walled, swollen, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 48 h. Colonies growing on MEA, reaching 3 cm diam. in 1 week at 16 °C. Mycelium superficial, surface smooth, circular, hairy, margin well defined, shiny, from above white, reverse pale yellow and grey in the middle.

Material examined: UZBEKISTAN, Surxondaryo, Boysun, Omonxona Village, South-Western Hissar Mountains, on dead branches of *Perovskia angustifolia* (Lamiaceae), 6 April 2016, Y. Gafforov, YG-S29-2 (TASM 6138, **holotype**; MFLU 17-0070, **isotype**), ex-type living culture (MFLUCC 18-1124).

GenBank numbers: ITS: MK101002, LSU: MK100999, SSU: MK100997.

Notes: *Muriphaeosphaeria angustifoliae* constitutes a strongly supported independent lineage closely nested with *M. ambrosiae* (MFLU 15-1971). *Muriphaeosphaeria ambrosiae* is only known from its asexual morph and cannot be compared to *M. angustifoliae*.

Muriphaeosphaeria angustifoliae is morphologically more similar to *M. galatellae* (Phukhamsakda et al. 2015) in having superficial ascumata and broadly fusiform multiseptate ascospores lacking a mucilaginous sheath. However, *M. angustifoliae* has larger ascumata (200–600 μm \times 200–500 μm v/s 114–180 \times 167–263 μm), a wider peridium (70–90 μm v/s 12–26 μm), narrower hamathecium (1–1.5 μm v/s 2–3 μm) and longer asci (125–175 \times 13–15 μm v/s 53–86 \times 9–17 μm). We therefore, introduce *M. angustifoliae* as a new species in Phaeosphaeriaceae.

Neosetophoma Gruyter et al.

Notes: *Neosetophoma* was introduced by de Gruyter et al. (2010) and is typified by *N. samararum* (Desm.) Gruyter, Aveskamp. & Verkley. *Neosetophoma* comprises 15 species (Wijayawardene et al. 2017a) and contains important plant pathogens, saprobes and soil fungi (Phookamsak et al. 2014; Karunarathna et al. 2017). The genus is characterized by globose to irregular conidiomata with papillate ostioles and yellowish conidia attenuated at one end (Wijayawardene et al. 2017a). In this study *Neosetophoma miscanthi* and *Neosetophoma salicis* are introduced.

Neosetophoma miscanthi Karun., C.H. Kuo & K.D. Hyde, **sp. nov.**

Index Fungorum number: IF556266; **Facesoffungi number:** FoF05848; Fig. 32

Etymology: Name reflects the host genus, *Miscanthus* from which the fungus was isolated.

Holotype: MFLU 18-2675

Saprobic on dead stems of *Miscanthus gigantius* (Poaceae), as raised, black, shiny globular structures on the host surface. **Sexual morph** *Ascumata* 90–130 μm high, 110–120 μm diam. (\bar{x} = 109.5 \times 115 μm , n = 5), solitary, gregarious, immersed under epidermis, becoming erumpent through host surface, subglobose, or polygonal at sides, uni-loculate, glabrous, ostiolate, with minute papilla; papilla 30–50 μm long (n = 5), carbonaceous, easily broken. *Peridium* 19–20 μm wide, thin-walled, of equal thickness, composed of few layers of dark brown to brown, pseudoparenchymatous cells of *textura angularis*. *Hamathecium* of dense, filamentous, septate, cellular pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 45–50 \times 10–12 μm (\bar{x} = 48 \times 10.5 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate to obclavate, slightly broad at the base with short rounded pedicel, apically rounded. *Ascospores* 18–21 \times 4.7–5.3 μm (\bar{x} = 20 \times 5 μm , n = 40), overlapping 1–2-seriate, hyaline, fusiform, with acute ends, occasionally 3-septate, cell near the septum slightly larger, smooth-walled, guttulate. **Asexual morph** Undetermined.

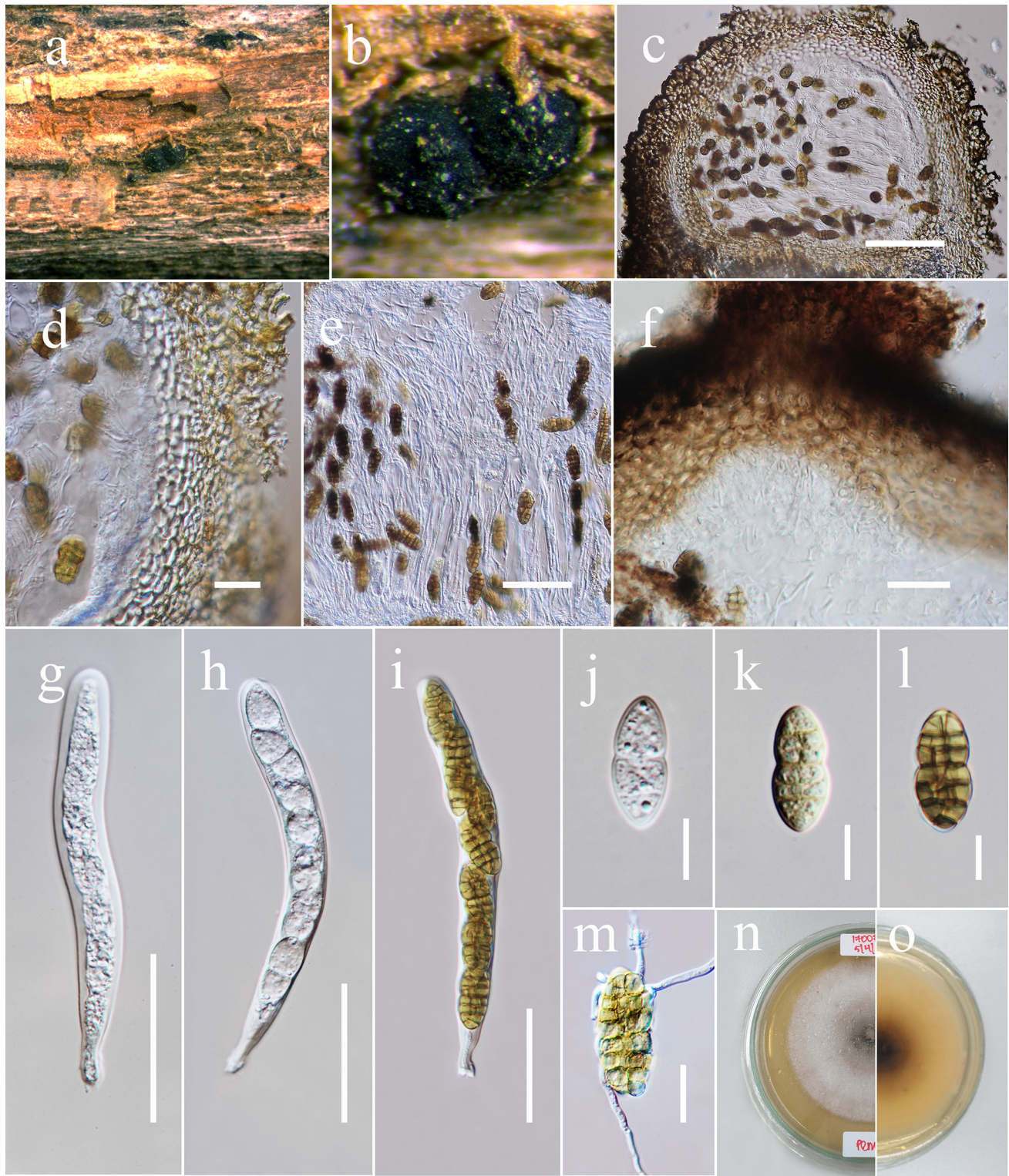


Fig. 31 *Muriphaeosphaeria angustifoliae* (TASM 6138, **holotype**). **a, b** Appearance of ascomata on host surface. **c** Section through an ascoma. **d** Peridium. **e** Hamathecium. **f** Ostiole. **g–i** Asci. **j–l** Ascospores. **m** Ascospore germination on MEA after 48 h. **n, o**

Culture characters on MEA (**n** from above view, **o** from below view). Scale bars: **a** = 2000 μ m, **b** = 500 μ m, **c** = 100 μ m, **g–i** = 50 μ m, **d, f, m** = 20 μ m, **e, j–l** = 10 μ m

Culture characteristics: Ascospores germinating on PDA within 12 h reaching 20 mm diam. after 7 d at 25 $^{\circ}$ C,

circular, floccose, flat with even margin, initially pale yellow becoming greenish grey; reverse yellowish grey.

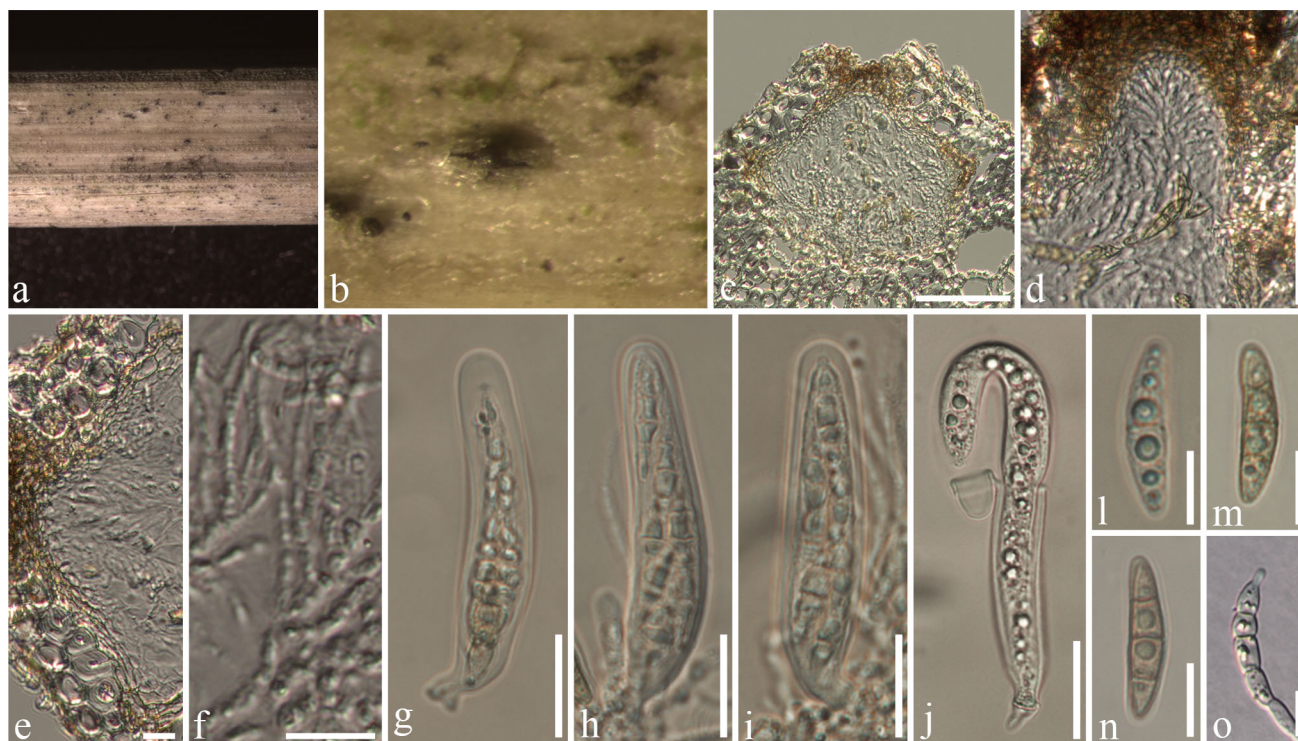


Fig. 32 *Neosetophoma miscanthi* (MFU 18-2675, **holotype**). **a, b** Appearance of ascomata on *Miscanthus giganteus*. **c**. Section through ascoma. **d**. Section through ostiole. **e**. Section through peridium. **f**.

Pseudoparaphyses. **g–j**. Different developing stages of the asci. **l–n**. Ascospores. **o**. Germinating ascospore. Scale bars: **c–e** = 50 µm, **f** = 20 µm, **g–o** = 10 µm

Material examined: TAIWAN, Chia Yi Province, Kwang Hwa, *Miscanthus giganteus* (Poaceae), 18 March 2018, A. Karunarathna AKTW 31 (MFLU 18-2675, **holotype**), ex-type living culture (FU31023).

GenBank numbers: ITS: MK503820, LSU: MK503826, SSU: MK503832.

Notes: *Neosetophoma miscanthi* is morphologically similar to *N. guiyangensis* but is distinct in its asci and ascospore characters. In *N. miscanthi* asci are cylindric-clavate to obclavate, broad at the base whereas the asci of *N. guiyangensis* are cylindrical to cylindric-clavate. Furthermore, *N. miscanthi* generally has smaller ascomata, peridia and asci parameters than *N. guiyangensis* (Hyde et al. 2018a). *Neosetophoma miscanthi* prominently consists with 3-septate ascospores, while *N. guiyangensis* prominently consisting with 1–3(–5)-septate ascospores. *Neosetophoma miscanthi* was found on Poaceae while *N. guiyangensis* was found on tree branches. In phylogenetic analysis the *N. miscanthi* and *N. guiyangensis* separates with high support (90% ML/0.99 BYPP)

Neosetophoma salicis Norphanphoun, Gafforov, T.C. Wen & K.D. Hyde, **sp. nov.**

Index Fungorum number: IF555517; **Facesoffungi number:** FoF06000; Fig. 33

Etymology: The specific epithet reflects the host genus.

Holotype: TASM 6147

Associated with twigs and branches. Sexual morph Undetermined. **Asexual morph** *Conidiomata* 8–10 × 3–4.5 µm, immersed in host tissue, scattered, erumpent, discoid, circular, with locules, ostiolate. *Ostioles* at the same level, with flattened top. *Peridium* brown to pale brown, comprising a few layers of cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, phialidic with prominent periclinal thickening and thick channel, globose to doliiform, 8–10 × 3–4.5 µm, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. *Conidia* (6.9–)8–10 × 2–2.8(–3.1) µm (\bar{x} = 8.7 × 2.8 µm, n = 30), unicellular, allantoid, hyaline, smooth-walled with thick layer.

Material examined: UZBEKISTAN: Surxondaryo Province, Boysun District, Qizilnaur Village, South-Western Hissar Mountains, twigs and branches of *Salix* sp. (Salicaceae), 17 June 2016, Y. Gafforov, YG-S109-2 (TASM 6147, **holotype**; MFLU 17-0118, **isotype**), ex-type living culture (MFLUCC).

GenBank numbers: ITS: MK608025, LSU: MK608026.

Notes: *Neosetophoma salicis* is introduced as a new species based on phylogenetic analysis, as it forms a separate branched as a sister taxon to *N. rosae* Jayasiri et al., which was isolated from twigs and branches of *Rosa canina* L. in Italy (isolate MFLUCC 17-0844, Wanasinghe

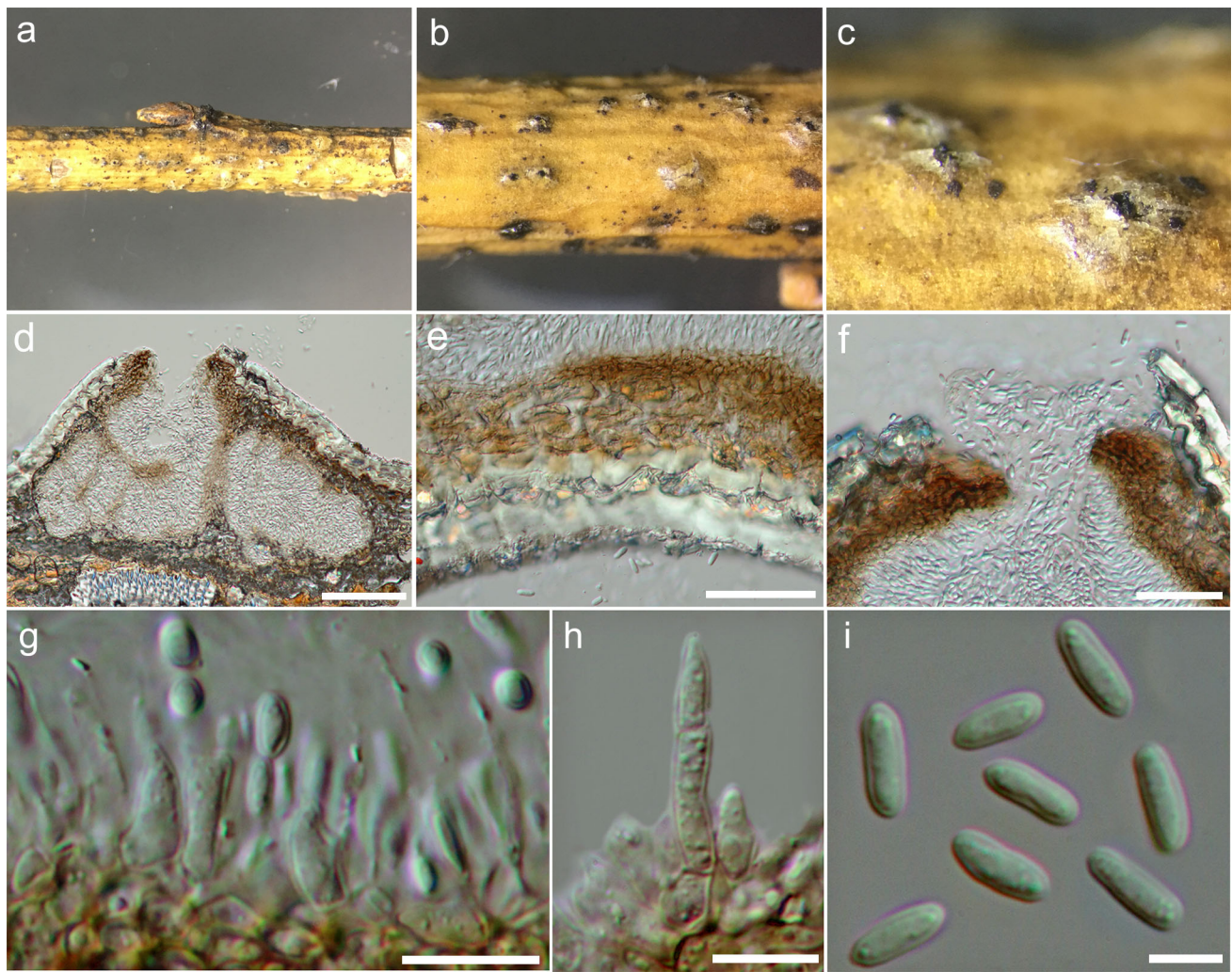


Fig. 33 *Neosetophoma salicis* (TASM 6147, **holotype**). **a** Stromatal habit in wood. **b** Fruiting bodies on host surface. **c** Surface of fruiting bodies showing the black ostioles. **d** Cross section of conidioma.

e Peridium. **f** Ostiolar. **g–h** Conidiogenous cell containing conidia. **i** Conidia. Scale bars: **d** = 100 μ m, **e**, **f** = 50 μ m, **g**, **h** = 10 μ m, **i** = 5 μ m

et al. 2018a) with strong support (Fig. 38). However, they are different in morphological characteristics, the conidia of *N. salicis* are shorter than *N. rosae* (8.7×2.8 versus 11.9×2.5 μ m) and conidia lack septa.

Nodulosphaeria Rabenh., Klotzschii Herb.

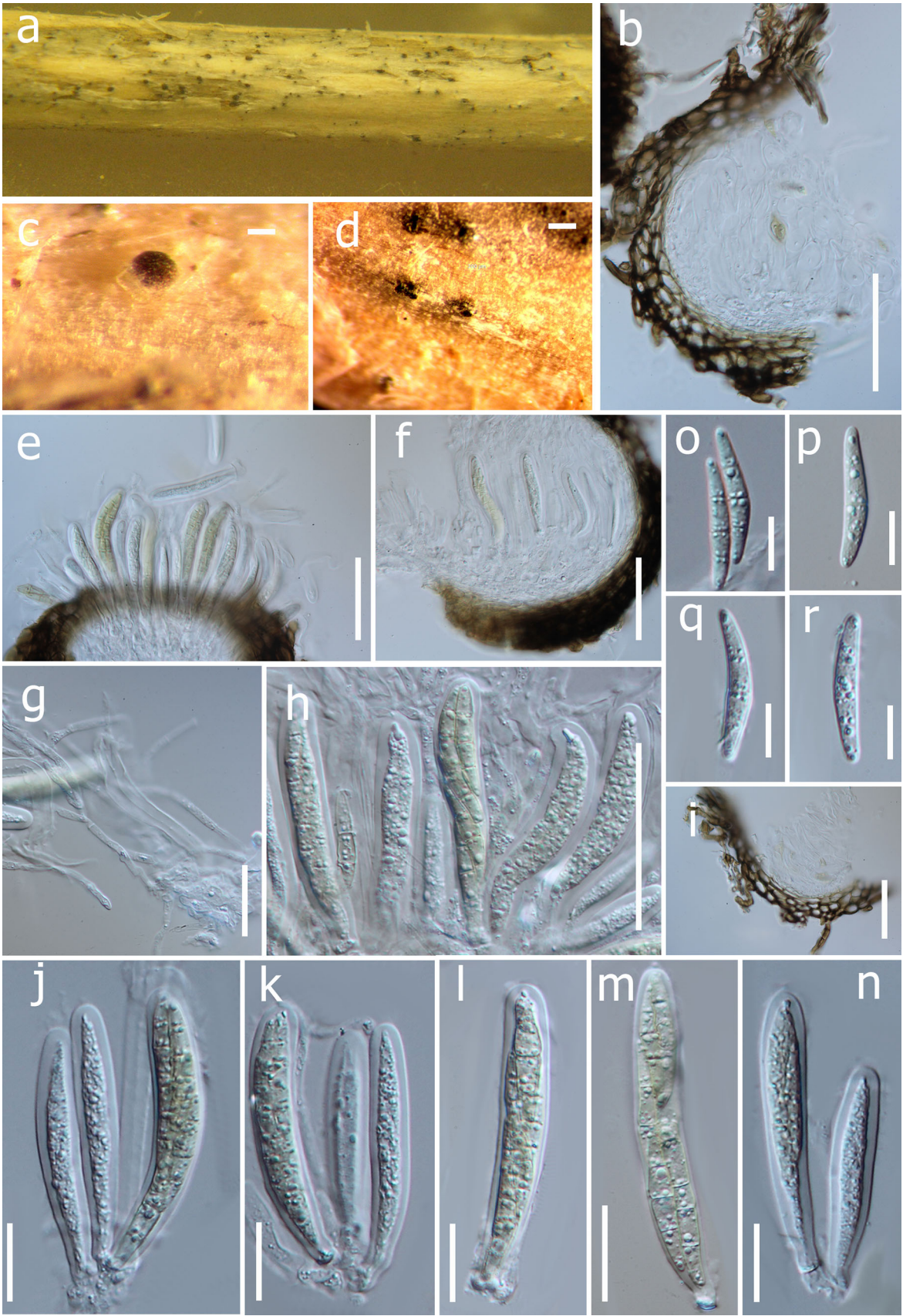
Notes: The genus *Nodulosphaeria* was introduced by Rabenhorst (1858) with *N. hirta* Rabenh. as type species. It is characterized by brown setae at the ascomata apex, and three- to multi-septate ascospores, with a swollen cell and some with terminal appendages (Holm 1961; Shoemaker 1984). The genus was re-examined by Zhang et al. (2012) and Phookamsak et al. (2014) based on type material of *N. hirta*. *Nodulosphaeria* was previously treated as a synonym of *Leptosphaeria*, but later reinstated by Holm (1957). *Nodulosphaeria* was accommodated in Phaeosphaeriaceae by Barr (1979) based on morphology and similarity to *Ophiobolus* as the ascospores form enlarged cell(s).

Shoemaker (1976) re-circumscribed *Nodulosphaeria* and transferred various species to *Ophiobolus*. Later, many species were added to the genus based on morphology (Shoemaker 1984; Shoemaker and Babcock 1987; Zhang et al. 2012). There are 71 epithets listed under *Nodulosphaeria* (Index Fungorum 2019). Mapook et al. (2016) revised the genus and confirmed its phylogenetic placement in Phaeosphaeriaceae.

Nodulosphaeria aquilegiae Chaiwan, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555508; **Facesoffungi number:** FoF05200; **Fig. 34**

Fig. 34 *Nodulosphaeria aquilegiae* (MFLU 17-1273, **holotype**). **a**, **c**, **d** Ascomata on a dead stem of *Aquilegia viscosa*. **b**, **i** Peridium. **e**, **f** Section of ascomata. **g** Pseudoparaphyses. **h–n** Asci. **o–r** Ascospores. Scale bars: **c**, **d** = 200 μ m, **b**, **e**, **f–i** = 50 μ m, **j–n** = 20 μ m, **o–r** = 10 μ m



Etymology: Name reflects the host from which the fungus was isolated.

Holotype: MFLU 17-1273

Saprobic on dead stem of *Aquilegia viscosa*. **Sexual morph** *Ascomata* 150–195 µm high × 95–195 µm diam. (\bar{x} = 167.8 × 142.2 µm, n = 5), superficial, solitary, scattered, uniloculate, globose to subglobose, dark brown to black, conspicuous on the host. *Ostioles* 50–60 × 45–60 µm (\bar{x} = 53.5 × 52.5 µm, n = 5), protruding from the centre of the ascomata, without setae. *Peridium* 40–80 µm wide, comprising several layers of brown to dark brown cells of *textura angularis*, outer layer darkened cells and inner layer pale brown to hyaline cells. *Hamathecium* comprising numerous, filiform, septate, hyaline pseudoparaphyses. *Asci* 70–100 × 7–11 µm (\bar{x} = 83 × 9 µm, n = 20), 8-spored, bitunicate, short pedicellate with club-shaped pedicel, or sessile, apically rounded. *Ascospores* 20–30 × 4.5–5.5 µm (\bar{x} = 25 × 5 µm, n = 20), overlapping 1–2-seriate, initially hyaline, becoming yellowish brown at maturity, fusiform, ellipsoidal to subcylindrical, slightly curved, upper part shorter and wider than the lower part, 4-transversely septate, constricted at the middle septum, ends remaining lighter and cone-shaped, with narrowly rounded ends, wall firm, smooth-walled, sometimes guttulate, with appendages (3–5 µm long, 3–4 µm wide) at both ends. **Asexual morph:** undetermined.

Material examined: ITALY, Province of Forlì-Cesena [FC], Passo la Calla - Santa Sofia, on a dead aerial stem of *Aquilegia viscosa* Gouan (Ranunculaceae), 14 July 2017, Erio Camporesi, IT3398 (MFLU 17-1273, **holotype**).

GenBank numbers: ITS: MK579853, LSU: MK579854, SSU: MK579855, TEF1- α : MK579856.

Notes: *Nodulosphaeria aquilegiae* was found on dead, aerial stems of *Aquilegia viscosa* in Italy. Ascomatal characteristics resemble *N. multiseptata* and *N. sambuci* in having superficial, solitary, uniloculate, globose to subglobose ascomata (Tibpromma et al. 2017). This is the first record of a *Nodulosphaeria* species on *Aquilegia viscosa*.

Nodulosphaeria thalictri D. Pem, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555433; **Facesoffungi number:** FoF05110; Fig. 35

Etymology: Name reflects the host from which the fungus was isolated.

Holotype: MFLU 17-1241

Saprobic on dead stems of *Thalictrum* sp. **Sexual morph** *Ascomata* 217–305 µm diam. × 185–304 µm high (\bar{x} = 263.7 × 217.9 µm, n = 10), immersed or semi-immersed, solitary or scattered, subglobose to obpyriform, dark brown to black, papillate. *Ostiole* 70–75 µm diam. (\bar{x} = 71.2 µm, n = 10), papillate, protruding from substratum with numerous internal brown to dark brown cells of

textura globulosa. *Peridium* 12–16 µm wide, comprising 4–5 layers of dark brown cells of *textura angularis*, flattened at the inside. *Hamathecium* comprising 1.5–2.5 µm wide, filiform, septate, branching pseudoparaphyses. *Asci* 77–100 × 7–12 µm (\bar{x} = 84.1 × 10.1 µm, n = 10), 8-spored, bitunicate, cylindric-clavate, slightly curved, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 29–35 × 4–5 µm (\bar{x} = 32.3 × 4.5 µm, n = 20), overlapping 3–4 seriate, hyaline when immature, becoming pale yellowish to greenish at maturity, long fusiform, 7–8 septate, straight or slightly curved, thick and smooth-walled, with terminal appendages. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h. at 16 °C and germ tubes produced from middle septa. Colonies growing on MEA, reaching 1 cm diam. in 1 week. Mycelium superficial, medium sparse, irregular, flat, smooth, effuse, slightly irregular margin, from above whitish, reverse yellowish to pale brown.

Material examined: ITALY, Province of Forlì-Cesena [FC], Lago Pontini – Bagno di Romagna, on dead aerial stems of *Thalictrum* sp. (Ranunculaceae), 5 July 2017, E. Camporesi (MFLU 17-1241, **holotype**; HKAS 97500, **isotype**), ex-type living culture (MFLUCC 18-1138).

GenBank numbers: ITS: MK 101000, LSU: MK 100998, SSU: MK 101001, TEF1- α : MK128971.

Notes: *Nodulosphaeria thalictri* is similar to *N. hirta* (type species of *Nodulosphaeria*) in having cylindric-clavate, slightly curved, short pedicellate asci and a peridium with dark brown cells of *textura angularis*, however *N. thalictri* has narrower pseudoparaphyses (1.5–2.5 µm v/s 2.5–3.5 µm), shorter and wider ascospores (\bar{x} = 32.3 × 4.5 µm v/s \bar{x} = 55 × 5 µm) and the presence of terminal appendages (Phookamsak et al. 2014). Our phylogenetic analyses place *N. thalictri* close to *N. aconiti* (MFLUCC 13–0728). *Nodulosphaeria thalictri* is similar to *N. aconiti* in having a peridium composed of cells of *textura angularis* and branching pseudoparaphyses (Mapook et al. 2016). However, *N. thalictri* has longer asci (84 × 10 µm v/s 69 × 9 µm), more septa in the ascospores septation (7–8 v/s 4–septate), has long fusiform ascospores rather than cylindric-fusiform and possesses terminal appendages, which are lacking in *N. aconiti*. *Nodulosphaeria thalictri* is unique in having an ostiole with numerous internal brown to dark brown cells of *textura globulosa*, protruding externally, a feature not recorded in other *Nodulosphaeria* species.

Phaeopoacea Thambug., Dissan. & K.D. Hyde

Notes: *Phaeopoacea* was introduced by Thambugala et al. (2017b) to accommodate the *Phaeopoacea* species occurring as a saprobe on Poaceae (Hyde et al. 2017b; Thambugala et al. 2017b). Currently, the genus comprises

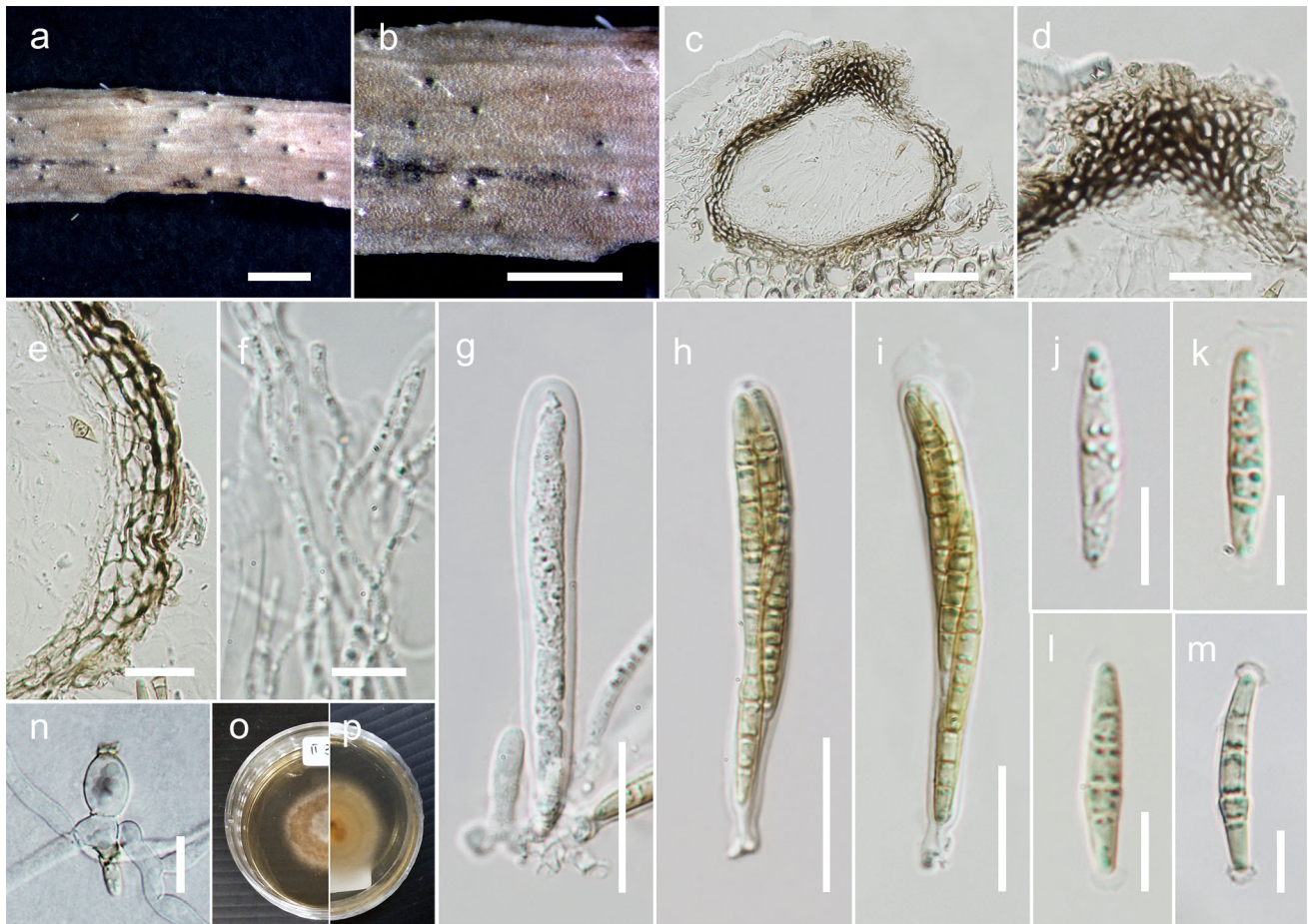


Fig. 35 *Nodulosphaeria thalictri* (MFLU 17-1241, **holotype**). **a, b** Appearance of ascomata on host surface. **c** Section through an ascoma. **d** Ostiole. **e** Peridium. **f** Hamathecium. **g–i** Asci. **j–m** Ascospores, arrow showing terminal appendages. **n** Germinated

ascospore on MEA after 24 h. **o, p** Culture characters (**o** from above view, **p** from below view). Scale bars: **a, b** = 500 μ m, **c** = 50 μ m, **d** = 30 μ m, **g–i** = 25 μ m, **e, n** = 20 μ m, **f, j–m** = 10 μ m

three species: *P. festucae* (type species), *P. phragmiticola* and *P. muriformis*. Sexual morphs of *Phaeopecta* are characterized by subepidermal ascomata with a central papillate ostiole, bitunicate asci and ascospores tapering towards the ends (Shoemaker and Babcock 1989; Hyde et al. 2017b). The asexual morphs from this genus have pycnidial conidiomata with brown conidia (Thambugala et al. 2017b). In this study, we introduce a novel species, *Phaeopecta asparagicola* from Asparagaceae (Fig. 39).

Phaeopecta asparagicola Phukhams., Akulov & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555501; *Facesoffungi* number: FoF04826; Fig. 36

Etymology: Name refers to the host plant, *Asparagus* sp.

Holotype: MFLU 18-1380

Saprobic on dead stems of *Asparagus* sp. **Sexual morph**

Ascomata 200–365 \times 110–314 μ m (\bar{x} = 283 \times 220 μ m, n = 10), semi-immersed to immersed under epidermal tissue, solitary or sometimes gregarious, confluent, scattered,

globose to compressed globose, coriaceous, dark brown to black, rough-walled, with short hyphae projecting from peridium, ostiolate. *Ostiole* centrally located, papillate, without periphysoids. *Peridium* 11–29 μ m wide, composed of 4–7 layers of reddish brown to dark brown cells of *textura angularis*, inner layer composed of hyaline gelatinous cells. *Hamathecium* composed of numerous, dense, long, 2–7 μ m wide (\bar{x} = 5 μ m, n = 50), filiform, transversely septate, branched, anastomosing, cellular pseudoparaphyses.

Asci 67–129 \times 12–16 μ m (\bar{x} = 98 \times 14 μ m, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate to broad cylindrical, with furcate pedicel, with ocular chamber visible when immature. **Ascospores** 22–33 \times 6–10 μ m (\bar{x} = 27 \times 8 μ m, n = 50), bi-seriate or overlapping, initially hyaline, becoming yellowish to brown at maturity, broad fusiform, narrow towards the apex, 3–7-transversely euseptate, constricted at the septa, with cell above central septum wider, smooth-walled, indentations present, surrounded by a 7–9 μ m wide, mucilaginous sheath. **Asexual morph** Undetermined.



◀**Fig. 36** *Phaeopoacea asparagicola* (MFLU 18-1380, **holotype**). **a** Appearance of ascomata on host surface. **b** Close up of ascomata. **c, d** Vertical sections of ascomata. **e** Section of partial peridium layer. **f** Cellular pseudoparaphyses. **g–i** Development state of asci. **j–o** Development state of ascospores. **p** Ascospores stained with india ink, sheath surrounding the entire ascospore. Scale bar: **b** = 500 μ m, **c, d** = 100 μ m, **e–i** = 50 μ m, **j–p** = 10 μ m

Culture characteristics: Colonies on MEA, reaching 50 mm diam. after 4 weeks at 18 °C. Culture olive-green radiating yellowish toward the edge, with dense mycelia, circular, flat, dull, fimbriate, radially furrowed, and slightly covered with white aerial mycelium; reverse black with radiating cream mycelium.

Material examined: UKRAINE, Odessa region, Lyman district, Regional landscape park Tiligulskyt, on the overwintered stems of *Asparagus* sp. (Asparagaceae), 1 May 2014, A. Akulov, EX CWU (MYC) AS 5825 (MFLU 18-1380, **holotype**), ex-type living culture (MFLUCC 16-0379).

GenBank numbers: ITS: MK443383, LSU: MK443379, RPB2: MK443387, SSU: MK443381, TEF1- α : MK443385.

Notes: *Phaeopoacea asparagicola* is introduced as a new species based on morphological and phylogenetic evidence. The species formed a moderately-supported clade with *P. festucae* and *P. phragmiticola* (MLBS = 66; BYPP = 0.99). The morphology of *P. asparagicola* is similar to *P. phragmiticola* in having sub-epidermal, globose, papillate ascomata, cylindrical with short stalk asci, and conical at the apex with pale brown ascospores (Shoemaker and Babcock 1989; Hyde et al. 2017b). Besides these characters, *P. asparagicola* can be distinguished from *P. phragmiticola* and *P. muriformis* by having larger ascomata and asci and ascospores only have longitudinal septa.

Phaeosphaeria I. Miyake

Notes: *Phaeosphaeria* was introduced by Miyake (1909) with *P. oryzae* I. Miyake as the type species (Phookamsak et al. 2014). Previously, *Phaeosphaeria* was considered as a synonym of *Leptosphaeria*. However, based on both morphology and molecular analyses, it was considered that *Phaeosphaeria* differs from *Leptosphaeria* in having pseudoparenchymatous peridium, stagonospora-like asexual morphs and mostly monocotyledonous hosts while *Leptosphaeria* has scleroplectenchymatous peridium, phoma-like asexual morphs and mostly dicotyledonous hosts (Schoch et al. 2009; Zhang et al. 2012). *Phaeosphaeria* species are probably cosmopolitan in distribution, since they have been recorded from both temperate and tropical countries (i.e. Canada, China, Germany, Japan, Thailand, and Switzerland) (Shoemaker and Babcock 1989; Phookamsak et al. 2014, 2019). There are 211 epithets for *Phaeosphaeria* in

Index Fungorum (2019). We follow the latest treatment and updated account of *Phaeosphaeria* in Phookamsak et al. (2019). *Phaeosphaeria penniseti* is introduced as a novel species based on morphological and phylogenetic evidence (Figs. 37, 38).

Phaeosphaeria penniseti Karun., C.H. Kuo & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF556267; **Facesoffungi number:** FoF05849; Fig. 37

Etymology: Name reflects the host genus, *Pennisetum*.

Holotype: MFLU 18-2674

Saprobic on dead stems of *Pennisetum purpureum* (Poaceae). **Sexual morph** Ascomata 133–184 μ m high 150–243 μ m diam. (\bar{x} = 158.5 \times 196.5 μ m, n = 5), black, immersed under host epidermis, visible as raised, to semi-immersed, solitary, subglobose to ampulliform, uni-loculate, ostiolate, with minute papilla. **Peridium** 18–20 μ m wide at the sides, comprising 3–5 layers, of brown to dark brown pseudoparenchymatous cells, of *textura angularis*, hyaline to pale brown, flattened towards the inner layers. **Hamathecium** comprising numerous, filamentous, branched, septate pseudoparaphyses. **Asci** 55–70 \times 10–15 μ m (\bar{x} = 62.5 \times 12.5 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, rounded at the apex and with a shallow ocular chamber. **Ascospores** 26–29 \times 4–5 μ m (\bar{x} = 28 \times 5 μ m, n = 40), overlapping, 2-seriate, hyaline, becoming brown at maturity, narrowly fusiform, 5-septate, slightly wider at the second cell from above, guttulate at the beginning, rounded at the ends. **Asexual morph:** Undetermined.

Material examined: TAIWAN, Chia Yi Province, Kwang Hwa, *Pennisetum purpureum* (Poaceae), 18 March 2018, A. Karunarathna AKTW 24 (MFLU 18-2674, **holotype**), ex-type living culture (FU31020).

GenBank numbers: ITS: MK503819, LSU: MK503825, SSU: MK503831.

Notes: In the NCBI BLAST search, *Phaeosphaeria penniseti* shows higher percentage identity to *P. oryzae* (99.80%). Phylogenetically, *Phaeosphaeria penniseti* forms a sister lineage with *P. oryzae*, the type species of the *Phaeosphaeria* with moderate support in maximum likelihood analysis (89% ML, Fig. 38). It differs from *P. oryzae* in having 5-septate ascospores, whereas, *P. oryzae* has 3-septate ascospores (Phookamsak et al. 2014).

Pseudoberkleasmiaceae Phukhams & K.D. Hyde, *fam. nov.*

Index Fungorum number: IF555489, **Facesoffungi number:** FoF05311

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Hyphomycetous*, dictyosporous. **Colonies** on natural substratum sporodochia, superficial,

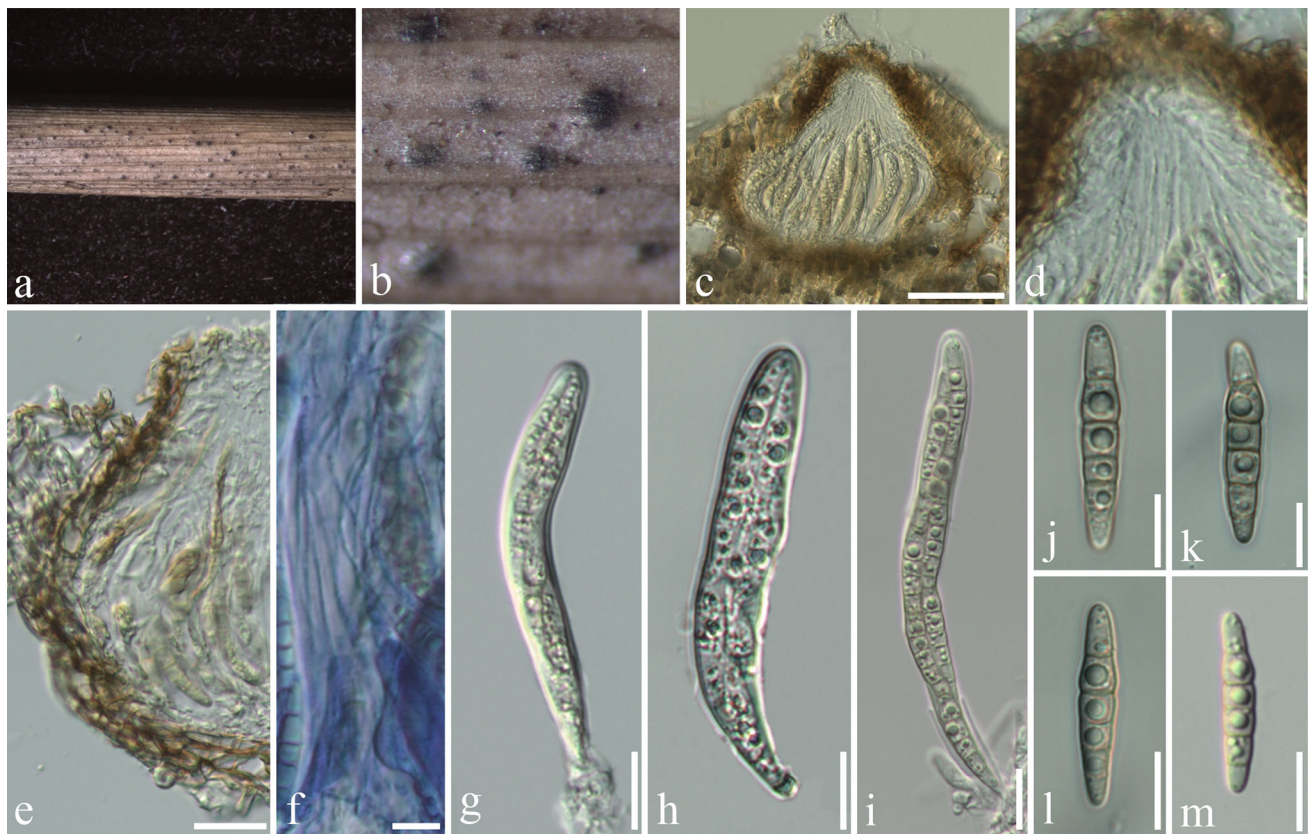


Fig. 37 *Phaeosphaeria penniseti* (MFLU 18-2674, **holotype**). **a, b** Appearance of ascomata on the host (*Pennisetum purpureum*, Poaceae). **c** Section through ascoma. **d** Section through ostiole.

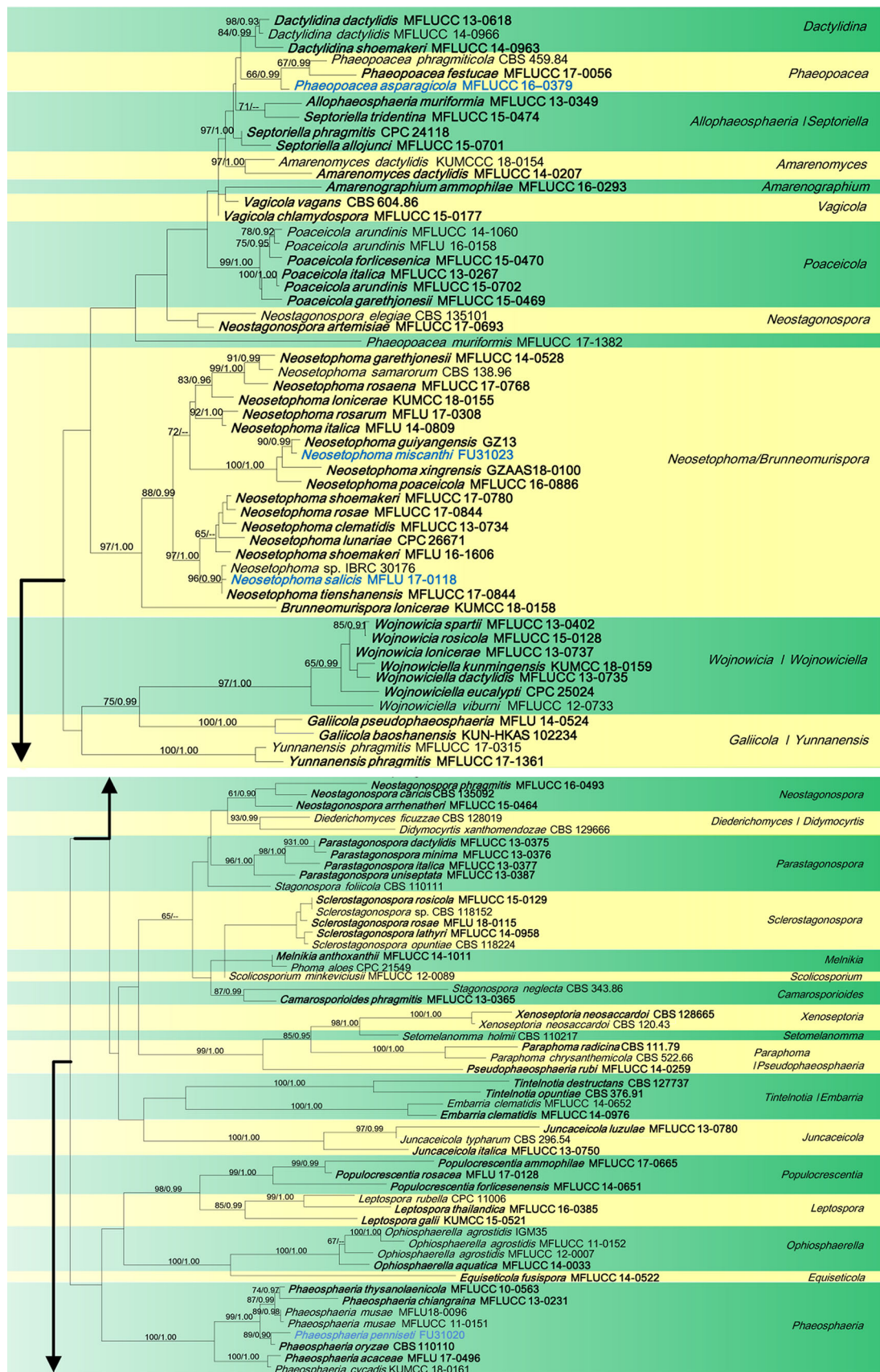
e Section through peridium. **f** Pseudoparaphyses (stained in cotton blue). **g–i** Different developing stages of the asci. **j–m** Ascospores. Scale bars: **c, d** = 50 µm, **e** = 25 µm, **f–m** = 10 µm

compact, scattered, irregular, dark-brown to black, glistening. *Mycelium* immersed in the substrate, septate, branched. *Conidiophores* micronematous, mononematous, reduced, hyaline. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate. *Conidia* acrogenous, solitary, broadly ellipsoidal to obovoid, muriform, guttulate, smooth-walled, brown, olivaceous green, with or without guttules, usually with conidiogenous cell attached.

Type genus: *Pseudoberkleasium pandanicola* Tibpromma & K.D. Hyde, Fungal Diversity: 52 (2018)

Notes: Pseudoberkleasmiaceae is introduced to accommodate a *berkleasium*-like hyphomycete that is phylogenetically placed in the order Pleosporales. The family comprises *Pseudoberkleasium chiangmaiense* and *P. pandanicola*, the latter as the generic type. *Berkleasium* is polyphyletic, with species having similar characteristics, but which are phylogenetically distinct (Pinnoi et al. 2007; Hu et al. 2010; Lu et al. 2018b). A study by Tanney and Miller (2017) was able to obtain several fresh collections of *Berkleasium* and compared those with the reference specimens of *Berkleasium concinnum*. Re-examination of the type species placed the generic type of *Berkleasium* in Tubeufiales. In this study, Pseudoberkleasmiaceae is

Fig. 38 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and TEF1- α sequence data for genera in Phaeosphaeriaceae. Related sequences are taken from Wanasinghe et al. (2018a) and Phookamsak et al. (2019). One-hundred and sixty-one strains are included in the combined analyses which comprise 3307 characters (419 characters for ITS, 824 characters for LSU, 990 characters for SSU, 1074 characters for TEF1- α) after alignment. *Staurosphaeria rhamnocola* (MFLUCC 17-0813, MFLUCC 17-0814) (Montagnulaceae, Pleosporales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -29921.960589 is presented. The matrix had 1190 distinct alignment patterns, with 23.56% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243950, C = 0.233656, G = 0.265190, T = 0.25720; substitution rates AC = 1.334366, AG = 3.046037, AT = 2.327147, CG = 0.800430, CT = 6.652827, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.527656$. Maximum parsimony analysis resulted 3276 constant characters and 629 informative characters. Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 65% are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.90 are in bold. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue



related to the family Hermatomyetaceae with relatively strong statistical support.

Pseudoberkleasmium Tibpromma & K.D. Hyde

Notes: The monotypic genus *Pseudoberkleasmium* was introduced by Tibpromma et al. (2018) with *P. pandanicola* Tibpromma & K.D. Hyde as the type species. *Pseudoberkleasmium* is characterized by hyaline subglobose conidiogenous cells and acrogenous, broadly ellipsoidal to obovoid, muriform, brown or olivaceous green, and guttulate conidia. In this paper, we introduce a new *Pseudoberkleasmium* species, *P. chiangmaiense*, based on phylogenetic and morphological evidence.

Pseudoberkleasmium chiangmaiense Y.Z. Lu & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555595; **Facesoffungi number:** FoF05310; **Fig. 39**

Etymology: *chiangmaiense*, referring to collecting site.

Holotype: MFLU 17-1118

Saprobic on decaying wood. **Sexual morph** Undetermined **Asexual morph** Hyphomycetous, dictyosporous. **Colonies** on natural substratum sporodochia, superficial, compact, scattered, irregular, black, glistening. **Mycelium** immersed in the substrate, composed of septate, branched, smooth, thin-walled, hyaline to pale brown, 2 µm wide hyphae. **Conidiophores** micronematous, mononematous, reduced, hyaline, smooth-walled. **Conidiogenous cells** 12–18 × 12–18 µm (\bar{x} = 15 × 14 µm, n = 20), holoblastic, monoblastic, integrated, terminal, determinate, subglobose, with guttulate, hyaline. **Conidia** 30–35 × 15–20 µm

(\bar{x} = 33 × 18 µm, n = 20), acrogenous, solitary, broadly ellipsoidal to obovoid, flattened, muriform, guttulate, smooth-walled, brown, usually with conidiogenous cell attached.

Culture characteristics: *Conidia* germinating on water agar and germ tubes produced from conidia within 12 h. **Colonies** growing on PDA, circular, with flat surface, edge entire, reaching 28 mm in 3 weeks at 28 °C, white to pale brown in PDA medium. **Mycelium** superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on decaying wood, 25 January 2017, Yong-Zhong Lu, MRC 23 (MFLU 17-1118, **holotype**), ex-type living culture (MFLUCC 17-1809).

GenBank numbers: ITS: MK131259, LSU: MK131260, TEF1- α : MK131261.

Notes: *Pseudoberkleasmium chiangmaiense* is similar to *P. pandanicola* in having hyaline subglobose conidiogenous cells and acrogenous, broadly ellipsoidal to obovoid, muriform, brown and guttulate conidia, but differs by its larger conidiogenous cells (12–18 × 12–18 µm vs 5–11 × 9–12 µm). Phylogenetically, *Pseudoberkleasmium chiangmaiense* shares a sister relationship to *P. pandanicola* with good bootstrap support (100% ML/1.00 BYPP) (Fig. 40); the phylogeny also indicates that they are distinct species.

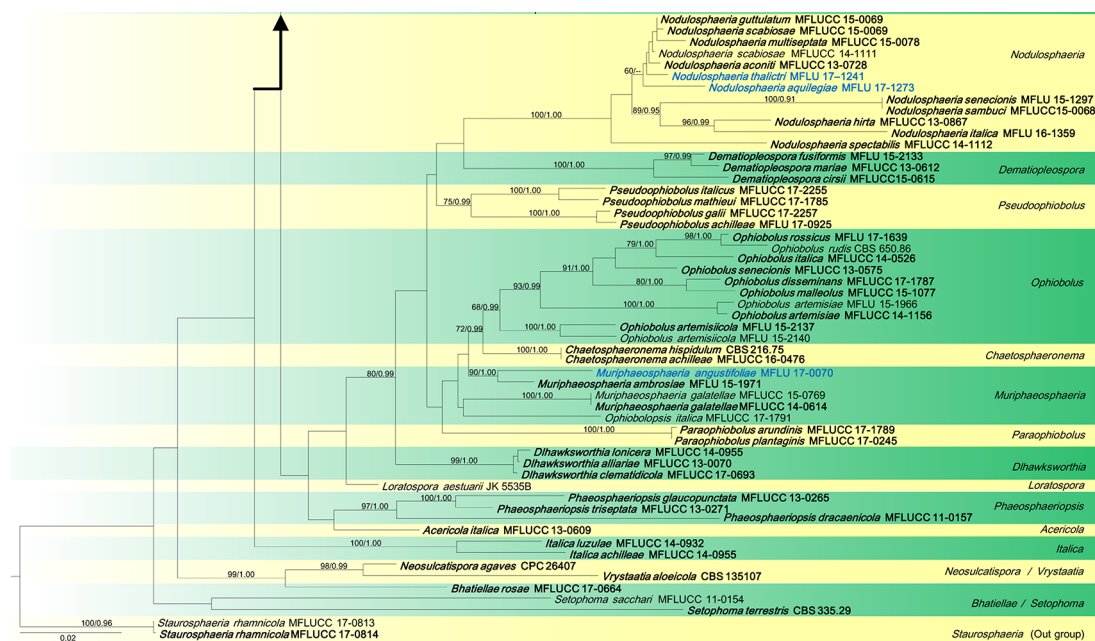


Fig. 38 continued

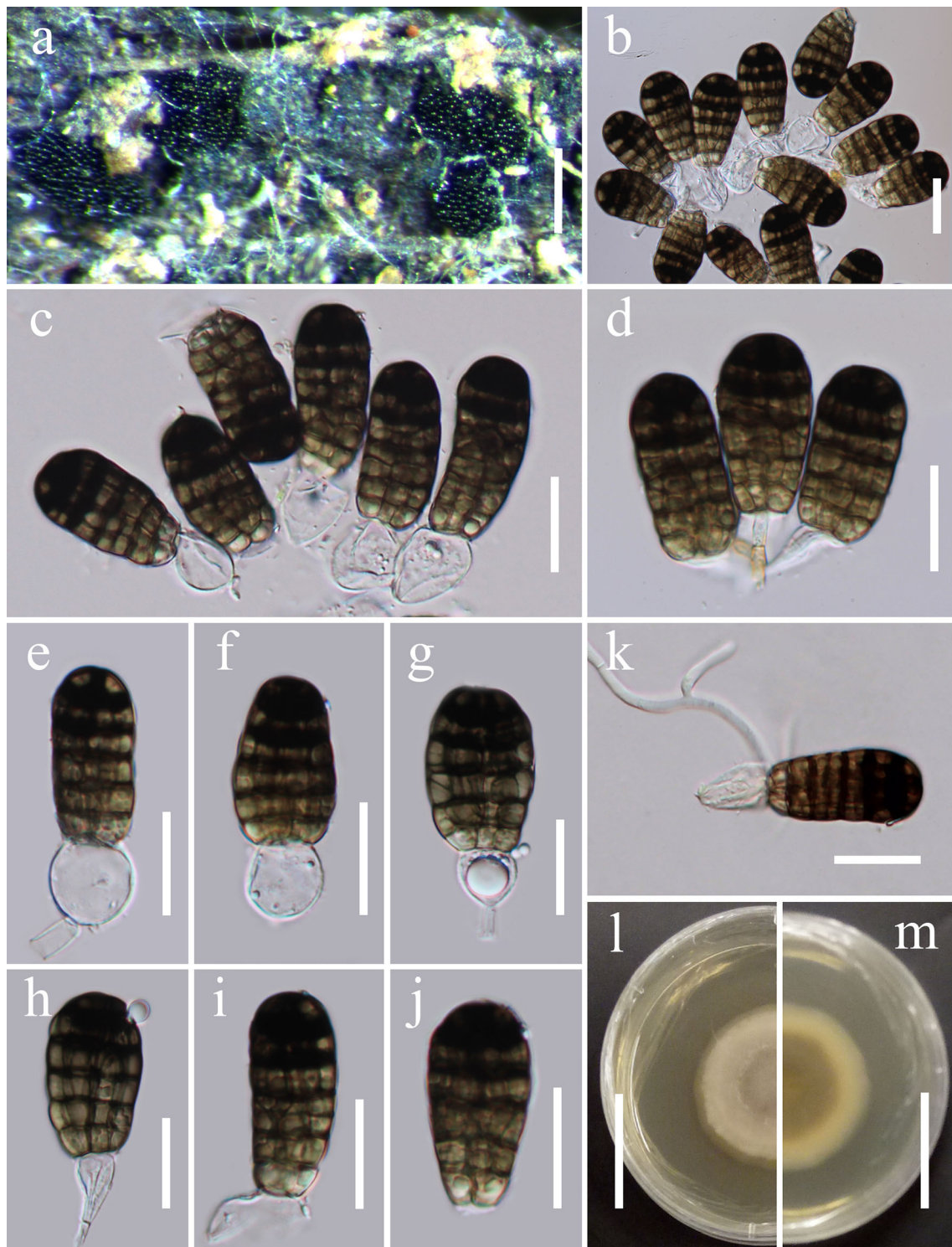
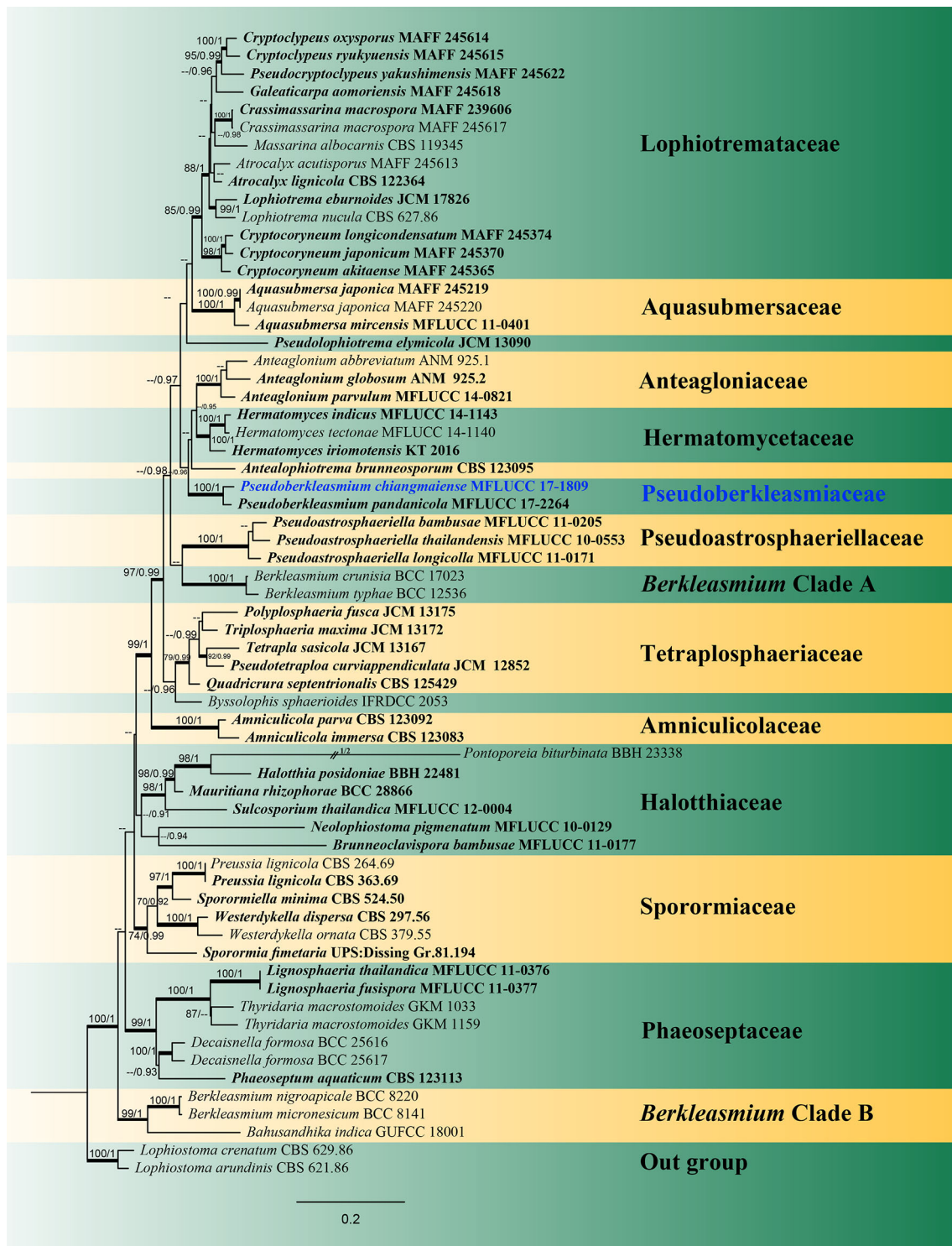


Fig. 39 *Pseudoberkleasmium chiangmaiense* (MFLU 17-1118, **holotype**). **a** Colonies on substrate. **b–j** Conidia. **k** Germinating conidium. **l, m** Colony on PDA (**l** from above view, **m** from below view). Scale bars: **a** = 200 μ m, **b–k** = 20 μ m, **l, m** = 20 mm

Pyrenochaetopsidaceae Valenzuela-Lopez, Crous, Cano, Guarro & Stchigel

Notes: ‘Cucurbitariaceae’ was revealed to represent five distinct families, i.e. the newly erected

Neopyrenochaetaceae, Parapyrenochaetaceae, Pseudopyrenochaetaceae and Pyrenochaetopsidaceae, and Cucurbitariaceae sensu stricto with a narrowed concept (Valenzuela-Lopez et al. 2018). *Pyrenochaetopsis* is the



◀**Fig. 40** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, TEF1- α , and RPB2 sequence data representing Pseudoberkleasmiaceae and the closely related families in Pleosporales order. Related sequences are taken from Tibpromma et al. (2018). Sixty-four strains are included in the combined analyses which comprise 4340 characters (842 characters for LSU, 1030 characters for SSU, 512 characters for ITS, 926 characters for TEF1- α , 1030 characters for RPB2) after alignment. *Lophiostoma crenatum* (CBS 629.86) and *L. arundinis* (CBS 621.86) in Lophiostomataceae (Pleosporales) are used as the outgroup taxa. Single gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood values of -38637.764110 is presented. The matrix had 1968 distinct alignment patterns, with 33.91% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245895, C = 0.251442, G = 0.271420, T = 0.231244; substitution rates AC = 1.592217, AG = 3.496391, AT = 1.418709, CG = 1.209916, CT = 8.405355, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.569582$. Bootstrap values for maximum likelihood (ML) equal to or greater than 70% and clade credibility values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian-inference analysis labelled on the nodes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

type genus of Pyrenochaetopsidaceae. The general characters of the family Pyrenochaetopsidaceae included glabrous or setose pycnidia with apapillate or papillate ostiolate necks, phialidic conidiogenous cells and aseptate, cylindrical to allantoid conidia. Members of Pyrenochaetopsidaceae are saprobes from various niches, such as water, plants, soil and air samples (de Gruyter et al. 2010, 2013; Valenzuela-Lopez et al. 2018). Some species e.g. *Pyrenochaetopsis poae*, have been repeatedly isolated as endophytes of graminaceous plants (Crous et al. 2014). Other species such as *P. globosa*, *P. paucisetosa* and *Neopyrenochaetopsis hominis*, have been isolated from sinusitis, toe nail and skin tissue of humans as weak pathogens (Valenzuela-Lopez et al. 2018).

Pyrenochaetopsis Gruyter, Aveskamp & Verkley

Notes: *Pyrenochaetopsis* was erected by de Gruyter et al. (2010) with *P. leptospora* (Sacc. & Briard) Gruyter, Aveskamp & Verkley as the type species (de Gruyter et al. 2010). The genus is characterized by setose pycnidia with apapillate or papillate ostioles, and simple, aseptate, cylindrical to allantoid conidia.

Pyrenochaetopsis sinensis G.S. Li, J.M. Liang & L. Cai, *sp. nov.*

Index Fungorum number: IF556011; **Facesoffungi number:** FoF05965; **Fig. 41**

Etymology: Named after the country where the type was collected.

Holotype: HMAS 248045

Saprobic on rhizosphere soil of turfgrasses. **Sexual morph** Undetermined. **Asexual morph** *Hyphae* pale white, smooth- and thin-walled, septate, 2–5 μm wide. *Conidiomata* pycnidial, pale brown, solitary or confluent, immersed (OA), subglobose or globose, 100–180 \times 100–155 μm , with apapillate ostiolar neck. *Pycnosclerotia* forming after 25 days culturing on OA, brown to dark brown, globose or subglobose, 55–60 μm in diam. *Setae* absent. *Pycnidial* wall of *textura angularis*, 3–5 layered, 15–25 μm thick, composed of brown, flattened polygonal cells of 3–6 μm diam. *Conidiogenous cells* phialidic, hyaline, smooth-walled, subglobose, 3–6 \times 2–5 ($\bar{x} = 4 \times 3$, $n = 30$) μm . *Conidia* aseptate, hyaline, smooth- and thin-walled, cylindrical to allantoid, 3–4.5 \times 1–2 ($\bar{x} = 4 \times 2$, $n = 40$) μm , usually with two guttules.

Culture characteristics: *Colonies* on OA reaching 23 mm diam. after 7 d at $25 \pm 1^\circ\text{C}$, flattened, greenish grey (26B2); reverse olive grey (26E3). *Colonies* on MEA reaching 19 mm diam. after 7 d at $25 \pm 1^\circ\text{C}$, floccose, pale grey (26B1) to olive (26C2); reverse olive (26F3). NaOH spot test negative. Crystals absent.

Material examined: CHINA, Beijing, in rhizosphere soil of *Poa pratensis* (Poaceae), 26 August 2017, J.M. Liang (HMAS 248045, **holotype**), ex-type living culture CGMCC 3.19296 = LC12199; Paratypes: China, Beijing, in rhizosphere soil of *Digitaria sanguinalis* (Poaceae), 21 August 2017, J.M. Liang LC12200; China, Beijing, in rhizosphere soil of *Poa pratensis* (Poaceae), 21 August 2017, J.M. Liang LC12197; *ibid.* LC12198.

GenBank numbers: ITS: MK348586, MK348587, MK348584, MK348584, LSU: MK348581, MK348580, MK348582, MK348583, RPB2: MK355077, MK355078, TUB2: MK348221, MK348220, MK348222, MK348223.

Notes: *Pyrenochaetopsis sinensis* is phylogenetically distinct from other species in this genus, clustering sister to *P. microspora* (Fig. 42). *Pyrenochaetopsis sinensis* is easily distinguished from *P. microspora* by the absence of setae covering on the surface of pycidium (Gruyter and Boerema 2002). In addition, *P. sinensis* is the only species of *Pyrenochaetopsis* producing pycnosclerotia.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray.

Notes: The family Tetraplosphaeriaceae accommodates seven genera viz. *Ernakulamia* Subram. (Subramanian 1994), *Polyplosphaeria* Kaz. Tanaka & K. Hiray. (Tanaka et al. 2009), *Pseudotetraploa* Kaz. Tanaka & K. Hiray. (Tanaka et al. 2009), *Quadricrura* Kaz. Tanaka, K. Hiray. & Sat. Hatak. (Tanaka et al. 2009), *Shrungabeeja* V.G. Rao & K.A. Reddy (Rao and Reddy 1981), *Tetraploa* Berk. & Broome, and *Triplosphaeria* Kaz. Tanaka & K. Hiray. (Tanaka et al. 2009). *Ernakulamia* is placed in this family based on morphological and phylogenetic analyses

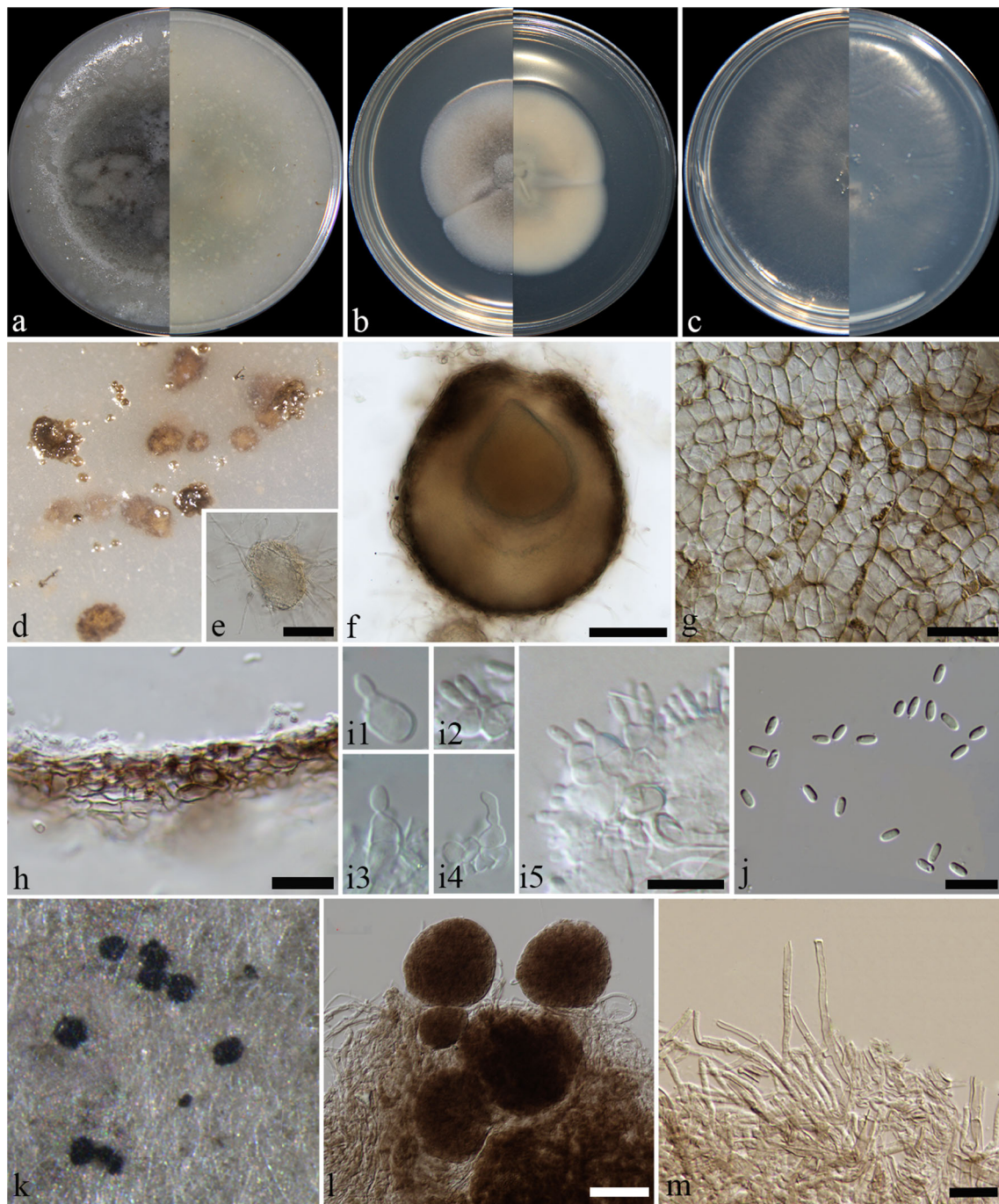


Fig. 41 *Pyrenochaetopsis sinensis* (HMAS 248045, holotype). **a–c** Colony on OA, MEA and SNA (front and reverse). **d** Pycnidia forming on OA. **e** Pre-pycnidial structures. **f** Pycnidia. **g, h** Pycnidia

wall. **i1–i5** Conidiogenous cell. **j** Conidia. **k** Pycnosclerotium on OA. **l–m** Pycnosclerotium. Scale bars: **e** = 50 μ m, **g** = 20 μ m (apply to **l**), **h** = 10 μ m (apply to **i, j, m, i1–i5**)

(Delgado et al. 2017). Although *Pseudotetraploa* and *Shrungabeeja* were not included in this family by Wijayawardene et al. (2018a), these genera should be retained. *Pseudotetraploa* is distinct from *Tetraploa* by its obpyriform to long obpyriform, pseudoseptate conidia composed of 4 to 8 columns with 4 (rarely 6 to 8) setose appendages (Hyde et al. 2013). *Pseudotetraploa* also

formed an independent clade in the molecular analysis and distinguished from *Tetraploa* (Tanaka et al. 2009). *Shrungabeeja* was identified as a distinctive genus within Tetraplosphaeriaceae in Ariyawansa et al. (2015). *Tetraploa*, *Polyposphaeria* and *Triplosphaeria* are characterized with almost hyaline 1(–3)-septate ascospores as *Massarina*-like sexual morphs and several setose

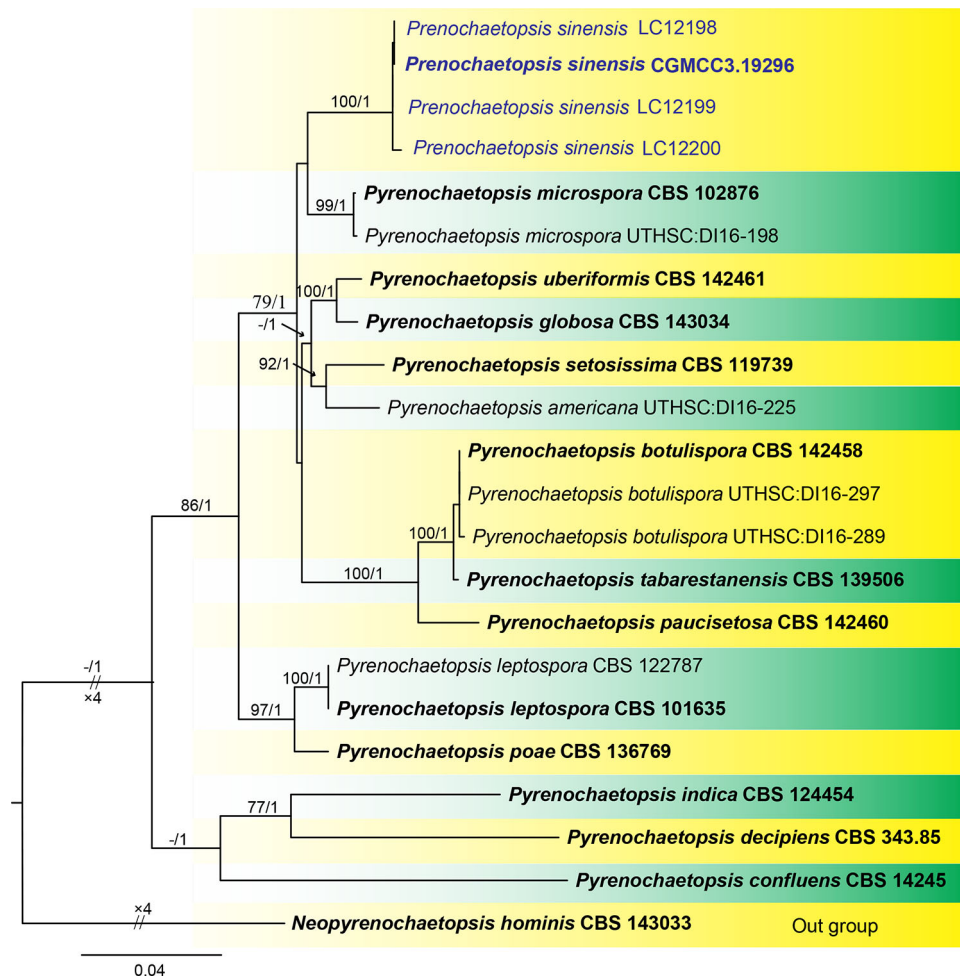


Fig. 42 Phylogram generated from maximum likelihood (ML) analysis inferred from a four-locus concatenated alignment (ITS, LSU, RPB2 and TUB2) for *Pyrenochaetopsis* species and closely related species. Related sequences are taken from Valenzuela-Lopez et al. (2018) and Crous et al. (2014). Twenty-two strains are included in the multi-locus analyses which comprise a total of 2454 characters (443 characters for ITS, 817 characters for LSU, 297 characters for TUB2 and 897 characters for RPB2) after alignment. *Neopyrenochaetopsis hominis* (CBS 143033) (*Pyrenochaetopsis* family, Pleosporales) is used as the outgroup taxon. Tree topology of the ML analysis is similar to

that of the Bayesian analysis. The best RAxML tree with a final likelihood value of -8929.890374 is presented. The matrix had 573 variable sites. Estimated base frequencies were as follows: A = 0.2382, C = 0.2531, G = 0.2663, T = 0.2423; substitution rates AC = 1.4907, AG = 4.6367, AT = 1.4907, CG = 1.0000, CT = 10.5414, GT = 1.0000; gamma distribution shape parameter $\alpha = 0.5740$. Bootstrap values (1000 replicates) over 75% for ML and Bayesian posterior probability (PP) over 0.95 are marked at the left of every node (ML/BYPP). Type strains are in bold and the newly generated sequences are indicated in blue

appendages as tetraploa-like asexual morphs (Tanaka et al. 2009; Hyde et al. 2013). The sexual morphs of the genera *Ernakulamia*, *Pseudotetraploa*, *Shrungabeeja* and *Quadricrura* are unknown. Most taxa of Tetraplosphaeriaceae were found on bamboo and grasses.

Tetraploa Berk. & Broome

Notes: Hyde et al. (2013) and Wijayawardene et al. (2014) recommended the use of *Tetraploa* over *Tetraplosphaeria* based on the close phylogenetic relationships between the type species of these two genera and there are more species accommodated in *Tetraploa*, having priority of the most named uses. Thus, Rossman et al. (2015b) adopted *Tetraploa* over *Tetraplosphaeria*. There

are 20 epithets listed under the genus in Index Fungorum (2019). However, only five species of *Tetraploa* have molecular data (NCBI: www.ncbi.nlm.nih.gov; accessed 1st May 2019). *Tetraploa* has relatively small globose ascomata, narrowly fusiform ascospores having appendage-like sheath, and conidia with four setose appendages and is mainly known from monocotyledons especially grasses and bamboo (Tanaka et al. 2009; Goonasekara et al. 2018; Farr and Rossman 2019). A new record of *Tetraploa nagasakiensis* from China is reported in this paper.

Tetraploa nagasakiensis (Kaz. Tanaka & K. Hirayama) Kaz. Tanaka & K. Hirayama

Facesoffungi number: FoF05080; Fig. 43

Basionym: *Tetraplosphaeria nagasakiensis* Kaz. Tanaka & K. Hiray., in Tanaka et al., Stud. Mycol. 64: 180 (2009)

Saprobic on dead bamboo branches. **Sexual morph**
Ascomata 170–200 μm high, 190–260 μm diam., immersed under host epidermis, solitary, scattered, visible as small minute black spots or papilla on host issue, dark

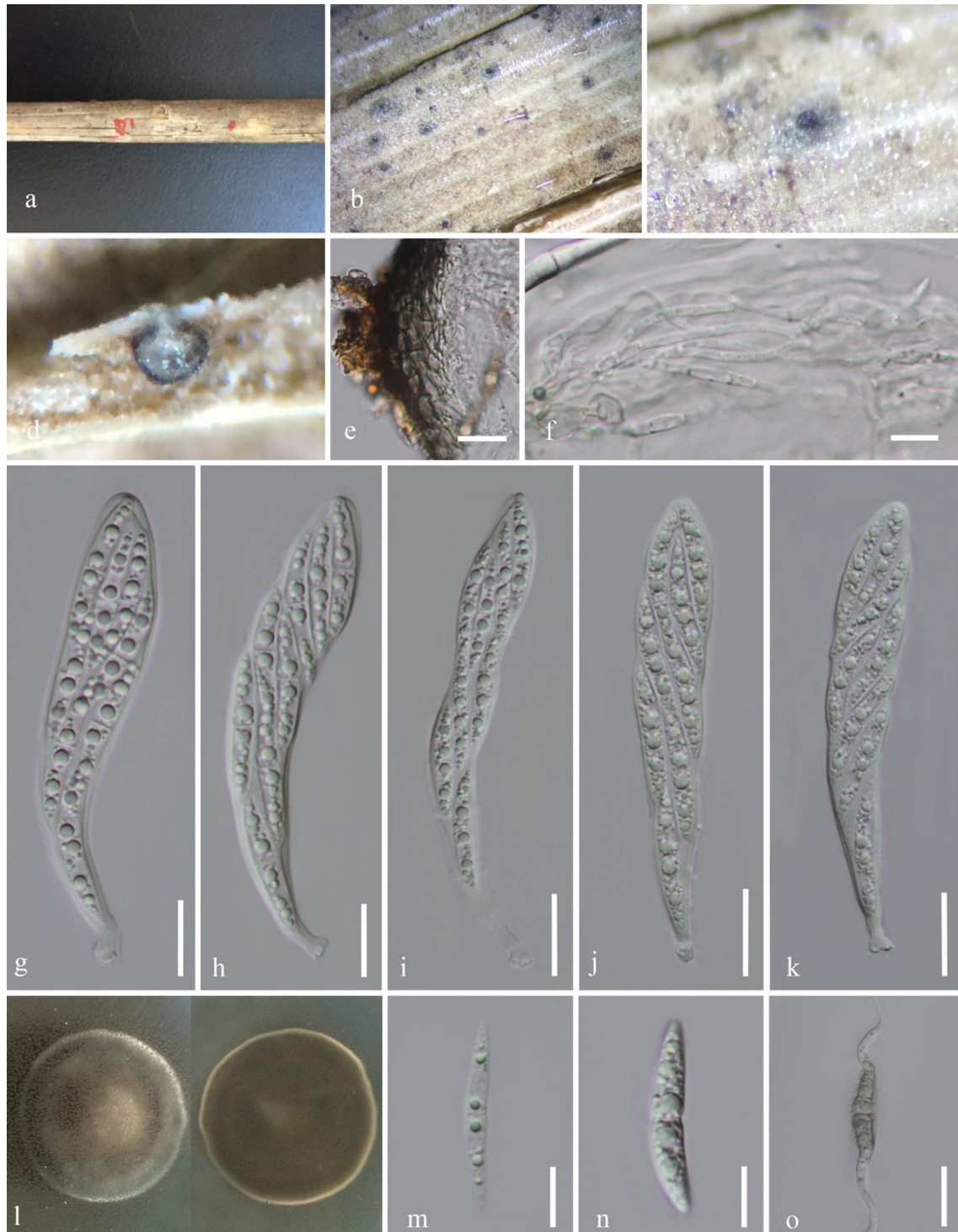


Fig. 43 *Tetraploa nagasakiensis* (HKAS 101756, new geographical record). **a–c** Host and ascomata. **d** Vertical section of ascoma. **e** Peridium of ascoma. **f** Pseudoparaphyses. **g–k** Asci. **l** Culture from

above and below views. **m, n** Ascospores. **o** Germinating ascospore. Scale bars: **i–k, o** = 20 μm , **e, g, h** = 15 μm , **f, m, n** = 10 μm

brown to black, uni-loculate, globose to subglobose or ampulliform, coriaceous, with ostiole. *Peridium* 17–24 µm wide, comprising several layers, with outer layers composed of dark brown to black cells of *textura angularis*, inner layers composed of light brown to hyaline pseudoparenchymatous cells arranged in *textura angularis*. *Hamathecium* of 1.7–2.4 µm, septate, branched, broad pseudoparaphyses, anastomosing near the apex. *Asci* 98–130 × 14–18 µm (\bar{x} = 114 × 16 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, pedicellate with furcate ends, apically rounded with well-developed ocular chamber. *Ascospores* 30–34.5 × 4–5 µm (\bar{x} = 32.3 × 4.6 µm, n = 20), overlapping 2–3-seriate, hyaline, 1-septate, narrowly fusiform, smooth-walled, multi-guttulate. **Asexual morph** Refer to Tanaka et al. (2009).

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on PDA reaching 30–35 mm diam. after 4 weeks at 20–25 °C, circular, slightly raised to umbonate, pale black at the middle, white at the margin from the above and below, no pigment in agar.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Pingbian County, nearby Tuanpo Reservoir, on dead bamboo branches, 21 September 2017, H.B. Jiang, Pb001 (HKAS 101756), living culture (KUMCC 18-0109).

GenBank numbers: ITS: MK079890, LSU: MK079891, SSU: MK079888.

Notes: Although the new collection (HKAS 101756) has eight different ITS base pairs as compared to the type strain of *Tetraploa nagasakiensis*, they are still close to each other in multi-phylogenetic analysis based on ITS, LSU and SSU sequenced data (Fig. 44). They are also morphologically very similar. *Tetraploa nagasakiensis* was reported only from Japan (Tanaka et al. 2009), but our new strain was collected in China.

Torulaceae Corda

Notes: The family Torulaceae was introduced by Corda (Sturm 1829). Two genera, *Dendryphion* Wallr. and *Torula* Pers., are accepted within this family. Su et al. (2016) and Li et al. (2016) introduced the genera *Neotorula* Ariyaw., Z.L. Luo & K.D. Hyde and *Sporidesmioides* Jin F. Li, Phook. & K.D. Hyde within Torulaceae, respectively.

Torula Pers.

Notes: The genus *Torula* was established by Persoon (1794), typified by *T. herbarum* (Pers.) Link as the type species. *Torula* is characterized by terminal or lateral, monoblastic or polyblastic conidiogenous cells, which have a basally thickened and heavily melanized wall, with the apex thin-walled and frequently collapsing and becoming coronate; these conidiogenous cells are consequently termed ‘corona cells’ (Crane and Miller 2016). This genus is problematic as many species await redescription (Seifert et al. 2011). More sequence data are required in the future

study of the genus. A key to *Torula* and similar genera was provided by Crane and Miller (2016).

Torula breviconidiophora C.G. Lin & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555428; **Facesoffungi number:** FoF05069; Fig. 45

Etymology: In reference to the short conidiophores.

Holotype: MFLU 18-1693

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Colonies effuse on the natural substrate, scattered, hairy, dark brown. **Mycelium** immersed to superficial, composed of pale brown, septate, branched hyphae. **Conidiophores** macronematous, mononematous, subcylindrical, erect, septate, smooth, straight or flexuous, subhyaline to dark brown, with ampulliform cells, 3.5–28 µm long, 3–8 µm wide at the widest part. **Conidiogenous cells** mono- to polyblastic, integrated, terminal, on conidiophores, terminal or intercalary in conidial chains, doliiform to ellipsoid, pale brown, collapsing in above half when old, 4–7 µm long, 3–7 µm wide. **Conidia** phragmosporous, in branched chains, acrogenous, dry, cylindrical, medium to dark brown, with apical cell subhyaline or pale brown, 1–4-septate, deeply constricted at septa, verrucose, rounded at both ends, easily separating, 8–21 µm long (\bar{x} = 15.2 µm, n = 60), 3.5–7 µm wide (\bar{x} = 5.2 µm, n = 60).

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA effuse, greyish brown to dark brown, reaching a diam. of 4–6 cm in 10 days at 25 °C.

Material examined: THAILAND, Chang Rai Province, Muang District, Mae Fah Luang University, near S7 building, on decaying wood, 20 July 2016, Chuangen Lin, ML 1-4 (MFLU 18-1693, **holotype**; HKAS 102196, **isotype**), ex-type living culture (KUMCC 18-0130).

GenBank numbers: ITS: MK071670, LSU: MK071672, SSU: MK071697, TEF1- α : MK077673.

Notes: This species is most similar to *T. mackenziei* which is characterized by greyish brown conidia composed of moniliform cells and 2–3 septa (Li et al. 2017). However, the conidia of *T. breviconidiophora* are medium to dark brown, with 1–4-septate, subhyaline or pale brown apical cells. From the phylogenetic trees of Bayesian inference, maximum parsimony and maximum likelihood analyses based on combined ITS, LSU, SSU and TEF1- α , this species is closest to *T. chromolaenae* and *T. mackenziei* (Fig. 47). *Torula chromolaenae* is distinct from other *Torula* species in having smaller and doliiform conidiogenous cells and 2–3-septate conidia (Li et al. 2017). *Torula breviconidiophora* differs from *T. chromolaenae* by its longer conidiophores (3.5–28 µm vs 5–6.3 µm).

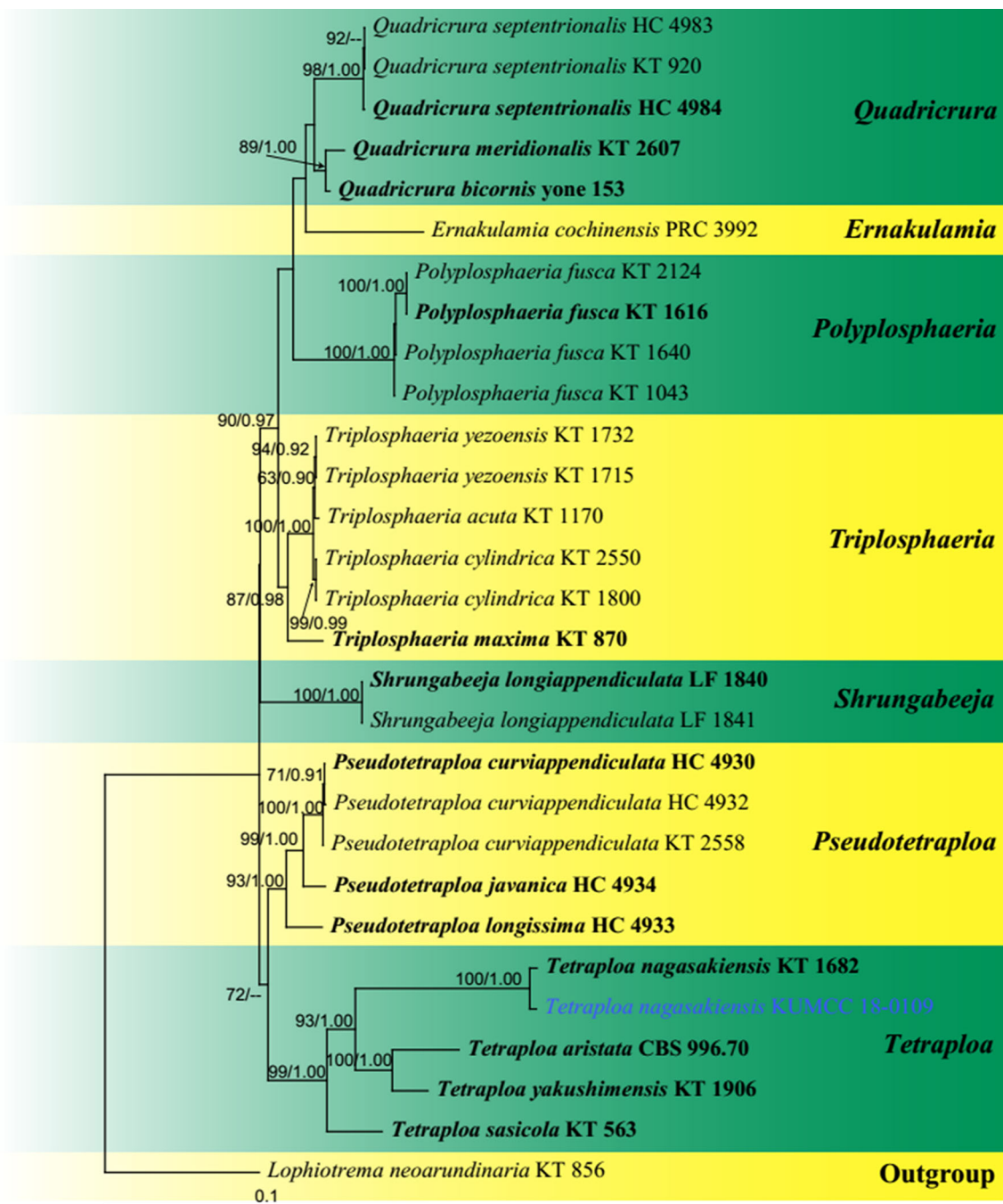


Fig. 44 Phylogram generated from maximum likelihood analysis based on a combined ITS, LSU, and SSU sequence dataset for *Tetraploa* species and several closely related genera in Tetraplophaeriaceae. Related sequences are taken from Tanaka et al. (2009) and Ariyawansa et al. (2015). Twenty-nine strains are included in the combined genes sequence analyses which comprise total 3225 characters including gaps (584 characters for ITS, 1300 characters for LSU, 1341 characters for SSU) after alignment. *Lophiotrema neoarundinaria* KT 856 (Lophiotremataceae, Pleosporales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis.

The best sorting RaxML tree with a final likelihood value of -8716.750658 is presented. The matrix had 430 distinct alignment patterns, with 15.62% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251593, C = 0.234741, G = 0.277315, T = 0.236350; substitution rates AC = 4.295630, AG = 4.189995, AT = 2.538258, CG = 1.455605, CT = 14.145092, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.501945$. Bootstrap values for maximum likelihood (ML) equal to or greater than 70% are shown on the left. Branches with Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are shown on the right. The ex-type strains are in bold and black. The newly generated sequence is indicated in blue.

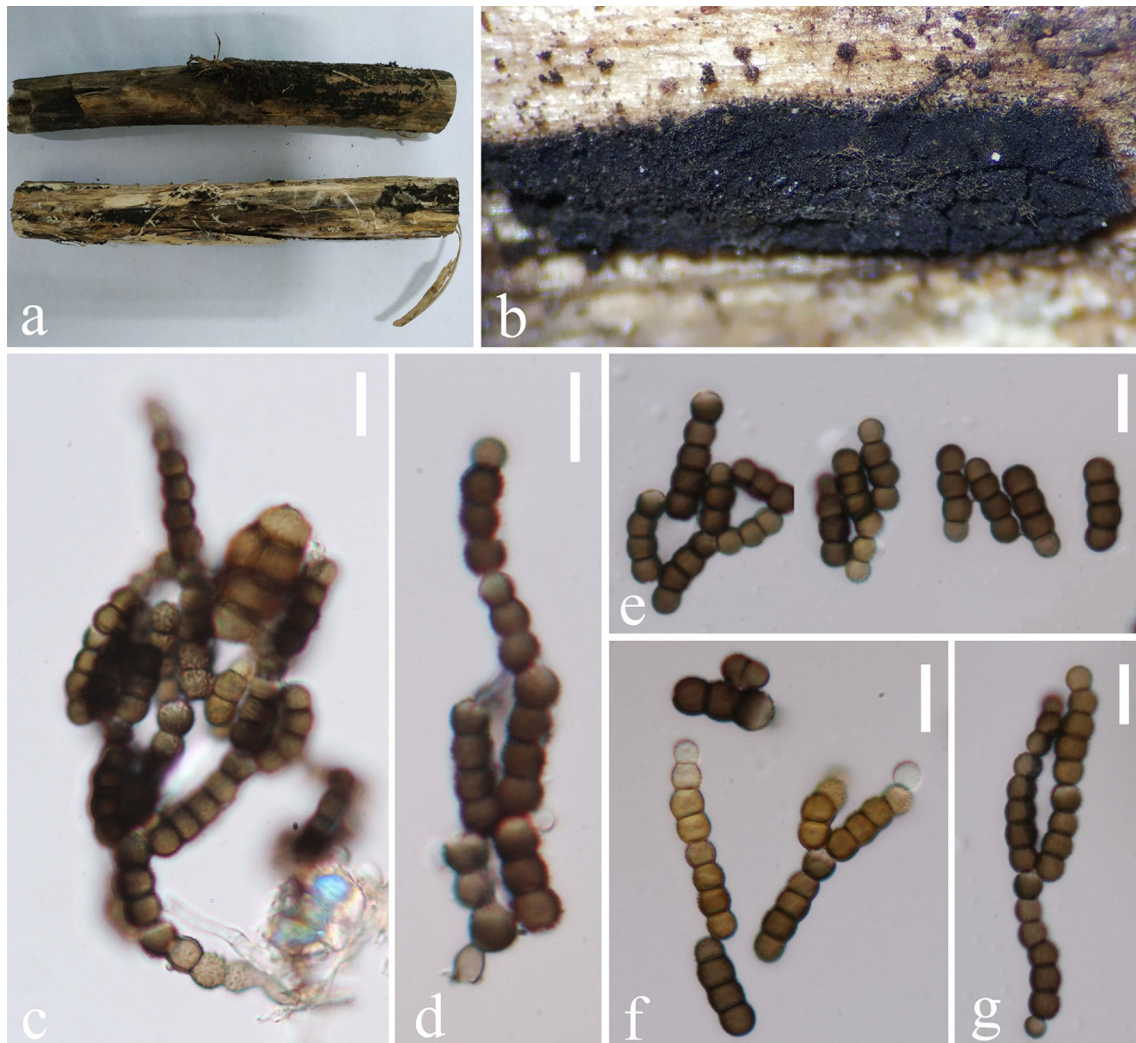


Fig. 45 *Torula breviconiophora* (MFLU 18-1693, **holotype**). **a, b** Host material. **b** Conidiophores on leaf surface. **c, d** Conidiophores, conidiogenous cells and conidia. **e–g** Conidia. Scale bars: **c–g** = 10 μ m

Torula polyseptata C.G. Lin & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555429, *Facesoffungi* number: FoF05070; Fig. 46

Etymology: In reference to the 2–8-septate conidia.

Holotype: MFLU 18-1694

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Colonies effuse on the natural substrate, scattered, hairy, dark brown. *Mycelium* immersed to superficial, composed of pale brown, septate, branched hyphae. *Conidiophores* macronematous, mononematous, subcylindrical, erect, septate, smooth, straight or slightly flexuous, dark brown to black, 10–40 μ m long, 3.5–8 μ m wide at the widest part. *Conidiogenous cells* holoblastic, mono- to polyblastic, integrated, terminal or intercalary in conidial chains, doliiiform, pale brown, collapsing in above half when old, 4.5–8.5 μ m long, 4.5–8 μ m wide. *Conidia* phragmosporous, in branched chains, acrogenous, dry, cylindrical, medium to dark

brown, 2–8-septate, deeply constricted at septa, verrucose, rounded at both ends, easily separating, 10–40 μ m long (\bar{x} = 19.3 μ m, n = 35), 3.5–7.5 μ m wide (\bar{x} = 5.5 μ m, n = 35).

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA effuse, greyish brown to dark brown, reaching a diam. of 4–6 cm in 10 days at 25 °C.

Material examined: THAILAND, Chang Rai Province, Muang District, Mae Fah Luang University, on decaying wood, 20 July 2016, Chuangen Lin, ML 21-2 (MFLU 18-1694, **holotype**; HKAS 102197, **isotype**), ex-type living culture (KUMCC 18-0131).

GenBank numbers: ITS: MK071671, LSU: MK071673, SSU: MK071698, TEF1- α : MK077674.

Notes: This species is most similar to *Torula pluriseptata* in their conidial morphology, however, the conidiophores of *T. polyseptata* are longer than *T. pluriseptata*

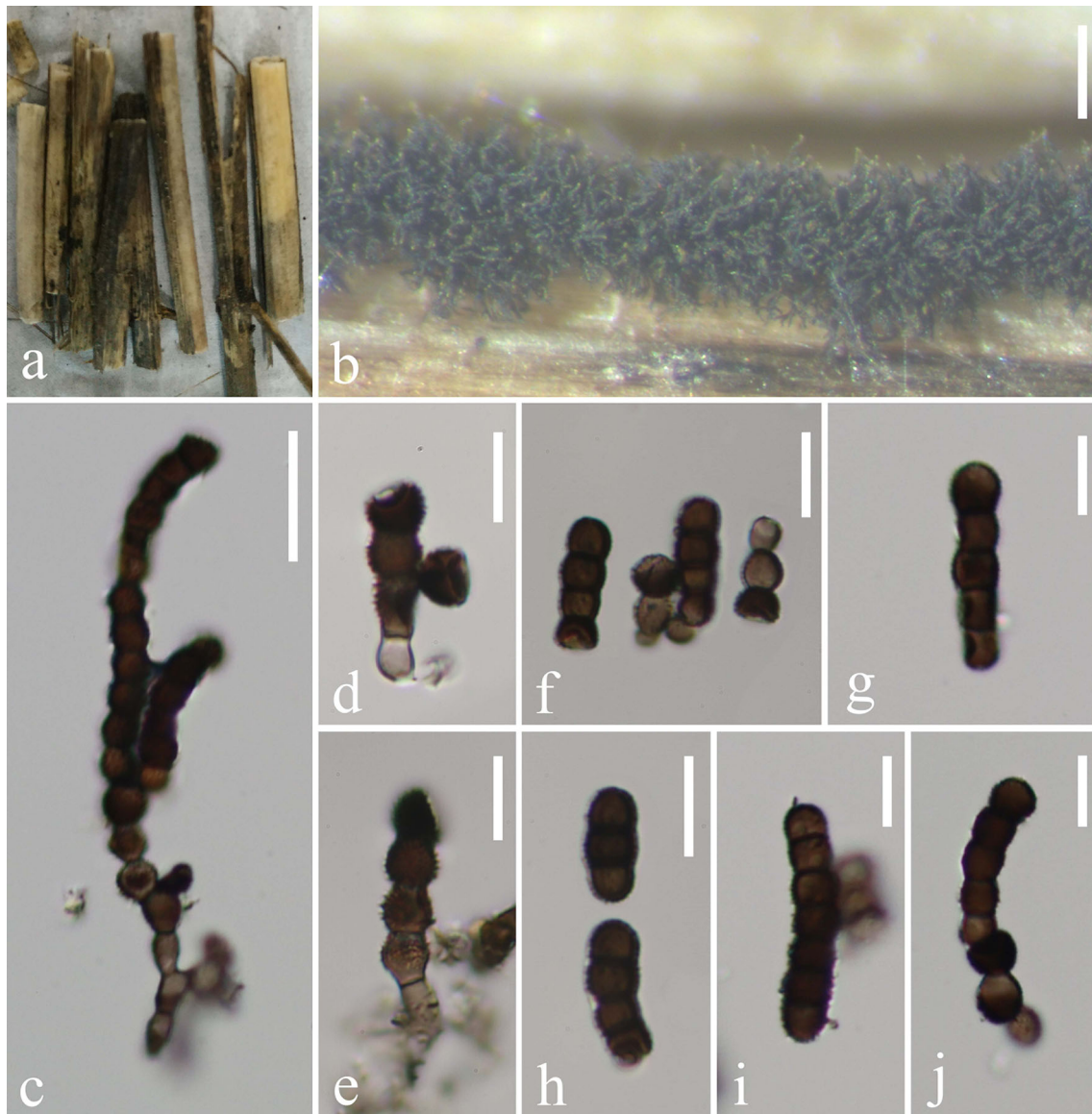


Fig. 46 *Torula polyseptata* (MFLU 18-1694, **holotype**). **a, b** Host material. **b** Conidiophores on leaf surface. **c–e** Conidiophores, conidiogenous cells and conidia. **f–j** Conidia. Scale bars: **c** = 20 µm, **d–j** = 10 µm

(10–40 µm vs 2.8–4.3 µm). *Torula polyseptata* forms a clade together with strains of *T. chiangmaiensis* with 98% MP bootstrap support, 97% ML bootstrap support and 0.97% Bayesian posterior probabilities within the genus *Torula* (Fig. 47). *Torula polyseptata* is distinct from *T. chiangmaiensis* by the size and number of septa in the conidia.

The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue. The tree is rooted with *Dendryphion nanum* (HKAS 84010).

Trematosphaeriaceae K.D. Hyde, Y. Zhang ter, Suetrong & E.B.G. Jones

Notes: Trematosphaeriaceae was introduced by Suetrong et al. (2011b) to accommodate the genera

Falciformispora K.D. Hyde, *Halomassarina* Suetrong et al. and *Trematosphaeria* Fuckel. These genera mainly comprise fungi inhabiting mangrove wood in marine environments and wood in freshwater (Hyde 1989; Suetrong et al. 2011b). The main distinguishing characters of this family are medium-sized rounded ascomata with a papillate ostiole, a relatively wide, coriaceous peridium, cellular pseudoparaphyses and cylindro-clavate asci. The ascospores are two-celled or many celled, hyaline or brown. We introduce *Falciformispora aquatica* as a new species based on evidence from morphology and phylogenetic analyses of combined LSU, SSU, RPB2 and TEF1- α sequence data (Fig. 49).

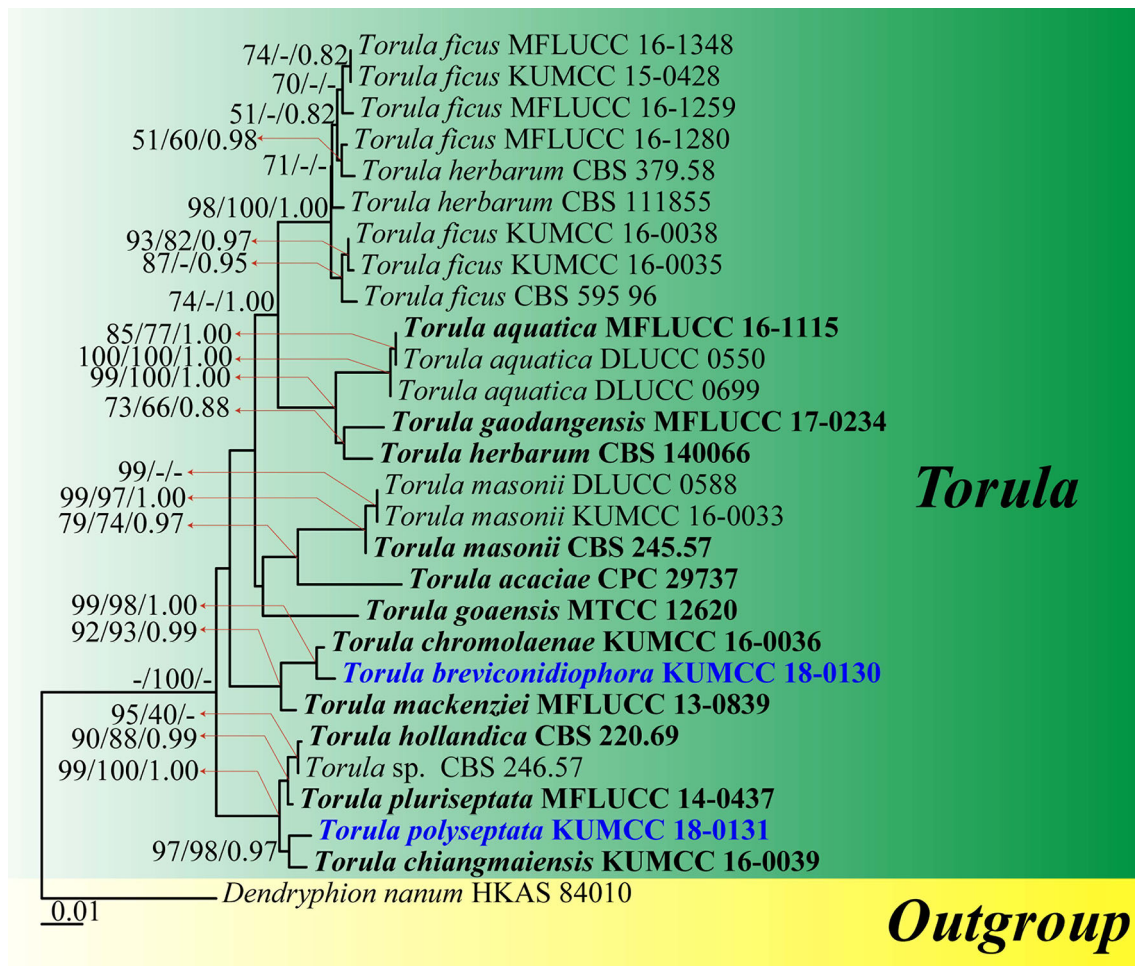


Fig. 47 Phylogenetic tree generated from ML analysis based on combined ITS, LSU, SSU and TEF1- α sequence data for the genus *Torula*. Related sequences are taken from Crane and Miller (2016), Su et al. (2016) and Li et al. (2017). Twenty-eight strains are included in the combined analyses which comprise 3139 characters (552 characters for ITS, 844 characters for LSU, 887 characters for SSU, 856 characters for TEF1- α) after alignment. The best RaxML tree with a final likelihood value of -7637.920840 is presented. The matrix had 454 distinct alignment patterns, with 31.43% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242476, C = 0.262534, G = 0.274745, T = 0.220245; substitution rates AC = 3.217101, AG = 3.132488, AT = 2.857294, CG = 1.885404, CT = 12.537654, GT = 1.000000; gamma distribution

shape parameter $\alpha = 0.02$. Maximum parsimony analysis of 2817 constant characters and 204 informative characters resulted in 126 equally most parsimonious tree of 567 steps (CI = 0.704, RI = 0.785, RC = 0.552, HI = 0.296). For the Bayesian analysis, two parallel runs with six chains were run for 1000,000 generations and trees were sampled every 100th generation, resulted in 20002 trees from two runs of which 15002 trees were used to calculate the posterior probabilities (each run resulted in 10001 trees of which 7501 trees were sampled). Bootstrap support values for maximum parsimony (MP) and maximum likelihood (ML) greater than 50% and Bayesian posterior probabilities greater than 0.8 are indicated above or below the nodes as MLBS/MPBS/BYPP

Falciformispora K.D. Hyde

Notes: *Falciformispora* was established by Hyde (1992) as a monotypic genus and was assigned to the Pleosporaceae when compared with *Setosphaeria*, which has an *Exserohilum* asexual morph and is exclusively parasitic on Gramineae. Subsequently, Raja et al. (2008) collected *Falciformispora* species in freshwater in Florida and found that it is closely related to *Chaetomastia* rather than *Setosphaeria*, but is distinct in having hyaline ascospores. Suetrong et al. (2009) recorded it from the terrestrial oil palm (*Elaeis guineensis*) in Thailand. Suetrong et al.

(2011b) showed that *Falciformispora* forms a well-supported clade with *Trematosphaeria pertusa* and *Halomasarina thalassiae* in Trematosphaeriaceae based on phylogenetic analysis. Therefore, this genus was placed in Trematosphaeriaceae. Currently, *F. lignatilis*, *F. senegalensis* and *F. tompkinsii* are listed in Index Fungorum (2019).

Falciformispora aquatica D.F. Bao, K.D. Hyde & H.Y. Su, *sp. nov.*

Index Fungorum number: IF555415; *Facesoffungi* number: FoF05059; Fig. 48

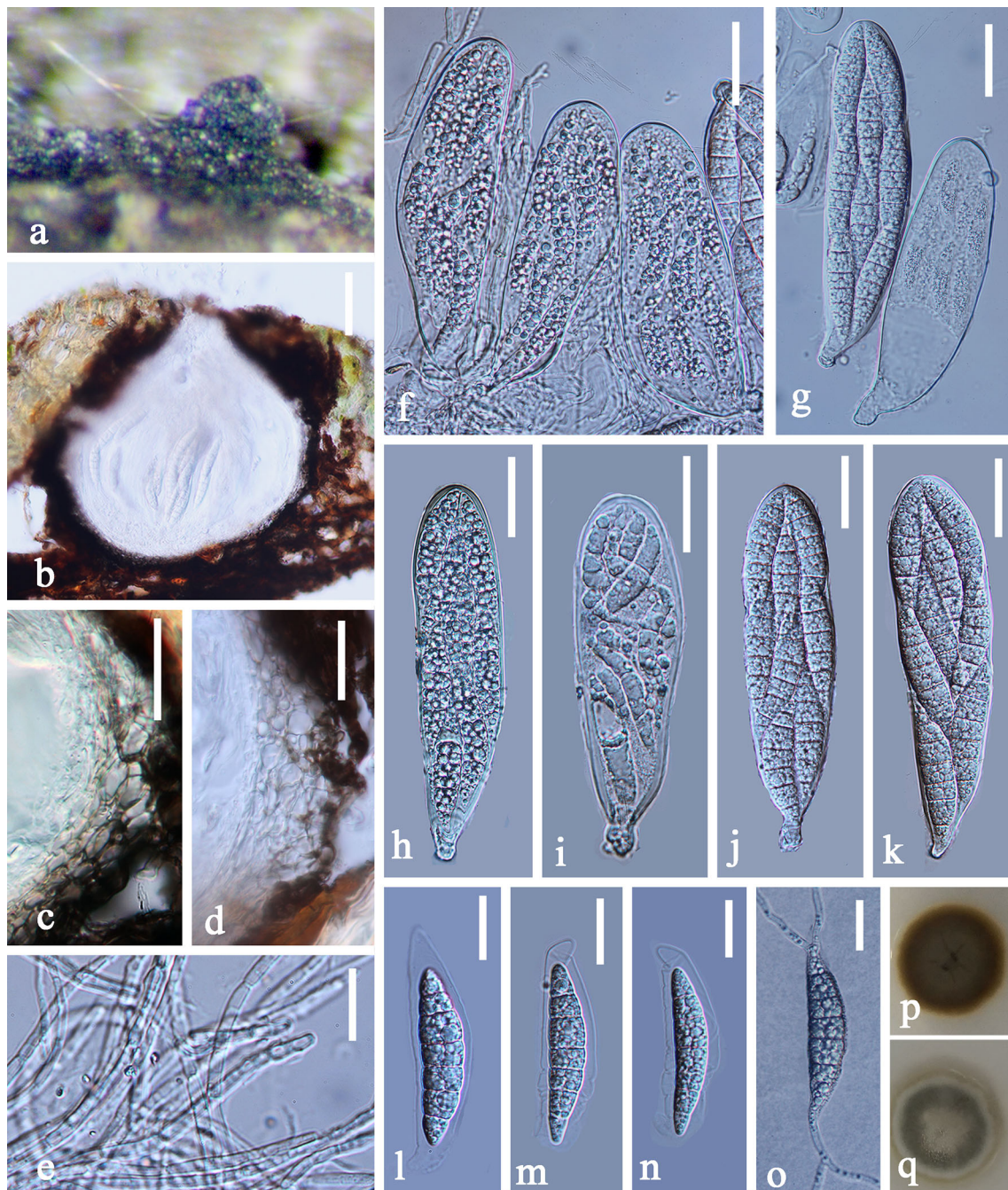


Fig. 48 *Falciformispora aquatica* (MFLU 18-1228, **holotype**). **a** Ascomata on submerged wood. **b** Section of ascoma. **c, d** Section of peridium. **e** Pseudoparaphyses. **f–k** Asci. **l–n** Ascospores.

o Germinating ascospore. **p, q** Culture on PDA. Scale bars: **b** = 100 μ m, **f–k** = 30 μ m, **c–e, l–o** = 20 μ m

Etymology: Referring to the aquatic habitat of this fungus.

Holotype: MFLU 18-1228

Saprobic on decaying wood, submerged wood in freshwater. **Asexual morph** Undetermined. **Sexual morph** **Ascomata** 260–330 μ m diam. 230–300 μ m high (\bar{x} = 286 \times 260 μ m, n = 10) solitary to gregarious, immersed in the host tissue, globose to subglobose,

coriaceous, papillate, ostiolate, dark grey to black. **Peridium** up to 25–30 μ m wide, composed of outer thick-walled angular or rounded greyish brown cells, and inner hyaline cells of *textura prismatica*. **Hamathecium** comprising 2–3.5 μ m wide, numerous, septate, cellular pseudoparaphyses, hyaline, branched, surrounded by a gelatinous matrix. **Asci** 115–167 \times 28–47 μ m (\bar{x} = 147 \times 36 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindro-clavate, short

pedicellate. *Ascospores* 48–59 × 10–16 µm (\bar{x} = 55 × 13 µm, n = 30), fusiform to clavate, hyaline, straight or slightly curved, 5–6-septate, mostly 6-septate, slightly constricted at all septa, tapering to narrow both of ends, surrounded by a mucilaginous sheath and a single scythe-like appendage at the apex.

Culture characteristics: *Ascospores* germinating on PDA within 24 h. Colonies on MEA at room temperature reaching 2.5 cm diam. in three weeks, mycelium pale brown to grayish brown after 3 weeks, composed brown to dark brown, septate, smooth or verrucose hyphae.

Material examined: Thailand, Prachuap Khiri Khan Province, Sai Khu Waterfall, on submerged decaying wood, August 2017, Vinit Kumar., site1–2–1, (MFLU 18–1228, **holotype**), ex-type living culture (MFLUCC 18–0212).

GenBank numbers: LSU: MK063643, RPB2: MK099810, TEF1- α : MK099811.

Notes: The phylogenetic analyses showed that *Falciformispora aquatica* grouped with members of *Falciformispora*, but separated in an independent lineage with relatively high bootstrap support (100% ML/1.00 BYPP, Fig. 49). *Falciformispora aquatica* is similar to *F. lignatilis*, as they have similar asci (bitunicate, fissitunicate, with a short pedicel) and ascospores (fusiform to clavate, hyaline). However, *F. aquatica* has larger asci (115–167 × 28–47 vs. 110–136 × 20–32 µm), and larger ascospores (48–59 × 10–16 vs. 42–50 × 7.5–10 µm). Moreover, *F. aquatica* ascospores are mostly 6-septate, whereas those of *F. lignatilis* over 7-septate.

Minutisphaerales Raja, Oberlies, Shearer & A.N. Mill.

Notes: The order Minutisphaerales was introduced by Raja et al. (2015) based on a LSU, ITS, SSU and MCM7 sequence dataset. It is typified by the sexual genus *Minutisphaera* with the chemical analysis carried out for *M. aspera* Raja, Oberlies, Shearer & A.N. Mill. and *M. parafimbriatispora* Raja, Oberlies, Shearer & A.N. Mill. Jayasiri et al. (2018) included a new family Acrogenosporaceae in Minutisphaerales.

Acrogenosporaceae Jayasiri & K.D. Hyde

Notes: Acrogenosporaceae is a monotypic family with *Acrogenospora* as the type genus. Rossman et al. (2015b) suggested to protect *Acrogenospora* over *Farlowiella* (Art. 59.1). Ellis (1972) reported an *Acrogenospora* asexual morph accompanies *F. australis* Dennis on the host substrate, while Mason (1941) showed the connection between *A. megalospora* (Berk. & Broome) Goh, K.D. Hyde & C.K.M. Tsui and *F. armichaeliana* (Berk.) Sacc. based on a cultural study. With seven strains related to this group, Jayasiri et al. (2018) carried out the phylogenetic analyses which supported the connection between *Acrogenospora* and *Farlowiella*.

Acrogenospora M.B. Ellis

Notes: The holomorph genus *Acrogenospora* is characterized by laterally compressed hysterothecia with a prominent sunken slit, aseptate, hyaline pedicellate ascospores, macronematous brown conidiophores, monoblastic, terminal or intercalary conidiogenous cells and globose, ellipsoid or obovoid, olivaceous to brown conidia. Among the available sequenced strains of the genus, many do not have any associated morphological descriptions. We therefore designate a reference specimen for the type species *A. sphaerocephala* and introduce a new taxon, *A. thailandica*, based on phylogenetic analyses and morphological characters.

Acrogenospora sphaerocephala (Berk. & Broome) M.B. Ellis, Dematiaceous Hyphomycetes: 114 (1971)

≡ *Monotospora sphaerocephala* Berk. & Broome, Ann. Mag. nat. Hist., Ser. 3 3: 361 (1859)

Index Fungorum number: IF308236; **Facesoffungi number:** FoF04687; Fig. 50

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Colonies sparse, scattered, black, glistening, hairy. Mycelium mostly immersed, consisting of septate, thin-walled, smooth, hyaline to pale brown hyphae. *Conidiophores* macronematous, monone-matous, (155–)215–320(–360) × (3.5–)4.8–7.5(–9.5) µm (\bar{x} = 275 × 6 µm, n = 15), solitary, erect, mostly flexuous, septate, slightly tapering towards the apex, mid to dark brown, paler and rounded at the apex, smooth, thick-walled at the base. *Conidiogenous cells* monoblastic, integrated, intercalary, mid brown, cylindrical, with percurrent proliferations, sometimes flexuous at the proliferation. *Conidia* acrogenous, 18–30 µm (\bar{x} = 24 µm, n = 40) diam., holoblastic, olive-green to brown, spherical or subspherical, unicellular, smooth and thick-walled, guttulate, truncate at the base.

Culture characteristics: Conidia germinating on PDA within 24 h. Germ tubes produced from both ends. Colonies on PDA, reaching 5–10 mm diameter after two weeks at 25 °C in natural light, with dense grayish green aerial mycelium on the surface, black in reverse with entire margin.

Material examined: THAILAND, Prachuap Khiri Khan Province, near 12°30.195'N, 99°31.350'E, on decaying wood submerged in a freshwater stream, 25 December 2014, Jaap van Strien, Site 5-14-2 (MFLU 18-1130, **reference specimen designated here**), living culture (MFLUCC 16-0179, GZCC 15-0071).

GenBank numbers: ITS: MH606233, LSU: MH606222, RPB2: MH626448.

Notes: The genus *Acrogenospora* includes 11 species and two of them have been linked to sexual morphs in *Farlowiella*. The synonymy of *Acrogenospora* with

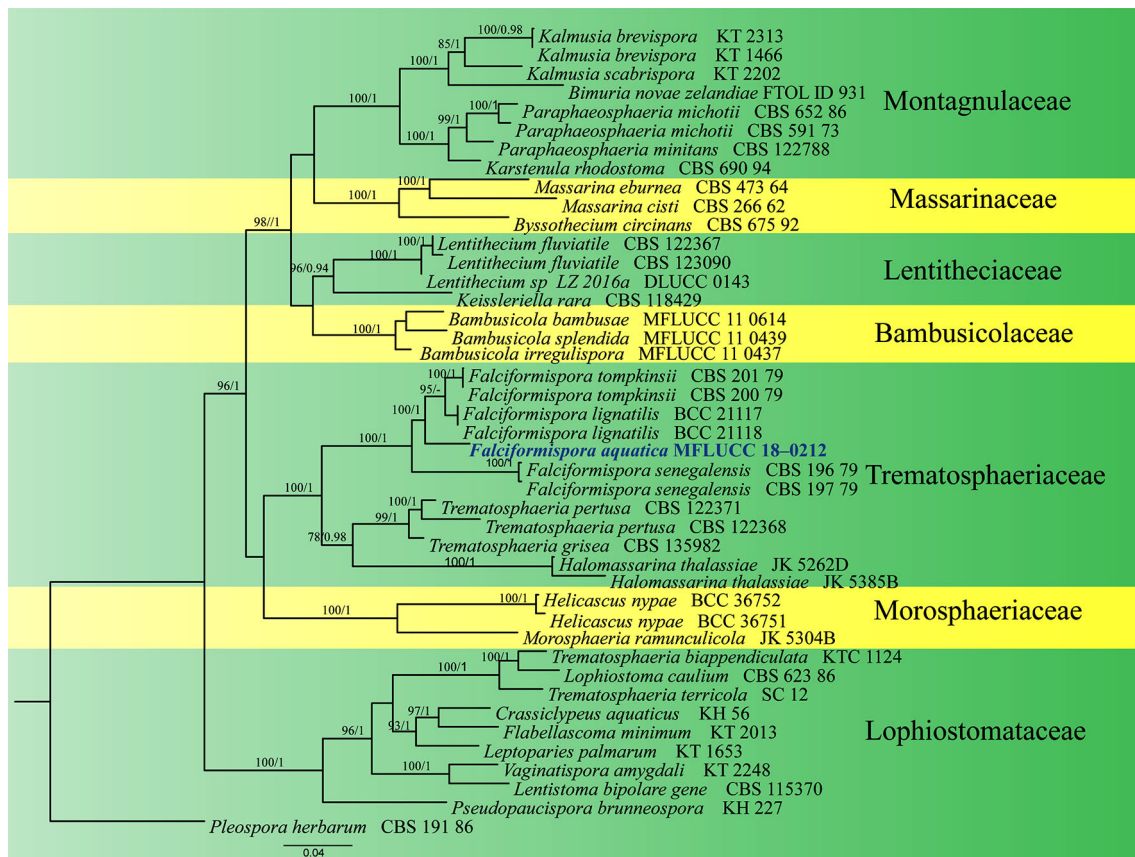


Fig. 49 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1- α and RPB2 sequence data for Trematosphaeriaceae and several closely related families in Dothideomycetes. Related sequences are taken from Suetrong et al. (2009) and Wanasinghe et al. (2018a), forty-three strains are included in the combined analyses which comprise total 3628 characters (1119 characters for LSU, 983 characters for SSU, 821 characters for TEF1- α , 705 characters for RPB2) after alignment. *Pleospora herbarum* (CBS 191.86) (Pleosporaceae, Pleosporales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the

Bayesian analysis. The best RaxML tree with a final likelihood value of -24083.791079 is presented. The matrix had 1258 distinct alignment patterns, with 18.62% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250098, C = 0.240190, G = 0.272034, T = 0.237678; substitution rates AC = 1.254339, AG = 3.593578, AT = 1.238765, CG = 1.071163, CT = 7.108157, GT = 1.000000; gamma distribution shape parameter α = 0.194764. Bootstrap values for maximum likelihood (ML) and equal to or greater than 75% and Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are placed above the branches. The newly generated sequence is indicated in bold and blue

Farlowiella has long been accepted based on the distinctive morphology of the asexual morphs (Ellis 1971, 1976; Goh et al. 1998a; Rossman et al. 2015b). The generic name *Acrogenospora* has been protected over its sexual morph *Farlowiella* (Rossman et al. 2015b). In this study, molecular data has been generated to support its asexual-sexual connection. *Acrogenospora sphaerocephala* was designated as the type species in the genus (Ellis 1971) and it is a frequently observed species with a worldwide distribution (Goh et al. 1998a).

Phylogenetic analyses indicate that our collection *A. sphaerocephala* (MFLUCC 16-0179) formed a distinctive branch in the genus, close to *A. carmichaeliana* (FMR 11021, CBS 179.73, CBS 164.76 and CBS 206.36). However, the identification of these *A. carmichaeliana*

(Berk.) Rossman & Crous collections is questionable as only molecular sequence data was provided and sequence data is unavailable for the ex-type strain. *Acrogenospora sphaerocephala* was thought to be the asexual morph of *F. carmichaeliana* due to the information in GenBank. It must be wrongly identified as *A. megalospora* was introduced as the asexual morph of *Farlowiella carmichaeliana* (Ellis 1971; Goh et al. 1998a) and the combination of the holomorph species was suggested as *Acrogenospora carmichaeliana* (Rossman et al. 2015b). Our collection was identified as *A. sphaerocephala* with the morphological characters well-matched with the original diagnosis. *Acrogenospora sphaerocephala* is morphologically similar to *A. megalospora* except *A. sphaerocephala* has globose conidia, while *A. megalospora* produces broadly ellipsoidal



Fig. 50 *Acrogenospora sphaerocephala* (MFLU 18-1130, reference specimen). **a** Colony on substrate. **b, c** Conidiophores with conidia. **d, e** Conidiophores. **f, g** Conidiogenous cells with conidia. **h–j** Conidia.

k Germinated conidium on PDA. **l, m** Culture (**l** from above view, **m** from below view). Scale bars: **a** = 200 μm , **b–d** = 100 μm , **e–g** = 50 μm , **h** = 30 μm , **k** = 20 μm , **i, j** = 10 μm

or obovoid conidia (Ellis 1971; Goh et al. 1998a; Cai et al. 2006). Additionally, our collection has similar size of conidiophores ($155\text{--}360 \times 3.5\text{--}9.5 \mu\text{m}$) with given by Ellis (1971) (up to $380 \mu\text{m}$ long, $5\text{--}8 \mu\text{m}$ wide at the apex and $9\text{--}11 \mu\text{m}$ wide at the base) and similar conidial size ($18\text{--}30 \mu\text{m}$, $\bar{x} = 24 \mu\text{m}$) with given by Ellis (1971) ($15\text{--}33 \times 14\text{--}33 \mu\text{m}$, $\bar{x} = 28 \times 27 \mu\text{m}$). Thus, a reference specimen for *A. sphaerocephala* is designated here.

Acrogenospora thailandica J. Yang & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555499; *Facesoffungi* number: FoF04676; Fig. 51

Etymology: Referring to the distribution in Thailand.

Holotype: MFLU 18-1129

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Colonies* sparse, scattered, dark brown, glistening, hairy. Mycelium mostly immersed, consisting of septate, hyaline to pale brown hyphae. *Conidiophores* $850\text{--}950 \times 3.5\text{--}8 \mu\text{m}$, macronematous, mononematous, solitary, erect, straight or slightly flexuous, septate, long cylindrical, slightly tapering towards the apex, pale to dark brown, paler towards the apex, smooth, thick-walled at the base. *Conidiogenous cells* monoblastic, integrated, intercalary, brown, cylindrical. *Conidia* acrogenous, $15.5\text{--}24.5 \mu\text{m}$ ($\bar{x} = 19 \mu\text{m}$, $n = 35$) diam., holoblastic, olive-green to dark brown, spherical or subspherical, unicellular, smooth and thick-walled, guttulate, truncate at the base.

Culture characteristics: Conidia germinating on PDA within 24 h. Germ tubes produced from both ends. Colonies on PDA slow growing, reaching 7–10 mm diameter after two weeks at 25°C in natural light, circular, with dark grayish green aerial mycelium on the surface, black in reverse with entire margin.

Material examined: THAILAND, Trat Province, Amphoe Ko Chang, $12^\circ08'\text{N}$, $102^\circ38'\text{E}$, on decaying wood submerged in a freshwater stream, 27 April 2017, Yong-Zhong Lu, YJT-30-2 (MFLU 18-1129, **holotype**; HKAS 102140, **isotype**), ex-type living culture (MFLUCC 17-2396).

GenBank numbers: ITS: MH606234, LSU: MH606223, RPB2: MH626449, SSU: MH606221.

Notes: Phylogenetic analyses indicate that *Acrogenospora thailandica* forms a basal branch in the genus together with its sister taxon *Acrogenospora* sp. (JX-43) with strong support. Yang et al. (2016c) reported *Acrogenospora* sp. (JX-43) with LSU, SSU and ITS sequence data and only mentioned that *Acrogenospora* sp. (JX-43) is morphologically similar to *A. sphaerocephala*. We therefore identify *Acrogenospora* sp. (JX-43) as *A. thailandica* based on the phylogenetic result (Fig. 52). *Acrogenospora thailandica* resembles *A. sphaerocephala* in having relatively long conidiophores, monoblastic, intercalary conidiogenous

cells and globose conidia of similar size, but *A. thailandica* has much longer conidiophores ($850\text{--}950 \mu\text{m}$ long) than those of *A. sphaerocephala* ($155\text{--}360 \mu\text{m}$ long).

Dothideomycetes orders *incertae sedis*

Asterinales M.E. Barr ex D. Hawksw. & O.E. Erikss.

Notes: The order Asterinales is poorly understood due to minimal sequence data and its taxonomic placement is mainly based on morphology. There are different interpretations of this order. Hongsanan et al. (2014) included only a single family Asteraceae in Asterinales, while Guatimosim et al. (2015) added Parmulariaceae to the order. The phylogenetic placement of Asterinales are also different in the above studies. Until now, there is no convincing evidence that can support the placement of this family and it is considered as a polyphyletic group. The enrichment of sequence data of taxa of Asterinales will make contributions towards further understanding the black mildews.

Asterinaceae Hansf.

Notes: The family Asterinaceae was established as a member of Myriangiales by Hansford (1946). Species of Asterinaceae are characterized by dark brown hyphae with hyphopodia, dark brown thyriothecia with stellate dehiscence and dark brown, 1-septate ascospores. Phylogenetic studies have provided several different interpretations of this family (Hongsanan et al. 2014; Guatimosim et al. 2015). There is presently no convincing evidence that can support the placement of this family and it is considered as a polyphyletic group. In this study, we provide two new collections with sequences data that cluster in Asterinales sensu lato.

Lembosia Lév.

Notes: *Lembosia* was established by Leveillé (1845) with descriptions of *L. dendrochili* Lév., *L. drimydis* Lév., *L. macula* Lév. and *L. tenella* Lév. The genus was placed in Lembosiaceae by Hosagoudar et al. (2001). The genus is characterized by oval, elongate thyriothecia with X-, Y-shaped, or longitudinal dehiscence and with lateral appressoria on the hyphae. Hongsanan et al. (2014) referred the genus in Asterinaceae and treated Lembosiaceae as a synonym.

Lembosia xyliae X.Y. Zeng, T.C. Wen & K.D. Hyde

Facesoffungi number: FoF00933; Figs. 53, 54

Colonies epiphyllous, circular, dense, single to confluent. *Hyphae* superficial, straight to substraight, dark brown, branching alternate to opposite at acute to wide angles, reticulate. *Hyphopodia* subglobose, 1-celled, alternate, lateral, antrorse. **Sexual morph** *Thyriothecia* dense, elongate, with stellate dehiscence, $350\text{--}500 \times 200\text{--}300 \mu\text{m}$ ($\bar{x} = 400 \times 250 \mu\text{m}$, $n = 20$). *Pseudoparaphyses* filiform,

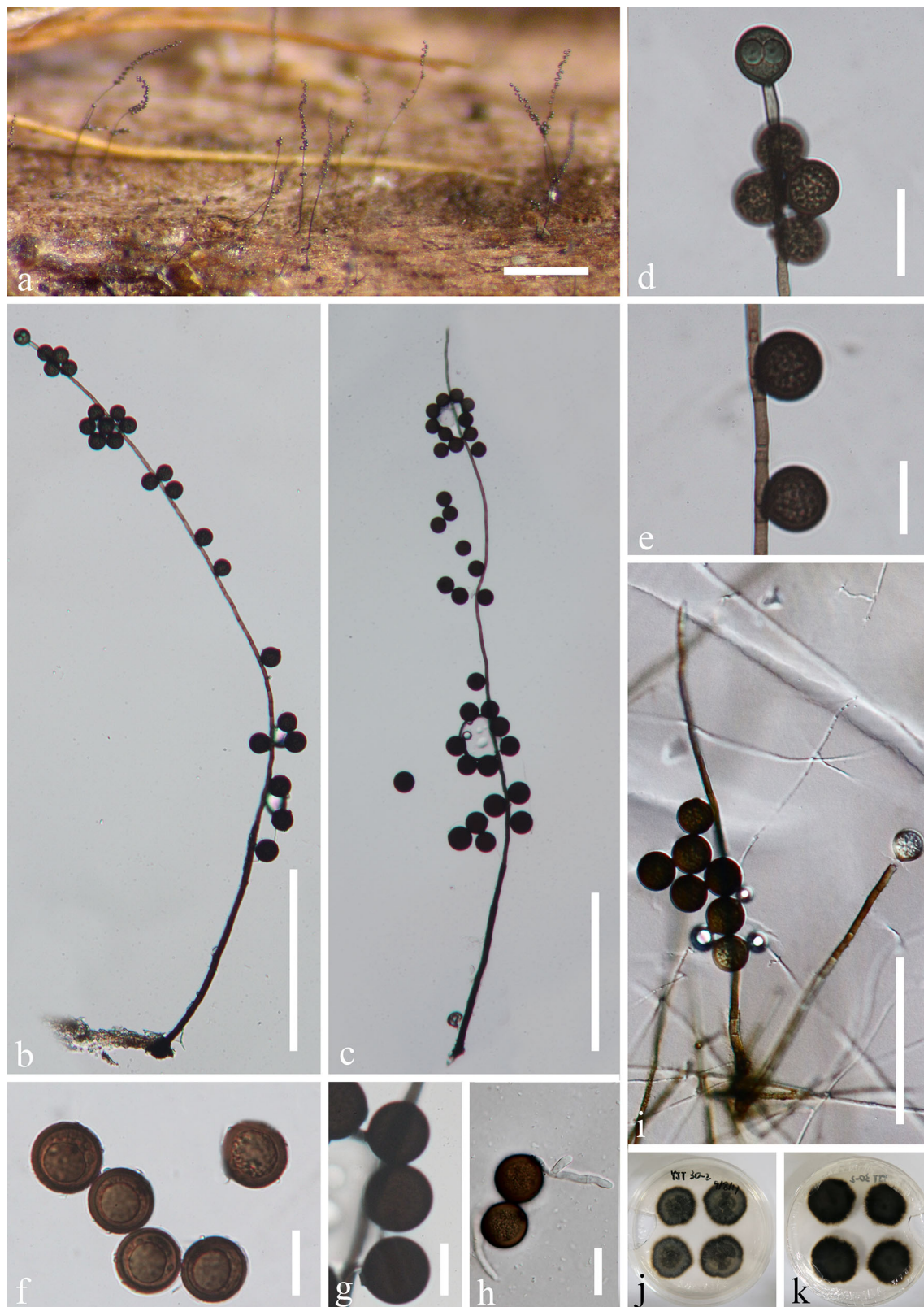


Fig. 51 *Acrogenospora thailandica* (MFLU 18-1129, **holotype**). **a** Colony on substrate. **b, c** Conidiophores with conidia. **d, e** Conidiogenous cells with conidia. **f, g** Conidia. **h** Germinated conidium on PDA. **i** Reproduced conidiophores and conidia from

culture. **j, k** Culture (**j** from above view, **k** from below view). Scale bars: **a** = 500 μ m, **b, c** = 200 μ m, **i** = 100 μ m, **d** = 30 μ m, **e–h** = 20 μ m

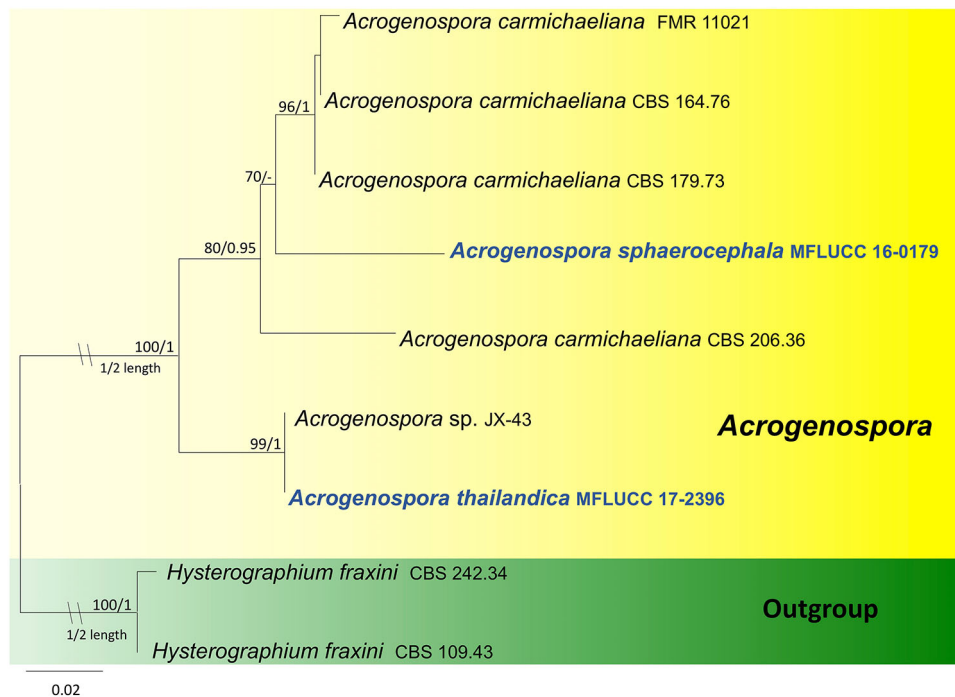


Fig. 52 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1- α and RPB2 sequence data for Acrogenosporaceae. Nine strains are included in the combined genes sequence analyses which comprise total 4150 characters. *Hystero-graphium fraxini* (CBS 242.32 and CBS 109.43) is selected as the outgroup taxa. Single gene analyses are carried out and the topology of each tree with clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best sorting RaxML tree with a final likelihood value of -8661.40414 is presented. The matrix had 269 distinct alignment patterns, with

44.96% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.259633, C = 0.231472, G = 0.273835, T = 0.235059; substitution rates AC = 27.402898, AG = 169.064131, AT = 43.635801, CG = 74.684163, CT = 684.643950, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.194764$. Bootstrap values for maximum likelihood (ML) and equal to or greater than 70% and Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are placed above the branches. The newly generated sequences are indicated in bold and blue

dense, numerous, septate, hyaline. *Asci* 8-spored, bitunicate, ellipsoid to subglobose, sessile, $40\text{--}60 \times 30\text{--}50 \mu\text{m}$ ($\bar{x} = 50 \times 40 \mu\text{m}$, $n = 30$). *Ascospores* obovoid to ellipsoid, 2-celled, slightly constricted at the septum, lower cell slightly longer and narrower, hyaline with two oil drops in each cell when immature, becoming brown at maturity, $25\text{--}32 \times 12\text{--}17 \mu\text{m}$ ($\bar{x} = 29 \times 14 \mu\text{m}$, $n = 30$). **Asexual morph** Undetermined

Material examined: THAILAND, Chiang Rai Province, Doi Mae Salong, on leaves of *Shorea roxburghii* (Dipterocarpaceae), 22 June 2015, XY Zeng (MFLU 16-0068); THAILAND, Amphoe Ko Chang, Yuttha Navi Ko Chang Memorial, on leaves of *Shorea roxburghii* (Dipterocarpaceae), 27 April 2017, XY Zeng (MFLU 17-1052).

GenBank numbers: ITS-LSU: MK660012 (MFLU 17-1052); LSU: MK660011 (MFLU 16-0068).

Notes: This species was introduced by Ariyawansa et al. (2015) with only a single LSU sequence data. The holotype was found on leaves of *Xylia* sp., but it seems incorrectly identified. In this study, we sequenced both the host and the fungal species by following Zeng et al. (2018). Results indicate that the species is associated with the host *Shorea*

roxburghii, which is very similar to *Xylia* species, and two new gene sequences (ITS and SSU) are generated. *Lembosia shoreae* (R.W. Ryan) B. Song & Hosag., which synonymized from *Morenoella shoreae*, is the only species reported from *Shorea*, but the original description is unavailable. Therefore, we would like to report a new host record and update sequence data for this species.

Morenoina Theiss.

Notes: A recent description of *Morenoina* was mentioned in Tibpromma et al. (2017) where the genus was placed in *Asterinales* genera *incertae sedis*.

Morenoina palmicola J. Fröhl., K.D. Hyde & Joanne E. Taylor

Facesoffungi number: FoF04833; Fig. 55

Isotype: MFLU 15-0030

Saprobic on petiole of *Salacca* sp. **Sexual morph** *Thyriothecia* 155–895 (up to 2400) μm long, 80–190 μm wide ($\bar{x} = 455 \times 135 \mu\text{m}$, $n = 30$), occurring on host surfaces, solitary, aggregated, or gregarious, easily removed from the host surface, superficial, ellipsoid, oblong, curved, X- or Y-shaped, flat, with longitudinal, slit-like opening,

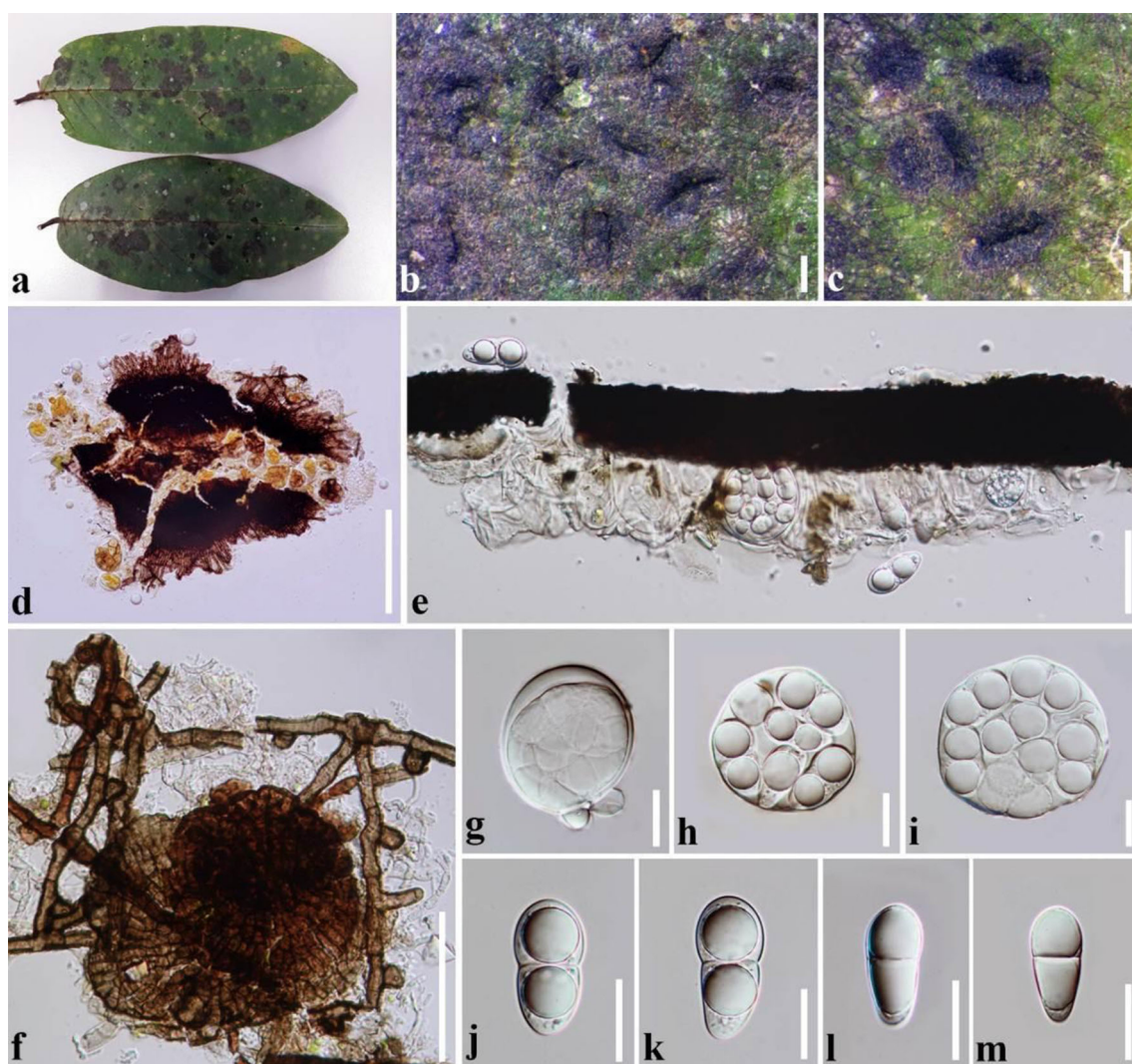


Fig. 53 *Lembosia xyliæ* (MFLU 16-0068, new host record). **a** Host leaves. **b**, **c** Thyriothecia on leaf surface. **d** Squash mount of thyriothecium. **e** Cross section of thyriothecium. **f** Hyphae with

hyphopodia. **g–i** Young asci. **j–m** Young ascospores. Scale bars: **b–d** = 200 μ m, **e**, **f** = 50 μ m, **g–m** = 20 μ m

linear fissure, which are branched at the margin, from the centre to the outer rim, free hyphae and appressoria at the margin. *Upper wall* comprises linear cells, with irregular, filiiform hyphae, radiating from the centre to the outer rim. *Asci* 19–26 \times 10–12 μ m (\bar{x} = 24 \times 11 μ m, n = 10), 8-spored, bitunicate, globose to subglobose or clavate, or saccate to globose, apedicellate, with a distinct, thickened apical region. *Ascospores* 9–14 \times 4–7 μ m (\bar{x} = 12 \times 6 μ m, n = 20), oblong or fusiform, wider at the apex, with slightly acute ends, 1-septate, with two large guttules in each cell, hyaline, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospore germinating on MEA within 24 h and germ tube produced from both end cells. Colonies on MEA reaching 3–4 cm diam., after two

weeks, grey to olivaceous, dense, with a fairly fluffy surface, hyphae, septate, branched, and smooth-walled.

Material examined: THAILAND, Krabi Province, on dead petiole of *Salacca* sp. (Arecaceae), 8 December 2014, Sirinapa Konta, KBR05 (MFLU 15-0030, **isotype**), ex-type living culture (MFLUCC 15-0284).

GenBank numbers: ITS: MK120273, LSU: MK120272, SSU: MK120299.

Notes: *Morenoina* has long taxonomic confusion concerning its familial placement. Until recently, there was no sequence data to confirm the relationships of this genus. Theissen (1913) introduced *Morenoina* with *M. antarctica* as the type species. Doidge (1942) synonymised *Morenoina* with *Lembosia* and Von Arx and Müller (1975) placed *Morenoina* in Leptopeltidaceae. Fröhlich and Hyde (2000) described and illustrated *M. palmicola* in

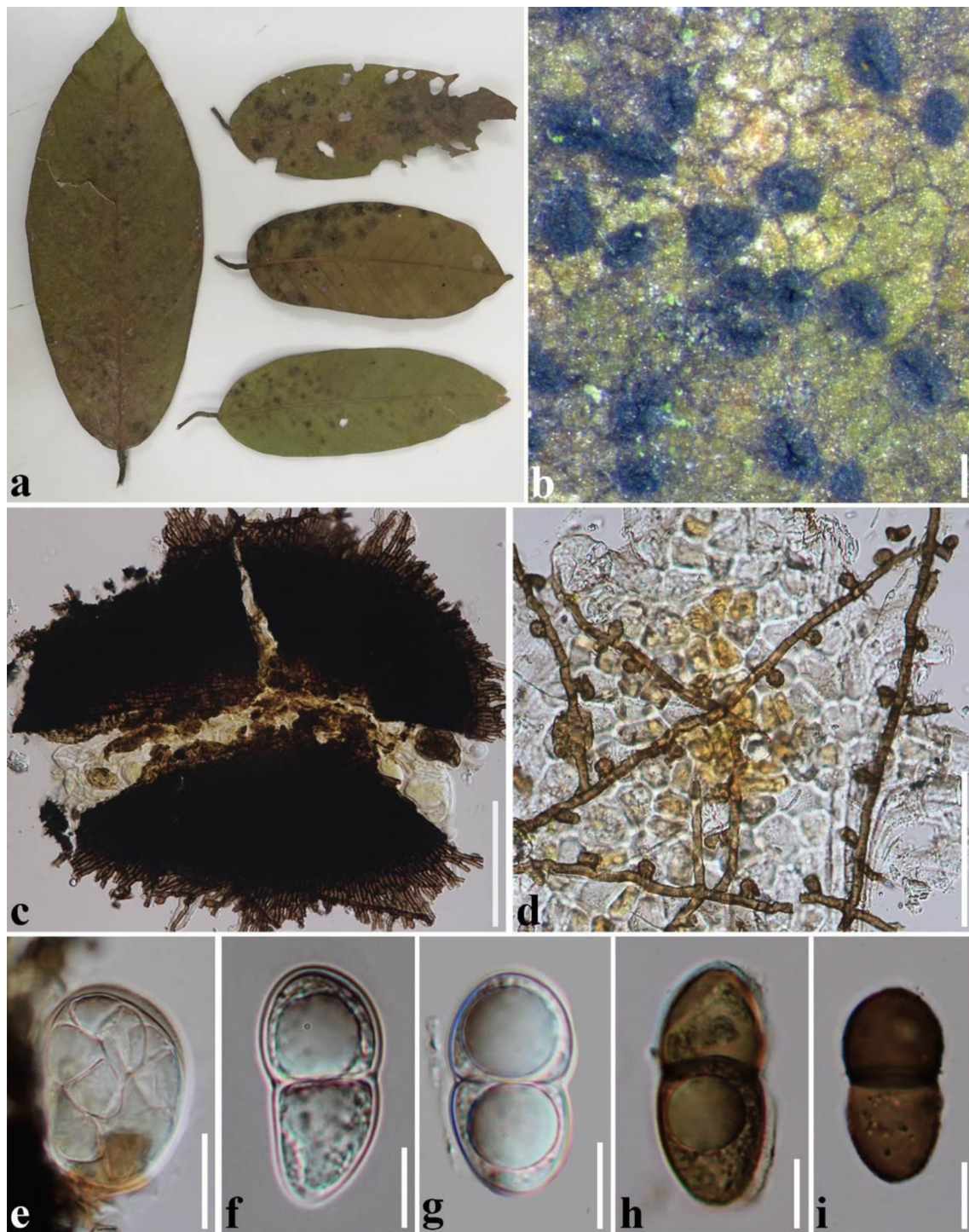


Fig. 54 *Lembosia xylicae* (MFLU 17-1052, new host record). **a** Host leaves. **b** Thyriothecia on leaf surface. **c** Squash mount of thyriothecium. **d** Hyphae with hyphopodia. **e** Young ascus. **f–i** Ascospores

from young to mature state. Scale bars: **b, c** = 100 μ m, **d** = 50 μ m, **e** = 20 μ m, **f–i** = 10 μ m

Asterinaceae. Lumbsch and Huhndorf (2010) also suggested that its placement should be in Asterinaceae. Hongsan et al. (2014) transferred *Morenoina* to Aulographaceae based on morphological characters. Tibpromma et al. (2017) introduced a new species *M.*

calamicola and showed its unstable phylogenetic placement. There are 26 epithets of *Morenoina* listed in Index Fungorum (2019). We collected a fresh specimen which is similar to *M. palmicola* J. Fröhl. et al. but from a dead petiole of *Salacca* (Arecaceae) collected in Krabi,

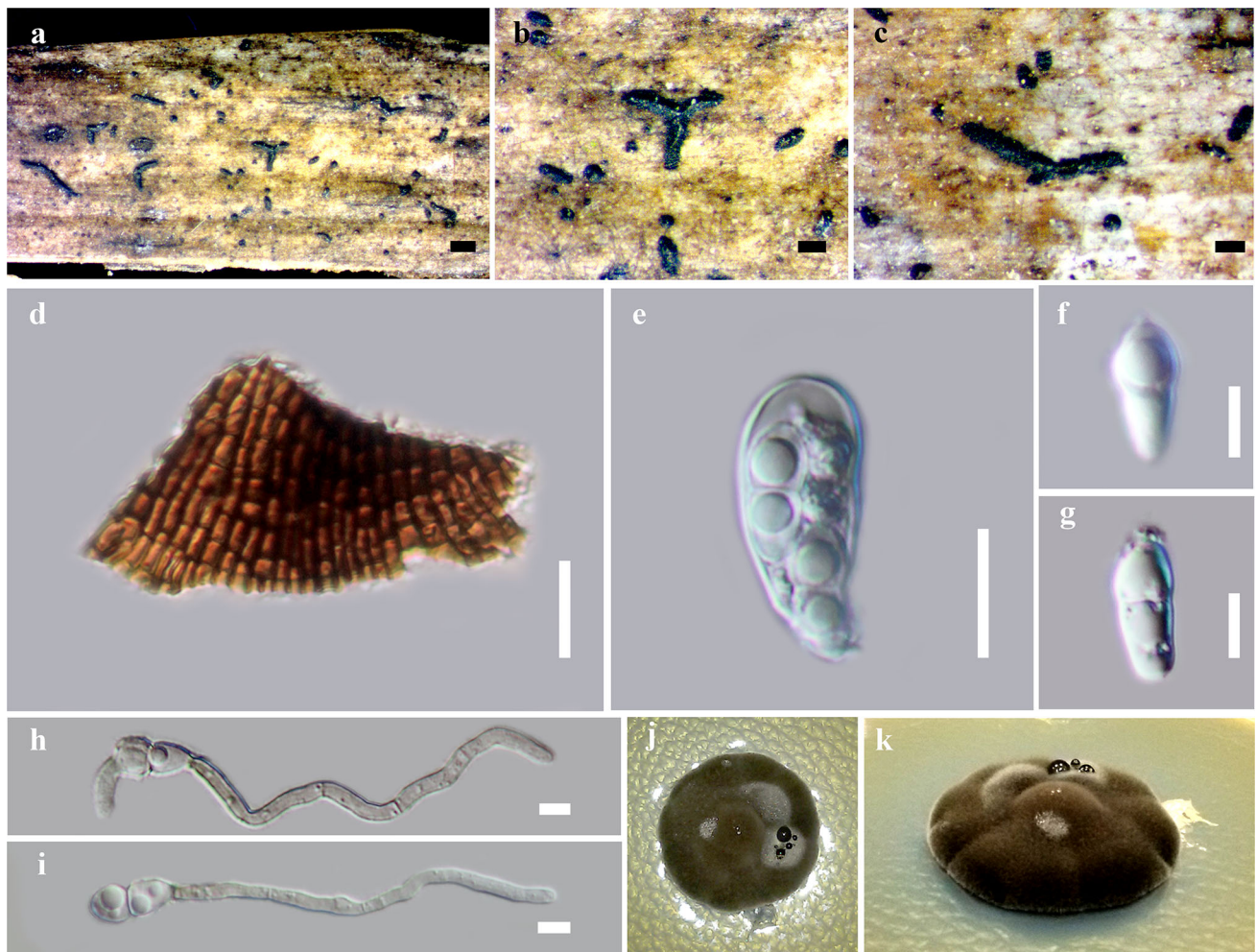


Fig. 55 *Morenoina palmicola* (MFLU 15-0013, new host record). **a** Appearance of thyrothecia on host substrate. **b, c** Close up of thyrothecia. **d** Cell walls of thyrothecium with radial arrangement.

e Asci. **f, g** Ascospores. **h, i** Germinated ascospores. **j, k** Culture on MEA. Scale bars: **a** = 500 μ m, **b, c** = 200 μ m, **d, e** = 10 μ m, **f–i** = 5 μ m

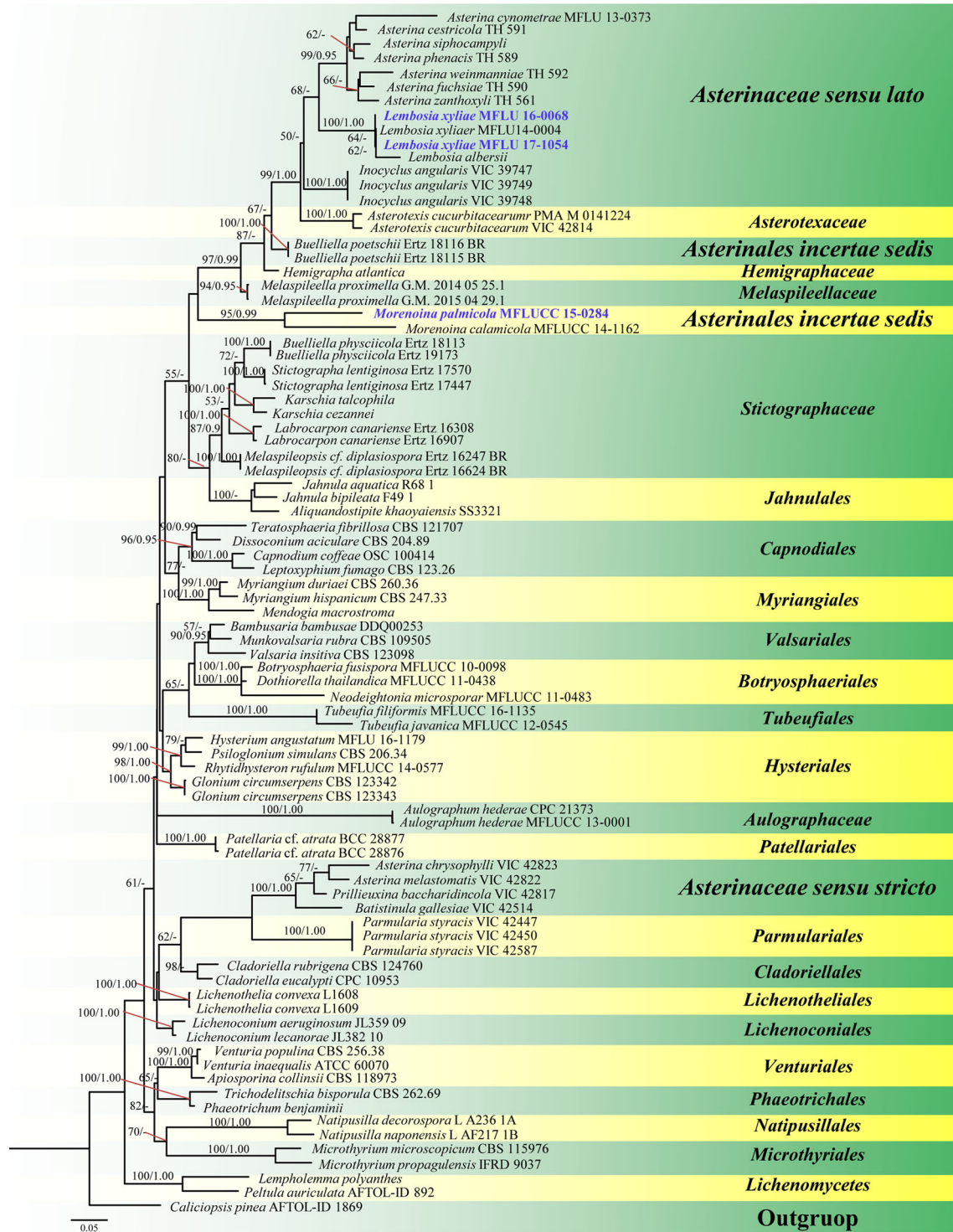
Thailand. The holotype was found on *Calamus* (Arecaceae) in Australia (Fröhlich and Hyde 2000). Since they have similar features it is wise to introduce our novel isolate as a new host record of *Morenoina palmicola* and this is the second species which has DNA based sequence data for phylogenetic analyses. In our analyses of combined LSU, and SSU sequence data, *Morenoina palmicola* and *M. calamicola* did not group in Asterinaceae sensu stricto. Both species have a close phylogenetic affiliation to Melaspileellaceae and Stictographaceae without statistical support (Fig. 56). Limited taxon sampling in the phylogenetic analyses may have resulted in inadequate resolution of this genus. Wider taxon sampling and accurate taxonomic information based on morphological examination of specimens, coupled with phylogenetic data are needed, to better integrate *Morenoina* into an appropriate taxonomic system.

Botryosphaeriales C.L. Schoch

Notes: Botryosphaeriales are considered as an important group in Dothidiomycetes due to the ecological and economic significance (Mehl et al. 2014). Many are classified as plant pathogens, known to cause many diseases on wide range of important plants. Some cause opportunistic infections in humans (de Hoog et al. 2000), and most are endophytes (Slippers & Wingfield 2007) and saprobes in plants. Based on morphological and molecular phylogenetic sequence data, Botryosphaeriales comprise six families, Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Phyllostictaceae, Planistromellaceae and Saccharataceae (Dissanayake et al. 2016, 2017a; Phillips et al. 2019).

Botryosphaeriaceae Theiss. & P. Syd.

Notes: Botryosphaeriaceae was introduced as a family in Botryosphaeriales by Schoch et al. (2006) and it represents the predominant family in the order in comprising 23



◀**Fig. 56** Phylogram generated from maximum likelihood analysis based on combined LSU, and SSU sequence data. Related sequences are taken from Dai et al. (2018). Eighty-five strains are included in the combined analyses which comprise a total of 3041 characters (1973 characters for LSU and 1068 characters for SSU) after alignment. *Caliciopsis pinea* (AFTOL-ID 1869) is used as the outgroup taxon. Single gene analyses were carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -27484.335626 is presented. The matrix had 1767 distinct alignment patterns, with 52.88% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.252599, C = 0.225029, G = 0.296253, T = 0.226118; substitution rates AC = 0.842370, AG = 2.253531, AT = 0.847156, CG = 1.108746, CT = 5.466539, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.400506$. Bootstrap values for maximum likelihood (ML) equal to or greater than 50 and Bayesian posterior probabilities (BYPP) equal to or greater than 0.9 are placed above the branches respectively. The newly generated sequences are indicated in bold and blue

genera and 187 species (Dissanayake et al. 2016). Species of Botryosphaeriaceae have a cosmopolitan distribution on a wide range of plant hosts, as endophytes, saprobes and plant pathogens.

***Dothiorella* Sacc., Michelia 2(6): 5 (1880)**

Notes: *Dothiorella* species are characterized by conidia that become pigmented and 1-septate, while they are still attached to the conidiogenous cells (Phillips et al. 2013). Presently, 30 species are accepted in the genus (Dissanayake et al. 2016). Wide host ranges and morphological plasticity within the genus have made it impossible to identify species based only on morphology. Phillips et al. (2008) have introduced the genus *Spencermartinsia* to accommodate the *Dothiorella*-like species but Yang et al. (2016b) have synonymized *Spencermartinsia* species into genus *Dothiorella* because they found that apiculate ascospores were not reliable to use for separating these two genera. Therefore we also have treated them as a single genus, *Dothiorella*.

Dothiorella plurivora (Abdollahz., Javadi & A.J.L. Phillips) Tao Yang & Crous, in Yang, Groenewald, Jami, Cheewangkoon, Abdollahzadeh, Lombard & Crous 2016

Facesoffungi number: FoF05785; Fig. 57

Saprobic on dead wood. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 155–260 μm diam., stromatic, superficial, unilocular, glabrous, brown to black, globose to subglobose, papillate. *Ostiole* central, short, lined with periphyses. *Wall of conidiomata* 20–45 μm membranaceous, composed of dark brown, or brown to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–9 \times 1.5–5 μm ($\bar{x} = 7.5 \times 3.5 \mu\text{m}$, $n = 30$), enteroblastic, phialidic, cylindrical to subcylindrical, hyaline, smooth-

walled, arising from the inner layers of conidioma. *Conidia* 14–22 \times 5–10 μm ($\bar{x} = 18 \times 8 \mu\text{m}$, $n = 50$), ellipsoidal to oval, hyaline when young, becoming to brown when mature, smooth-walled, guttulate, 1-septate.

Culture characteristics: Ascospores germinating on PDA (potato dextrose agar) within 2 days at 23 °C. Sporulation after 1 week, colony 2 cm diam. gray from above and reverse, with white mycelia radiating outwards, with irregular form of margin, filamentous mycelium, with rough surface.

Material examined: CHINA, Yunnan Province, Kunming, Songhuaba Lake; on dead wood, 3 September 2017; S.K. Huang (KUN HKAS 99572), living culture (KUMCC 18-0013).

GenBank numbers: ITS: MK459467, LSU: MK459468.

Notes: *Spencermartinsia plurivora* has been isolated from soil in Iran (Abdollahzadeh et al. 2014). Multi-gene analysis showed that *Spencermartinsia* to have close affinities with *Dothiorella* (Phillips et al. 2013; Slippers et al. 2013). Therefore, Yang et al. (2016b) placed *Spencermartinsia* as a synonym of *Dothiorella*. In phylogenetic analysis of *Dothiorella*, our strain clusters with the ex-type strain of *Dothiorella plurivora* (IRAN 1557C). *Dothiorella plurivora* is characterized by 7–10 \times 3–5 μm conidiogenous cells and ellipsoid to ovoid, brown, 1-septate conidia (20–25 \times 10–13 μm) (Abdollahzadeh et al. 2014). Morphological similarities reveal it is similar to our taxon.

Dothiorella rhamni Wanas., Bulgakov, E.B.G. Jones & K.D. Hyde, in Li et al., Fungal Diversity 78: 253 (2016)

Facesoffungi number: FoF01668; Fig. 58

Saprobic or weak pathogen on dead twigs of *Cercis canadensis* L. (Fabaceae). **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 310–370 μm high \times 360–500 μm diam. ($\bar{x} = 339 \times 425 \mu\text{m}$, $n = 10$), pycnidial, stromatic, mostly solitary, semi-immersed to immersed in the host, dark brown to black, apapillate. *Peridium* multi-layered 50–57 μm wide at the base, 68–83 μm wide in sides, comprising 8–10 layers, heavily pigmented, thick-walled, comprising blackish to dark brown, *textura angularis* cells. *Conidiogenous cells* 9–15 μm high \times 2–4 μm wide, holoblastic, cylindrical to subcylindrical, hyaline, the first conidium produced holoblastically and subsequent conidia enteroblastically, swollen at the base, discrete, producing a single conidium at the apex. *Conidia* 15–24 \times 7–11 μm ($\bar{x} = 20.9 \times 8.9 \mu\text{m}$, $n = 30$), initially hyaline, unicellular, becoming cinnamon to sepia and 1-septate, while still attached to conidiogenous cells; detached conidia, hyaline, sepia or dark brown, unicellular or 1-septate moderately thick-walled, wall externally smooth, roughened on the inner surface, oval to ovoid, widest in the centre, apex obtuse, base truncate or rounded.

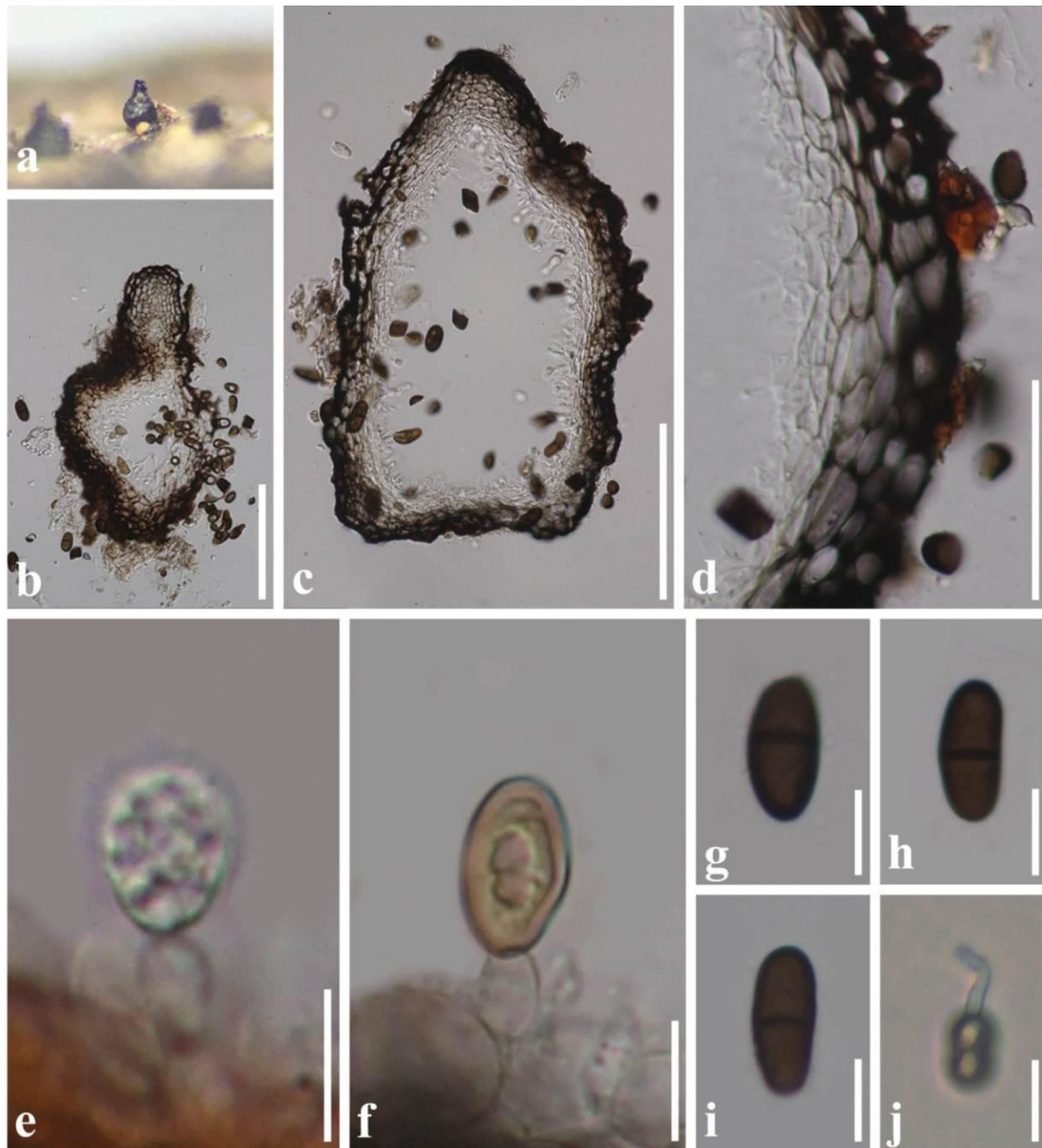


Fig. 57 *Dothiorella plurivora* (HKAS 99572, new record). **a** Appearance of conidiomata on host. **b, c** Conidiomata in vertical section. **d** Wall of conidioma. **e–f** Conidiogenous cells with

developing conidia. **g–i** Conidia. **j** Germinated conidia. Scale bars: **b, c** = 100 μ m, **d** = 50 μ m, **j** = 20 μ m, **e–i** = 10 μ m

Culture characteristics: Colonies on PDA, circular, fimbriate, crenate edged, initially both surfaces white and turning to grey towards centre after 4 days, fast growing, reach 70 mm diam. in 6 days at 28 °C.

Material examined: RUSSIA, Rostov region, Shakhty City, Alexandrovsky (Central) Park (47.7058991 N, 40.2053368°E), on dead and dying twigs of *Cercis canadensis* L., 1 March 2016, Timur S. Bulgakov (MFLU 16–1545), living culture (MFLUCC 19-0001).

GenBank numbers: ITS: MK064561, TEF1- α : MK078544.

Notes: *Dothiorella rhamni* was introduced by Li et al. (2016). There are several records of this species from *Rhamnus cathartica* in Russia, *Tamarix gallica* and *Rhamnus alaternus* in Italy (Dissanayake et al. 2016; Li et al. 2016). Based on our phylogenetic analysis of combined ITS and TEF1- α sequence data of *Dothiorella* species (Fig. 61), our strain (MFLUCC 19-0001) clustered with the ex-type strain of *D. rhamni* (MFLUCC 14-0902) and the two specimens share similar morphological characters.



Fig. 58 *Dothiorella rhamni* (MFLU 16-1545, **new record**). **a** Appearance of conidiomata on host substrate. **b** Vertical section of a conidioma. **c** Peridium of conidioma. **d**, **e** Immature and mature

conidia attached to conidiogenous cells. **f**, **g** Mature conidia. **h** Culture characters on PDA. Scale bars: **b**, **c** = 50 μ m, **d** = 20 μ m, **f** = 20 μ m, **e**, **g** = 10 μ m

Dothiorella styphnolobii Brahmanage, Bulgakov & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555482; *Facesoffungi* number: FoF05095; Fig. 59

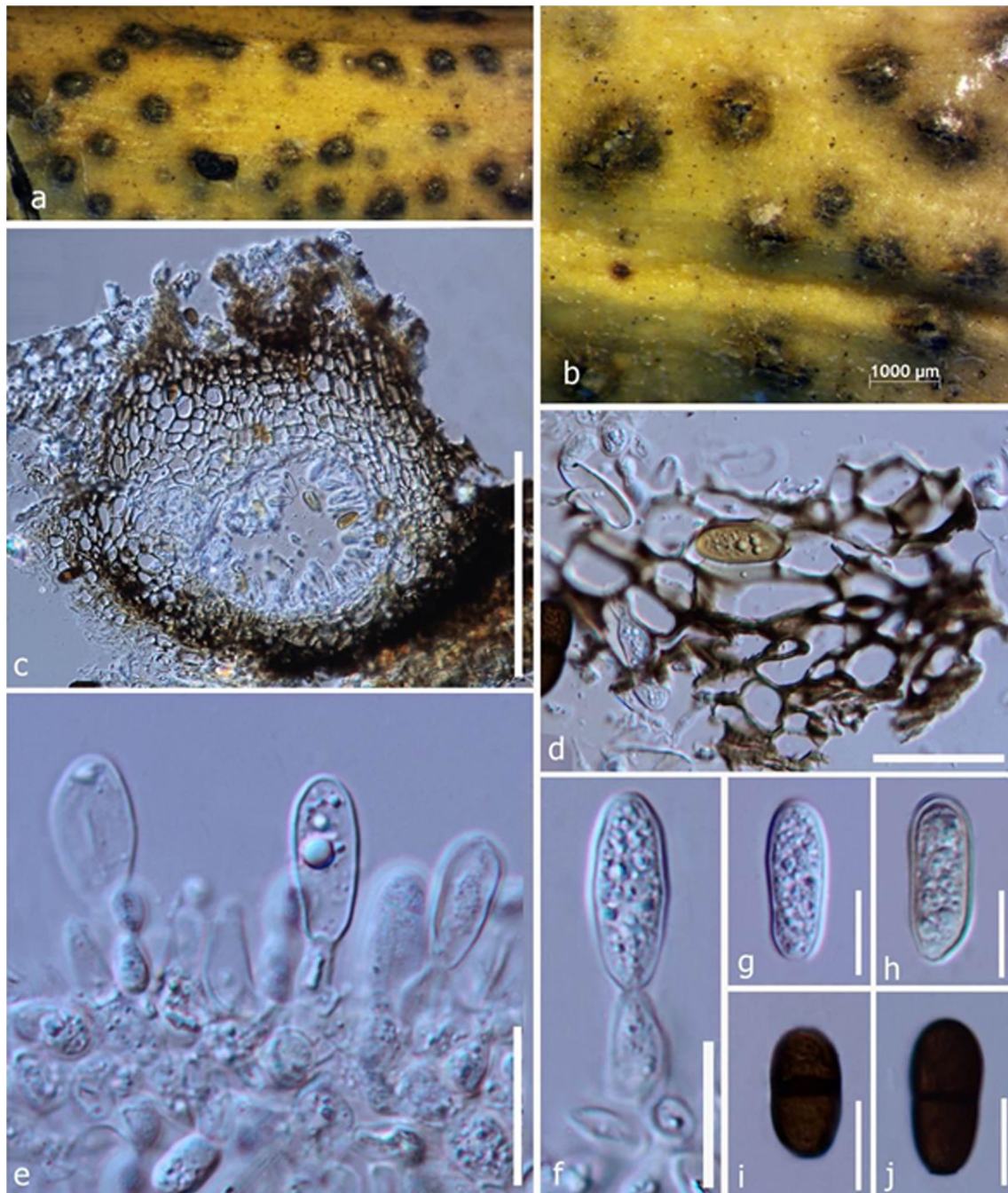


Fig. 59 *Dothiorella styphnolobii* (MFLU 17-2256, **holotype**). **a, b** Appearance of conidiomata on *Styphnolobium japonicum*. **c** Vertical section of conidioma. **d** Peridium. **e** Developing stages of conidia on

conidiogenous cells. **f** Immature conidium attach to conidiogenous cells. **g–j** Conidia. Scale bars: **b** = 1000 µm, **c** = 100 µm, **d**, **e** = 20 µm, **f–j** = 10 µm

Etymology: The specific epithet “styphnolobii” refers to the host plant genus *Styphnolobium*.

Holotype: MFLU 17-2256

Saprobic on dead twigs and branches of *Styphnolobium japonicum* (L.) Schott (Fabaceae). **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 425–500 × 160–180 µm (\bar{x} = 460 × 170 µm, n = 30), pycnidial, stromatic, mostly solitary, semi-immersed to immersed, dark brown

to black, ostiolate. *Ostiole* apapillate. *Peridium* 30–65 µm wide, comprising 6–8 layers of heavily pigmented, thick-walled, blackish to dark brown, angular cells. *Conidiogenous cells* 7–9 × 2–4 µm, holoblastic, conical, hyaline, swollen at the base, discrete, producing a single conidium at the apex, proliferating at the same level giving rise to periclinal thickenings. *Conidia* 18–22 × 8–10 µm (\bar{x} = 20 × 8 µm, n = 30), initially hyaline, unicellular,

guttulate, becoming pale brown and 1-septate, while still attached to conidiogenous cells; detached conidia, hyaline, dark brown, unicellular or 1-septate, slightly concentric, oval to ovoid, apex obtuse, base truncate or rounded.

Culture characteristics: Colonies on PDA at 25 °C reaching 5 cm in 7 days, ash at first, becoming blackish when mature and reverse ash becoming blackish when mature.

Material examined: RUSSIA, Republic of Crimea, Feodosia Municipality, Karadag Nature Reserve, the park of Karadag Biological Station, on dead and dying twigs and branches of *Styphnolobium japonicum* (L.) Schott, 21 June 2016, Timur S. Bulgakov (MFLU 17-2256, **holotype**), ex-type living culture (JZB3150013).

GenBank numbers: ITS: MH880849, TEF1- α : MK069594.

Notes: Our new collection shares similar morphological characters with *Dothiorella*, such as 1-septate conidia that are dark at an early stage of development (Phillips et al. 2005, 2013). In our phylogenetic analyses, *D. styphnolobii* showed close phylogenetic affinities to *D. juglandis* (Fig. 61). *Dothiorella styphnolobii* resembles *D. italica* in the characteristics of conidiomata and conidia, but are distinct in the shape of conidiogenous cells that are sub-cylindrical in *D. italica* and conical in *D. styphnolobii* (Dissanayake et al. 2017a). *Dothiorella styphnolobii* can also be distinguished from *D. italica* by the conidiomatal width (160–180 μ m vs 680 μ m), conidiogenous cells (7–9 \times 2–4 μ m vs 8–15 \times 3–6 μ m) and conidia (18–22 \times 8–10 μ m vs 28.7–43.2 \times 13.2–17.5 μ m) (Dissanayake et al. 2017a). However, they formed two distinct lineages in our phylogram with the maximum likelihood support of 80% ML (Fig. 61).

Dothiorella symphoricarposicola W.J. Li, J.K. Liu & K.D. Hyde, *Cyptogamie Mycologie* 35(3): 265 (2015)

Facesoffungi number: FoF04935; Fig. 60

Saprobic on dead, aerial branch of *Laburnum anagyroides* Medik. **Sexual morph** Undetermined. **Asexual morph** **Conidiomata** 0.17–0.53 mm (\bar{x} = 0.39 mm, n = 10) diam., solitary, scattered, immersed to semi-immersed, partially erumpent at maturity, pyriform, unilocular, globose, black, ostiolate. **Ostiole** 30–60 μ m diam., single, central, with a well-developed neck, thick-walled, sometimes papillate. **Peridium** multi-layered, 45 μ m wide at the base, 20–38 μ m wide in sides, outer layer composed of 4–5 layers of thick, brown cells, inner 3–4 layers of hyaline cells of *textura angularis*, cells towards inner layer become paler. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** 9–14 \times 3–5.3 μ m (\bar{x} = 11.5 \times 4.2 μ m, n = 10), phialidic, cylindrical, sometimes slightly curved, hyaline, smooth, thick-walled, formed from the inner most layer of pycnidial wall.

Conidia 14–21 \times 7–11.5 μ m (\bar{x} = 18.4 \times 9 μ m, n = 30), ovoid, straight or slightly curved, guttulate, initially aseptate, hyaline, becoming 1-septate, pale to dark brown at maturity, smooth-walled, rounded at both ends.

Culture characteristics: Colonies on PDA, circular, fimbriate, crenate edged, with both surfaces white at first, becoming grey towards centre and finally becoming black, fast growing, and reach 6 cm diam. after 4 days at 28 °C.

Material examined: ITALY, Forlì-Cesena Province, Corniolo – Santa Sofia, on dead, aerial branch of *Laburnum anagyroides* Medik. (Fabaceae), 15 May 2016, Erio Camporesi, IT-2971 (MFLU 16-1355), living culture (MFLUCC 18-0092, KUMCC 18-0414).

GenBank numbers: ITS: MH819800, TEF1- α : MH853685.

Notes: *Dothiorella symphoricarposicola* was introduced by Li et al. (2014). There are several records of this species from *Symphoricarpos* sp., *Sambucus nigra*, *Laurus nobilis* and *Laburnum alpinum* in Italy (Li et al. 2014; Dissanayake et al. 2016). Here we introduce *D. symphoricarposicola* as a new host record. Based on our phylogenetic analysis of combined ITS and TEF1- α sequence data of Botryosphaeriaceae species (Fig. 61), our strain (MFLUCC 18-0092) clusters with the ex-type strain of *D. symphoricarposicola* (MFLUCC 13-0497). The two strains share similar morphological characters. However, our strain has slightly larger conidiomata (0.17–0.53 mm) and conidiogenous cells (9–14 \times 3–5.3 μ m) compared to the conidiomata (0.2–0.3 mm) and conidiogenous cells (4–12 \times 1.5–6 μ m) of the ex-type strain (Li et al. 2014).

Lasiodiplodia Ellis & Everh.

Notes: This genus comprises 53 species (Dissanayake et al. 2017a). Both sexual and asexual morphs have been reported within the genus (Alves et al. 2008; Tennakoon et al. 2016b). For the species differentiation morphology is not a reliable character and species can be resolved using combined ITS and TEF1- α sequence data (Phillips et al. 2013; Slippers et al. 2014).

Lasiodiplodia iraniensis Abdollahz., Zare & A.J.L. Phillips [as ‘iranensis’], *Persoonia* 25: 8 (2010)

Facesoffungi number: FoF04922; Fig. 62

Saprobic on dried pods of *Cassia* sp. **Sexual morph** Undetermined. **Asexual morph** Appearing as raised spots on the host. Coelomycetous. **Conidiomata** 210–405 μ m high \times 90–336 μ m diam. (\bar{x} = 283 \times 194 μ m, n = 10), stromatic, pycnidial, immersed, aggregated, unilocular, globose to depressed globose. **Peridium** 20–55 μ m wide, composed of 3–6-layers of pale brown to brown, smooth-walled cells of *textura angularis*. **Pseudoparaphyses** 2.1–3.9 μ m wide, aseptate, hyaline. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** 10–22 μ m \times 3–6.3 μ m (\bar{x} = 13 \times 4.4 μ m, n = 20), lining the pycnidial



Fig. 60 *Dothiorella symphoricarposicola* (MFLUCC 18-0092, new host record). **a** Appearance of conidiomata on dead branch of *Laburnum anagyroides*. **b** Longitudinal section of a conidioma. **c** Longitudinal section of a conidioma wall showing cell organization.

cavity, holoblastic, subcylindrical, hyaline, smooth-walled. *Conidia* 14–28 × 8–14.5 μm (\bar{x} = 22.5 × 12, n = 25) ovoid, rarely subovoid to ellipsoid-ovoid, with a broadly

d–f Conidiogenous cells with developing conidia. **g** Conidia. **h, i** Colony on PDA (**h** from below view, **i** from above view). Scale bars: **a** = 0.5 mm, **b** = 100 μm, **c–g** = 20 μm

rounded apex and truncate base, hyaline, thick-walled, smooth-walled.

Culture characteristics: Colonies on PDA reaching 55 mm diam. after 7 days at 25 °C, circular, smooth

margin, white at first, ash to greenish black after 2 weeks, flat on the surface, with aerial mycelium, reverse black.

Material examined: THAILAND, Chiang Rai Province, on dried pods of *Cassia* sp. (Fabaceae), 22 December 2016, R.H. Perera, RHP 37 (MFLU 17-2847), living culture (MFLUCC 18-0586).

GenBank numbers: ITS: MH107831, LSU: MH107832, TEF1- α : MH107833, TUB2: MH107834.

Notes: The new collection is a typical *Lasiodiplodia* species, and it shares the similar morphology with *Lasiodiplodia iraniensis* which the dimensions of their conidiophores and conidia are almost identical (Abdollahzadeh et al. 2010). Conidia of *L. iraniensis* become 1-septate and dark brown with longitudinal striations with the time (Abdollahzadeh et al. 2010). However, we did not observe released mature conidia in our collection. The multi-gene phylogenetic analysis showed that our newly obtained strain (MFLUCC 18-0586) clustered together with *Lasiodiplodia iraniensis* (Fig. 63). Therefore, we identify our collection as *L. iraniensis* and it is reported here as a new record to Thailand and *Cassia* sp.

Jahnulales K.L. Pang, Abdel-Wahab, El-Shar., E.B.G. Jones & Sivichai

Notes: Jahnulales was erected by Pang et al. (2002) which comprises freshwater lignicolous ascomycetes (Huang et al. 2018). This order is phylogenetically related to the Dothideales, Patellariales, and Pleosporales (Campbell et al. 2007). Jahnulales species often occur on rotting or soft submerged corticated or decorticated wood (Inderbitzin et al. 2001; Suetrong et al. 2011a; Tanaka et al. 2015; Huang et al. 2018). They produce ascomata with multi-layered peridial walls, composed of large cells, stalked and/or sessile bitunicate asci, and one-septate ascospores with appendages or gelatinous sheaths (Pang et al. 2002; Suetrong et al. 2011a; Jones et al. 2015). Two families, Aliquandostipitaceae and Manglicolaceae are currently accepted within this order (Jones et al. 2015; Wijayawardene et al. 2018a).

Aliquandostipitaceae Inderb.

Notes: Aliquandostipitaceae, typified by *Aliquandostipite* Inderb. is characterized by globose to subglobose ascomata, and one-septate ascospores (Inderbitzin et al. 2001). The sexual morph genera, *Aliquandostipite*, *Jahnula* and *Megalohypha* (Kirschstein 1936; Inderbitzin et al. 2001; Ferrer et al. 2007), and asexual morph genera, *Brachiosphaera*, *Speiropsis* and *Xylomyces* are currently accommodated within this family (Tubaki 1958; Descals et al. 1976; Goos et al. 1977; Campbell et al. 2007; Suetrong et al. 2011a; Wijayawardene et al. 2018a).

Jahnula Kirschst.

Notes: *Jahnula* was introduced by Kirschstein (1936) and typified by *Jahnula aquatica* (Kirschst.) Kirschst. *Jahnula* species have been reported from wood or decorticated wood in freshwater habitats (Hawksworth 1984; Hyde 1993; Hyde and Goh 1998; Ho et al. 2002; Suetrong et al. 2011a; Fournier et al. 2015; Huang et al. 2018). The genus is polyphyletic, however, *Jahnula* sensu stricto accommodates *J. aquatica*, *J. granulosa*, and *J. rostrata* (Suetrong et al. 2011a). We introduce an additional taxon to this genus from decaying wood submerged in a river in Australia.

Jahnula queenslandica Dayarathne, Fryar & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555384; **Facesoffungi number:** FoF04945; Fig. 64

Etymology: The name queenslandica refers to the geographic location where the specimen was collected.

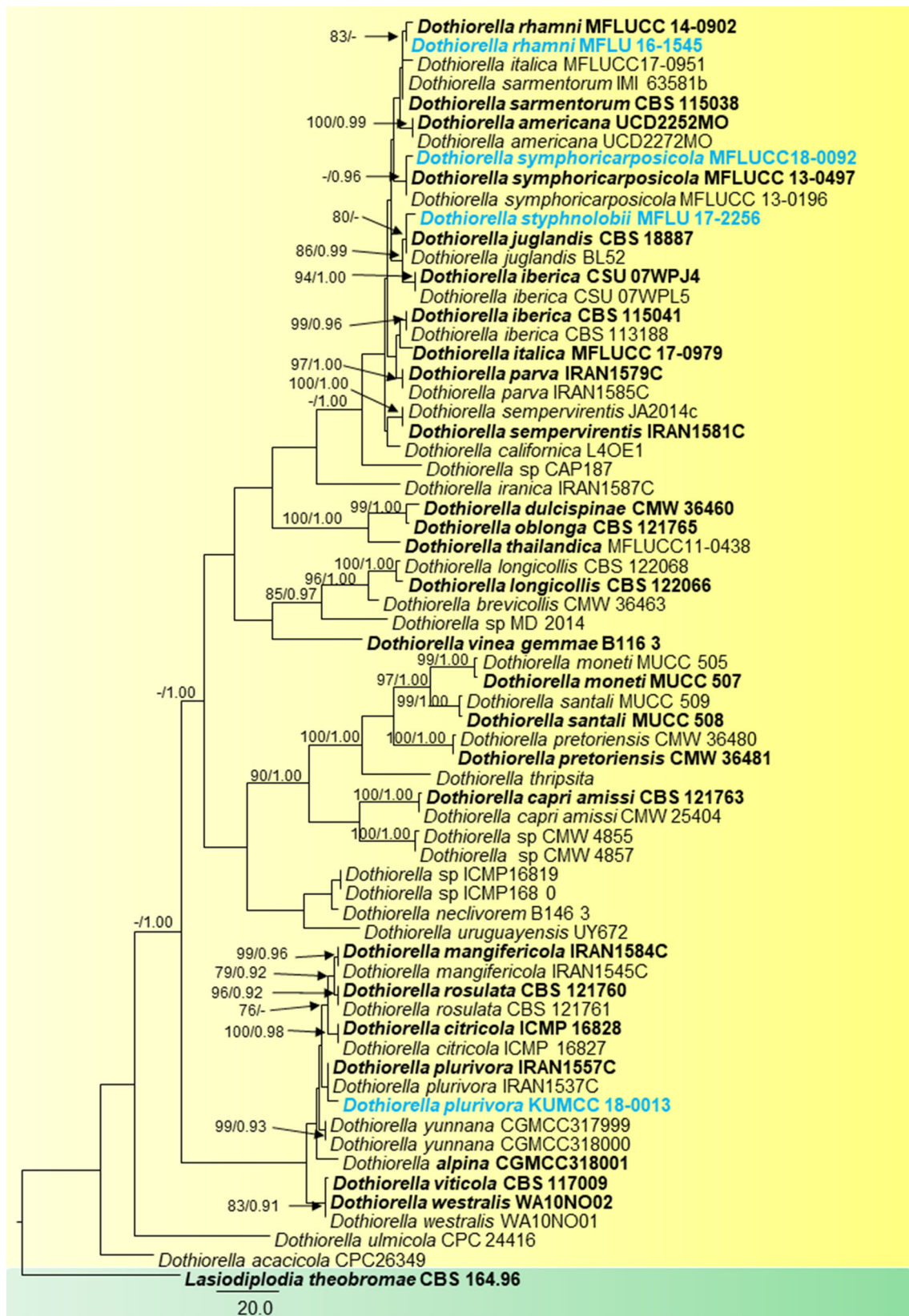
Holotype: AQ522780

Saprobic on dead wood. **Sexual morph** *Ascomata* 280–330 × 200–300 μm (\bar{x} = 350 × 250 μm , n = 5), perithecial, solitary, superficial to semi-immersed, unilocular, obpyriform to subglobose, dark brown to black, papillate, ostiolate. *Ostiole* central, composed of hyaline periphyses. *Peridium* 28–40 μm thick, membranous, composed of brown cells of *textura angularis*. *Hamathecium* comprising 1.5–2 μm wide, septate, branched, filiform pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 140–200 × 12–22 μm (\bar{x} = 180 × 16 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate, rounded at apex, with a distinct ocular chamber. *Ascospores* 20–34 × 8–16 μm (\bar{x} = 25 × 12 μm , n = 30), uniseriate, initially light brown, becoming dark brown at maturity, oval to broadly ellipsoid, aseptate, with a mammiform apex, slightly curved, smooth-walled, often with two large guttules, apiosporous, rounded at lower end, with hyaline cell at lower end, up to 2–3 μm , lacking a sheath. **Asexual morph** undetermined.

Material examined: AUSTRALIA, Queensland, Daintree National Park, fast running stream with clear water and a rocky base, S 16.170779, E 145.405268, on decaying wood submerged in a river, 14 April 2015, Sally Fryar and Toby Cawson, CT110 (AQ522780, **holotype**; MFLU 18-1692, **isotype**).

GenBank numbers: LSU: MH878780, ITS: MH878782.

Notes: *Jahnula queenslandica* has obpyriform to subglobose ascomata, septate, branched, filiform pseudoparaphyses, cylindrical asci and oval to broadly ellipsoid ascospores that are characteristic of *Jahnula* (Raja et al. 2008; Sivichai and Boonyuen 2010; Suetrong et al. 2011a;



◀**Fig. 61** Phylogram generated from maximum parsimony analysis based on combined ITS and TEF1- α sequence data for *Dothiorella* species in family Botryosphaeriaceae. Related sequences are taken from Wanasinghe et al. (2018a) and GenBank. Sixty-six strains are included in the combined analyses which comprise 828 characters after alignment. *Lasiodiplodia theobromae* (CBS 164.96) (Botryosphaeriaceae and Botryosphaeriales) is used as the outgroup taxon. Values for maximum likelihood equal to or greater than 60 and Bayesian posterior probabilities equal or greater than 0.90 are placed. Maximum parsimony analysis of 85 parsimony informative characters resulted in a most parsimonious tree (CI = 0.545, RI = 0.824, RC = 0.449, HI = 0.455). The ex-type strains are in bold and black. The newly generated sequences are in bold and blue

Fournier et al. 2015; Huang et al. 2018). However, *J. queenslandica* is unique from other *Jahnula* species by having apiospores. According to our phylogram (Fig. 65) *J. queenslandica* (MFLU 18-1692) is closely related to *J. sunyatsenii* (UBC F13876) (Inderb.) K.L. Pang, E.B.G. Jones & Sivichai with high statistical support (91% ML/0.99 BYPP). *Jahnula queenslandica* can be distinguish from *J. sunyatsenii* by its aseptate, dark brown apiospores, while ascospores of *J. sunyatsenii* are 1-septate, light brown with two bipolar, helmet-shaped appendages, tending to unite over the respective ends (Raja and Shearer 2006).

Tubeufiales Boonmee & K.D. Hyde

Notes: The order Tubeufiales was introduced by Boonmee et al. (2014) for a single family, Tubeufiaceae. Later, Suetrong et al. (2014) introduced the second family Wiesneriomycetaceae into Tubeufiales. Recently, based on divergence time estimates, Liu et al. (2017) synonymized the orders Bezerromycetales and Wiesneriomycetales under Tubeufiales.

Tubeufiaceae M.E. Barr

Notes: Barr (1979) introduced the family Tubeufiaceae typified by *Tubeufia*. According to recent study by Lu et al. (2018b) this family comprises 38 genera. The sexual morphs of Tubeufiaceae are characterized by having superficial ascomata, pseudoparaphysate hamathecium, bitunicate asci, and multi-septate, hyaline to pale brown cylindrical ascospores (Barr 1980; Lu et al. 2017; Liu et al. 2018; Brahmanage et al. 2017; Phookamsak et al. 2018). Hyphomycetous asexual morphs of Tubeufiaceae are often helicosporous, while some are chlamydosporous and phragmosporous (Boonmee et al. 2011, 2014; Brahmanage et al. 2017; Doilom et al. 2017; Luo et al. 2017; Liu et al. 2018; Lu 2018).

Kamalomyces R.K. Verma, N. Sharma & Soni

Notes: The genus *Kamalomyces* introduced by Verma et al. (2008), is typified by *K. indicus* R.K. Verma, N. Sharma & Soni. *Kamalomyces* has a unique set of

characters, such as ascomata on a subiculum of black hyphae, with solitary, gregarious, subglobose to lemoniform ascomata with short stalks and lacking ostioles, bitunicate, broadly cylindrical to clavate asci and hyaline, vermiform, crowded, septate ascospores (Verma et al. 2008; Dubey and Neelima 2013; Boonmee et al. 2011, 2014; Phookamsak et al. 2018; Lu et al. 2018a, b). *Kamalomyces* currently comprises four species viz. *K. bambusicola* Phook., Y.Z. Lu & K.D. Hyde, *K. indicus*, *K. mahabaleshwarensis* Rashmi Dubey & Moonamb. and *K. thailandicus* Phook., Y.Z. Lu & K.D. Hyde (Verma et al. 2008; Dubey and Neelima 2013; Phookamsak et al. 2018). The phylogenetic relationships of *Kamalomyces* were reported by Phookamsak et al. (2018). We introduce a novel marine species to this genus based on combined LSU, ITS and TEF1- α sequence data.

Kamalomyces mangrovei Dayarathne & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555385; **Facesoffungi number:** FoF04946; Fig. 66

Etymology: Epithet derived from the mangrove habitat that species found.

Holotype: MFLU 18-1691

Saprobic on decaying, submerged wood in a mangrove stand. **Sexual morph** *Ascomata* 280–315 × 250–300 μ m, superficial, solitary to gregarious, embedded in a subiculum of crowded, black, septate, thick-walled hyphae, superficial, solitary, gregarious, globose to subglobose, glabrous, short-stalked, apapillate, with indistinct ostiolate. *Peridium* 30–45 μ m wide, comprising light brown cells of *textura angularis*, and inwardly small, subhyaline cells of *textura prismatica*. *Hamathecium* comprising numerous, 1.5–2 μ m wide, filiform, septate, branched, hyaline pseudoparaphyses. *Asci* 148–180 × 16–20 μ m (\bar{x} = 165 × 18 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 52–67 × 6.5–8.5 μ m (\bar{x} = 62 × 7.5 μ m, n = 30), 2–3-seriate, hyaline becoming light brown when mature, elongate cylindrical to fusiform-clavate, tapering towards the lower cells, enlarged at the 4th and 5th cell, straight or slightly curved, 8–9 septa, distoseptate.

Culture characteristics: Colonies on PDA reaching 3 cm diam. after 30 days at 25 °C, circular, smooth margin white at first, dark gray to black after 6 weeks, flat on the surface, without aerial mycelium, reverse brownish black.

Material examined: THAILAND, Ranong Province, Maung District, Mu 4 Tombol Ngao, Ranong Mangrove Research Center (GPS: 9°43' to 9°57'N; 98°29' to 98°39'E) on decaying, submerged wood of mangrove, 7 December 2016, Monika C. Dayarathne, MCD 053 (MFLU 18-1691, **holotype**), ex-type living culture (MFLUCC 17-0407, TBRC).

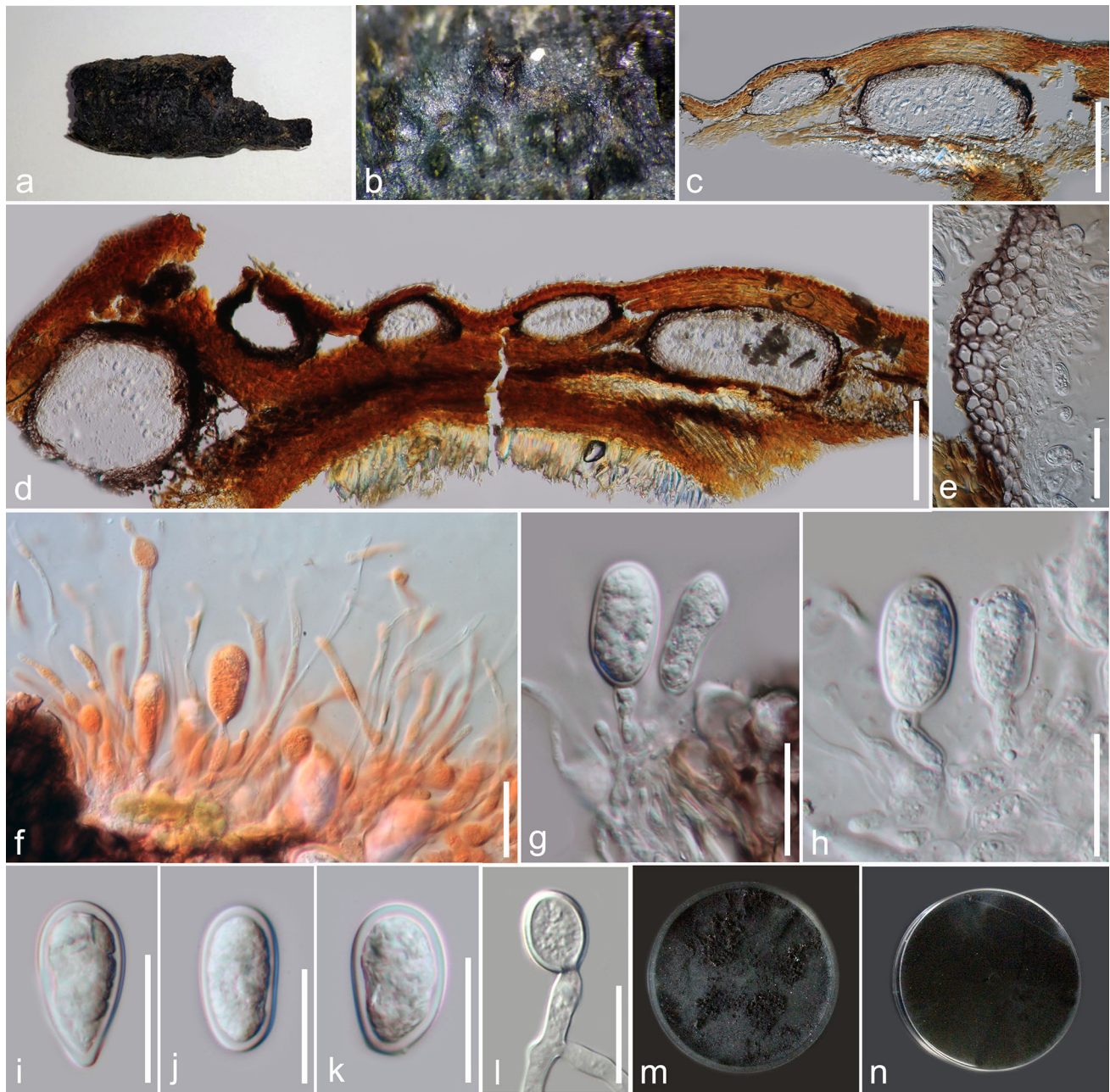


Fig. 62 *Lasiodiplodia iraniensis* (MFLU 17-2847, **new host/geographical record**). **a** Herbarium material. **b** Conidiomata on host substrate. **c, d** Sections through conidiomata. **e** Peridium. **f** Paraphyses

in Congo red. **g, h** Conidiophores with conidia. **i–k** Conidia. **l** Germinating conidium. **m, n** Colony on PDA. Scale bars: **c, d** = 200 μ m, **e** = 50 μ m, **f–i** = 20 μ m

GenBank numbers: ITS: MH878781, LSU: MH878779, SSU: MH878796, TEF1- α : MH886508.

Notes: *Kamalomycetes mangrovei* is characterized by solitary to gregarious, globose to subglobose, short-stalked ascomata, lacking ostioles embedded in a subiculum of black hyphae, bitunicate, cylindrical to clavate asci and hyaline, elongate cylindrical to fusiform-clavate, septate ascospores. *Kamalomycetes mangrovei* is morphologically best fit *Kamalomycetes* (Verma et al. 2008; Dubey and Neelima 2013; Boonmee et al. 2011, 2014, Phookamsak

et al. 2018; Lu et al. 2018b). *Kamalomycetes mangrovei* closely resembles *K. bambusicola* Y.Z. Lu & K.D. Hyde and *K. thailandicus* Phook., Y.Z. Lu & K.D. Hyde due to its ascomatal characters, asci and ascospore shape. However, *K. mangrovei* differs significantly from *K. bambusicola* and *K. thailandicus* by having fewer ascospore septa (8–9 vs 27–30 and 33–36 septa) and being swollen at the 4th and 5th cells. The novel species occurred on a mangrove species while *K. bambusicola* and *K. thailandicus* have been reported from bamboo. This is the first record of

Tubeufiaceae from a marine habitat (Jones et al. 2015, 2019). According to our phylogenetic analyses with concatenated LSU, ITS and TEF1- α sequence data, *K. mangrovei* clustered within the genus *Kamalomycetes* with high statistical support (84% ML/75% MP/0.99 BYPP, Fig. 67).

Eurotiomycetes O.E. Erikss. & Winka

Chaetothyriomycetidae Doweld

Chaetothyriales M.E. Barr

Notes: Barr (1987) established the order Chaetothyriales based on the presence of periphysoids in the ascomata. However, Loculoascomycetes was suggested to be paraphyletic and Chaetothyriales had closer affinity with Eurotiales based on SSU sequence data (Haase et al. 1995; Spatafora et al. 1995; Berbee 1996; Silva-Hanlin and Hanlin 1999). Doweld (2001) introduced the subclass Chaetothyriomycetidae for Chaetothyriales. Chaetothyriales comprises ecologically diverse species including opportunistic pathogens on humans (Réblová et al. 2013; de Hoog 2014; Hyde et al. 2018a, b). Five families are currently recognized in Chaetothyriales, viz. Chaetothyriaceae, Cyphellophoraceae, Epibryaceae, Herpotrichiellaceae, and Trichomeriaceae (Teixeira et al. 2017).

Herpotrichiellaceae Munk

Notes: The family Herpotrichiellaceae was introduced by Munk (1953), based on the type genus *Herpotrichiella* Petr., along with *Berlesiella* Sacc., *Capronia* Sacc., *Dicthyotrichiella* Munk and *Didymotrichiella* Munk. Sexual morphs in this family are characterized by ascomata with setae and ostioles, bitunicate, saccate to ovoid asci with a thickened apex and pale grey to brown ascospores (Munk 1953), while asexual morphs are diverse dematiaceous hyphomycetes (Gueidan et al. 2014; Klaubauf et al. 2014; Liu et al. 2015; Tian et al. 2016; Dong et al. 2018). However, the classification of some hyphomycetes in this family has been controversial. Some previously morphologically-based species were excluded from Herpotrichiellaceae with molecular evidence. For example, *Veronaea simplex* Papendorf was transferred to Venturiaceae (Arzanlou et al. 2007). Some genera, e.g. *Cladophialophora* and *Exophiala* require further study to confirm their natural classification (Liu et al. 2015; Hyde et al. 2016; Tian et al. 2016; Dong et al. 2018). Currently, Herpotrichiellaceae comprises 15 genera and resides in the order Chaetothyriales (Liu et al. 2015; Hyde et al. 2016; Wijayawardene et al. 2018a).

Thysanorea Arzanlou

Notes: Arzanlou et al. (2007) studied ramichloridium-like species and revealed that the genus *Periconiella* was polyphyletic. *Thysanorea* was therefore introduced to accommodate *Periconiella papuana* Aptroot as *T. papuana* (Aptroot) Arzanlou, W. Gams & Crous (Arzanlou et al.

2007). *Thysanorea* differs from *Periconiella* in branching pattern of conidiophores and prominent denticle-like conidiogenous loci (Arzanlou et al. 2007). Dong et al. (2018) introduced the second species, *T. aquatica* W. Dong, H. Zhang & K.D. Hyde from an aquatic habitat. Only two species were accepted in *Thysanorea* (Arzanlou et al. 2007; Dong et al. 2018).

Thysanorea uniseptata N.G. Liu & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555387; **Facesoffungi number:** FoF04949; Fig. 68

Etymology: Named after the fact that conidia are 1-septate.

Holotype: MFLU 18-1723

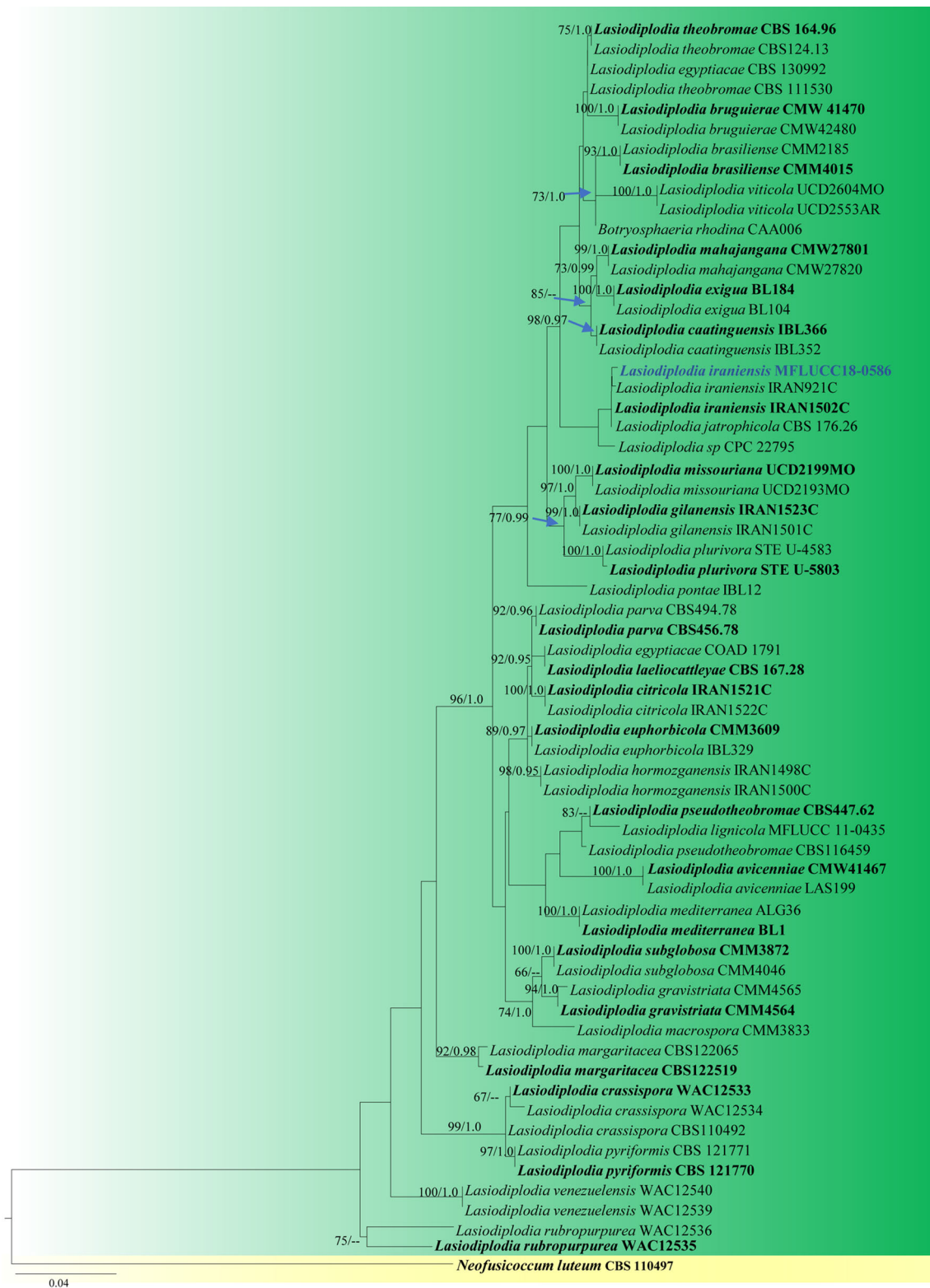
Saprobic on submerged wood. **Sexual morph** Undetermined. **Asexual morph** Colonies on natural substrate effuse, scattered, velvety, dark brown to black, with greyish white, glistening heads of conidia at apex. Mycelium partly immersed, partly superficial, composed of pale brown to brown, branched, septate, smooth hyphae. **Conidiophores** up to 310 μm long, 5.5–8 μm wide at base, 3–5 μm wide in upper half, macronematous, mononematous, branched at apex, erect, straight or broadly curved, septate, constricted at septa near apex, not constricted at septa below, thick-walled, smooth-walled, brown below, paler towards apex. **Conidiogenous cells** 6–11.5 \times 2–4 μm (\bar{x} = 8.9 \times 3.2 μm , n = 15), polyblastic, terminal or intercalary at main stem and fertile branches, hyaline or subhyaline, urniform, conidiogenous loci obvious. **Conidia** 6.5–9 μm long, 2–3 μm wide at the septum (\bar{x} = 7.6 \times 2.5 μm , n = 30), acropleurogenous, solitary, pyriform, hyaline and aseptate when young, subhyaline, (0–)1-septate when mature, not constricted at the septa, broadly round at the apex, attenuate and narrowly truncate at the base, with darkened hilum, smooth-walled.

Culture characteristics: Conidia germinated on water agar media within 24 h. Germ tubes produced from one or both ends of conidium. Colonies growing on PDA circular, edge entire, with umbonate surface, greyish brown to brown from above, dark brown from reverse, mycelium dense, fluffy.

Material examined: THAILAND, Chiang Rai Province, Muang District, Ban Nang Lae Nai, on decaying wood submerged in a freshwater stream, 6 March 2018, N.G. Liu, CR067 (MFLU 18-1723, **holotype**), ex-type living culture (MFLUCC 18-0701).

GenBank numbers: ITS: MH883033, LSU: MH883031, SSU: MH883049.

Notes: *Thysanorea uniseptata* resembles *T. aquatica* and *T. papuana* in having obvious denticle-like conidiogenous loci and pyriform, (0–)1-septate conidia. However, conidia of *T. aquatica* have prominent guttules and are constricted at septa, features that distinguish it from *T. uniseptata*.



◀**Fig. 63** Phylogram generated from maximum parsimony analysis based on combined ITS and TEF1- α sequence data for *Lasiodiplodia* species in family Botryosphaeriaceae. Related sequences are taken from Wanasinghe et al. (2018a). Sixty-three strains are included in the combined analyses which comprise 1300 characters after alignment. *Neofusicoccum luteum* (CBS 110497) (Botryosphaeriaceae and Botryosphaeriales) is used as the outgroup taxon. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. Maximum parsimony analysis of 575 constant characters and 79 informative characters resulted in most parsimonious tree (CI = 0.551, RI = 0.769, RC = 0.423, HI = 0.449). The best RaxML tree with a final likelihood value of -4380.160038 is presented. The matrix had 317 distinct alignment patterns, with 36.03% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.215525, C = 0.287133, G = 0.258862, T = 0.238480; substitution rates AC = 0.872639, AG = 3.555191, AT = 1.330285, CG = 1.135935, CT = 5.468515, GT = 1.000000; gamma distribution shape parameter α = 0.196200. Bootstrap values for maximum parsimony (MP) and maximum likelihood (ML) equal to or greater than 65 and Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are placed below the branches respectively. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Thysanorea uniseptata differs from *T. papuana* in having hyaline or subhyaline conidiogenous cells, while the latter are golden to dark brown. Moreover, *T. uniseptata* has smaller conidiogenous cells and larger conidia than those of *T. papuana* (6–11.5 vs 5–20 μ m long and 6.5–9 vs 5–6 μ m long). Phylogenetic analysis showed that *T. uniseptata* is phylogenetically distinct from *T. aquatica* and *T. papuana* (Fig. 69).

Eurotiomycetidae Geiser & Lutzoni

Eurotiales G.W. Martin ex Benny & Kimbr.

Notes: Currently, the order Eurotiales comprise three families, Aspergillaceae Link, Thermoascaceae Apinis and Trichocomaceae E. Fisch (Houbraken and Samson 2011). Some species in the Eurotiales are able to grow in extreme environments, such as low water activity, low acidity, low levels of oxygen, or at extreme high temperatures (Houbraken and Samson 2011; Houbraken et al. 2014).

Aspergillaceae Link

Notes: The family Aspergillaceae was erected by Link (1826) and belongs to Eurotiales. The most well-known species of this family belongs to genera *Aspergillus* P. Micheli ex Haller and *Penicillium* Link (Houbraken and Samson 2011; Houbraken et al. 2014). Several species belong to Aspergillaceae have the ability to produce a diversity of secondary metabolites (or extrolites), organic acids and diverse enzymes that degrade a wide variety of complex biomolecules (Geiser et al. 2006; Pitt and Hocking 2009; Samson et al. 2010; Houbraken and Samson 2011), while others can cause disease in humans.

Penicillium Link

Notes: The genus is subdivided in two subgenera (*Aspergilloides* and *Penicillium*) and 26 sections (Houbraken and Samson 2011; Houbraken et al. 2016). Species of *Penicillium* are ubiquitous and known to cause rot in fruits and bulbs of plants, including *P. expansum* (apples and pears), *P. digitatum*, *P. italicum* and *P. ulaiense* (citrus fruits), *P. tulipae* (tulip bulbs) and *P. allii* (garlic) (Balgrie 2003; Samson and Frisvad 2004; Valdez et al. 2006). Currently, the genus contains more than 350 accepted species (Visagie et al. 2014).

Section *Fasciculata* contains species that are found on stored or manufactured foods, and have rough-walled conidiophore stipes and subglobose conidia (Houbraken et al. 2016). Species in this section are able to grow at low water activities, and low temperature (with the exception of species in series *Verrucosa*) (Houbraken et al. 2016). Section *Fasciculata* is subdivided in four series: *Camemberti*, *Corymbifera*, *Viridicata*, *Verrucosa*. Six species are currently accepted in series *Corymbifera* (*P. alboconemium*, *P. allii*, *P. hirsutum*, *P. hordei*, *P. radicola*, *P. tulipae*) and most of those species (except *P. hordei*) have a strong association with flower bulbs and other plant roots (Houbraken et al. 2016).

During an investigation of the fungal diversity on roots of deodeok (*Codonopsis lanceolata*), rotten apple (*Malus pumila*), freshwater, and soil in Korea, five new species of *Penicillium* were isolated and these are described here based on phylogenetic analyses (Figs. 70, 71, 72, 73) and morphological characteristics (Figs. 74, 75, 76, 77, 78).

Penicillium circulare Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen *sp. nov.*

Index Fungorum number: IF555413; **Facesoffungi number:** FoF05793; Fig. 74

Etymology: *circulare*, referring to the formation of two concentric rings on YES media.

Holotype: CNUFC-GEU220-1

Macromorphology: CYA, 25 °C: Sporulation on CYA moderate; green in sporulating area with white mycelium in centre, yellow at the margins; radial wrinkles; exudate absent; soluble pigment absent; reverse orange to dark orange brown, wrinkled towards the edges; YES, 25 °C: Weak sporulation on YES; exudate absent; soluble pigments absent; reverse buff, two concentric rings. MEA, 25 °C: Sporulation on MEA strong; mycelium white turns pale yellow at the margins; exudate absent; soluble pigments absent; reverse pale brown or orange brown towards the centre.

Micromorphology: *Sclerotia* absent. *Conidiophores* monoverticillate, stipe smooth, 2.5–3.5 μ m wide, unbranched or with one or two branches 25–58 μ m long.

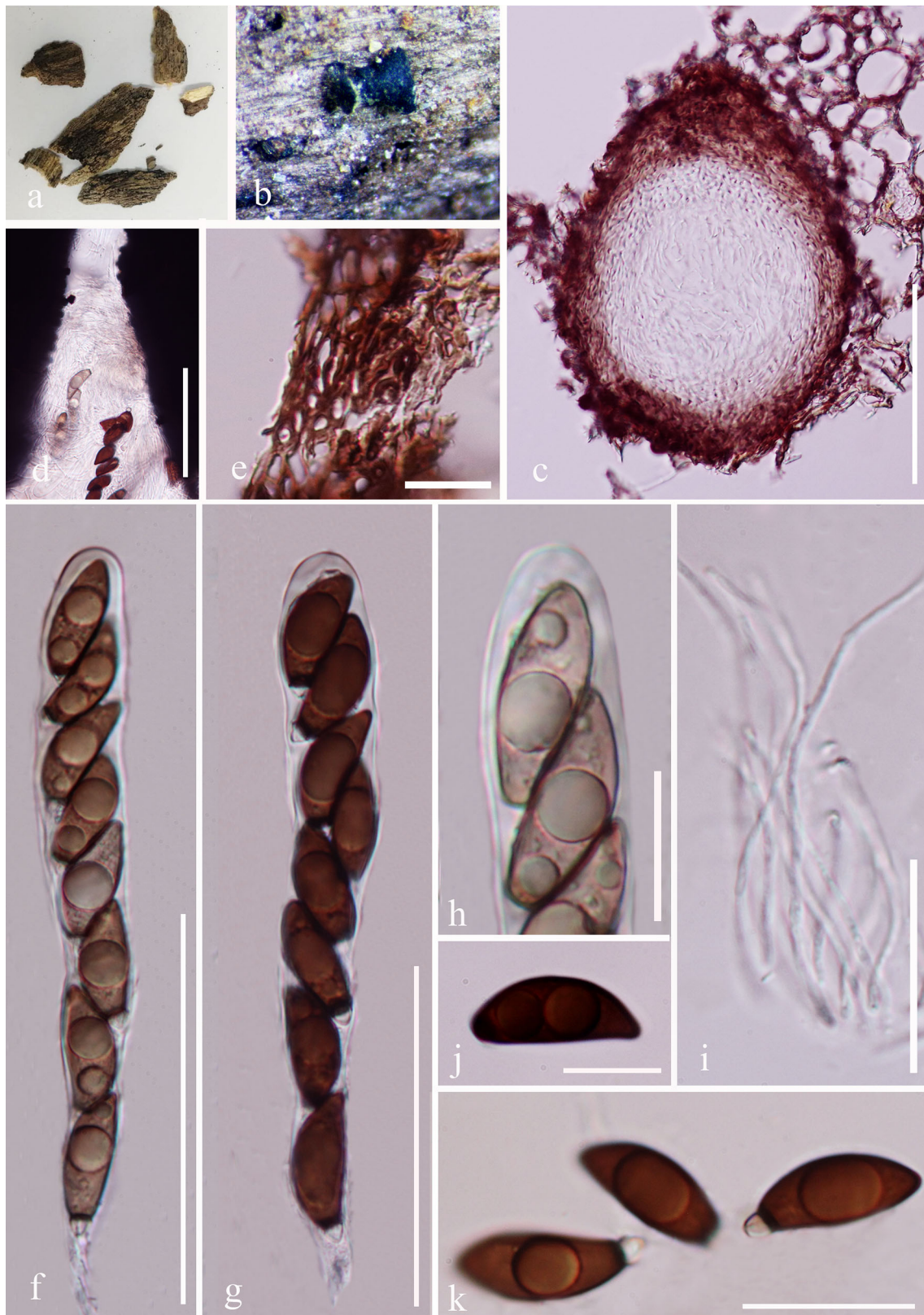


Fig. 64 *Jahnula queenslandica* (MFLU 18-1692, holotype). **a** Host. **b** Appearance of ascomata on host. **c** Section of ascoma. **d**Periphysate ostiolar region. **e** Peridium. **f, g** Asci. **h** Apex of an ascus.

i Pseudoparaphyses. **j, k** Apiosporous ascospores. Scale bars: **c, f, g, i** = 100 μ m, **d** = 50 μ m, **e** = 20 μ m, **h, j, k** = 10 μ m

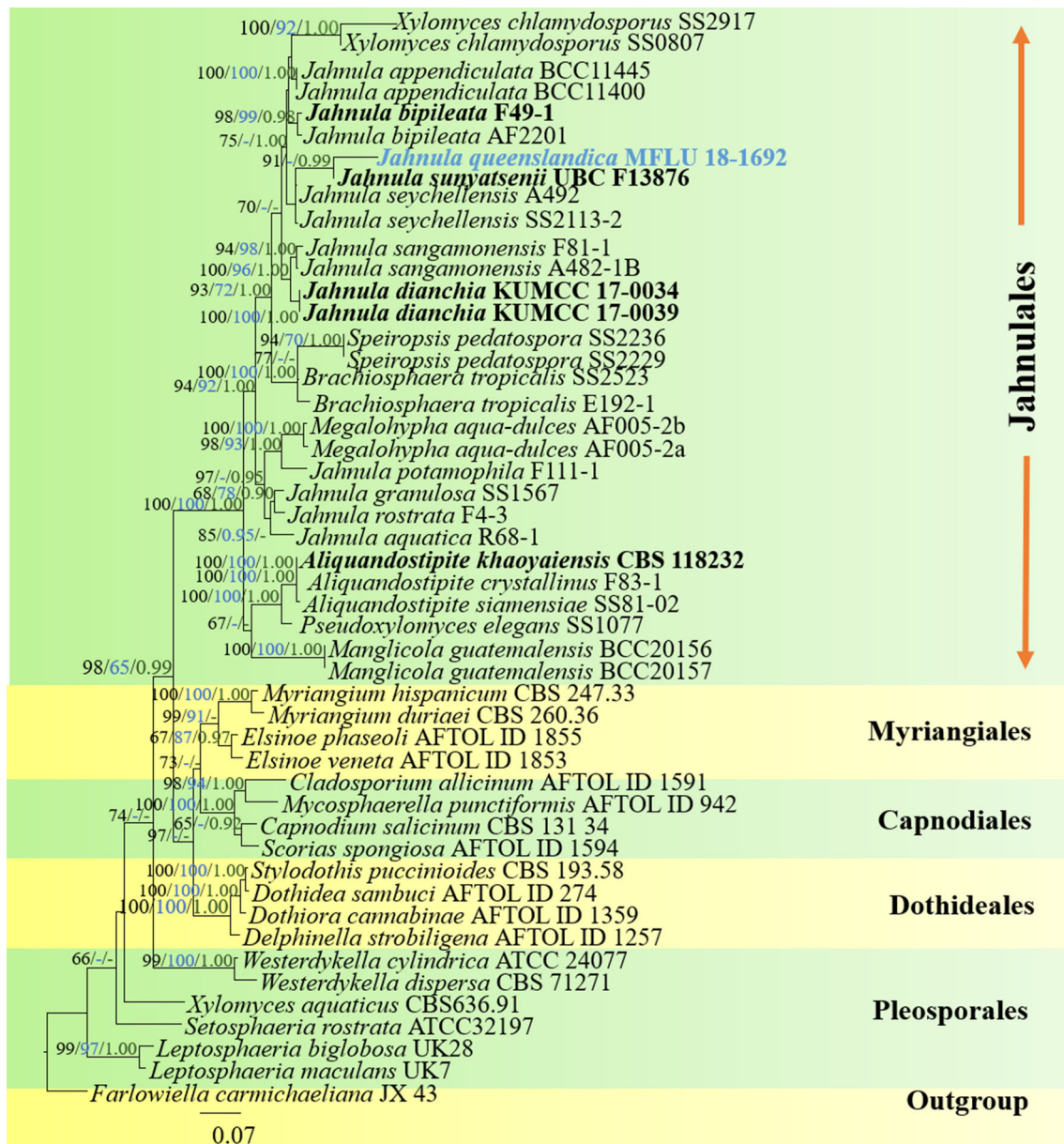


Fig. 65 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data of selected taxa. Related sequences are obtained from GenBank. Forty-nine strains are included in the analyses, which comprise 1159 characters including gaps. Single gene analyses are carried out and compared with each species, to compare the topology of the tree and clade stability. The tree is rooted with *Farlowiella carmichaeliana* (JX 43). Tree topology of the ML analysis is similar to the MP and BI. The best scoring RAXML tree with a final likelihood value of -9016.535047 is presented. The matrix had 607 distinct alignment patterns, with 27.68% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244145, C = 0.229207, G = 0.302247, T = 0.224401; substitution rates AC = 0.875220, AG = 1.547245,

AT = 1.078795, CG = 0.865551, CT = 4.551536, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.372555$. The maximum parsimonious dataset consisted of constant 604, 385 parsimony-informative and 170 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 1569 steps (CI = 0.556, RI = 0.754, RC = 0.420, HI = 0.444) in the first tree Maximum parsimony bootstrap (MPBT, blue) values > 65%, Bayesian posterior probabilities (PP, green) > 0.80% and maximum likelihood bootstrap (ML, black) values > 65%) are given above the nodes. The scale bar indicates 0.07 changes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Phialides ampulliform to cylindrical shaped, 3–10 per metula, $7.5\text{--}11.5 \times 2.5\text{--}3.5 \mu\text{m}$. *Conidia* globose $2.5\text{--}3.5 \mu\text{m}$.

Culture characteristics: The isolate grew over a wide range of temperatures with varying growth rates on MEA, CYA, and YES. The average growth rates of CNUFC-GEU220-1 on MEA, CYA, and YES medium at 25 °C



Fig. 66 *Kamalomyces mangrovei* (MFLU 18-1691, holotype). **a, b** Ascomata. **c.** Section of ascoma. **d** Section through peridium. **e–g** Asci and pseudoparaphyses. **h–k** Ascospores. **l** Germinating

ascospore. **m, n** Cultures on PDA (**m** from above view, **n** from below view). Scale bars: **a** = 500 µm, **c** = 200 µm, **b** = 100 µm, **e–g** = 50 µm, **d, h–l** = 20 µm

were 12, 26, and 10.5 mm per 7 days, respectively. Optimal growth was observed around 25 °C, slow growth was observed at below 10 °C, and no growth at 37 °C.

Material examined: REPUBLIC OF KOREA, Geumsan Park, Jeju Island, from forest soil, 27 March 2018 (CNUFC-GEU220-1, **holotype**), ex-type living culture preserved as glycerol stock at *Rhizophydium koreanum* 80 °C in the CNUFC.

GenBank numbers: CAL: MK481061, RPB2: MK481053, MK481054, TUB2: MK481057, MK481058.

Notes: *Penicillium circulare* belongs to section *Sclerotia* and is phylogenetically related to *P. jacksonii*, but differs by the production of two concentric rings on YES. In addition, it produces monoverticillate conidiophores with one or two branches, in contrast to a single branch of *P. jacksonii*.

Penicillium geumsanense Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen **sp. nov.**

Index Fungorum number: IF555412; **Facesoffungi number:** FoF05794; Fig. 75

Etymology: *geumsanense*, referring to its collection location, Geumsan Park, Jeju Island from where the species was isolated (Korea).

Holotype: CNUFC-GEU2229-1

Macromorphology: CYA, 25 °C: Sporulation on CYA moderate; dark grey green; velvety floccose in centre; mycelium white; soluble pigment absent; reverse orange to dark orange brown; MEA, 25 °C: Colonies grey green; velvety; floccose in centre; strongly fasciculate; soluble pigment absent; reverse dark orange brown and light yellow; YES, 25 °C: Sporulation on YES strong; mycelium white, radially sulcate; soluble pigments absent; reverse white to dark orange brown.

Micromorphology: *Sclerotia* absent. *Conidiophores* mostly terverticillate, sometimes mono- or biverticillate, occasionally with a divaricate branch, branches 22 µm long, stipe 3.0–4.5 µm wide. *Metulae* mostly 2–3, 9.0–17.5 × 2–4 µm. *Phialides* ampulliform shaped, 1–5 per metula, 7.5–10.5 × 2–3.5 µm. *Conidia* ellipsoidal, 3.5–4.0 × 3.0–3.5 µm.

Culture characteristics: The isolate was observed to grow over a wide range of temperatures with varying growth rates on MEA, CYA, and YES. The average growth rates of CNUFC-GEU2229-1 on MEA, CYA, and YES medium at 25 °C were 6.5, 11.5, and 13.5 mm per 7 days, respectively. Optimal growth was observed around 25 °C, slow growth was observed at below 10 °C, and no growth at 37 °C.

Material examined: REPUBLIC OF KOREA, Geumsan Park, Jeju Island, from forest soil, 27 March 2018

(CNUFC-GEU2229-1, **holotype**), ex-type living culture preserved as glycerol stock at – 80 °C in the CNUFC.

GenBank numbers: CAL: MK481062, MK481063, RPB2: MK481055, MK481056, TUB2: MK481059, MK481060.

Notes: *Penicillium geumsanense* belongs to section *Robsamsonia* and is phylogenetically related to *P. glandicola*, a new species described below. It differs from *P. glandicola* by producing terverticillate, monoverticillate or biverticillate conidiophores, in contrast to the terverticillate conidiophores of *P. glandicola*, in addition, grows more slowly than *P. glandicola* on all media.

Penicillium mali-pumilae Hyang B. Lee, T.T.T. Nguyen & Houbraken, **sp. nov.**

Index Fungorum number: IF555410; **Facesoffungi number:** FoF05790; Fig. 76

Etymology: *mali-pumilae*, referring to *Malus pumila*, the type was isolated from rotten fruit of apple.

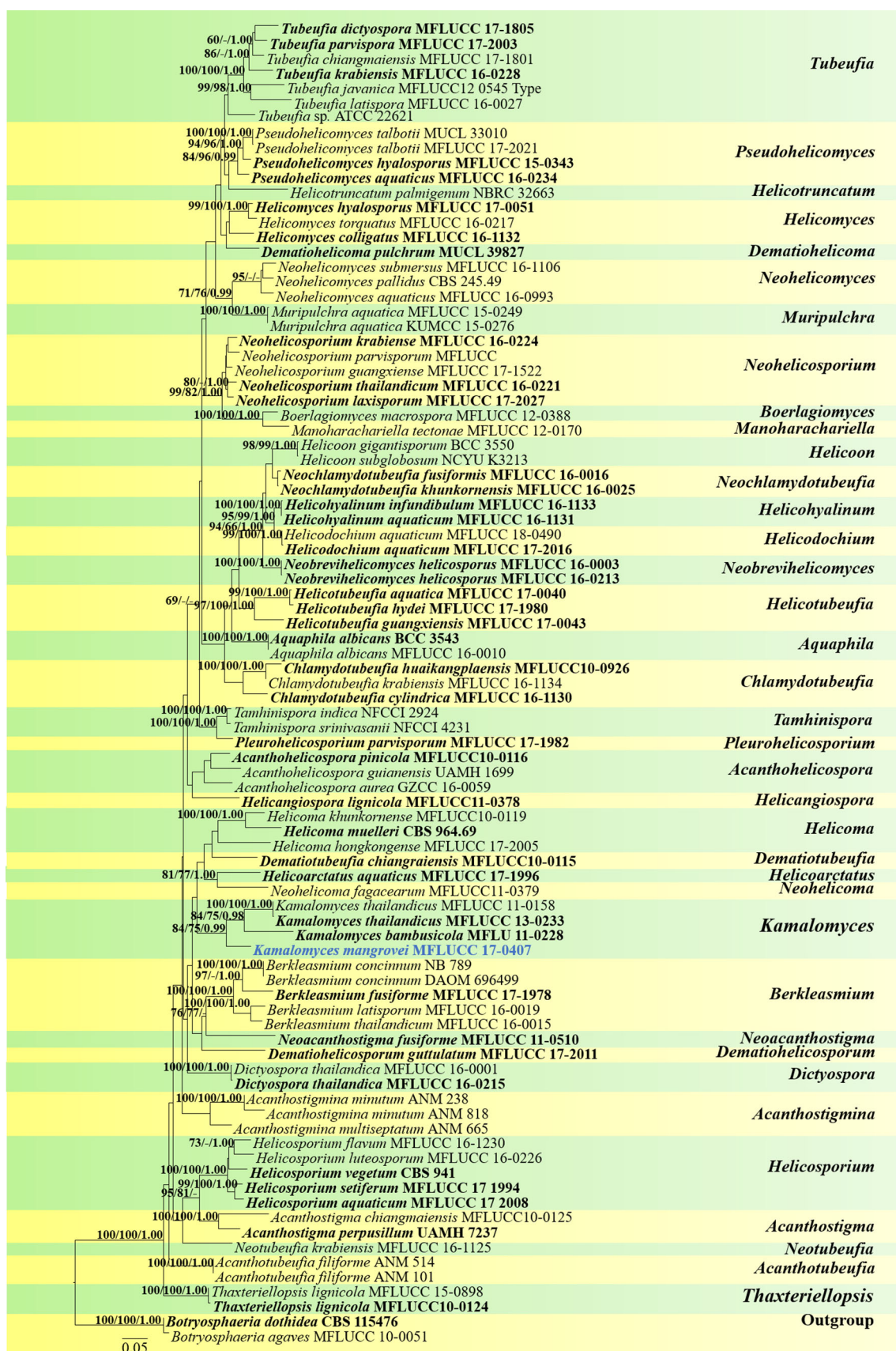
Holotype: CBS H-22503

Macromorphology: CYA, 25 °C: Colonies plane; sporulation on CYA strong; colony texture fasciculate; mycelium white; exudate present as large clear or pale yellow droplets; soluble pigment absent; radial sulcate; margin entire; conidia green to dull blue green; reverse pale brown with (dark) brown in centre. YES, 25 °C: Sporulation absent, mycelium (pale) yellow in centre, white near edge; exudate present as yellow pigments; soluble pigments absent; reverse pale brown, sometimes with brown centre. MEA, 25 °C: Sporulation on MEA strong; colony texture fasciculate; mycelium white; exudate present as large pale yellow or brown droplets; soluble pigments absent; conidia green occasionally blue-green; reverse yellow with pale brown centre or pale brown with brown centre. DG18, 25 °C: Sporulation absent or poor; texture fasciculate; mycelium white or pale yellow, conidia dull green; reverse (pale) yellow.

Micromorphology: *Sclerotia* absent. *Conidiophores* mostly long, with rough walled stipes, non-vesiculate, predominantly terverticillate, branches 20 µm long, stipe 2.5–3.5 µm wide. *Metulae* 4–10, 9–13 × 2.5–4 µm. *Phialides* flask shaped, 3–8 per metula, 8–12 × 2.5–3.5 µm. *Conidia* in long, distorted chains, smooth walled or very finely roughened, globose to subglobose, 3–3.5 µm.

Colony diameters: 7 d, in mm: CYA 22–32; CYA15 °C 26–31; CYA30 °C 4–15; CYA37 °C no growth; DG18 21–31; MEA 19–28; YES 21–32; CYAS 20–28; creatine agar 10–20, weak growth, poor acid production, base formation absent.

Material examined: NETHERLANDS, *Lilium* bulb, Aalsmeer, CBS 127.90 = IBT 12175; REPUBLIC OF KOREA, rot apple (*Malus pumila*), stored in refrigerator



◀**Fig. 67** Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and TEF1- α sequence data of selected taxa. Related sequences are obtained from GenBank. Data set comprises 2530 characters including gaps. Single gene analyses are carried out and compared with each species, to compare the topology of the tree and clade stability. Tree is rooted with *Botryosphaeria agaves* (MFLUCC 10-0051) and *B. dothidea* (CBS 115476). Tree topology of the ML analysis is similar to the MP and BI. The best scoring RAXML tree with a final likelihood value of -27950.184903 is presented. The matrix had 1137 distinct alignment patterns, with 26.87% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234676, C = 0.258513, G = 0.266669, T = 0.240142; substitution rates AC = 1.053687, AG = 4.072971, AT = 3.048439, CG = 0.739670, CT = 8.539737, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.712704$. The maximum parsimonious dataset consisted of constant 1587, 768 parsimony-informative and 175 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 5615 steps (CI = 0.273, RI = 0.584, RC = 0.160, HI = 0.727) in the first tree. Maximum likelihood bootstrap (ML, left), maximum parsimony bootstrap (MP, middle) values $> 65\%$, and Bayesian posterior probabilities (BYPP, right) $> 0.80\%$ are given above the nodes. The scale bar indicates 0.05 changes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

(4 °C), Yesan, 2012, CBS 140671 = DTO 327-D1 = EML-MP6080-1.

GenBank numbers: CAL: KP900992, ITS: KP900991, RPB2: MK033522, TUB2: KP900993.

Notes: *Penicillium mali-pumilae* resembles *P. psychrotrophicum* and detailed notes are given in the description of that species.

Penicillium psychrotrophicum Hyang B. Lee, H.Y. Mun, J.C. Frisvad & Houbraken, *sp. nov.*

Index Fungorum number: IF555409; **Facesoffungi number:** FoF05789; Fig. 77

Etymology: *psychrotrophicum*, refers to its ability to grow at low temperature conditions.

Holotype: CBS H-22504

Macromorphology: CYA, 25 °C: Colonies plane; sporulation on CYA strong; colony texture fasciculate; mycelium white; exudate present as large clear droplets; soluble pigment absent; radial sulcate; margin entire; conidia green; reverse pale brown, brown in centre. YES, 25 °C: Sporulation poor, mycelium white; exudate absent; soluble pigments absent; conidia dull green; reverse brown. MEA, 25 °C: Sporulation on MEA strong; colony texture fasciculate; mycelium white; exudate present as large clear droplets; soluble pigments absent; conidia green; reverse yellow with pale brown centre. DG18, 25 °C: Sporulation moderate; texture fasciculate; mycelium white, conidia dull green; reverse yellow-orange.

Micromorphology: *Sclerotia* absent. *Conidiophores* 100–200 μm long, with rough walled stipes, non-

vesiculate, terverticillate, branch up to 20 μm long, stipe 2.5–3.5 μm wide. *Metulae* 4–10, 9–15 \times 2.5–4 μm . *Phialides* flask shaped, 3–8 per metula, 7.5–9.5 \times 2–3 μm . *Conidia* in long, distorted chains, finely rough to rough, often with spiral striations, ovoidal to fusiform, often with a connective on one side, 2.5–3.5 μm .

Colony diameters: 7 d, in mm: CYA 27–31; CYA15 °C 33–37; CYA30 °C 8–12; CYA37 °C no growth; DG18 31–36; MEA 23–28; YES 34–39; CYAS 29–34; creatine agar 20–25, weak growth, poor acid production, base formation absent.

Material examined: REPUBLIC OF KOREA, Deodeok root (*Codonopsis lanceolata*), Cheongyang, 2011, (CBS H-22504, **holotype**), ex-type living culture (CBS 140670 = DTO 327-C9 = EML-COD3 = IBT 33673).

GenBank numbers: CAL: KP900994, ITS: KP941754, RPB2: MK033521, TUB2: KP900995.

Notes: *Penicillium psychrotrophicum* belongs to series *Corymbifera* and is phylogenetically related to *P. tulipae*, *P. radicola* and *P. mali-pumilae*, a new species described below. *Penicillium psychrotrophicum* differs from *P. tulipae* and *P. radicola* (and *P. hirsutum*) by having smaller colonies on CYA, CYA incubated at 30 °C and MEA. *Penicillium mali-pumilae* is phenotypically similar but differs by having smaller colonies on CYAS (29–34 vs 20–28 mm), DG18 (31–36 vs 21–31 mm) and CYA incubated at 15 °C (33–37 vs 26–31 mm). Furthermore, *P. psychrotrophicum* produces (pale) yellow mycelium on YES, while *P. mali-pumilae* has white coloured mycelium and the reverse of *P. psychrotrophicum* on DG18 has a shade of orange and this is lacking in *P. mali-pumilae*.

The taxonomy of *P. tulipae* and *P. radicola* needs attention. Both species can be recognized using TUB2 sequences; however, these species can not be differentiated using CAL sequences only. Three groups of strains are present in the combined phylogram, though the relationship is not resolved. A further complication is the position of a strain (presumably) representing the type of *P. virescens* Bainier (non Sopp, 1912), CBS 109553 (= NRRL 974). This strain belongs to the *P. tulipae*-*P. radicola* clade and the name might thus have priority over the other two. CBS 109553 differs from both *P. tulipae* and *P. radicola* by having a (dark) brown reverse on CYA and CYAS and brown soluble pigment production. *P. hirsutum*, another member of series *Corymbifera*, also has a brown reverse on CYA; however, these reverses are in shades of yellow-brown or orange-brown. Sporulation on YES is poor and this feature is shared with *P. radicola*, while *P. tulipae* colonies sporulate moderately or strong sporulation on YES. Base production on CREA is shared with *P. tulipae* and *P. virescens*; a feature absent in *P. radicola*. More research is needed to resolve the taxonomy of this clade.

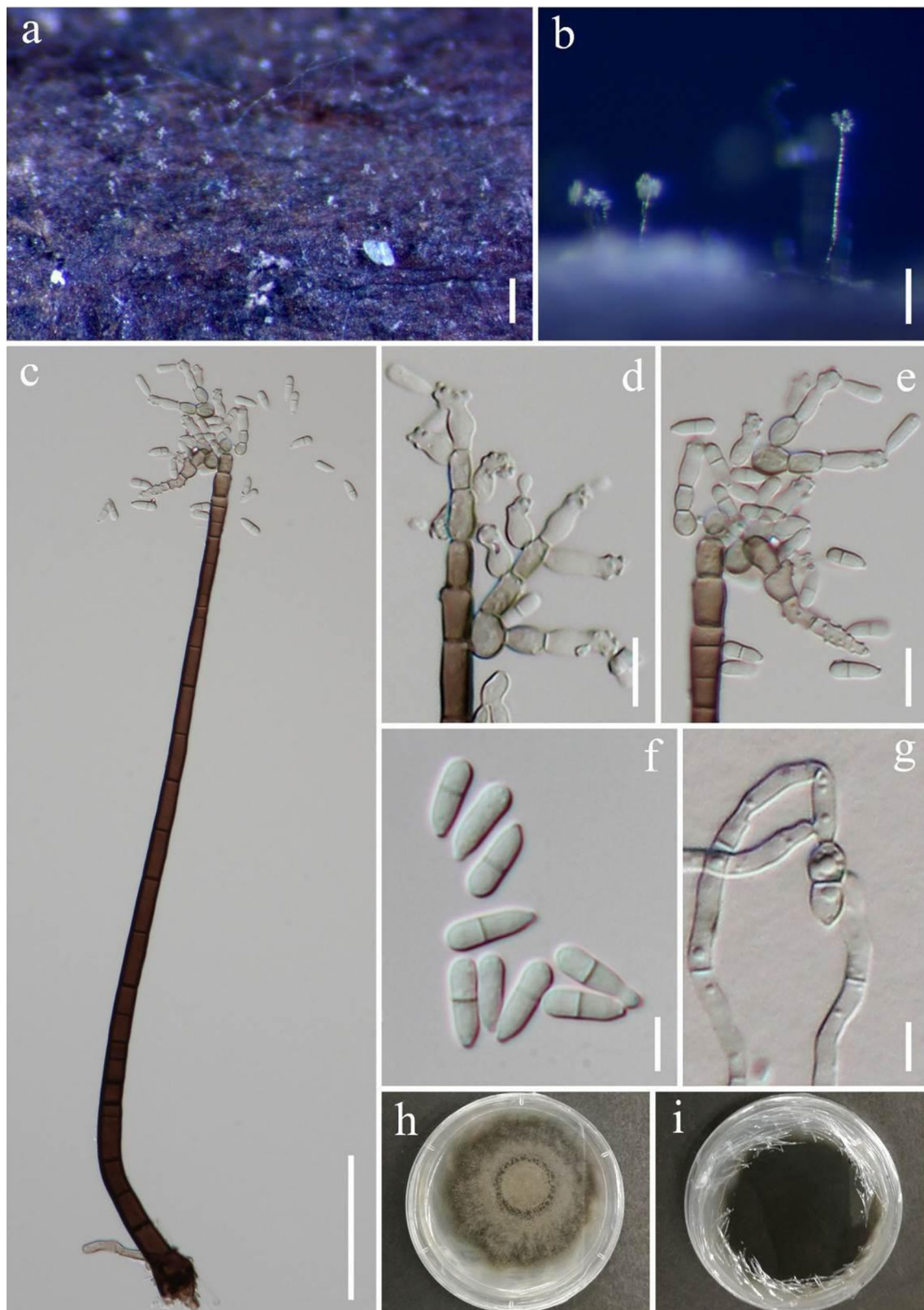


Fig. 68 *Thysanorea uniseptata* (MFLU 18-1723, holotype). **a, b** Colonies on natural substrate. **c** Conidiophore with conidia. **d, e** Conidiogenous cells with conidia. **f** Conidia. **g** Geminated conidium.

h, i Colony on PDA (**h** from above view, **i** from below view). Scale bars: **a** = 250 μm , **b** = 100 μm , **c** = 50 μm , **d, e** = 10 μm , **f, g** = 5 μm

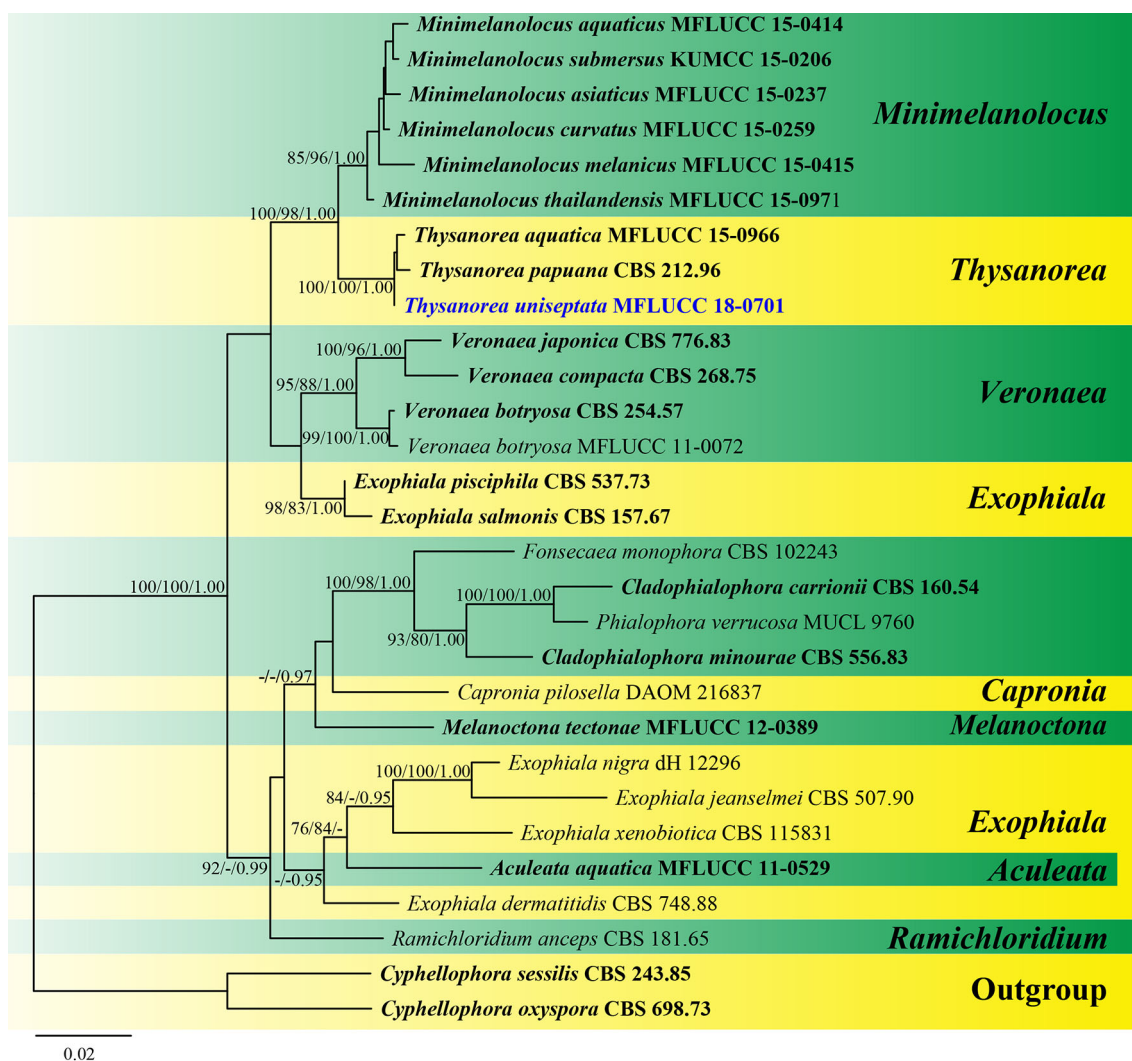


Fig. 69 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data representing Herpotrichiellaceae. Related sequences are taken from Liu et al. (2015), Tian et al. (2016) and Dong et al. (2018). Twenty-nine strains are included in the combined analyses which comprise 3634 characters (674 characters for ITS, 1361 characters for LSU, 1599 characters for SSU) after alignment. *Cyphellophora oxyspora* (CBS 698.73) and *C. sessilis* (CBS 243.85) (Cyphellophoraceae, Chaetothyriales) are used as the outgroup taxa. Single gene analyses were carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -11580.668860 is presented. The matrix had 664 distinct alignment patterns, with

28.94% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.255728, C = 0.221018, G = 0.274376, T = 0.248878; substitution rates AC = 1.635663, AG = 2.578277, AT = 1.796079, CG = 1.025171, CT = 6.468570, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.513924$. Maximum parsimony analysis of 3080 constant characters and 182 informative characters resulted in one equally most parsimonious tree (CI = 0.610, RI = 0.675, RC = 0.411, HI = 0.390). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75% are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Penicillium wandoense Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen, *sp. nov.*

Index Fungorum number: IF555411; *Facesoffungi* number: FoF05791; Fig. 78

Etymology: *wandoense*, referring to its collection location, Wan island (*Wando*) from where the species was isolated (Korea).

Holotype: CNUFC-WT31-1

Macromorphology: CYA, 25 °C: Sporulation on CYA moderate; colonies radially sulcate; surface texture velutinous; mycelium white; soluble pigment absent; reverse yellow brown to reddish brown; MEA, 25 °C: Sporulation on MEA strong; colonies pale green; margins low, wide, irregular; velvety to floccose texture; reverse pale red or pale yellow; YES, 25 °C: Sporulation poor, mycelium

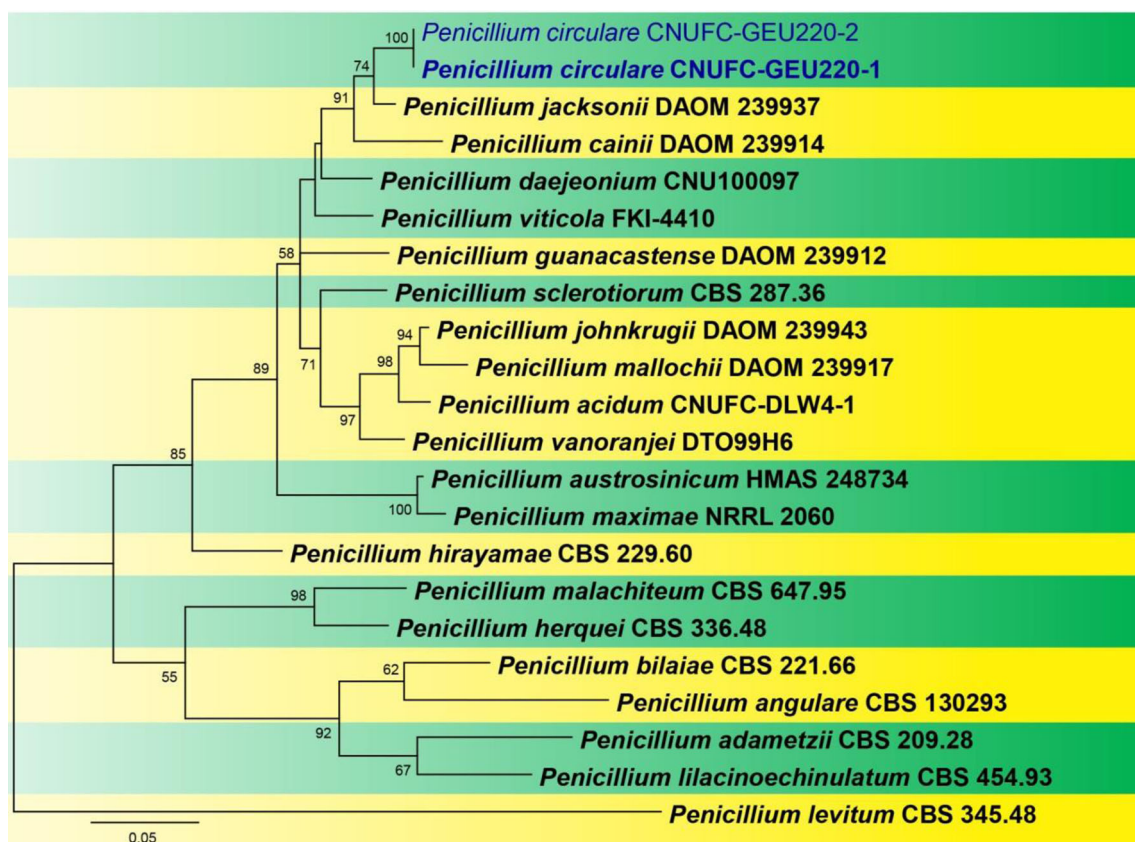


Fig. 70 Phylogram generated from maximum likelihood analysis based on combined TUB2, CAL, and RPB2 sequence data for *Penicillium circularis* and related species within the sect. *Sclerotiora*. *Penicillium levitum* (CBS 345.48) was used as outgroup taxon.

Bootstrap values for maximum likelihood (ML) greater than 50% are placed above the branches. Type strains are in bold. The newly generated sequences are indicated in blue

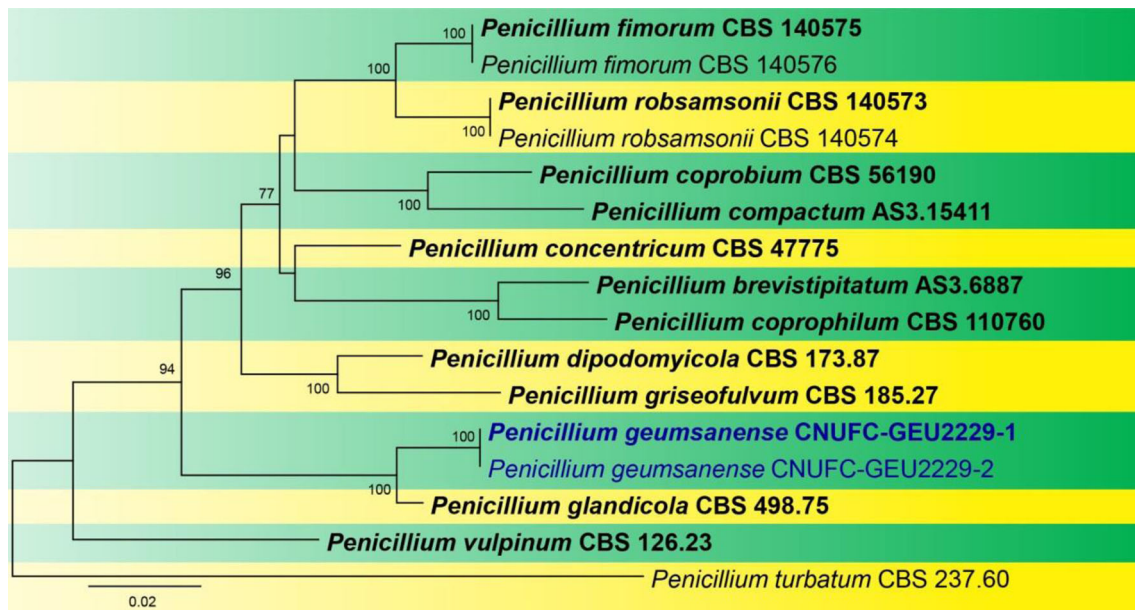


Fig. 71 Phylogram generated from maximum likelihood analysis based on combined TUB2, CAL, and RPB2 sequence data for *Penicillium geumsanense* and related species within the sect. *Robsamsonia*. *Penicillium turbatum* (CBS 237.60) was used as outgroup

taxon. Bootstrap values for maximum likelihood (ML) greater than 50% are placed above the branches. Type strains are in bold. The newly generated sequences are indicated in blue

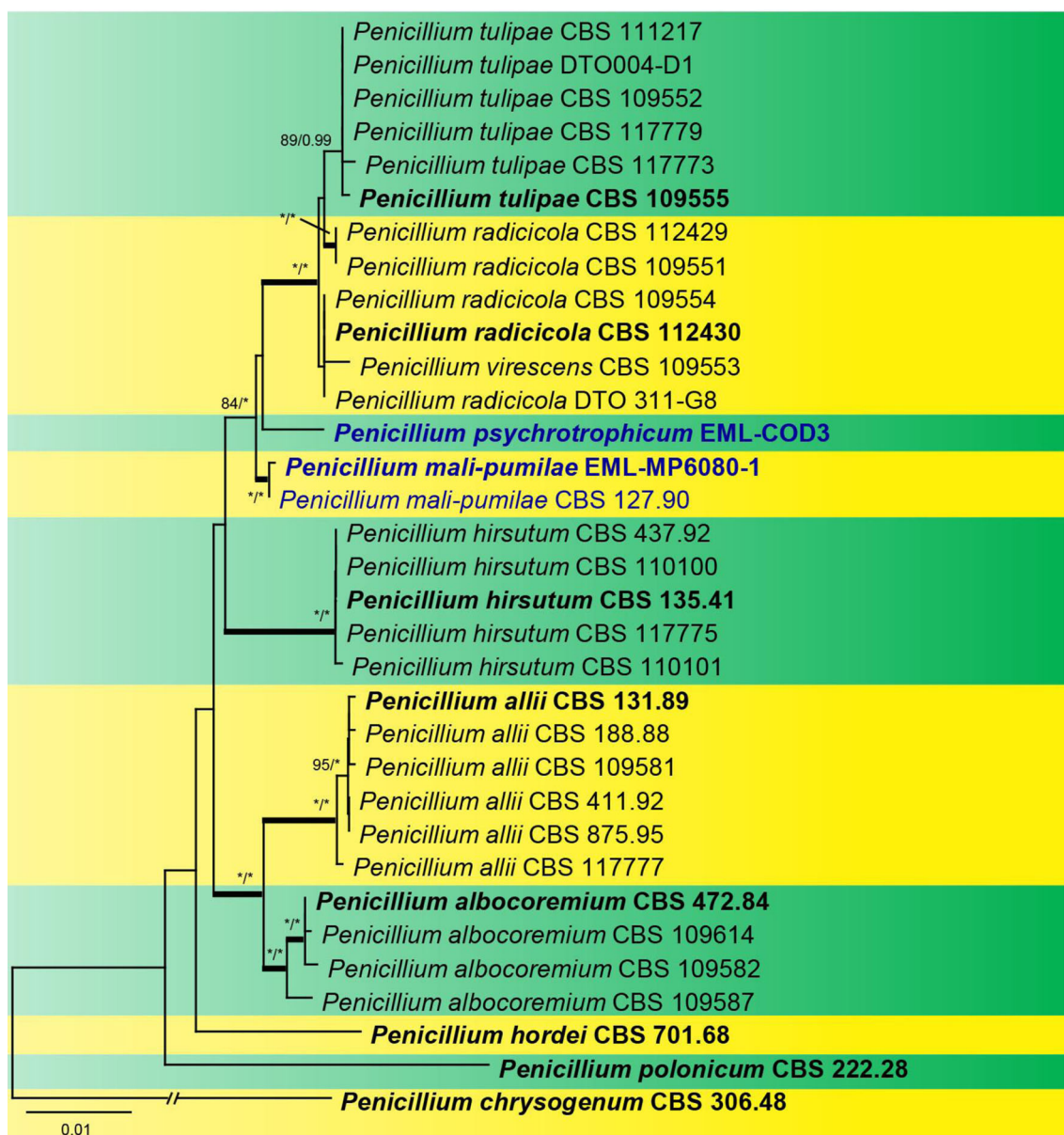


Fig. 72 Phylogram generated from maximum likelihood analysis based on combined TUB2, CAL, and RPB2 sequence data for *Penicillium psychrotrophicum* and *P. mali-pumilae* and related species within the sect. *Fasciculata* series *Corymbifera*. *Penicillium chrysogenum* (CBS 306.48) was used as outgroup taxon. Bootstrap

values for maximum likelihood (ML) equal to or greater than 70% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are in bold. Type strains are in bold. The newly generated sequences are indicated in blue

white; surface texture velutinous; reverse yellow brown to reddish brown.

Micromorphology: *Sclerotia* absent. *Conidiophores* arising from agar surface, predominantly biverticillate, but also many monoverticillate, branch up to 26.5 μm long, stipe 2.5–3.5 μm wide. *Metulae* 2–4, 9.5–15.5 \times 2.5–4.0 μm . *Phialides* ampulliform shaped, 2–5 per metula, 6.5–9.5 \times 2–3.5 μm . *Conidia* subglobose to ellipsoidal, 3–4 \times 2.5–3.5 μm .

Culture characteristics: The isolate grew over a wide range of temperatures with varying growth rates on MEA, CYA, and YES. The average growth rates of CNUFC-WT31-1 on MEA, CYA, and YES medium at 25 $^{\circ}\text{C}$ were 34.5, 23, and 21 mm per 7 days, respectively. Optimal growth was observed around 25 $^{\circ}\text{C}$, slow growth was observed at below 10 $^{\circ}\text{C}$, and at 37 $^{\circ}\text{C}$.

Material examined: REPUBLIC OF KOREA, Wando island (34 $^{\circ}$ 19'1.20" N 126 $^{\circ}$ 45'0.00" E), from freshwater, 24 August 2018 (CNUFC-WT31-1, **holotype**), ex-type living

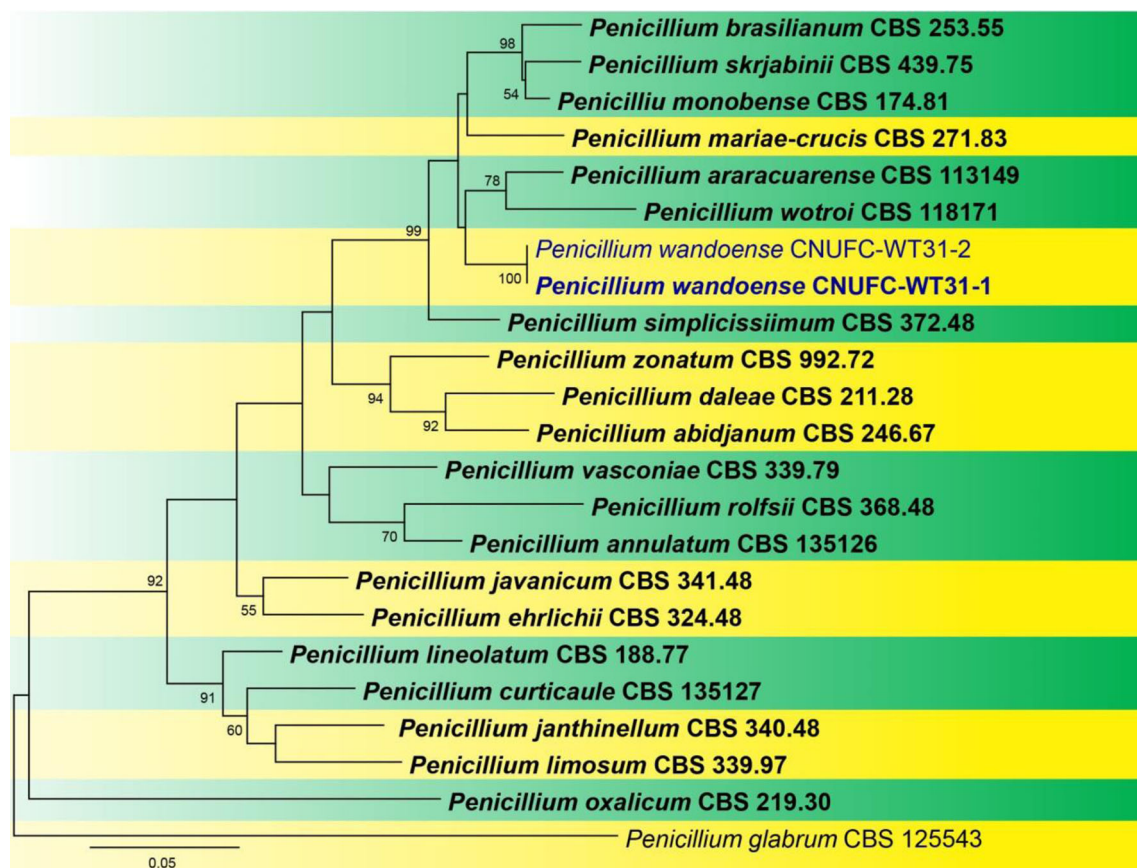


Fig. 73 Phylogram generated from maximum likelihood analysis based on combined TUB2, CAL, and RPB2 sequence data for *Penicillium wandoense* and related species within the sect. *Lanata-Divariata*. *Penicillium glabrum* (CBS 125543) was used as outgroup

taxon. Bootstrap values for maximum likelihood (ML) greater than 50% are placed above the branches. Type strains are in bold. The newly generated sequences are indicated in blue

culture preserved as glycerol stock at -80°C in the CNUFC.

GenBank numbers: CAL: MK080564, MK080565, RPB2: MK080566, MK080567, TUB2: MK080562, MK080563.

Notes: *Penicillium wandoense* differs from *P. araracuarensense*, and *P. wotroi* by its pale red or pale yellow reverse on MEA. In the phylogenetic tree based on multiple genes, the strain formed a separate branch from other species of the genus and is considered to represent a new species.

Laboulbeniomycetes Engl.

Laboulbeniales Lindau

Notes: The order Laboulbeniales includes about 2100 described species of obligate ectosymbionts on Arthropods. The Laboulbeniales sensu Lindau comprehended all the Laboulbeniomycetes, but recently the class has been splitted in three orders as a result of molecular analysis (Goldmann and Weir 2018; Haelewaters et al. 2019). However, the great majority of species is still classified in

the Laboulbeniales, while the two new orders include only a few of the known species (less than 3%).

Laboulbeniaceae G. Winter

Notes: A full taxonomic treatment of the family is more than 30 years old (Tavares 1985), but this classification has been recently questioned in the papers reported above. Although a new comprehensive taxonomy the group has not yet been advanced, the two genera considered below can still be safely included in the family Laboulbeniaceae.

Prolixandromyces R. K. Benjamin 1970, Aliso 7: 174 [MB 4369]

= *Monandromyces* R. K. Benjamin 1999, Aliso 18: 72 [MB 28387] **syn. nov.**

Notes: The genus *Monandromyces* was erected by R.K. Benjamin in 1999 to accommodate *Autophagomyces microveliae* Thaxt. and ten new species. The given diagnosis (page 72) is as follows: “Receptacle consisting of three in-line superposed cells (I, II, III) bearing distally on one side a stalked peritheciium and on the other side a simple, free appendage; basal (I) and suprabasal (II) cells

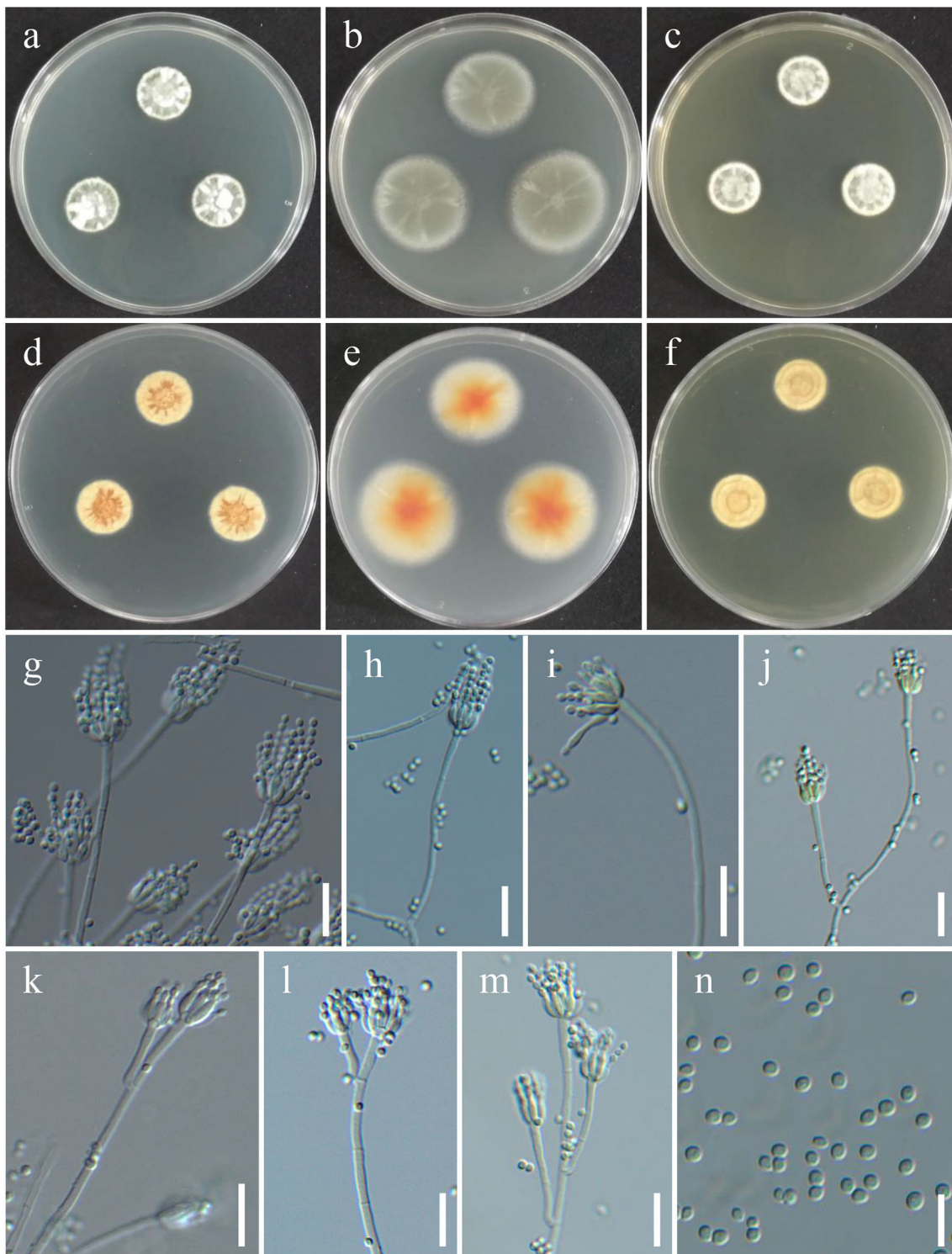


Fig. 74 *Penicillium circulare* (CNUFC-GEU220-1, holotype). **a, d** Colonies in Czapek yeast agar (CYA). **b, e** Colonies in malt extract agar (MEA). **c, f** Colonies in yeast extract sucrose agar (YES). **g–m** Conidiophores. **n** Conidia. Scale bars: **g–m** = 20 μ m, **n** = 10 μ m

strongly obliquely superposed; cell II subtending the perithegium; terminal cell (III) subtending the appendage. Appendage consisting of three superposed cells and a single, terminal, simple, flask-shaped antheridium; basal

cell small, broader than long to nearly isodiametric; median cell elongate, several times longer than broad; terminal cell small, nearly isodiametric or \pm elongate, always less than length of median cell; antheridium flask shaped with an

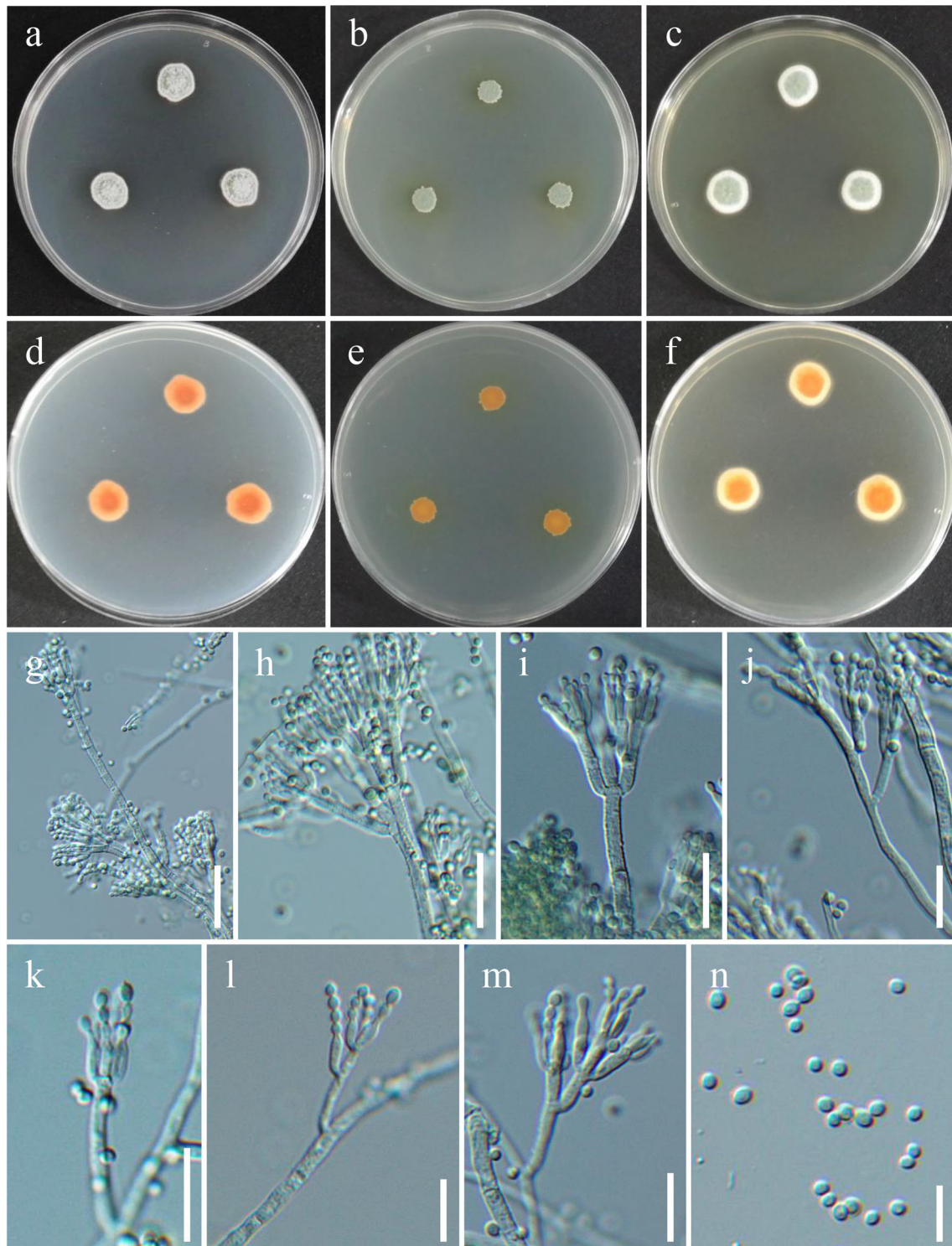


Fig. 75 *Penicillium geumsanense* (CNUFC-GEU2229-1, **holotype**). **a, d** Colonies in Czapek yeast agar (CYA). **b, e** Colonies in malt extract agar (MEA). **c, f** Colonies in yeast extract sucrose agar (YES). **g–m** Conidiophores. **n** Conidia. Scale bars: **g–m** = 20 µm, **n** = 10 µm

elongate, slender efferent tube. Perithecium with two stalk cells (VI, VII), three persistent basal cells (m, n, n'), and four vertical rows of outer wall cells of five cells each.".

The recent description of four new species in the genus *Prolixandromyces* (Kaishian and Weir 2018) and the consequent emendation of the genus, now including also a species with a single, terminal antheridium (i.e.

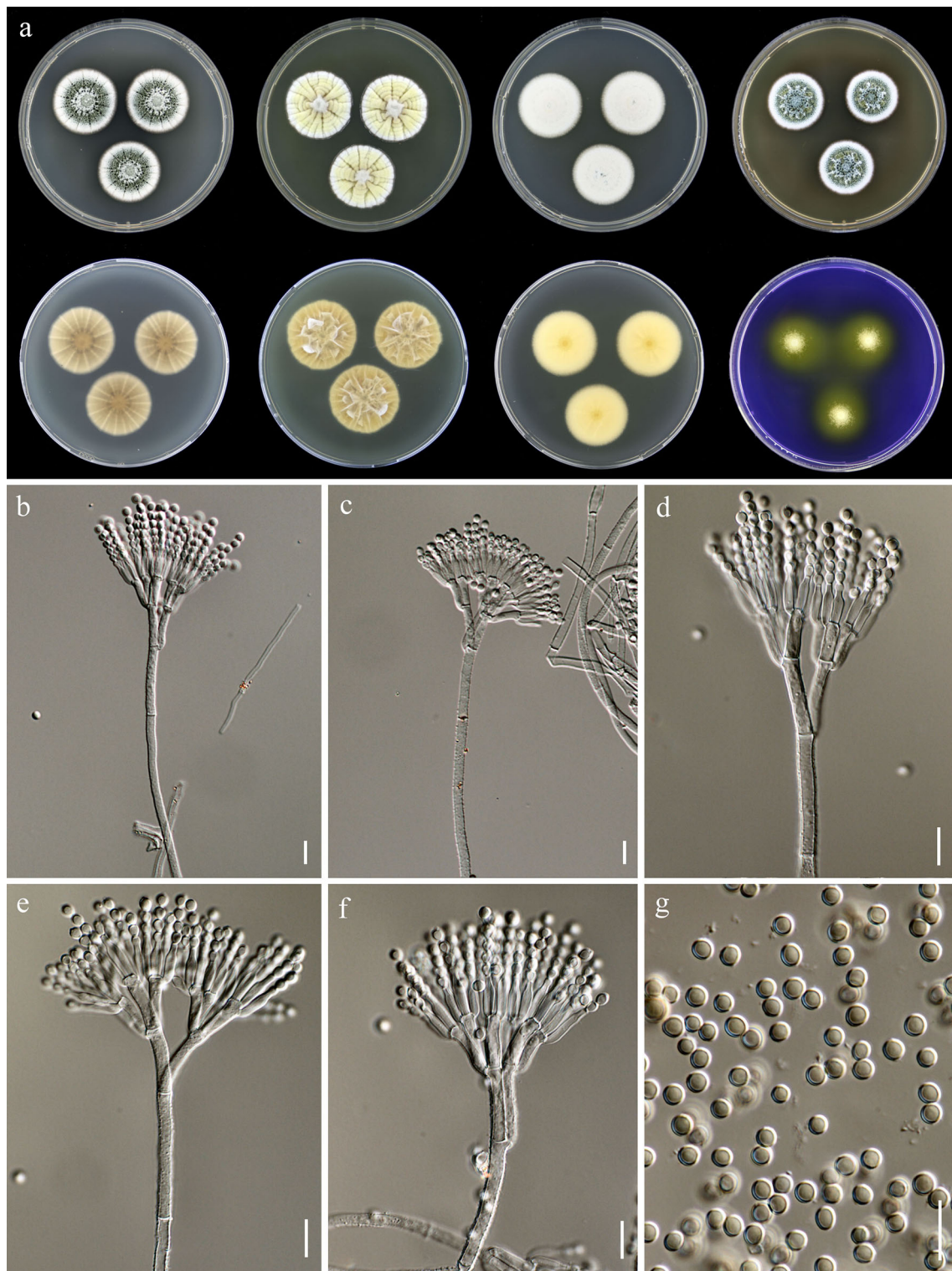


Fig. 76 *Penicillium mali-pumilae* (EML-MP6080-1, **ex-type culture**). **a** 7 d old cultures, 25 °C, left to right; first row, all obverse, Czapek yeast agar (CYA), yeast extract sucrose agar (YES), dichloran

18% glycerol agar (DG18), malt extract agar (MEA); second row, CYA reverse, YES reverse, DG18 reverse, CREA obverse. **b–f** Conidiophores. **g** Conidia. Scale bars: **b–g** = 10 µm

P. bromelicola A. Weir & Kaishian), removes any difference between *Monandromyces*, (characterized by a single antheridium) and *Prolixandromyces*. In the emended

diagnosis (page 223) is written: “The uppermost cell in the series either producing a single, simple, terminal antheridium in the 3-celled appendage or more frequently

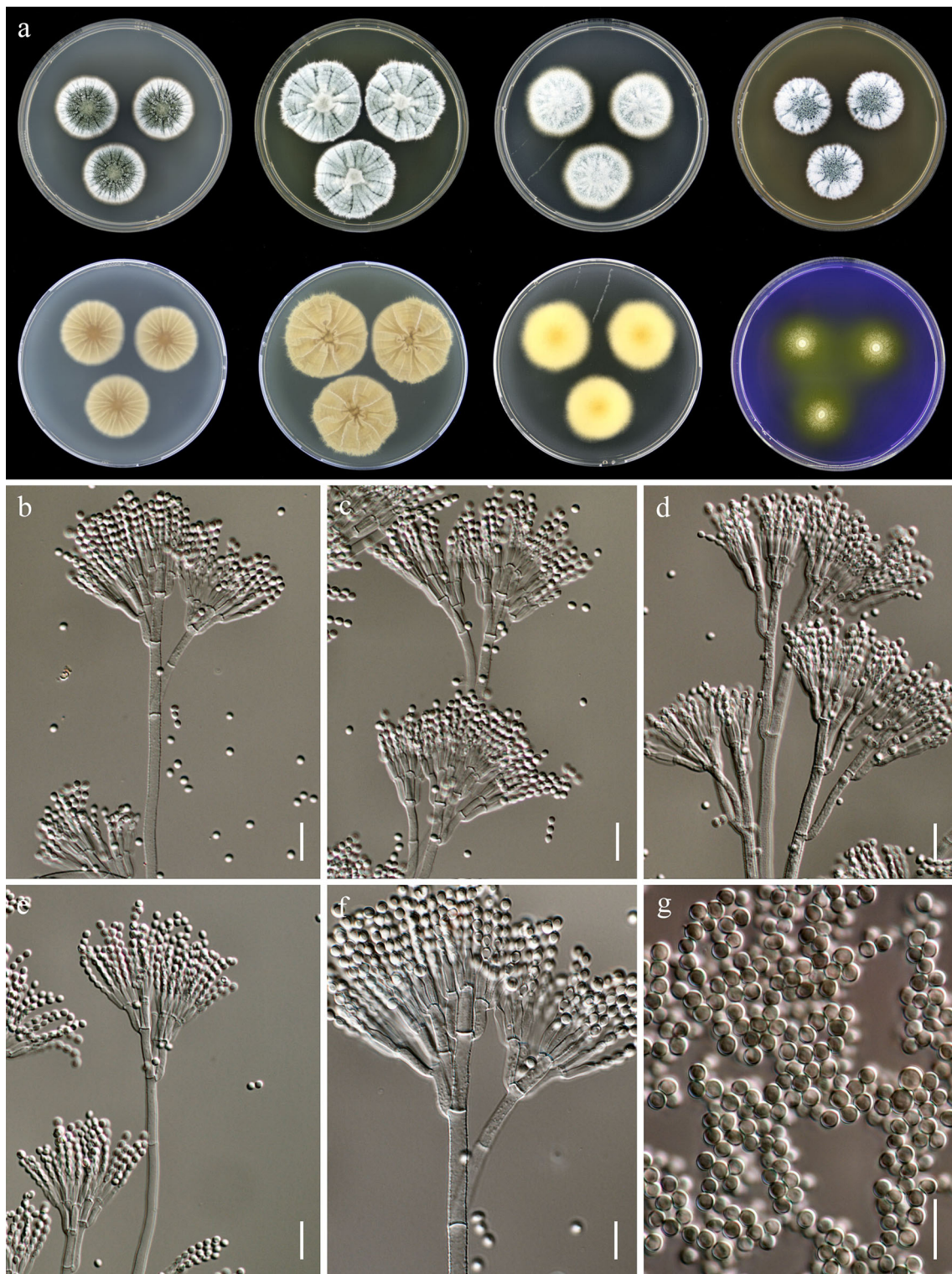


Fig. 77 *Penicillium psychrotrophicum* (EML-COD3, **ex-type culture**). **a** 7 d old cultures, 25 °C, left to right; first row, all obverse, Czapek yeast agar (CYA), yeast extract sucrose agar (YES), dichloran

18% glycerol agar (DG18), malt extract agar (MEA); second row, CYA reverse, YES reverse, DG18 reverse, CREA obverse. **b–f** Conidiophores. **g** Conidia. Scale bars: **b–g** = 10 µm

in the 4–11-celled appendage giving rise to both a terminal and a lateral antheridium”. All the other features are

identical, as it is identical the family of most of the host insects: the Veliidae (semiaquatic bugs). As a consequence

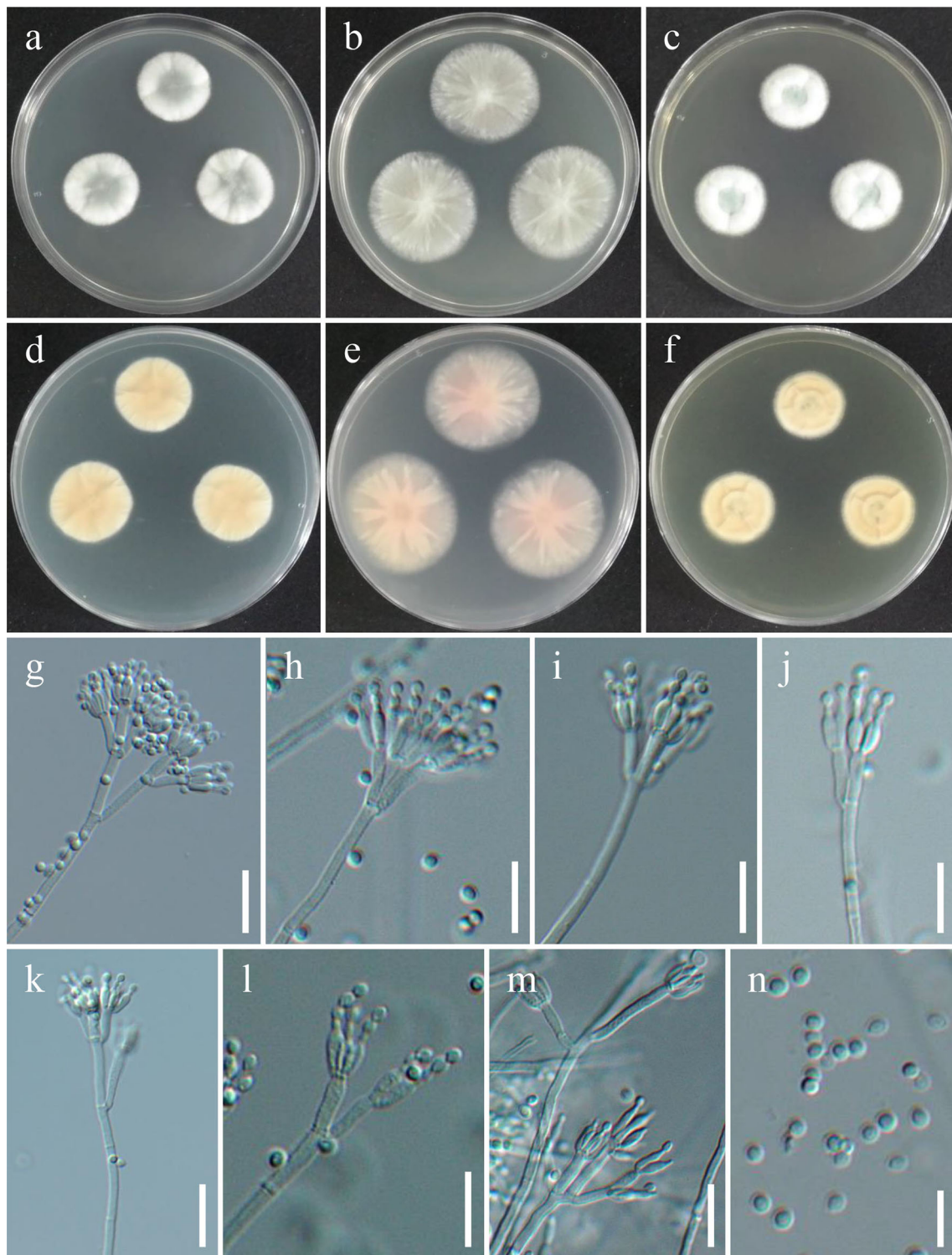


Fig. 78 *Penicillium wandoense* (CNUFC-WT31-1, **holotype**). **a, d** Colonies in Czapek yeast agar (CYA). **b, e** Colonies in malt extract agar (MEA). **c, f** Colonies in yeast extract sucrose agar (YES). **g–m** Conidiophores. **n** Conidia. Scale bars: **g–m** = 20 μm, **n** = 10 μm

of the new synonymy all the species of *Monandromyces* are transferred to the genus *Prolixandromyces* with the following new combinations.

Prolixandromyces australis (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces australis* R.K. Benjamin 1999, Aliso 18: 78 [MB 459855]; *Index Fungorum* number: IF556540

Prolixandromyces elongatus (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces elongatus* R.K. Benjamin 1999, Aliso 18: 86 [MB 459861]; *Index Fungorum* number: IF556541

Prolixandromyces falcatus (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces falcatus* R.K. Benjamin 1999, Aliso 18: 77 [MB 459854]; *Index Fungorum* number: IF556542

Prolixandromyces longispinae (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces longispinae* R.K. Benjamin 1999, Aliso 18: 87 [MB 459862]; *Index Fungorum* number: IF556543

Prolixandromyces microveliae (Thaxter) W. Rossi, **comb. nov.**

≡ *Autophagomyces microveliae* Thaxter 1931, Mem. Amer. Acad. Arts Sci. 16: 96

= *Monandromyces microveliae* (Thaxter) R.K. Benjamin 1999, Aliso 18: 74 [MB 459852]; *Index Fungorum* number: IF556544

Prolixandromyces neoalardi (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces neoalardi* R.K. Benjamin 1999, Aliso 18: 82 [MB 459859]; *Index Fungorum* number: IF556545

Prolixandromyces polhemorum (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces polhemorum* R.K. Benjamin 1999, Aliso 18: 79 [MB 459856]; *Index Fungorum* number: IF556546

Prolixandromyces protuberans (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces protuberans* R.K. Benjamin 1999, Aliso 18: 81 [MB 459858]; *Index Fungorum* number: IF556547

Prolixandromyces pseudoveliae (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces pseudoveliae* R.K. Benjamin 1999, Aliso 18: 84 [MB 459860]; *Index Fungorum* number: IF556548

Prolixandromyces tenuistipitis (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces tenuistipitis* R.K. Benjamin 1999, Aliso 18: 80 [MB 459857]; *Index Fungorum* number: IF556549

Prolixandromyces umbonatus (R.K. Benjamin) W. Rossi, **comb. nov.**

≡ *Monandromyces umbonatus* R.K. Benjamin 1999, Aliso 18: 74 [MB 459853]; *Index Fungorum* number: IF556550

Stigmatomyces H. Karst., Chemismus Pfl.-Zelle: 78 (1869)

Notes: After the recent description of *Stigmatomyces coronatus* (Rossi and Bernardi 2018), the accepted species are 148 distributed in all continents, all occurring on flies (Diptera) with the only exceptions being *S. caudicola* Speg. and *S. euconni* F. Picard, two species that certainly do not belong to the genus *Stigmatomyces*. *Stigmatomyces succini* is the only known fossil species of the Laboulbeniales reported so far (Rossi et al. 2005). Very few sequences are available for species in the genus.

Stigmatomyces chamaemyiae W. Rossi & M. Leonardi, **sp. nov.**

Index Fungorum number: IF828160; *Facesoffungi* number: FoF05175; Fig. 79

Etymology: From the name of the genus of the host insects, *Chamaemyia*.

Holotype: FI WR3847

Receptacle, distal portion of the free appendage ad perithecial apex almost hyaline; stalk and basal cell of the free appendage and perithecial venter rusty or amber yellow; the rest of the fungus is very diluted reddish or amber yellow. Receptacle very variable in length, slightly tapering to the foot, with the suprabasal cell longer than the basal. Stalk cell of the appendage relatively small, distally prominent, strongly tapered below, its outer margin almost straight. Free appendage usually turned sidewise, with the axis consisting of five cells (rarely four), each bearing two anteridia, the uppermost of which is spinose. Stalk cell of the perithecium distinctly broader than long, separated by the secondary stalk-cell by a concave septum; the cells above it subequal in size and shape, the two outer of which are more or less prominent. Perithecial venter finely granular, oblong, slightly and symmetrically inflated, passing without abrupt transition to the spreading base of the paler and longer neck, which is slightly curved dorsally and slightly swollen at its junction with the tip; the latter is asymmetrical, with the ventral side more convex; the apex short, rather abruptly narrower, distinctly turned towards the dorsal side, ending in four, small, paired, subtruncate lips. Total length 205–440 µm; perithecium 45–75 × 130–220 µm; free appendage 50–65 µm; ascospores 30–35 µm.

Material examined: MALTA, Ghajn Tuffieha Bay, sea level, 1 May 2001, B. Merz, on legs and apex abdomen of *Chamaemyia flavicornis* (Strobl) (Diptera, Chamaemyidae) (FI WR3533 & WR3534, **paratypes**). FRANCE, Pyrénées Orientales, La Bastide, Col de Palomère, high grassland, 10 June 2007, J. C. Deeming, on legs of *C. juncorum* (Fallén) (FI WR3142, **paratype**). PORTUGAL, Monte Gordo, V.

Fig. 79 *Stigmatomyces chamaemyiae* (FI WR3847, **holotype**). Scale bar = 50 μ m



R. S. Antonio, 11 May 2012, R. Andrade, on various parts of *C. flavipalpis* (Haliday) (FI WR3848, **paratype**); Sintra, Almargem do Bispo, 21 August 2013, R. Andrade, on various parts of *C. polystigma* (Meigen) (FI WR3847, **holotype**).

Notes: The thalli on the tergites of *C. flavipalpis* from Portugal are very long (up to 590 μ m) because of a very

long receptacle (up to 350 μ m). *Stigmatomyces chamaemyiae* is the first species of the Laboulbeniales reported on Chamaemyidae. Among the described species, the species most similar to *S. chamaemyiae* seems to be *S. aphaniosomae* W. Rossi & A. Weir occurring on Chyromyidae. In the latter species, however, the perithecial apex is very different, the free appendage is shorter, with the axis

consisting of three cells, and the basal cell of the receptacle is usually longer than the suprabasal (Rossi and Weir 2011). Twenty-four species of *Stigmatomyces* are recorded from Portugal, while eleven are from France; to date, none of the species of *Stigmatomyces* have been reported from Malta (Castaldo et al. 2004; Rossi et al. 2013).

Stigmatomyces cocksii* W. Rossi & M. Leonardi, *sp. nov.

Index Fungorum number: IF828161; *Facesoffungi* number: FoF05176; Fig. 80

Etymology: Named after the Australian entomologist Graeme Cocks, who collected the new species.

Holotype: CAMB WR4074a

Thallus grayish yellow: the perithecial venter, the stalk cell and lower cell of the appendage are darker, the basal cell of the receptacle (cell I) and the free appendage are paler, while the suprabasal cell of the receptacle (cell II) is hyaline or almost so. Receptacle very variable in length; basal cell regularly tapering to the foot and rather abruptly constricted at the septum with the suprabasal, which is of nearly uniform diameter although variably elongate. Stalk cell of the appendage stout, broadly heart-shaped, distally prominent. Free appendage reaching the summit of the perithecial venter, with the axis consisting of four cells, the lower of which is about twice longer than broad, the others slightly broader than long and gradually smaller; each axial cell bears two antheridia except the uppermost, which bears a third, terminal antheridium. Perithecial stalk and basal cells relatively small, not strongly unequal in size, distinctly prominent externally. Perithecial venter regularly elliptical in outline, its surface distinctly warty, the wart-like elevations disposed transversely forming darker ridges; the neck abruptly narrower, longer than the venter, almost isodiametric, transversely striate, slightly enlarged at its junction with the tip, which tapers gradually to a subtruncate apex. Total length 175–345 µm; perithecial venter 38–62 × 40–58 µm; perithecial neck, up to 155 µm; free appendage 48–57 µm; ascospores 29–31 µm.

Material examined: AUSTRALIA, Queensland, Hermit Park, 44 Marks St., Malaise trap, 23 December 2015, G. Cocks, on *Notiochyromya* sp. nova (Diptera, Chyromyidae) (CAMB WR4074a, **holotype**; FI WR4074a, **isotype**), Same data as the type, 20 November 2015 (FI WR4073, **paratype**).

Notes: Because of the transverse ridges formed by wart-like elevations, *Stigmatomyces cocksii* bears a superficial resemblance to *S. micrandrus* Thaxt. and *S. rugosus* Thaxt., both parasitic on shore flies (Ephydriidae). However, in the two latter species these ridges are smaller and more numerous, the appendage is distinctly shorter than the perithecial venter, the apex of perithecium bearing relatively large with diverging lips (Thaxter 1908).



Fig. 80 *Stigmatomyces cocksii* (CAMB WR4074a, **holotype**). Scale bar = 50 µm

The only previously described species of *Stigmatomyces* on flies of the family Chyromyidae is *S. aphaniosomae*. The latter is very different from *S. cocksii*: among other distinguishing features, it has a smooth surface of the perithecial venter or almost so, a shorter perithecial neck, a shorter free appendage, the perithecial apex bearing

unequal and diverging lips (Rossi and Weir 2011). The identified species of *Stigmatomyces* reported from Australia thus far are three: *S. limnophorae* Thaxt., *S. rugosus* Thaxt. (Rossi et al. 2013), and *S. zaleae* W. Rossi & A. Weir (Rossi and Weir 2007).

Stigmatomyces papei W. Rossi & M. Leonardi, *sp. nov.*

Index Fungorum number: IF828162; *Facesoffungi number*: FoF05178; Fig. 81

Etymology: Named after the Danish dipterologist Thomas Pape, who collected the new species.

Holotype: FI WR4044

Perithecium pale reddish brown; the rest of the thallus is almost hyaline or faintly tinged with reddish brown, with the exception of the lower cell of the free appendage which stands out with brilliant rusty red. Receptacle rather short and stocky, tapering throughout, the basal cell subtriangular with its content contracted above, the suprabasal distinctly longer. Stalk-cell of the appendage relatively long and narrow, distally prominent. Free appendage slender and attenuate, straight or sigmoid, its axis usually

consisting of 9 cells, each bearing a pair of slightly diverging antheridia arranged in two rows, except for the uppermost cell, which bears three superimposed antheridia. Stalk-cell of the perithecium large, longer than broad, its outer margin overlapped for most of its length by the secondary stalk-cell, which is only slightly smaller. Perithecial basal cells subequal, large, longer than broad. Perithecium longer than the rest of the thallus, slender and elongate, the venter oblong, the neck hardly distinguished, about as long as the venter, very slightly tapering towards the tip and ending with two large and unequal outgrowths, of which the shorter is broadly ovoid, the other bean-shaped and bending outwards. Total length 575–640 μm ; perithecium 60–70 \times 340–380 μm ; free appendage 105–140 μm ; ascospores 55 μm .

Material examined: TANZANIA, Morogoro Region, Udzungwa Mts. Natl. Park, Mizimu Camp, 769 m, 30–31 July 2015, T. Pape, N. Scharff & al., on tergites of *Plagiostenoptera submetallica* (Loew) (Diptera, Platystomatidae) (FI WR4044, **holotype**).

Fig. 81 *Stigmatomyces papei* (FI WR4044, **holotype**). **a** Whole thallus. **b** Upper portion of a syntype. Scale bars: **a**, **b** = 50 μm



Notes: A few thalli occurring on the upper surface of the right wing of the host are smaller and stockier, with the larger of the perithecial outgrowths longer and slenderer. The two large perithecial outgrowths are unique in the genus and make *Stigmatomyces papei* distinguishable at first sight. It is likely allied with *S. ortalidanus* Thaxt. described 100 years ago on *Plagiostenoptera vicaria* Hendel (= *P. nigripes* Enderlein) from the Cameroons and never reported since, with which it shares the structure of the free appendage, the shape of the perithecial venter and the elongation of the perithecial basal cells. However, the latter fungus lacks the two peculiar perithecial outgrowths, it is much longer (up to 1 mm), with very long suprabasal cell and perithecial stalk-cell, wall cells of the perithecium spirally twisted, and surface of the perithecial neck distinctly corrugated (Thaxter 1931).

Stigmatomyces papei is the first species of *Stigmatomyces* reported thus far from Tanzania.

***Stigmatomyces tschirnhausii* W. Rossi & M. Leonardi, sp. nov.**

Index Fungorum number: IF828163; **Facesoffungi number:** FoF05177; **Fig. 82**

Etymology: Named after the German dipterologist Michael von Tschirnhaus.

Holotype: FI WR3542

Receptacle, distal portion of the free appendage ad perithecial apex almost hyaline; the rest of the fungus is unequally colored with diluted rusty red, with the perithecial venter and lower cell of the free appendage distinctly darker. Receptacle tapering throughout, the basal cell abruptly narrow just above the foot, the suprabasal longer, the horizontal septum dividing the two cells associated with a slight constriction. Stalk-cell of the appendage rather short and stout, broadly heart-shaped, very prominent distally. Axis of the appendage consisting of four cells, the lower distinctly larger and darker, about twice as long as broad, the others gradually smaller, each bearing a pair of relatively large antheridia with strongly curved necks, the uppermost of which is spinose. Stalk-cell of the perithecium flattened and subtriangular; the cells above distinctly prominent externally. Perithecial venter relatively short and stout, symmetrically inflated, the spiral wall cells separated by thin furrows; the neck distinctly longer, almost isodiametric above the slightly spreading base; the tip very slightly bent and tapering; the lips strongly unequal, two being short, flattened and divergent, the other two elongate, forming together a tooth-like, suberect prolongation. Total length 280–400 μ m; perithecium 50–70 \times 175–225 μ m; free appendage 55–70 μ m.

Material examined: KENYA, Western Region, Kakamega District, Kakamega Forest, Kisere Forest, about 20 km NE' Kakamega, about 90 km SSE' Mount Elgon



Fig. 82 *Stigmatomyces tschirnhausii* (FI WR3542, **holotype**). Scale bar = 50 μ m

summit, 1597 m asl, forest, Malaise trap, 00°23'07"N, 34°53'16"E, 16 April–16 May 2003, M. Kraemer, on sternites near apex abdomen, antennae and legs of *Dasiops* sp. (Diptera, Lonchaeidae) (FI WR3542, **holotype**).

Notes: The perithecial apex of *Stigmatomyces tschirnhausii* bearing two pairs of lips of very unequal length is reminiscent of the apex of *S. dacinus* Thaxt. The latter, occurring on Tephritidae, shares with the new species also the spirally twisted wall-cells of the perithecial venter, but is quite different in other features, such as the very long

stalk-cell of the appendage, the free appendage longer with the axis consisting of a higher number of cells, the basal of which is sterile, the twist of the perithecial venter extending to the neck (Thaxter 1931). *Stigmatomyces tschirnhausii* is the first species of this genus reported on flies of the family Lonchaeidae. The species of *Stigmatomyces* reported from Kenya to date are four: *S. rugosus* (Rossi

1988), *S. limnophorae* (Rossi et al. 2013), *S. limosinae* Thaxt. and *S. dacinus* (Rossi and Leonardi 2018).

Stigmatomyces vikhrevii* W. Rossi & M. Leonardi, *sp. nov.

Index Fungorum number: IF828164; *Facesoffungi* number: FoF05179; Fig. 83

Fig. 83 *Stigmatomyces vikhrevii* (FI WR3694, paratype). Scale bars = 50 μ m



Etymology: Named after the Russian dipterologist Nikita Vikhrev, who collected the new species.

Holotype: FI WR3691

Receptacle almost hyaline; the rest of the fungus is unequally colored with diluted rusty red, with the perithecial venter and lower cell of the free appendage distinctly darker. Receptacle rather stout, nearly uniform, with the basal cell abruptly tapered at the base and the suprabasal longer, sometimes slightly broader above. Stalk-cell of the appendage short and stout, its outer margin more or less convex. Free appendage also short and stout, with the axis composed of three cells, the lower distinctly darker, each producing a pair of large antheridia, the uppermost of which bears a tiny spine. Stalk-cell of the perithecium much compressed, the secondary stalk-cell larger, with lower and outer convex margins. Perithecial venter elliptical in outline, its wall cells very slightly spiral with a verruculose surface, the verrucosity disposed more or less transversely; passing without abrupt transition to the base of the paler, smooth and shorter neck; the latter erect, its margins very slightly concave, distally broader at its junction with the stout, tapering tip; the subtruncate apex ends in four lips, three of which are very small, subequal and flattened, the fourth rounded and more prominent. Total length 210–415 μm ; perithecium $45\text{--}60 \times 140\text{--}220 \mu\text{m}$; free appendage 50–55 μm ; ascospores 40–45 μm .

Material examined: MALAYSIA, Borneo, Sabah, Kota Kinabalu, 5.99 N, 116.09E, 26–30 December 2011, N. Vikhrev, on the tergites near the apex of the abdomen of *Discomyza maculipennis* (Wiedemann) (Diptera, Ephydriidae) (FI WR3691, **holotype**; FI WR3692, WR3693, WR3694, **paratype**).

Notes: *Stigmatomyces vikhrevii* bears a superficial resemblance to *S. compressus* Thaxt. reported on Jamaican shore-flies, which however has a more slender habit, a different perithecial apex, and a much longer free appendage (Thaxter 1931).

The species of *Stigmatomyces* reported thus far from Malaysia are seven. These are *S. ilythae* Thaxt. (Thaxter 1917), *S. dacinus* Thaxt., *S. limosinoides* Thaxt., *S. tortimasculus* Thaxt. (Thaxter 1918), *S. sygmoideus* Thaxt., *S. subinflatus* Thaxt. (Thaxter 1931) and *S. neurochaetae* W. Rossi et A. Weir (Rossi and Weir 2007). Actually, *S. subinflatus* was described twice: in the first description the host (*Drosophila* sp.) is reported from Cameroon (Thaxter 1918, p. 740), while in the second the collecting place was transferred to “Sarawak, Borneo” (Thaxter 1931, p. 134). The right place seems the second because this is the one reported on the label of the type slide of *S. subinflatus* (Thaxter no. 2180 = FH 6409).

Lecanoromycetes O.E. Erikss. & Winka

Notes: This class represents most of the lichenized members within Ascomycota (Lücking et al. 2017). However, it also includes some non-lichenized ascomycetes (Kirk et al. 2008). Most of the taxa are characterised by apothecial ascomata, while a few form perithecia (Ekanayaka et al. 2017).

Subclass Lecanoromycetidae

Notes: The subclass Lecanoromycetidae with in Lecanoromycetes was established by Hibbett et al. (2007). This subclass comprises Caliciales, Lecanorales, Lecideales, Leprocaulales, Peltigerales, Rhizocarpaceles and Teloschistales (Jaklitsch et al. 2016).

Caliciales Bessey

Notes: This order includes both mazaediate and non-mazaediate genera of both crustose, fruticose and foliose lichenized genera in various habitats (Jaklitsch et al. 2016; Ekanayaka et al. 2017). However the taxa in this order are highly varied in their morphological characters.

Caliciaceae Chevall.

Notes: This family was established by Chevallier (1826) and currently comprises 29 genera and 630 species (Jaklitsch et al. 2016; Wijayawardene et al. 2018a). Taxa are mostly lichenized and form crustose to squamulose, foliose, or fruticose lichen thalli. Ascomata are mostly apothecial (Jaklitsch et al. 2016). Species are widely distributed in temperate, subtropical, and tropical regions, especially on bark, rocks and wood (Jaklitsch et al. 2016).

Buellia De Not.

Notes: The lichen genus *Buellia* was introduced by De Notaris (1846). Currently this genus includes around 400 species. The genus is characterized by black lecideine apothecia, septate, oblong to ellipsoid, rarely citriform, hyaline to brownish ascospores and a deep reddish brown to yellow or yellowish green to rarely hyaline hypothecium (Joshi et al. 2010).

Buellia viridula Ekanayaka & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555467; **Facesoffungi number:** FoF05082; Fig. 84

Etymology: The specific epithet *viridula* refers to the pigment colour in hymenium layer of apothecia.

Holotype: MFLU 16-0587

Saprobic on dead stems. **Sexual morph** **Apothecia** 300–350 \times 110–160 μm (\bar{x} = 331.7 \times 132.6 μm , n = 10), arising singly, erumpent, sessile, black when fresh. **Receptacle** pulvinate, black. **Disc** flat to slightly convex, black. **Margins** black. **Excipulum** 22–38 μm (\bar{x} = 31.5 μm , n = 10) wide at margins and flanks, composed of black cells of *textura angularis*. **Hymenium** blackish green. **Paraphyses** 1–3 μm wide (\bar{x} = 2.1 μm , n = 20), numerous, branched, septate.

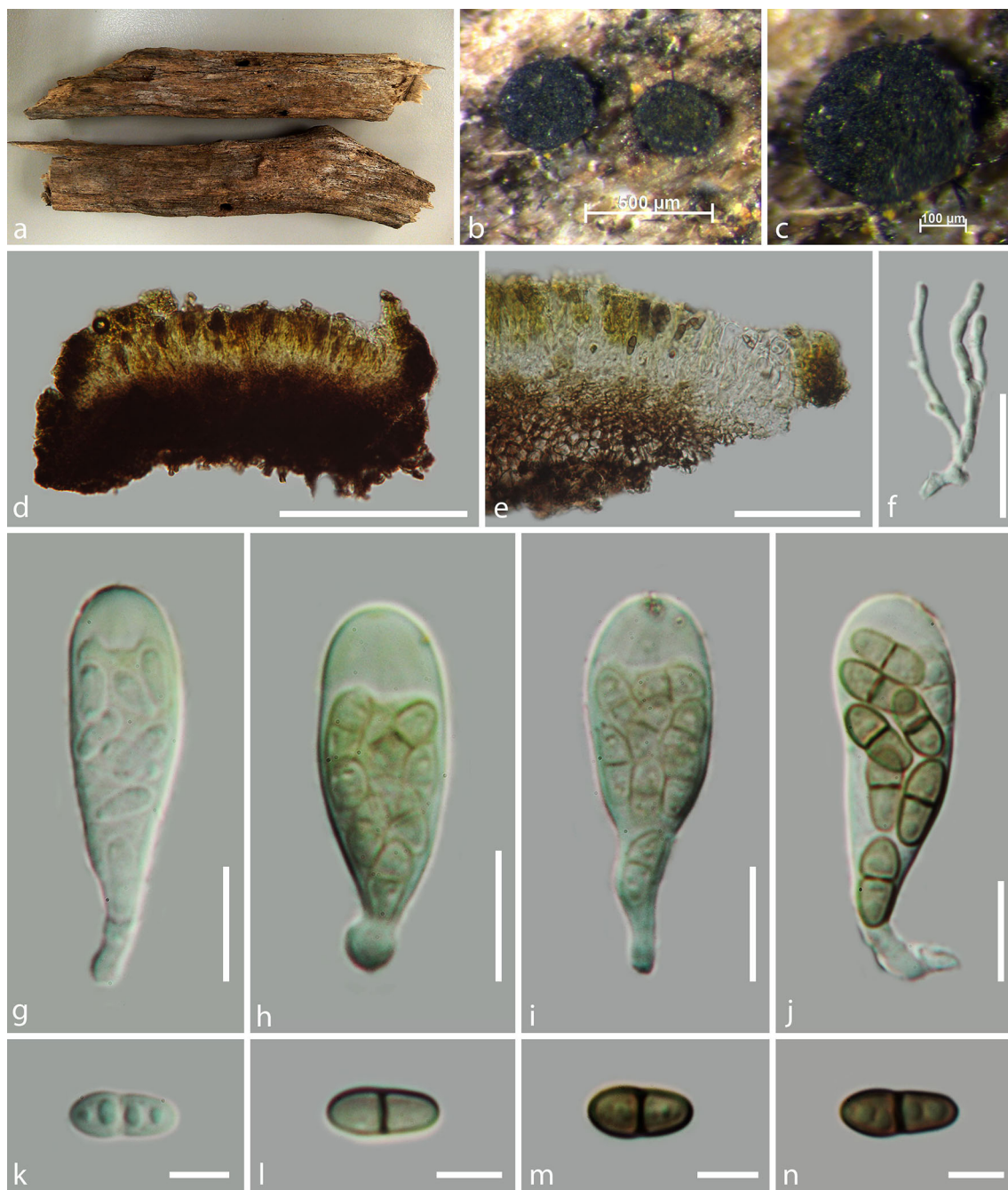


Fig. 84 *Buellia viridula* (MFLU 16-0587, holotype). **a** Substrate. **b**, **c** Ascomata on wood. **d** Cross section of an ascoma. **e** Close up of the cross section of ascoma at margins. **f** Cylindrical paraphyses. **g–j**

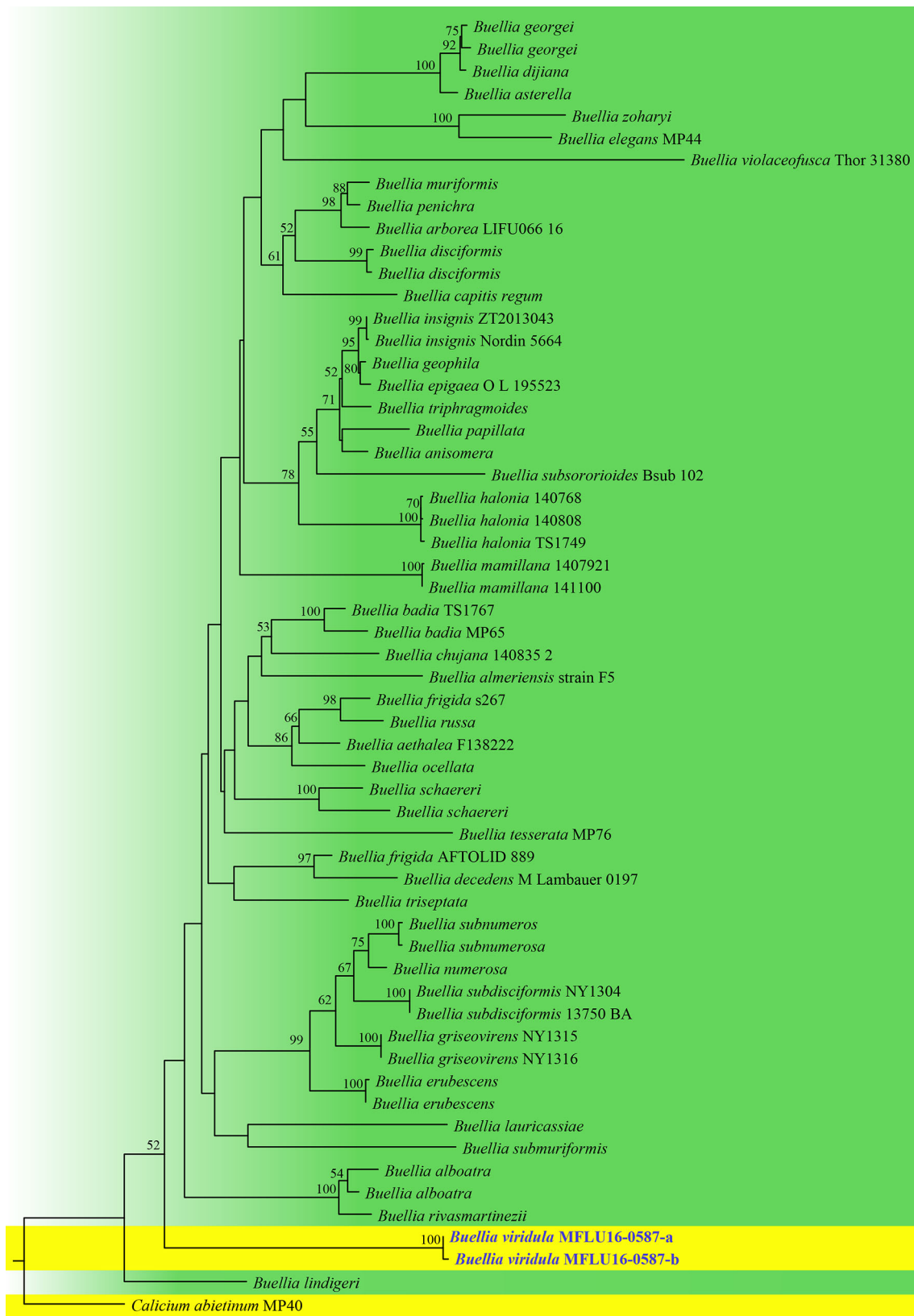
Cylindric-clavate asci. **k–n** Obvoid ascospores. Scale bars: **b** = 500 μ m, **d** = 150 μ m, **c** = 100 μ m, **e** = 60 μ m, **f** = 20 μ m, **g–j** = 10 μ m, **k–n** = 5 μ m

Asci 24–50 \times 8–14 μ m (\bar{x} = 34.3 \times 10.4 μ m, n = 30), 8-spored, globose, long stipitate, apex rounded, inoperculate, amyloid ring absent at the apex. *Ascospores* 7–11 \times 3–4 μ m (\bar{x} = 9.5 \times 3.7 μ m, n = 40), multiseriate, obvoid, immature spore hyaline, greenish brown at maturity, smooth-walled, 1-septate, guttules present. **Asexual morph** undetermined.

Material examined: THAILAND, Chiang Rai Province, Doi Mae Suai, on dead stems, 22 June 2015, A.H. Ekanayaka, HD0026 (MFLU 16-0587 **holotype**; HKAS 104247, **isotype**).

GenBank numbers: ITS: MK075947 (MFLU 16-0587-a), MK075948 (MFLU 16-0587-b).

Notes: *Buellia viridula* is characterized by sessile black apothecia, a blackish excipulum, a blackish green



0.2

◀**Fig. 85** Phylogram generated from a maximum likelihood analysis based on ITS sequence data. The newly generated nucleotide sequences are compared against the GenBank (<http://www.ncbi.nlm.nih.gov/>) database using the Mega BLAST program. Related sequences were obtained from GenBank. Fifty-eight strains were included in the sequence analyses, which comprised 655 characters including gaps. *Calicium abietinum* (MP40) is used as the outgroup taxon. The best scoring RAXML tree with a final likelihood value of -9417.010515 is presented. The matrix had 460 distinct alignment patterns, with 21.50% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.223, C = 0.287, G = 0.258, T = 0.232; substitution rates AC = 1.600208, AG = 2.778296, AT = 1.882342, CG = 0.827224, CT = 6.521407, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.407728$. Bootstrap support values for ML equal or greater than 50% are given above the nodes. The newly generated sequences are in blue

hymenium, globose asci and ellipsoid greenish ascospores. *Buellia viridula* is similar to *B. ocellata* and *B. jugorum* by having coloured hymenium, but the latter two species have ornamented ascospores (Scheidegger 1993). The phylogenetic analysis clearly establishes *B. viridula* as a new species (Fig. 85).

Lecanorales Nannf.

Notes: This order was established by Nannfeldt (1932). Taxa form lichen thalli with protococcoid green photobionts (Crespo et al. 2010; Miadlikowska et al. 2014). The members are widely distributed (Kirk et al. 2008; Ekanayaka et al. 2017).

Lecanoraceae Körb.

Notes: This family was established by Körber (1855). The members of the family are widely distributed and commonly found on rocks, soil or bark (Kalb et al. 2011). Species are characterised by apothecial ascomata, sparingly branched paraphyses, semifissitunicate cylindrical to clavate asci, and ellipsoid, subglobose or bacilliform, hyaline ascospores (Kalb et al. 2011).

Lecidella yunnanensis Ekanayaka, & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555468; **Facesoffungi number:** FoF05083; Fig. 86

Etymology: The specific epithet *yunnanensis* refers to the province where type specimen collected.

Holotype: MFLU 17-1910

Saprobic on dead stems. **Sexual morph** 300–500 × 150–200 µm ($\bar{x} = 368 \times 181$ µm, $n = 10$). **Apothecia** arising singly or in small groups, sessile, slightly erumpent from the substrate, pulvinate, black with shiny appearance. **Receptacle** convex. **Margin** distinct, black. **Hymenium** upper part dark brown and lower part hyaline, within a thick gelatinous matrix. **Ectal excipulum** composed of small, thin-walled, blackish cells of *textura angularis*, with algal cells. **Medullary excipulum** composed of narrow, long, thin-walled, hyaline cells of *textura*

intricata. **Paraphyses** 1–2 µm wide ($\bar{x} = 1.6$ µm, $n = 20$), numerous, filiform, propoloid, septate, slightly swollen at the apices, apices are glued together to develop a pseudoeptithecium. **Asci** 40–50 × 9–13 µm ($\bar{x} = 45 \times 12$ µm, $n = 30$), 8-spored, cylindric-clavate, narrowed to the base, short pedicellate, rounded at the apex, amyloid ring absent at the ascus apex, croziers present at the base of asci. **Ascospores** 10–15 × 5–6 µm ($\bar{x} = 12 \times 5.4$ µm, $n = 40$), hyaline when immature, greenish brown at maturity, smooth walled, ellipsoid, 1-septate, guttulate.

Material examined: CHINA, Kunming, Yunnan Province, 25 April 2016, A.H. Ekanayaka, HC 001, HC004 (MFLU 17-1910, **holotype**).

GenBank numbers: ITS: MK075945, LSU: MK075949 (MFLU 17-1910-a); ITS: MK075946, LSU: MK075950 (MFLU 17-1910-b).

Notes: *Lecidella yunnanensis* is characterized by black, sessile, pulvinate apothecia, with a black disk with a shiny appearance, propoloid septate paraphyses, cylindric-clavate asci and ellipsoid ascospores. *Lecidella yunnanensis* is similar to *Lecidella enteroleuella*, however *L. enteroleuella* differs from *L. yunnanensis* by having black, greenish to reddish brown to olive disks and a hyaline hymenium layer (Nash et al. 2004). In the phylogenetic analysis, *L. yunnanensis* groups clearly distinct from known species of *Lecidella* (Fig. 87).

Pilocarpaceae Zahlbr.

Notes: Pilocarpaceae is a family of mainly crustose lichens, including mostly foliicolous lineages, plus the bulk of species currently classified in the genus *Micarea*, previously placed in a separate family Micareaceae (Andersen and Ekman 2004, 2005; Miadlikowska et al. 2014).

Micarea Fr.

Notes: The genus *Micarea* itself is highly heterogeneous, with several lineages falling outside the genus in its proper sense and even outside the Pilocarpaceae; the monophyletic core group also possibly represents more than one genus (Czarnota and Guzow-Krzemińska 2010; Schmull et al. 2011; Ekman and Svensson 2014). Here, we introduce a new species with squamulose thallus that forms an isolated lineage within the monophyletic *Micarea* core clade (Fig. 89). It might well represent a separate genus, but further data are required to resolve this entire clade taxonomically.

Micarea squamulosa Aptroot, Lücking & M. Cáceres, *sp. nov.*

Index Fungorum number: IF555463; **Facesoffungi number:** FoF05966; Fig. 88

Etymology: Referring to the squamulose thallus.

Holotype: M. E. S. Cáceres & A. Aptroot ISE 40719 (ISE)



Fig. 86 *Lecidella yunnanensis* (MFLU 17-1910, **holotype**). **a** Substrate. **b** Ascomata on wood. **c** Cross section of an ascoma. **d** Close up of a vertical section of the ascoma at margin. **e** Aseptate paraphyses.

f–i Short pedicellate asci. **j–m** Ovate ascospores. Scale bars: **c**, **d** = 100 µm, **e** = 20 µm, **f–i** = 15 µm, **j–m** = 6 µm

Terricolous squamulose *Micarea* with loose to agglutinated, olive-green lobes which are flat to terete and solid to hollow, without rhizines; apothecia immarginate, dark brown, ascospores hyaline, ellipsoid, $11\text{--}12 \times 6\text{--}6.5$ µm. *Thallus* squamulose, terricolous, extending up to 2 cm diam., consisting of loose to crowded and occasionally agglutinated, simple to plicate or lobate flat to ascending squamules of c. 0.4–1.2 mm diam. *Squamules* entire to shallowly incised, partly saddle-shaped to erect, olive green, not pruinose, smooth but not shiny; margins rather thick and rounded, of the same colour as the upper surface; lower surface dull, pale olive green, without rhizines; medulla whitish, often becoming hollow, up to 300 µm

thick; marginal lobes more often flat, solid and elongate than the central lobes which are more often erect and hollow. *Photobiont* green. *Ascomata* apothecia, superficial on the thallus, solitary and centrally on the squamules, round to irregular in outline, 0.2–0.6 mm diam.; disc dark brown to dark grey, convex, dull; margin c. 0.1 mm wide, dark brown (paler inside), glossy, not visible from above. *Hymenium* hyaline, c. 60 µm high; epihymenium olive brown; excipulum dark brown outside, hyaline inside; hypothecium contiguous with the excipulum, hyaline. *Paraphyses* rather agglutinated. *Asci* cylindrical, with 8 ascospores. *Ascospores* hyaline, ellipsoid, $11\text{--}12 \times 6\text{--}6.5$ µm, thin-walled, without gelatinous sheath

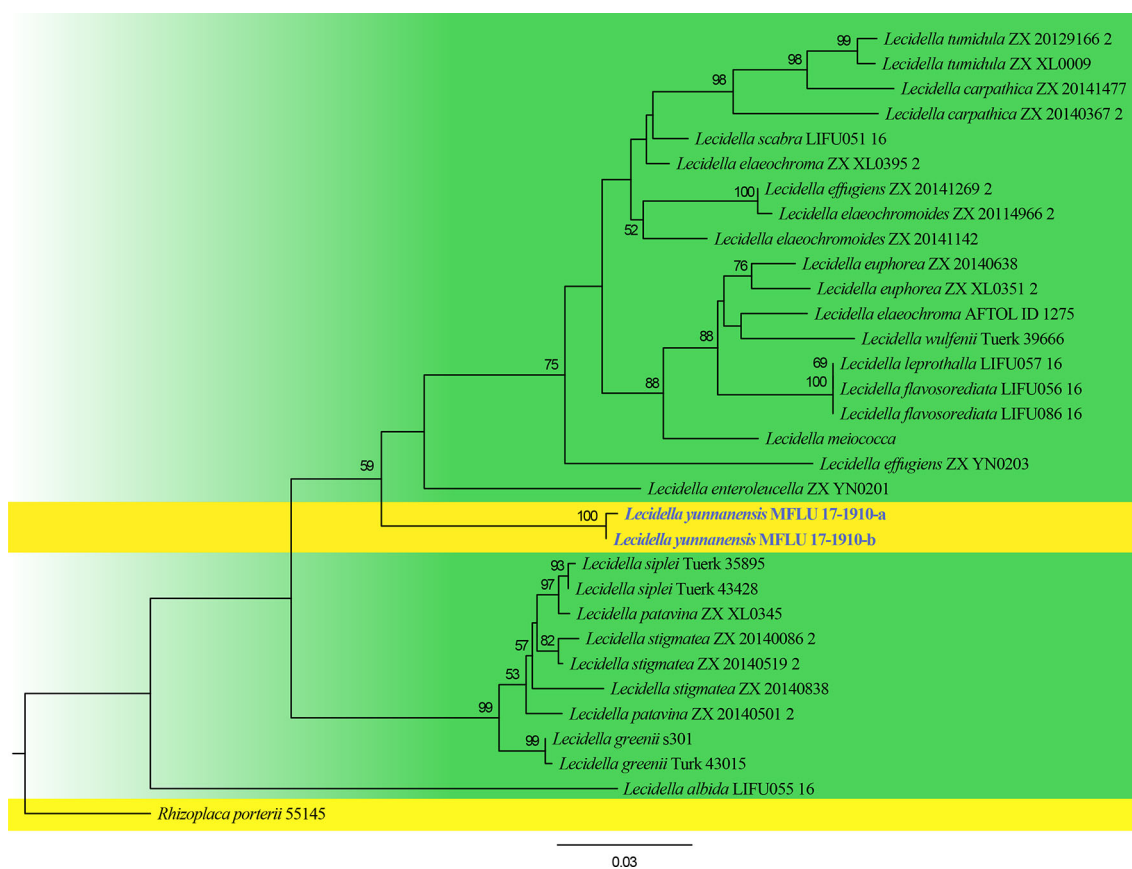
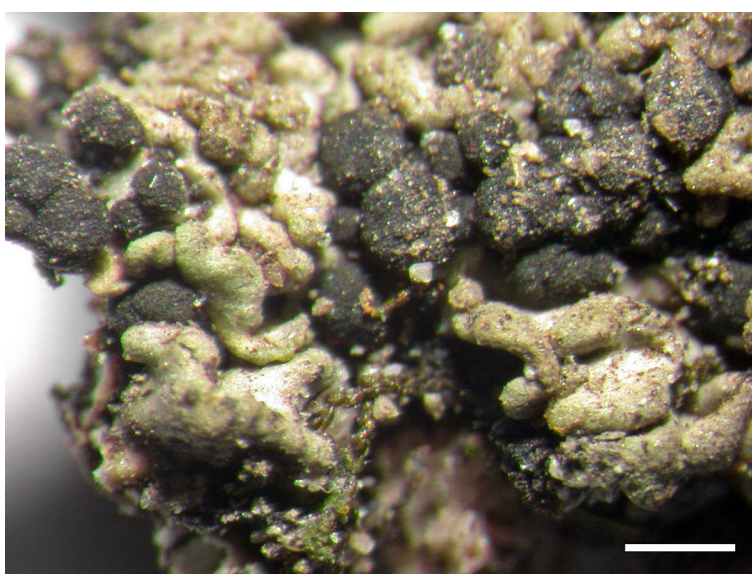


Fig. 87 Phylogram generated from a maximum likelihood analysis based on combined ITS and LSU sequence data. The newly generated nucleotide sequences are compared against the GenBank database using the Mega BLAST program. Related sequences were obtained from GenBank. Fifty-eight strains were included in the sequence analyses, which comprised 1397 (ITS-1-607, LSU-608-1397) characters including gaps. *Rhizoplaca porterii* 55145 is used as the outgroup taxon. The best scoring RAXML tree with a final likelihood

value of -5739.681991 is presented. The matrix had 462 distinct alignment patterns, with 31.86% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234, C = 0.258, G = 0.284, T = 0.224; substitution rates AC = 1.101172, AG = 2.447560, AT = 1.586081, CG = 0.813290, CT = 8.452097, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.205506$. Bootstrap support values for ML equal or greater than 50% are given above the nodes. The newly generated sequences are in blue

Fig. 88 *Micarea squamulosa* (isotype). Habitus. Scale bar = 0.5 mm



but usually with a central vacuole/oil droplet. *Pycnidia* not observed. *Secondary chemistry*: Cortex and medulla K–, P–, C–, UV–. TLC: Atranorin, gyrophoric acid and skyrin; all apparently in concentrations which are too low for spot reactions.

Material examined: BRAZIL. BAHIA: Chapada Diamantina, Lençóis, Cachoeira do Mosquito; 12°23' S, 41°22'40" W, alt. c. 450–500 m; 22 July 2017, on siliceous soil, M.E.S. Cáceres & A. Aptroot ISE 40719 (**ISE holotype**; **ABL isotype**).

Notes: This species looks strongly like a small species of *Toninia*, especially because of the olive-green, often contorted squamules with rounded margins and often hollow medulla. Timdal (1991) did not accept any of the ten species originally described from Brazil in this genus; they were partly referred to other genera by him, and partly excluded without alternative generic dispositions. Aptroot (2002) referred some of these to the genera *Bacidiopsis* and *Micarea*. The first genuine *Toninia*, *T. massata* (Tuck) Herre, was reported from Brazil only recently by Cáceres et al. (2017), from Ceará state. The present species differs from all previously reported toninioid species from the country. Sequence data of the mitochondrial small subunit rDNA (GenBank accession: MK080110) place this taxon

in the Pilocarpaceae, in the monophyletic *Micarea* core clade (Fig. 89); however, no distinctly squamulose taxa were known in this clade before. This clade remains unresolved and may include several genera, apart from *Micarea* s.str., which is represented by the strongly supported *M. prasina* subclade. In that case, the squamulose taxon may represent a separate genus. The species previously reported as *Toninia* from Brazil or similar taxa elsewhere also need to be resampled, to test whether some of these are related to the *M. bullata* lineage.

The species was found in the Chapada Diamantina, an area in the state of Bahia in tropical northeastern Brazil representing the second largest conserved area in the country outside the Amazon (Funch et al. 2009). The natural vegetation of the Chapada Diamantina includes various types of evergreen moist and semi-deciduous dry tropical forest, belonging to the Caatinga, Cerrado and Atlantic rain forest biomes and the Restinga-like Capitinga (Funch et al. 2009). The siliceous bedrock, geologically mostly of precambrian origin, surfaces in many parts in the form of isolated inselbergs surrounded by forest. These inselbergs are usually only up to 500 m higher than the surrounding landscape, but the meso- and microclimate on the often rather flat tops and the generally very steep slopes

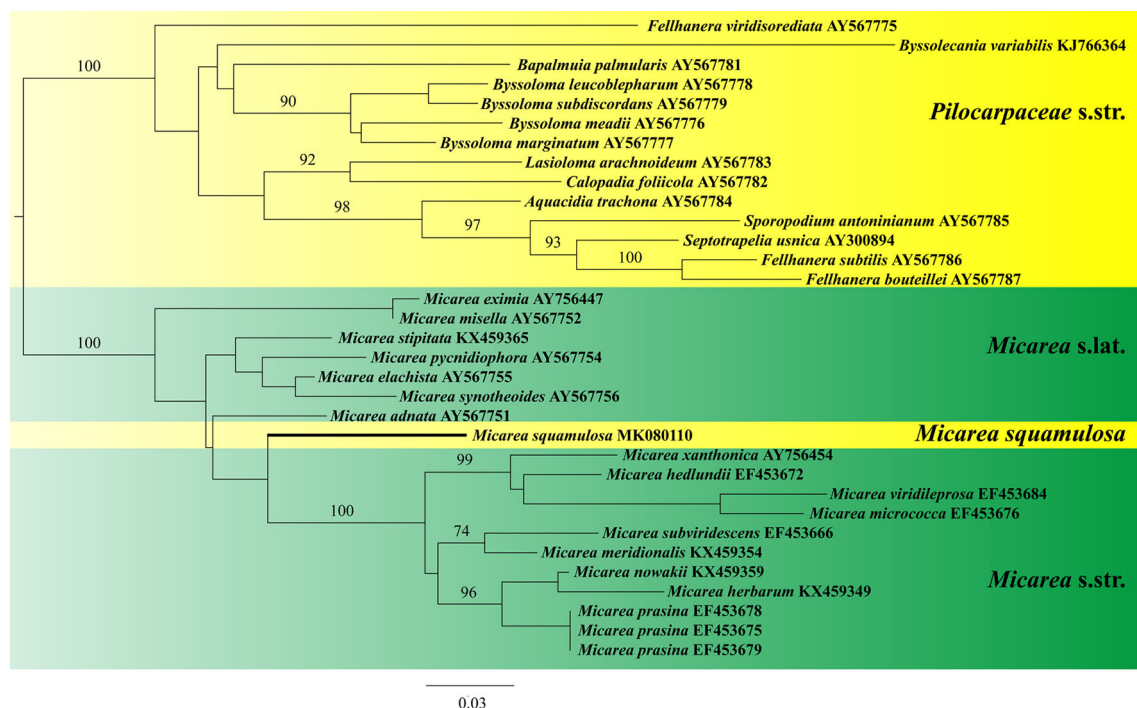


Fig. 89 Best-scoring maximum-likelihood tree of a subset of Pilocarpaceae based on mtSSU sequence data, including the Pilocarpaceae core (as outgroup or sister clade) and the *Micarea* core clade, showing the position of the new species, *M. squamulosa*. GenBank accession numbers are indicated in the tree figure. The final alignment comprised 914 columns, with 450 distinct alignment patterns, and the final likelihood was –6458.814273. Estimated base

frequencies were as follows: A = 0.335039, C = 0.150256, G = 0.201024, T = 0.313681, and substitution rates as follows: AC = 1.022403, AG = 4.972129, AT = 1.612594, CG = 0.507417, CT = 4.968323, GT = 1.000000, with the gamma distribution shape parameter α = 0.290696. Bootstrap values based on 1000 pseudoreplicates are placed above the branches

differs markedly from that in the surrounding areas, leading to the presence of so-called campos rupestres, to some extent resembling elfin forest but dominated by sclerophyllous small trees and shrubs adapted to the particular edaphic and climatic conditions of this habitat (Conceição et al. 2007; Funch et al. 2009). So far, around 300 lichenized species have been reported from the region (Kalb 1986; Ahti and Oksanen 1990; Kashiwadani and Kalb 1993; Mendonça et al. 2016; Aptroot and Cáceres 2018a, b; Kalb and Aptroot 2018), many from a single field trip during which also the following enigmatic squamulose lichen was collected, on vertical soil at a raised ledge in the middle of a river. The new species was found on wet sand with bryophytes and a possibly undescribed Gyalideopsis on a vertical ledge, in crevices between sandstone bedrock, on a small island in a broad river near a waterfall. The location is very wet and poor in nutrients.

Ostropomycetidae V. Reeb, Lutzoni & Cl. Roux

Notes: *Ostropomycetidae* is the second largest subclass in class *Lecanoromycetes*, including six orders with mostly lichenized taxa but also some secondarily delichenized lineages (Lücking et al. 2017).

Ostropales Nannf.

Notes: *Ostropales* is the largest order of subclass *Ostropomycetidae*, with 11 families, approximately 140 genera, and well over 3200 accepted species (Lücking et al. 2017). Among the largest families are Graphidaceae and Porinaceae, with a new genus in Graphidaceae and a new species in Porinaceae introduced below.

Porinaceae Rchb.

Notes: *Porinaceae* is a mid-sized family of approximately 360 known species, currently classified in six genera (Lücking et al. 2017). The generic concept is in flux and based on molecular data, at least 15 genus-level lineages can be distinguished (Sobreira et al. 2018). All *Porinaceae* produce perithecioid ascomata and are rather uniform in their internal morphology; some lineages also reproduce vegetatively by means of isidia or isidioid structures and rarely soredia. The latter are characteristic of the genus *Myeloconis* (McCarthy and Elix 1996) but otherwise unknown in the family. Here we describe a new species with exposed, black perithecia and a sorediate thallus (Fig. 90) which based on ITS sequence data belongs in the *Porina byssophila* clade (Fig. 91), representing an unnamed genus (Sobreira et al. 2018) corresponding to *Pseudosagedia* subgen. *Limosagedia* Hafellner & Kalb (1995).

Porina sorediata Aptroot, Lücking & M. Cáceres, *sp. nov.*

Index Fungorum number: IF555464; *Facesoffungi* number: FoF05967; Fig. 90

Etymology: Referring to the sorediate thallus, an unusual feature in the family except in the genus *Myeloconis*.

Holotype: M. E. S. Cáceres & A. Aptroot ISE 42451 (ISE)

Porina with capitate soralia and black semiglobose perithecia with 3-septate, somewhat curved ascospores with rounded ends, of $14\text{--}15 \times 3.5\text{--}4\ \mu\text{m}$. *Thallus* covering areas of bark of up to 20 cm diam., mostly smooth and often somewhat glossy, greyish green, not surrounded by a differentiated prothallus; photobiont tentepohlioid, globiose to usually ellipsoid, c. $7\text{--}12 \times 6\text{--}8\ \mu\text{m}$. *Soralia* numerous, round, globose, somewhat paler than the thallus, especially when abraded, c. 0.2–0.5 mm diam. *Soredia* farinose, globose to usually ellipsoid, c. $17\text{--}27 \times 10\text{--}18\ \mu\text{m}$, consisting of one trentepohlioid algal cell of c. $7\text{--}12 \times 6\text{--}8\ \mu\text{m}$, surrounded by dozens of hyaline, semiglobose to somewhat angular hyphal cells with lumina of c. $2\text{--}3\ \mu\text{m}$. *Ascomata* uncommon, perithecia, black, semiglobose, c. 0.2 mm diam., c. 0.1 mm high. *Wall* clearly differentiated into a proper ascoma wall and an involucrellum which covers the exposed half of the ascoma with a separate layer; both layers purple-brown, unchanged in KOH. *Ascospores* 8/ascus, hyaline, 3-septate, somewhat curved with rounded ends, $14\text{--}15 \times 3.5\text{--}4\ \mu\text{m}$.

Material examined: Brazil, Alagoas, Quebrangulo, Reserva Biológica de Pedra Talhada, private area, $9^{\circ}15'S$, $36^{\circ}25'35''W$, on tree bark, c. 600 m alt., 21–23 Oct 2017, M.E.S. Cáceres & A. Aptroot ISE 42451 (**ISE holotype**; **ABL isotype**); Same locality and details, ISE 42328, 42450 & 42675 (ISE, ABL).

Notes: Only three species in the family *Porinaceae* are known to form soredia, all in the genus *Myeloconis* (McCarthy and Elix 1996). Species of the latter genus have brightly pigmented soredia and medulla, perithecia with pale walls, and large, muriform ascospores, thus quite different from the new species. Species with exposed, black perithecia occur in several lineages of *Porinaceae*, including the genera *Pseudosagedia* and *Trichothelium* and the *Porina byssophila* clade (Sobreira et al. 2018). Unfortunately, we were unable to generate mtSSU data for the present taxon, and the nuLSU primers sequenced a fungal contaminant. However, the ITS data (GenBank accession: MK080109) place the new species in the *P. byssophila* clade, together with *P. guentheri* (Fig. 91). This is notable, as the *P. byssophila* clade, in spite of its very different morphology, is closely related to the genus *Myeloconis* based on mtSSU data (Sobreira et al. 2018), and hence the molecular phylogeny brings the lineages with soredia rather close together. Hafellner and Kalb (1995) established subgenus *Limosagedia* for a subgroup of species within *Pseudosagedia*, with *Porina linearis* (Leight.) Zahlbr. as type but including also *P. byssophila*. The stated difference was the K + bluish outer perithecial wall. Thus,

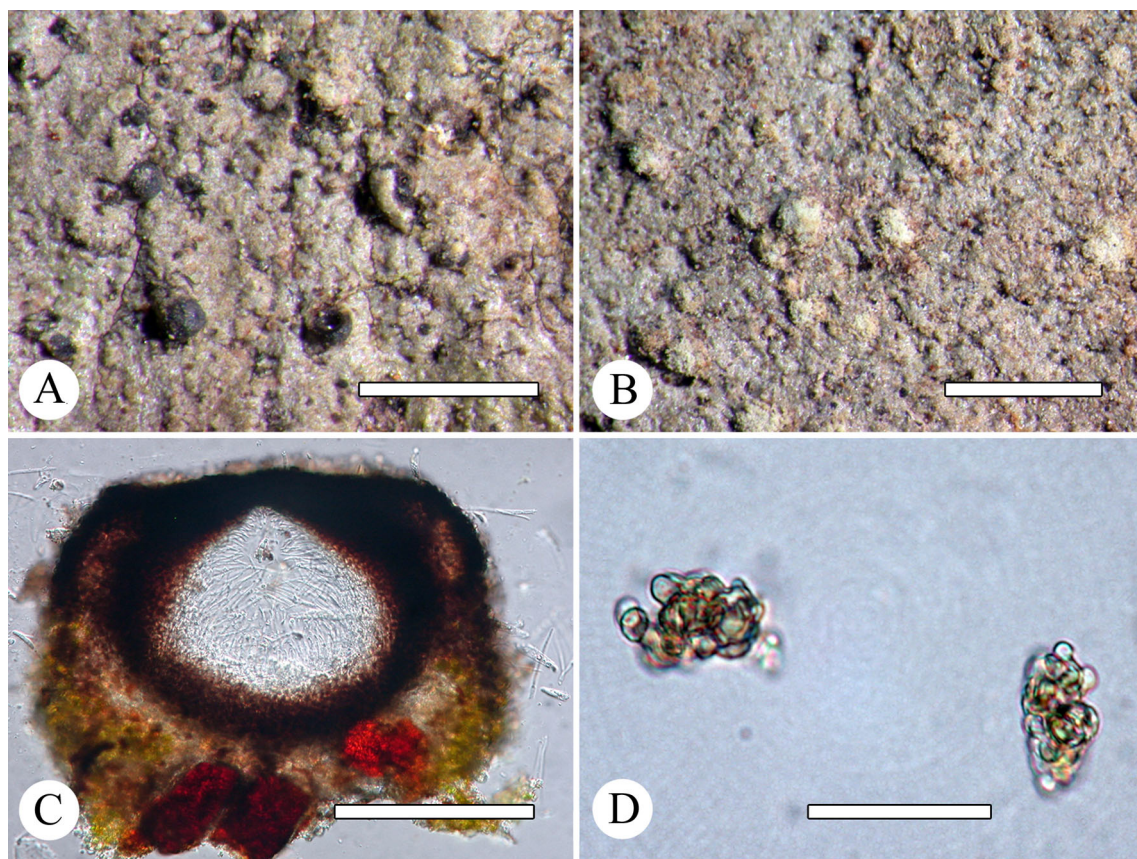


Fig. 90 *Porina soredata* (isotype). **a** Thallus with ascomata and soralia. **b** Thallus with soralia. **c** Section through ascoma. **d** Soredia. Scales bars: **a**, **b** = 1 mm, **c** = 0.2 mm, **d** = 50 μ m

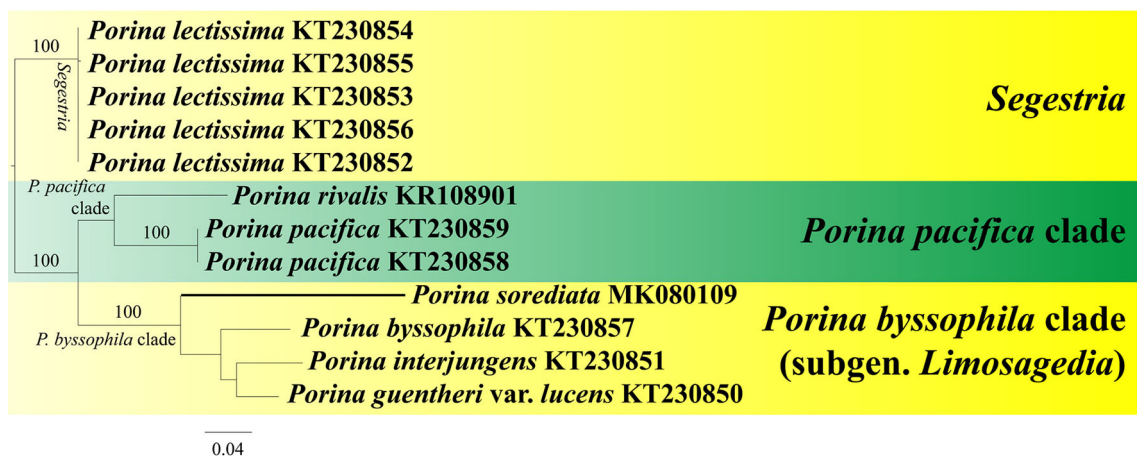


Fig. 91 Best-scoring maximum-likelihood tree of available subset of Porinaceae based on ITS sequence data, showing placement of *P. soredata* in the *P. byssophila* clade which, based on mtSSU sequence data, is closely related to the genus *Myeloconis* (Sobreira et al. 2018). The final alignment comprised 534 columns, with 210 distinct alignment patterns, and the final likelihood was −1903.538679.

Estimated base frequencies were as follows: A = 0.187911, C = 0.338406, G = 0.295727, T = 0.177956, and substitution rates as follows: AC = 1.312730, AG = 3.551014, AT = 2.797834, CG = 1.299677, CT = 6.511396, GT = 1.000000, with the gamma distribution shape parameter α = 0.330010. Bootstrap values based on 1000 pseudoreplicates are placed above the branches

Limosagedia could potentially be a name available for this clade when raised to genus level; however, in the present species no such K-reaction was observed. The new taxon

was found in the Pedra Talhada Biological Reserve in the state of Alagoas, northeastern Brazil, where it was locally quite common on shaded bark of various trees, but it has

not been observed in any other site in this locality, a phenomenon also known from other species that appear to represent local endemics. Pedra Talhada Biological Reserve is ecologically quite unique, representing one of the larger remnants of Atlantic rain forest in northeastern Brazil, with various phytophysiognomies formed on inselbergs built from precambrian gneiss (Nusbaumer et al. 2015; Studer et al. 2015). The new species is thus far only known only from Brazil.

Graphidaceae Dumort.

Notes: Graphidaceae is the second largest family of lichenized *Ascomycota*, containing over 2000 known species and about 80 genera (Lücking et al. 2017). Although most lineages have been sequenced, odd taxa that do not fit any of the genera now recognized continue to be encountered on a regular basis (Lumbsch et al. 2014). Here we describe a new genus based on sequenced material found in the same area as *Porina sorediata*, described elsewhere in this paper. The species was identified as the rare *Thelotrema cryptotrema* Nyl., later recombined as *Ocellularia cryptotrema* (Nyl.) Kalb and more recently as *Schizotrema cryptotrema* (Nyl.) Rivas Plata & Mangold (Rivas Plata et al. 2010). Sequence data show that the taxon is unrelated to *Thelotrema* or *Schizotrema* and instead forms a novel lineage in tribe *Ocellulariae*, related to the *Ocellularia profunda* and *O. praestans* clades (Fig. 93). The latter two are not members of *Ocellularia* sensu stricto and will require new genera placement as well, but here we formally describe a new genus for *Thelotrema cryptotrema*, which in addition to its phylogenetic placement also exhibits some unusual features within tribe *Ocellularieae* (Fig. 92).

Cryptoschizotrema Aptroot, Lücking & M. Cáceres, *gen. nov.*

Index Fungorum number: IF555465; **Facesoffungi number:** FoF05968

Etymology: Referring to the anatomical resemblance with *Schizotrema* species, due to the partially carbonized and concentrically layered, fissured excipulum, and the notion that the *Schizotrema*-like excipulum is hidden beneath a covering layer.

Type species: *Cryptoschizotrema cryptotrema* (Nyl.) Aptroot, Lücking & M. Cáceres.

Cryptoschizotrema cryptotrema (Nyl.) Aptroot, Lücking & M. Cáceres, *comb. nov.*

Index Fungorum number: IF555466; **Facesoffungi number:** FoF05969; **Fig.** 92

= *Thelotrema cryptotrema* Nyl., Ann Sci Nat Bot Sér 5, 7: 318 (1867).

= *T. secoligella* Müll. Arg., Hedwigia 34: 31 (1895).

= *T. annulatum* Müll. Arg., J Linn Soc Bot 30: 453 (1895).

New genus in Graphidaceae with myriotremoid to porinoid, immersed-erumpent ascomata with a narrow pore, dark brown to partially (apically) carbonized, fissured and becoming concentrically layered excipulum lacking periphysoids, muriform, subdistoseptate, I-negative (non-amyloid) ascospores with thin walls and septa, and psoromic acid chemistry. *Thallus* light greenish grey, uneven-verrucose, with dense, prosoplectenchymatous cortex. *Ascomata* immersed-erumpent, rounded, disc covered by narrow pore, invisible; proper margin covered by whitish thalline layer, not visible, when abraded seen as brown to black, fissured lobules forming concentric layers in older ascomata. *Columella* absent. *Excipulum* prosoplectenchymatous, brown to partially (apically) carbonized, becoming layered (striate) in older ascomata; periphysoids absent. *Hymenium* clear; paraphyses unbranched. *Ascospores* 1–2(–4)/ascus, richly muriform, up to 100 × 30 µm, oblong-ellipsoid, distoseptae with rather thin walls and septa and angular lumina, colorless, I– (non-amyloid). **Secondary chemistry:** psoromic acid (thallus P + yellow).

Material examined: Brazil, Alagoas, Quebrangulo, Reserva Biológica de Pedra Talhada, private area, 9°15'S, 36°25'35"W, on wooden pole, c. 550 m alt., 21–23 Oct 2017, M.E.S. Cáceres & A. Aptroot ISE 42655 (**ABL, B, ISE**).

Notes: Tribe *Ocellularieae* largely comprises the taxa previously classified in the collective genera *Myriotrema* and *Thelotrema* (Hale 1980; Lumbsch et al. 2014). Both are highly polyphyletic, as shown by Frisch et al. (2006) and Rivas Plata et al. (2012), and even after formally segregating several lineages as new genera, quite a number of orphaned lineages remain unnamed. Our results show that *Thelotrema cryptotrema* (nuLSU Genbank accession: MK080108) represents an additional lineage in this heterogeneous assembly, related to the *O. profunda* and *O. praestans* clades. This topology would theoretically allow to include the latter two clades together with *T. cryptotrema* in a single genus, for which the here established name would then be available. However, at this time we refrain from placing additional species in *Cryptoschizotrema*, since the long branches leading to each clade (Fig. 93) do not suggest a single genus to be involved and the differences between *Cryptoschizotrema* and the other two clades are substantial, including the massive, fully carbonized and non-striate excipulum and the distoseptate, I + violet-blue (amyloid) ascospores in *O. profunda* and *O. praestans* and relatives.

This monospecific new genus is thus far only known from Central and South America. It is tropical lowland to montane species growing on bark or wood; the sequenced specimen was found in Brazilian Atlantic Rain Forest, on a

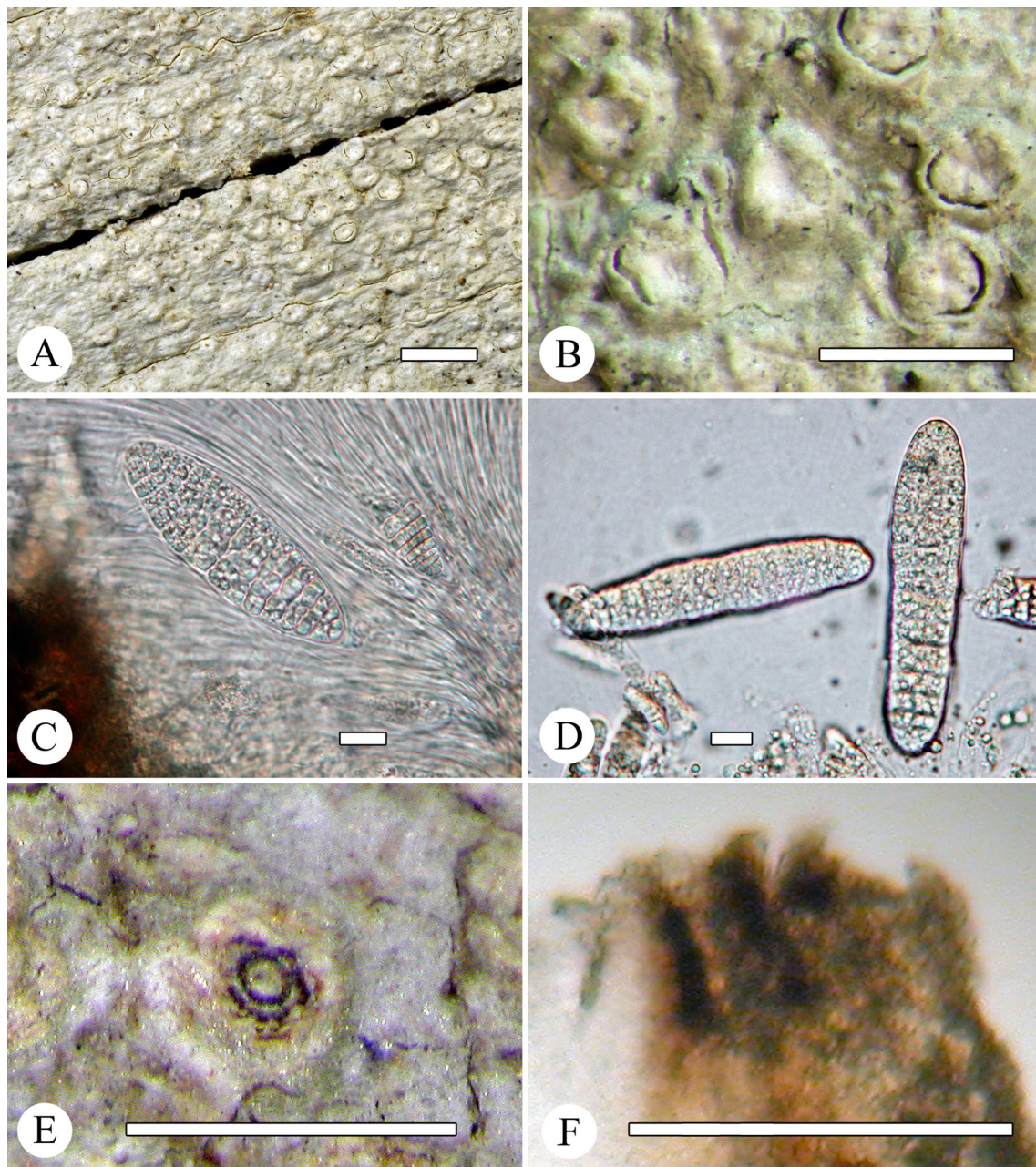


Fig. 92 *Cryptoschizotrema cryptotrema*. **a–d** Cáceres & A. Aptroot ISE 42655. **e, f** isotype of *T.annulatum* in BM). **a** Thallus with ascomata. **b** Ascomata enlarged. **c** Hymenium with asci and ascospores. **d** Ascospores. **e** Abraded ascoma showing schizotremoid

proper margin (photograph A. Mangold). **f** Section through ascoma showing striate, apically carbonized excipulum (photograph A. Mangold). Scale bars: **a** = 1 mm, **b, e** = 0.5 mm, **c, d** = 10 μ m, **f** = 100 μ m

wooden pole of a fence dividing different parts of the reserve.

Leotiomyces O.E. Erikss. & Winka

Notes: Leotiomyces is the largest the largest class of inoperculate discomycetes, a group of nonlichenized ascomycetes (Eriksson and Winka 1997; Lumbsch et al. 2005; Zhang and Wang 2015; Ekanayaka et al. 2017).

Wijayawardene et al. (2018a) accepted 11 orders and 44 families in Leotiomyces.

Helotiales Nannf.

Notes: Helotiales species are abundant in humid areas as saprobes on dead leaves and shoot on herbaceous and woody plants (Webster 2007). In addition, they occur as plant pathogens and endophytes. Helotiales is a highly

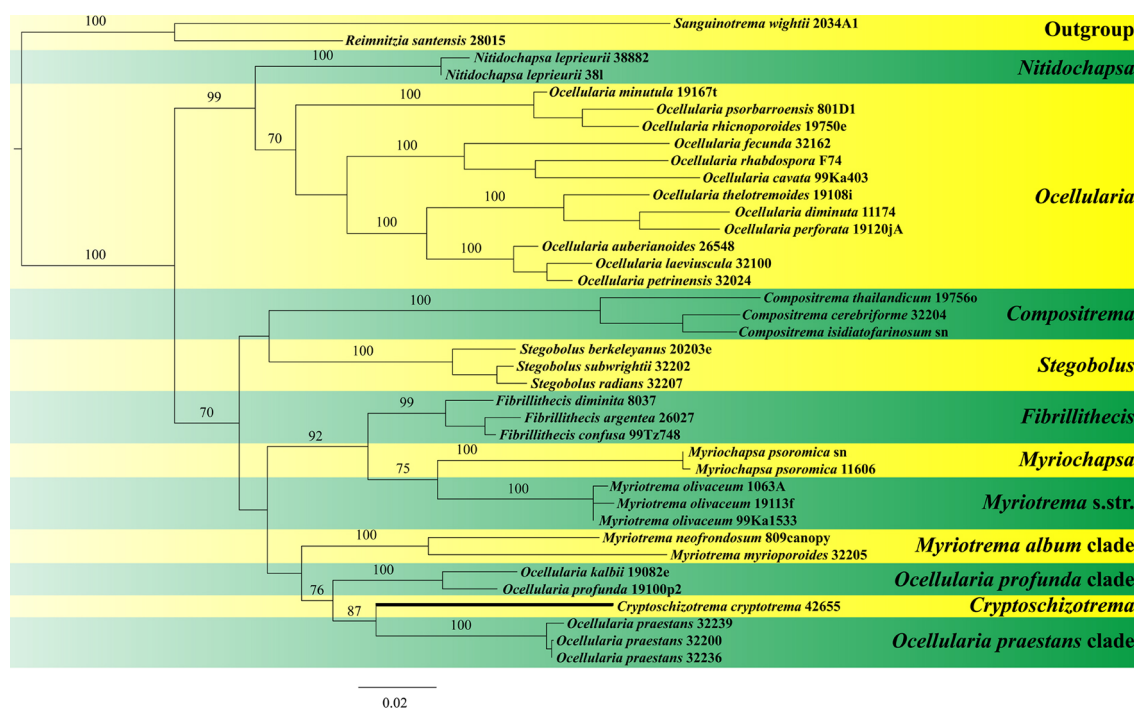


Fig. 93 Best-scoring maximum-likelihood tree of subset of Graphidaceae tribe *Ocellularieae* based on three markers (mtSSU, nuLSU, RPB2), showing placement of *Cryptoschizotrema cryptotrema* near the *O. profunda* and *O. praestans* clades. The final alignment comprised 2618 columns, with 983 distinct alignment patterns, and the final likelihood was -14732.747014 . Estimated base frequencies

were as follows: A = 0.289260, C = 0.202949, G = 0.260731, T = 0.247061, and substitution rates as follows: AC = 0.929088, AG = 3.966253, AT = 2.046683, CG = 0.790669, CT = 7.857784, GT = 1.000000, with the gamma distribution shape parameter $\alpha = 0.231216$. Bootstrap values based on 1000 pseudoreplicates are placed above the branches

diversified order and accommodates 27 families (Ekanayaka et al. 2017; Wijayawardene et al. 2018a).

Chaetomellaceae Baral, P.R. Johnst. & Rossman

Notes: Chaetomellaceae was introduced by Baral et al. (2015) with its type genus *Chaetomella* Fuckel to accommodate non-lichenized discomycetes as a family *insertae sedis* in Leotiomyces. ITS and LSU based phylogenetic study revealed that the family consists of four genera viz. *Chaetomella* (= *Zoellneria*), *Pilidium* Kunze (= *Discohainesia*), *Sphaerographium* Sacc. and *Synchaetomella* Decock & Seifert. Wijayawardene et al. (2018a) accepted the family in the Helotiales (Leotiomyces).

Pilidium Kunze

Notes: The genus *Pilidium* was introduced with *P. acerinum* (Alb. & Schwein.) Kunze as the type species with a *Hainesia* synasexual, and *Discohainesia* sexual morphs (Rossman et al. 2004; Johnston et al. 2014). Currently, 22 accepted *Pilidium* species have been reported as saprobes and pathogens on various hosts (Wijayawardene et al. 2017a).

Pilidium concavum (Desm.) Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 124: 148 (1915)

Facesoffungi number: FoF05212; Fig. 94

Saprobic on dead flower petals and leaves of *Rosa* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* sporodochial, 175–200 μm high (\bar{x} = 185 μm , n = 10), 122–140 μm diam. (\bar{x} = 133.5 μm , n = 10), 48–56.5 μm (\bar{x} = 52.5 μm , n = 5) wide at the base, superficial, scattered, sessile, relatively sphaerical, initially yellowish brown, turning brownish or almost black, initially convex cap turning to concave. *Peridium* thick, *textura angularis*. *Conidiophores* 11.2–19.8 \times 1.0–1.4 μm (\bar{x} = 15.6 \times 1.2 μm , n = 10), a dense palisade, hyaline to pale brown, tapering distally. *Conidiogenous cells* 2.2–3.3 \times 0.8–1.1 μm (\bar{x} = 2.6 \times 0.9 μm , n = 10), enteroblastic, phialidic, hyaline, tapering towards the apex, terminal and lateral. *Conidia* 4.8–7.4 \times 1.5–2.4 μm (\bar{x} = 6.1 \times 1.9 μm , n = 40), L/W 3.2, 1-celled, hyaline, fusoid to allantoid, slightly falcate, apex acute, base obtuse, thin-walled, guttules at both ends, formed singly on the conidiogenous cells.

Culture characteristics: Colonies reaching to 36.5 mm after 2 weeks at 28 °C on PDA with two zones. Inner zone dirty yellow to light brown, flat, slightly clock wise rotate sparse mycelia, reverse light brown; outer layer dirty white, flat, smooth, lobate margin, reverse dirty white. Later, zonate, dirty white, flat surface, smooth with light brown patches, reverse dark brown centre and light brown margin.

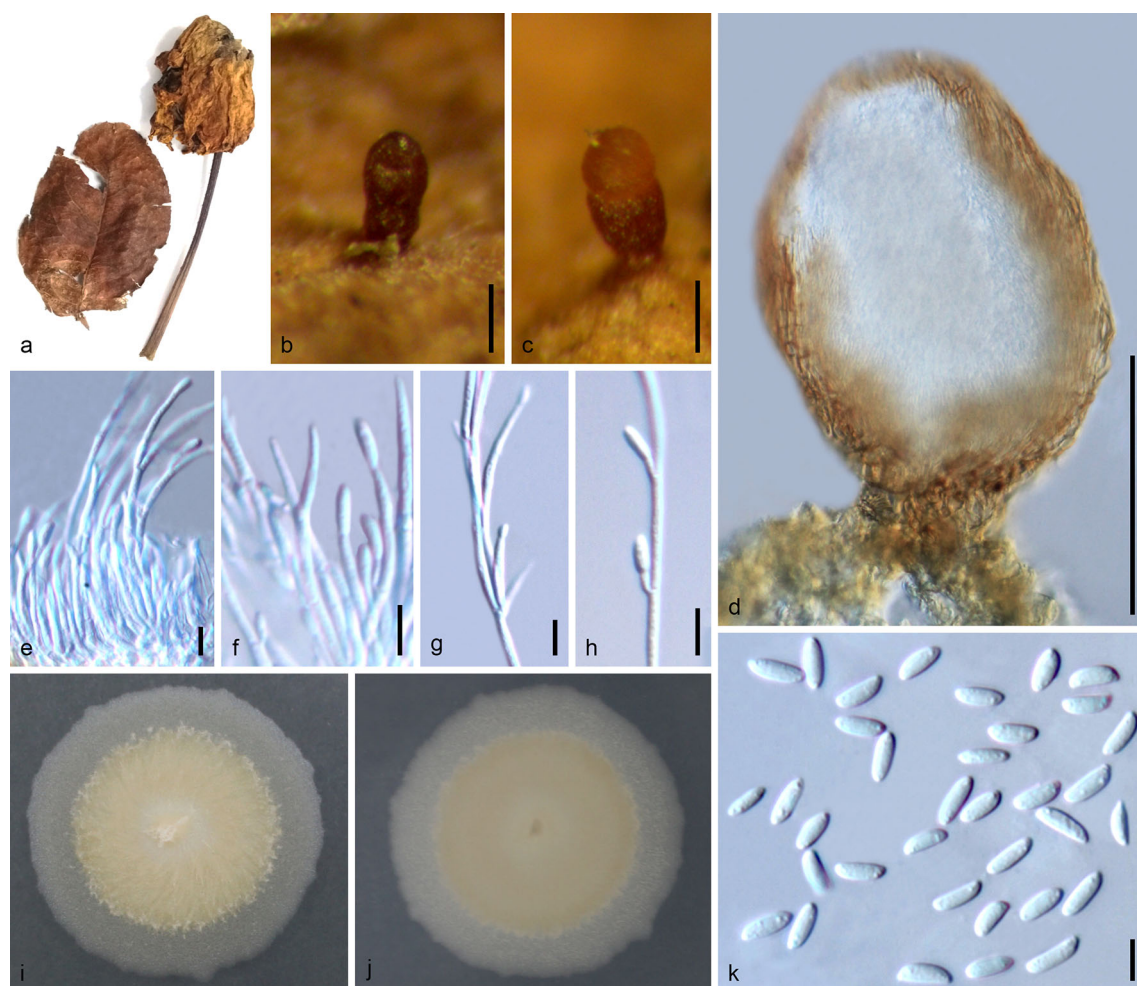


Fig. 94 *Pilidium concavum* (MFLU 18-0106, **new geographical record**). **a** Host. **b, c** Appearance of conidiomata on host surface. **d** Vertical section through the conidioma. **e–h** Conidiophores and

conidiogenous cells. **i, j** Culture on PDA (**i** from above view, **j** from below view). **k** Conidiospores. Scale bars: **b–d** = 100 μ m, **e–h**, **k** = 5 μ m

Material examined: THAILAND, Chiang Rai Province, Muang District, Tha Sut Sub-district, (20° 03' 24.7''N, 99° 52' 23.5''E), dead petals and leaves of *Rosa* sp. (Rosaceae), 20 August 2017, MC. Samarakoon, SAMC017 (MFLU 18-0106, HKAS 102341), living culture (MFLUCC 17-2671).

GenBank numbers: ITS: MK100327, LSU: MK108192, SSU: MK108189.

Notes: *Pilidium concavum* (synanamorph *Hainesia lythri* (Desm.) Höhn.; sexual morph *Discohainesia oenotherae* (Cooke and Ellis) Nannf.), is an interesting species with morphological differentiation due to genetic control (Sutton 1980; Palm 1991; Rossman et al. 2004). The species is often pathogenic and occasionally saprobic on flowers, fruits and oil and forest plants (Cardin et al. 2009; Geng et al. 2012; Lopes et al. 2010; Ayoubi et al. 2016). *Pilidium concavum* has been recorded mainly in temperate regions and on many hosts. Palm (1991) reports *P. concavum* on *Rosa* leaves from the United Kingdom and

Connecticut (USA). The strain isolated from petals and leaves of *Rosa* sp. in this study is similar in morphology and phylogeny to *P. concavum*. The ITS-LSU multi-locus phylogenetic studies reveal that strain MFLUCC 17-2671 is closely related (86% ML/0.99 BYPP) to *P. concavum* and the *P. lythri* clade (Fig. 95). Morphological characterizations, especially the conidia, overlap with the consistency measurements ($5.5\text{--}7.2 \times 1.4\text{--}1.8 \mu\text{m}$) described by Palm (1991). Thus, we report this as *P. concavum* on petals and leaves of *Rosa* sp. as a saprobe from Thailand, a new geographical record.

Pezizomycetes O.E. Erikss. & Winka

Notes: Pezizomycetes is the representative operculate discomycete of Ascomycota. It is characterized by apothecial ascomata or deformed apothecia and asci with an apical slit or operculum (Hansen and Pfister 2006). Presently, 21 families are accepted in this class (Ekanayaka et al. 2018). Phylogenetic studies based on multiple genes

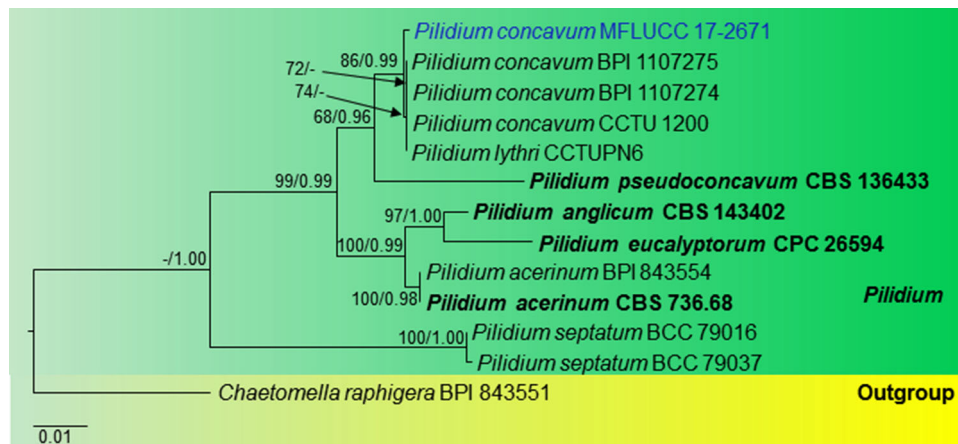


Fig. 95 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data for *Pilidium* species. Related sequences are taken from Marin-Felix et al. (2017). Thirteen strains are included in the combined analyses which comprise 1250 characters (465 characters from ITS, 785 characters for LSU) after alignment. *Chaetomella raphigera* (BPI 843551) (Chaetomellaceae, Helotiales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value

of -3008.149666 is presented. The matrix had 128 distinct alignment patterns, with 1.3% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.258502, C = 0.211927, G = 0.278401, T = 0.251171; substitution rates AC = 3.685184, AG = 2.311128, AT = 2.325507, CG = 0.504055, CT = 5.692118, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.02$. Bootstrap values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are placed respectively on the branch. Type strains are bold. The newly generated sequence is indicated in blue

indicate the Pezizomycetes is a monophyletic group (Ekanayaka et al. 2018).

Pezizales J. Schröt.

Notes: Phylogenetic analyses by Ekanayaka et al. (2018) show six clades in this order. All operculate taxa and some non-apothecial taxa are included in Pezizales. In addition to genera from 21 families with a resolved placement, 15 genera are unresolved and listed as *Pezizales incertae sedis* (Jaklitsch et al. 2016; Wijayawardene et al. 2017a).

Ascodesmidaceae J. Schröt. [as ‘Ascodesmidacei’]

Notes: The family Ascodesmidaceae was introduced by Schröter (1893) and is typified by *Ascodesmis* Tiegh. with *Ascodesmis aurea* Tiegh. as type species. This family is characterized by small ascomata, straight or curved paraphyses and smooth or ornamented ascospores (Güngör et al. 2014; Ekanayaka et al. 2018). Currently, twelve genera are listed in this family, but just four have sequence data. (Ekanayaka et al. 2018; Wijayawardene et al. 2018a). Phylogenetically, this family is close to Pyrenomataceae Corda and Otideaceae Eckblad within Pezizales (Ekanayaka et al. 2018).

Boubovia Svrček

Notes: The genus *Boubovia* was established by Svrček (1791) for *Boubovia luteola* Svrček which is characterized by glabrous to setaceous ascomata, inamyloid asci and smooth or ornamented ascospores with a cyanophilic sheath (Korf and Zhuang 1984; Yao and Spooner 1996; Kristiansen 2016). Six species, *Boubovia ascoboloides*

(Korf & W.Y. Zhuang) Y.J. Yao & Spooner, *B. luteola* Svrček, *B. nicholsonii* (Masse) Spooner & Y.J. Yao, *B. ovalispora* (Boud.) Van Vooren, *B. subprolata* (Korf & W.Y. Zhuang) Y.J. Yao & Spooner and *B. vermiphila* Brumm. & R. Kristiansen are known. Three species have available molecular data (Perry et al. 2007; Hansen et al. 2013; Kušan et al. 2018).

Boubovia gelatinosa M. Zeng, Q. Zhao & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555488; **Facesoffungi number:** FoF05174; **Fig. 96**

Etymology: The epithet refers to ascospores surrounded by gelatinous sheath.

Holotype: HKAS 102407

Saprobic on sheep dung. **Sexual morph** Ascomata superficial, scattered. **Disc** pulvinate, yellowish to orange, shiny, up to 1 mm high, 0.5 mm broad, with 1–2 mm long setaceous hairs, exceeding the disc. **Medullary excipulum** of *textura intricata*. **Ectal excipulum**, hyaline, J⁻, comprised of 8–12 × 6–8 μm cells of *textura angularis* to *globulosa*. **Paraphyses** 2–3 μm broad, filiform, septate, straight, hyaline, J⁻. **Asci** 108–160 × 18–23 μm, 8-spored, subcylindrical to clavate, operculate, inamyloid. **Ascospores** [20/1/1, in H₂O] (16.3–)16.6–18.9(–21.1) × (7.7–)8.9–10.4(–11.0) (Q = 1.65–2.30, Q = 1.84 ± 0.15), ellipsoid to subglobose, uniseriate to biseriate or irregular, smooth-walled, enveloped by gelatinous sheath or over 2/3 part surrounded by sheath, deBary-bubbles present. **Asexual morph** Undetermined.

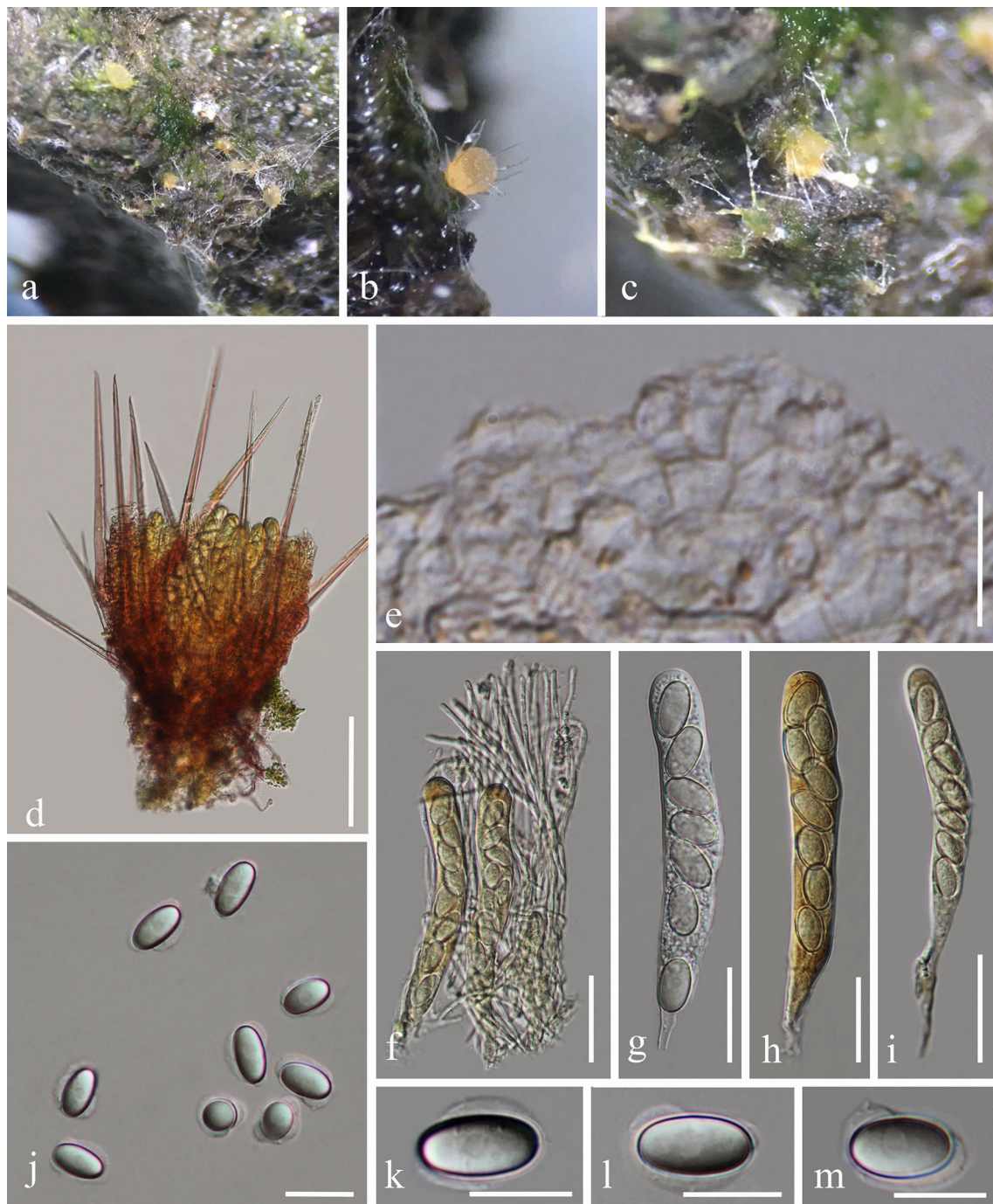


Fig. 96 *Boubovia gelatinosa* (HKAS 102407, **holotype**). **a–c** Typical mature specimens. **d** Squash of ascomata in Melzer's reagent. **e** Receptacle surface of pileus. **f** Asci and paraphyses in Melzer's

reagent. **g–i** Asci (**h, i** Asci in Melzer's reagent). **j–m** Ascospores. Scale bars: **d** = 100 μm, **e**, **j** = 20 μm, **k–m** = 15 μm

Material examined: CHINA, Jiuzhaigou, Sichuan, on sheep dung, 22 August 2018; Ming Zeng, ZM1d (HKAS 102407, **holotype**).

GenBank numbers: ITS: MK093850, LSU: MK093851, SSU: MK093852, TEF1- α : MK093853.

Notes: This species is distinguished by orange shiny ascomata with long hairs, straight paraphyses and ellipsoid,

smooth wall ascospores with sheath. The phylogenetic tree shows a close relationship with *Coprotus ochraceus* (P. Crouan & H. Crouan) J. Moravec (Fig. 97), but morphologically, this species is more similar to *Boubovia* species. *Boubovia* may yet prove to be synonym of *Coprotus* or more than two genera may exist here, but further collections are needed. *Boubovia vermiphila* differs in its

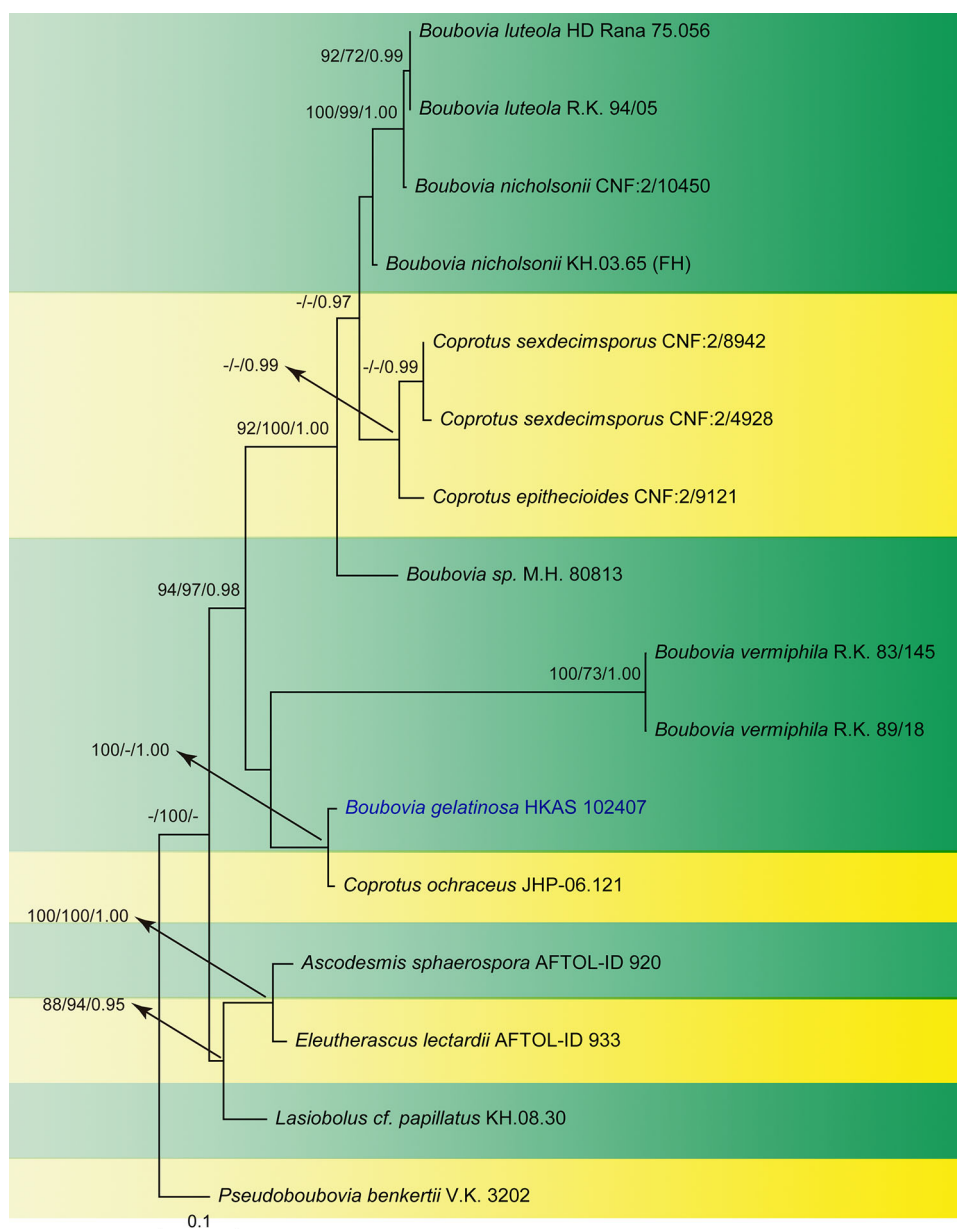


Fig. 97 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and TEF1- α sequence data for *Boubovia* species and several closely related genera in Ascodesmidae. Related sequences are taken from Perry et al. (2007), Hansen et al. (2013), Lindemann et al. (2015) and Kušan et al. (2018). Sixteen strains are included in the combined analyses which comprise 3584 characters (669 characters for ITS, 890 characters for LSU, 1043 characters for SSU, 982 characters for TEF1- α) after alignment. *Pseudoboubovia benkertii* (V.K. 3202) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -12041.925019 is presented. The matrix had 891 distinct alignment

patterns, with 51.43% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246462, C = 0.237728, G = 0.271829, T = 0.243980; substitution rates AC = 0.807419, AG = 1.258958, AT = 1.238671, CG = 0.599522, CT = 3.934755, GT = 1.000000; gamma distribution shape parameter α = 0.201448. Maximum parsimony analysis of 2717 constant characters and 600 informative characters resulted in two equally most parsimonious tree of 1614 steps (CI = 0.778, RI = 0.704, RC = 0.547, HI = 0.222). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.90. The newly generated sequence is indicated in blue

glabrous ascomata, curved paraphyses, ornamented ascospores with 1–2 oil drops and large apical ascospore caps (Brummelen and Kristiansen 1999; Kristiansen 2016).

Boubovia ascoboloides and *B. ovalispora* differ in their glabrous ascomata and curved paraphyses (Korf and Zhuang 1984; Kristiansen 2016). *Boubovia subprolata*

differs in its pinkish glabrous ascomata and curved paraphyses (Korf and Zhuang 1991).

Sordariomycetes O.E. Erikss. & Winka

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde

Notes: The subclass Diaporthomycetidae was introduced to accommodate ten orders and 26 families (Maharachchikumbura et al. 2015). Diaporthales, initially placed in the subclass Sordariomycetidae, where it formed a sister group with Magnaporthaceae, has been transferred and established as type order of the subclass Diaporthomycetidae (Zhang et al. 2006). Species of this subclass are saprobic, endophytic, parasitic or pathogenic in plants, animals or humans (Maharachchikumbura et al. 2015). The sexual morphs comprise stromata made up of orange, brown or black parenchymatous tissues and seldom pyriform ascomata. The ascospores are 2–3 seriate, aseptate or septate, of different shapes, and may or may not have appendages or sheaths. The asexual morphs are ceolomycetes, where conidiomata are acervuli or pycnidial with annellidic or phialidic proliferating conidiogenous cells, or as hyphomycetes, where conidiophores originate from hyphae with occasionally coloured terminal or lateral conidiogenous cells (Maharachchikumbura et al. 2015).

Diaporthales Nannf.

Notes: Diaporthales is a well-supported monophyletic clade within the Diaporthomycetidae and members of this order are saprobes and soil inhabitants, pathogens, parasites or endophytes in plants (Zhang et al. 2006; Rossman et al. 2007; Maharachchikumbura et al. 2015). Some are also pathogenic to humans and animals (Rossman et al. 2007). Diaporthalean microfungi are currently accommodated within 21 families. Among all the species in this order, *Cryphonectria parasitica* (Murrill) M.E. Barr is probably the most well-known chestnut blight fungus which destroyed the whole population of American chestnut trees [*Castanea dentata* (Marsh.) Borkh.] within a short period of time (Anagnostakis 1987). Taxa belonging to this order have yellowish brown to black valsooid or diatrypoid pseudo- or asco-stromata, brown to black perithecial fruiting bodies, regularly immersed in stromata of leafy or woody substrates with papillate ostioles swollen at the apex. The mature 2–32 spored asci with a J- refractive apical apparatus, float freely and become dehiscent at maturity (Barr 1978; Samuels and Blackwell 2001; Senanayake et al. 2017). The asexual states are usually ceolomycetous, with conidiophores arising from the top-most cell layer of basal or parietal tissue or from under the developing scutellum; otherwise, they are reduced to enteroblastic, holoblastic, phialidic or annellidic hyaline or olivaceous conidiogenous cells (Sogonov et al. 2008; Senanayake et al. 2017).

Diaporthaceae Höhn.

Notes: The family Diaporthaceae currently comprises 14 genera (Maharachchikumbura et al. 2016; Senanayake et al. 2017, 2018; Dissanayake et al. 2017b).

Diaporthe Nitschke

Notes: *Diaporthe* includes economically important plant pathogens, endophytes, and saprobes (Udayanga et al. 2014; Hyde et al. 2016). They have a broad range of hosts from cultivated crops to ornamental plants (Dissanayake et al. 2017b). Rossman et al. (2015a) prioritized the older name *Diaporthe* over *Phomopsis*, while the latest account is provided in Fig. 100. An updated phylogenetic tree for *Diaporthe* species with new records and new species is presented in Fig. 100.

Diaporthe italiana Chethana, Camporesi & K. D. Hyde, *sp. nov.*

Index Fungorum number: IF555376; **Facesoffungi number:** FoF04934; Fig. 98

Etymology: The specific epithet ‘italiana’ was given after the country, where the fungus was collected.

Holotype: MFLU 17-0311

Saprobic on dead aerial branch of *Morus alba* L. **Sexual morph** *Perithecia* 0.2–0.42 mm (\bar{x} = 0.311 mm, n = 10), solitary, scattered, immersed to semi-immersed, partially erumpent, globose, black, with tapering perithecial necks. *Peridium* multi-layered, 20 μ m wide at the top, 10–12 μ m wide in sides, outer layer composed of 4–5 layers of thick, brown cells, inner 3–4 layers of hyaline cells of *textura angularis*, cells towards inner layer lighter. *Asci* 45–55 \times 6–8.5 μ m (\bar{x} = 51 \times 7.7 μ m, n = 20), 8-spored, unitunicate, sessile, cymbiform to clavate. *Ascospores* 10.5–13 \times 2.7–4.5 μ m (\bar{x} = 12.1 \times 3.5 μ m, n = 40), overlapping biseriate, hyaline, fusiform to allantoid, slightly curved, 2-celled, widest near the centre, with acute rounded ends, 1-median septate, rarely bi-guttulate, often tetra-guttulate, with larger guttules at centre and the smaller towards the ends, smooth-walled. **Asexual morph** not observed.

Culture characteristics: Colonies on the PDA, circular, fluffy, aerial, white mycelium with fimbriate margin, olivaceous to grey olivaceous reverse, relatively slow growing, reach 3 cm diam. after 7 days at 25 °C.

Material examined: ITALY, Forlì-Cesena Province, Forlì, via Friuli, on dead, aerial branch of *Morus alba* L. (Moraceae), 19 January 2017, Erio Camporesi, IT 3217 (MFLU 17-0311, **holotype**), ex-type living culture (MFLUCC 18-0090, KUMCC 18-0002); (HKAS 101460, **isotype**), ex-isotype living culture (MFLUCC 18-0091, KUMCC 18-0003).

GenBank numbers: CAL: MH853690, ITS: MH846237, TEF1- α : MH853686, TUB2: MH853688 (MFLUCC

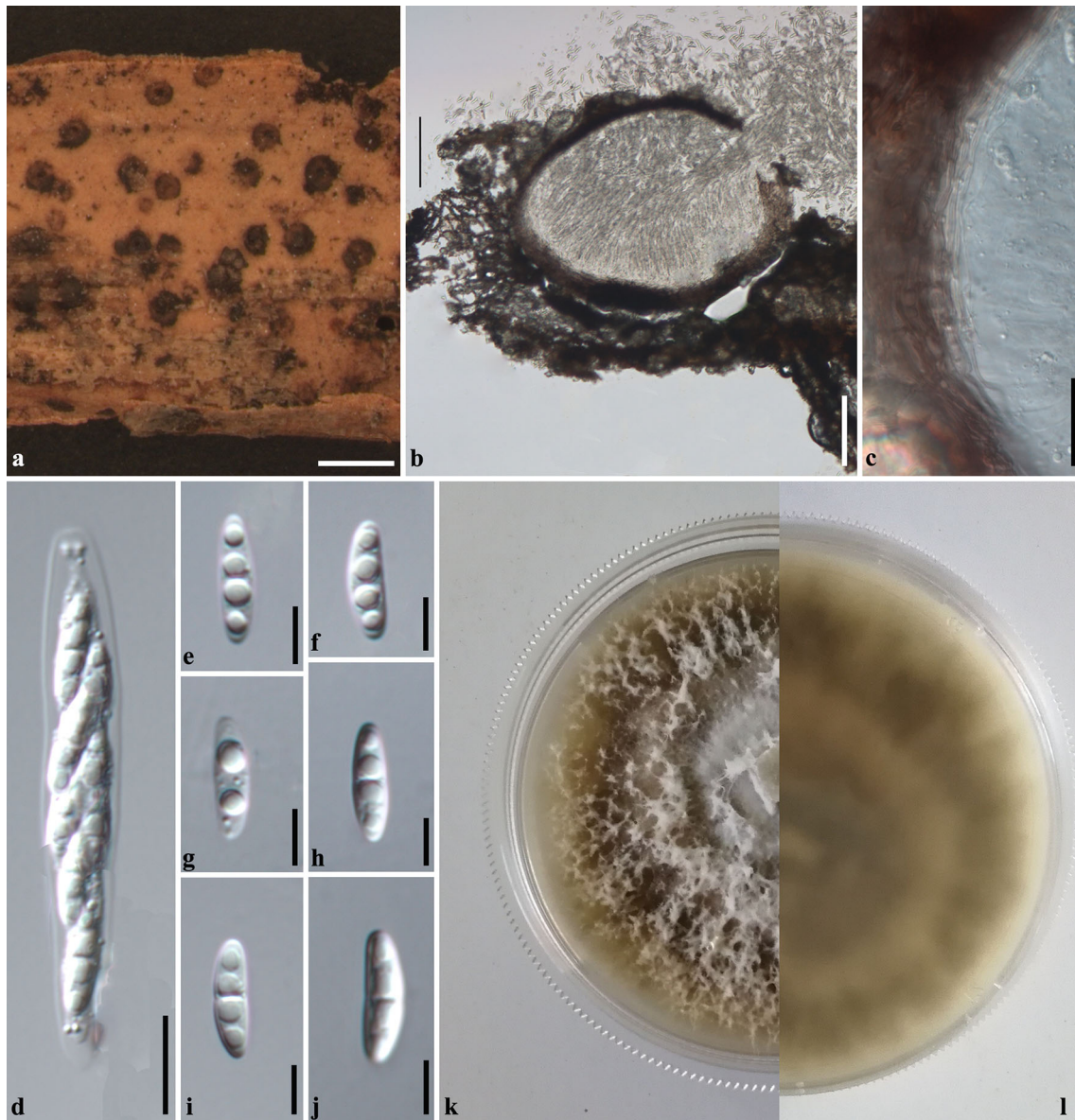


Fig. 98 *Diaporthe italiana* (MFLUCC 18-0090, holotype). **a** Appearance of perithecia on dead branch of *Morus alba*. **b** Longitudinal section of a perithecium. **c** Longitudinal section of a perithecium wall

showing cell organization. **d** Bi-seriate asci. **e–j** Ascospores. **k, l** Colony on PDA (**k** from above view, **l** from below view). Scale bars: **a** = 1 mm, **b** = 100 μ m, **c** = 20 μ m, **d** = 10 μ m, **e–j** = 5 μ m

18-0090); CAL: MH853691, ITS: MH846238, TEF1- α : MH853687, TUB2: MH853689 (MFLUCC 18-0091).

Notes: *Diaporthe italiana* is phylogenetically closely related to *D. rudis*, but is clearly distinguished based on the morphology and phylogeny. In our phylogenetic analysis of combined ITS, TEF1- α , TUB2, and CAL sequence data of *Diaporthe* species (Fig. 100), our strains (18-0090 and 18-0091) cluster together with the ex-type strain of *Diaporthe rudis* (AR3422) with relatively high bootstrap and Bayesian probabilities (100% ML/1.00 BYPP). Sequence comparison for ITS region between *D. rudis* (AR3422) and *D. italiana* (MFLUCC 18-0091) showed 2.11% base pair differences. Our collection is distinct from *D. rudis* in

having smaller asci (45–55 \times 6–8.5 μ m), and smaller ascospores (10.5–13 \times 2.7–4.5 μ m), in contrast to larger asci (53.5–58.5 \times 10.6–12 μ m), and larger ascospores (12–14.2 \times 3.5–3.7 μ m) of *D. rudis* (Udayanga et al. 2014). A *Diaporthe* species named *Diaporthe mori* Berl. (current name *Phomopsis moricola* (Sacc.) Grove) has been identified from *Morus alba* and *M. nigra* (Bargagli-Petrucchi 1915). However, they differ from our species in having smaller, immersed perithecia (0.18–0.2 mm), smaller asci (36–40 \times 7 μ m), and smaller, bi-guttulate ascospores (7–8 \times 3–3.5 μ m). Since, this species were introduced in 1915, DNA sequences were unavailable in

the databases. Therefore, they were not included in the phylogenetic analysis.

Diaporthe rumicicola Manawasinghe, Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555379; *Facesoffungi* number: FoF04940; Fig. 99

Etymology: Name reflects the host genus.

Holotype: MFLU 18-0739

Saprobic on dead leaves of woody plants. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* on host pycnidial, 98–280 µm diam. (\bar{x} = 208 µm, n = 10), ampulliform, scattered, immersed, ostiolate, with elongate

black neck. *Pycnidial wall* comprising 2–3 layers, heavily pigmented, thick-walled, comprising dark brown cells of *textura angularis*, with lighter cells towards the inside, with inner layer composed of 2–5 layers, hyaline, thin-walled cells of *textura angularis*. *Conidiophores* on host reduced to conidiogenous cells. *Pycnidia* in culture black, immersed, solitary or merged, exudated. *Paraphyses* observed on culture. *Conidiogenous cells* enteroblastic with percurrent annellations, integrated, clustered, hyaline, smooth-walled. *Alpha conidia*, on host 3–5 × 2–3 µm (\bar{x} = 3.5 × 2.5 µm, n = 30), hyaline, smooth-walled, mono or bi-guttulate. *Beta conidia* not observed.

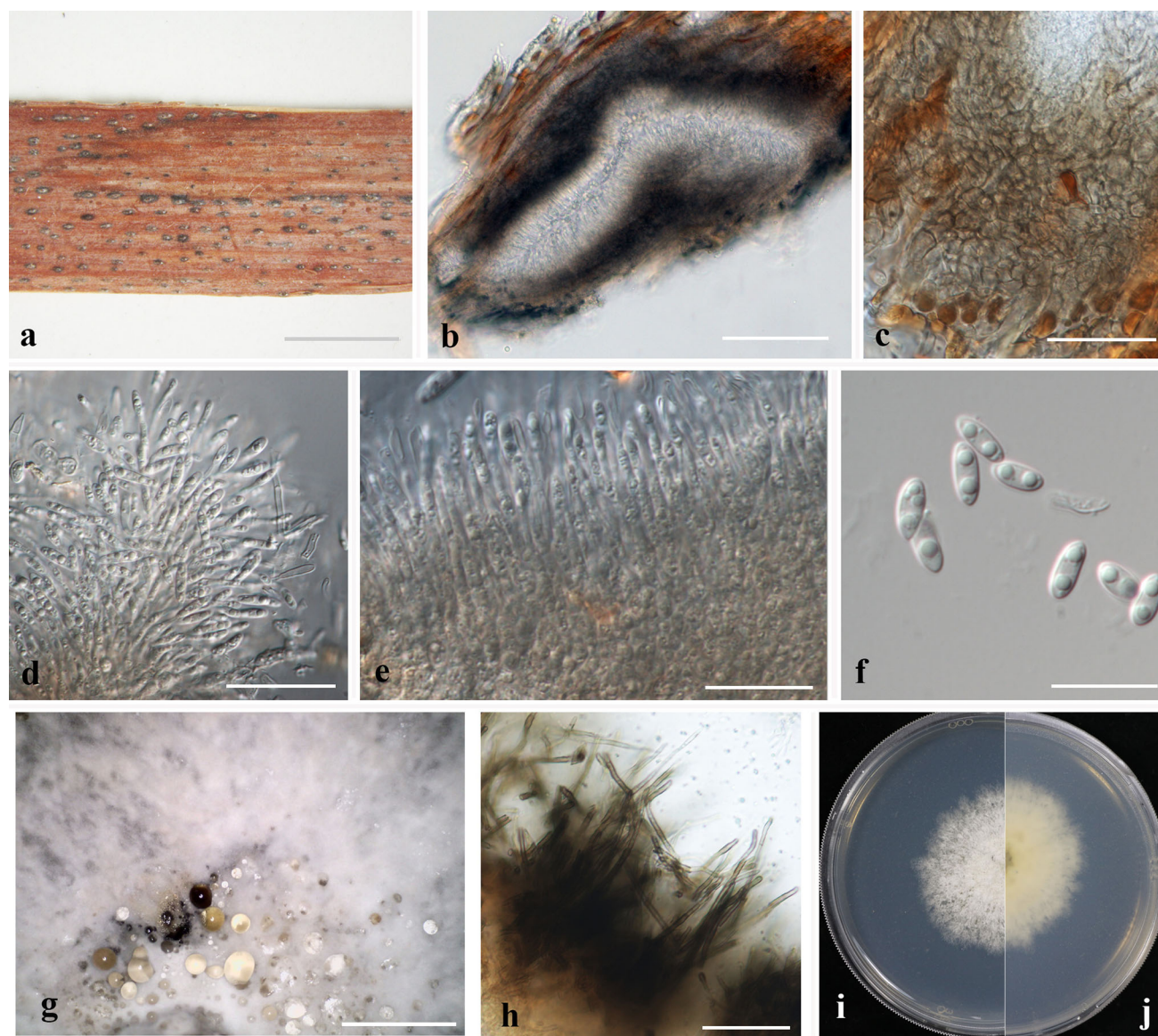


Fig. 99 *Diaporthe rumicicola* (MFLU 18-0739, holotype). **a** Appearance of conidiomata on dead branch of *Rumex* spp. **b** Cross section of conidioma on host. **c** Pycnidial wall on host. **d, e** Conidiogenous cells with developing conidia. **f** Conidia on host. **g** Pycnidia on PDA.

h Appearance of paraphysis. **i, j** Colony on PDA (**i** from above view, **j** from below view). Scale bars: **a** = 2000 µm, **b** = 200 µm, **g** = 100 µm, **c–e, h** = 20 µm, **f** = 10 µm

Culture characteristics: Colonies on PDA 50 mm diam., after 7 days at 25 °C, cream to white cottony mycelium, irregular and lobate at the margins, white at the centre; reverse yellowish and concentric lines on conidial formation can be observed when colony getting old.

Material examined: ITALY, near Castrocaro Terme (province of Forlì-Cesena), on dead aerial stem of *Rumex* sp. (Polygonaceae), 19 February 2018, Camporesi Erio IT (MFLU 18-0739, **holotype**), ex-type living culture (MFLUCC 18-1566, JZB320005).

GenBank numbers: ITS: MH84623, TEF1- α : MK049554, TUB2: MK049555.

Notes: *Diaporthe rumicicola* was isolated from dead branch of *Rumex* sp. from Forlì-Cesena of Italy. Morphologically, this species is similar to genus *Diaporthe*, and the combined gene sequence analysis of ITS, TEF1- α , CAL and TUB2 genes placed the taxon in *Diaporthe* (Fig. 100). The current species develop a sister clade with *Diaporthe foeniculina* with 100% bootstrap value in ML analysis and 1.0 Bayesian probabilities in Bayesian analysis (Fig. 99). Morphologically the current species is differing with developing smaller alpha conidia ($3.5 \times 2.4 \mu\text{m}$) compared to *D. foeniculina* ($8.5\text{--}9 \times 2.3\text{--}2.5 \mu\text{m}$) (Udayanga et al. 2014). In addition to that this is the first time that *Diaporthe* species recorded on *Rumex* sp. (Farr and Rossman 2019).

Gnomoniaceae G. Winter

Notes: The family Gnomoniaceae, typified by the genus *Gnomonia* Ces. & De Not., encompasses fungi with immersed black perithecia which are solitary or aggregated with or without a stromatic tissue (Sogonov et al. 2008). The neck of the perithecial bodies extends beyond the host epidermis and may be short or long with an upright, oblique or parallel positioning to the host surface (Sogonov et al. 2008). The asexual morphs of species of Gnomoniaceae produce acervular or pycnidial fruiting bodies (Monod 1983). Species belonging to this family have mainly been reported from north America and Europe, with only few originating from Asia (Walker et al. 2014). Most of the species are host-specific (Senanayake et al. 2017) and commonly occur as endophytes, pathogens or saprobes, even though, they sometimes behave as parasites or opportunistic pathogens (Sieber 2007; Senanayake et al. 2018).

Plagiostoma Fuckel

Notes: *Plagiostoma* (Gnomoniaceae, Diaporthales) encompasses microfungal members of pathogenic, endophytic or saprobic nature inhabiting stems, branches, twigs and leaves of woody and herbaceous plants belonging to various families which occur mostly temperate regions of the northern hemisphere as well as some parts of Asia (Mejía et al. 2011; Walker et al. 2014). The genus, typified

by *P. euphorbiae* (Fuckel) Fuckel, currently accommodates 32 species (Mejía et al. 2011; Walker et al. 2014; Senanayake et al. 2017). These species produce perithecial and pycnidial fruiting bodies on overwintered leaves and twigs (Walker et al. 2014) and the genus primarily distinguishes itself from other genera in the family by neck characters of the perithecia along with ascospore morphology (Mejía et al. 2011). Other than these, presence or absence of stroma, geographical location or host are secondary differentiating features (Mejía et al. 2011). In this study, we report *Plagiostoma salicellum* (Fr.) Sogonov for the first time from a new geographical area in Europe, notably Italy.

Plagiostoma salicellum (Fr.) Sogonov, Stud. Mycol. 62: 73 (2008)

Facesoffungi number: FoF05761; Fig. 101

Saprobic on dead branches of *Salix caprea*. **Sexual morph**

Ascomata 205–350 \times 260–330 μm (\bar{x} = 275 \times 290.5 μm , n = 6), perithecial, mostly solitary, scattered, immersed in bark, producing a faint elevation of the periderm, each comprising of a convergent, protruding neck, black, subglobose. **Neck** 110–120 μm long (\bar{x} = 113 μm , n = 6), 76–126 μm diam. at the base (\bar{x} = 97.3 μm , n = 6) and 88–131 μm diam. at apex (\bar{x} = 103.8 μm , n = 6), cylindrical, eccentric to lateral, straight to very slightly twisted, not surrounded by a stroma. **Peridium** 18–29 μm wide, thick, comprising 4–6 layers, outer layer heavily pigmented, thick walled, consisting of dark brown to blackish cells of *textura angularis*, cells towards inside lighter, inner layer composed of 1–2 layers, pale brown to hyaline, flattened, thin-walled cells of *textura angularis*. **Asci** 32–55 \times 5–15 μm (\bar{x} = 43.7 \times 8.7 μm , n = 34), 8-spored, cylindrical to clavate, clavate-elongated, straight to slightly curved, broadly rounded apex with a conspicuous J- refractive apical ring, 1.7–4.3 μm diam., often consisting of a short but not necessarily persistent, tapered and pointed stipe. **Ascospores** 12–18 \times 1–4 μm (\bar{x} = 15.8 \times 2.5 μm , n = 54), obliquely parallel or irregularly seriate, hyaline, ellipsoid-elongated, tapering slightly towards rounded ends, 1-septate, slightly constricted at median to sub-median septum, with granular cytoplasm, without any sheath or appendage. **Asexual morph** Undetermined.

Material examined: ITALY, Province of Forlì-Cesena [FC], Monte Fumaiolo, on dead aerial branch of *Salix caprea* L. (Salicaceae), 27 August 2017, Erio Camporesi, IT 3454 (MFLU 17-1601).

GenBank numbers: ITS: MK080111, TEF1- α : MK424970, TUB2: MK424971.

Notes: *Plagiostoma salicellum* is characterised by a cylindrical neck surrounded by a white stroma and narrow ellipsoid-elongated ascospores often having short appendages (Mejía et al. 2011). However, in our specimen no

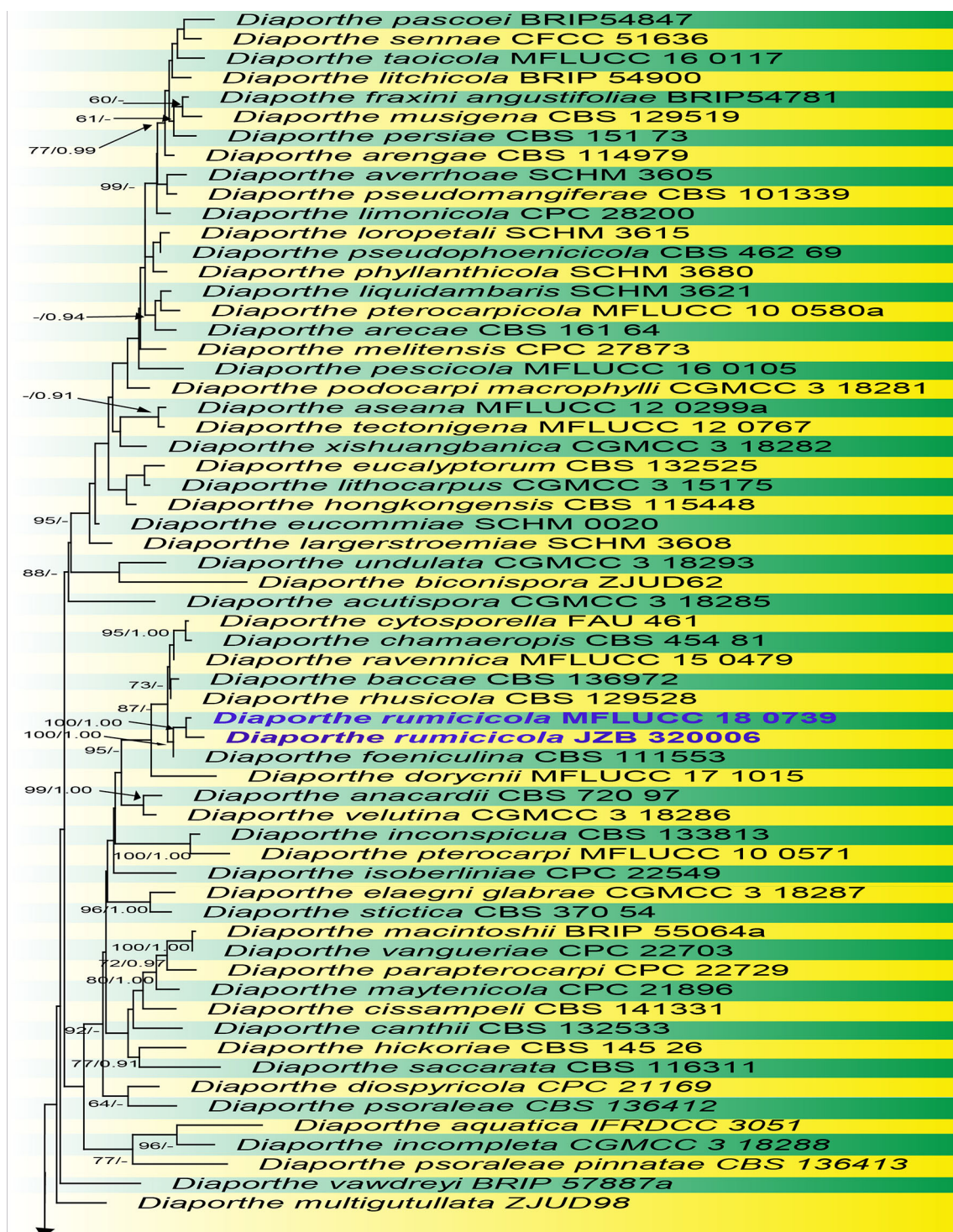


Fig. 100 Phylogenetic tree generated by maximum likelihood analysis of combined ITS, TEF1- α , TUB2 and CAL sequence data of *Diaporthe* species. Sequences were obtained from GenBank. One-hundred and ninety-two strains are included in the analyses, which comprise 2603 characters including gaps. Single gene analyses are carried out to compare the topology of the tree and clade stability. Tree was rooted with *Diaporthe corylina* (CBS 121124). Tree topology of the Bayesian analysis was similar to the RAXML. The best scoring RAXML tree with a final likelihood value of =

– 60797.442221 is presented. The matrix had 2107 distinct alignment patterns, with 40.98% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.228179, C = 0.282550, G = 0.268109, T = 0.221162; substitution rates AC = 0.854574, AG = 3.369047, AT = 0.975280, CG = 0.800183, CT = 3.251377, GT = 1.000000; gamma distribution shape parameter α = 0.881490. RAXML and Bayesian posterior probabilities values $\geq 60\%$ (ML) and 0.9 (BYPP) are shown respectively near the nodes. The newly generated sequences are indicated in blue

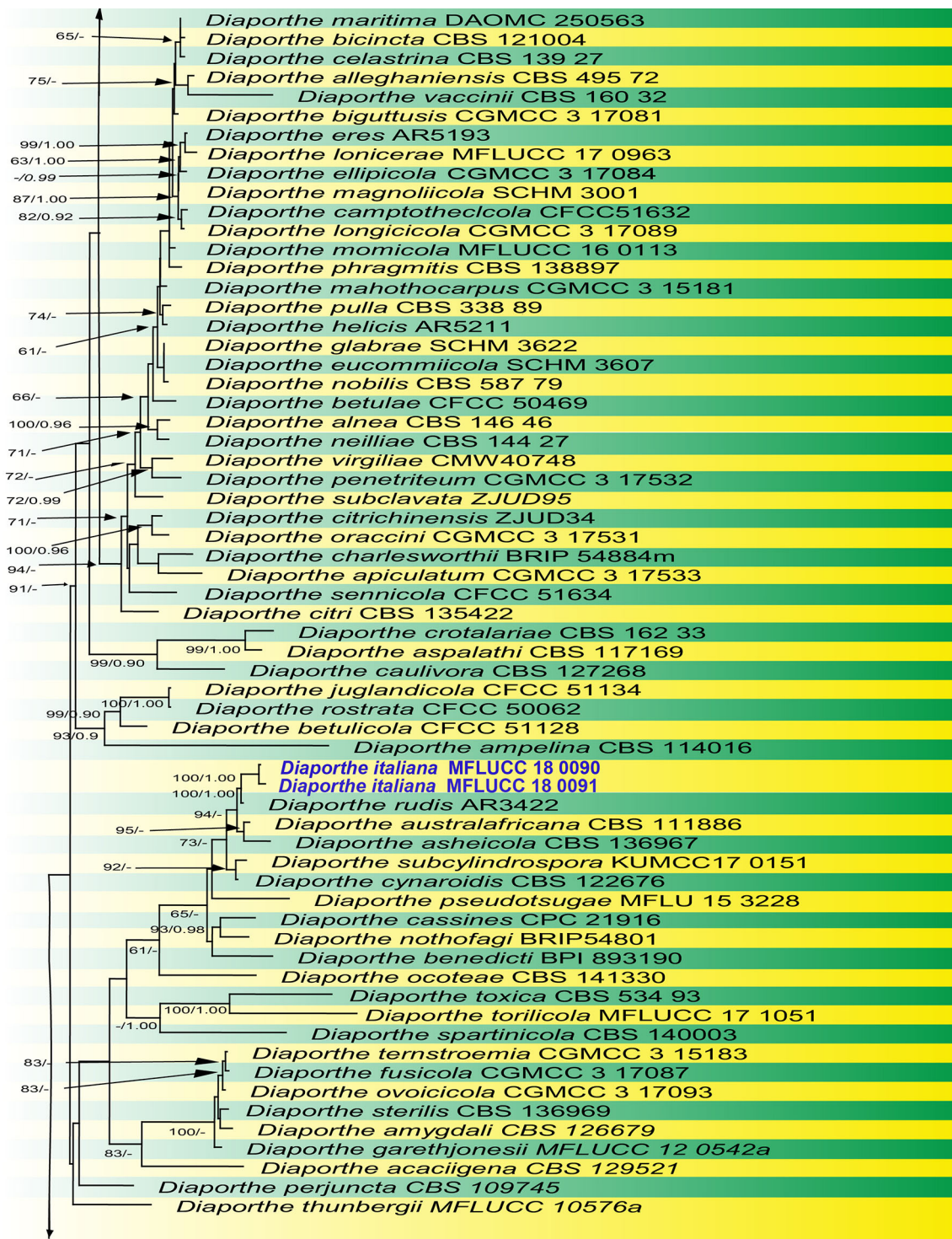


Fig. 100 continued

stroma was observed around the perithecial neck which was also shorter $\bar{x} = 113 \mu\text{m}$ (this study) vs $\bar{x} = 177 \mu\text{m}$ (Mejía et al. 2011)] and broader both at the base $\bar{x} = 97.3 \mu\text{m}$ (this study) vs $\bar{x} = 81 \mu\text{m}$ (Mejía et al. 2011)] and at the apex $\bar{x} = 103.8 \mu\text{m}$ (this study) vs $\bar{x} = 79 \mu\text{m}$ (Mejía et al. 2011)] as compared to the lectotype and

epitype of *P. salicellum* described by Mejía et al. (2011). The perithecia were mostly solitary rather than aggregated and narrower in diameter $\bar{x} = 290.5 \mu\text{m}$ (this study) vs $\bar{x} = 397 \mu\text{m}$ (Mejía et al. 2011)]. The asci also were shorter and narrower ($\bar{x} = 43.7 \times 8.7 \mu\text{m}$ (this study) vs $\bar{x} = 55.0 \times 13.0 \mu\text{m}$ (Mejía et al. 2011)]. The ascospores

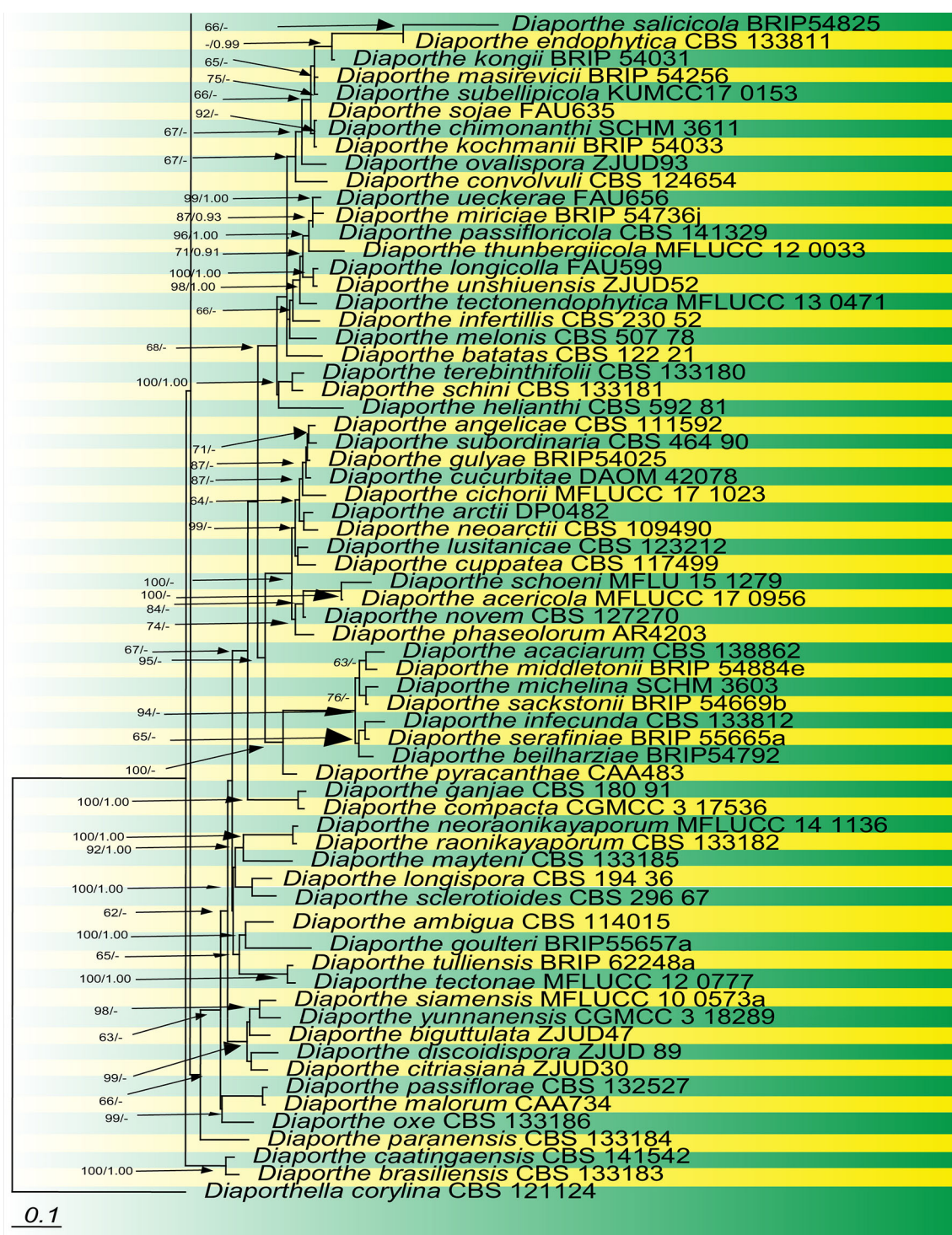


Fig. 100 continued

of *P. salicellum* (MFLU 17-1601) did not have an appendage unlike those of the lectotype and epitype of *P. salicellum* and they were smaller $\bar{x} = 15.8 \times 2.5 \mu\text{m}$ (this study) vs $\bar{x} = 18.5 \times 3.5 \mu\text{m}$ (Mejía et al. 2011)]. However, the length of the ascospores may not be a key distinguishing factor since Mejía et al. (2011) observed that

length and width of ascospores of *P. salicellum* may vary, even within an ascus. The combined data set of ITS, TUB2 and TEF1- α sequences in our phylogenetic analyses has not clearly separated our strain (MFLU 17-1601) with significant bootstrap support from the strains of *P. salicellum* (AR 3828) and (LCM 449.01) (Fig. 102). The morphological

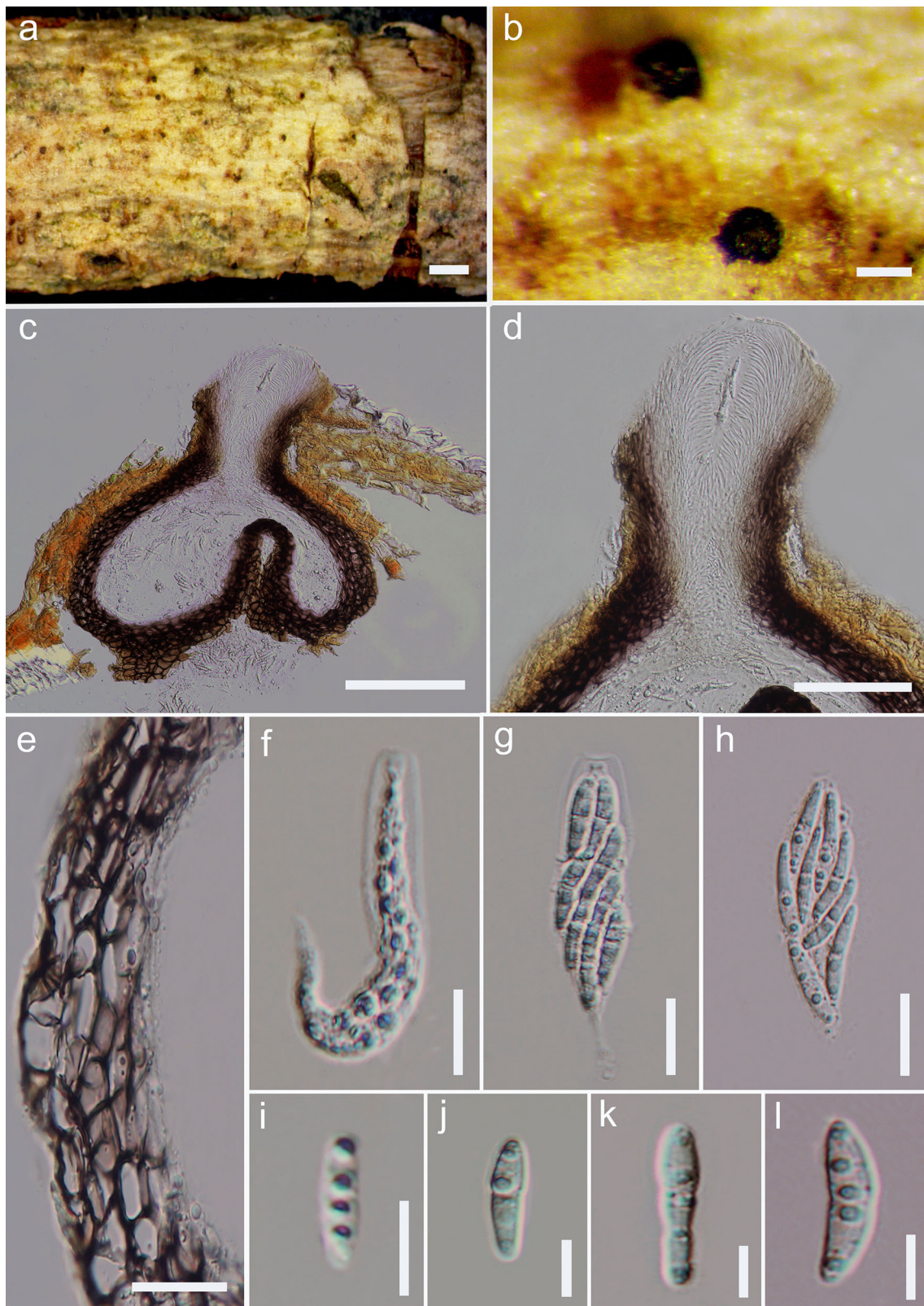
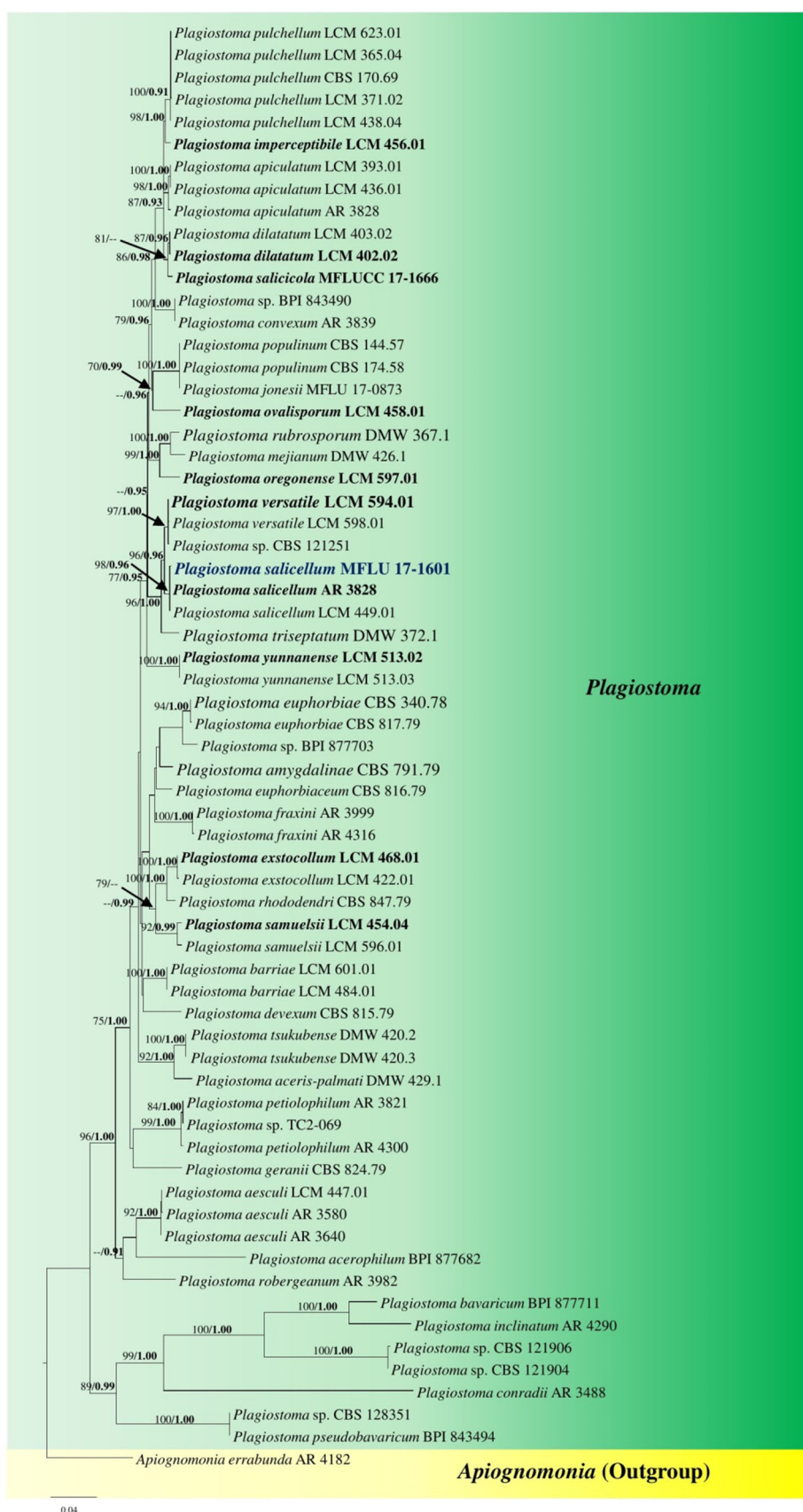


Fig. 101 *Plagiostoma salicellum* (MFLU 17-1601, new geographical record). **a** Appearance of ascomata on host substrate. **b** Close-up of ascoma on host substrate. **c** Section of an ascoma. **d** Section through

ostiole. **e** Peridium. **f–h** Asci. **i–l** Ascospores. Scale bars: **a** = 500 µm, **b, c** = 200 µm, **d** = 100 µm, **i–l** = 20 µm, **e–h** = 10 µm

Fig. 102 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and TEF1- α sequence data for *Plagiostoma* species in Gnomoniaceae. Related sequences were taken from Sogonov et al. (2008), Mejía et al. (2011) and Walker et al. (2014). Sixty-five strains are included in the combined analyses which comprise 1948 characters (511 characters for ITS, 777 characters for TUB2, 660 characters for TEF1- α) after alignment. *Apiognomonia errabunda* (AR 4182) (Gnomoniaceae, Diaporthales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -12805.418798 is presented. The matrix had 982 distinct alignment patterns, with 17.73% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.220722, C = 0.299844, G = 0.226468, T = 0.252965; substitution rates AC = 0.958759, AG = 3.395596, AT = 0.951907, CG = 1.027587, CT = 4.491882, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.409235$. Bootstrap values for maximum likelihood (ML) equal to or greater than 60 are placed above and below the branches. Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are in bold. The newly generated sequence is indicated in bold and blue



differences mentioned above may be the result of phenotypic plasticity arising from a need to adapt to the climatic conditions in Italy (Jeewon & Hyde 2016). Due to lack of significant molecular support, we therefore report our strain as *P. salicellum*, collected for the first time from Italy. It is also known from Canada, Europe (Austria, Belgium, Bulgaria, Czech Republic, Germany, Poland, Sweden, Switzerland, UK and USA (Sogonov et al. 2008).

Diaporthomycetidae, families incertae sedis

Distoseptisporaceae K.D. Hyde & McKenzie

Notes: Distoseptisporaceae was established to accommodate a group of sporidesmium-like hyphomycetous taxa, which are phylogenetically distinct from Sporidesmiaceae and characterized by darker conidia with slightly paler rounded apices and indeterminate length, and especially with most species having relatively short conidiophores (Su et al. 2016). Subsequently, a series of new species (Hyde et al. 2016; Yang et al. 2018b; Luo et al. 2018) were introduced to this monotypic family, and Yang et al. (2018b) provided an emendation of *Distoseptispora* according to much longer, percurrently proliferating conidiophores and euseptate conidia. Two new taxa are introduced to this monotypic family herein, namely *Distoseptispora dehongensis* and *D. palmarum*, which were found from freshwater and palm habitats, respectively.

Distoseptispora K.D. Hyde, McKenzie & Maharachch.

Notes: *Distoseptispora* is typified by *D. fluminicola* Mckenzie, H.Y. Su, Z.L. Luo & K.D. Hyde (Su et al. 2016) and currently 16 species are recorded in Index Fungorum (2019). In addition, *D. adscendens* (HKUCC 10820) and *D. leonensis* (HKUCC 10822) were also included in this genus based on evidence of phylogeny (Su et al. 2016). Members in this genus are commonly encountered in freshwater habitats and are hyphomycetous, which have olivaceous, brown or yellowish/reddish brown conidia, euseptate or distoseptate, obclavate or cylindrical with rounded apex, and are of indeterminate length (Su et al. 2016; Luo et al. 2018; Tibpromma et al. 2018; Yang et al. 2018b).

Distoseptispora dehongensis W. Dong, H. Zhang & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555406; **Facesoffungi number:** FoF05057; Fig. 103

Etymology: Name reflects Dehong, from where the species was isolated.

Holotype: HKAS 101738

Saprobic on decaying wood submerged in freshwater.

Sexual morph Undetermined. **Asexual morph** Colonies gregarious or scattered, effuse, hairy, olivaceous. *Mycelium* mostly immersed, consisting of branched, septate, smooth, hyaline hyphae. *Conidiophores* 45–80 µm long (\bar{x} = 59 µm, n = 10), 4–5 µm wide (\bar{x} = 4.5 µm, n = 10),

macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, smooth-walled, brown to pale olivaceous, septate, slightly constricted at septa, thin-walled. *Conidiogenous cells* 13–20 µm long (\bar{x} = 16 µm, n = 10), 3–5 µm wide (\bar{x} = 4.5 µm, n = 10), monoblastic or polyblastic, terminal, determinate, cylindrical, brown to pale olivaceous. *Conidia* 17–30 µm long (\bar{x} = 25 µm, n = 15), 7.5–10 µm wide (\bar{x} = 9.2 µm, n = 15), acrogenous, solitary, obpyriform to obclavate, broad cylindrical or irregular, straight or curved, 3–5-distoseptate, olivaceous, thick-walled, smooth, rounded at the apex, truncate at the base.

Culture characteristics: On PDA, colony circular, reaching 40 mm in 45 days at 25 °C, grey from above, dark grey from below, surface rough, dry, raised, edge entire.

Material examined: CHINA, Dehong, on submerged wood in a stream, 25 November 2017, G.N. Wang H10A (HKAS 101738, **holotype**), ex-type living culture (KUMCC 18-0090).

GenBank numbers: ITS: MK085061, LSU: MK079662, TEF1- α : MK087659.

Notes: *Distoseptispora dehongensis* is phylogenetically, a strongly supported member in Distoseptisporaceae (100 ML/1.00 BYPP) in Fig. 105. Morphological characteristics of *D. dehongensis* (such as cylindrical, unbranched, septate conidiophores and distoseptate conidia) matches well with those in *Distoseptispora*. It can be easily distinguished from the other taxa in *Distoseptispora* by its fewer distosepta (3–5-distoseptate vs. > 7-distoseptate) and shorter length (17–30 µm vs. > 35 µm) of conidia (Hyde et al. 2016; Su et al. 2016; Yang et al. 2018b; Luo et al. 2018). *Distoseptispora dehongensis* has similar conidial dimensions to *D. martinii*. However, they differ in conidial shape (Xia et al. 2017). In our multi-gene phylogenetic analyses, *D. dehongensis* has a close phylogenetic affinity to *D. obpyriformis* and *D. rostrata* with weak support (Fig. 105), and they can be distinguished in conidial shape, size and number of distosepta (Luo et al. 2018).

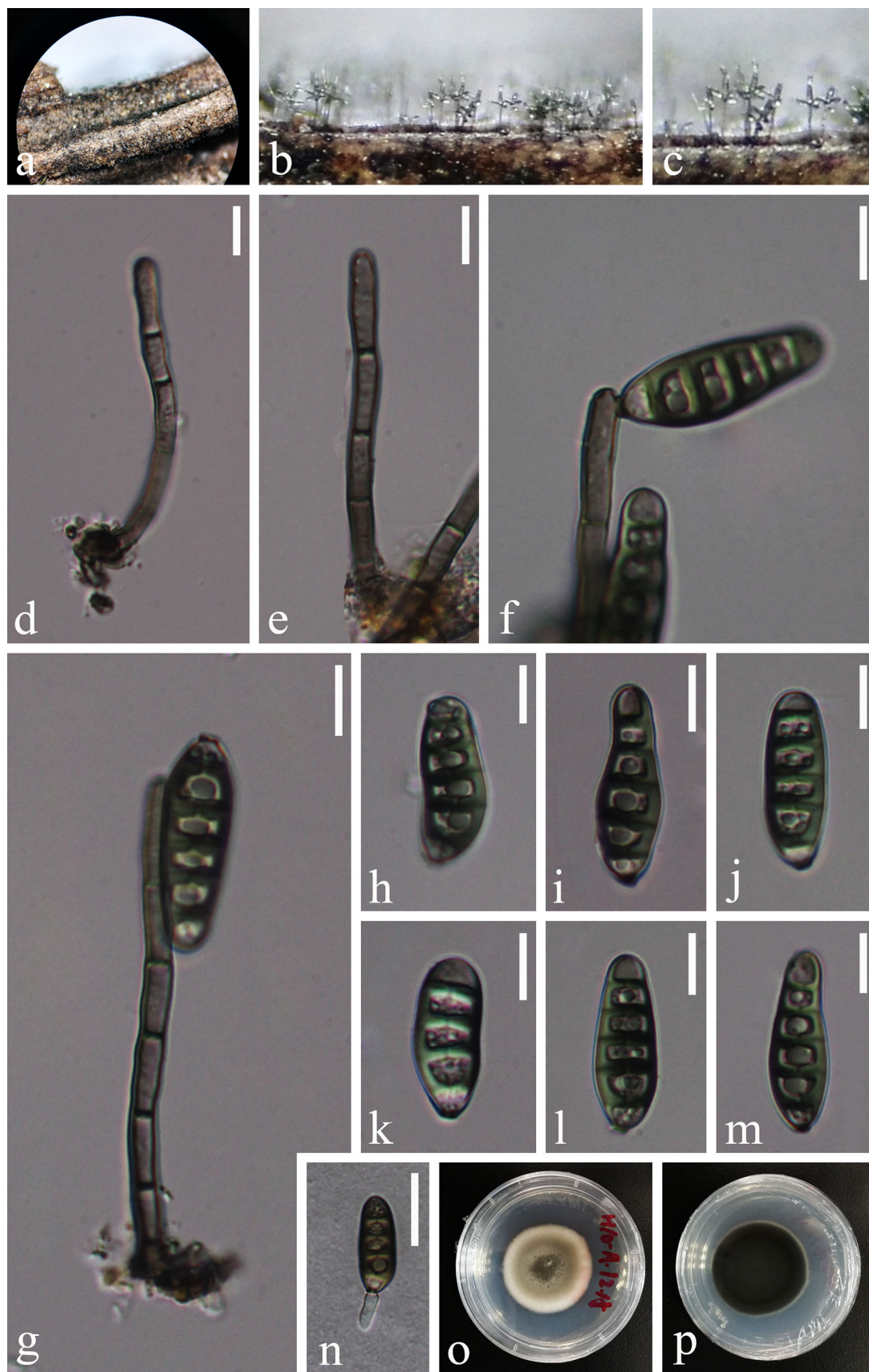
Distoseptispora palmarum S.N. Zhang, K.D. Hyde & J.K. Liu, *sp. nov.*

Index Fungorum number: IF555431; **Facesoffungi number:** FoF05090; Fig. 104

Etymology: The epithet reflects the host plant.

Holotype: MFLU 18-1588

Colonies on the substratum superficial, effuse, hairy or velvety, black. *Mycelium* mostly immersed, composed of branched, septate, smooth, pale brown hyphae. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* 90–165 µm long (\bar{x} = 125 µm, n = 10), 4–7 µm wide (\bar{x} = 5.5 µm, n = 10), macronematous, mononematous, septate, unbranched, single or in groups of 2 or 3, erect,



◀**Fig. 103** *Distoseptispora dehongensis* (HKAS 101738, **holotype**). **a–c** Colonies on substrate. **d, e** Conidiophores. **f, g** Conidiophores with conidia. **h–m** Conidia. **n** Germinated conidium. **o, p** Colony on PDA (**o** from above view, **p** from below view). Scale bars: **n** = 20 μ m, **d–m** = 10 μ m

straight or flexuous, smooth, brown, cylindrical, robust at the base. *Conidiogenous cells* polyblastic, integrated, determinate, terminal, pale brown to brown, cylindrical. *Conidia* 35–180 μ m long (\bar{x} = 76.3 μ m, n = 32), 7–11 μ m wide (\bar{x} = 8.6 μ m, n = 32), acrogenous, dry, oblong, obclavate, cylindrical or rostrate, elongated, straight or

curved, truncate at the base, rounded at the apex, 7–27-distoseptate, smooth, greenish black to brown, paler towards the apex, thick-walled.

Culture characteristics: Colonies on PDA, 20–25 mm diameter after 21 days at 25 °C, mycelium sparse, dark brown to black, reverse concolourous.

Material examined: THAILAND, Trat Province, Koh Chang, on rachis of *Cocos nucifera* (Arecaceae), 27 April 2017, S.N. Zhang, SNT128 (MFLU 18-0588, **holotype**), ex-type living culture (MFLUCC 18-1446); *ibid.* (HKAS 102209, **isotype**).



Fig. 104 *Distoseptispora palmarum* (MFLU 18-1588, **holotype**). **a** Colonies on substrate surface. **b, c** Conidiophores with conidiogenous cells bearing conidia. **d** Conidiophores. **e** Conidiogenous cells. **f–i** Conidia. Scale bars: **a** = 200 μ m, **b–d, i** = 50 μ m, **f–h** = 20 μ m, **e** = 10 μ m

GenBank numbers: ITS: MK085062, LSU: MK079663, RPB2: MK087670, SSU: MK079661, TEF1- α : MK087660.

Notes: *Distoseptispora palmarum* shares similar conidial features to other species of *Distoseptispora*, but its conidiophores are longer than most *Distoseptispora* species (Luo et al. 2018; Tibpromma et al. 2018; Yang et al. 2018b; Phookamsak et al. 2019). *Distoseptispora palmarum* is similar to *D. leonensis* (\equiv *Ellisembia leonensis*) (McKenzie 1995; Shenoy et al. 2006; Su et al. (2016), *D. suoluensis* and *D. guttulata* (Yang et al. 2018b). However, *D. palmarum* is distinct because of its polyblastic conidiogenous cells. Multi-gene analysis based on LSU, ITS, TEF1- α and RPB2 indicates that *D. palmarum* and *D. leonensis* constitute a well-supported independent lineage (Fig. 105). However, *D. palmarum* differs from *D.*

leonensis in the length and number of distosepta in the conidia.

Hypocreomycetidae O.E. Erikss. & Winka

Notes: Eriksson and Winka (1997) introduced this subclass with four orders. In the classification of Eriksson (2006), the subclass Hypocreomycetidae comprised four orders (i.e. Coronophorales, Halosphaeriales, Hypocreales and Microascales) (Maharachchikumbura et al. 2015, 2016). Most of the taxa of the Hypocreomycetidae have light coloured perithecia, nonamyloid apical rings in the asci when apical rings are present and the absence of true paraphyses (Zhang et al. 2006)

Glomerellales Chadeff. ex Reblova et al.

Notes: We follow the updated classification by Wijayawardene et al. (2018a).

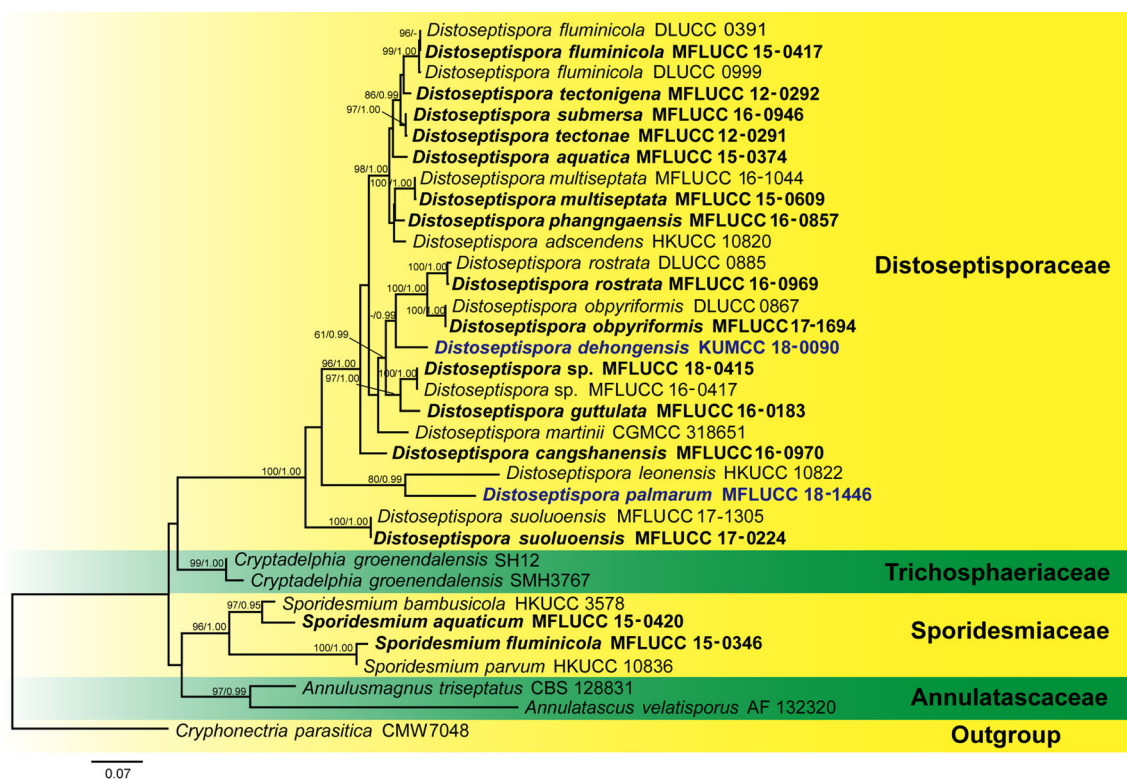


Fig. 105 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, TEF1- α and RPB2 sequence data for Distoseptisporaceae species and several related families. Related sequences are taken from Hyde et al. (2016), Su et al. (2016), Xia et al. (2017), Yang et al. (2018b) and Luo et al. (2018). Thirty-four strains are included in the combined analyses which comprise 3612 characters (897 characters for LSU, 694 characters for ITS, 946 characters for TEF1- α , 1075 characters for RPB2) after alignment. *Cryphonectria parasitica* (CMW 7048) (*Cryphonectriaceae*, *Diaporthales*) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the

Bayesian analysis. The best RaxML tree with a final likelihood value of -15208.000555 is presented. The matrix had 1181 distinct alignment patterns, with 45.45% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240242, C = 0.262790, G = 0.284086, T = 0.212881; substitution rates AC = 0.955762, AG = 2.559225, AT = 1.264794, CG = 0.896334, CT = 7.954863, GT = 1.000000; gamma distribution shape parameter α = 0.214652. Bootstrap values for maximum likelihood (ML) equal to or greater than 60 and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are placed above the branches, respectively. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

Plectosphaerellaceae W. Gams et al.

Notes: Several asexual morph genera in this family have verticillate conidiophores such as *Acrostalagmus* Corda and *Verticillium* Nees. *Stachylidium bicolor*, the type of its genus, produces erect, roughened, verticillate conidiophores, often with additional verticillate axes emerging from the main stipe; this results in a more complex conidiophore than in other similar genera (Réblová et al. 2011).

***Acrostalagmus* Corda**

Notes: Based on the phylogenetic analyses of Réblová et al. (2011), the common tropical hyphomycete described and illustrated by Seifert (1985) as *Stilbella annulata* was revealed as a member of Plectosphaerellaceae and a sister species to *Acrostalagmus luteoalbus*, the type of the genus. Both *Stilbella annulata* and *Acrostalagmus luteoalbus*

produce ameroconidia in bright orange to reddish slimy masses; in both species the reddish pigmentation sometimes also colours the phialides.

Acrostalagmus annulatus (Berk. & M.A. Curtis) Seifert, *Studies in Mycology* 68: 186 (2011)

Facesoffungi number: FoF05253; Fig. 106

Saprobic on decaying fruit. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, forming rounded pale reddish brown slimy heads, oval. **Conidiophore** axis erect, repeatedly branched, pale reddish brown at the base and hyaline at the apex, full-grown conidiophore stipes 4–5 μm wide at the base, tapering to 3 μm . **Conidiogenous cells** phialidic 9–26 \times 2–3.5 μm , narrowly flask-shaped in the widest part, arising in whorls of 1–5 at several levels along the main stipe and its branches. **Conidia** 6–8 \times 3–

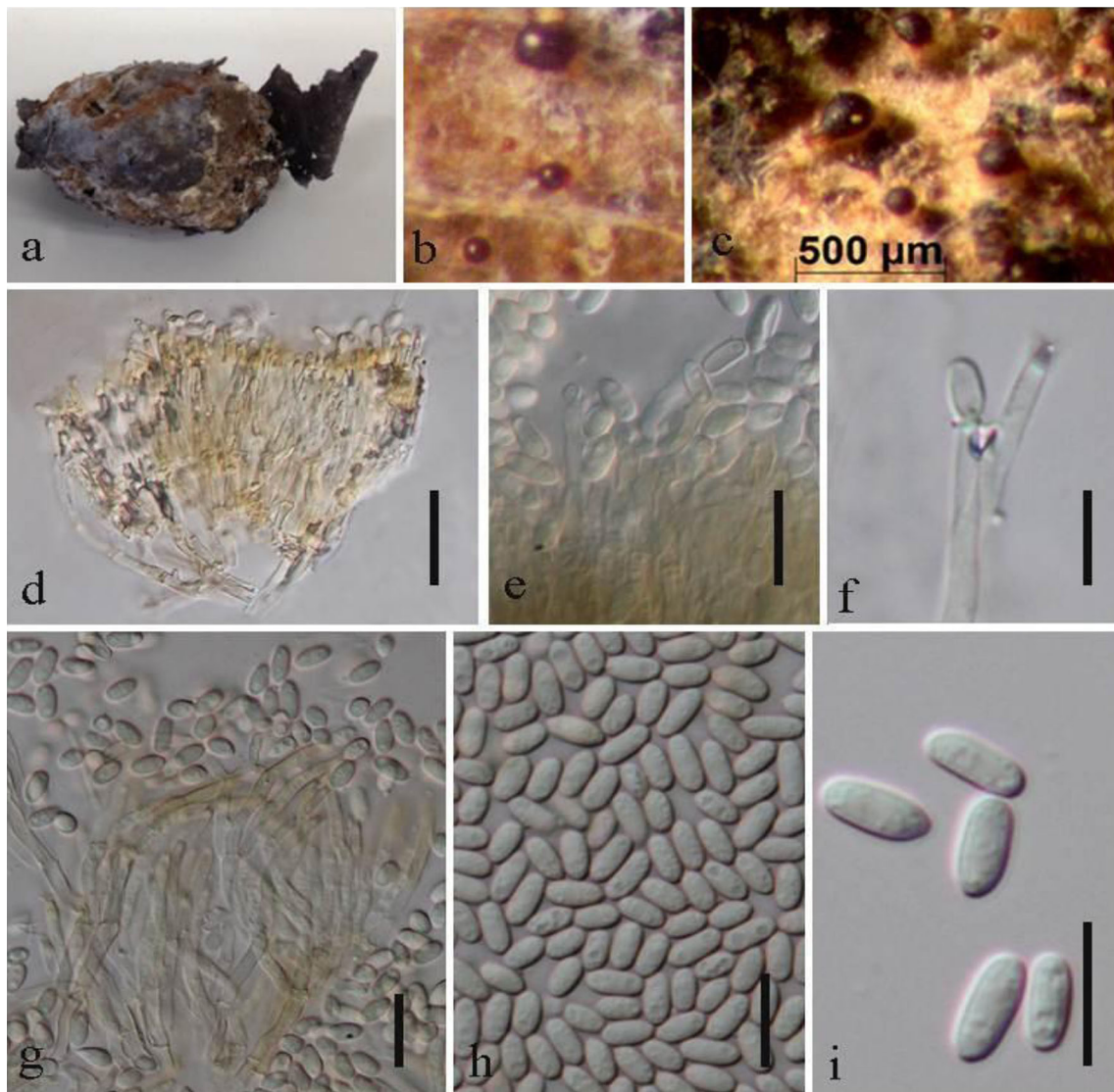


Fig. 106 *Acrostalagmus annulatus* (MFLU 16-0952, new geographical record). **a** Host fruit. **b, c** Conidiomata on host surface. **d** Conidiophores. **e–g** Conidiogenous cells and conidiophores with conidia. **h, i** Conidia. Scale bars: **d** = 20 μm , **e–i** = 10 μm

4 μm ($\bar{x} = 7.4 \times 3.6 \mu\text{m}$, $n = 30$), hyaline, sub-globose to cylindrical, single-celled.

Culture characteristics: Conidia germinated on MEA. On MEA colonies are appressed, circular, flat surface, edge entire, first cream then become dark brown and rise in the centre with mycelium, reverse brown reaching 2 cm in 2 weeks at 18 °C.

Material examined: THAILAND, Chiang Mai Province, Doi Suthep, 22 December 2015, decaying fruits of unknown species, Subashini C. Jayasiri, C 132 (MFLU 16-0952), living culture (MFLUCC 16-0612).

GenBank numbers: ITS: MK607614, LSU: MK607617, RPB2: MK607616, SSU: MK607615.

Notes: The new isolate of *Acrostalagmus annulatus* fits with the type description in having erect, roughened, verticillate conidiophores, phialidic conidiogenous cells and oblong-ellipsoidal conidia accumulate in slime (Seifert

1985; Réblová et al. 2011). *Acrostalagmus annulatus* (MFLUCC 16-0612) forms a sister clade to *A. annulatus* (DAOM 212126) and an environment sample with high statistical support (100% ML/1.00 BYPP) in Fig. 107. In here based on morphology and phylogenetic affinity introduced a new record of *Acrostalagmus annulatus* from Thailand.

Hypocreales Lindau

Notes: The order Hypocreales (Hypocreomycetidae) comprise highly diverse species in the tropics, subtropics and temperature regions (Pöldmaa 2011) and comprise the families Bionectriaceae, Clavicipitaceae, Cordycipitaceae, Flammocladiaceae, Hypocreaceae, Nectriaceae, Niessliaceae, Ophiocordycipitaceae, Stachybotriaceae and Tilachliaceae with 237 genera (Kirk et al. 2008; Maharachchikumbura et al. 2015, 2016)

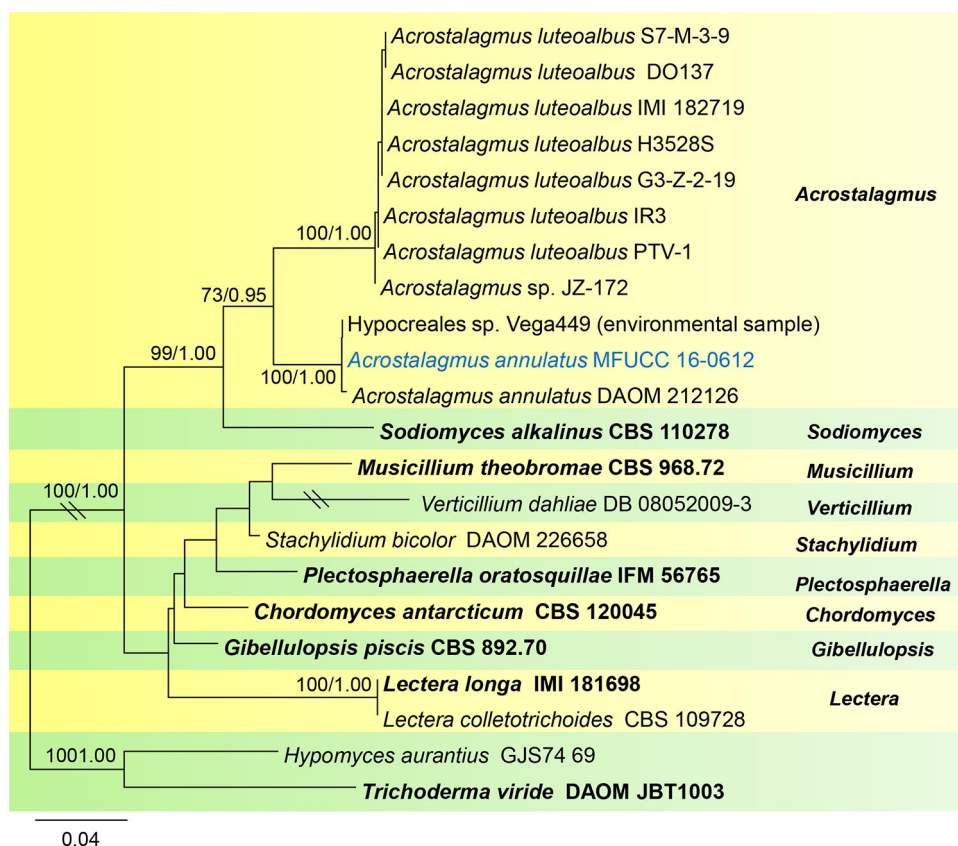


Fig. 107 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of selected taxa of Plectosphaerellaceae. Related sequences were obtained from GenBank. Twenty-two strains are included in the analyses, which comprise 1299 characters including gaps. Tree was rooted to *Hypomyces aurantius* (GJS74 69) and *Trichoderma viride* (DAOM JBT1003). Tree topology of the ML analysis is similar to the BI. The best scoring RAxML tree with a final likelihood value of -4999.737002 is presented. The matrix had 345 distinct alignment patterns, with 41.99% of undetermined characters or gaps. Estimated

base frequencies were as follows; A = 0.222188, C = 0.278776, G = 0.279137, T = 0.219898; substitution rates AC = 0.918516, AG = 1.868080, AT = 2.187888, CG = 0.896478, CT = 5.118188, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.637862$. Maximum likelihood bootstrap (MLBS) values $> 70\%$ and Bayesian posterior probabilities (BYPP) $\geq 0.95\%$ are given near the nodes respectively. The scale bar indicates 0.04 changes. The ex-type strains are in bold and black. The newly generated sequence is indicated in blue

Cordycipitaceae Kreisel ex G.H. Sung et al.

Notes: The family Cordycipitaceae was first described by Kreisel (1969). However, Cordycipitaceae was validly segregated from Clavicipitaceae by Sung et al. (2007) based on morphological and multi-gene phylogenetic analyses. Most of the species in the family are entomogenous and produce stalked, erect, stromatic ascomata or reduced stipes or subiculate stromata (Kepler et al. 2017). Stroma are fleshy or subiculate and pallid or brightly coloured (Sung et al. 2007; Kepler et al. 2017). Kepler et al. (2017) included 11 genera in this family. Wijayawardene et al. (2017a) included 17 genera in this family.

Cordyceps Fr.

Notes: Cordyceps was validly published by Link (1833) and formally moved to Cordycipitoideae by Sung et al. (2007) with the type species *Cordyceps militaris* (L.) Fr. Kepler et al. (2017) synonymised *Isaria* Pers., *Microhilum* H.Y. Yip & A.C. Rath., *Phytocordyceps* C.H. Su & H.H. Wang and *Evlachovaea* B.A. Borisov & Tarasov under *Cordyceps* using phylogenetically-based results.

Cordyceps succavus Y.P. Xiao, T.C. Wen & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555420; **Facesoffungi number:** FoF05065; Fig. 108

Etymology: The specific epithet refers to the feature of the stromata (inside hollow after mature).

Holotype: MFLU 18-1890

Parasitic in an unknown insect buried in the upper 1 cm of soil, forming yellowish to yellow stromata. **Sexual morph:** Stromata 4–5 cm long, 3–6 mm wide, yellowish to yellow, fleshy, mostly solitary, stipitate, inside hollow after mature. Stipe 2–3 cm long, 3–5 mm wide, fleshy, yellowish to white, clavate, with stromata on the top. Fertile head 1.5–2 cm long, 4–5 mm wide, fleshy, solitary, cylindrical, yellow to yellowish. Stroma 3–3.4 × 2.4–2.7 mm (\bar{x} = 3.2 × 2.6 µm, n = 30) in vertical section, yellow to yellowish. Perithecia 534–655 × 179–278 µm (\bar{x} = 594 × 229 µm, n = 30), half-embedded, ampulliform to ovoid, yellow to yellowish, thick-walled, with ostiole on the top. Peridium 23–36 µm wide (\bar{x} = 29 µm, n = 60), two layers, *textura porrecta* in first layer, *textura angularis* in secondary layer. Asci 486–600 × 3.6–4.9 µm (\bar{x} = 543 × 4.3 µm, n = 60), 8-spored, hyaline, narrow cylindrical, with a thick apex. Apical cap 3.1–4.1 × 3.3–4.5 µm (\bar{x} = 3.6 × 3.9 µm, n = 60) µm diam., hyaline. Ascospores 466–594 × 0.9–1.2 µm (\bar{x} = 530 × 1.1 µm, n = 60), filiform, smooth, hyaline, septate, breaking into secondary spores. Secondary spores 2.8–4.9 × 0.9–1.2 µm (\bar{x} = 3.8 × 1.1 µm, n = 60), cylindrical, smooth, hyaline, one-celled. **Asexual morph:** Undetermined.

Material examined: THAILAND, Chiang Mai Province, Samoeng, on larvae (Lepidopteran), 10 July 2017, Y.P. Xiao, CM0752 (MFLU 18-1890, **holotype**); *ibid.* CM0752b, HKAS 96376 (MFLU 18-1891, **isotype**).

GenBank numbers: ITS: MK086060, LSU: MK086062, RPB1: MK084616, RPB2: MK079353, SSU: MK086058.

Notes: According to morphology and phylogenetic analysis (Fig. 110), the new collection is closely related to *Cordyceps grylli*, which was collected from adults of Gryllidae in China (Teng 1936; Mains 1959), but the phylogenetic analyses supports two different species. *Cordyceps succavus* is characterized by yellow to yellowish, longer stromata, not becoming grayish when dry, yellow ampulliform to ovoid perithecia, longer asci and shorter ascospores (Table 3). *Cordyceps grylli* has yellow stromata, becoming grayish when dry, with half-embedded, light brown or chestnut brown, ovoid perithecia, cylindrical asci and filiform ascospores breaking into 1-celled secondary spores (Mains 1959) (Table 3). Therefore, we propose *Cordyceps succavus* as a new species.

Blackwellomyces Spatafora & Luangsa-ard

Notes: This genus was introduced by Kepler et al. (2017) with two species with ascospores not disarticulating into secondary spores at maturity and with irregularly spaced septa.

Blackwellomyces lateris Y.P. Xiao, T.C. Wen & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555421; **Facesoffungi number:** FoF05066; Fig. 109

Etymology: The specific epithet refers to the feature of the stroma (unilateral on the stipe).

Holotype: MFLU 18-0663

Parasitic in a larvae (Lepidoptera) buried in the upper 2 cm of soil, dark to dark-brown host, forming yellow to yellowish stromata. **Sexual morph** *Thallus* within host, without mycelium cover. Stromata 5–6 cm long, 1.5–2 mm wide, fleshy, mostly branched, yellow to yellowish, stipitate arising from head of the host. Stipe 3.5–4 cm long, 1.5 mm wide, fleshy, yellow to yellowish, clavate, with stromata on the side face. Fertile head 0.5–2.5 cm long, 1.5–2 mm wide, fleshy, solitary or branched, cylindrical, yellow to yellowish, unilateral on the stipe. Stroma 713–822 × 939–1106 µm (\bar{x} = 767 × 1023 µm, n = 30) in vertical section, yellow to yellowish, unilateral. Perithecia 287–343 × 138–184 µm (\bar{x} = 315 × 161 µm, n = 30), embedded, ampulliform to ovoid, yellow to yellowish, thick-walled, with ostiole on the top. Peridium 17–29 µm wide (\bar{x} = 23 µm, n = 60), three layers, *textura porrecta* in first layer, *textura angularis* in middle layer, *textura intricata* in third layer. Asci 166–223 × 3.7–5.1 µm (\bar{x} = 195 × 4.4 µm, n = 60), 8-spored, hyaline, narrow cylindrical, with a thin apex. Apical cap 2.2–3.0 × 3.3–

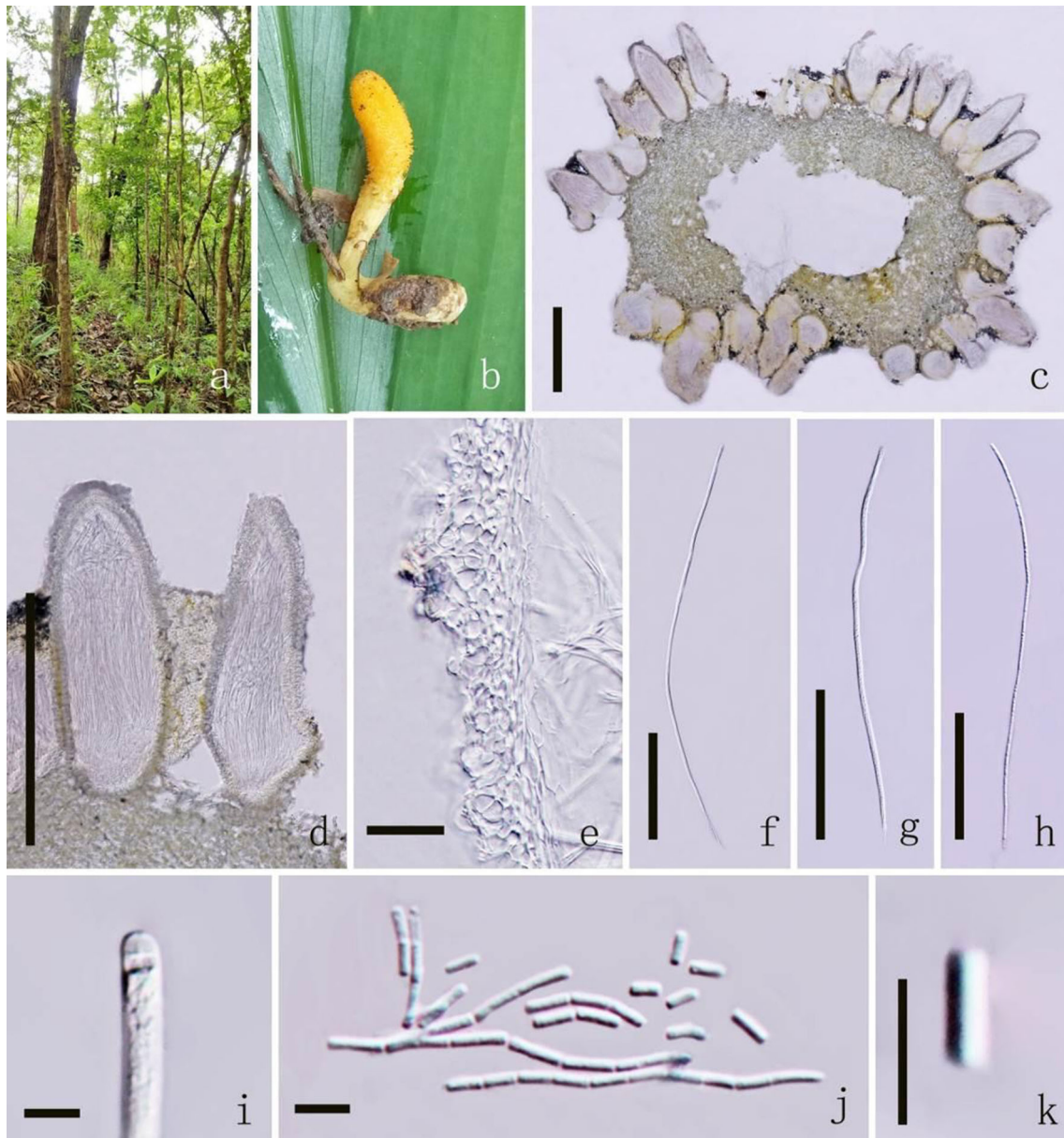


Fig. 108 *Cordyceps succavus* (MFLU 18-1890, **holotype**). **a** Habitat of *Cordyceps succavus*. **b** Stromata without infected insect. **c** Vertical section of stroma. **d** Vertical sections showing the semi-immersed

perithecia. **e** Perithecium wall. **f, g** Asci. **h** Part of ascospores. **i** Apical cap of asci. **j, k** Secondary ascospores. Scale bars: **c, d** = 500 µm, **f, g** = 200 µm, **h** = 50 µm, **e** = 20 µm, **i–k** = 5 µm

4.4 µm (\bar{x} = 2.2 × 3.3 µm, n = 60), hyaline. *Ascospores* 160–217 × 1.0–1.5 µm (\bar{x} = 188 × 1.2 µm, n = 60) cylindrical, smooth-walled, hyaline, without septa, not breaking into secondary part spores. **Asexual morph** Undetermined.

Material examined: THAILAND, Chiang Mai Province, The Mushroom Research Centre, on larvae (Lepidopteran), 12 June 2017, Y.P. Xiao, MRC170617 (MFLU 18-0663, **holotype**); *ibid.* MFLU 18-0664, MRC170617b, (HKAS 96376, **isotype**).

GenBank numbers: ITS: MK086059, LSU: MK086061, RPB1: MK084615, RPB2: MK079354, SSU: MK086057, TEF1- α : MK069471.

Notes: According to morphological and phylogenetic analysis (Fig. 110), *Blackwellomyces lateris* is closely related to *B. cardinalis* and *B. pseudomilitaris*, and characterized by yellow to yellowish, longer stromata; yellow to yellowish, longer fertile head with stromata in side face; embedded, ampulliform to ovoid perithecia; shorter asci; aseptate ascospores (Table 4). Molecular data indicate that *Blackwellomyces lateris* has 16 bp in ITS region, 2 bp in nrSSU, 10 bp in nrLSU, 11 bp in TEF1- α , 12 bp in RPB1,

Table 3 Synopsis of *Cordyceps* species discussed in the paper

Species	Host	Stromata	Fertile head (mm)	Stipe (mm)	Perithecia (μm)	Asci (μm)	Ascospores (μm)	Secondary spores (μm)	References
<i>C. grylli</i>	Gryllidae (Orthoptera)	Yellow when fresh becoming grayish		1–2 thick	Ovoid, partly embedded (up to one-half), light brown or chestnut-brown 400–700 × 300–350	Cylindric, 300–400 × 4	Filiform, break into fragments	1-celled, 4–5 × 1	Zang and Kinjo (1998)
<i>C. succavus</i>	Unknown insect	Yellowish to yellow 4–5 cm long, 3–6 mm wide	15–20 long, 4–5 wide, fleshy, solitary, cylindrical, yellow to yellowish	20–30 long, 3–5 wide	Half-embedded, ampulliform to ovoid, yellow to yellowish 534–655 × 179–278	Cylindrical 486–600 × 3.6–4.9	Filiform, multiseptate, 466–594 × 0.9–1.2	1-celled, 2.8–4.9 × 0.9–1.2	This study

20 bp in RPB2 that are different from *B. cardinalis* (OSC 93610), and has 30 bp in ITS region, 17 bp in nrSSU, 10 bp in nrLSU, 35 bp in RPB1 that are different from *B. pseudomilitaris* (NBRC 101509). *Blackwellomyces lateris* has good support in the phylogenetic tree and, therefore, we propose it as a new species.

Hypocreales genera incertae sedis

Sarocladium W. Gams & D. Hawksw.

Notes: *Sarocladium* was erected by Gams and Hawksworth (1975) and *S. oryzae* selected as the type species. *Sarocladium* is classified in Hypocreales, family *incertae sedis* (Maharachchikumbura et al. 2015, 2016). This genus encompasses 22 species according to Index Fungorum (2019). *Sarocladium attenuatum* was however, confirmed as synonym of *S. oryzae* (Bills et al. 2004). Therefore, 20 species are accepted. *Sarocladium* species resembles *Acremonium* species, but differ in their elongated, solitary phialides, sparsely or repeatedly branched conidiophores, abundant adelophialides and elongated conidia (Giraldo et al. 2015). Colony and conidial morphology can be the primary characters to identify species. Phylogenetic analysis based on a LSU-SSU and LSU-ITS dataset resolves intraspecific identification (Summerbell et al. 2011; Giraldo et al. 2015; Liu et al. 2017). Species of this genus are rice plant pathogens (Saravanakumar et al. 2009), saprobes, mutualistic endophytes (Yeh and Kirschner 2014) and human opportunistic pathogens (Giraldo et al. 2015). Some endophytes even have a potential as biological control agents against plant pathogens (Kelemu et al. 2001).

Sarocladium kiliense (Grütz) Summerb, Stud. Mycol. 68: 158 (2011)

≡ *Acremonium kiliense* Grütz, Dermatol. Wochenschr. 80:774. 1925.

Facesoffungi number: FoF05816; Fig. 111

Holotype: CBS 122.29

Culture characteristics: Colonies attaining a diam of 2.6 cm in 12 days at 22 °C, entire margin, circular, dense, moist, with radial wrinkles on the surface, pink from above and reverse. *Mycelium strands* form at the central of colonies from which the phialides are produced. *Phialides* 20–46 × 1–2 μm (\bar{x} = 34 × 1.7 μm, n = 50) phialidic, slender, tapering towards the apex. *Conidia* 2–6 × 1–2 μm (\bar{x} = 4 × 1.5 μm, n = 100), abundant, cylindrical to elliptical, aseptate, hyaline, smooth-walled, straight to curved, with round end, tending to gather in slimy head at the tip of phialide.

Material examined: CHINA, Yunnan Province, Kunming Institute of Botany, on scarred leaves of an unidentified plant, 10 September 2017. Rungtiwa Phookamsak, Dry culture (HKAS 101476), living culture (KUMCC 18-0031).

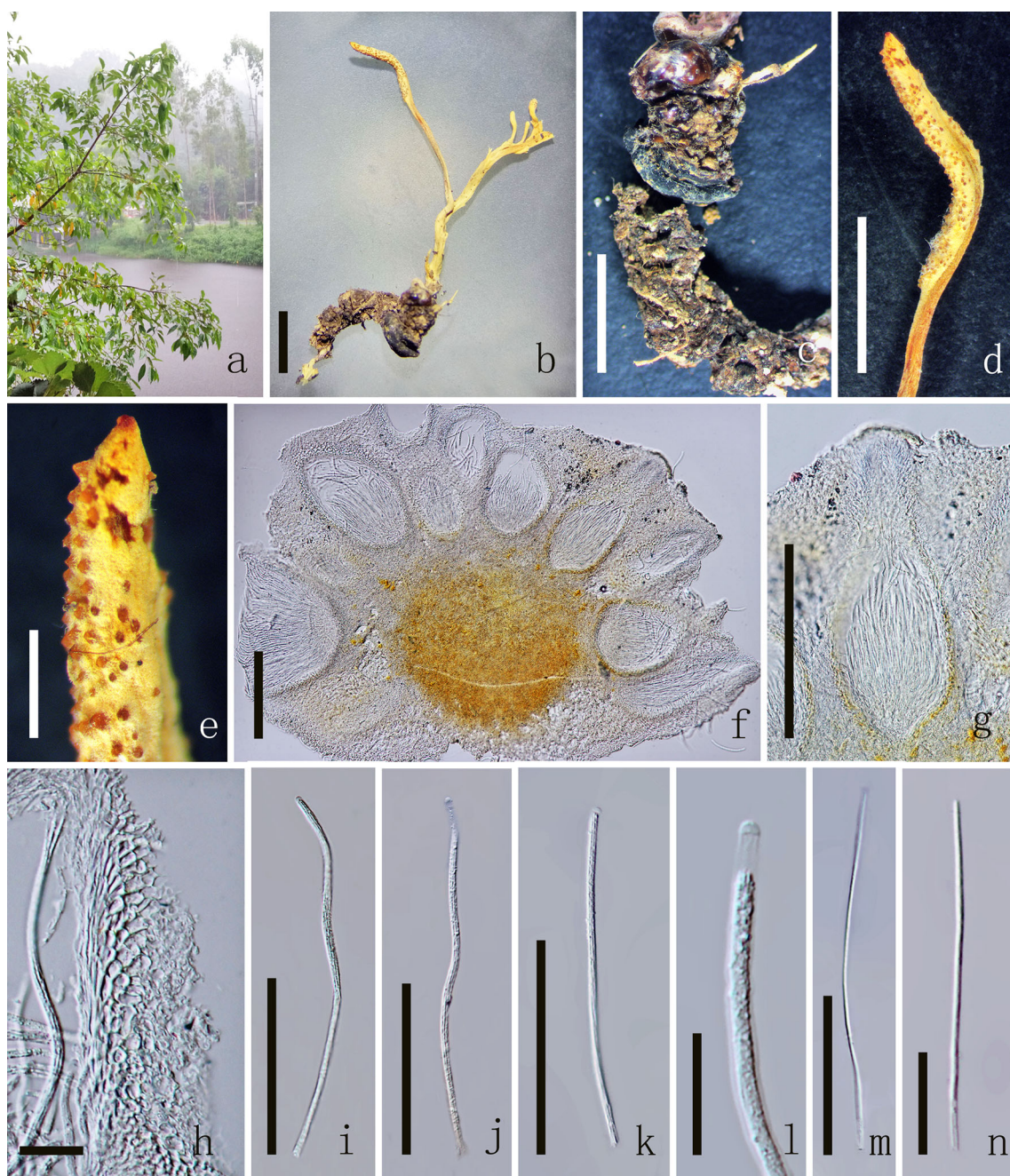


Fig. 109 *Blackwellomyces lateris* (MFLU 18-0663, **holotype**). **a** Habitat of *Blackwellomyces lateris*. **b** Overview of the host and stromata. **c** Host. **d, e** Stromata. **f** Vertical section of stroma. **g** Vertical sections showing the immersed perithecia. **h** Perithecium.

i–k Asci. **l** Apical cap of asci. **m, n** Ascospores. Scale bars: **b–d** = 1 cm, **e** = 2 mm, **f, g** = 200 μ m, **i–k** = 100 μ m, **m** = 50 μ m, **h, l, n** = 20 μ m

GeneBank numbers: ITS: MK616348, LSU: MK616474.

Notes: Our isolate has a close affinity with *Sarocladium kiliense* (CBS 122.29) based on the analysis of a combined LSU and ITS sequence data (Fig. 112). Comparison of ITS sequence showed 1/519 bp nucleotides differ from the type strain of *S. kiliense* (CBS 122.29 = MUCL 9724). *Sarocladium kiliense* is a combined species which initially proposed by Summerbell et al. (2011) based on the

phylogenetic analysis of a combined LSU and SSU sequences. The morphological descriptions of *Sarocladium kiliense* such as strain MUCL 9724 (Perdomo et al. 2011) and strain IR5 (Ebrahimi and Fotouhifar 2016) were given. Our isolates morphologically resemble type strain MUCL 9724 by having cylindrical, smooth, hyaline, conidia with rounded ends which is in slimy heads and dirty white to pale orange colony, but differ in absent of adelophialides

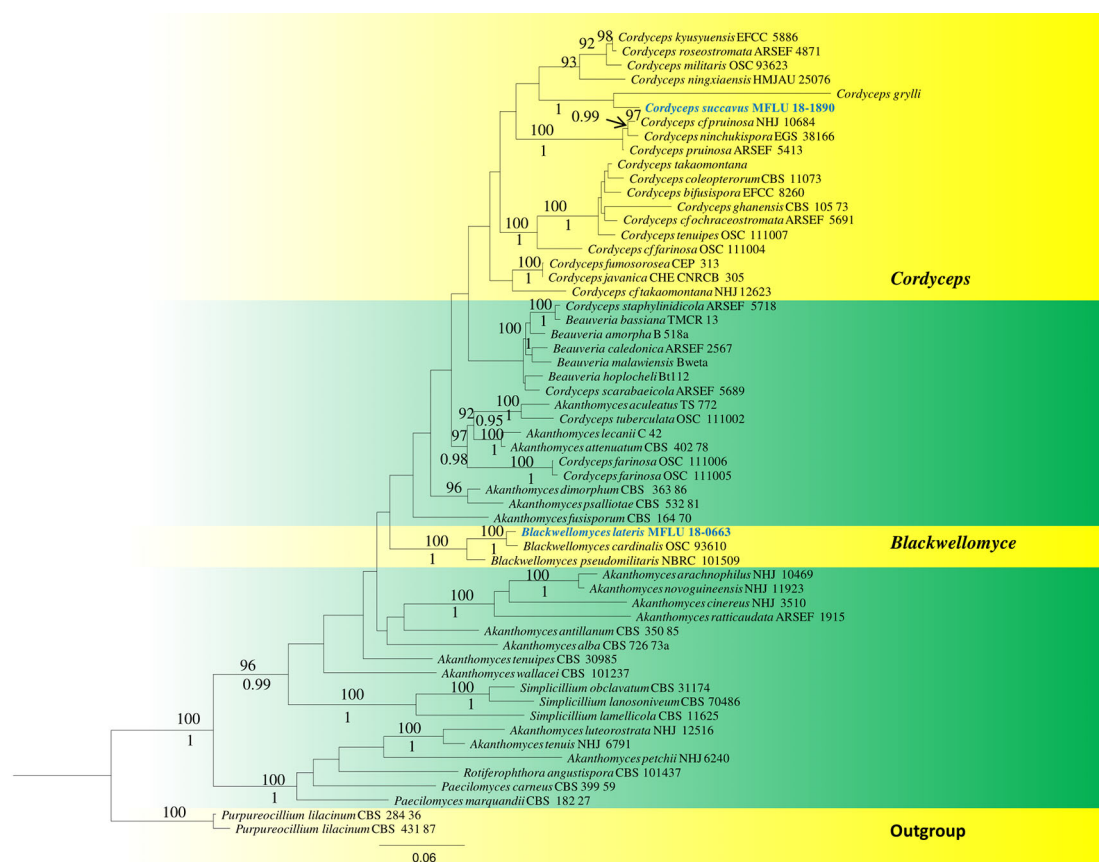


Fig. 110 Phylogram generated from maximum likelihood analysis based on combined ITS, SSU, LSU, TEF1- α , RPB1 and RPB2 sequence data for *Ophiocordyceps* species and *Blackwellomyces*. Related sequences are taken from Sung and Spatafora (2004), Sung et al. (2007) and Kepler et al. (2017). Fifty-seven strains are included in the combined genes sequence analyses which comprise total 4558 characters (1002 characters for SSU, 716 characters for LSU, 494 characters for ITS, 920 characters for TEF1- α , 570 characters for RPB1 and 856 characters for RPB2) after alignment. *Purpureocillium lilacinum* (CBS 284.36) and *P. lilacinum* (CBS 431.87) are used as outgroup taxa. Tree topology of the maximum likelihood analysis is

similar to the Bayesian analysis. The best sorting RaxML tree with a final likelihood value of -37381.826537 is presented. The matrix had 1832 distinct alignment patterns, with 29.69% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244626, C = 0.262958, G = 0.266932, T = 0.225484; substitution rates AC = 1.386955, AG = 3.678399, AT = 1.009103, CG = 1.080113, CT = 7.048074, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.209990$. Bootstrap values for maximum likelihood and Bayesian equal to or greater than 75 are placed above and below the branches respectively. The newly generated sequences are indicated in bold and blue

and chlamydospores. Our isolates also similar as strain IR5 in colonial characters as well as the shape and size of phialides (tapering toward apex, $19\text{--}48 \times 1\text{--}2 \mu\text{m}$) and conidia (cylindrical with round end, $3\text{--}7 \times 1\text{--}2 \mu\text{m}$), but differ in absents of chlamydospores (Ebrahimi and Fotouhifar 2016). Historically, *Sarocladium kiliense* can be an endophytes (strain CanL-10b, China) on *Brassica napus* (Zhang et al. 2014b), a pathogen such as strain IR5 (Iran) on *Malus domestica* leaf (Ebrahimi and Fotouhifar 2016), strain CBS 400.52 (England) on *Ficus carica* (Lombard et al. 2015), strain CBS 122.29 (Germany) on skin infection of man (Herrera et al. 2013), strain FMR 10426 (USA) on blood of human or animal (Irinnyi et al. 2015). *Sarocladium kiliense* have close association with human infections and plant scab, the detailed morphological description is necessary for rapid diagnosis of agent which

causes disease (Perdomo et al. 2011). Herewith we introduce our isolate as a new collection of *Sarocladium kiliense*.

Pleurotheciales Réblová & Seifert

Notes: Réblová et al. (2016) introduced the order Pleurotheciales with a single family Pleurotheciaceae Réblová & Seifert based on morphological data and phylogenetic analyses.

Pleurotheciaceae Réblová & Seifert

Notes: Members of the family Pleurotheciaceae share the following morphological characters: perithecial, astromatic, immersed to superficial ascomata, a hamathecium of paraphyses, unitunicate asci, with a non-amyloid apical ring and hyaline or versicolorous, transversely multi-septate ascospores with polar cells hyaline or brown central

Table 4 Synopsis of *Blackwellomyces* species discussed in this paper

Species	Host	Stromata	Fertile head (mm)	Stipe (mm)	Perithecia (µm)	Asci (µm)	Ascospores (µm)	Reference
<i>B. cardinalis</i>	Lepidoptera	Reddish orange to reddish,	Reddish orange to reddish, cylindrical, elliptical to fusiform, 2–9 × 1–4	Orange to red, cylindrical to enlarging apically 4–50 × 0.5–1.5	Embedded, elliptical to fusiform to obclavate, 230–540 × 110–240	175–330 × 3–5	Irregularly multiseptate, 160–320 × 1	Sung and Spatafora (2004)
<i>B. pseudomilitaris</i>	Lepidoptera	Orange	Orange, cylindrical, 2–8 × 1.2–4		Superficial with one-quarter to one-third immersed, elongate ellipsoid to elongate ovoid, 290–570 × 120–245	290–410 × 5–6	Multiseptate, 280–390 × 1	Hywel-Jones (1994)
<i>B. lateris</i>	Lepidoptera	Yellow to yellowish, 50–60 × 1.5–2	Yellow to yellowish, cylindrical, elliptical to fusiform, 5–25 × 1.5–2	Yellow to yellowish, clavate, with stromata on the side face 35–40 × 1.5	Embedded, ampulliform to ovoid, 287–343 × 138–184	166–223 × 3.7–5.1	Aseptate, 160–217 × 1.0–1.5	This study

cells. The asexual morph is characterized by macronematous or semi-macronematous conidiophores, loosely fasciculate or aggregated in indeterminate synnemata, and conidiogenous cells producing conidia holoblastically, conidial secession rhexolytic on short denticles or rachis on sympodially extending polyblastic conidiogenous cells and conidia hyaline, brown or versicolorous, septate or aseptate (Réblová et al. 2016).

Phaeoisaria Höhn.

Notes: *Phaeoisaria* was introduced by von Höhnelt (1909) for a collection on *Gigantochloa* sp. (Bambusae) and is typified by *P. bambusae* Höhn. This dematiaceous hyphomycete genus presently includes 19 species that produce indeterminate synnemata with septate or aseptate ellipsoidal, obovoidal, fusiform-cylindrical or falcate conidia formed on a sympodially extending rachis, occurring on decaying wood, plant debris or soil sediments (Sutton 1973; Deighton 1974; Castañeda et al. 2002; Seifert et al. 2011; Mel'nik 2012; Cheng et al. 2014; Liu et al. 2015; Réblová et al. 2016). Réblová et al. (2012) described the genus *Pleurotheciella* for two new species, *P. rivularia* and *P. centenaria*.

Phaeoisaria siamensis Jayasiri & K.D. Hyde, *sp. nov.*

Index fungorum number: IF555710; *Facesoffungi number:* FoF05324; Fig. 113

Etymology: With reference to country ('Siam' earlier name of Thailand) where the specimen was collected.

Holotype: MFLU 16-0953

Saprobic on decaying fruits. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* scattered, indeterminate, erect, rigid, superficial, dark brown composed of compact appressed conidiophores. *Conidiophores* 330–380 µm high, 20–25(–30) µm (\bar{x} = 360 × 24.5 µm, n = 20) wide, macronematous, in synnematus conidiomata, scattered, synnemata subulate or cylindrical, indeterminate, at the base 13–15 µm beneath the fertile portion with conidiogenous cells, composed of medium to dark brown, smooth, septate parallel hyphae, 2–2.5(–3) µm wide, splaying out at the middle to apex. *Conidiogenous cells* 8–12 × 2–2.5 µm (\bar{x} = 10.5 × 2.3 µm, n = 20), integrated, terminal and intercalary, poly-blastic, sympodial, cylindrical or somewhat attenuated toward the tip, pale brown near base, subhyaline at the apex, denticulate, denticles conspicuously cylindrical, 2–2.5 × 1–1.5 µm. *Conidia* 5–8 × 3–4 µm (\bar{x} = 6.2 × 3.5 µm, n = 30), globose to subglobose, hyaline, aseptate.

Culture characteristics: Conidia germinated on MEA. Colonies are appressed, circular, flat surface, edge entire, first cream then become dark brown and rise in the centre with mycelium, reverse brown reaching 10 mm in 2 weeks at 18 °C.

Material examined: THAILAND, Chiang Mai Province, Doi Suthep, 22 December 2015, decaying fruits of

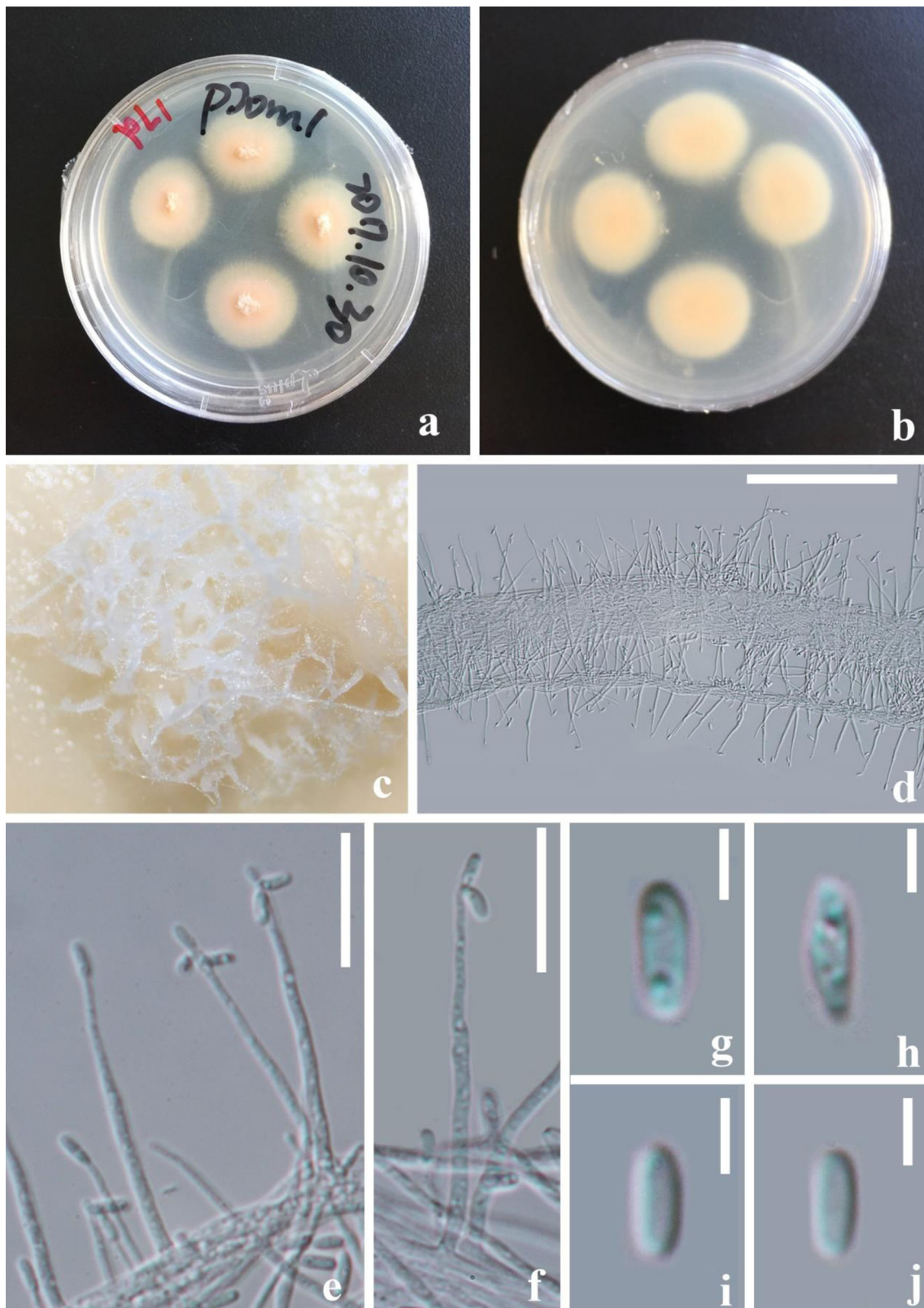


Fig. 111 *Sarocladium kiliense* (HKAS 101476, new record). **a, b** Upper and reverse view of culture on PDA after 17 days. **c** Mycelium strand form at centre of colony. **d** Phialides arising from mycelium

strand. **e, f** Phialides bearing conidia. **g–j** Conidia. Scale bars: **d** = 100 μ m, **e, f** = 15 μ m, **g–j** = 3 μ m

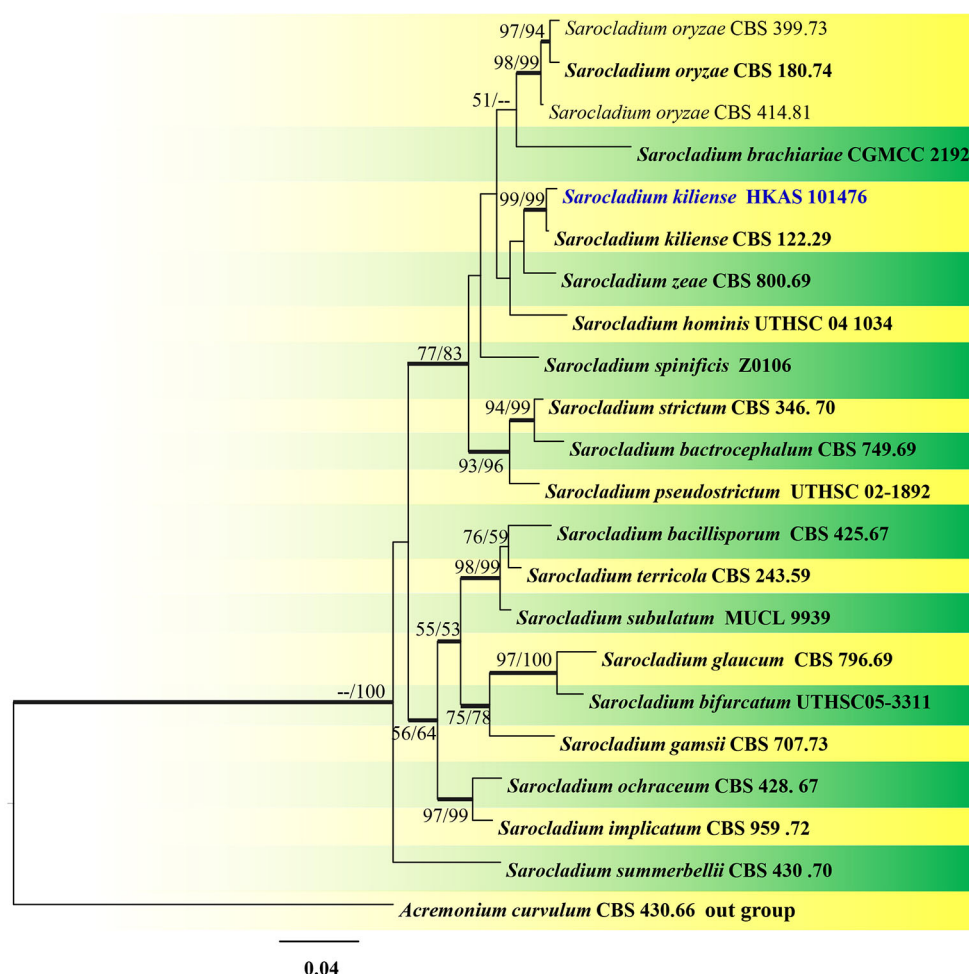


Fig. 112 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data for *Sarocladium* species. Related sequences were referred to Liu et al. (2017). Twenty-two strains are included in the combined genes sequence analyses which comprise total 1086 characters (517 characters for LSU, 569 characters for ITS) after alignment. *Acremonium curvulum* (CBS 430.66) (*Incertae sedis*, Hypocreales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree with clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best sorting RaxML tree with a final likelihood value of -4666.270461 is presented. The matrix had 300 distinct alignment patterns, with 3.01% undetermined characters

or gaps. Estimated base frequencies were as follows: A = 0.232286, C = 0.271554, G = 0.293432, T = 0.202727; substitution rates AC = 1.861270, AG = 2.197180, AT = 2.893484, CG = 0.997016, CT = 6.880061, GT = 1.000000; gamma distribution shape parameter α = 0.179594. Maximum parsimony analysis of 791 constant characters and 142 informative characters resulted in two equally most parsimonious tree of 153 steps (CI = 0.614, RI = 0.643, RC = 0.395, HI = 0.386). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 50 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.90 are in bold. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Meliaceae sp., Subashini C. Jayasiri, C 128 (MFLU 16-0953, **holotype**), ex-type living culture (MFLUCC 16-0607).

GenBank numbers: ITS: MK607610, LSU: MK607613, RPB2: MK607611, SSU: MK607612.

Notes: *Phaeoisaria siamensis* fits with the generic description of *Phaeoisaria* in having indeterminate synnemata with aseptate ellipsoidal, obovoidal, fusiform-cylindrical or falcate conidia formed on a sympodially extending rachis. *Phaeoisaria siamensis* (MFLUCC 16-0607) forms a sister clade to *P. aquatica* (MFLUCC

16-1298) with high statistical support (99% MLBS/1.0 BYPP) in Fig. 114. *Phaeoisaria aquatica* differs from *P. siamensis* in having compactly and parallelly adpressed conidiophores, with flared conidiogenous cells in the above half (Luo et al. 2018). A comparison of the ITS and RPB2 nucleotides of these two strains reveals 8 (1.6%) and 13 (1.5%) nucleotide differences which justifies the new species following the guidelines of Jeewon and Hyde (2016).

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

Notes: The order Savoryellales was introduced by Boonyuen and Pang (2011) to accommodate three sexual genera viz. *Ascotaiwania* Sivan. & H.S. Chang, *Ascothailandia* Sri-indr., Boonyuen, Sivichai & E.B.G. Jones (now *Canalisporium* Nawawi & Kuthub.), *Savoryella* E.B.G. Jones & R.A. Eaton and an asexual genus *Canalisporium* based on multi-gene phylogenies. It was placed in subclass Hypocreomycetidae (Sordariomycetes) (Boonyuen and Pang 2011), and subsequently raised to subclass Savoryellomycetidae (Sordariomycetes) by Hongsanan et al. (2017) based on phylogenetic analyses and its stem age (267 MYA) reported in Hyde et al. (2017a). This was also confirmed by Dayarathne et al. (2019a).

Savoryellaceae Jaklitsch & Réblová

Notes: The family Savoryellaceae has a worldwide distribution in freshwater, marine and brackish water habitats (Ranghoo 1998; Abdel-Wahab and Jones 2000; Cai et al. 2003; Jones et al. 2015). The family was reviewed by Dayarathne et al. (2019a) with morpho-molecular and molecular clock analyses. It comprises three genera *Ascotaiwania* Sivan. & H.S. Chang, *Canalisporium* Nawawi & Kuthub. and *Savoryella* E.B.G. Jones & R.A. Eaton (Dayarathne et al. 2019a).

Canalisporium Nawawi & Kuthub.

Notes: *Canalisporium* was proposed to accommodate *Berkleasium caribense* Hol.-Jech. & Mercado, *B. pulchrum* Hol.-Jech. & Mercado and *C. elegans* Nawawi & Kuthub. and typified by *C. caribense* (Hol.-Jech. & Mercado) Nawawi & Kuthub. Twelve species are accepted in the genus, nine of which have molecular data in GenBank. *Canalisporium* is characterized by muriform conidia and with sexual morph formerly known in *Ascothailandia* (Sri-indrasutdhi et al. 2010).

Canalisporium dehongense W. Dong, H. Zhang & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555407; **Facesoffungi number:** FoF05058; **Fig. 115**

Etymology: Name reflects Dehong, from where the species was isolated.

Holotype: MFLU 18-1189

Saprobic on decaying wood submerged in freshwater.

Sexual morph Undetermined. **Asexual morph** *Conidiomata* sporodochial, scattered, punctiform, pulvinate, granular, black, shiny. *Mycelium* immersed in natural substrate, consisting of branched, septate, thin-walled, smooth, hyaline to pale brown hyphae. *Conidiophores* up to 65 µm long, micronematous, mononematous, vesiculate, consisted of 1–9 subglobose, smooth, hyaline cells, unbranched, septate, constricted at the septa. *Conidigenous cells* 7–16 × 7–14 µm (\bar{x} = 12 × 10 µm, n = 15), holoblastic, monoblastic, terminal, determinate,

subglobose, ellipsoidal, sometimes swelling to globose, hyaline, smooth, thin-walled. *Conidia* 20–30 × 12–19 µm (\bar{x} = 25 × 16 µm, n = 40), solitary, acrogenous, ellipsoidal to obovoid, muriform, smooth, brown, 1 straight column of vertical septa and 3–5 rows of transverse septa, slightly constricted at the septa, darkened and thickly banded at the septa, canals in the septa obscured by dark pigmentation; basal cell single, cuneiform, sometimes swollen, pale brown to hyaline.

Culture characteristics: On PDA, colony circular, 10 mm in 40 days at 25 °C, brown to grey from above, black from below, raised, felty wooly, fairly dense.

Material examined: CHINA, Yunnan Province, on submerged wood in a small river, 25 November 2017, G.N. Wang, H158D (MFLU 18-1189, **holotype**), ex-type living culture, (MFLUCC 18-1396), *ibid.*; H158D (HKAS 101725, **isotype**), ex-isotype living culture (KUMCC 18-0075).

GenBank numbers: ITS: MK051033, LSU: MK051034, SSU: MK051035.

Notes: *Canalisporium dehongense* is morphologically similar to *C. caribense* (Hol.-Jech. & Mercado) Nawawi & Kuthub. and *C. exiguum* Goh & K.D. Hyde in having muriform conidia with one longitudinal septum, two cells at the apex and darkened bands at the septa (Goh et al. 1998b; Sri-indrasutdhi et al. 2010). However, it differs from *C. caribense* by its smaller conidia (20–30 × 12–19 µm vs. 24–51 × 15–29 µm) and from *C. exiguum* by having more rows of transverse septa (3–5 vs. 2–3). A comparison of nucleotides of *C. dehongense* with *C. caribense* SS03839, *C. caribense* SS03683 and *C. exiguum* SS00809 also reveals a difference of 94, 101 and 82 bp in the ITS gene region, respectively. The species clusters as a distinct clade within the genus *Canalisporium* (Fig. 116) with high statistical support (0.99 BYPP).

Sordariomycetidae O.E. Erikss. & Winka

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Notes: The order Chaetosphaeriales was introduced by Huhndorf et al. (2004) to accommodate Chaetosphaeriaceae Réblová, M.E. Barr & Samuels. Maharachchikumbura et al. (2015) indicated that Chaetosphaeriaceae and Helminthosphaeriaceae Samuels, Cand. & Magni were sister families within Chaetosphaeriales clade. Subsequently, Konta et al. (2017) introduced another two families, Leptosporrellaceae Konta & K.D. Hyde and Linocarpaceae Konta & K.D. Hyde into Chaetosphaeriales based on LSU and ITS sequence data. Besides these four families, Chaetosphaeriales also comprises some genera *incertae sedis*, e.g. *Caudatispora* J. Fröhl. & K.D. Hyde, *Erythromada* Huhndorf, A.N. Mill., F.A. Fernández &

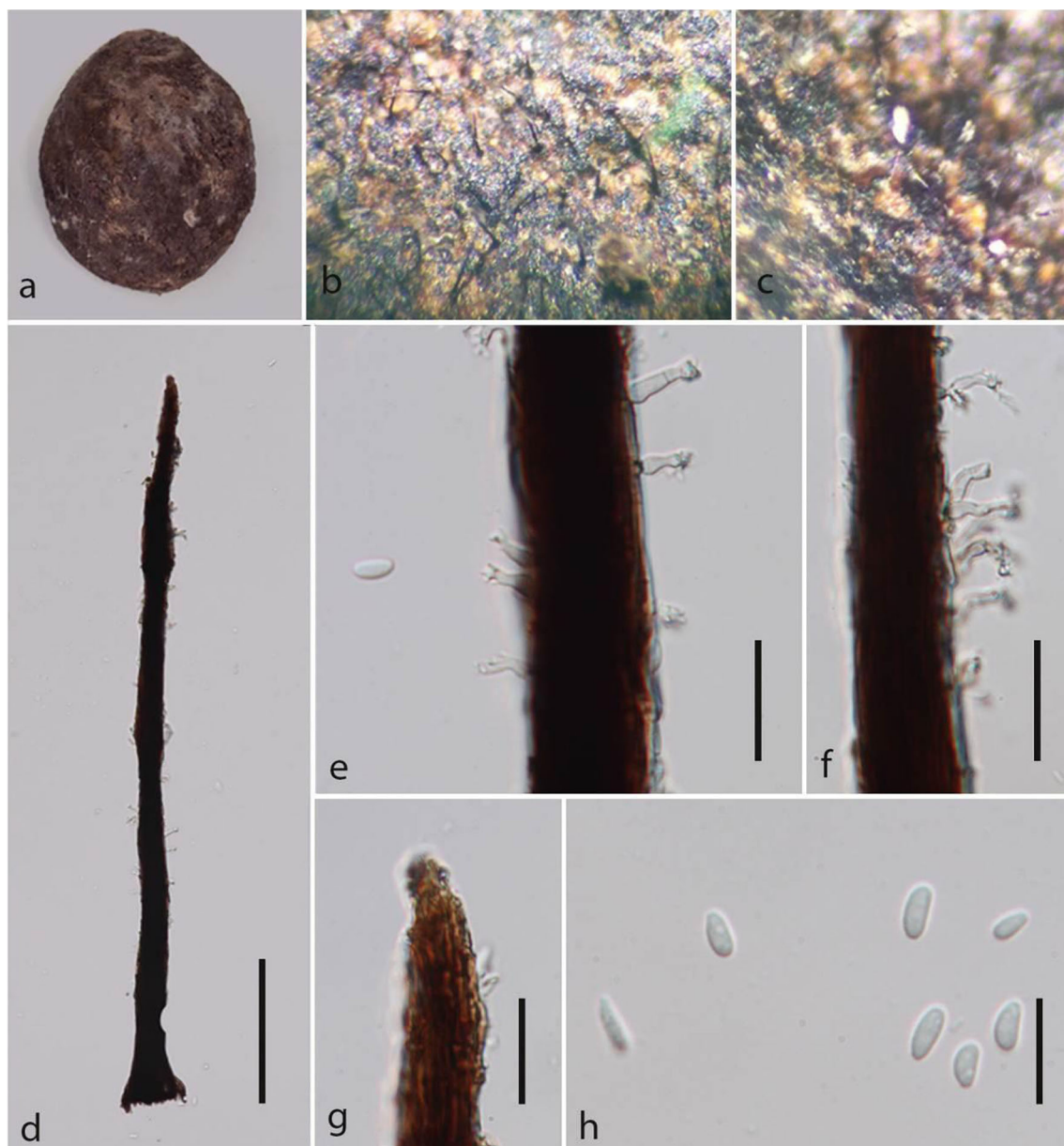


Fig. 113 *Phaeoisaria siamensis* (MFLU 16-0953, **holotype**). **a** Host fruit. **b, c** Conidiomata on host surface. **d** Conidiophore. **e–g** Conidiogenous cells arranged on conidiophores. **h** Conidia. Scale bars: **d** = 100 µm, **e–g** = 10 µm

Lodge, and *Lasiosphaeriella* Sivan. (Maharachchikumbura et al. 2015, 2016).

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Notes: Thirty-eight genera are presently accepted in Chaetosphaeriaceae (Maharachchikumbura et al. 2015, 2016; Wijayawardene et al. 2018a; Yang et al. 2018a). Recent studies are those of Liu et al. (2016), Lu et al. (2016), Luo et al. (2016, 2019), Wei et al. (2018) and Yang et al. (2016, 2018).

Sporoschisma Berk. & Broome

Notes: Most *Sporoschisma* species have been reported from freshwater habitats (Goh et al. 1997; Ho et al. 2002; Luo et al. 2016, 2019; Yang et al. 2016a). Thirteen species are accepted within this genus (Luo et al. 2016, 2019). *Sporoschisma* resides in Chaetosphaeriaceae (Chaetosphaeriales) (Maharachchikumbura et al. 2015, 2016).

Sporoschisma chiangraiense N.G. Liu & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF555386; *Faceoffungi number:* FoF04950; Fig. 117

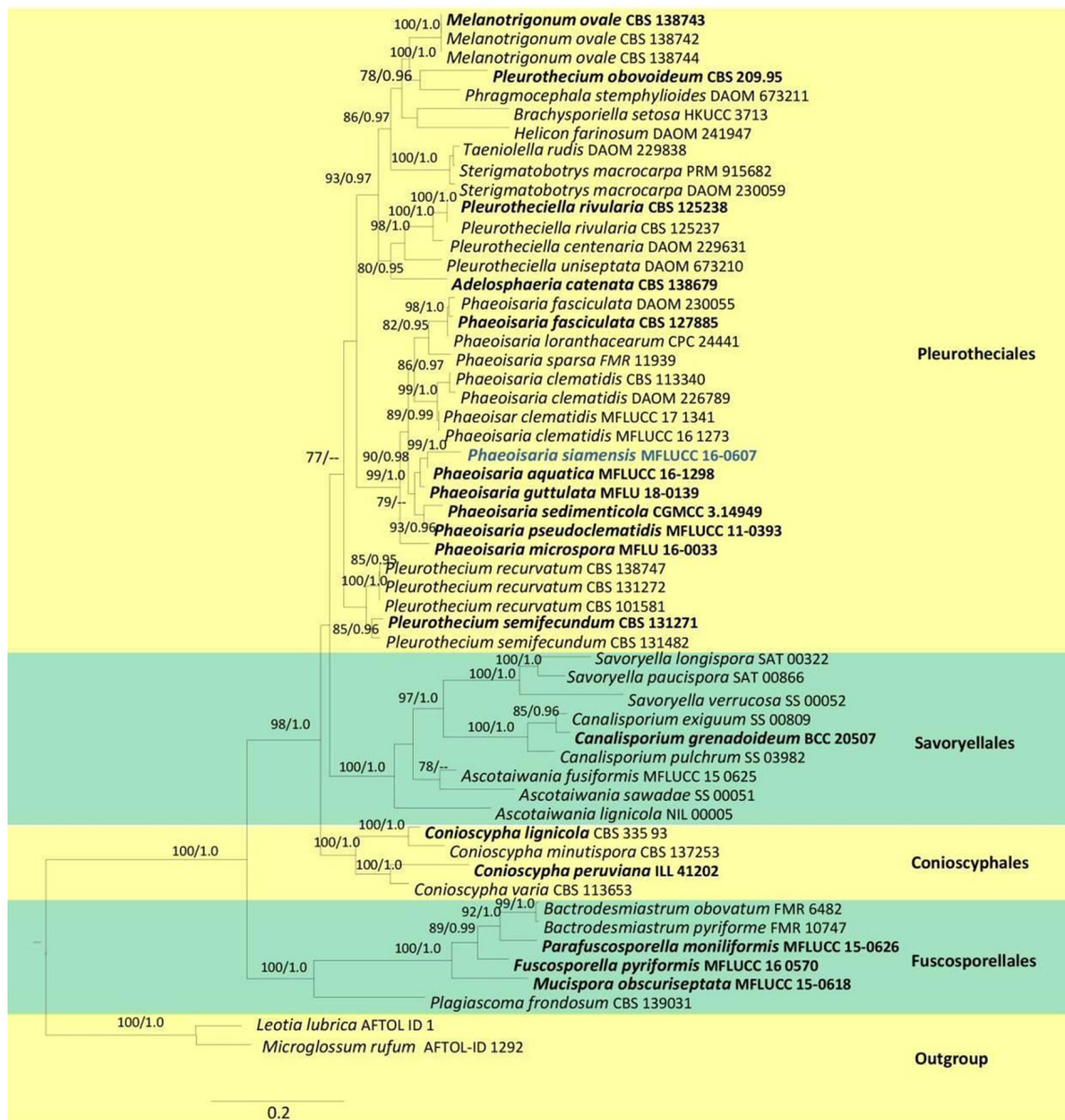


Fig. 114 Simplified phylogram showing the best RAXML maximum likelihood tree obtained from the combined SSU, ITS, LSU and RPB2 matrix of 55 taxa of the orders Pleurotheciales, Savoryellales, Conioscyphales and Fuscosporellales. The matrix comprised 3920 characters including alignment gaps. The tree was rooted to *Leotia lubrica* (AFTOLID 1) and *Microglossum rufum* (AFTOL-ID 1292). The best scoring RAXML tree with a final likelihood value of – 32124.131818 is presented. The matrix had 1958 distinct alignment

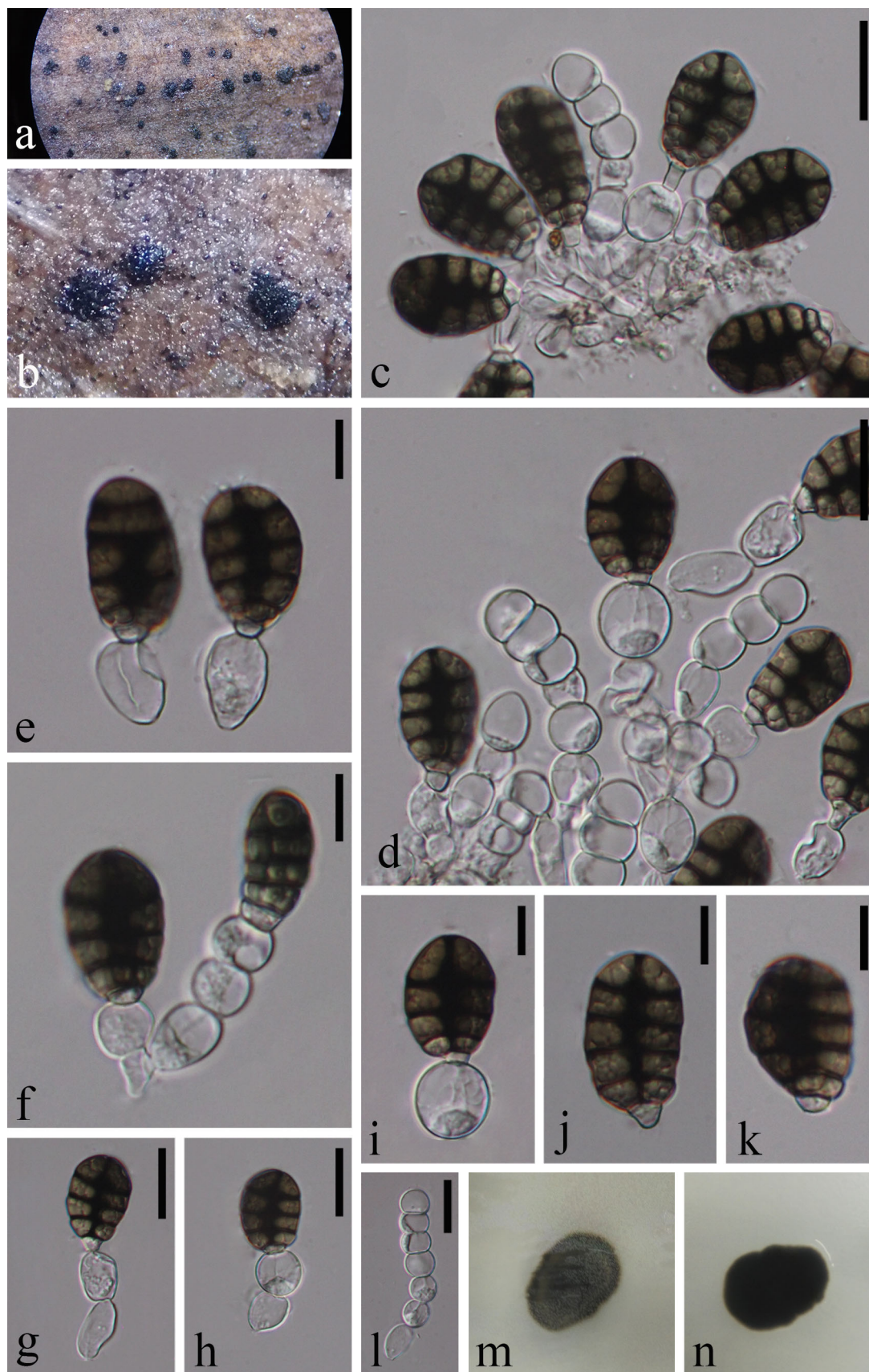
patterns, with 38.37% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237765, C = 0.258447, G = 0.293741, T = 0.210047; substitution rates AC = 1.443319, AG = 2.967467, AT = 1.388359, CG = 1.234302, CT = 7.043503, GT = 1.000000. MLBS equal to or greater than 70% (first set) and BYPP values equal to or greater than 0.95 (second set) are given at the nodes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Etymology: The name refers to the place that fungus was collected, Chiang Rai, Thailand.

Holotype: MFLU 18-1722

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Colonies on natural substrate effuse, black, hairy, with long chains of conidia. **Mycelium** immersed, composed of hyaline, guttulate, branched, 1.5–3 wide hyphae. **Setae** 85–150 × 3.5–8 µm,

scattered or in groups mixed with conidiophores, capitate, sometimes surrounded by hyaline mucilage at the swollen apex, smooth, median brown, paler towards the apex, straight or flexuous, septate. **Conidiophores** 100–220 µm long, 5–8 µm wide below venter, 11–13.5 µm wide above, and 13–16 µm wide at venter, macronematous, monone-matous, smooth, dark brown to black, paler at the torn apex, straight or slightly flexuous, solitary or in groups of



◀**Fig. 115** *Canalisporium dehongense* (MFLU 18-1189, **holotype**). **a**, **b** Colonies on submerged wood. **c–i** Conidia with conidiogenous cells. **j**, **k** Conidia. **l** Conidiophore. **m**, **n** Colony on PDA (**m** from above view, **n** from below view). Scale bars: **c**, **d**, **g**, **h**, **l** = 20 μm , **e**, **f**, **i–k** = 10 μm

2–3, arising from dark brown to black bulbous base, composed of a cylindrical stipe and a swollen venter with a long cylindrical neck, erect, sometimes proliferating percurrently. *Conidiogenous cells* monophialidic, percurrent, integrated, brown, lageniform, frayed at the apex. *Conidia* 15.5–30 \times 8.5–12.5 μm (\bar{x} = 23.8 \times 10.7 μm , n = 30), formed in chains, cylindrical, aseptate, hyaline, verruculose, smooth-walled, with a conspicuous guttule at centre when young, 1-septate, brown, with conspicuous, circular guttules in each cell when mature, conspicuously darkened and slightly constricted at the septa, thickened at both ends (Fig. 117).

Culture characteristics: Conidia germinating on water agar media within 48 h. One or two germ tubes produced randomly from conidium wall. Colonies growing on PDA white, irregular, circular, edge entire, mycelium fluffy, dense in the centre, becoming sparse at the edge.

Material examined: THAILAND, Chiang Rai Province, Muang District, Ban Nang Lae Nai, on decaying wood submerged in a freshwater stream, 6 March 2018, N.G. Liu, CR066 (MFLU 18-1722, **holotype**), ex-type living culture (MFLUCC 18-0703).

GenBank numbers: ITS: MH883032, LSU: MH883030, SSU: MH883048.

Notes: *Sporoschisma chiangraiense* is phylogenetically related to *S. aquaticum* and *S. palauense* (Fig. 118). Comparisons of ITS sequences showed that there are 106 bp differences with gaps of total 558 bp between *S. chiangraiense* and *S. aquaticum*, and 58 bp differences with gaps of total 563 bp between *S. chiangraiense* and *S. palauense*. *Sporoschisma chiangraiense* differs from *S. aquaticum* and *S. palauense* in having 1-septate conidia when mature, while the latter two are 3-septate, and 1–3-septate respectively (Luo et al. 2016; Yang et al. 2016a). Conidia of *S. chiangraiense* have conspicuous guttules, a feature absent in *S. aquaticum*.

Ellisembia Subram., Proc. Indian Natn Sci. Acad., Part B. Biol. Sci. 58(4): 183 (1992)

Notes: *Ellisembia*, based on *E. coronata*, was segregated from the widely circumscribed *Sporidesmium* by Subramanian (1992) and delimited to species with brown, distoseptate conidia and conidiophores with none or percurrent and irregular extension. It comprises saprobic species on wood, bamboo culm or plant remnants in terrestrial and freshwater habitats. Based on the evidence from molecular DNA data, the difference between

euseptate vs. distoseptate conidia among *Sporidesmium*-like species does not seem significant (Su et al. 2016; Yang et al. 2018). The genus *Ellisembia* is polyphyletic, it comprises 65 species but only some of them could be positioned in the system based on DNA sequence data. Currently, members of *Ellisembia* are placed in four clades in *Sordariomycetes*, i.e. in Chaetosphaeriaceae under the name *Ellisembia*, Distoseptisporaceae as *Distoseptispora*, Sporidesmiaceae as *Sporidesmium* and Xylariales as *Ellisembia calyptrata* (Réblová and Winka 2001; Shenoy et al. 2006; Su et al. 2016; this study). Until the systematic positions of the type species of *Ellisembia* and *Sporidesmium* are revealed, we recommend using the name *Ellisembia* for species grouped in a strongly supported monophyletic clade in Chaetosphaeriaceae, experimentally linked with sexual morphs having multiseptate, versicolourous ascospores in asci with a non-amyloid apical annulus, persistent paraphyses and immersed ascomata.

Ellisembia aurea Réblová & J. Fourn., **sp. nov.**

Mycobank number: MB827909; **Facesoffungi number:** FoF05783; Figs. 119, 120

Etymology: *Aureus* (L) golden, referring to the colour of the golden-yellow pigment covering necks and surrounding substrate.

Holotype: PRA-14744

Saprobic on decaying wood partly submerged in freshwater. **Sexual morph** *Ascomata* immersed with protruding necks or becoming superficial, solitary or in small groups. Venter 600–750 μm diam., 320–400 μm high, subglobose, upright or decumbent. *Neck* central, 170–200 μm wide, 300–600(–1000) μm long, upright or decumbent, cylindrical, sometimes tapering towards the apex, with a distinct pore at the apex. Neck often basally swollen up to 320–400 μm , conical, surrounded by a dark brown to black stroma formed of densely interwoven, dark brown, septate, thick-walled hyphae 2.5–3.5 μm wide of textura intricata. Stroma covered by erect, dark brown conidiophores. Neck covered irregularly by a layer of golden-yellow granules which disappear with age; granules of the same pigment are also staining the surrounding substrate. *Ostiole* periphysate. *Ascomatal wall* leathery, 20–27 μm , two-layered; outer layer consisting of brown, thick-walled, polyhedral cells with opaque walls of textura angularis; towards the interior cells more flattened of textura prismatica. Inner layer consisting of several rows of thin-walled, hyaline, flattened cells. *Paraphyses* hyaline, branched, anastomosing, septate, 2.5–3.5 μm wide, tapering to ca. 2.0 μm . *Asci* (165–)170–205 \times 23–25.5(–27.5) μm (mean \pm SD = 190.4 \pm 14.2 \times 24.6 \pm 1.6 μm), (150–)154–175 μm (mean \pm SD = 163.1 \pm 8.5 μm) long in the sporiferous part, truncate at the apex, cylindrical to clavate, stipitate; with 8 obliquely uniseriate or biseriate ascospores; apical

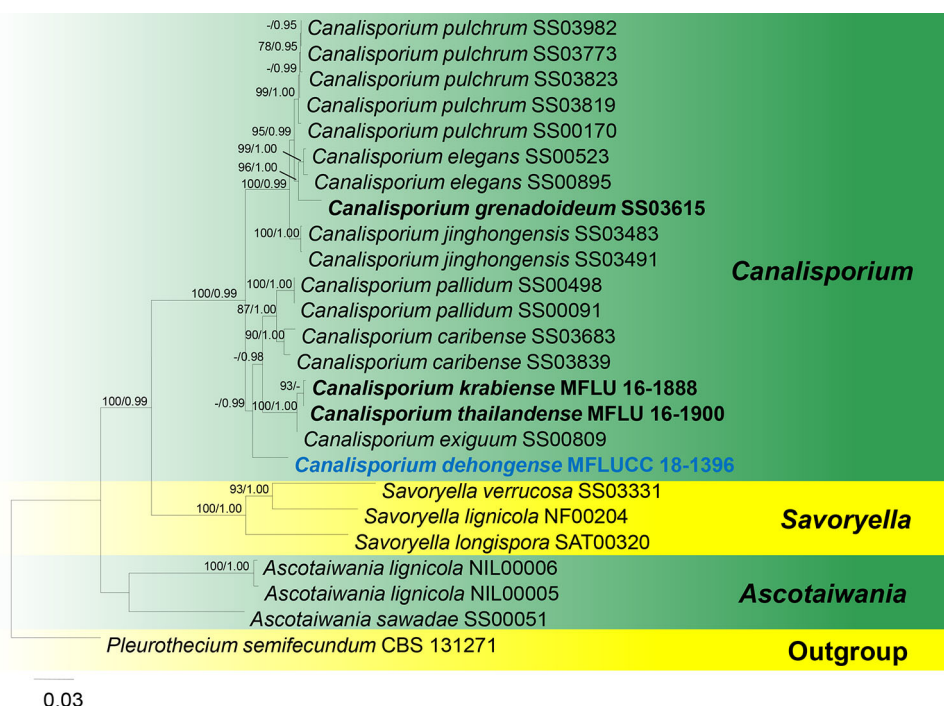


Fig. 116 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data for *Canalisporium* species and several related genera. Related sequences are taken from Sri-indrasudthi et al. (2010) and Boonyuen and Pang (2011). Twenty-five strains are included in the combined sequence analyses which comprise total 2757 characters after aligned. *Pleurothecium semifecundum* (CBS 131271) (Pleurotheciaceae, Pleurotheciales) is used as the outgroup taxon. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best scoring RaxML tree with a final likelihood value of -11890.841233 is presented. The matrix had 828 distinct alignment patterns, with 10.21%

undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.225725, C = 0.259821, G = 0.307021, T = 0.207433; substitution rates AC = 1.748411, AG = 3.032505, AT = 1.758208, CG = 1.095962, CT = 6.405200, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.244920$. Bootstrap values for maximum likelihood (ML) equal to or greater than 70 and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are placed above the branches, respectively. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

annulus 6.5–7.5(–8) μm wide, 2.0–2.5 μm high, non-amyloid. Outer wall of the ascus fragile, often rupturing basally resulting in a prolonged stipe and apically causing a release of the apical content with the annulus. *Ascospores* (33–)36–38(–40) \times 9.5–11.5(–12) μm (mean \pm SD = $37.1 \pm 2.0 \times 10.6 \pm 0.6 \mu\text{m}$), ellipsoidal, sometimes inequilateral, 5(–7)-septate, not constricted at the septa, with a large globule in each cell obscuring the septa, versicolorous prior to discharge, middle cells brown to olivaceous brown with hyaline polar cells, smooth-walled, without mucilaginous sheath or appendages. **Asexual morph** *Conidiophores* macronematous, mononematous, 92–155 μm long, 6.5–7.5 μm wide, unbranched, upright or slightly bent, seldom with a percurrent extension, septate, dark brown, paler and tapering towards the tip, (3.5–)5.0–5.5 μm wide at the apex, truncate. *Conidia* holoblastic, secession schizolytic, (65–)70–97(–103) \times 11–16(–17.5) μm (mean \pm SD = $85.0 \pm 10.2 \times 14.8 \pm 2.3 \mu\text{m}$), (3.5–)4.5–5.0 μm wide at the base, obclavate to fusiform to lanceolate, truncate at the base, tapering apically with a terminal extension which might be up to 26 μm long,

brown to reddish brown, with the darkest basal cell, paler at the apex, 11–13(–15)-distoseptate, smooth-walled.

Culture characteristics: Colonies on Modified Leonia's Agar (MLA) 7–8 mm diam. after 28 d, convex, circular to slightly irregular. Aerial mycelium abundant, lanose, floccose, partially decumbent, colony yellow, surrounded by a yellow-orange pigment diffused into the agar; margin entire to slightly undulate; reverse yellow-orange. Sporulation after 60 d; conidiophores arise at the margin of the colony. Colonies on potato-carrot agar (PCA) 12–13 mm diam. after 28 d, convex, circular. Aerial mycelium abundant around the centre and on the inoculation block, velvety, loose to almost cobwebby towards the margin, colony yellow-orange, surrounded by a yellow zone of submerged growth and deep yellow pigment diffused into the agar; margin filiform; reverse yellow. Sporulation absent. **Vegetative mycelium** hyaline, some hyphae pale brown, 1.5–2.5 μm wide. *Conidiophores* 24–40 μm long, 6–10 μm wide in the broadest part, seldom macronematous, mostly semimacronematous reduced to a conidiogenous cell sometimes with 1–2 supporting cells, conidiogenous cell

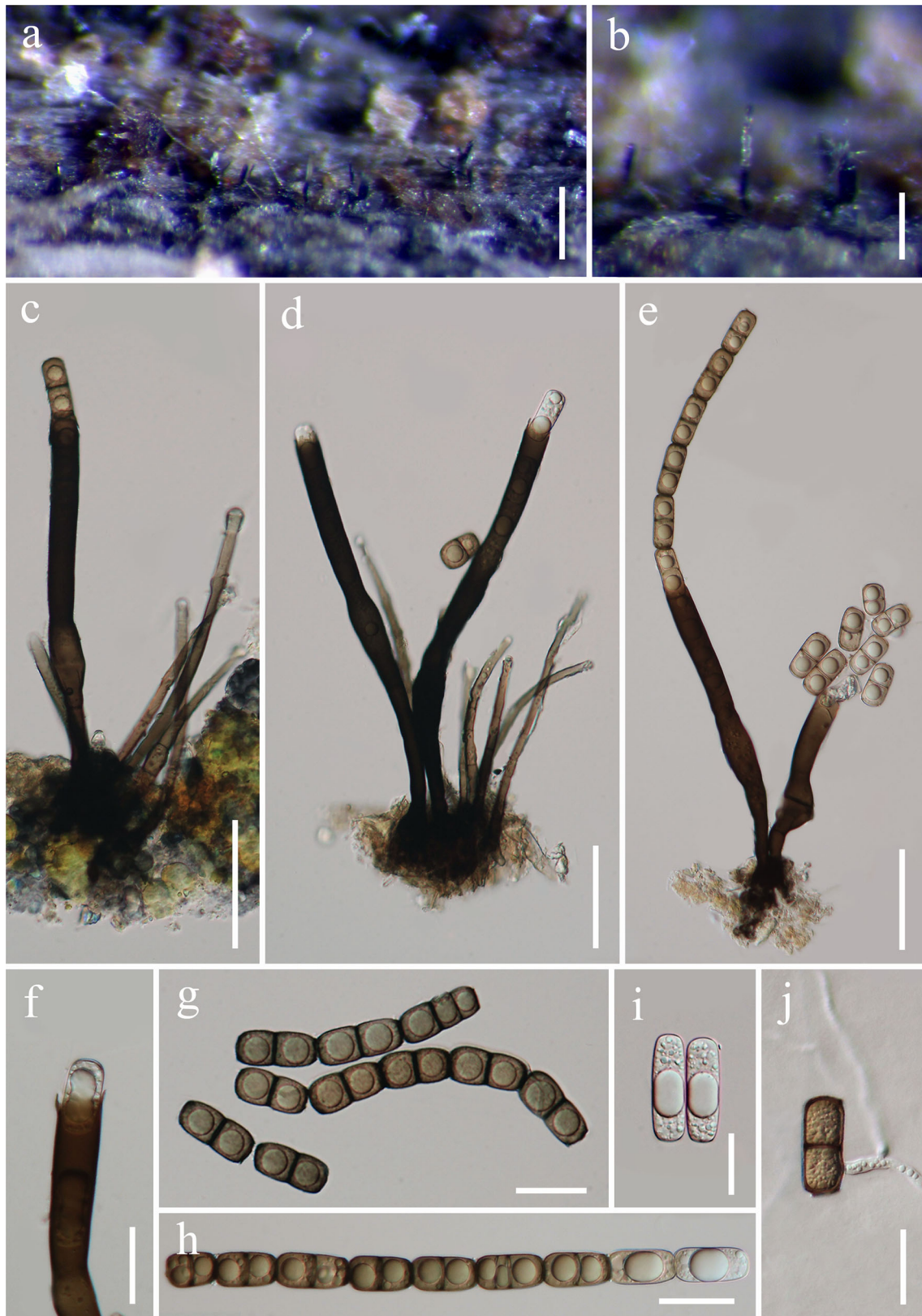


Fig. 117 *Sporoschisma chiangraiense* (MFLU 18-1722, **holotype**). **a, b** Colonies on natural substrates. **c, d** Conidia and conidiophores with setae. **e** Conidiophores and conidia. **f** Portion of phialide

producing conidium. **g–i** Conidia. **j** Germinated conidium. Scale bars: **a** = 200 μ m, **b** = 100 μ m, **c–e** = 50 μ m, **f–h** = 25 μ m, **i, j** = 20 μ m

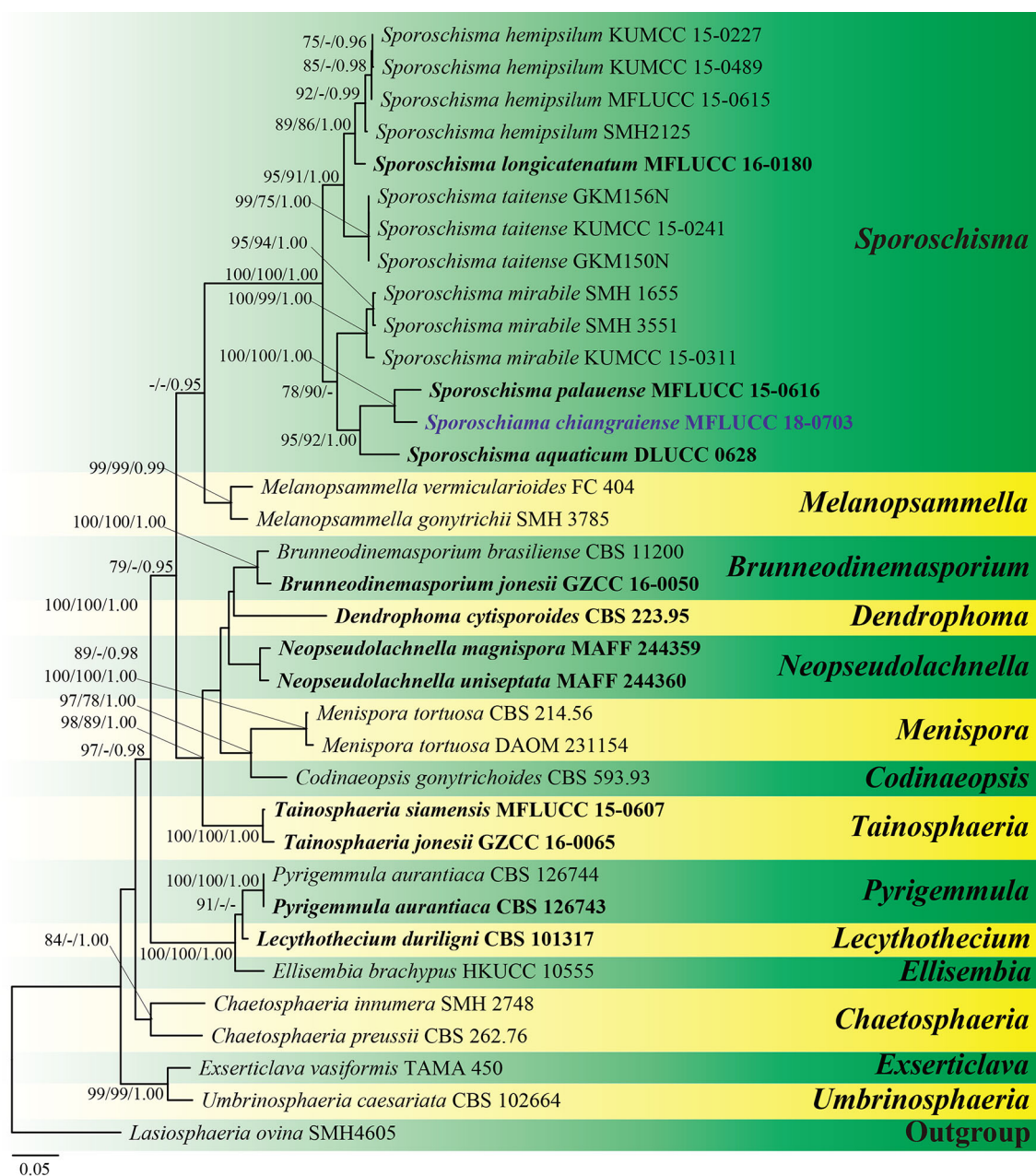


Fig. 118 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing Chaetosphaeriaceae. Related sequences are taken from Liu et al. (2016), Lu et al. (2016), Luo et al. (2016) and Yang et al. (2016a). Thirty-five strains are included in the combined analyses which comprise 1635 characters (1028 characters for LSU, 607 characters for ITS) after alignment. *Lasiosphaeria ovina* (SMH4605) (Lasiosphaeriaceae, Sordariales) is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -8025.509056 is presented. The matrix had 607 distinct alignment patterns, with

24.38% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.228162, C = 0.260607, G = 0.308790, T = 0.202441; substitution rates AC = 1.613577, AG = 2.168568, AT = 1.347260, CG = 0.833554, CT = 8.019859, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.534284$. Maximum parsimony analysis of 1148 constant characters and 117 informative characters resulted in nine equally most parsimonious trees (CI = 0.591, RI = 0.751, RC = 0.443, HI = 0.409). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 75 are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are in bold. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

swelled in the middle, dark brown, with a cup-shaped percurrent extension. *Conidia* (95–)105–128(–

137) \times 11.5–13.5(–16.5) μm (mean \pm SD = $124.0 \pm 11.8 \times 12.9 \pm 1.5 \mu\text{m}$), 3.5–4.5(–5) μm wide at the base,

long-fusiform, truncate at the base, tapering apically, brown, with the darkest cell at the base, paler towards the apex, (12–)15–18-distoseptate, smooth-walled, apex sometimes extended into a hyaline filiform appendage 56–85 µm long, 2.0–2.5 µm wide, conidia with an appendage 186–230(–268) µm long (mean \pm SD = 221 \pm 36.5).

Material examined: FRANCE, Ariège, Rimont, La Maille brook, 42.97706, 1.307167, ca. 550 m a.s.l., on partly submerged wood of a decorticated branch of *Sambucus nigra*, 4 August 2017, J. Fournier, J.F. 17058 (PRA-14744, **holotype**), ex-type living culture (CBS 144403).

GenBank numbers: ITS: MH836375, LSU: MH836376.

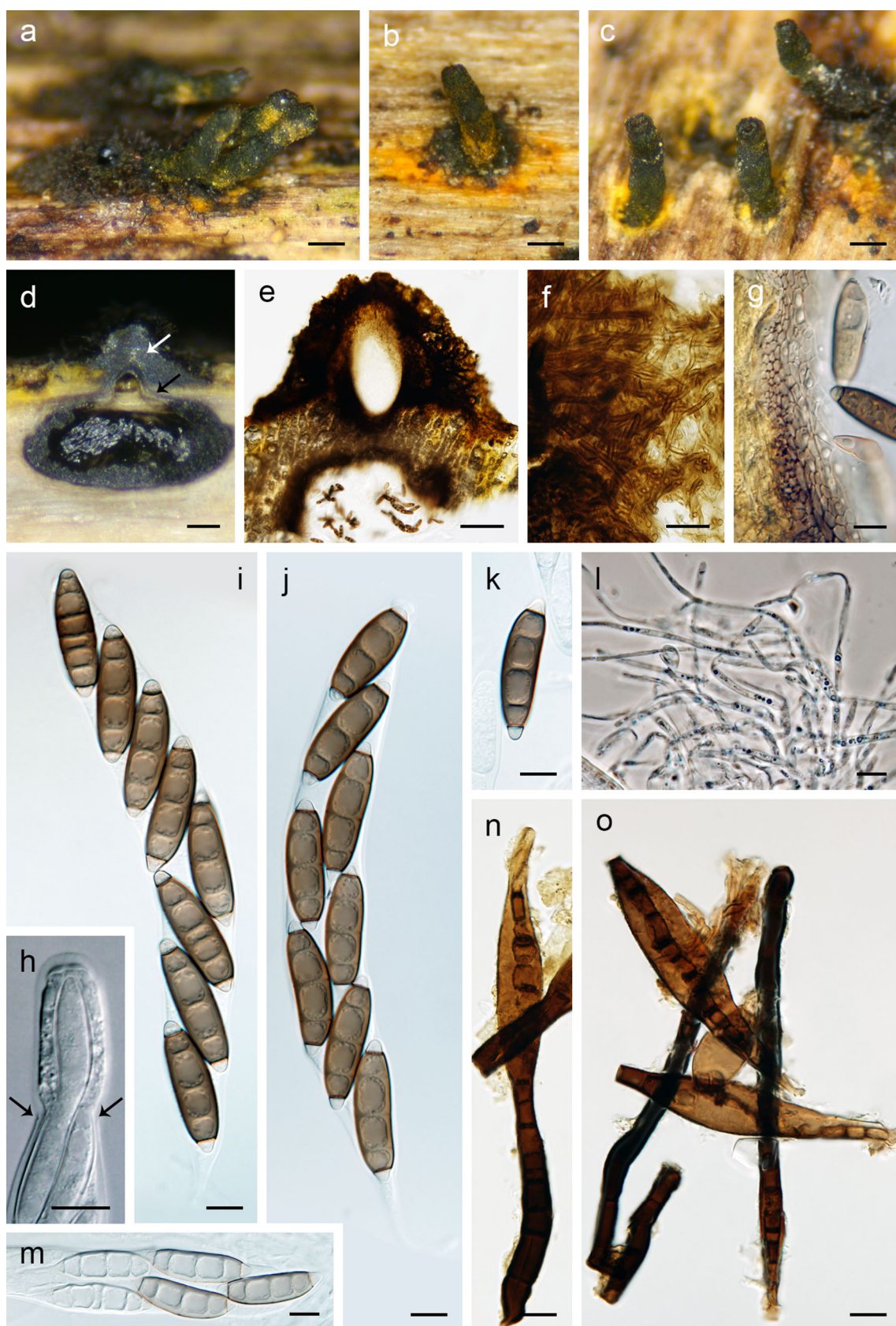
Notes: Conidia that are formed on nature substrate are shorter, usually fusiform to lanceolate, tapering apically with a short terminal extension and with less distosepta compared to conidia formed in MLA culture, which are mostly long-fusiform, wider at the distal end, which sometimes extends into a hyaline filiform appendage. The conidiophores formed in vivo are macronematous and cylindrical compared to usually semimacronematous and swollen conidiophores with a frequent percurrent extension formed in vitro. In the ITS-LSU phylogeny (Fig. 121), *E. aurea* is positioned in Chaetosphaeriaceae in a strongly supported clade together with *Ellisembia brachypus*, *E. foliiculata* and *Pyrigemmula aurantiaca*.

Besides *E. foliiculata* (Réblová and Winka 2001), *E. aurea* is another *Ellisembia* species experimentally linked with a sexual morph with versicolarous ascospores. *Ellisembia aurea* resembles *E. foliiculata* in the morphology of immersed ascomata, size of ascospores and morphology of brown, distoseptate conidia but the latter species differs from *E. aurea* in having flask-shaped ascomata, regularly 7-septate ascospores, shorter and narrower asci and cylindrical to clavate or obclavate, shorter conidia without a rostrum or appendage at the distal end. Hughes and Illman (1974a) reported the characteristic yellowish colour of the substrate surrounding the colonies of *E. foliiculata*, similar to the golden-yellow pigment released in vitro and found in wood surrounding ascomata of *E. aurea*. Among *Ellisembia* species having conidia with a distal rostrate end, *E. aurea* resembles *E. brachypus*, which differs in having somewhat shorter conidia (as *E. deightonii* 50–90 µm *vide* Ellis 1958, 45–65 µm *vide* Hughes and Illman 1974b) with fewer, 5–8 distosepta. The conspecificity of *E. aurea* and *E. brachypus* (HKUCC 10555, Shenoy et al. 2006) is not supported in our phylogeny.

Subramanian (1992) segregated *Ellisembia*, typified by *E. coronata*, from the widely circumscribed *Sporidesmium* to accommodate species with distoseptate conidia and conidiophores with none or percurrent and irregular extension. However, such delimitation based purely on asexual morphological characters is not supported by molecular DNA data (Su et al. 2016; Yang et al. 2018b). Su

et al. (2016) resurrected Sporidesmiaceae (Fries 1849) with the single genus *Sporidesmium* to accommodate taxa with euseptate or distoseptate conidia and accepted *Ellisembia* as its synonym. However, the type species of neither *Sporidesmium* nor *Ellisembia* were included. In the same publication, a new family Distoseptisporaceae and the genus *Distoseptispora* were introduced (Su et al. 2016), delimiting a group of *Sporidesmium*-like taxa in having exclusively distoseptate conidia, and two former *Ellisembia* species were included. However, Yang et al. (2018b) expanded the generic concept of *Distoseptispora* by including species with euseptate conidia. At present, species formerly classified in *Ellisembia* are accommodated in four different clades in the Sordariomycetes, i.e. *E. adscendens* and *E. leonensis* in *Distoseptispora* in Distoseptisporaceae, *E. bambusicola* and *E. minigelatinosa* in *Sporidesmium* in Sporidesmiaceae (Shenoy et al. 2006; Su et al. 2016), *E. aurea*, *E. foliiculata* and *E. brachypus* in Chaetosphaeriaceae (Réblová and Winka 2001; Shenoy et al. 2006; this study) and *E. calyptrata* in Xylariales (Shenoy et al. 2006). Moreover, various sexual morphs have been linked with *Ellisembia*. Those with hyaline, septate ascospores and superficial or immersed ascomata are currently placed in Distoseptisporaceae, i.e. *D. adscendens* with *Miyoshiella triseptata* sexual morph (as *Lasiosphaeria*, Shoemaker & White 1985), and in Sporidesmiaceae, i.e. *S. bambusicola* with *Miyoshiella fusispora* sexual morph (Kawamura 1929) and *Sporidesmium thailandense* of which only the sexual morph is known (Yang et al. 2018b). The position of *Sporidesmium larvatum* with *Miyoshiella larvata* sexual morph (Reblova 1999) is unknown. Furthermore, *Ellisembia* sexual morphs with versicolarous ascospores and immersed ascomata were so far exclusively placed in Chaetosphaeriaceae. Despite the proposed synonymy of *Ellisembia* with *Sporidesmium* (Su et al. 2016) and also with similar *Imicles* (Shoemaker and Hambleton 2001; Wu and Zhuang 2005), in the absence of molecular DNA data of their type species, their relationship is unclear and these genera should be retained as separate taxa following Seifert et al. (2011).

For the time being, we use the name *Ellisembia* for taxa attributed to Chaetosphaeriaceae and characterized by pigmented, distoseptate conidia, macronematous conidiophores with or without percurrent extension and multi-septate, versicolarous ascospores in asci with a non-amyloid apical annulus, persistent paraphyses and immersed ascomata. Members of the *Ellisembia* clade in Chaetosphaeriaceae are congeneric with the morphologically similar *Pyrigemmula* typified by *P. aurantiaca* (Magyar et al. 2011). The generic name *Pyrigemmula* is available and recommended for use to accommodate *Ellisembia* p. p. and related fungi if its separate position from *E. coronata* is confirmed in the future.



◀**Fig. 119** *Ellisembia aurea* (PRA-14744, **holotype**). **a–c** Ascomata. **d** Vertical section of ascoma (white arrow indicates stroma, black arrow indicates ascomal wall). **e** Vertical section of the lower part of the neck with visible stroma. **f** Stroma consisting of interwoven hyphae in detail **g** Vertical section of the ascomatal wall. **h** Ascal apex with apical annulus (arrows indicate ruptured outer wall and released ascal content). **i, j** Asci. **k** Ascospore. **l** Paraphyses. **m** Ascus with immature ascospores. **n, o** Conidia and conidiophores on nature substrate. Scale bars: **a–c** = 200 μm , **d** = 100 μm , **e** = 50 μm , **f** = 20 μm , **g–o** = 10 μm

Linocarpaceae Konta & K.D. Hyde

Notes: Konta et al. (2017) introduced this family to accommodate *Linocarpon* Syd. & P. Syd. and *Neolinocarpon* K.D. Hyde and placed it in Chaetosphaeriales. Senwanna et al. (2018) introduced the novel species, *Neolinocarpon phayaoense* Senwanna & K.D. Hyde.

Neolinocarpon K.D. Hyde

Notes: *Neolinocarpon* was included in Linocarpaceae based on DNA sequence data (Konta et al. 2017) and this was confirmed by Senwanna et al. (2018).

Neolinocarpon rachidis Konta & K.D. Hyde

Facesoffungi number: FoF05114; Fig. 122

Saprobic on petiole of *Cocos nucifera* L. **Sexual morph** **Ascomata** 320–460 μm high \times 230–290 μm diameter (\bar{x} = 415 \times 265 μm , n = 10), solitary, deeply immersed, with a central raised, black, globose-subglobose papilla, with a central ostiole. **Papilla** 157–223 μm high \times 127–198 μm diameter at the base (\bar{x} = 160 \times 140 μm , n = 5), black, shiny, with hyaline periphyses. **Peridium** 14–30 μm wide (\bar{x} = 22 μm , n = 10), outer cells merging with the host epidermal cells, composed of dark brown to black cells of *textura angularis*. **Hamathecium** comprising numerous, 1–3 μm diameter (\bar{x} = 2 μm , n = 20), hypha-like, septate, unbranched, paraphyses, longer than asci. **Asci** 95–180 \times 9–17 μm (\bar{x} = 145 \times 13 μm , n = 20), 8-spored, unitunicate, cylindrical, long pedicellate, with a wedge-shaped, J-, subapical ring. **Ascospores** 123–140 \times 2–4 μm (\bar{x} = 106 \times 3 μm , n = 20), parallel in ascus, becoming spiral when mature, filiform, straight or curved, hyaline, aseptate, containing numerous refringent septum-like bands, rounded at the apex, pointed at the base, lacking appendage sheath, smooth-walled. **Appressoria** 3–5 \times 2–5 μm (\bar{x} = 4 \times 3.5 μm , n = 20), globose to subglobose, hyaline. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h and produced appressoria-like structures at each tips of germ tube. Colonies on MEA reaching 2.5–3 cm diameter after two weeks at 25–28 °C, white at the edge, brown in the middle with strong radiations outwards. After 3 weeks of incubation, colonies smooth, flat, margin undulate, white to gray in the centre, white at the

margin, mycelium becoming red-brown when they produced into media, hyphae septate, branched, smooth-walled.

Material examined: THAILAND, Prachaupkhirikhan Province, on dead of petiole, *Cocos nucifera* (Arecaceae), 30 July 2015, Sirinapa Konta, PJK04i (MFLU 15-2347, **isotype**), ex-isotype living culture (MFLUCC 15-0814).

GenBank numbers: ITS: MK106342, LSU: MK106353, MK106354, SSU: MK106367, MK106368.

Notes: *Neolinocarpon rachidis* was introduced as a new species by Konta et al. (2017) and in this study *N. rachidis* was found on *Cocos nucifera* (Arecaceae) in Prachaupkhirikhan Province, Thailand. Appressorium structures were produced by germ tubes indicating that are endophytes. Phylogenetically, *N. rachidis* strain MFLUCC 15-0814 clustered with *N. rachidis* MFLUCC 15-0332 with high support (Fig. 123). Therefore, a record of *N. rachidis* on coconut host is reported.

Xylariomycetidae O.E. Erikss & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Notes: Eriksson and Hawksworth (1986) introduced the order Amphisphaeriales. However, it was synonymized with Xylariales by Eriksson and Hawksworth (1987). Based on molecular and morphological data, these orders were separated and Amphisphaeriales was resurrected (Senanayake et al. 2015). Currently, this order includes six families, namely: Amphisphaeriaceae, Clypeosphaeriaceae, Bartaliniaceae, Discosiaceae, Phlogicylindriaceae and Pestalotiopsidaceae (Senanayake et al. 2015).

Amphisphaeriaceae G. Winter

Notes: Winter (1884–1886) introduced the family Amphisphaeriaceae to accommodate the type genus *Amphisphaeria*. For an account of Amphisphaeriaceae G. Winter see Senanayake et al. (2015). In this manuscript we introduce a new monotypic genus *Trochilispora*.

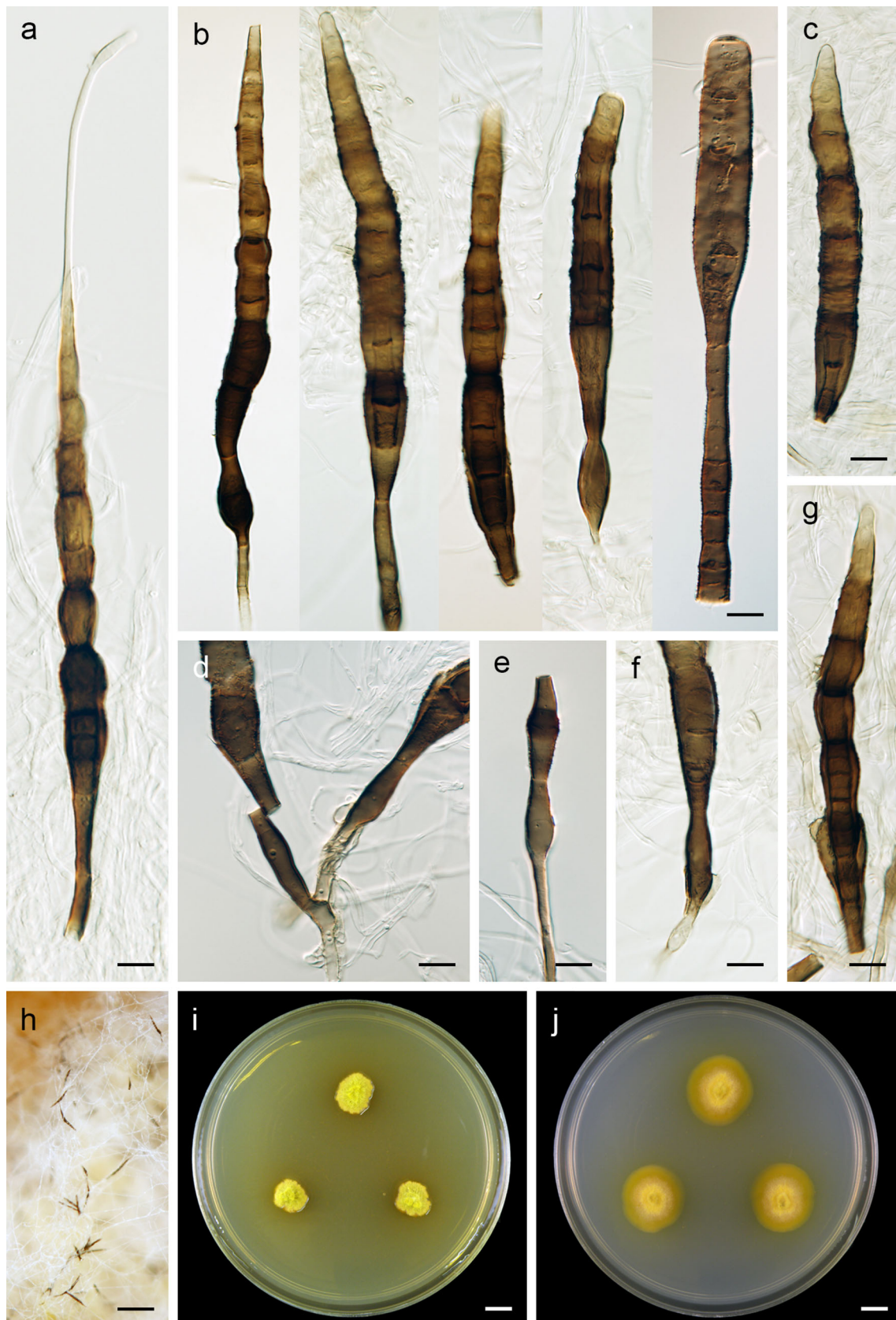
Trochilispora VP Abreu, AWC Rosado & OL Pereira, **gen. nov.**

Index Fungorum number: IF555484; **Facesoffungi number:** FoF04859

Etymology: From the family Trochilidae (hummingbirds) and -spora.

Type species: *Trochilispora schefflerae* Abreu VP, Rosado AWC & Pereira OL

Asexual morph Associated with leaf spot disease on *Schefflera morototoni* (Fig. 125a). **Conidiomata** acervular (Fig. 127c), epiphyllous, scattered and occasionally confluent, subepidermal in origin, erumpent, rounded to oval in outline, unilocular, brown or black, basal stroma thick, of *textura angularis*, cells thick-walled and almost colourless; lateral walls thick, cells thick-walled, pale brown to brown. **Conidiophores** cylindrical to subcylindrical, formed in the



◀ **Fig. 120** *Ellisembia aurea* (CBS 144403, **ex-holotype**). **a** Conidium with appendage. **b, c** Conidia. **d, e** Conidiophores. **f, g** Conidiophores with visible percurrent extension. **h** Conidia formed on aerial mycelium. **i, j** Colonies on MLA and PCA after 28 d. Scale bars: **a–g** = 10 μ m, **h** = 100 μ m, **i, j** = 0.5 cm

concavity of the conidioma, unbranched, hyaline, smooth-walled. *Conidiogenous cells* discrete, annellidic with 2 annellations, hyaline, thin- and smooth-walled. *Conidia* fusiform, straight or slightly curved, 3–4-septate, concolourous, smooth, bearing apical appendage tubular, fili-form, single, not centric, unbranched and basal appendage absent; basal cell hyaline to subhyaline, obconic to conic, smooth and thin-walled; 2–3 median cells doliiform, smooth, concolourous, brown, septa darker than the rest of the cell; apical cell hyaline to subhyaline, subconical to hemisphaerical, thin- and smooth-walled. **Sexual morph** Undetermined.

Trochilisporea schefflerae VP Abreu, AWC Rosado & OL Pereira, **sp. nov.**

Index Fungorum number: IF555485; *Facesoffungi* number: FoF04860; Fig. 124

Etymology: Name derived from its host genus, *Schefflera*.

Holotype: VIC 44384

Asexual morph *Conidiomata* acervular, epiphyllous, scattered and occasionally confluent, subepidermal in origin, erumpent, rounded to oval in outline, 49–88 \times 79–235 μ m diam., unilocular, brown or black, basal stroma thick, of *textura angularis*, cells thick-walled and almost colourless; lateral walls 3–5 cells thick, cells thick-walled, pale brown to brown. *Conidiophores* cylindrical to subcylindrical, (8.5–15.5 \times 1.5–2 μ m), formed in the concavity of the conidioma, unbranched, hyaline, smooth-walled. *Conidiogenous cells* discrete, annellidic with 2 annellations, (3.5–11.5 \times 1.5–3 μ m), hyaline, thin- and smooth-walled. *Conidia* fusiform, straight or slightly curved, concolourous, smooth, bearing apical appendage, and basal appendage absent; 3-septate (13–19 \times 3.5–5), bearing: [basal cell obconic to conic, hyaline to subhyaline,

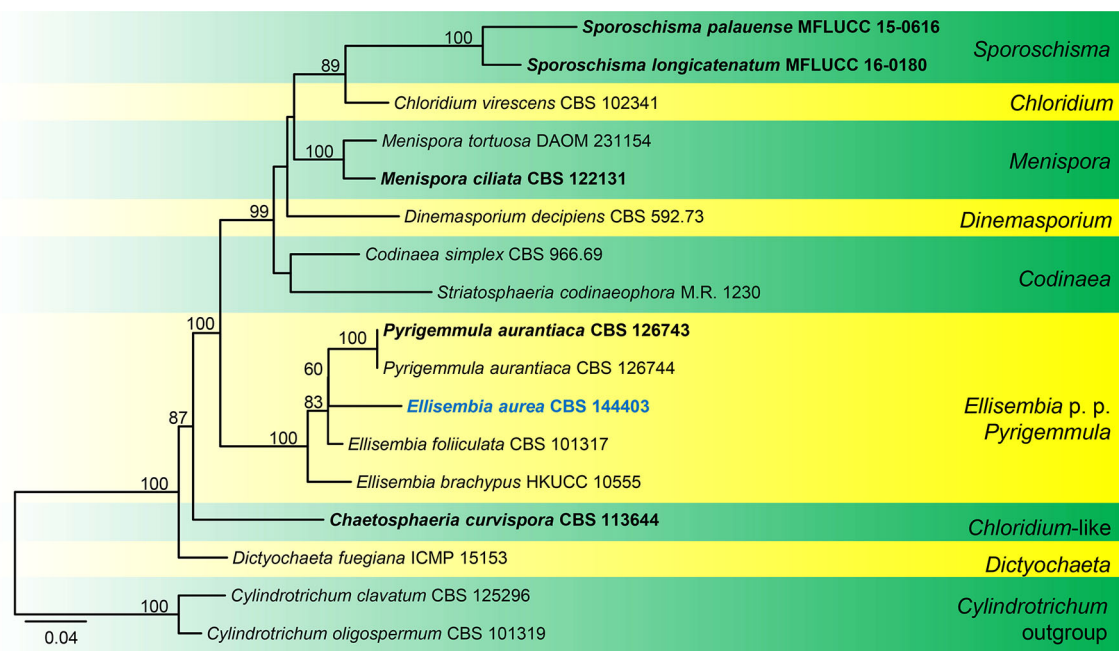


Fig. 121 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data for *Ellisembia aurea* and members of Chaetosphaeriaceae. Related sequences are taken from Réblová and Winka (2000, 2001), Réblová (2004), Réblová and Seifert (2008), Schoch et al. (2009), Magyar et al. (2011), Réblová et al. (2011), Yang et al. (2016a) and Vu et al. (2019). Seventeen strains are included in the combined gene sequence analysis, which comprises total 1837 characters including gaps (628 for ITS, 1209 for LSU) and 528 unique characters. *Cylindrotrichum clavatum* (CBS 125296) and *C. oligospermum* (CBS 101319) are used as the outgroup taxa. The best RAxML tree with a final likelihood value of

– 7216.460156 is presented. Estimated base frequencies for the two partitions were as follows: the ITS partition A = 0.214700, C = 0.306167, G = 0.262251, T = 0.216881; substitution rates AC = 4.616604, AG = 5.194154, AT = 5.725980, CG = 3.570615, CT = 13.113689, GT = 1.000000; the LSU partition A = 0.242254, C = 0.240274, G = 0.317255, T = 0.200218; substitution rates AC = 0.504038, AG = 1.058491, AT = 0.427775, CG = 0.207895, CT = 3.855638, GT = 1.000000. Branch support in nodes \geq 50% maximum likelihood bootstrap support is indicated above branches. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

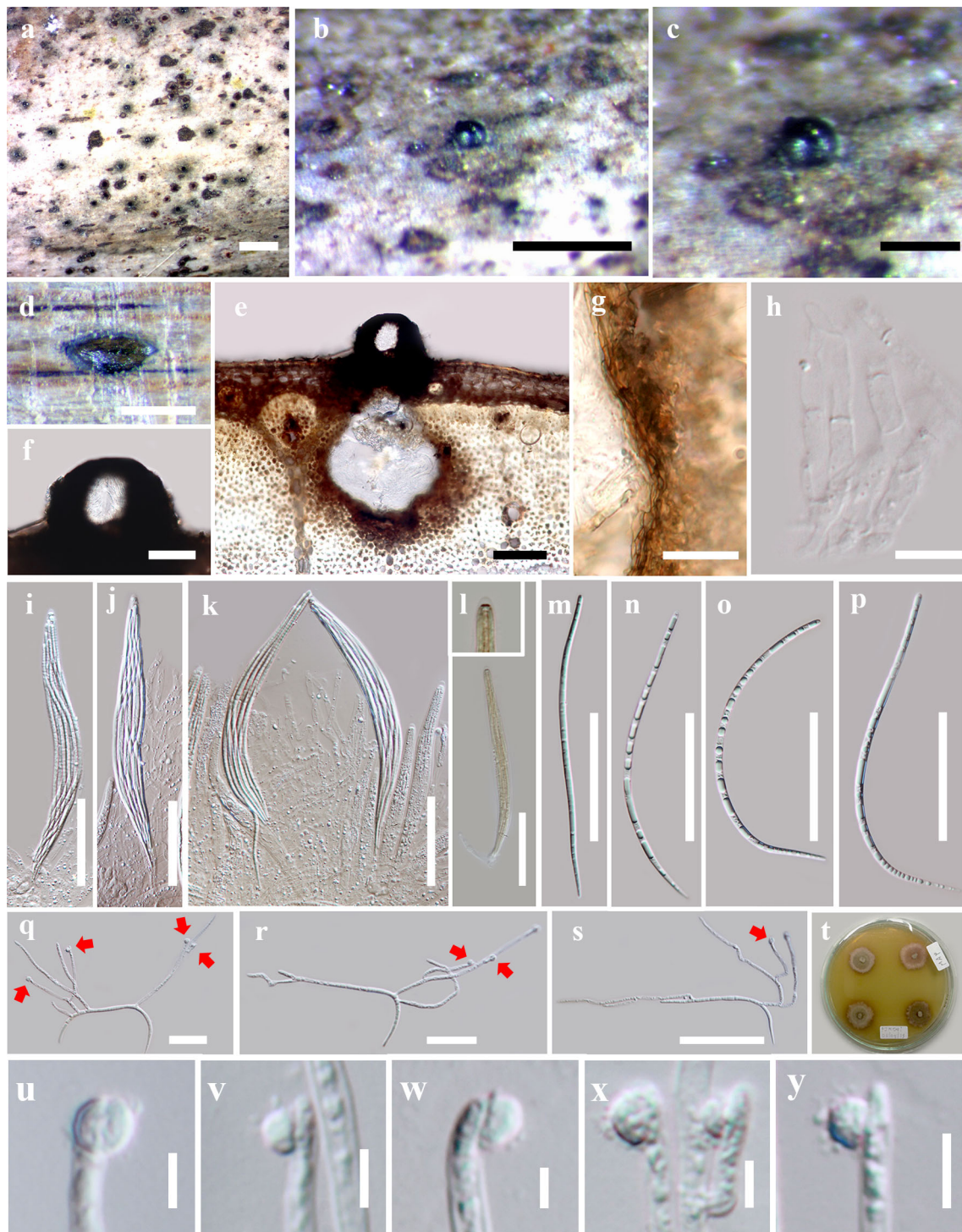


Fig. 122 *Neolinocarpon rachidis* (MFLU 15-2347, **isotype**). **a** Appearance of ascomata on host substrate. **b, c** Close up of ascomata. **d** Yellowish ascospore mass. **e** Section of ascoma. **f** Papilla. **g** Peridium. **h** Paraphyses. **i–k** Asci. **l** J- reaction of apical ring. **m–**

p Ascospores. **q** Germinated ascospore (appressoria at red arrow). **u–y** Appressoria. Scale bars: **a** = 1000 μ m, **b, d** = 500 μ m, **c** = 200 μ m, **e** = 100 μ m, **f, i–s** = 50 μ m, **g** = 20 μ m, **h** = 10 μ m, **u–y** = 5 μ m

smooth and thin-walled, 2–4 μ m long; two median cells doliiform, 8.5–12.5 μ m long, smooth, concolourous, brown, septa darker than the rest of the cell (second cell from base brown, 3.5–5.5 μ m long; third cell brown,

4.5–7 μ m long); apical cell 2–3.5 μ m long, hyaline to subhyaline, subconical to hemispherical, thin- and smooth-walled; with 1 tubular apical appendage, arising from the apical crest, not centric, unbranched, filiform, 2–6.5 μ m

long; basal appendage absent], or 4-septate (15.5–21 × 4–5), bearing: [basal cell obconic to conic, hyaline to subhyaline, smooth and thin-walled, 2–5 µm long; three median cells doliiform, 10–13 µm long, smooth, concolourous, brown, septa darker than the rest of the cell (second cell from base brown, 4–6 µm long; third cell brown, 2.5–4 µm long; fourth cell brown, 2.5–4.5 µm long); apical cell 2.5–3.5 µm long, hyaline to subhyaline, subconical to hemispherical, thin- and smooth-walled; with 1 tubular apical appendage, arising from the apical crest, not centric, unbranched, filiform, 2.5–7.5 µm long; basal appendage absent. **Sexual morph** Undetermined.

Culture characteristics: Colonies cultured on PDA reaching 38 mm diam. after 1 wk at 25 °C with a photoperiod of 12 h; regularly margins; with dense aerial mycelium; white; colonies fertile (Fig. 124b). Colonies cultured on MEA reaching 40 mm diam. after 1 wk at 25 °C with a photoperiod of 12 h; regularly and submerged margins; with scarce and sebaceous aerial mycelium; pale yellowish; colonies fertile.

Material examined: BRAZIL, Minas Gerais, Paraopeba, Floresta Nacional de Paraopeba (FLONA-Paraopeba), on leaves of *Schefflera morototoni* (Araliaceae), 30 January 2016, V.P. Abreu & O.L. Pereira (VIC 44384, **holotype**), ex-type living culture (COAD 2371).

GenBank numbers: ITS: MH128360, LSU: MH084761, TEF1- α : MH231216, TUB2: MH231215.

Notes: *Trochilisporea* is introduced as a new genus based on morphology and phylogenetic support (LSU and ITS sequence data). Based on phylogenetic analyses, *Trochilisporea schefflerae* COAD 2371 grouped in a well-supported clade including *Hymenopleella hippophaeicola* CBS 140410 (Fig. 125), but different genera can be grouped in the same clade as for example, *Morinia* and *Zetiaspizna*; *Truncatella* and *Broomella*; among others. Unfortunately, Jaklitsch et al. (2016) did not observed the asexual morph of *Hymenopleella hippophaeicola*, but the authors cite the *Hymenopleella sollmannii* species reported by Shoemaker and Müller (1965). The phylogenetic position of the *Trochilisporea* family is still unclear. *Trochilisporea schefflerae* COAD 2371 differs from *Hymenopleella sollmannii* by having conidia formed in conidiomata acervular with lateral walls 3–5 cells thick of brown hyphae; conidiophores smaller; conidiogenous cells discrete, annellidic with 2 annellations; conidia fusiform, straight or slightly curved, 3–4-septate, with medium brown central cells and hyaline to subhyaline end cells, apical cell with an appendage tubular, filiform, single, not centric, unbranched, not septum and basal cell without appendage basal. Our phylogenetic tree built using LSU and ITS data, and morphological features corroborated that our isolate represents a new genus and a new species belonging to Amphispheariaceae (Fig. 125).

Sporocadaceae Corda.

Notes: Jaklitsch et al. (2016) proposed Sporocadaceae based on morphological observations and phylogenetic analyses of ITS-LSU sequence data. This group of fungi comprises different asexual morph genera which are acervular coelomycetes having hyaline, pale or dark brown, septate conidia. The type genus is *Seimatosporium* Corda (Jaklitsch et al. 2016). Jaklitsch et al. (2016) accepted *Bartalinia*, *Monochaetia*, *Neopestalotiopsis*, *Pseudopestalotiopsis*, *Pestalotiopsis*, *Seiridium* and many other conidial appendage bearing asexual morph genera (Jaklitsch et al. 2016; Wijayawardene et al. 2017a, 2018a). Wijayawardene et al. (2018a) listed 22 genera in this family.

Pestalotiopsis Steyaert

Notes: Based on conidial features, Steyaert (1949) divided *Pestalotia* De Not., into three genera, *Pestalotia* De Not., *Pestalotiopsis* Steyaert, and *Truncatella* Steyaert. Species with 5-celled conidia (4-septate) was grouped within *Pestalotiopsis*. Based on a multilocus phylogenetic and morphological analysis of pestalotiopsis-like species, Maharachchikumbura et al. (2014) divided the complex into three genera: *Pestalotiopsis* Steyaert, *Neopestalotiopsis* Maharachch., K.D. Hyde & Crous and *Pseudopestalotiopsis* Maharachch., K.D. Hyde & Crous based on morphology of conidial median cells and LSU sequence data. *Pestalotiopsis* is characterized by median cells concolourous, i.e. three pale-pigmented median cells. *Pestalotiopsis* is a complex genus and has considerable phenotypic diversity (Maharachchikumbura et al. 2014). Thus, the identification is complemented with DNA sequence data and phylogenetic analysis based on the combination of three gene regions (ITS, TUB2 and TEF1- α) (Jeewon et al. 2003; Maharachchikumbura et al. 2011, 2012, 2013; Geng et al. 2013).

Pestalotiopsis aggestorum F. Liu & L. Cai, Nature Scientific Reports 7: 870 (2017)

Facesoffungi number: FoF05991; Fig. 126

Saprobic on dead leaves of unknown host. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* acervuli, 130–150 µm diam., pycnidial, superficial to semi-immersed, visible as black spots on the host. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–4 × 1–2 µm (\bar{x} = 2.4 × 1.3 µm), phialidic, discrete, cylindrical, hyaline. *Conidia* 17–22 × 7–9 µm (\bar{x} = 21.0 × 8.2 µm), fusiform, tapering at both ends, 4-septate; basal cell 3–5 µm long (\bar{x} = 4.1 µm), conic, hyaline and smooth-walled; three median cells together 11–15 µm long (\bar{x} = 13.7 µm), doliiform, light brown, rough-walled; second cell from base 3–5 µm long (\bar{x} = 4.4 µm); third cell 3–5 µm long (\bar{x} = 4.6 µm); fourth cell 3–5 µm long (\bar{x} = 4.0 µm); apical cell 3.2–4.7 µm long

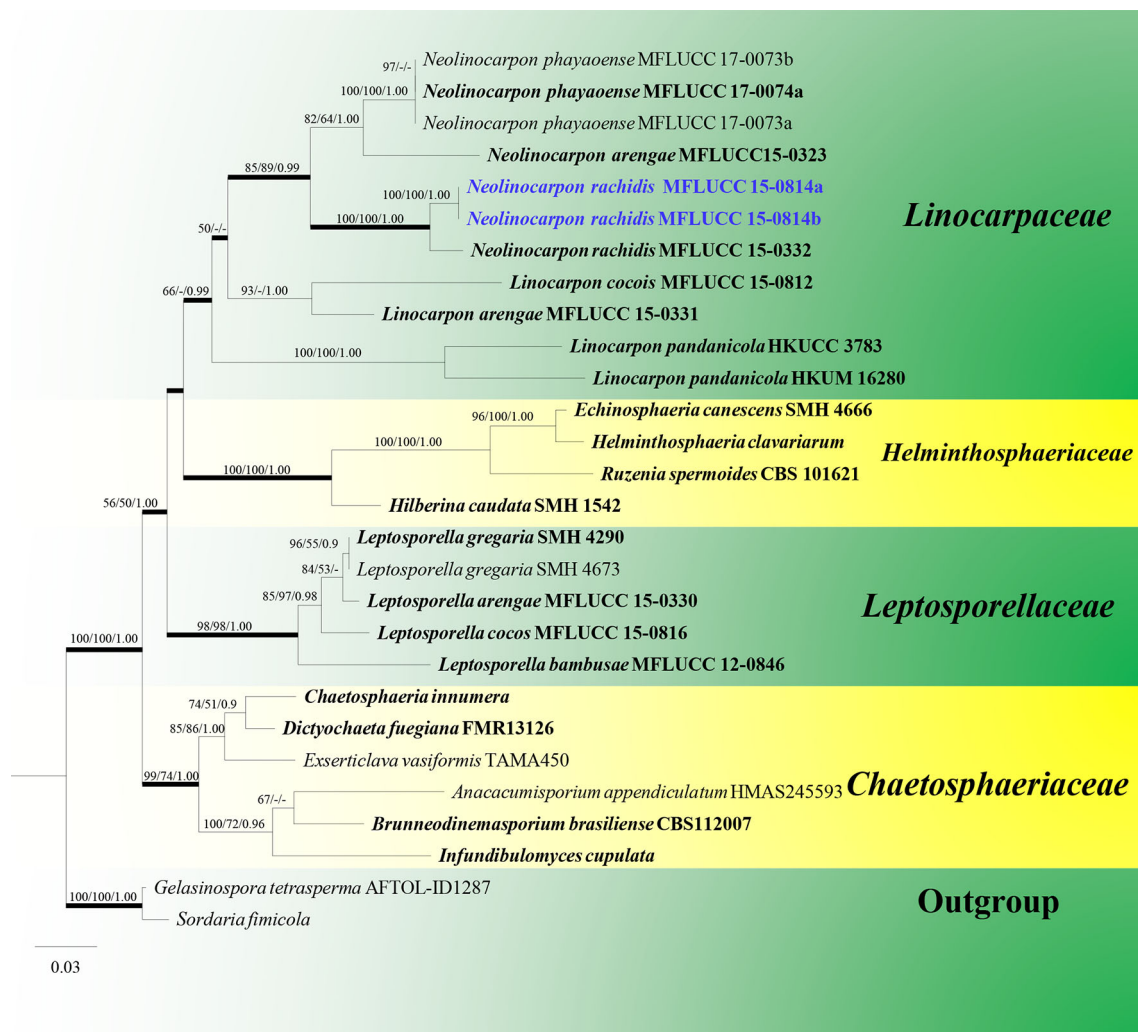


Fig. 123 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and TEF1- α sequence data for *Neolinocarpon* species and several closely related genera in Linocarpaceae and all families in Chaetosphaeriales. Related sequences were referred from Konta et al. (2017) and Senwanna et al. (2018). Twenty-eight strains are included in the combined analyses which comprise 3673 characters (666 characters for ITS, 1005 characters for LSU, 1043 characters for SSU, 946 characters for TEF1- α) after alignment. *Sordaria fimicola* and *Gelasinospora tetrasperma* (AFTOL-ID 1287) (Sordariaceae, Sordariales) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best RaxML tree with a final likelihood value of -14985.889953 is presented. The matrix had

1082 distinct alignment patterns, with 55.45% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231817, C = 0.269309, G = 0.304861, T = 0.194013; substitution rates AC = 0.889100, AG = 1.588862, AT = 0.616066, CG = 1.035174, CT = 4.437165, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.281924$. Maximum parsimony analysis of 3673 constant characters and 649 informative characters resulted in two equally most parsimonious tree of 2562 steps (CI = 0.702, RI = 0.690, RC = 0.484, HI = 0.298). Bootstrap values for maximum likelihood (ML) and maximum parsimony (MP) equal to or greater than 50, Bayesian posterior probabilities (BYPP) equal to or greater than 0.9 are placed above the branches respectively. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

(\bar{x} = 4.0 μ m), conic, hyaline and smooth-walled; 2–3 apical appendages 9–17 μ m long (\bar{x} = 15 μ m), tubular, filiform; basal appendage 5–8 μ m long (\bar{x} = 6.2 μ m), single, central, tubular, filiform.

Culture characteristics: Colonies on PDA 35 mm diameter after 7 days at 25 °C, circular, raised, dense aerial mycelia with fluffy appearance with circular edge, white; reverse white.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang District, Doi Mae Salong, on dead leaves of unknown host, 23 September 2016, N. I de Silva, NI104 (MFLU 17-0674), living culture (MFLUCC 17-0869).

GenBank numbers: ITS: MK334672.

Notes: Our strain clusters with the type of *Pestalotiopsis aggestorum* in the combined ITS, TUB2 and TEF1- α phylogenetic analyses (Fig. 127). *Pestalotiopsis*

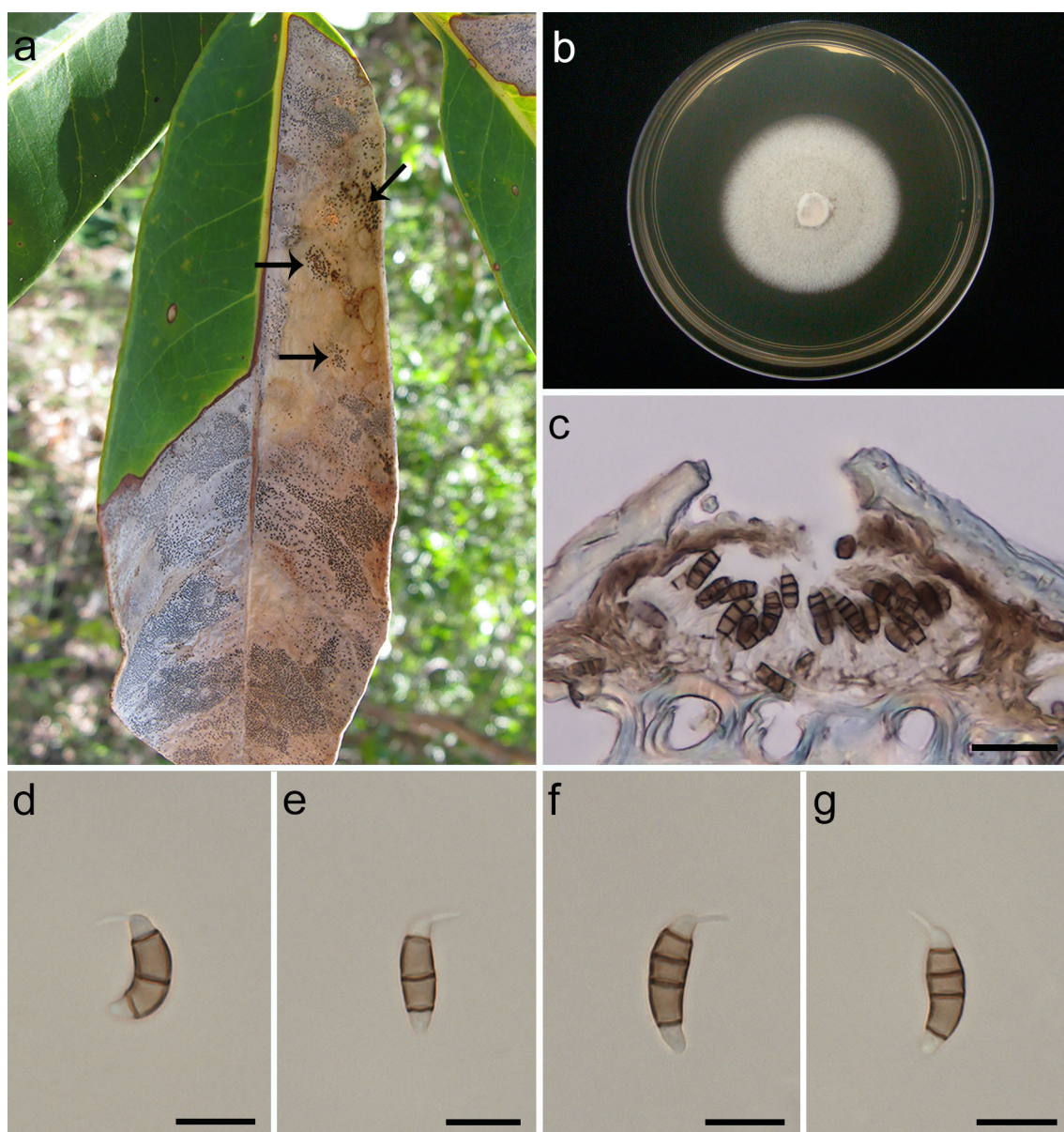


Fig. 124 *Trochilisporea schefflerae* (VIC 44384, **holotype**). **a** Leaves of *Schefflera morototoni* in Floresta Nacional de Paraopeba, state of Minas Gerais, Brazil (the arrows indicate the reproductive structures of the fungus). **b** Colony on PDA after 1 wk at 25 °C with a

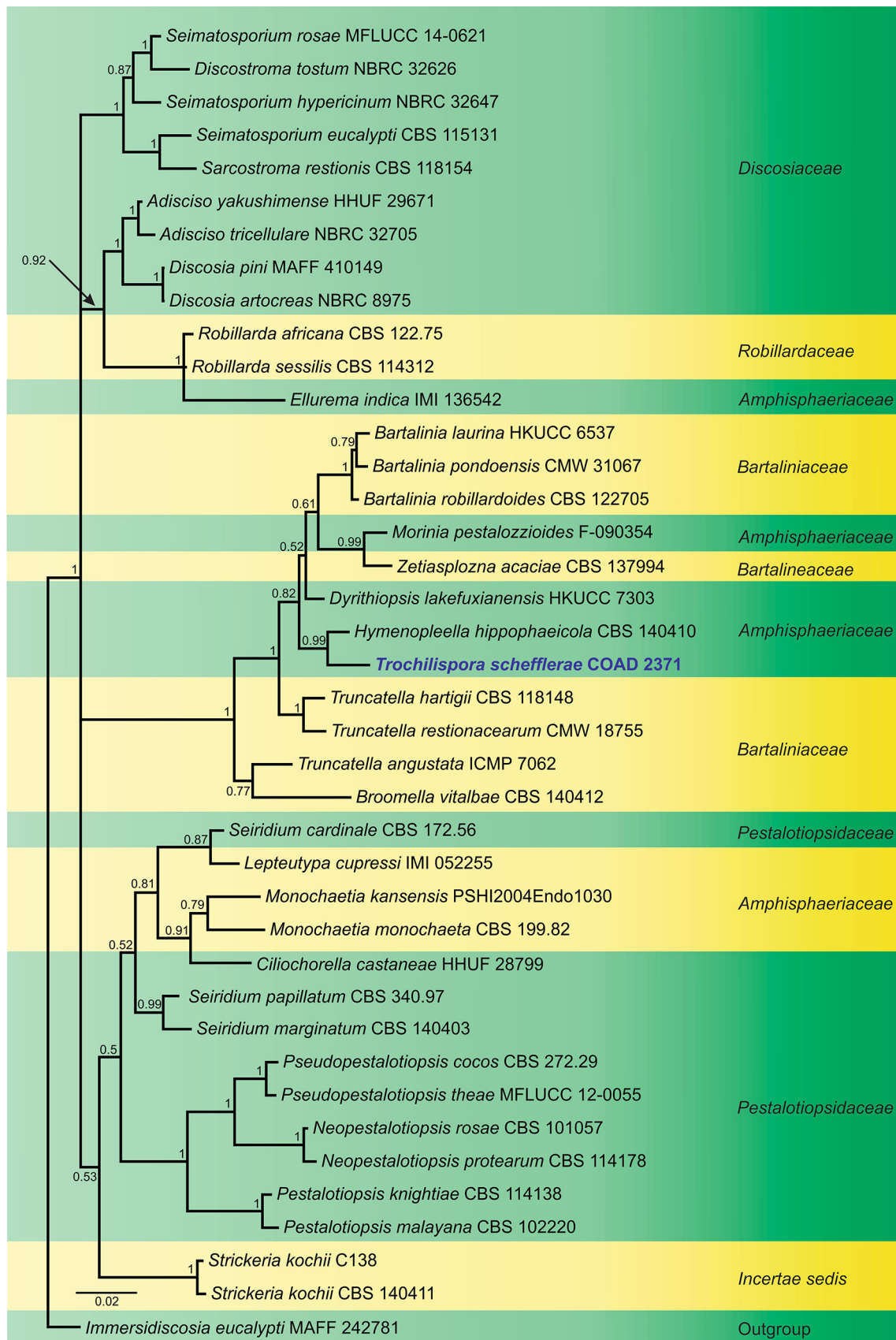
photoperiod of 12 h in the dark in Petri dishes (90 × 15 mm) (COAD 2371). **c** Cross section of the conidioma. **d–g** Conidia. Scale bars: **c** = 50 µm, **d–g** = 10 µm

aggestorum was isolated from leaves of tea (*Camellia sinensis*) in Yunnan, China. Our strain has fusiform, 4-septate conidia with overlap dimensions. However, our strain has smaller apical appendages (9–17) µm than *P. aggestorum* (18–28 µm; Liu et al. 2017). The current collection of *P. aggestorum* was isolated from dead leaves of unknown forest plant in Chiang Mai, as a new collection from Thailand.

Xylariales Nannf.

Castanediellaceae Hern.-Restr., Guarro & Crous

Notes: The phylogenetic position based on analysis of LSU sequence data shows it belongs to Xylariales and is distinct from Beltraniaceae. The typical asexual morph features are: conidiophores macronematous, mononematous or aggregated in sporodochia, branched, brown to pale brown. Conidiogenous cells mono or polyblastic, sympodial, discrete, solitary or in whorls, cylindrical to lageniform, hyaline to subhyaline. Conidia are unicellular or septate transversely, cylindrical, fusiform or lunate, and are



◀**Fig. 125** Phylogram generated from Bayesian Inference analysis based on combined ITS and LSU sequence data for several closely related genera in Amphisphaeriales. Sequence data of ex-type or ex-epitype cultures are taken from Senanayake et al. (2015) and the closest hits of GenBank database were included in this study. The combined genes sequence analysis included 40 taxa, which comprise 1405 characters (591 characters for ITS, 814 characters for LSU), and outgroup taxon *Immersidiscosia eucalypti* (MAFF 242781). Bayesian posterior probability are indicated at the nodes, and values equal or greater than 0.95 are in bold. Isolate numbers are indicated after species names. The ex-type or ex-epitype strains are in bold and black. The newly generated sequence is indicated in bold and blue

hyaline. In Castanediellaceae there is single genus *Castanediella* (Wanasinghe et al. 2018a).

Castanediella Hern.-Restr., Crous & M.J. Wingf.

Notes: The genus *Castanediella* was introduced by Hernández-Restrepo et al. (2015), with *Castanediella acaciae* as type species. Species of *Castanediella* are differentiated on conidiophores and conidia features. Species belonging to this genus are characterized by branched conidiophores and falcate, cylindrical or fusiform, straight to slightly curved, 0–1-septate conidia. Commonly, species are isolated from wood or leaves and 12 species are currently accepted (Costa et al. 2018; Wanasinghe et al. 2018a).

While evaluating the diversity of fungi related to *Melipona scutellaris* substrates (honey, pollen, surface of nest) living Atlantic Forest, Pernambuco, Brazil, a new species was isolated and it is described based on morphological characteristics and its phylogeny is inferred based on ITS/LSU sequence data.

Castanediella meliponae J.E. Felinto-Santos, R.N. Barbosa & N.T. Oliveira, *sp. nov.*

Index Fungorum number: IF555426; **Facesoffungi number:** FoF05765; **Fig. 128**

Etymology: “*meliponae*” referring to substrate related the *Melipona scutellaris*.

Holotype: URM 91974

Sexual morph Undetermined. **Asexual morph** Colonies mycelium white, velvety, margin regular, slowly growth, good sporulation, on PDA (potato dextrose agar), MEA (malt extract agar) and OA (Oats Meal Agar) at 25 °C in fourteen days. *Mycelium* hyaline, septate, smooth, 2–5 µm diam. *Conidiophores* hyaline, erect, 35–100 × 2–3.5 µm diam., 1–2 septate, branched apex, *Conidiogenous cells* hyaline, cylindrical, defined shape, smooth 2–3 × 6–30 µm diam. *Conidia* hyaline, solitary, one celled, falcate, straight to slightly curved with subobtusate apex, smooth, 3–4 × 5–10 µm diam.

Culture characteristic: Colonies growing on MEA, surface white, reverse brown with white margins, 29–31 µm

diam. On OA surface brown centre and white margin, reverse in brown centre and white margin, 30–35 µm diam. On PDA centre of the dark beige colony and white to light beige margin, reverse with white centre and beige light margin, 20–23 µm diam. Exudates and soluble pigment absent in all media. Cultures incubation at 25 °C in 14 days in incubator type Biological Oxygen Demand.

Material examined: BRAZIL, Paulista, Pernambuco state, on surface of nest of *Melipona scutellaris*, native stingless bees from to Brazilian Atlantic Forest, 29 November 2017, J.E. Felinto-Santos, FIBIO 002-B3 (URM 91974, **holotype**), ex-type living culture (URM 7933).

GenBank numbers: ITS: MH992664, LSU: MH988746.

Notes: *Castanediella meliponae* distinguishes of *C. cagnizarii*, *C. hyalopenicillata* and *C. eucalypti* with respect to conidiophores, conidiogenous cells and conidia morphology. The conidiophores of *C. cagnizarii* and *C. eucalypti* are pale brown to brown medium while *C. meliponae* are predominantly hyaline. *Castanediella hyalopenicillata* has conidiophores prostrate, while *C. meliponae* is erect. The conidiogenous cells of *C. meliponae* distinguish of *C. hyalopenicillata*, *C. cagnizarii*, and *C. eucalypti* in form, absence of denticles in apex, colour and absent of scars. *C. hyalopenicillata* has conidia fusiform with 0–1 septate. Conidia of *C. cagnizarii* are cylindrical to filiform with 0–1 septate. Conidia of *C. meliponae* are falcate and one celled. Furthermore, the conidia of *C. meliponae* are shorter than *C. cagnizarii*, *C. hyalopenicillata* and *C. eucalypti*. In our phylogenetic analyses (Fig. 129) *C. meliponae* is positioned close to *Synnemadiella eucalypti*, however some morphological differences were observed between those. *Synnemadiella eucalypti* produces synnemata and conidia granular, ellipsoid, but inequilateral, base truncate, 0.5 µm diam. These features are not observed in *C. meliponae* (Fig. 128) and take together with ITS and LSU sequences we consider as new species.

Diatrypaceae Nitschke

Notes: Taxa in Diatrypaceae can be distinguished by perithecial ascomata, usually embedded in a black stroma, cylindric-clavate to clavate, long pedicellate asci and allantoid ascospores (Glawe and Rogers 1984; Rappaz 1987; Mehrabi et al. 2015; de Almeida et al. 2016). Both coelomycetes (*Libertella*, *Cytosporina*) and hyphomycetes (*Phaeoisaria*) have been reported as asexual morphs of Diatrypaceae (Glawe and Rogers 1984; Wijayawardene et al. 2017a,b; de Almeida et al. 2016; Mehrabi et al. 2016). Currently this family comprises 18 genera (Wijayawardene et al. 2018a; Dayarathne et al. 2019b).

Diatrypella (Ces. & De Not.) De Not.

Notes: We follow the latest treatment and updated accounts of *Diatrypella* in Senwanna et al. (2017).

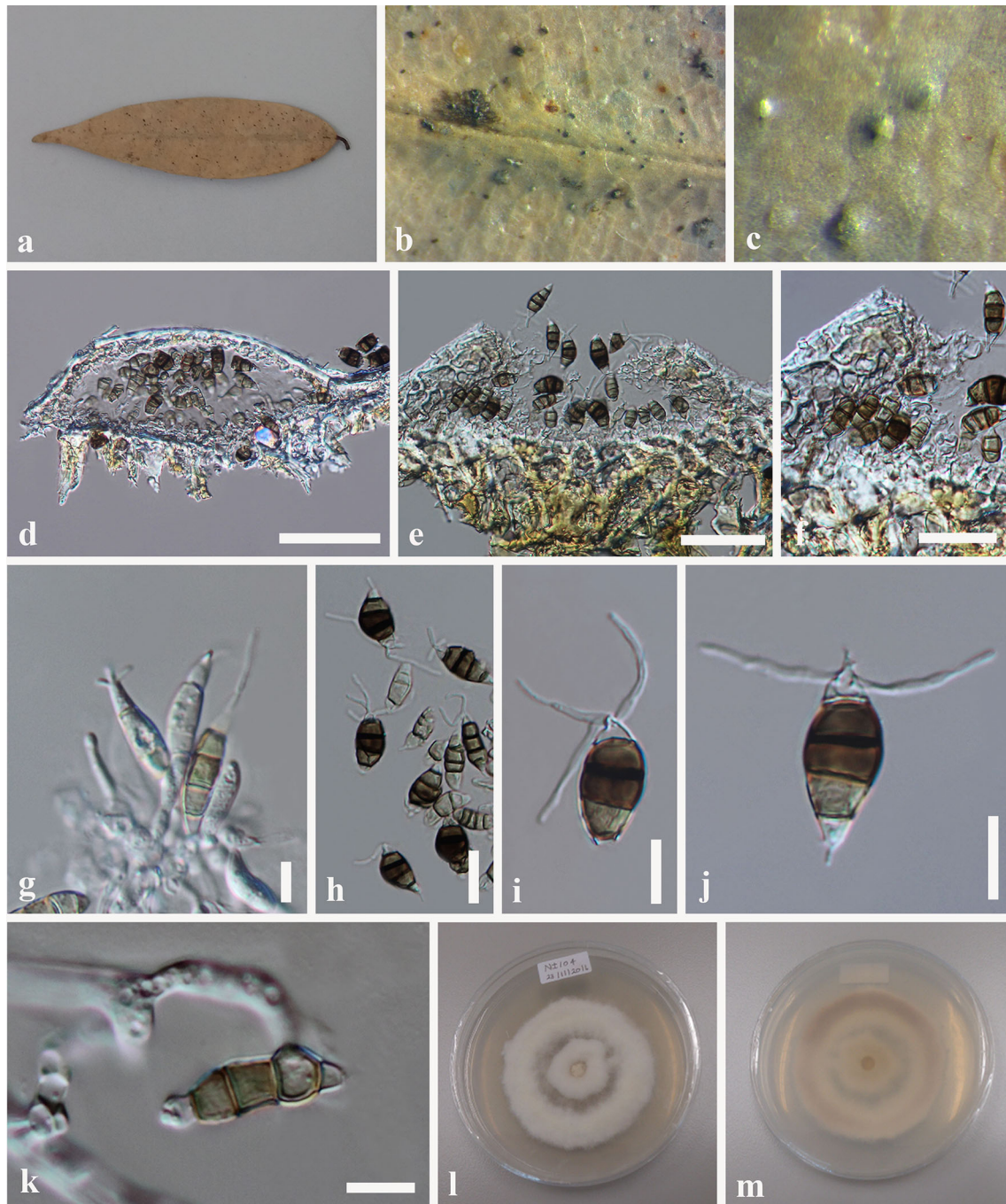


Fig. 126 *Pestalotiopsis aggestorum* (MFLU 17-0674, new geographical record). **a** The specimen. **b, c** Conidiomata on the host. **d–f** Section of conidiomata. **g** Conidiogenous cells. **h–j** Conidia.

k Germinating conidia. **l, m** Colony on PDA (**l** from above view, **m** from below view). Scale bars: **d, e** = 50 μ m, **f, h** = 20 μ m, **i–k** = 10 μ m, **g** = 5 μ m

Key to the related species of *Diatrypella*

- | | |
|---|--------------------------------|
| 1. Ascospores 4–5 μ m long on average..... | <i>Diatrypella major</i> |
| 1. Ascospores 6–10 μ m long on average..... |2 |
| 2. Entorostroma yellowish or olive-green..... |3 |
| 2. Entorostroma white..... |4 |
| 3. Asci larger, 120–150 \times 15.5–21.5 μ m..... | <i>D. tectonae</i> |
| 3. Asci smaller, 40 \times 8–12 μ m..... | <i>D. frostii</i> |
| 4. Stromata small, up to 2 mm diam..... |5 |
| 4. Stromata larger than 2 mm..... | <i>D. vulgaris</i> |
| 5. 1–4 ascomata per stromata, on twigs of <i>Hevea brasiliensis</i> | <i>D. heveae</i> |

5. 3–4 ascomata per stromata, on seed pods of *Delonix regia*.....*D. delonicis*

Diatrypella delonicis R.H. Perera & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF552536; *Facesoffungi number:* FOF02658; Fig. 130

Etymology: Named after the host genus.

Holotype: MFLU 16-1016

Saprobic on dried seed pods of *Delonix regia*. **Sexual morph** Stromata 0.65–1.28 mm wide, solitary or gregarious on host, immersed, with 3–4 ascomata immersed in a single stroma, comprising of outer, dark brown to black, small, tightly packed, thin parenchymatous cell layer, with inner white, loosely packed, parenchymatous cells. Ascomata 243–340 µm high, 217–380 µm diam., (\bar{x} = 310 × 331 µm, n = 20), perithecial, immersed in stromatic tissues, aggregated, globose to subglobose, sometimes with flattened base, pale to dark brown, carbonaceous, ostioles not prominent. Peridium 16–24 µm wide (\bar{x} = 18 µm, n = 20), 2 layered, inner 3–6 layers of hyaline, flattened, elongate, thin-walled cells of *textura angularis*, outer 4–7 layers of pale to dark brown, flattened, thick-walled cells of *textura angularis*. Hamathecium comprising 8.2–13 µm wide (\bar{x} = 9.8 µm, n = 20), septate, paraphyses, longer than the asci, tapering towards the apex, wider at the base. Asci 95–100 × 14–20 µm (\bar{x} = 100 × 18 µm, n = 25), multi-spored, unitunicate, clavate, with narrow, long, thin-walled pedicel, with swollen upper portion, apex rounded, without an visible apical apparatus. Ascospores 6.2–7.4 × 1.4–1.8 µm (\bar{x} = 6.7 × 1.6 µm, n = 20), overlapping, pale brown, allantoid to cylindrical, unicellular, with small, fat globules at the ends, smooth-walled, without sheath or appendages.

Asexual morph Undetermined

Culture characters: Ascospores germinated on PDA within 18 h and germ tube produced from one or both ends of the ascospore. Reaching 6.5 cm within 14 days on PDA, at 25 °C, colonies medium dense, circular, flat, with diffuse margin, white, below similar in color, not zonate, not producing pigmentation on PDA media.

Material examined: THAILAND, Chiang Rai Province, Muang District, Mae Fah Luang University, in front of S7 building, on dried seed pods of *Delonix regia* (Boj. ex Hook.) Raf. (Fabaceae), 10 December 2014, R.H. Perera, RHP 75 (MFLU 16-1016, **holotype**), ex-type living culture (MFLUCC 15-1014); *ibid.* RHP 77 (MFLU 16-1032).

GenBank numbers: ITS: MH812994, LSU: MH812996, TUB2: MH847790 (MFLUCC 15-1014); ITS: MH812995, LSU: MH812997, TUB2: MH847791 (MFLU 16-1032).

Notes: *Diatrypella delonicis* clusters with *D. major*, *D. frostii* and *D. vulgaris* within *Diatrypella* sensu stricto (Fig. 131). DNA sequences of *D. delonicis* and putative strain of *D. major* (1058) differed in 2 nucleotides in the

ITS region. DNA sequences of *D. delonicis* and putative strain of *D. frostii* (UFMGCB 1917) differed in 10 nucleotides in the ITS region. Sequence data of the TUB2 region of *D. major* and *D. frostii* are not available in the GenBank for the comparison. *Diatrypella delonicis* and ex-type strain of *D. vulgaris* (HVGRF03) showed 1 nucleotide difference in the ITS region, and 14 different nucleotides in the TUB2 region. DNA sequences of *D. delonicis* and ex-type strain of *D. tectonae* (MFLUCC 12-0172a) differed in 7 nucleotide positions of the ITS region. DNA sequence data of *D. heveae* (ex-type MFLUCC 17-0368) differed in 11 nucleotides in the ITS region and 33 in the TUB2. A key to species is provided above including the phylogenetically closely related species and the taxa were described from Thailand, *D. heveae* and *D. tectonae*.

Peroneutypa Berl.

Notes: *Peroneutypa* is typified by *P. bellula* (Desm.) and currently there are 47 estimated species (Wijayawardene et al. 2017a). The asexual morphs for the genus are unknown. The species within *Peroneutypa* are saprobes, pathogens and are widely distributed in terrestrial habitats (Lumbsch and Huhndorf 2010; Maharachchikumbura et al. 2015; Shang et al. 2017). Cultures and sequences for the genus are available, but are lacking for the type.

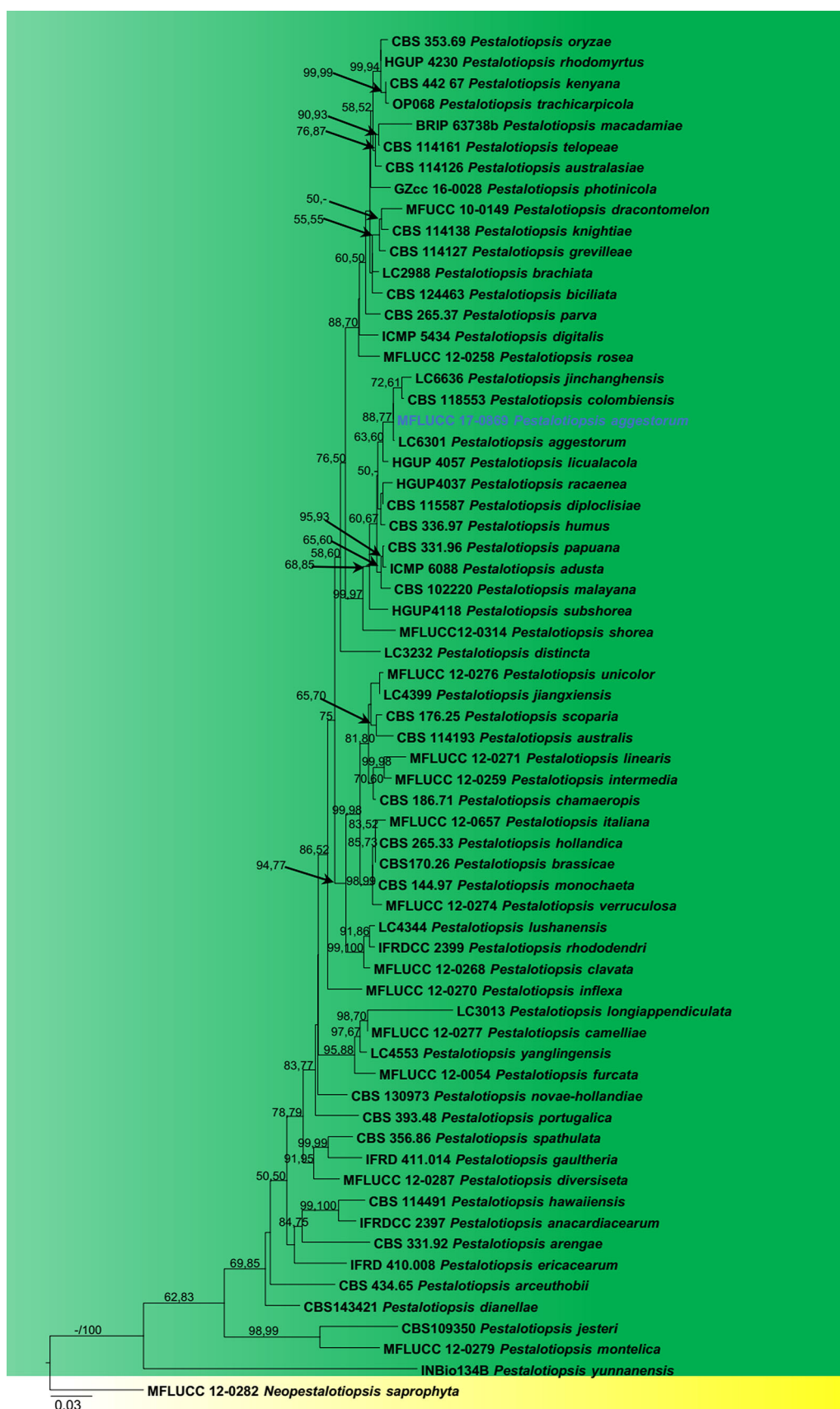
Peroneutypa scoparia Carmarán & A.I. Romero (2006)

Facesoffungi number: FoF01998; Fig. 132

Holotype: MFLU 19-0623

Saprobic on decayed wood at a mangrove stand. **Sexual morph** Ascomata 234–347 × 347–439 µm, solitary to scattered, lacking stromatic tissues, deeply immersed, dark brown to black, globose to subglobose, uni to multi-loculate, ostiolate, papillate. Ostioles central, apex composed of brown outer amorphous layer and inner yellow cells of *textura porrecta* and ostiolar canal filled with periphyses, 195–530 µm high, 330–720 µm wide. Peridium up to 25–35 µm wide, thick, 3-layered, incorporating occasionally in the host tissues. Paraphyses 1.5–2 µm wide, arising from the base of perithecia, short, thin-walled cells, guttulate, unbranched with apex blunt. Asci 19.5–23 × 3.2–5 µm (\bar{x} = 21 × 4.2 µm, n = 20), 8-spored, unitunicate, clavate, long pedicellate, apically rounded, with J-, subapical ring, initially deliquescing. Ascospores 2.8–4.8 × 1.4–1.9 µm (\bar{x} = 4.2 × 1.4 µm, n = 40), overlapping, allantoid, hyaline to light brown, aseptate, not constricted at the septum, smooth-walled with one to few small guttules at the both ends, straight to slightly curved. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA, reaching 10 cm diam. after 2 weeks at 20–25 °C, medium dense, irregular to regular, slightly raised, surface slightly rough, with uneven edge, undulate margin, cottony, colony from above: pale grey at the margin, greenish-grey at the centre;



◀**Fig. 127** Phylogram of maximum likelihood analysis based on ITS, TUB2 and TEF1- α sequences for *Pestalotiopsis* species. Related sequences were obtained from Maharachchikumbura et al. (2012, 2014). *Neopestalotiopsis saprophyta* (MFLUCC 12-0282) is used as the outgroup taxon. Sixty five strains are included in the combined analyses which comprise 1545 characters (565 characters for ITS, 472 characters for TUB, 508 characters for TEF1- α) after alignment. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the maximum parsimony analysis. The best RaxML tree with a final likelihood value of -10917.490545 is presented. The matrix had 716 distinct alignment patterns, with 12.01% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.234122, C = 0.292180, G = 0.213547, T = 0.260152; substitution rates AC = 1.238816, AG = 3.435200, AT = 1.254551, CG = 1.048645, CT = 4.518698, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.803705$. Maximum parsimony analysis of 945 constant characters and 384 informative characters resulted in two equally most parsimonious tree of 1643 steps (CI = 0.525, RI = 0.685, RC = 0.360, HI = 0.475). Bootstrap support values for ML (first set) and MP equal to or greater than 50% are given above the nodes. The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

from below: yellow to brown; mycelium greenish-grey, not produced pigmentation on PDA media.

Material examined: THAILAND, Phetchaburi Province, Cha-am District, from a dieback diseased marine wood, 11 January 2018, Vin. Kumar, KRB010 (MFLU 19-0623), living culture (MFLUCC 18-1111).

GenBank numbers: ITS: MK603519, TUB2: MK101307.

Notes: The species *Peroneutypa scoparia* (MFLUCC 18-1111) is similar to the type of *P. scoparia* (MFLUCC 11-0478) in Diatrypaceae, based on molecular data and morphology. It is characterized by immersed ascomata with a cylindrical or subconical, periphysate ostiole, apically rounded, clavate asci and allantoid, aseptate, and hyaline to light brown ascospores. *Peroneutypa aeriensis* has unique ascomatal characters with multiple, short necks. Phylogenetically *P. scoparia* (MFLUCC 18-1111) shares the same clade with *P. scoparia* (MFLUCC 11-0478) with a close affinity. Our isolate grouped within the *Peroneutypa* clade with low statistical support. This species is associated to the dieback symptoms. Here we add a TUB2 sequence with our entry. This is the first *Peroneutypa* species reported from a mangrove habitat (Jones et al. 2015, 2019).

Xylariales Nannf., genera *incertae sedis*

Notes: Xylariales have been revised by several recent studies researchers (Tang et al. 2009; Maharachchikumbura et al. 2015, 2016; Senanayake et al. 2015; Wendt et al. 2018; Daranagama et al. 2018; Voglmayr et al. 2018; Wijayawardene et al. 2018a; Doilom et al. 2018). Maharachchikumbura et al. (2016) accepted 24 genera,

while Wijayawardene et al. (2018a) listed 44 genera in Xylariales, genera *incertae sedis*.

Fasciatispora K.D. Hyde

The most recent account of this genus are by Daranagama et al. (2018) who we follow here.

Fasciatispora arengae Konta & K.D. Hyde

Facesoffungi number: FoF05113; Fig. 133

Culture characteristics: Ascospores germinated on MEA within 24 h and germ tube was produced from both ends. Colony on MEA, at first whitish, felty, azonate, with fluffy margins, hyphae, septate, branched, and smooth.

Material examined: THAILAND, Phang-nga Province, on dead leaflet of *Arenga pinnata* (Arecaceae), 5 December 2014, S. Konta, PHR07 g (MFLU 15-0301), ex-type living culture (MFLUCC 15-0326).

GenBank numbers: ITS: MK120275, MK120276, MK120277, LSU: MK120300, MK120301, MK120302, SSU: MK120304, MK120305, MK120306.

Notes: Doilom et al. (2018) introduced *Fasciatispora arengae* from southern Thailand based on morphology. Phylogenetic analyses indicated that *F. arengae* clustered with other species in the '*Fasciatispora*' clade; *F. nypae* and *F. calami* (99 MP/1.00 BYPP, Fig. 134). Accordingly, Hyde (1991), Wijayawardene et al. (2018a) and Doilom et al. (2018) assigned *Fasciatispora* to Amphisphaeriales genera *incertae sedis*, which was confirmed by Daranagama et al. (2018). Subsequently, several studies transferred *Fasciatispora* to Xylariaceae (Alias et al. 1994; Hyde 1995a; Hidayat et al. 2007; Hyde and Wong 1999; Kang et al. 1999; Liu et al. 2015; Hyde et al. 2017a). In this study, phylogenetic analysis of combined four gene regions (TUB2, ITS, LSU, and RPB2) showed that *Fasciatispora* did not form a clade close to Amphisphaeriaceae as was mentioned in Daranagama et al. (2018), it formed a separate between the Graphostromataceae and '*Hypoxylon*' clades (Fig. 134). *Fasciatispora* is, therefore, best accommodated in Xylariales genera *incertae sedis*.

Basidiomycota R.T. Moore

Agaricomycetes Doweld

Agaricomycetidae Parmasto

Agaricales Underw.

Cortinariaceae R. Heim ex Pouzar

Notes: The limits of the family Cortinariaceae remain unknown. Most species in this family are in the genus *Cortinarius*, with a cosmopolitan distribution and over 2000 described species. Many genera formerly placed in the Cortinariaceae, (e.g., *Phaeocollybia*, *Hebeloma*, *Galerina*) have been transferred to other families in Agaricales (Matheny et al. 2015). Furthermore, the sequestrate genera, *Thaxterogaster*, *Quadrispora*, *Protoglossum* and *Hymenogaster pro parte* as well as *Cuphocybe*, *Rapacea*

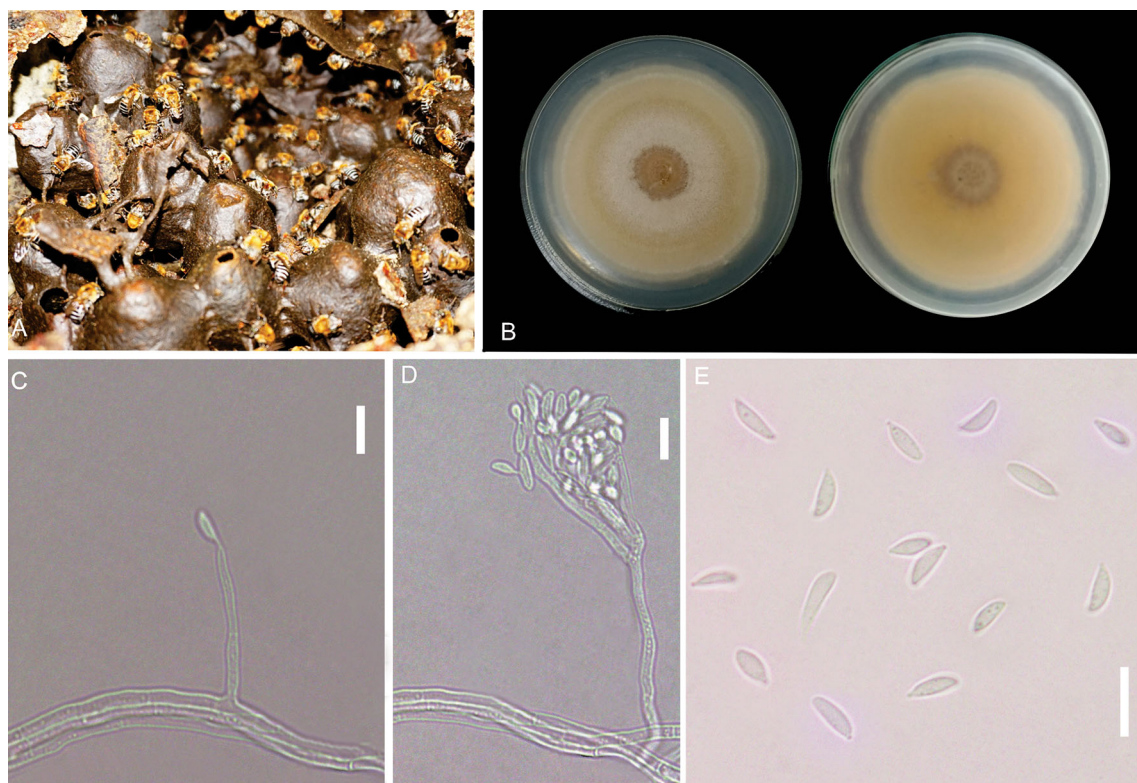


Fig. 128 *Castanediella meliponae* (URM 91974, holotype). **a** Surface of nest of *Melipona scutellaris*. **b** (Left to right) Surface and reverse of colony growth on PDA. **c** Conidiogenous cell and conidia. **d** Conidiophore and conidia. **e** Conidia. Scale bars: **c–e** = 10 μ m

and species of *Rozites*, once thought to be genera within the Cortinariaceae, are currently included in the genus *Cortinarius* (Peintner et al. 2001, 2002). The basidiocarps range from agaricoid to sequestrate, and many have poorly to well-developed veils. The basidiospores are typically ornamented and cinnamon brown in deposit.

Cortinarius (Pers.) Gray

Notes: *Cortinarius* species are important ectomycorrhizal fungi and are associated with different trees and shrubs, belonging to the families Fagaceae, Salicaceae, Caesalpiniaceae, Cistaceae, Dipterocarpaceae, Myrtaceae, Rhamnaceae, Rosaceae and Pinaceae, as well as some herbaceous plants in the Cyperaceae and Polygonaceae (Frøslev et al. 2006). The basidiocarps range from agaricoid to sequestrate, and many have poorly to well-developed veils. The basidiospores are typically ornamented and cinnamon brown in deposit. Hundreds of species are still undescribed and below we present two new species belonging to *Cortinarius* subgenus *Telamonina*, sect. *Safranopedes* (Bidaud, Moënne-Loec. & Reumaux) Liimat., Kytöv. & Niskanen from Europe.

Cortinarius minusculus Liimat. & Niskanen, *sp. nov.*

Index Fungorum number: IF555637; **Facesoffungi number:** FoF05970; Fig. 135a

Etymology: Name based on a Latin adjective *minusculus*, meaning rather small.

Holotype: K. Liimatainen & T. Niskanen 12-032 (H)

Pileus 0.7–1.5 cm wide, at first conical to somewhat convex, later planoconvex, often with an acute umbo, red-brown, paler at the margin, hygrophanous. **Lamellae** medium spaced, adnexed to emarginated, brown. **Stipe** 2.5–5 cm long, 0.15–0.3 cm thick, cylindrical, at first very pale greyish brown, covered with silky, white fibrils, later darker, especially at the lower ½ of the stipe. **Context:** in pileus red brown, in stipe yellow brown, dark brown at the base when older. **Universal veil** white, forming often distinct complete and incomplete on the stipe. **Odour** in lamellae indistinct. **Exsiccatae:** pileus brown, stipe greyish brown. **Basidiospores** (7.5–)8–9(–9.5) \times 4.7–5.3 μ m, av. = 8.5 \times 4.9 μ m, Q = 1.63–1.8, Qav. = 1.74, ellipsoid to obovoid-ellipsoid, moderately verrucose, more strongly at apex, somewhat dextrinoid. **Lamellar trama hyphae** encrusted.

ITS sequence (GenBank MK211177, holotype) distinct from other members of *C.* sect. *Safranopedes*. With a sister group relationship to *C. scotoides* and deviating from it by 10 substitutions and indels.

Ecology and distribution: In hemiboreal and temperate mixed forests with *Betula*, *Corylus*, *Populus* and *Pyrola rotundifolia* on mull soil. Known from northern Europe.

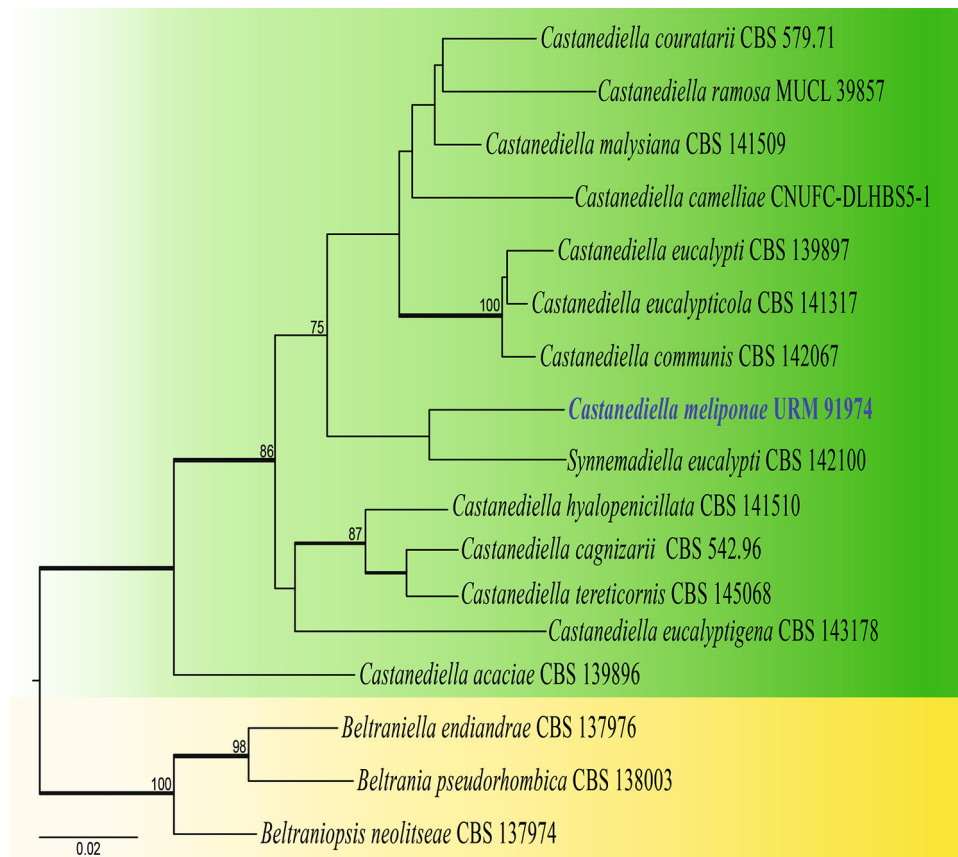


Fig. 129 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data for *Castanediella* species and several closely related genera. Related sequences are taken from Hernández-Restrepo et al. (2017) and Wanasinghe et al. (2018a). Seventeen strains are included in the combined analyses which comprise 1037 characters (557 characters for ITS, 480 characters for LSU) after alignment. *Beltraniella endiandrae* (CBS 137976) (Amphisphaeriaceae, Amphisphaeriales), *Beltrania pseudorhombica* (CBS 138003) (Beltraniaceae, Sordariales) and *Beltraniopsis neolitsea* (CBS 137974) (*Incertae sedis*) are used as the outgroup taxa. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum

likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood value of -3681.798352 is presented. The matrix had 245 distinct alignment patterns, with 6.62% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.284691, C = 0.205176, G = 0.254615, T = 0.255518; substitution rates AC = 0.678292, AG = 2.785917, AT = 1.405179, CG = 0.578526, CT = 3.212102, GT = 1.000000; gamma distribution shape parameter $\alpha = 3.725904$. Bootstrap values for maximum likelihood (ML) equal to or greater than 75 are placed above the branches respectively. The newly generated sequence is indicated in bold and blue

Material examined: Finland, Uusimaa, Vantaa, Tammisto, Tammisto's Nature Reserve Area, herb-rich mixed forest with *Quercus*, *Corylus*, *Betula*, *Pinus* and *Populus*, 17 September 2012, K. Liimatainen & T. Niskanen 12-032 (H, **holotype**; K, **isotype**).

GenBank numbers: ITS: MK211177 (loc. cit. 12-031 (H)), MK211178.

Notes: *Cortinarius minusculus* is a small and slender medium brown *Telamonia* with distinct white veil, indistinct odour, and ellipsoid to obovoid-ellipsoid spores. It grows on mull soil with several different deciduous trees and *Pyrola*. The species formed a well-supported monophyletic group within *C.* sect. *Safranopedes* in our phylogenetic analysis.

***Cortinarius subscotoides* Niskanen & Liimat. sp. nov.**

Index Fungorum number: IF555638; **Facesoffungi number:** FoF05971; Fig. 135b

Etymology: The name refers to the affinity to *C. scotoides*.

Holotype: K. Liimatainen & T. Niskanen 12-010 (H)

Pileus 2–4 cm wide, at first conical, later planoconvex, with an acute umbo, dark brown, paler at the margin, hygrophanous. **Lamellae** medium spaced, adnexed to emarginated, at first pale greyish brown, later brown. **Stipe** 2.5–5 cm long, 0.5–0.9 cm thick, cylindrical, at first silky whitish fibrillose, soon brown, especially at the base of the stipe. **Context:** in pileus dark brown, in stipe brown, darker brown at the base. **Universal veil** white, rather thin, forming a complete girdle on the middle part of the stipe.

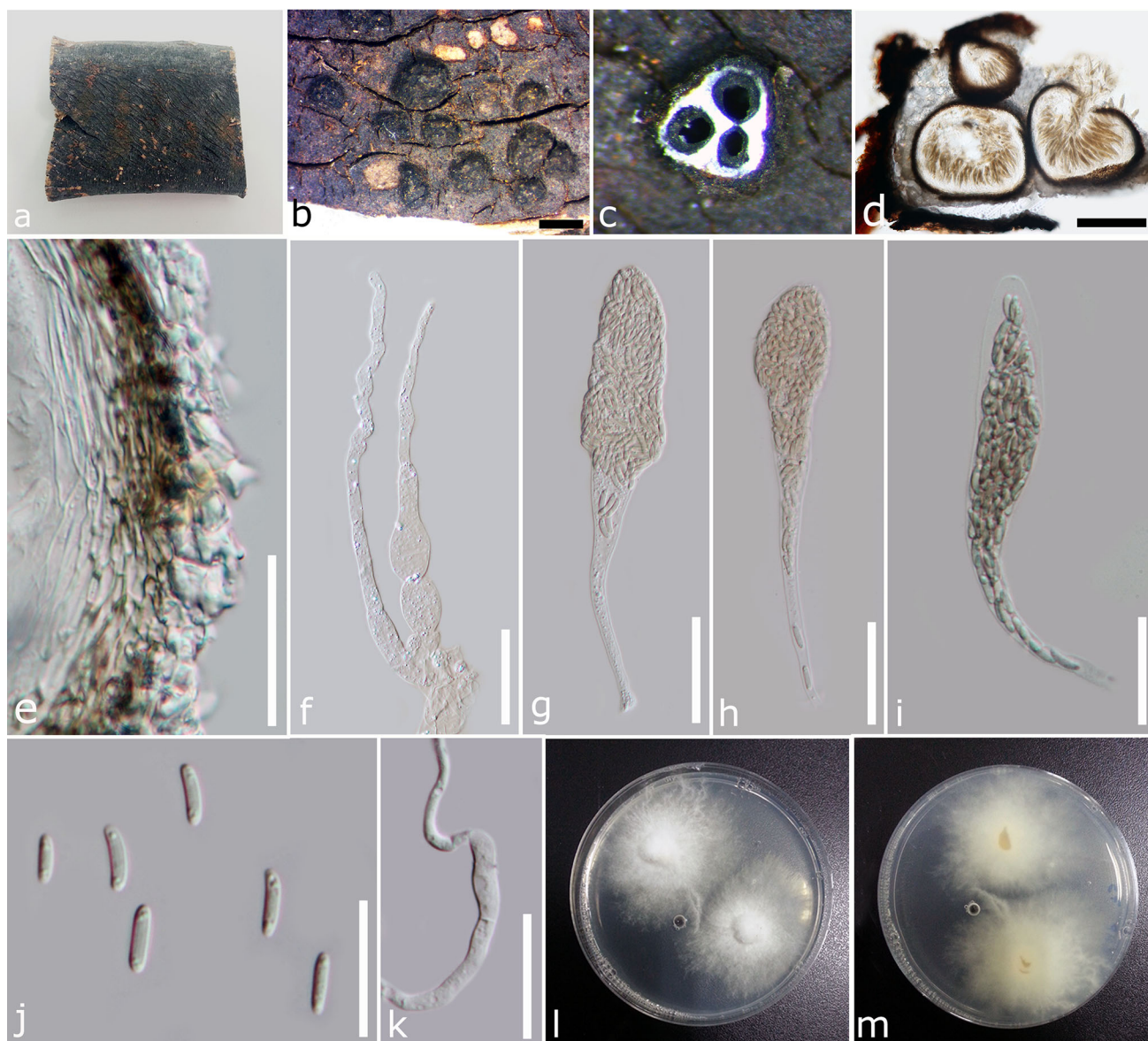


Fig. 130 *Diatrypella delonicis* (MFLU 16-1016, **holotype**). **a** Herbarium material. **b** Appearance of ascomata on host substrate. **c** Longitudinal section through stroma with ascomata. **d** Vertical section through ascomata. **e** Close up of the peridium. **f** Paraphyses. **g–i** Asci.

j Ascospores. **k** Germinating ascospore. **l, m** Colony on PDA (**l** from above view, **m** from below view). Scale bars: **b** = 1 mm, **d** = 500 μ m, **e–i, k** = 20 μ m, **j** = 10 μ m

Odour in lamellae indistinct. *Exsiccatae*: pileus dark brown, stipe greyish brown. *Basidiospores* $7\text{--}8 \times 4.8\text{--}5.3 \mu\text{m}$, $\bar{x} = 7.5 \times 5.1 \mu\text{m}$, $Q = 1.4\text{--}1.6$, $\bar{x} = 1.47$, lacrymoid to shortly obovoid-ellipsoid, strongly verrucose, somewhat dextrinoid. *Lamellar trama hyphae* encrusted. *ITS sequence* (GenBank MK211175, **holotype**) distinct from other members of *C.* sect. *Safranopedes*. With a close relationship to *C. scotoides* and deviating from it by five substitutions and indels.

Ecology and distribution: In hemiboreal and temperate mixed forests with *Corylus* on mull soil. Known from northern Europe.

Material examined: Finland, Varsinais-Suomi, Lohja, Virkkala, Pähkinäniemi, *Corylus* forest with some *Betula*, *Populus* and *Picea* on calcareous ground, 16 September 2012, K. Liimatainen & T. Niskanen 12-010 (H, **holotype**; K, **isotype**).

GenBank numbers: ITS: MK211175 (*loc. cit.* K. Liimatainen & T. Niskanen 12-015 (H)), MK211176.

Notes: *Cortinarius subscotoides* has a dark brown pileus, short but stout stipe, indistinct smell, and lacrymoid to shortly obovoid-ellipsoid, strongly verrucose spores. It grows on mull, calcareous soil at least with *Corylus*. In our

phylogenetic analysis the species formed a well-supported clade within *C. sect. Safranopedes* (Fig. 136).

Psathyrellaceae Vilgalys et al.

Notes: Psathyrellaceae was proposed by Redhead et al. (2001) based on molecular phylogenetic studies. Initially, the family comprised the genera *Psathyrella* (Fr.) Quél., *Lacrymaria* Pat., *Coprinellus* P. Karst., *Coprinopsis* P. Karst., and *Parasola* Redhead et al. The latter three genera were segregated from the polyphyletic genus *Coprinus* Pers. s. lat. in the same paper. Only a few species (*Coprinus comatus* (O.F. Müll.) Pers. and related taxa) remained in the *Coprinus* sensu stricto, and the genus was transferred to Agaricaceae Chevall. Subsequently, several smaller genera were added to Psathyrellaceae. According to Kirk et al. (2008), it comprises 12 genera.

Coprinopsis P. Karst.

Notes: Members of the genus *Coprinopsis* live as saprotrophs on various substrata such as wood, soil, dung, herbal remnants or burnt ground. Its basidiomes are agaricoid, brittle, and often short lived and/or deliquescent, with blackish to black spore print (Vesterholt 2012). The genus contains around 200 species globally (Kirk et al. 2008). The phylogenetic tree is shown in Fig. 137.

Coprinopsis psammophila Mešić & Tkalčec, *sp. nov.*

Index Fungorum number: IF555781; **Facesoffungi number:** FoF05972; Fig. 138

Etymology: The species is named after its substrate, sandy soil in a desert shrubland.

Holotype: CNF 1/6401

Pileus 10–25 mm broad at maturity, subglobose to ellipsoid at first, later obtusely or truncately conical, often with inflexed margin before expanding, finally subapplanate and radially splitting, partially deliquescent, surface finely and shallowly plicate-sulcate except at the centre, pale grey-brownish to light brown at first, later grey to grey-brown, finally black(ish), entirely covered with a delicate, poorly developed, whitish to cream coloured, silky veil. **Lamellae** free, rather crowded, up to 2.5 mm broad, soon becoming black, partially deliquescent. **Stipe** 20–70 × 1.5–3.5 mm, cylindrical, mostly with a broadened (bulbous to subcylindrical) base (up to 6 mm wide), with rather long, completely distinctly narrower or gradually narrowing pseudorhiza, central, widely hollow, whitish, dry, minutely fibrillose-floccose, sometimes striate; basal part always buried in the sand, but often also its lower half, or even most of it. **Context** very thin. **Odour** and **taste** not recorded. **Spore print** black.

Basidiospores [300/3/1] (8.5–)8.8–9.8–10.9(–11.2) × 5.8–6.4–7.2(–7.5) µm (in KOH 2.5%), averages of different basidiomes 9.5–10 × 6.3–6.6 µm, $Q = 1.31$ – 1.52 – 1.71 , av. $Q = 1.47$ – 1.56 , ellipsoid or suboblong

(subcylindrical), more rarely (sub) ovoid, not flattened, with rounded to slightly acute base and very obtuse apex, smooth, slightly to moderately thick-walled (up to 0.6 µm), with wide (2–3.2 µm in KOH, 1.4–2.5 µm in H₂O) and central germ-pore, brown-black in KOH, dark red-brown in H₂O, opaque, non-amyloid and non-dextrinoid. **Basidia** 13–28 × 6–10 µm, clavate, 4-spored, thin-walled, hyaline, surrounded by (3–)4–6(–7) hymenophysalides (pseudoparaphyses). **Cheilocystidia** not observed. **Pleurocystidia** conical or fusiform, up to ca. 100 µm long and 18–45 µm wide, thin-walled, hyaline, rather abundant (but scattered) to scarce. **Pileipellis** a cutis, composed of repent, hyaline, thin-walled, 2–20 µm wide hyphae, with narrowest hyphae on the surface. **Veil hyphae** 1–9 µm broad, occasionally branched, not or only slightly constricted at the septa, thin-walled to slightly thick-walled (up to 0.5 µm), sparsely diverticulate (excrescences pretty wide with rounded tip), hyaline, mostly smooth, sometimes finely to coarsely encrusted. **Clamp connections** absent.

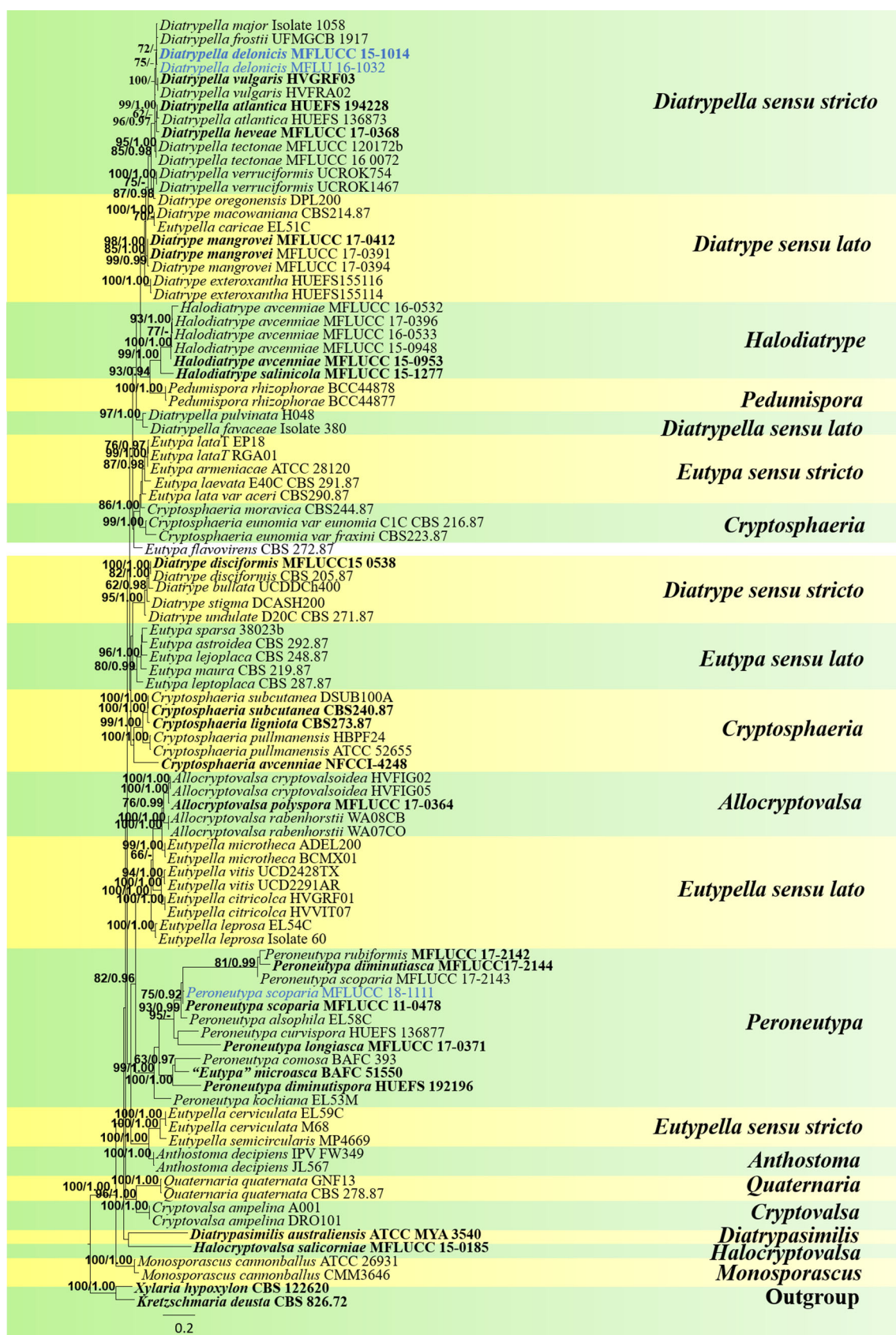
Habit and habitat: In a scattered group (approximately 30 basidiomes at a radius of ca. 10 m), terrestrial, on a sandy soil among sparse herbaceous plants and low bushes in an arid, lowland, Mediterranean desert shrubland.

Distribution: known only from the type locality in Libya, Sirte District.

Material examined: LIBYA, Sirte District, by Qasr Abu Hadi town, 13.9 km S-SE from Sirte, 31°05'55"N, 16°39'54"E, 46 m a.s.l., on sandy soil in a desert shrubland, 14 November 2008, leg. M. Čerkez (CNF 1/6401, **holotype**).

GenBank numbers: ITS: MK491274, LSU: MK492278.

Notes: Morphologically and ecologically, *Coprinopsis psammophila* is characterised by occasionally branched and sparsely diverticulate veil hyphae (sect. *Alachuani* (Singer) D.J. Schafer), mostly ellipsoid or suboblong (subcylindrical), smooth basidiospores with very obtuse apex and wide germ-pore, absence of clamp connections, presence of pseudorhiza, often bulbous stipe base, and terrestrial growth on sandy soil. This set of characters clearly differentiate *C. psammophila* from all other species in the genus. Among all known species in the section *Alachuani*, only *C. alcobae* (A. Ortega) Valade also lives on sandy soil, but has no pseudorhiza, and differs in other morphological characters. Furthermore, only the poorly known *Coprinus dryophilus* Pat. has a rooting stipe, but lives on wood and also differs in other morphological characters. A megablast search of NCBI's GenBank nucleotide database, using the ITS sequence from our holotype collection of *C. psammophila*, showed no closely related species. The closest hit was *C. verticillata* (Schulz-Wedd.) Redhead et al. (GenBank Number MH861734, Identities = 653/725(90%), Gaps = 23/725(3%)). In phylogenetic tree of *Coprinopsis* species based on ITS



◀**Fig. 131** Phylogram generated from maximum likelihood analysis based on combined ITS and TUB2 sequence data of selected taxa. Related sequences were obtained from GenBank. Ninety-five strains are included in the analyses, which comprise 971 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree was rooted with *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122620). Tree topology of the ML analysis was similar to BI. The best scoring RAxML tree with a final likelihood value of -9028.552721 is presented. The matrix had 404 distinct alignment patterns, with 11.19% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.232808, C = 0.250740, G = 0.235523, T = 0.280930; substitution rates AC = 1.126828, AG = 3.047992, AT = 1.477104, CG = 0.932402, CT = 3.736033, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.466736$. The maximum parsimonious dataset consisted of constant 316, 546 parsimony-informative and 109 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 2920 steps (CI = 0.407, RI = 0.751, RC = 0.306, HI = 0.593) in the first tree Maximum likelihood bootstrap (ML) values > 65% and Bayesian posterior probabilities (PP) > 0.90% and are given above the nodes. The scale bar indicates 0.2 changes. The ex-type strains are in bold and black. The newly generated sequences are indicated in bold and blue

sequences (Fig. 139) *C. psammophila* is nested near two other species of sect. *Alachuanii*, *C. strossmayeri* (Schulzer) Redhead et al. and *C. picacea* (Bull.) Redhead et al.

Coprinopsis villosa L. Nagy, Desjardin, Vágvölgyi & Papp, in Nagy et al., Mycologia 105(1): 120 (2013)

Index Fungorum number: IF487717; *Facesoffungi* number: FoF05973; Fig. 140

Pileus up to 20 mm high and 7 mm broad when still unexpanded, narrowly ellipsoid at first, then narrowly conical (never expanded in our collection), plicate-sulcate except at the centre, white at first, then becoming brownish-grey to grey, covered with medium abundant, rather loosely attached, floccose veil, reddish brown all over or light brown at the wider central zone and whitish around. *Lamellae* free, crowded, white at first, black at maturity, with whitish edge. *Stipe* up to 32×3 mm, cylindrical or somewhat tapering towards the base, central, widely hollow, dry, tomentulose, white. *Odour* and *taste* not observed. *Spore print* black.

Basidiospores [100/2/1] $8.6\text{--}10.1\text{--}11.4 \times 6.2\text{--}7\text{--}7.8$ μm (in KOH 2.5%), averages of different basidiomes $9.6\text{--}10.7 \times 6.7\text{--}7.3$ μm , $Q = 1.30\text{--}1.45\text{--}1.57$, av. $Q = 1.42\text{--}1.47$, ellipsoid to ovoid in frontal view, often (sub) amygdaloid in side view, not flattened, with rounded to slightly conical base and rounded apex, smooth, thick-walled ($1\text{--}1.2$ μm), with $1.2\text{--}1.8$ μm wide, central germ-pore, medium rusty brown in H_2O , medium brown in KOH, semi-transparent, non-amyloid and non-dextrinoid. *Basidia* $17\text{--}33 \times 8\text{--}11$ μm , clavate or spatulate with rounded or subcylindrical upper part, 4-spored, thin-walled, hyaline,

surrounded by 3–5(–6) hymenophysalides (pseudoparaphyses). *Cheilocystidia* up to ca. 40 μm in diameter, mostly subglobose or ellipsoid, thin-walled, hyaline, very delicate and easily collapsing in our material. *Pleurocystidia* $30\text{--}65 \times 20\text{--}45$ μm , ovoid, conical, oblong (subcylindrical) or ellipsoid, thin-walled, hyaline, rather abundant but scattered. *Veil* on pileus composed of two types of elements: (1) ellipsoid to elongated cells, often inflated and/or constricted at septa, arranged in chains forming tufts, up to 90 μm wide, gradually narrowing towards the pointed tuft tip (to only a few μm), not branched or diverticulate, subhyaline to yellow–brown (with intracellular pigment), thin-walled to moderately thick-walled (up to 1 μm), and (2) narrow, 1–6 μm wide, branched, sparsely diverticulate, hyaline, thin-walled to moderately thick-walled (up to 0.8 μm) hyphae laying on the broader ones. *Pileipellis* a cutis, composed of repent, ellipsoid to elongated, mostly inflated, hyaline, thin-walled to moderately thick-walled (up to 1 μm), 4–50 μm wide hyphae. *Clamp connections* present and rather abundant in all tissues.

Material examined: CROATIA, Zagreb County, 800 m W-NW from Kostanjevac Podvrški (near Samobor), $45^\circ 49' 51''\text{N}$, $15^\circ 35' 17''\text{E}$, 250 m a.s.l., 13 October 2007, leg. M. Čerkez (CNF 1/4862, **new country record**).

Habit and habitat: On horse dung (Nagy et al. 2013). Our collection was composed of five immature basidiomes (spores matured after sampling) growing from a heap of horse dung mixed with straw.

Distribution: Hitherto known from Croatia, Germany, Hungary, Spain, Sweden and USA (Hawaii) (Nagy et al. 2013; Ruiz & Cerdán 2016).

GenBank numbers: ITS: MK491273, LSU: MK492277.

Notes: ITS sequence obtained from our material of *Coprinopsis villosa* is identical to the sequence from the type material (GenBank number HQ847031). *C. villosa* is characterised by fimicolous habitat (horse dung), brown veil on the pileus (at least near the centre), smooth and medium-sized basidiospores, veil composed of two types of elements (broader, unbranched, non-diverticulate cells in chains together with a narrower, branched and sparsely diverticulate cells), and the presence of clamp connections. According to the dominant type of velar elements, it belongs to the section *Lanatuli* (Fr.) D.J. Schafer. The only other known *Coprinopsis* species that has a veil on the pileus composed of sausage like elements together with a branched and diverticulate elements is *C. candidolanata* (Doveri & Uljé) Keirle et al. However, it has a pure white veil, densely diverticulate narrower veil hyphae, no clamp connections, and it occurs on deer and sheep dung. In the protologue of *C. villosa*, Nagy et al. (2013) wrote that they did not see clamp connections. However, in Croatian, Spanish (Ruiz & Cerdán 2016) and Hawaiian material (Keirle et al. 2004; mentioned in the protologue under

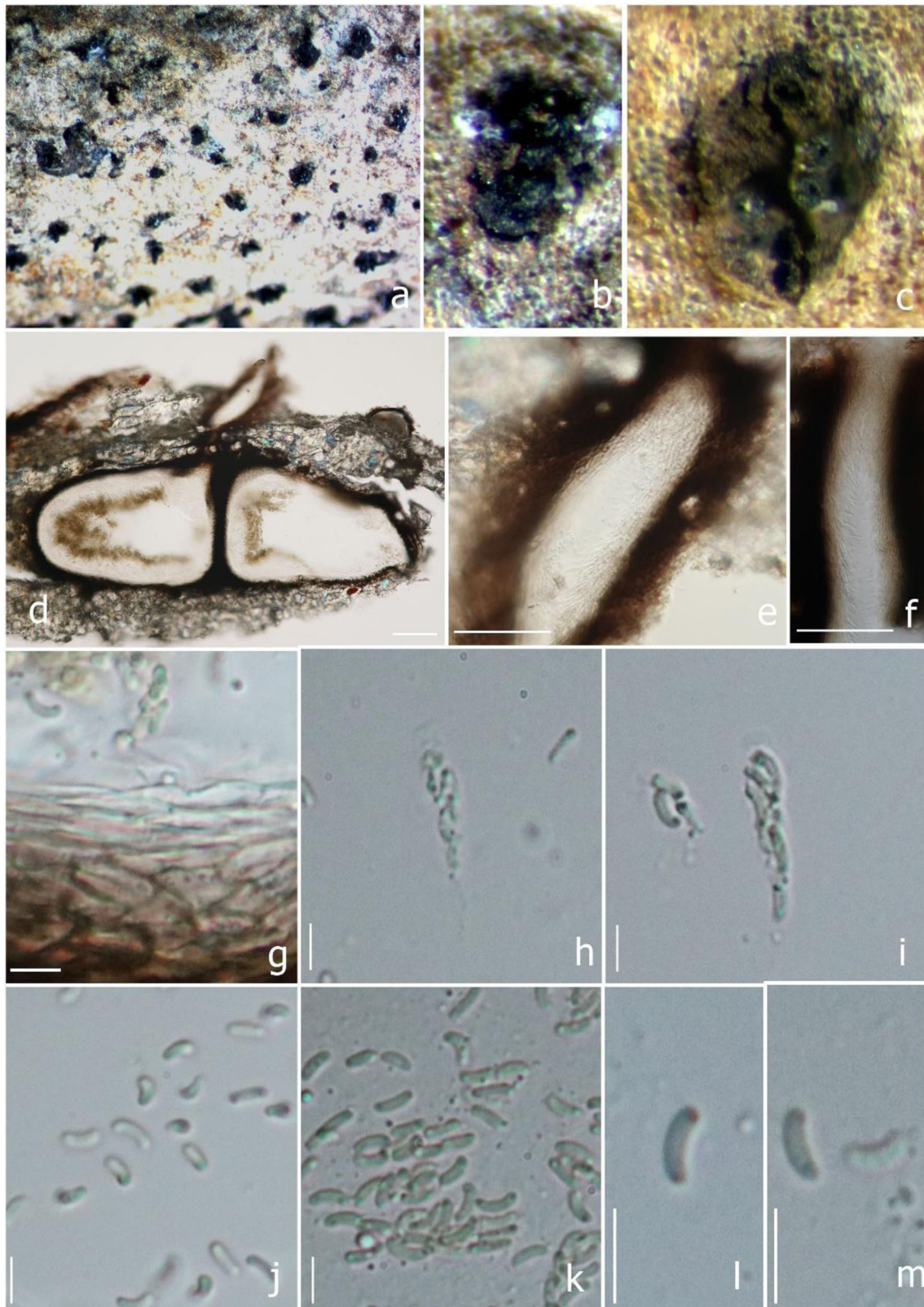


Fig. 132 *Peroneutypa scoparia* (MFLU 19-0623, new record). **a–c** Appearance of ascomata on host. **d** Vertical section through ascoma. **e, f** Ostiole, section through neck with periphyses. **h, i** Asci. **j–m** Ascospores. Scale bars: **d** = 100 μ m, **e, f** = 50 μ m, **g–m** = 5 μ m

“Other specimens examined”) clamp connections are present. A length/width ratio (Q) of basidiospores is another difference worth mentioning between the original description and the description of Croatian material. Basidiospores reported in original description are more elongated ($Q = 1.47\text{--}1.57\text{--}1.64$) than those measured in Croatian material ($Q = 1.30\text{--}1.45\text{--}1.57$). *C. villosa* is reported here as new to Croatian mycobiota. An overview of coprinoid taxa recorded for Croatia until 2000 is given by Mešić & Tkalc̃ec (2003).

Cantharellales Gäum.

Notes: The order Cantharellales represents most likely the oldest lineage among homobasidiomycetes and equally the oldest lineage in which the ectomycorrhizal mode of nutrition has been acquired. However, this lineage also harbours few lichen-forming, several lichenicolous as well as many saprotrophic and parasitic species (Hibbett et al. 2014). Also referred to as the cantharelloid clade, this lineage typically contains species producing basidia with a variable number of spores depending on the genus. Two sterigmata are found in many *Clavulina* and *Membranomyces*, for example, as well as in some rare tropical African *Cantharellus*, but a variable number from four to eight sterigmata per basidium in a single species is the situation that predominates in *Cantharellus*, *Craterellus*, *Botryobasidium* and *Sistotrema*.

Botryobasidiaceae Jülich.

Notes: It was first introduced as subfamily Botryobasidioideae of the Corticiaceae in 1958, and was validly published by Parmasto (1968). Later on, Jülich (1982) raised the status of subfamily to the rank of family, as the Botryobasidiaceae. Corticioid genera *Botryobasidium*, *Botryodontia*, *Botryohypochnus* (considered a synonym of *Botryobasidium*), *Candelabrochaete*, *Suillosporium*, and *Waitea*, were described based mainly on similarities in the their basidiocarp micromorphology. *Botryobasidium* has smooth spores and is usually 6–8 sterigmata, while *Botryophypochnus* produces spiny spores and contains 4-sterigmate basidia. Langer (1994) based on molecular data analysis suggested for synonymization and proved *Botryobasidium* as paraphyletic. Almost all species produce thin and delicate basidiomata with distinct wide hyphae. Many species are associated with asexual morph genera like *Haplotrichum*, *Acladium*, etc. The proposed taxon has somewhat similar in morphological features of *Acladium*, but molecular data strongly supports to be distinct from all other known genera of Botryobasidiaceae. Therefore, this taxon is being proposed as new genus.

Neoacladium P.N. Singh & S.K. Singh, *gen. nov.*

Index Fungorum number: IF556212; **Facesoffungi number:** FoF5687

Etymology: Name refers to its morphological similarity to the genus *Acladium*.

Type species: *Neoacladium indicum* P.N. Singh & S.K. Singh

Saprobic on dead bark of tree of terrestrial habitats. **Asexual morph.** Colonies effuse, cottony or velvety, rhizoidal, light yellow, powdery, reverse greyish orange. **Mycelium** mostly semi-immersed or immersed, single or interwoven, light olivaceous. Stroma none. **Chlamydospores** produced from lateral hyphae, bulbous and inflated, simple to branched, constricted near septa, pigmented, trident shaped, subhyaline to light olivaceous. Setae and hyphopodia absent. **Conidiophores** semi-macronematous, mononematous, fasciculate, dichotomously loosely interwoven, branched, straight or flexuous, subhyaline to light olivaceous, smooth, septate. **Conidigenous cells** integrated to terminal sometimes discrete, determinate, acropleurogenous, polyblastic, inflated or sometimes cylindrical, persistent occasionally sessile, denticulate, denticles numerous. **Conidia** solitary or catenate, dry, variously shaped, sub-globose- globose, clavate-obclavate, lenticular, pyriform to ampulliform, smooth-walled, pigmented, sub-hyaline to light olivaceous. **Sexual morph** Undetermined.

Notes: Phylogenetic analysis of ITS and LSU sequence data indicates that *Neoacladium* is a distinct genus in Botryobasidiaceae, which forms a clade sister to *Botryobasidium*. *Neoacladium* is close to *Acladium*, but differs from all other allied genera in having subhyaline to light olivaceous variously shaped conidia, viz. globose to sub-globose, clavate, obclavate, lenticular, ampulliform and pyriform, catenate conidia, dentate and phialidic conidigenous cells and presence of abundant trident like pigmented chlamydospores.

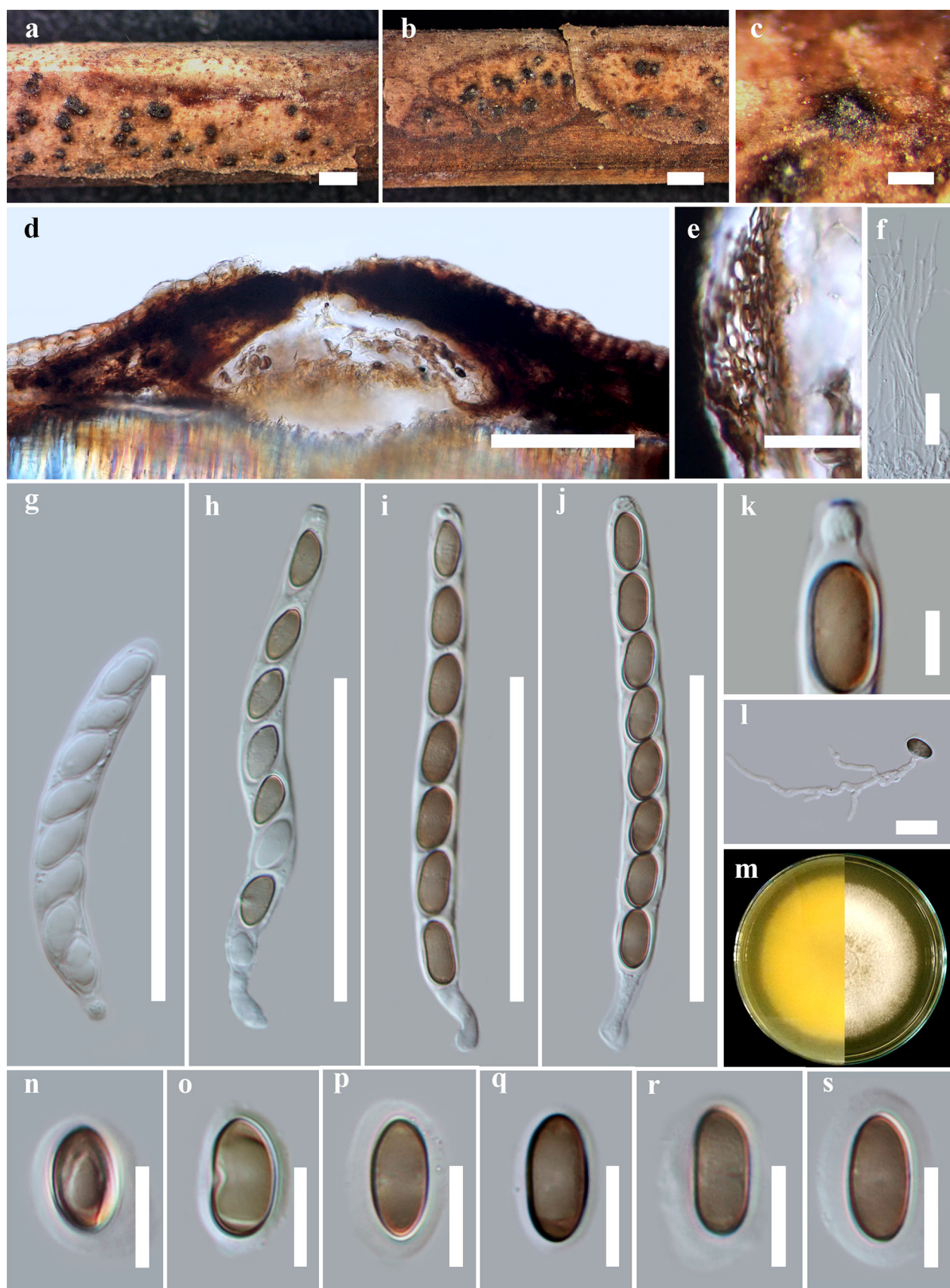
Neoacladium indicum P.N. Singh & S.K. Singh, *sp. nov.*

Index Fungorum number: IF556211; **Facesoffungi number:** FoF5688; Figs. 139, 141

Etymology: Specific epithet “*indicum*” refers to the country of origin.

Holotype: AMH 10054

Saprobic on dead bark of *Leucaena leucocephala* L. **Asexual morph** Colonies uniformly spread on dead bark, yellow, velvety. **Conidiophores** semi-macronematous, mononematous, fasciculate, dichotomously branched, loosely interwoven, straight to flexuous, subhyaline to light olivaceous, smooth-walled, septate, $337\text{--}752 \times 9\text{--}13 \mu\text{m}$.



◀Fig. 133 *Fasciatispora arengae* (MFLU 15-0301, new record). **a, b** Appearance of ascomata on host substrate. **c** Close up of ascomata. **d** Section of ascoma. **e** Peridium. **f** Paraphyses. **g–j** Asci. **k** J + reaction with Melzer's reagent in apical ring. **l** Germinated ascospore. **m** Colony on culture. **n–s** Ascospores. Scale bars: **a, b** = 1000 μ m, **c** = 200 μ m, **d** = 100 μ m, **g–j** = 50 μ m, **e, f** = 20 μ m, **l, n–s** = 10 μ m, **k** = 5 μ m

Conidiogenous cells integrated to terminal, sometimes discrete, determinate, acropleurogenous, polyblastic, inflated, sometimes cylindrical, persistent, occasionally sessile, denticulate, denticles numerous, 1–2 celled, 0–1 septate, subhyaline to light olivaceous, 7.48–62.92 μ m (\bar{x} = 20.52 \times 6.32 μ m, n = 30). Conidia solitary or produced in short chains, variously shaped, globose to sub-globose,

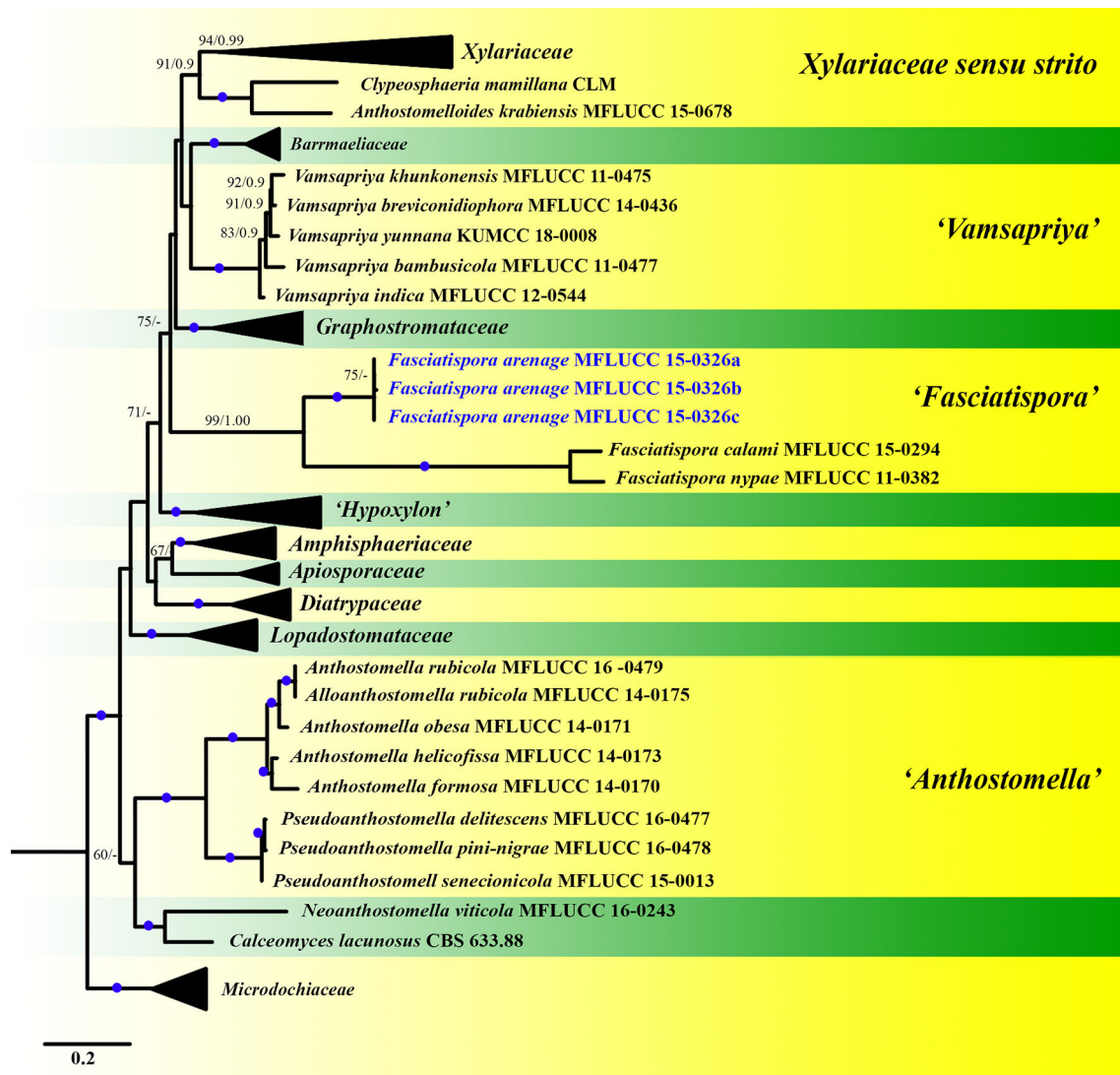


Fig. 134 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, RPB2 and TUB2 sequence data for *Fasciatispora* species and several closely related genera in Xylariales. Related sequences are taken from Voglmayr et al. (2018), Wendt et al. (2018) and Daranagama et al. (2018). One hundred and fifty-seven strains are included in the combined analyses which comprise 7548 characters (1288 characters for ITS, 2397 characters for LSU, 1246 characters for RPB2, 2617 characters for TUB2) after alignment. Microdochiaceae is used as the outgroup taxon. Single gene analyses are carried out and the topology of each tree had clade stability. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood

valued of -156397.840016 is presented. The matrix had 4604 distinct alignment patterns, with 59.36% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239282, C = 0.272288, G = 0.248516, T = 0.239913; substitution rates AC = 1.231573, AG = 3.991205, AT = 1.258243, CG = 0.936670, CT = 5.480741, GT = 1.000000; gamma distribution shape parameter α = 0.408051. Bootstrap values for maximum likelihood (ML) equal to or greater than 50, Bayesian posterior probabilities (BYPP) equal to or greater than 0.9 are placed above and below the branches respectively. Our strains generated sequences are indicated in blue. Branches with 100% MLBS and 1.00 BYPP are shown as blue nodes

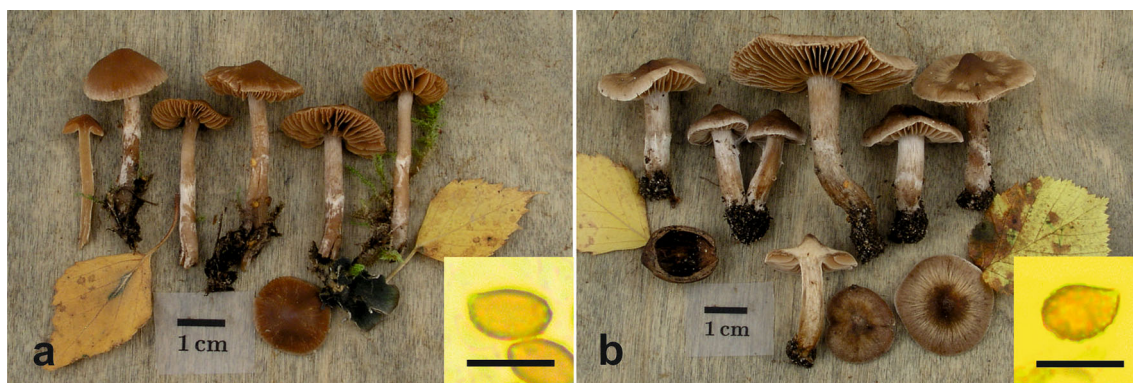


Fig. 135 Basidiomata and basidiospores (in MLZ). of **a** *Cortinarius minusculus* (K. Liimatainen & T. Niskanen 12-032, H). **b** *Cortinarius subscotoides* (K. Liimatainen & T. Niskanen 12-015, H). Photographs Kare Liimatainen. Scale bar: **a**, **b** (basidiospores) = 10 µm

clavate, obclavate, pyriform, lenticular, sometimes broadly ellipsoidal to ampulliform, pigmented, smooth-walled, base truncate, subhyaline to light olivaceous, $10.5\text{--}25.88 \times 9.36\text{--}16.5 \mu\text{m}$ ($\bar{x} = 15.75 \times 13.55 \mu\text{m}$, $n = 30$).

Sexual morph Undetermined

Culture characteristics: Conidia germinating on malt extract agar (MEA). Colonies light yellow (4A4), reaching 4.2 cm diam. in 10 days at 25 °C, rhizoidal with irregular margin, surface powdery, reverse greyish orange (5B5). **Hyphae** septate, unbranched to branched, pigmented, smooth and thin walled, subhyaline to light olivaceous, $5\text{--}5.62 \mu\text{m}$ wide.

Material examined: INDIA, Maharashtra, Pune District, on dead bark of *Leucaena leucocephala* (Fabaceae), 30 July 2017, P.N. Singh; (AMH 10054, **holotype**), ex-type living culture (NFCCI 4480).

GenBank numbers: ITS: MK391496, LSU: MK391493.

Notes: The proposed taxon is compared with the asexual genus *Acladium* in having subhyaline to light olivaceous ampulliform to pyriform conidia produced from tubular to inflated and conidiogenous cells which are persistent, and occasionally sessile. Chlamydospores in the proposed taxon produced laterally and form trident like structure, which are pigmented. Most of these features are absent in

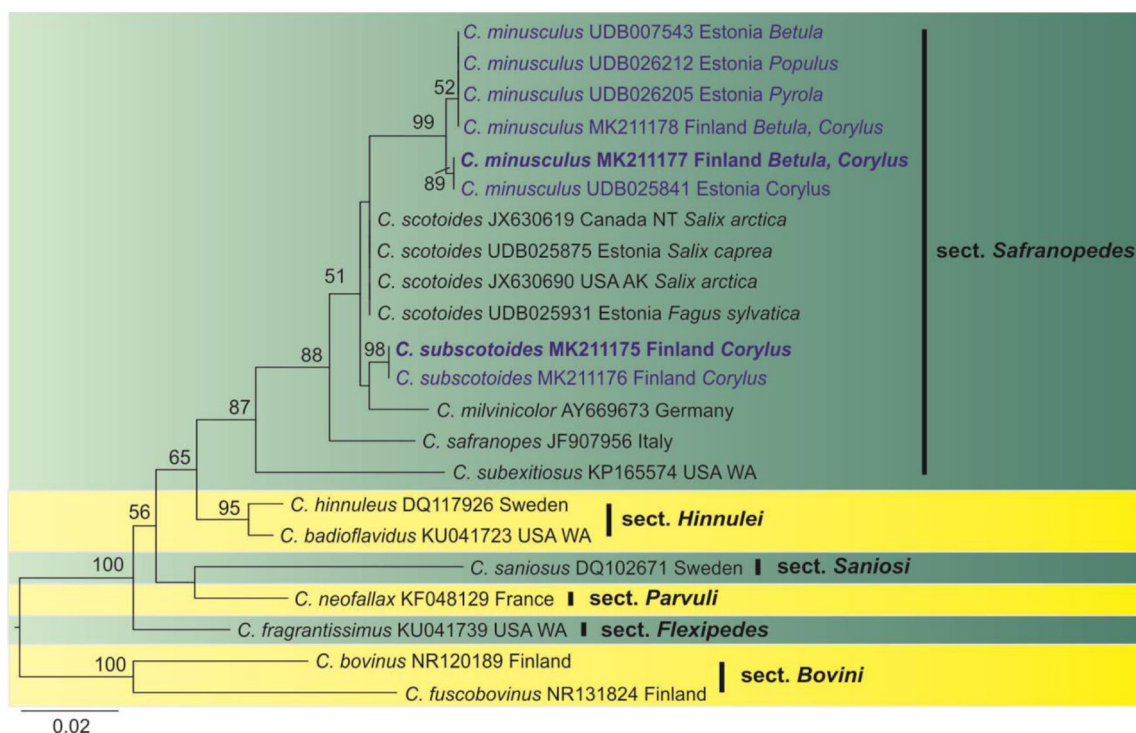


Fig. 136 Phylogram resulting from the RaXML (Stamatakis 2014) analysis of ITS regions. Bootstrap values greater than 50% are indicated above branches. The names in blue represent the new species of *Cortinarius* and the specimens in boldface the type

specimens of the species. The tree is rooted with *C.* section *Bovini*. The ex-type strains are in bold. The newly generated sequences are indicated in blue

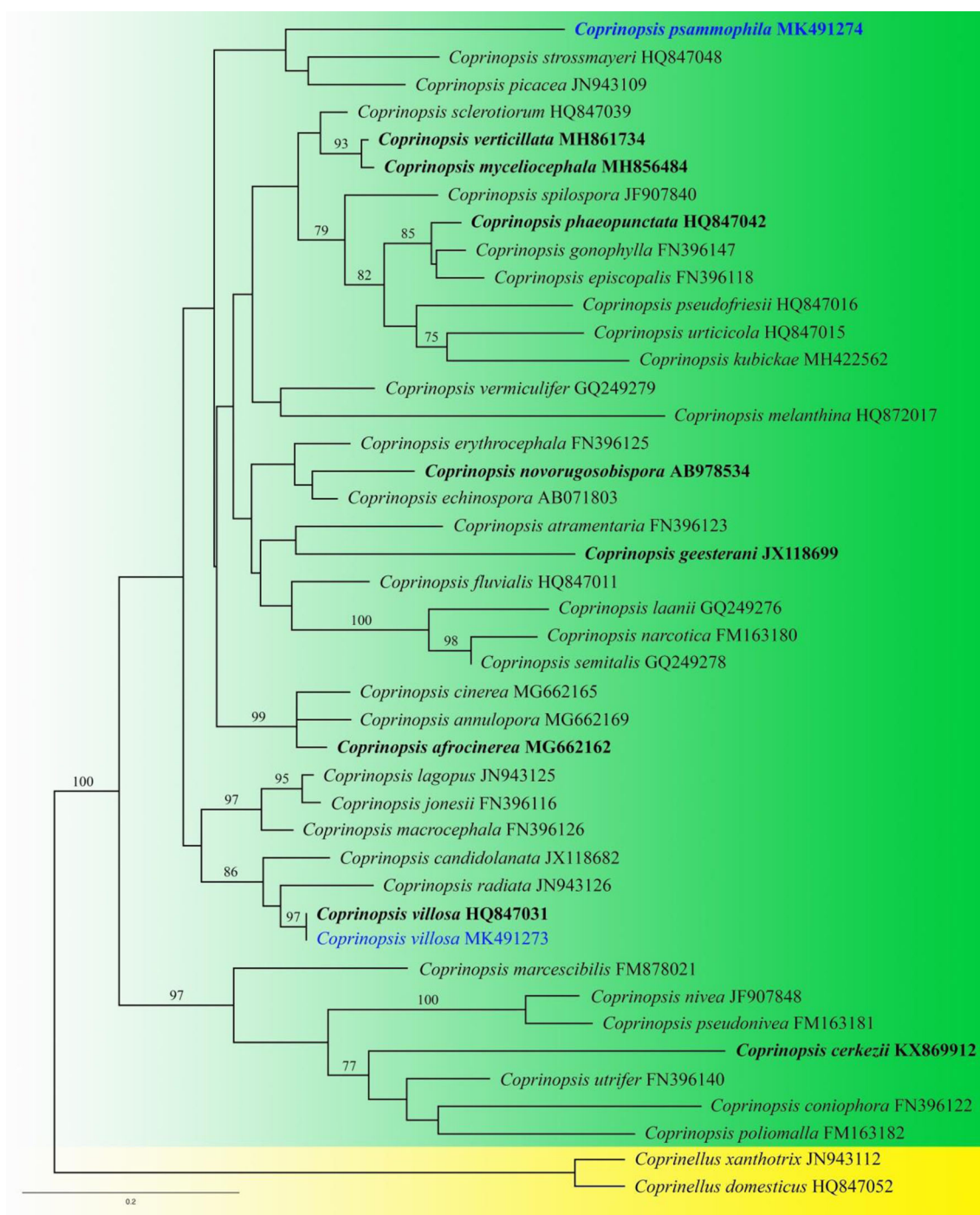


Fig. 137 Maximum likelihood phylogenetic tree of *Coprinopsis* species based on an ITS1–5.8S–ITS2 DNA sequence alignment and calculated with PhyML software (Guindon et al. 2010). Related sequences are taken from Nagy et al. (2011, 2012, 2013), Raut et al. (2011), Osmundson et al. (2013), Raut et al. (2015), Tibpromma et al. (2017), Phookamsak et al. (2019) and Vu et al. (2019). Forty-three strains are included in the gene sequence analyses with total of 737 characters after alignment. The tree is rooted with *Coprinellus xanthotrix* (SZMC-NL-3417) and *C. domesticus* (SZMC-NL-1292). The best PhyML tree with a final likelihood value of -3591.26595 is

presented. Estimated base frequencies were as follows: A = 0.23036, C = 0.22632, G = 0.21420, T = 0.32912; substitution rates AC = 1.48357, AG = 3.68147, AT = 1.56733, CG = 0.64802, CT = 4.50774, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.570$; proportion of invariant is 0.348. The ex-type strains are indicated in bold. The newly generated sequences are indicated in blue. Maximum likelihood bootstrap values greater than 70% are indicated at the nodes. The bar indicates the number of nucleotide substitutions per site

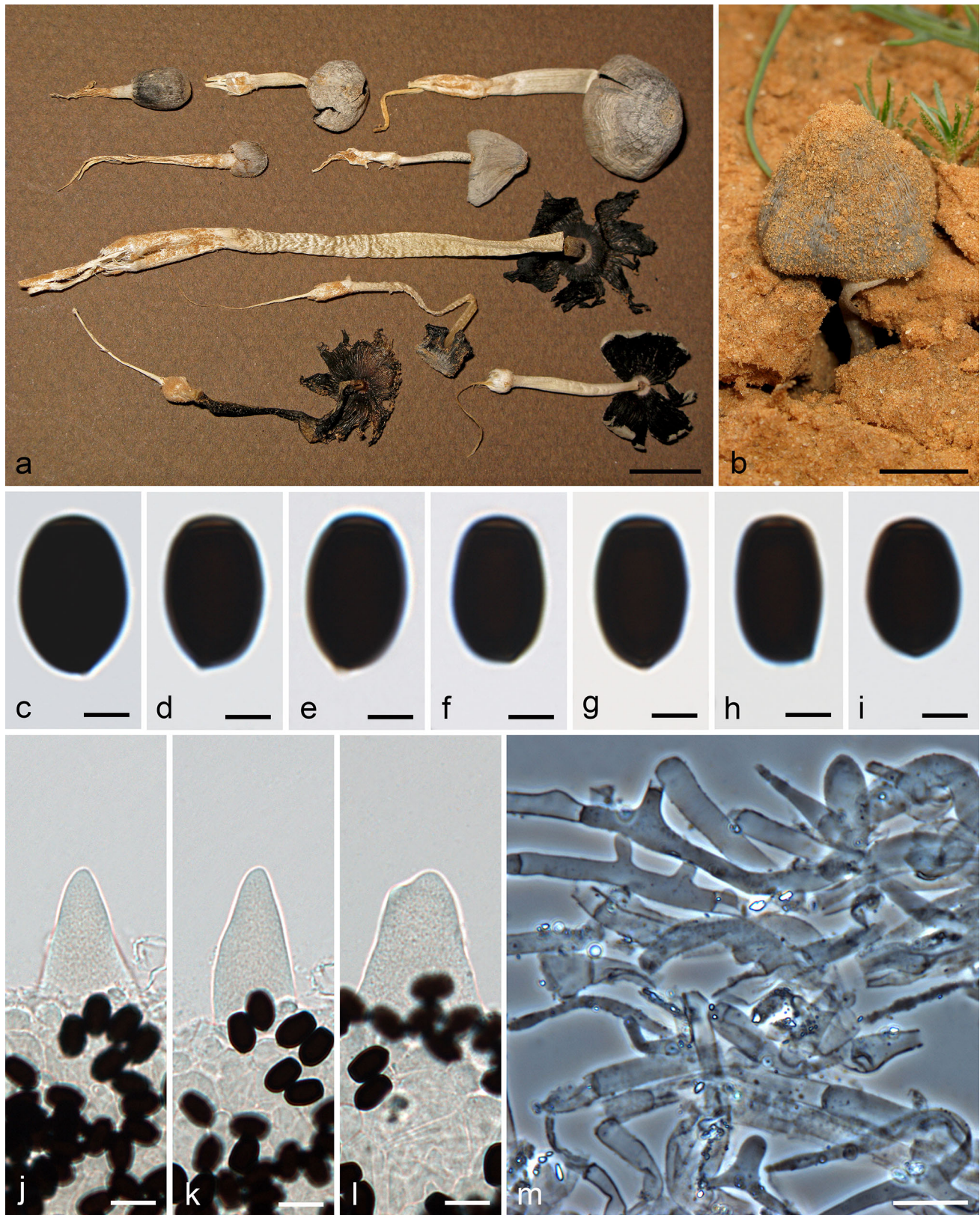


Fig. 138 *Coprinopsis psammophila* (CNF 1/6401, holotype). **a, b** Basidiomes. **c–i** Basidiospores. **j–l** Pleurocystidia. **m** Veil on the pileus (phase contrast). Scale bars: **a** = 10 mm, **b** = 5 mm, **c–i** = 3 μ m, **j–m** = 10 μ m

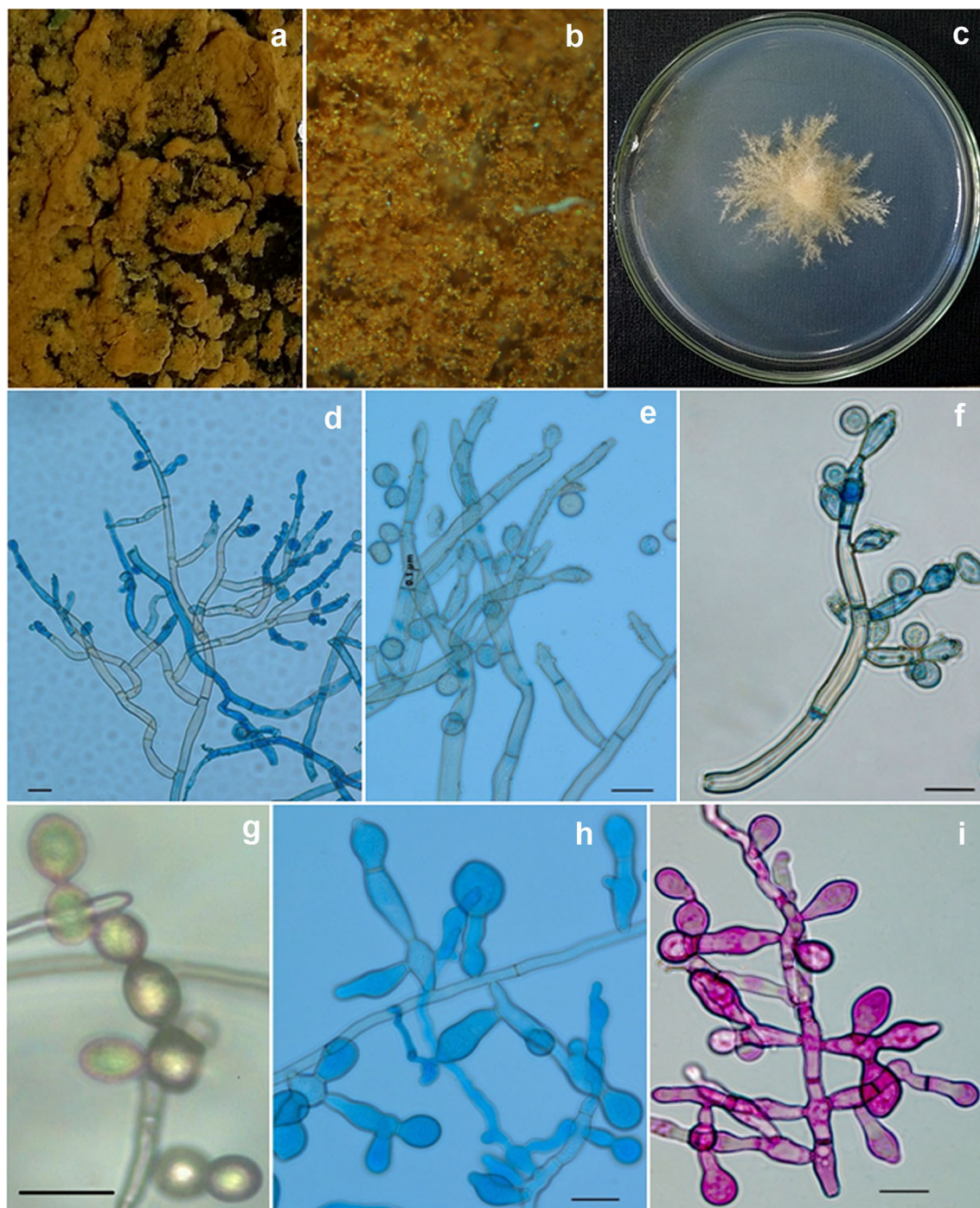


Fig. 139 *Neoaccladium indicum* (AMH 10054, **holotype**). **a** Yellow velvety fungal colonies spreaded on outer bark surface. **b** Stereoscopic surface view of fungal colonies from substratum. **c** Colony morphology (above view). **d** Dichotomously branched conidiophores. **e** Enlarged microscopic view of dichotomously branched conidiophores

with intercalary, lateral and terminal dentate conidiogenous cells and conidia. **f** A detached branch of conidiophore bearing conidiogenous cells and conidia. **g** Catenate conidia. **h–i** Trident shaped and inflated chlamydospores. Scale bars: **d–i** = 20 μ m

Acladium. However, the conidial shape, length–width are very much variable in *N. indicum*, which separate it from other reported taxa in this group. Proposed taxon is also distinct from other genera in this group, like *Burgoa*, *Minimedusa*, *Ceratobasidium*, (Rogers 1935; Weresub and

LeClair 1971) in having non-bulbuliferous vegetative parenchymatous propagules. During this study the sexual stage *Botryobasidium* of *Acladium* was not encountered.

The proposed *N. indicum* (AMH 10054 **holotype**), is different from other *Botryobasidium* species based on the

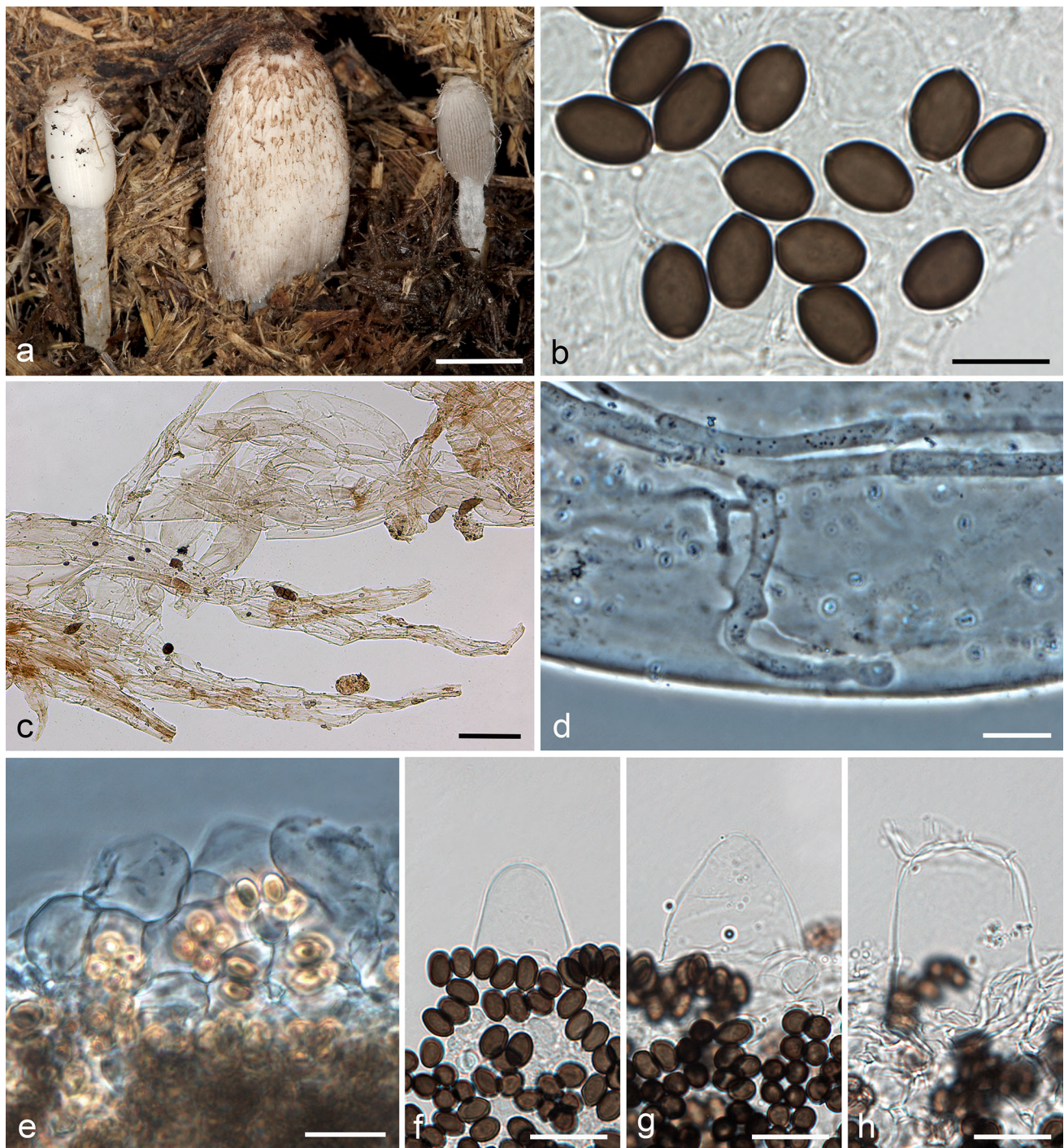


Fig. 140 *Coprinopsis villosa* (CNF 1/4862, new geographical record). **a** Basidiomes. **b** Basidiospores. **c** Veil on the pileus. **d** Veil on the pileus (phase contrast). **e** Cheilocystidia (phase contrast). **f–h** Pleurocystidia. Scale bars: **a** = 3 mm, **c** = 100 μ m, **e–h** = 20 μ m, **b**, **d** = 10 μ m

sequence analyses. On megablast analysis, ITS sequence of *N. indicum* showed 80% (524/651) identity and 53 gaps (8%) with *B. subcoronatum*, 84% (343/410) identity and 27 gaps (6%) with *B. simile* (GEL2348), and 81% (521/645) identity 54 gaps (8%) with *B. intertextum* UC2022959. The phylogenetic analysis clearly establishes *Neoaccladium* as a

novel genus, and *N. indicum* as the type species with strong bootstrap values (Figs. 142, 143).

Hydnaceae Chevall.

= Clavulinaceae Donk, Beih. Nova Hedwigia 1(4): 407 (1970)

= Cantharellaceae J. Schröt., in Cohn, Krypt.-Fl. Schlesien (Breslau) 3.1 (25–32): 413 (1888) [1889]

= Sistotremataceae Jülich, Bibl. Mycol. 85: 390 (1982)

= Pterygellaceae Jülich, Bibl. Mycol. 85: 386 (1982),

= Heteroacanthellaceae P. Roberts, Mycologist 12(4): 147 (1998)

= Repetobasidiaceae Jülich, Bibl. Mycol. 85: 388 (1982)

Notes: Index Fungorum (<http://www.indexfungorum.org>) and MycoBank (www.mycobank.org) are still considering Hydnaceae in a different, much narrower sense, whereas recent phylogenetic studies (Moncalvo et al. 2006; Hibbett et al. 2014; Lawrey et al. 2016) have demonstrated that *Hydnum* L., the type genus of Hydnaceae, belongs in the core lineage of the cantharelloid clade. Hence, the older family name “Hydnaceae” has nomenclatural priority over other family names that could be considered to name the family that groups members of this core clade. The morphological character that seems to support this lineage is the stichic nature of basidia (Pine et al. 1999), although this is only based on observations for very few species. The family is principally comprised of edible species (all *Craterellus*, *Cantharellus* and *Hydnum*). Type genus: *Hydnum* L., Species Plantarum: 1178 (1753)

Cantharellus Adans.

Notes: *Cantharellus* is an ectomycorrhizal genus of edible mushrooms and is reputed for its high culinary and commercial value. The genus has a worldwide distribution and is one of the prominent fungal genera in Africa (De Kesel et al. 2016) and Madagascar (Buyck et al. 2015), with several species being sold along roads and in local markets in large quantities. The genus is infamous for the difficulty of species delimitation and identification (Olariaga et al. 2016). The recent use of DNA sequences for the delimitation of species has more than doubled the number of worldwide accepted species over the past ten years, with numerous species continuing to be described from the African continent (e.g. Buyck et al. 2017; Das et al. 2018a). Sequencing of recent collections from Africa and Madagascar has also allowed for the epitypification of many of the earlier species (e.g. Buyck and Hofstetter 2018; Buyck et al. 2018).

Cantharellus goossensiae (Beeli) Heinem., Bull. Jard. Bot. Etat Brux. 28(4): 406 (1958).

Mycobank number: MBT385407; **Index Fungorum number:** IF556561; Figs. 144, 145

Basionym: *Hygrophorus goossensiae* Beeli, Bull. Société Royale Botanique Belge 61: 99 (1928).

Iconography: HEINEMANN (1958, Fig. 42; 1959, pl. XXVII, Fig. 3).

Original diagnosis: « Pileo carnosus crasso, convexe, glabro levi, atro-violacea, 5–6 cm lato; stipite crasso solida dein cavo, sulcato, ochraceo, 3–4 × 2 cm; lamellis crassis decurrentibus venoso connexis, ochraceis; sporis

ellipsoideis, hyalinis, levis, 8–9 × 4–5 µm; carne ochraceopallida contactu aeris rubescente. »

Original description (freely translated from French) “-Pileus thick and fleshy, unevenly convex, smooth, glabrous, dark violaceous, 5–6 cm diam.; stipe thick, solid then hollowing, ochraceous, 3–4 × 2 cm; gills thick, decurrent, interveined, yellowish ochre; spores ellipsoid, hyaline, smooth, 8–9 × 4–5 µm; flesh becoming pinkish when cut or exposed.”

Epitype description, Figs. 144, 145

Basidiomata fleshy and firm, dispersed or solitary. *Pileus* 82 mm diam., with strongly inrolled margin, at surface dull, tomentose to fibrillose, yellowish brown with olive tinges, slightly paler in the centre (4–5DE series), toward the margin rather dull yellowish to grayish brown, musterd brown (5E6–4, 5F4–5). *Hymenophore* composed of slightly higher radial gill folds compared to the strongly developed interstitial venation, nearly off-white to pale cream when young, then developing ochraceous tints. *Stipe* thick and massive, 30 × 11–26 mm, surface splitting in horizontally arranged patches or rims in the upper portion, smooth elsewhere, slightly paler than pileus and developing dark grayish brown to orange brown tinges, not hollowing. *Context* off-white to pale cream, moderately yellowing, finally turning ferruginous when cut, 6–7 mm thick above the upper stipe-hymenophore transition. *Smell* faint, but typical and fruity. *Taste* mild. *Spore print* insufficient but very pale.

Spores ellipsoid to narrowly ellipsoid, (5.8)6.2–6.57–7.0(7.3) × (3.8)4.0–4.38–4.7(5.0) µm, Q = (1.3)1.4–1.51–1.6(1.7), smooth, hyaline. *Basidia* narrowly clavulate, measuring mostly 40–55(63) × 7–8(9) µm, predominantly 4–5-spored. *Subhymenium* filamentous. *Cystidia* not observed. *Pileipellis* composed of long, multi-celled hyphal extremities, aggregating together in trichoids or tufts, composed of subcylindrical, thin-walled cells; the terminal cell variable in length, mostly 30–70 µm long, ca 10–20 µm wide and most often wider than the subterminal cells, often slightly constricted in the middle portion, sometimes even clavate, broadly obtuse at the tip, rarely subcylindrical or somewhat narrowing upward. *Clamp connections* present everywhere.

Epitype: CENTRAL AFRICAN REPUBLIC. Dzanga-Sangha Forest Reserve, near Bayanga, close to Bai-Hakou base camp, N2.859934 – E16.467492, under monospecific *Gilbertiodendron dewevrei* forest, on bare sandy soil, 19 May 2016, 1648/Buyck 16.064 (PC 0125008), **epitype is designated here !**; Democratic Republic of the Congo. Central African forest district, near Selenge-Lukolela, isolated on the soil of the *Gilbertiodendron dewevrei* forest, August 1925, M. Goossens-Fontana 372 (BR), **holotype**.

Additional material examined and sequenced: CENTRAL AFRICAN REPUBLIC. Dzanga-Sangha Forest Reserve, near Bayanga, close to Bai-Hakou base camp, N2.859934 – E16.467492, under monospecific

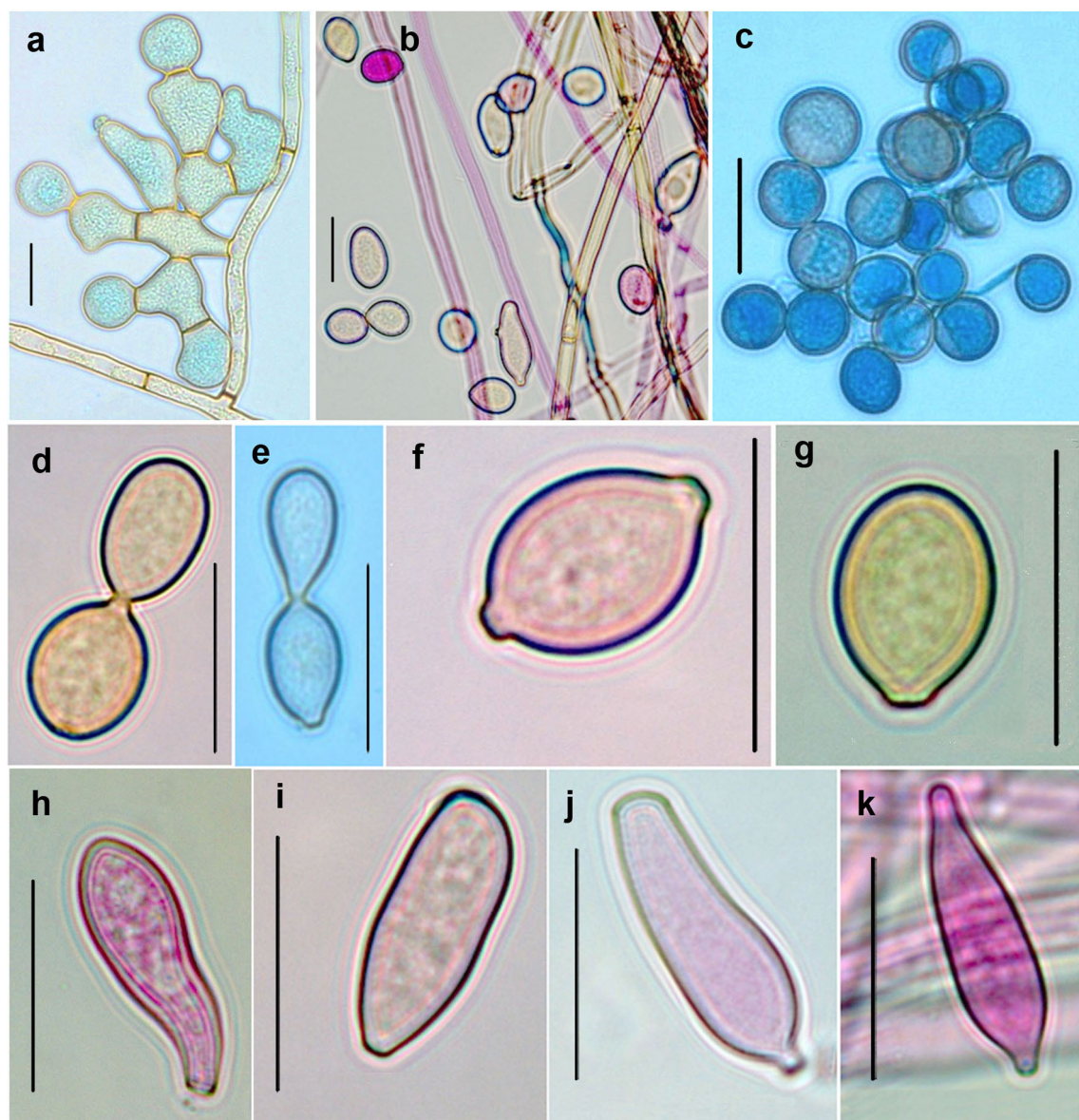


Fig. 141 *Neoaccladium indicum* (AMH 10054, **holotype**). **a** Branched chlamydospores. **b** Hyphae and different types of conidia. **c** Numerous globose to sub-globose conidia. **d**, **e** Catenate conidia.

f Lenticular conidium. **g** Pyriform conidium. **h**, **i** Clavate conidia. **j**, **k** Obclavate conidia with protuberant hila. Scale bars: **a–k** = 20 μ m

Gilbertiodendron dewevrei forest, on bare sandy soil, 16 May 2016, 1644/, Buyck 16.032 (PC 0124999); id., 1647/Buyck 16.063 (PC 0125002), 18 May 2016, 1655/Buyck 16.080 (PC 0125003); id., 1660/Buyck 16.087 (PC0125001); id., 1662/Buyck 16.091 (PC0125004); id., 19 May 2016, 1664/Buyck 16.096 (PC0125000); id., 1665/Buyck 16.097 (PC0125007); id., 26 May 2016, 1679/Buyck 16.127 (PC0125005); id., 24 May 2016, Buyck 16.114 (PC0125006).

Notes: This species, which was first described as a *Hygrophorus* (Beeli 1928), seems locally quite common in the *Gilbertiodendron dewevrei* rain forest. The original description was based on a watercolor sketching a single, very

juvenile fruiting body. The latter, therefore, is hardly representative for what this species might look like when fully mature, particularly when considering the impressive variability of the general field habit repeatedly reported already for other chanterelles (Buyck et al. 2016b, 2016c; Das et al. 2018b; Olariaga et al. 2015). Moreover, the original description was very succinct, both for macro- and microscopic features, and sketches a species characterized by a convex, irregularly lobed and dark violet young cap sitting on top of an ochraceous yellow, short and fleshy stipe and having a similarly colored, strongly veined-anastomosing hymenophore.

Yet, the feature that has most frequently been emphasized as characteristic for this species (Eyssartier 2001;

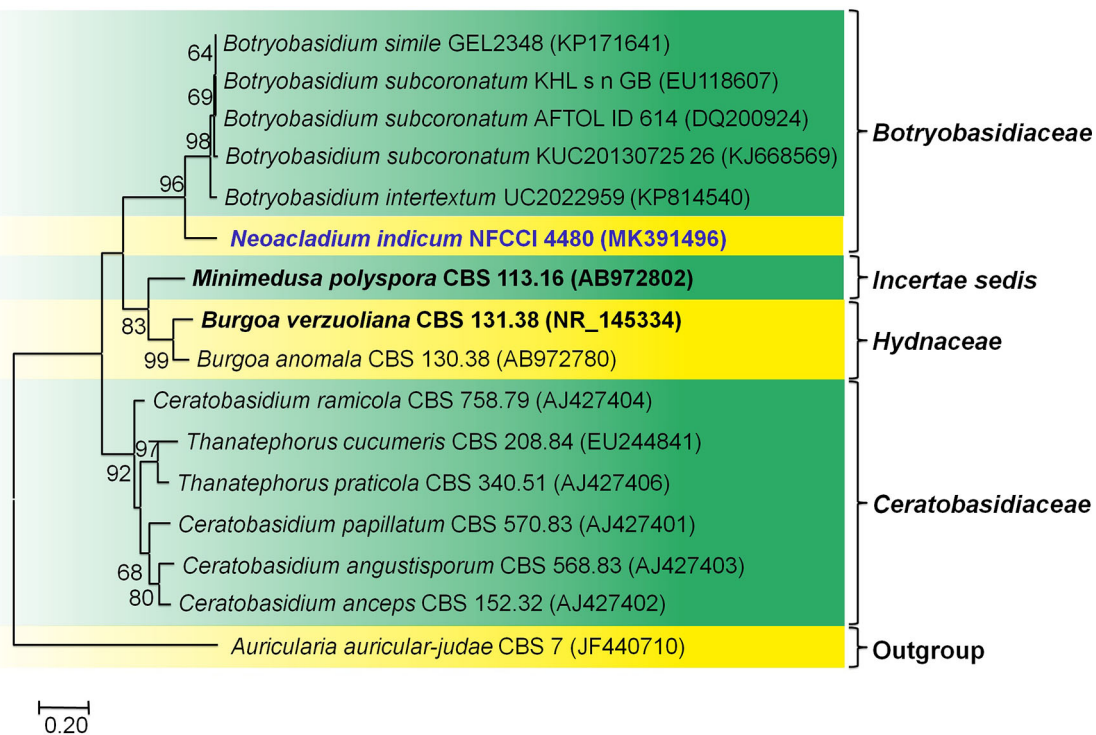


Fig. 142 Molecular phylogenetic analysis of ITS gene region of *Neoacladium indicum* (AMH 10054, **holotype**) by Maximum likelihood method. Sixteen strains are included in the sequence analyses which comprise 668 positions after alignment. *Auricularia auricular-judae* CBS 7 (JF440710) (Auriculariaceae, Auriculariales) is used as the outgroup taxon. Bootstrap values for maximum likelihood (ML) greater than 50 are placed along the branches, respectively. The

evolutionary history was inferred by using the Maximum likelihood method based on the Jukes-Cantor model (Jukes and Cantor 1969). The tree with the highest log likelihood (− 4900.5990) is shown. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

Buyck et al. 2012; De Kesel et al. 2016) is the mention - in the original description - of the unusual pinkish reddening of its context when exposed, as opposed to the yellowing context of most other Central African chanterelles with similar colors. As already previously discussed (Buyck et al. 2012), we think that this pinkish red context is probably a secondary and perhaps unimportant or even ill-interpreted character. Very similar examples were recently discussed for two North American species (Buyck et al. 2016b), including *C. septentrionalis* A.H.Sm., for which the type description equally mentions a characteristic pinkish lilac tinge in the context.

Fortunately, however, the microscopic features of *C. goossensiae* allow to distinguish it rather easily from other tropical African chanterelles as it offers the unique combination of comparatively small, ellipsoid spores and a pileipellis composed of thin-walled, clamped hyphal extremities terminating frequently in rather short but quite wide (11–13 µm diam.), obtusely rounded terminal cells (Heinemann 1958; Buyck et al. 2012) as here indeed illustrated again for the epitype (Fig. 147c). The spores of the holotype are clearly smaller than mentioned in the original description, viz. 5.5–6.72–8 × 3–3.97–5 µm,

Q = 1.37–1.71– 2.0 (see Eyssartier (2001)). The small spore size is here confirmed by our collections and is a useful feature to distinguish this species from *C. cyanoxanthus* (see Buyck et al. (2012)).

During a recent field trip in the Central African rain forest, not so far from where this species was originally described, Buyck collected many specimens sharing identical microscopic features with the holotype of *C. goossensiae*. One of these included a juvenile specimen that corresponded exactly to the published watercolor of the holotype (see Fig. 145a). As a result, we have no doubt about the correctness of our identification as *C. goossensiae* and we can finally epitypify this enigmatic species and assess its phylogenetic affinities and morphological variability using molecular sequencing.

The epitype description is based on the epitype only, but we have obtained (near-) identical sequences from all of our collections, (seven sequences have been used to represent the species in our phylogenetic analysis, Fig. 146). These sequences confirm the impressive field variability of this species, both in size and general color. Variations in size concern not only the stipe, which can exceptionally be more slender and up to 6 cm long, but also the pileus which

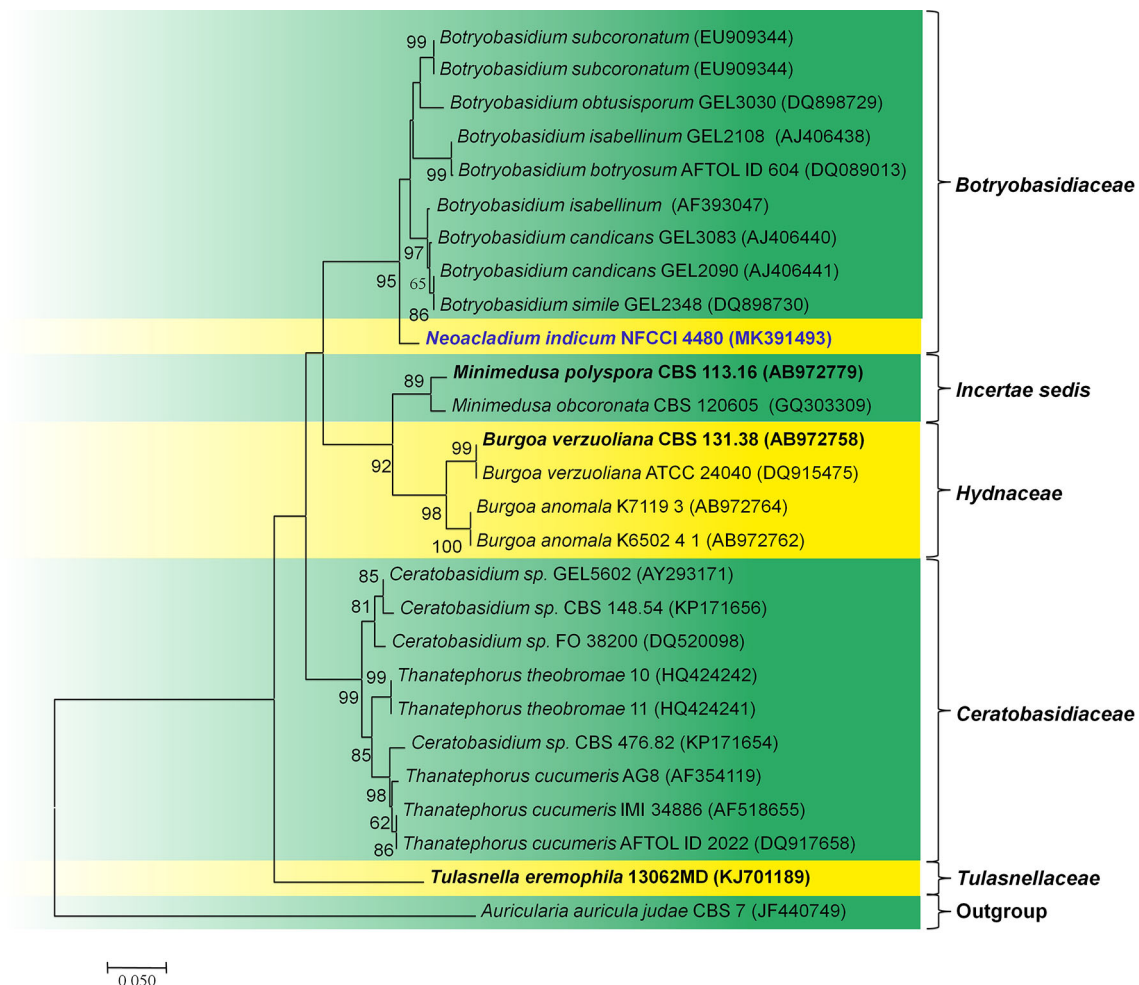


Fig. 143 Molecular Phylogenetic analysis of LSU of *Neoacladium indicum* (AMH 10054, **holotype**) by Maximum likelihood method. Twenty seven strains are included in the sequence analyses which comprise 2176 positions after alignment. *Auricularia auricular-judae* CBS 7 (JF440710) (Auriculariaceae, Auriculariales) is used as the outgroup taxon. Bootstrap values for maximum likelihood (ML) greater than 50 are placed along the branches respectively. The

evolutionary history was inferred by using the Maximum likelihood method based on the Kimura 2-parameter model (Kimura 1980). The tree with the highest log likelihood (−3161.4740) is shown. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). The ex-type strains are in bold and black. The newly generated sequence is indicated in bold and blue

reached 15 cm diam. in one collection). Moreover, *C. goossensiae* is another example of a species that changes drastically in general appearance between very young and more adult stages, exactly as for the closely related and recently neotypified African *C. miniatescens* (Buyck et al. 2016a). Very young stages of the latter species are entirely velutinous and dark wine red, while the adult stages develop into nearly smooth, bright yellow basidiomata (for illustrations, see Buyck et al. (2016a)). This is exactly what happens in *C. goossensiae* where very young stages are dark violet and tomentose, but then tend to become smooth and much paler with age, usually turning brownish to yellow or even pale cream in one collection. The explanation of this metamorphosis lies in both cases with the dense fibrillose to tomentose layer that entirely covers the young cap of both species. This surface layer is of a very

different color compared to the color of the underlying cap surface which will be gradually exposed as it expands. Secondly, depending on the intensity of the yellowing of the context (in which we could not detect any pinkish tinges), the overall color of the mature pileus varies greatly, from pale cream over yellow to reddish brown.

For somebody acquainted with European chanterelles, some specimens of the African *C. goossensiae* are reminiscent of *C. amethysteus* in the field because of a similar, robust stature and identical, violet-purplish tinges on the pileus surface (see Olariaga et al. (2016)). Notwithstanding the fact that both species share the omnipresence of clamp connections in their tissues, they belong in different subgenera (Fig. 146). Indeed, *C. goossensiae* appears to belong in the exclusively African subg. *Pseudocantharellus*. The species is strongly reminiscent of *C. miniatescens*,

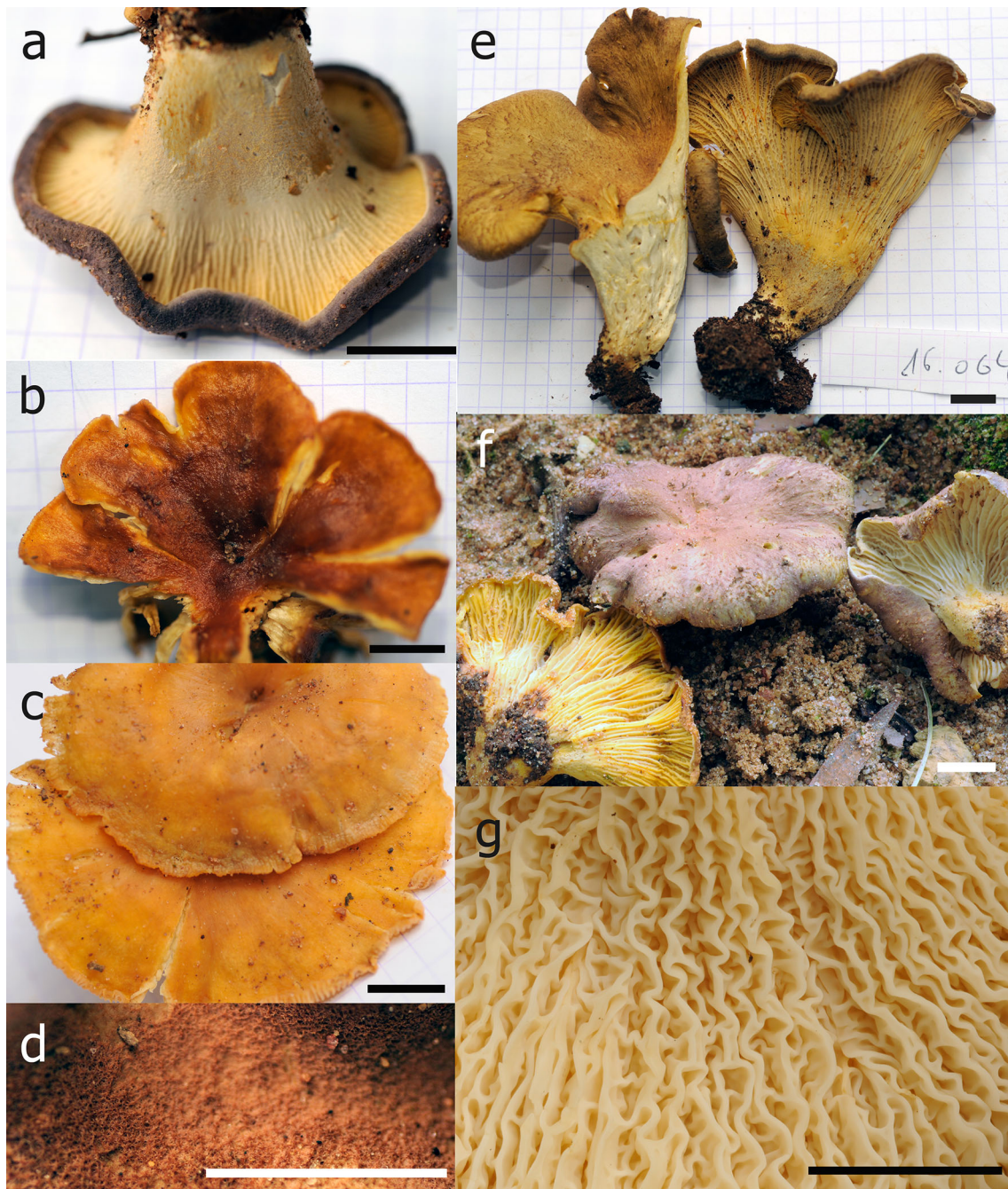


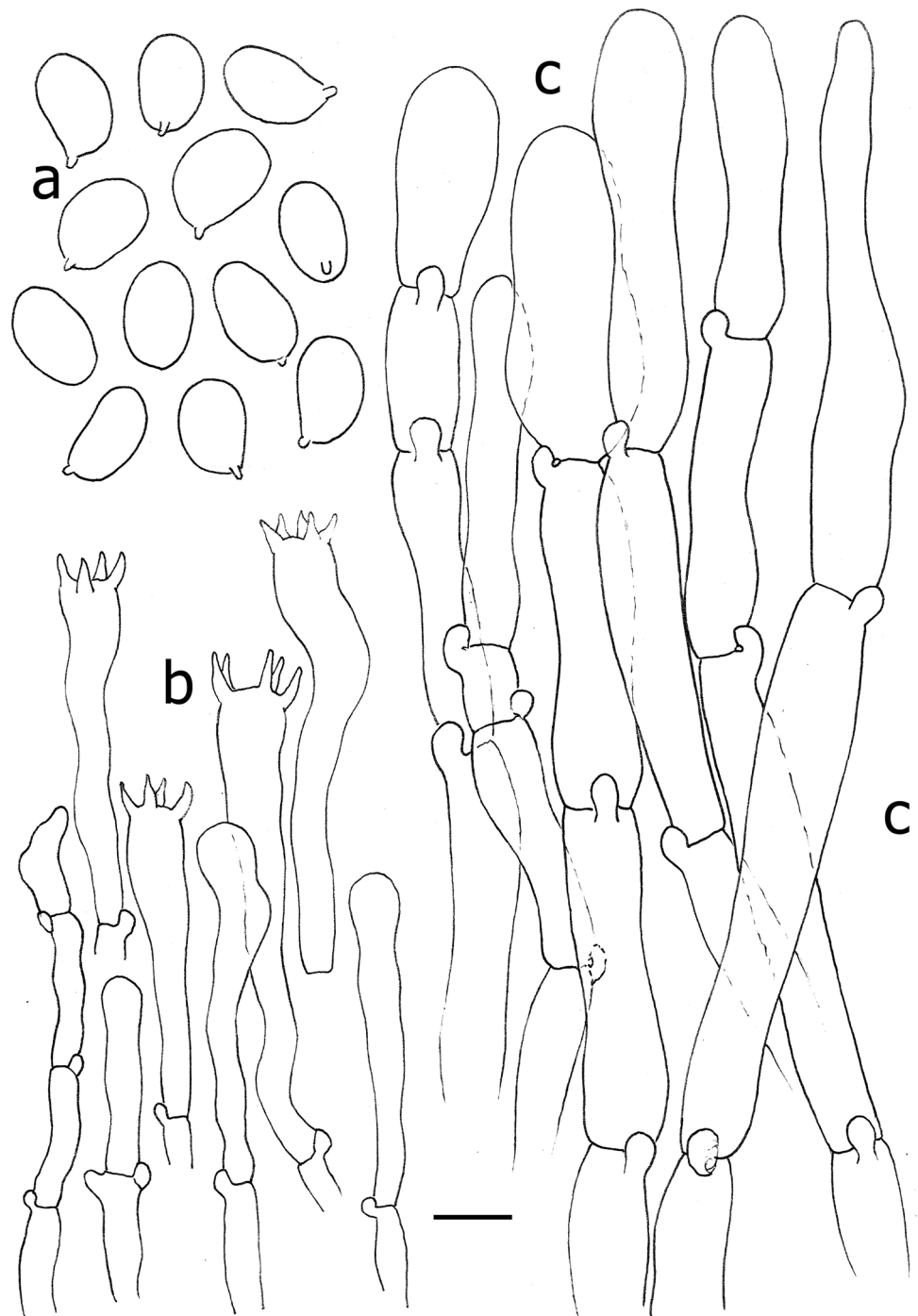
Fig. 144 *Cantharellus goossensiae*. **a** Young specimen (Buyck 16.087) showing the typical dark violet pileus and short, fleshy, yellowish stipe as illustrated (Heinemann 1959) for the **holotype**. **b** Mature rusty brown discolored form (Buyck 16.080). **c** Mature yellow discolored form (Buyck 16.096). **d** Detail of the hairy pileus

covering in young specimens (Buyck 16.087). **e** Epitype (Buyck 16.064). **f** typical, amethysteus-like form (Buyck 10.063). **g** detail of a mature specimen (Buyck 16.127) with a strongly veined hymenophore. Photos B. Buyck. Scale bars: **a–g** = 1 cm

in particular because both share a strongly veined-anastomosing hymenophore that is off-white when young. However, *C. goossensiae* forms much more robust, fleshy fruiting bodies that lack the long and slender stipe and the very thin pileus typical of the latter species. Fully grown specimens of *C. goossensiae* are also more variable in color

compared to *C. miniatescens* as the latter never develops the brown to olive tinges observed in several collections of the former (see Fig. 144b, c, e). Some collections of *C. goossensiae* developed a typical orange tinge in its upper part of the stipe, something that appeared to be a good feature for the correct identification of specimens that lost

Fig. 145 *Cantharellus goossensiae* (epitype). Microscopic features. **a** Spores. **b** Basidia and basidiola. **c** Hyphal extremities of the pileus surface. Drawings B. Buyck. Scale bar = 10 μ m, but only 5 μ m for spores



their violet pileus color. In addition, *C. goossensiae* generally lacks the dispersed remains of the red fibrillose tomentum that are visible near the cap centre or near the very cap margin of mature or older *C. miniatescens* (see for illustrations Buyck et al. (2016a)). The latter species also has narrower spores and more slender hyphal extremities composed of more elongated cells at the pileus surface.

Cantharellus brunneopallidus Buyck, Randrianjohany & V. Hofst., *sp. nov.*

Mycobank number: MB829484; *Facesoffungi number*: FoF05997; Figs. 147, 148a–c

Etymology: Referring to the brownish color when young, fading to yellowish cream, isabelline or dirty whitish with age.

Holotype: MADAGASCAR. Tampolo, S 17.28724 – E49.40868, growing on sandy soil between grass and

amongst dead leaves under *Intsia*, 4 July 2011, Buyck, Hofstetter & Randrianjohany leg., Buyck 1053/BB11.105 (PC0085584, **holotype**).

Fruiting bodies rather small, less than 30 mm high, in groups of several to many dispersed to aggregated individuals. *Pileus* less than 30 mm diam., regular in outline, more rarely lobed or wavy-undulate, first convex, then becoming progressively more depressed in the centre, finally often infundibuliform; margin strongly inrolled, plane or slightly wavy, the marginal zone of the cap remaining often downturned in age; surface finely fibrillose, slimy when wet, when young often unevenly coloured in patches of yellowish brown to reddish brown or even dark brown (5CD6–7, 7DEF6–8), later sometimes locally retaining these colors, elsewhere gradually paler, discolouring to pale cream or isabelline between pale brownish squamae. *Hymenophore* decurrent, rather low and mostly ca 1 mm high, quite abruptly delimited from the sterile stipe surface, composed of crowded (25–35/cm), frequently forking and thin gill folds, whitish and with concolorous, even edges, without anastomosing-veined pattern in between gills or on gill sides. *Stipe* shorter than the cap diam., 9–15(19) × 3–5(7) mm, subcylindrical or slightly narrowing downward, slimy when wet, particularly in lower half also covered with similar, fibrillose-erected to appressed, pale brownish squamulae as the pileus surface, off-white, but soon yellowing with age below, sometimes brownish in lower half when strongly squamulose, not hollowing. *Context* white, rather firm, relatively thick (2–3 mm just outside the pileus centre), strongly bruising chrome yellow when handled on the whole surface of the fruiting bodies or in lower tissues from insect damage, but not entirely becoming yellow. *Taste* mild. *Smell* weak. *Spore print* not obtained.

Spores ellipsoid, (6.2)6.4–**6.68**–6.9(7.0) × (3.9)4.2–**4.47**–4.8(5.0) μm , $Q = (1.36)1.41$ –**1.50**–1.59(1.70), smooth, hyaline. *Basidia* small and short, mostly 35–42 × 6–7 μm , usually six-spored. *Cystidia* none. *Subhymenium* more pseudoparenchymatic than filamentous. *Pileipellis* composed of thin-walled to refringent, intertwining, septate and mostly slender generative hyphae, (4)6–9(12) μm diam., with many free endings and occasional ramifications; terminal cell mostly (30)40–65 μm long, rounded obtuse or slightly tapering at the apex, thin-walled to refringent, but very few clearly thick-walled, mostly quite regular in outline, sometimes locally undulating or more abruptly inflated. *Clamp connections* absent from all tissues.

Additional material examined: MADAGASCAR. Tam-polo, S 17.28724 – E49.40868, growing on sandy soil between grass and amongst dead leaves under *Intsia*, 6 July 2018, 1054/Buyck 11.116 (PC0085585, **paratypus**).

Notes: The description is based on the holotype. The paratype has similar features, including a near identical spore size of (6.0)6.3–**6.66**–7.0(7.3) × (3.9)4.1–**4.49**–4.7(4.8) μm , $Q = (1.35)1.42$ –**1.52**–1.63(1.70). This species is strongly reminiscent of the tropical African *C. densifolius* (sensu lato) because of the equally crowded gill folds and overall color, and it is thus not surprising that it was originally mistaken for that species when we collected it in the field. Nevertheless, the very strong yellowing when bruised is more typical of the Malagasy *C. albidolutescens* Buyck, Eyssart. & V. Hofst., but the latter has less crowded gill folds (see Buyck et al. (2015)). Our phylogeny now shows that it is clearly an independent species. As we never have found *C. brunneopallidus* in other habitats or with other host trees during the many years of collecting in Madagascar, it is possible that it might be a strict associate on the island of the ectomycorrhizal tree genus *Intsia* Thouars (Fabaceae), a very small tree genus with an indopacific distribution (Asamoah et al. 2012), but more sites with *Intsia* need to be studied in Madagascar to confirm this. *Intsia bijuga* (Colebr.) Kuntze, the host species on our collecting site, is known to have survived in a few remaining remnants of low elevation humid forests along Madagascar's east coast. This tree was always heavily exploited for its high quality wood. It is listed for many years already on the IUCN Red List of Threatened Species and is believed to risk worldwide extinction within the next 20 years without appropriate action to stop illegal logging (see *Intsia bijuga* page on Wikipedia for more details).

Cantharellus griseotinctus Buyck, Randrianjohany & V. Hofst. **sp. nov.**

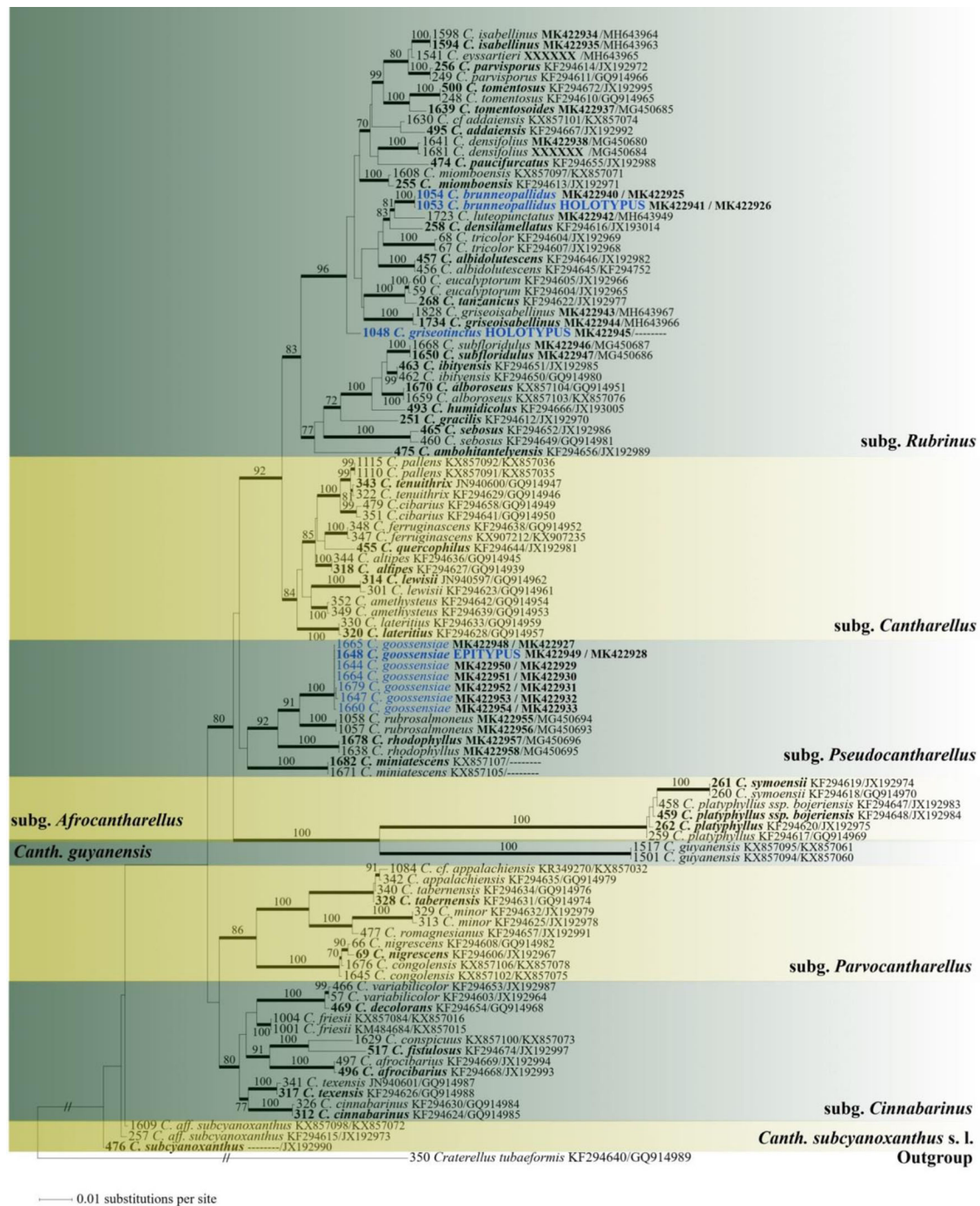
Mycobank number: MB829483; *Facesoffungi number*: FoF05998; Figs. 148d–f, 149

Etymology: griseo- and -tinctus, referring to the greyish tinges of the pileus surface.

Holotype: PC0085579

Diagnosis: differs from *C. albolutescens* in the less crowded and better developed, less forked gill folds with distinct rib-like anastomoses on the gill sides, as well as in the much shorter terminal cells of the hyphal extremities in the pileipellis.

Fruiting bodies medium-sized, growing single or in small groups. *Pileus* relatively fleshy and firm, up to 45 mm diam., first convex, than plano-convex or becoming slightly depressed in the centre, surface a pale brown to brownish gray (6–7DE4–7) or pale gray to grayish cream toward the margin, from centre to margin gradually more areolate-fissured, pileus centre distinctly warty-scurfy, fading to hardly visible squamae to almost smooth toward the margin, rarely developing strongly strigose-squamose rims in concentric arrangement. *Hymenophore* decurrent, composed of well-developed, relatively thick gill folds, up



◀**Fig. 146** Most likely phylogram ($-\ln = 12014.27555$) inferred from combined analyses of nucLSU and TEF1- α for 106 cantharelloid taxa, using *Craterellus tubaeformis* as the outgroup taxon. The combined gene sequence analyses comprise 1840 characters after exclusion of ambiguously aligned regions (1211 characters for nucLSU, 629 characters for TEF1- α). Phylogenetic analyses were all conducted in PhyML (Guindon and Gascuel, 2003) under GTR evolutionary model with the number of substitutions categories, the proportion of invariable sites and the gamma shape parameters estimated during the searches. No significant conflict was detected between nucLSU and TEF1- α based on comparison of bootstrap values recovered from bootstrap analyses of individual gene (200 bootstrap replicates with conflict assumed when two different relationships, one being monophyletic and the other being non-monophyletic, for the same set of taxa were both supported with significant bootstrap values equal or greater than 70%; Mason-Gamer and Kellog 1996). Searches for the most likely tree included three independent runs. Model parameters for the most likely tree were as follows: proportion of invariable sites = 0.412; gamma shape parameter = 0.409; A = 0.26337, C = 0.22919, G = 0.27754, T = 0.22990 for base frequencies; A–C = 1.09799, A–G = 5.55043, A–T = 1.56560, C–G = 1.10930, C–T = 10.70297, G–T = 1.00000 for substitution rates. The newly generated sequences are indicated in bold and the taxa discussed in bold blue. GenBank accessions for nucLSU/TEF1- α follow taxon names. Branches that received significant support (equal or greater than 70%) based on 500 BS replicates are in bold and BS values indicated along the branches

to 4 mm high, unequal and shorter gills of variable length present, radially undulate –wavy due to rib-like veins running down the gill sides, off-white to pale cream with even smooth edges, furcations frequent only near the pileus margin. *Stipe* stout, shorter than the pileus diam., less than 20 mm long, 4–7 mm diam., surface white, minutely warty – fibrillose, not hollowing. *Context* relatively firm, white, but near the surface strongly bruising yellow when handled. *Taste* mild. *Smell* weak. *Spore print* not obtained.

Spores rather small, $(6.0)6.3\text{--}6.64\text{--}7.0(7.5) \times (3.7)4.0\text{--}4.43\text{--}4.8(5.2) \mu\text{m}$, $Q = (1.30)1.39\text{--}1.51\text{--}1.62(1.72)$, ellipsoid, smooth, with a small apiculus. *Basidia* clavulate, small to almost medium-sized, $35\text{--}50(60) \times 7\text{--}8 \mu\text{m}$, mostly six-spored; sterigmata robust. *Cystidia* none. *Subhymenium* more pseudoparenchymatic than filamentous. *Pileipellis* composed of ramifying, intermingled, strongly thick-walled hyphal extremities, that are densely septate (with > 10 consecutive thick-walled cells) but easily fragmenting when making preparations, sparsely branching, measuring mostly $(4)6\text{--}8(10) \mu\text{m}$ diam.; cells becoming gradually shorter toward the apex, with the terminal cell rarely longer than $30 \mu\text{m}$, tapering and more or less conical, or also sometimes more ellipsoid and inflated. *Clamp connections* absent from all tissues.

Materials examined: MADAGASCAR. East Coast, Analalava, 7 km West of Mahovelona (Foulpointe), $17^{\circ}42\text{S}\text{--}49^{\circ}27\text{E}$, in low altitude humid forest, in small

groups among herbs on muddy, stony, steep slope, Buyck 1048/BB 11.054 (PC0085579, **holotype** !).

Notes: This species strongly resembles *C. albido-lutescens*, (see Buyck et al. (2015)) but it differs from it because of the less crowded and better developed, less forked gill folds with distinct rib-like anastomoses on the gill sides. The more spaced gills also immediately exclude *C. densifolius* and look-alikes as a possible identification. It was collected on the outer limit of one of the few remnants of low altitude humid forests on the east coast. This forest remnant near Analalava, not far from Foulpointe, is known for its high biodiversity and conservation value, which is well documented in particular for the many rare palm species that are growing there (Rakotoarinivo et al. 2010).

Hymenochaetales Oberw.

Notes: The order was set up by Frey et al. (1977), based on Hymenochaetaceae Donk, the most species in the order have xanthochroic reaction. But recent molecular analyses showed that more families without xanthochroic reaction were included in the order (Miettinen and Larsson 2011).

Hymenochaetaceae Donk, Bull. bot. Gdns Buitenz.

Notes: The family Hymenochaetaceae was introduced by Donk (1948), based on the type genus *Hymenochaete* Lév. It is the most important family in Hymenochaetales, because it has the major species in the order, many species in the family are medicinal fungi and some are forest pathogens (Dai et al. 2007, 2009). The xanthochroic reaction is the most important characteristic of the family. Currently around 20 genera and 500 species are accepted in the family (Larsen and Cobb-Pouille 1990; Léger 1998; Parmasto 2005; Kirk et al. 2008; Dai 2010; Cui et al. 2011; He and Dai 2012; Ji et al. 2017, 2018; Zhou et al. 2016a, b, c).

Fomitiporia Murrill, N. Amer. Fl.

Notes: *Fomitiporia* was included in *Phellinus* Quél. sensu lato previously, but is characterized by subglobose to globose, hyaline, thick-walled, strongly dextrinoid and cyanophilous basidiospores, and accepted as an independent genus (Fasson & Niemelä 1984; Dai 2010; Amalfi & Decock 2013; Chen & Cui 2017).

Fomitiporia carpinea X.H. Ji, X.M. Tian & Y.C. Dai, *sp. nov.*

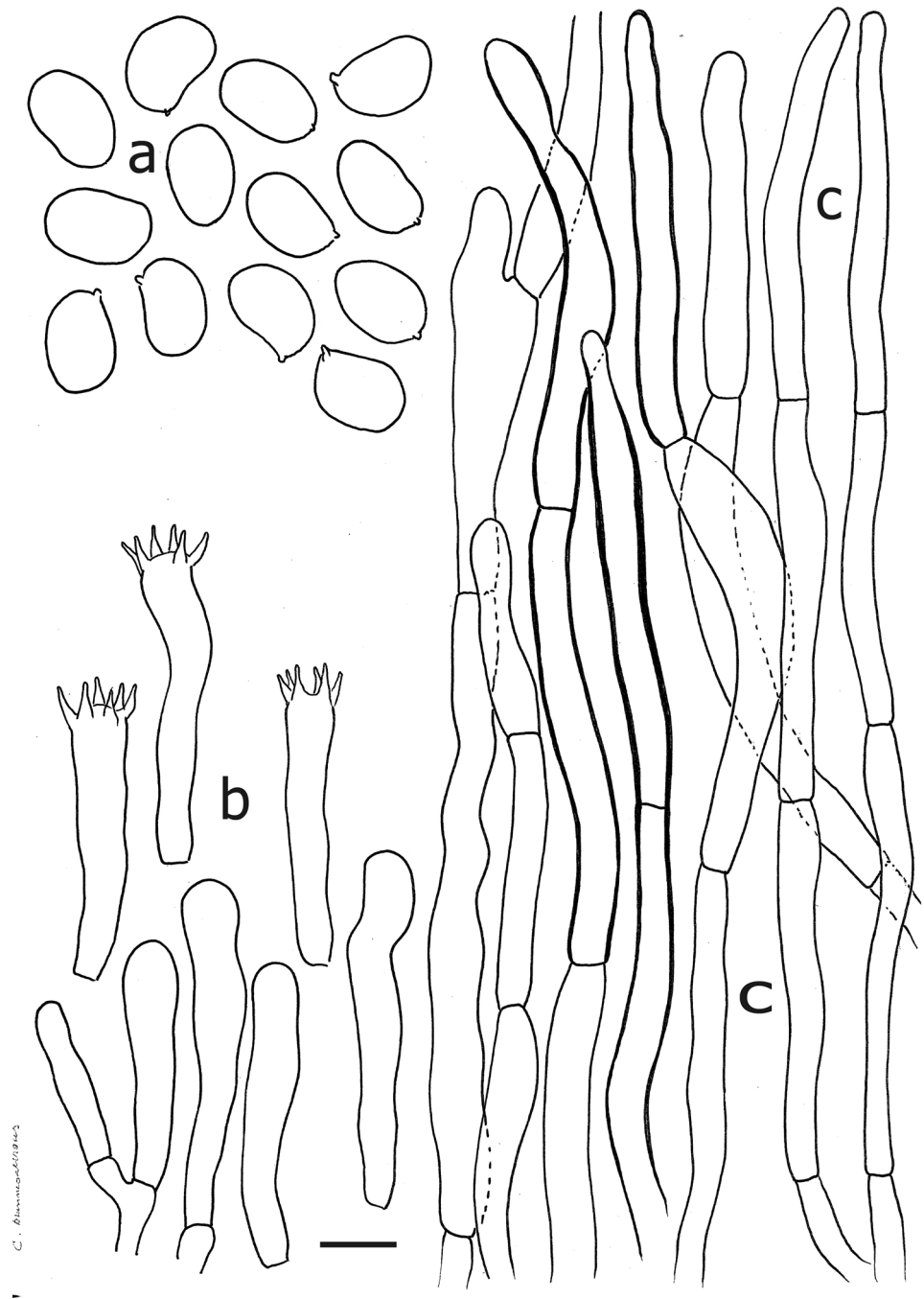
Index Fungorum number: IF555462; *Facesoffungi number*: FoF04971; Fig. 150

Etymology: Referring to the species growing on *Carpinus*.

Holotype: BJFC 025552.

Basidiocarp perennial, resupinate, inseparable, without odour or taste when fresh, consistency woody hard, light in weight when dry, up to 10 cm long, 4 cm wide and 7 mm thick at centre, becoming more or less cushion-shaped with

Fig. 147 *Cantharellus brunneopallidus* (PC0085584, **holotype**). Microscopic features. **a** Spores. **b** basidia and basidiola. **c** Hyphal extremities at pileus surface. Drawings B. Buyck. Scale bar = 10 μ m, but only 5 for spores



age; margin receding, brown, up to 2 mm wide. Pore surface dark brown to bay when fresh, becoming yellowish brown to umber up on drying, distinctly shining; pores circular, 4–6 per mm; dissepiments thin and entire. Subiculum brown, up to 2 mm thick. Tubes concolorous with pore surface, stratified, up to 5 mm long. Hyphal system dimitic in all parts; generative hyphae simple septate, skeletal hyphae negative in Melzer's reagent, acyanophilous in Cotton Blue; tissue darkening but otherwise unchanged in KOH. Subicular generative hyphae

infrequent, hyaline to pale yellowish brown, thin- to slightly thick-walled, occasionally branched, simple septate, 3–4 μ m in diam.; skeletal hyphae yellowish brown, thick-walled, with a wide lumen, unbranched, regularly arranged, 3–5 μ m in diam. Tramal generative hyphae hyaline to pale yellow brown, thin- to slightly thick-walled, occasionally branched, frequently simple septate, 2.5–3.5 μ m in diam.; skeletal hyphae yellowish brown, thick-walled, with a narrow lumen, rarely branched, interwoven, 3–4.5 μ m in diam. Hymenial setae absent;

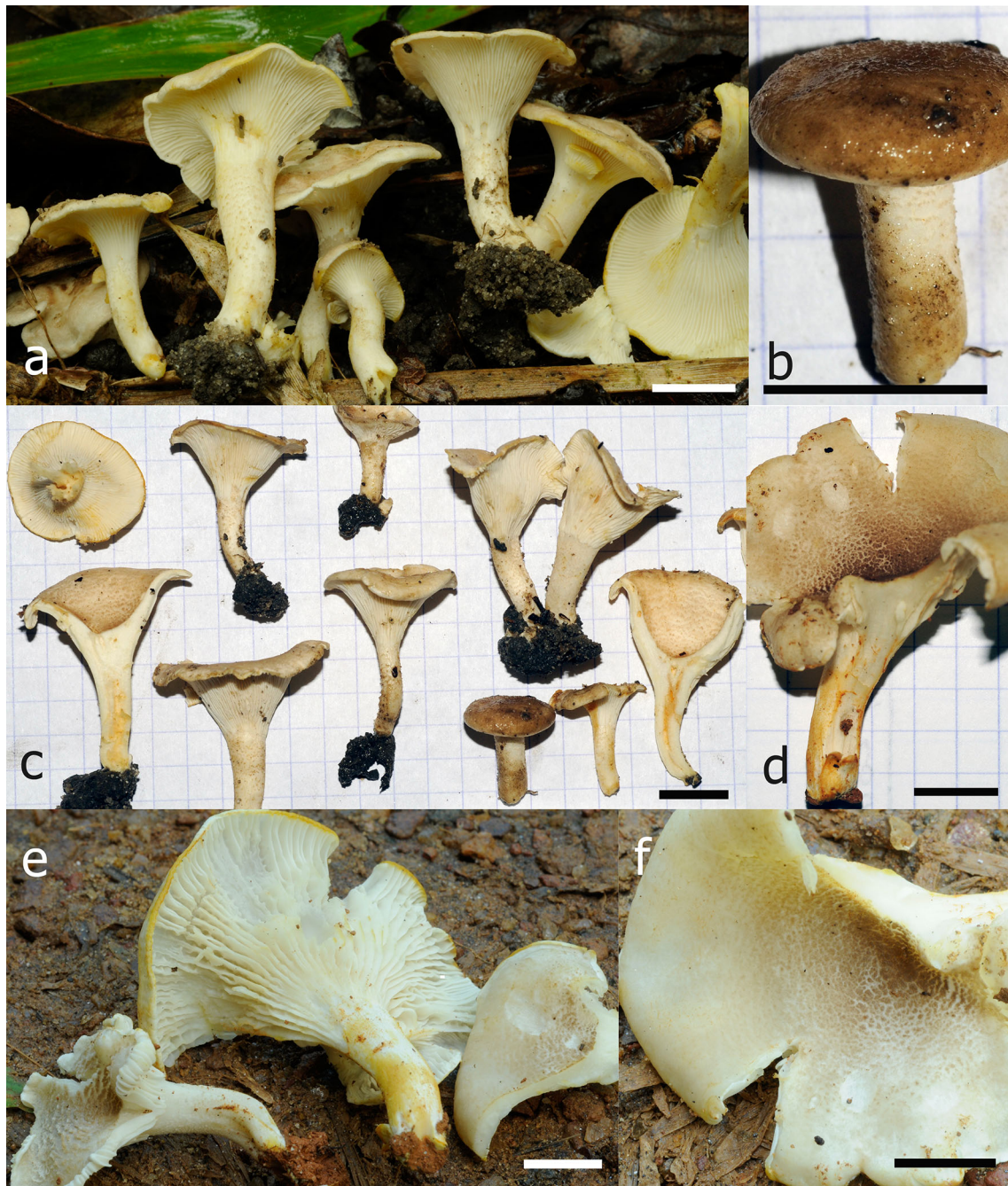


Fig. 148 *Cantharellus brunneopallidus* (PC0085584, **holotype**). **a** Freshly collected specimens. **b** Young specimen showing the dark pileus. **c** holotype overview. **d–f** *Cantharellus griseotinctus*

(PC0085579, **holotype**). **d** showing color change after one day with respect to the freshly collected specimens depicted in e–f (photos B. Buyck) Scale bars: 1 cm

cystidioles present, ventricose, hyaline, thin-walled, $10\text{--}18 \times 3\text{--}5 \mu\text{m}$; basidia short clavate to capitate, with a basal simple septum and four sterigmata, $12\text{--}16 \times 8.5\text{--}11 \mu\text{m}$; basidioles in shape similar to basidia, but slightly smaller, big irregular or rhombic crystals present among trama. Basidiospores globose, hyaline, thick-walled, smooth, dextrinoid in Melzer's reagent, cyanophilous in

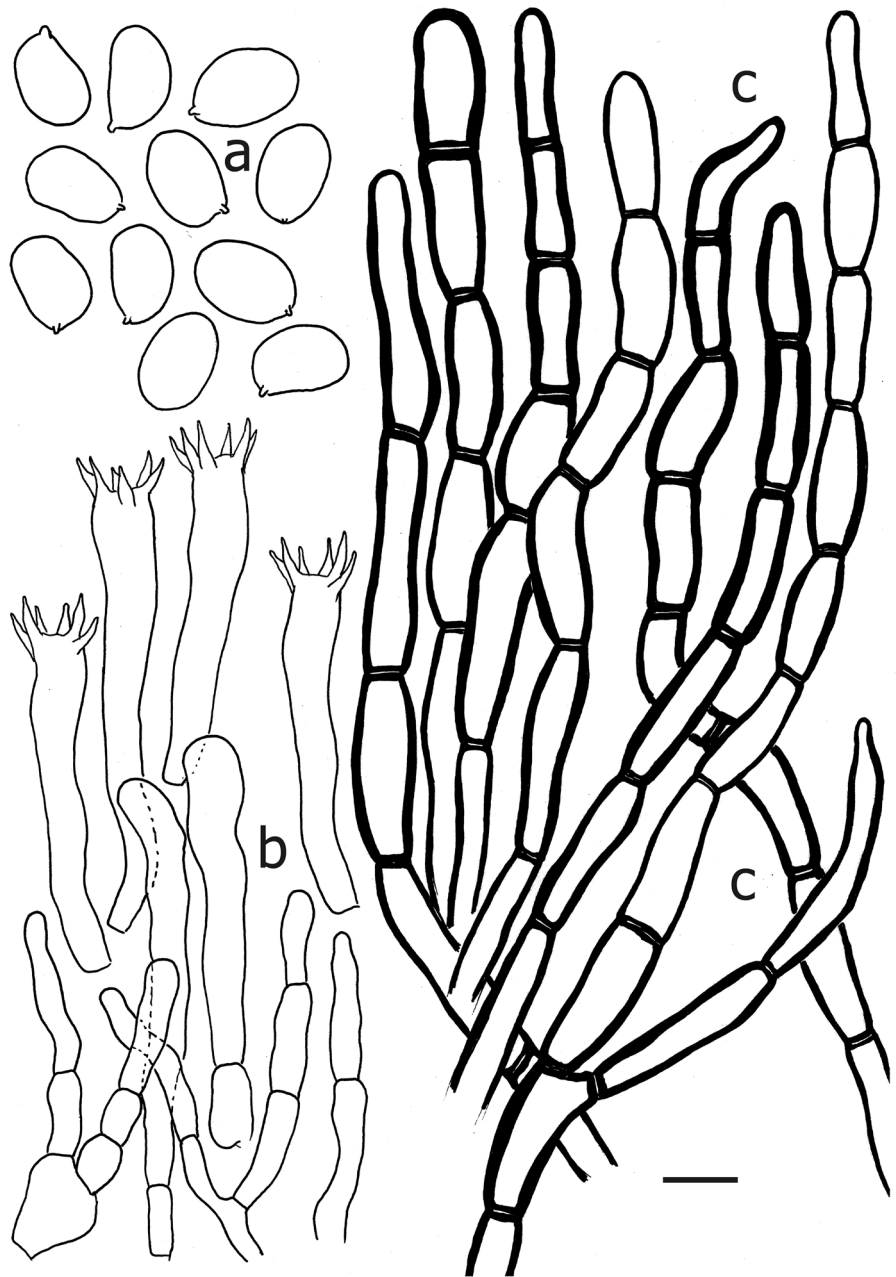
Cotton Blue, $(6.1\text{--})6.5\text{--}7.8(\text{--}8) \times (5.5\text{--})6\text{--}7.5(\text{--}7.8) \mu\text{m}$, $L = 7.06 \mu\text{m}$, $W = 6.7 \mu\text{m}$, $Q = 1.05$ ($n = 30/1$).

Material examined: CHINA, Gansu Province, Pingliang, Kongtongshan Forest Park, on stump of *Carpinus*, 2 Sept 2017, Dai 18023 (BJFC 025552, **holotype**).

GenBank numbers: ITS: MH930812, LSU: MH930810.

Notes: *Fomitiporia carpinea* is similar to *F. punctata* (P. Karst.) Murrill in sharing perennial, resupinate, cushion-

Fig. 149 *Cantharellus griseotinctus* (PC0085579, holotype). Microscopic features. **a** Spores. **b** basidia and basidiola. **c** Hyphal extremities at pileus surface. Drawings B. Buyck. Scale bars = 10 μ m, but only 5 for spores



shaped basidiocarps, the approximately the same size basidiospores, and occurring in temperate forests (Dai 2010, 2012). However, the latter species has smaller pores (6–8 per mm), interwoven hyphae in subiculum, lacks cystidioles, while *F. carpinea* has bigger pore (4–6 per mm), hyphae regularly arranged in subiculum, the presence of cystidioles. Phylogenetically *F. carpinea* formed a distinct terminal lineage (Fig. 152), and is distant from *F. punctata*.

Fomitiporia lagerstroemiae X.H. Ji, X.M. Tian & Y.C. Dai, *sp. nov.*

Index Fungorum number: IF555461; *Facesoffungi* number: FoF04972; Fig. 151

Etymology: Referring to the species growing on *Lagerstroemiae*.

Holotype: BJFC 025858

Basidiocarp perennial, resupinate, inseparable, without odour or taste when fresh, consistency woody hard, light in weight when dry, up to 5 cm long, 3 cm wide and 8 mm

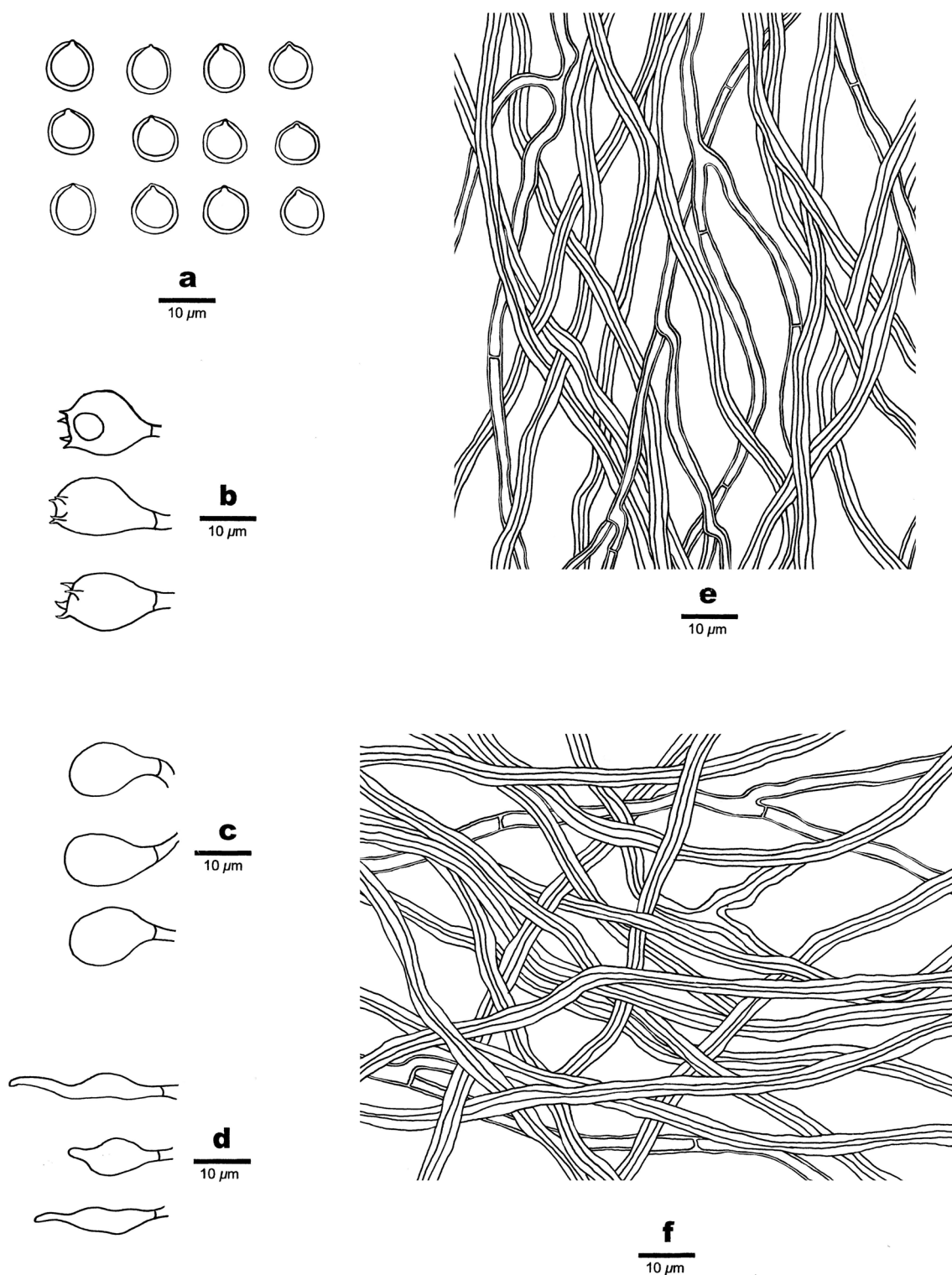
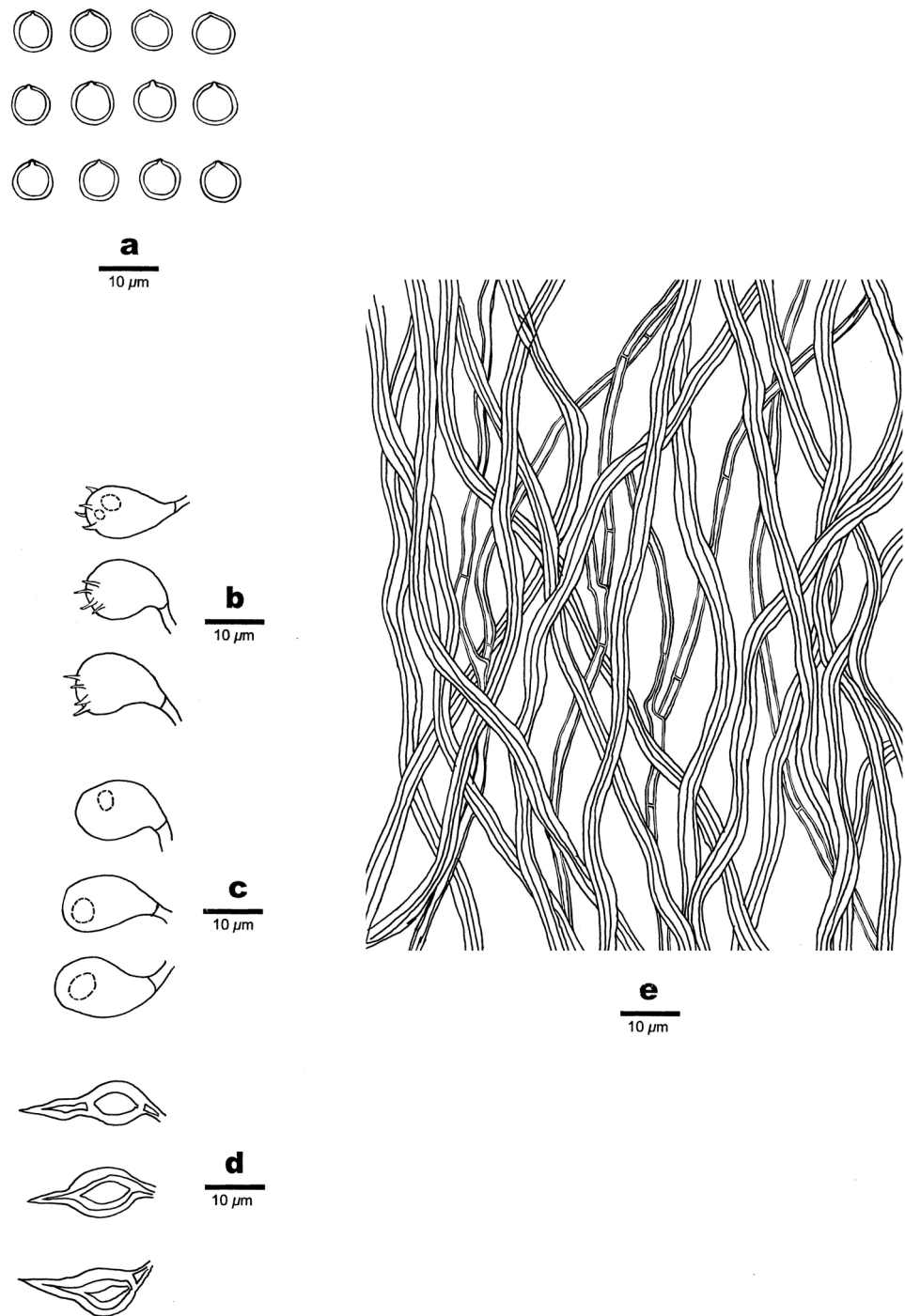


Fig. 150 Microscopic structures of *Fomitiporia carpineae* (BJFC 025552, **holotype**). **a** Basidiospores. **b** Basidia. **c** basidioles. **d** Cystidioles. **e** Hyphae from trama. **f** Hyphae from subiculum

thick at centre, becoming more or less cushion-shaped with age; margin receding, dark brown, up to 2 mm wide. Pore surface snuff brown when dry, distinctly shining; pores

circular, 7–9 per mm; dissepiments thin and entire. Subiculum brown, very narrow to almost lacking. Tubes concolorous with pore surface, stratified, up to 8 mm long.

Fig. 151 Microscopic structures of *Fomitiporia lagerstroemiae* (BJFC 025858, **holotype**). **a** Basidiospores. **b** Basidia. **c** Basidioles. **d** Hymenial setae. **e** Hyphae from subiculum



Hyphal system dimitic in all parts; generative hyphae simple septate, skeletal hyphae negative in Melzer's reagent, acyanophilous in Cotton Blue; tissue darkening but otherwise unchanged in KOH. *Subicular* generative hyphae infrequent, hyaline to pale yellowish brown, thin- to slightly thick-walled, occasionally branched, simple septate, 2.5–4 μm in diam.; skeletal hyphae yellowish brown, thick-walled, with a wide lumen, unbranched, loosely interwoven, 3–4.5 μm in diam. *Tramal* generative

hyphae hyaline to pale yellow brown, thin- to slightly thick-walled, occasionally branched, frequently simple septate, 2.5–3 μm in diam.; skeletal hyphae yellowish brown, thick-walled, with a narrow to medium size lumen, rarely branched, interwoven, 3–4 μm in diam. Hymenial setae frequent, ventricose, thick-walled, dark brown, 15–22 \times 5–7 μm ; cystidioles absent, basidia barrel-shaped, with a basal simple septum and four sterigmata, 9.5–11.5 \times 6.5–9 μm ; basidioles in shape similar to

basidia, but slightly smaller. Basidiospores subglobose, hyaline, thick-walled, smooth, dextrinoid in Melzer's reagent, cyanophilous in Cotton Blue, $(4.8\text{--}5\text{--}6(-6.2) \times (4\text{--}4.5\text{--}5.5(-6)) \mu\text{m}$, $L = 5.86 \mu\text{m}$, $W = 5.13 \mu\text{m}$, $Q = 1.14$ ($n = 30/1$).

Material examined: VIETNAM, Dong Nai Province, Dinh Quan District, Thac Mai Preservation Park, on stump of *Lagerstroemia*, 14 Oct 2017, Dai 18335 (BJFC 025858, **holotype**).

GenBank numbers: ITS: MH930812, LSU: MH930810.

Notes: *Fomitiporia lagerstroemiae* is similar to *Fomitiporia hainaniana* B.K. Cui & Hong Chen in sharing

perennial, resupinate, basidiocarps, the approximately the same size pores, the presence of hymenial setae, interwoven tramal hyphae and occurring in tropical forests (Chen and Cui 2017). However, *Fomitiporia hainaniana* has smaller basidiospores ($4\text{--}5 \times 3.8\text{--}4.4 \mu\text{m}$), and grows on angiosperm wood rather than *Lagerstroemia* (Chen and Cui 2017). The phylogenetic analysis of ITS and LSU sequence (Fig. 152) shows that *Fomitiporia lagerstroemiae* is closely related to *Fomitiporia bannaensis* Y.C. Dai, and both species has perennial, resupinate, basidiocarps, the approximately the same size pores and hymenial setae. However, *Fomitiporia bannaensis* has smaller

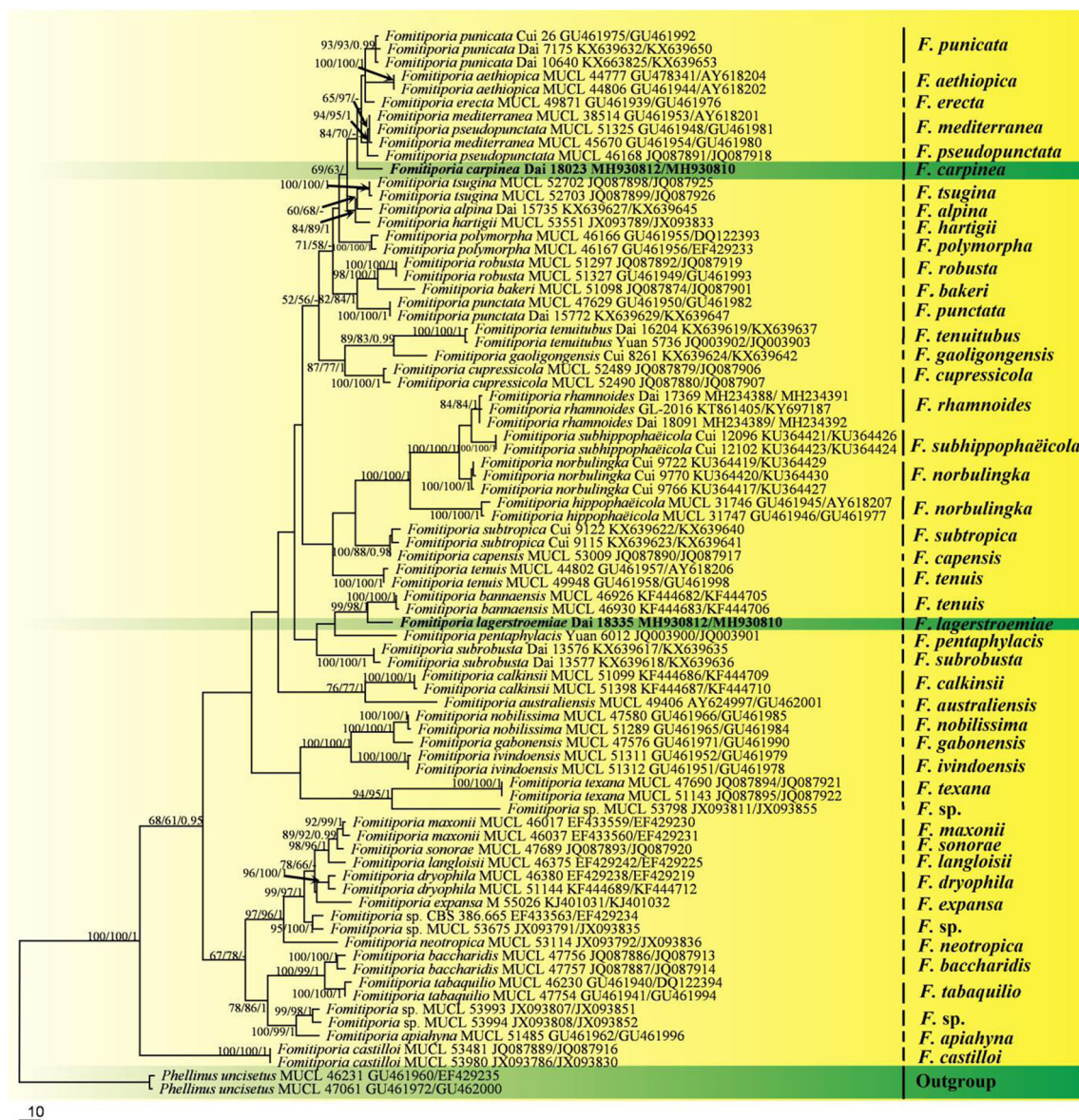


Fig. 152 Phylogenetic position of *Fomitiporia carpinea* (**holotype**) and *Fomitiporia lagerstroemiae* (**holotype**) inferred from the ITS and LSU sequences. Bootstrap support values for ML and MP greater than 50% and Bayesian posterior probabilities greater than 0.95 are given

near nodes respectively. The tree is rooted with *Phellinus uncisetus* (MUCL 46231) and *P. uncisetus* (MUCL 47061). The new isolates are in bold and black

basidiospores $(4.2\text{--}5.2 \times 3.8\text{--}4.9 \mu\text{m})$, $L = 4.68 \mu\text{m}$, $W = 4.24 \mu\text{m}$), the presence of cystidioles (Dai 2010).

Polyporales Gäum.

Notes: Polyporales is a large group of Agaricomycetes with about 1800 described species (Kirk et al. 2008; Justo et al. 2017). This order includes species with a wide variety of basidiomata (pileate, stipitate, resupinate or multiple flabelliform lobes) and hymenophore (poroid, hydroid, lamellate, merulioid or smooth) shapes (Binder et al. 2013; Hibbett et al. 2014). Most of the species are saprotrophic wood-decay fungi, while few are plant pathogens. Polyporales has been the focus of many phylogenetic studies which have confirmed it as a strongly supported monophyletic clade of Agaricomycetes (Binder et al. 2013; Hibbett et al. 2014; Justo et al. 2017).

Polyporaceae Fr. ex Corda

Notes: Polyporaceae (Polyporales) was proposed by Fries (1838) with *Polyporus* P. Micheli as the type genus. The family currently includes about 45 genera (Justo et al. 2017). Phylogenetic analyses have shown that Polyporaceae belongs to the “core polyporoid” within Polyporales (Binder et al. 2013). Species in the family have poroid, irregular or lamellate, occasionally corticioid hymenophore. The hyphal system is rarely monomitic, mostly dimitic or trimitic, and cystidia are generally lacking. The species are saprobes and cause white rot (Cannon and Kirk 2007; Justo et al. 2017).

Grammothele Berk. & M.A. Curtis

Notes: *Grammothele*, typified by *G. lineata* Berk. & M.A. Curtis (Berkeley and Curtis 1869), is a genus with about 22 species (www.indexfungorum.org), with thin and

strongly adherent basidiomata, and shallow pores (Ryvarden 2015). The hyphal system is dimitic to trimitic, with clamped generative hyphae, skeletal hyphae thick-walled to solid, hyaline, darkening with age, dextrinoid or not. Dendrohyphidia and others sterile elements are absent or present and the basidiospores are ellipsoid to cylindrical, thin-walled, smooth and non-amyloid. This tropical genus occurs on mono- and dicotyledons (Karasinsk 2015; Ryvarden 2015; Wu et al. 2016).

Grammothele aurantiaca A.M.S. Soares, *sp. nov.*

Index Fungorum number: IF555479; **Facesoffungi number:** FoF05974; Fig. 153

Etymology: aurantiacus L. = orange, referring to the colour of the basidiomata.

Holotype: MG 232015

Basidiomata annual, resupinate, strongly adnate, hard and brittle when dried, up to 8 cm long, 4.5 cm wide, 1 mm thick; pore surface salmon to orange (5C5), becoming dark orange with the age (5B8); margin narrow to almost lacking, rust orange (5C4). Pores shallow, almost invisible to the naked eye, round to angular, 6–8 per mm, dissepiments thin, tubes concolorous, up to 1 mm deep. Basidiospores scarce, subglobose, hyaline, thin-walled, with tiny or without apiculus, smooth, IKI-, 4–5 μm wide ($L = 4.66 \mu\text{m}$, $W = 4.33 \mu\text{m}$, $Q = 1.07$, $n = 10/2$). Basidia not seen. Hyphal system dimitic, generative hyphae thick-walled, up to 3 μm wide, without clamps, IKI-; skeletal hyphae thick-walled 4–5 μm , tightly interwoven, cherry red in KOH, IKI-. Dendrohyphidia absent. Cystidia and others sterile elements absents.

Material examined: BRAZIL, Amapá: Serra do Navio, Serra dos Veados, on dead wood, 00° 55' 39,96" N and 51°

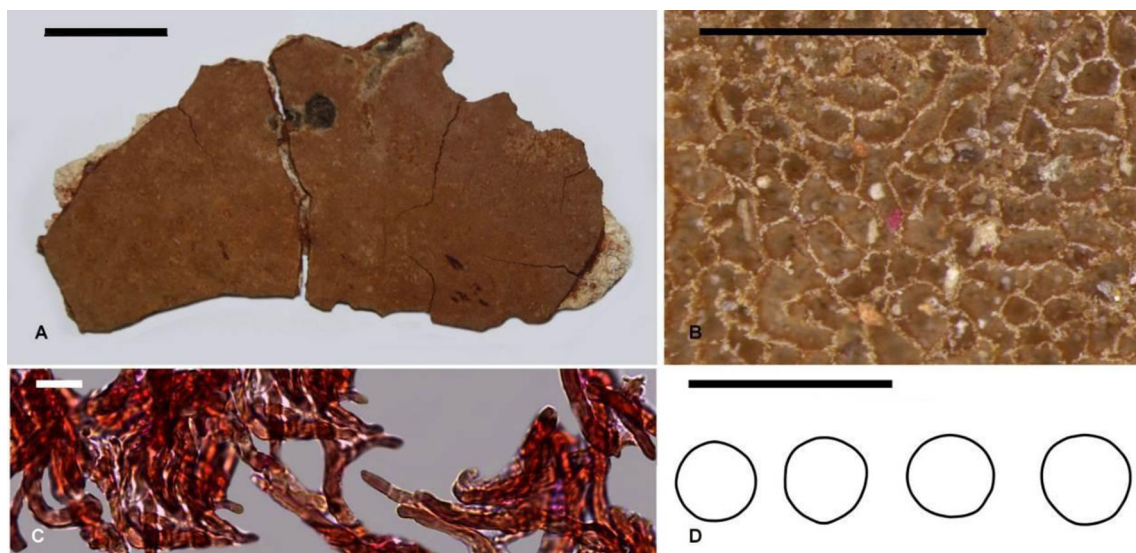


Fig. 153 *Grammothele aurantiaca* (MG 232015, holotype). **a** Basidioma. **b** Pores. **c** Hyphae from the sub-hymenium in KOH **d** basidiospores. Photos: A.M.S. Soares; Drawing: R.L. Alvarenga. Scale bars: **a** = 1 cm, **b**, **c** = 10 μm , **d** = 5 μm

59' 20,79" W, October 2014, W. Xavier, WX 2014-115, (MG 232015, **holotype**; **isotype** in URM).

Additional specimens examined: *Grammothele aurantiaca* – BRAZIL, Amapá: Serra do Navio, Serra dos Veados, on dead wood, February 2015, W. Xavier, WX 2015-88 (MG 226148). *Porogramme lateritia* – COSTA RICA, Alajuela: Bijagua, Parque Nacional Volcan Arenal La Fortuna de San Carlos, July 2001, L. Ryvarden, 43 (O F18637). DOMINICAN REPUBLIC: November 1892, Elliot (O F903299). FRANCE, Guadeloupe: Camp Jacob, sur un tronc d'un *Synplocus maritimiersii*, Duss 592 (O F505994, **holotype**); Basse terre: October 1976, A. David, 2189 LY-AD (O F505992). VENEZUELA, Aragua: dead hardwood, February 2006, L. Ryvarden (O F506199).

GenBank numbers: LSU: MH844886, ITS: MH842137.

Notes: *Grammothele aurantiaca* is characterized by the salmon to dark orange basidiomata, dimitic hyphal system, generative hyphae simple-septate, and skeletal hyphae cherry red in KOH. *Porogramme lateritia* (Pat.) Pat. has similar colour, however the pores are smaller [10–15(–20 per mm)], the hyphal system is monomitic with clamps and the basidiomata become greyish to reddish when dried (Lowe 1964; Ryvarden 1983). Besides, in the phylogenetic tree (Fig. 156), *G. aurantiaca* clustered in the *Grammothele* clade with good support (1.00/89%) and is distantly

related to the *Porogramme* clade, with *P. albocincta* (Cooke & Massee) Gibertoni (1.00/95%) (Fig. 156) as the type species of the genus.

***Grammothele micropora* A.M.S. Soares & W.K.S. Xavier sp. nov.**

Index Fungorum number: IF555480; **Facesoffungi number:** FoF05975; Fig. 154

Etymology: mikrós Gr. = small + poros L. = pore, referring to the tiny pores.

Holotype: MG 232012

Basidiomata annual, resupinate, effuse, strongly adnate, hard and brittle when fresh and when dried, up to 15 cm long, 8 cm wide, 1 mm thick; pore surface black when fresh, dark-bluish when dried (1F1); margin narrow, concolorous with the pore surface becoming slightly whitish with the age. Pores shallow, invisible to the naked eye, irregular, round, sometimes angular to hexagonal, 25–30 per mm, dissepiments thin, tubes concolorous, up to 1 mm deep. **Basidiospores** subglobose, hyaline, thick-walled, smooth, with tiny or without apiculus, IKI–, (3.0–) 3.5–4(–4.5) × 3–3.5 (–4) µm (L = 3.81 µm, W = 3.14 µm, Q = 1.21, n = 15/1). **Basidia** narrowly clavate, 7–10 × 3–5 µm, with four sterigmata, 2.5–3 µm long. Hyphal system dimitic, generative hyphae, thin-walled,

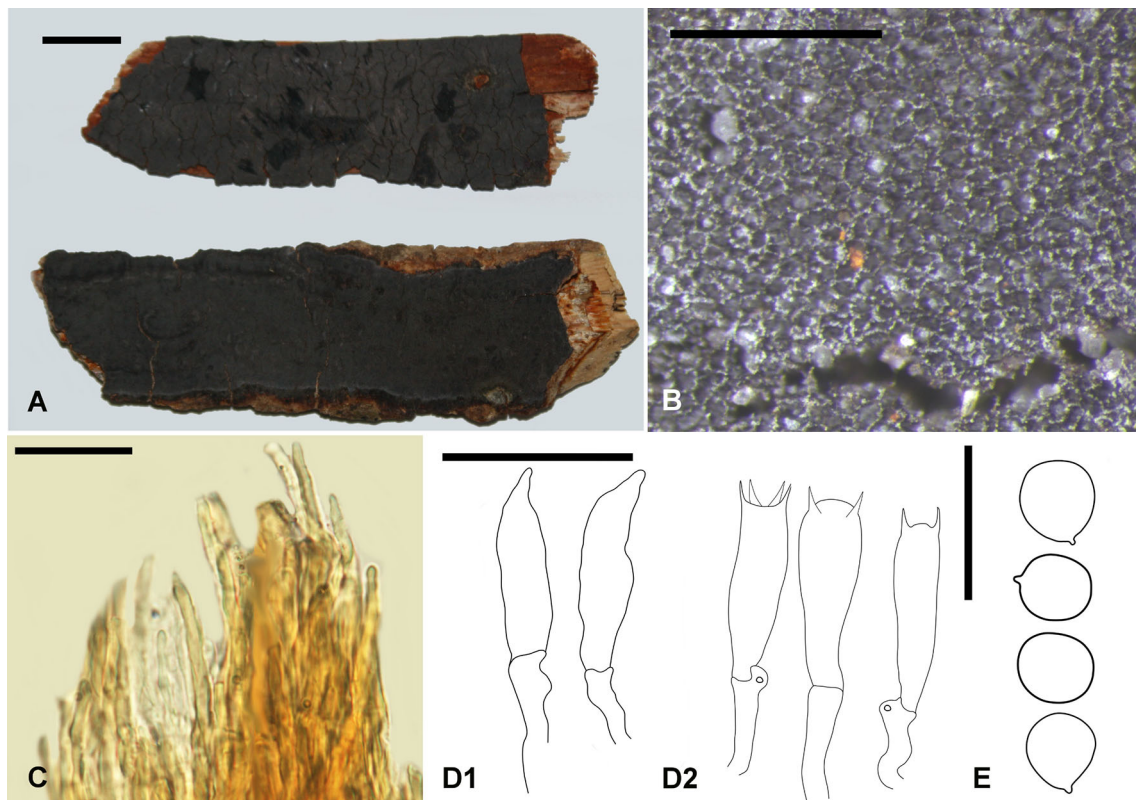


Fig. 154 *Grammothele micropora* (MG 232012, **holotype**). **a** Basidiomata. **b** Pores. **c** Hyphae from the sub-hymenium. **d1** Cystidioles. **d2** Basidia. **e** Basidiospores. Photos: A.M.S. Soares; Drawings: R.L. Alvarenga. Scale bars: **a** = 1 cm, **b**, **c** = 10 µm, **d**, **e** = 5 µm

hyaline, clamped, 2–3 μm wide, IKI-; skeletal hyphae dominating, thick-walled, brown to black in KOH, 5–7 μm wide IKI-. Dendrohyphidia absent. Cystidia absent, but fusoid cystidioles present, 6–9 \times 4–5 μm .

Material examined: BRAZIL, Amapá: Serra do Navio, 0° 55' 9.95"N and 51° 59' 19.8"W, on dead wood, October 2014. W. Xavier, WX 2014-116 (MG 232012, **holotype**; **isotype** in URM).

Additional specimens examined: BRAZIL, Amapá: Porto Grande, Floresta Nacional do Amapá, July 2009, H. Sotão, H2009-256A (MG 232558). BRAZIL, Amapá: Porto Grande, Floresta Nacional do Amapá, September 2011, A.M.S. Soares, M146 (MG 232692).

GenBank numbers: ITS: MH842144, LSU: MH842144.

Notes: the dark bluish to black basidiomata, the small pores and basidiospores, among the smallest in the genus, are characteristic of this species. Initially, *G. micropora* was identified as *Porogramme albocincta* (Cooke & Massée) Gibertoni because of its dark bluish grey basidiomata and very small pores (8–20 per mm). Nevertheless, *G. micropora* has even smaller pores and dimitic hyphal system, whereas *P. albocincta* is monomitic and its basidiospores are longer [4–6 (6.5) \times 3–3.5 μm] (Ryvarden 1979). *Grammothele boliviana* Karasinski has similar colour (grey to bluish grey), however the basidiospores are broadly ellipsoid to ovate and larger [8.4–10.8(–11.5) \times 6–7.2(–7.5) μm]. Differently from the new species, *G. boliviana* has hyphidia and dendrohyphidia and is reported on palms

(Karasinski 2015). Additionally, in the phylogenetic tree, *G. micropora* clustered within the *Grammothele* clade (1.00/76%) and grouped with low to moderate support with *G. brasiliensis* Ryvarden (0.95/70%) (Fig. 156). The type species of the *G. brasiliensis* is from Brazil's southeast (state of São Paulo) and it is characterized by the dark grey basidiomata, pores 5–6 per mm and cylindrical basidiospores (5–6 \times 2.5–3 μm) (Ryvarden 2015).

Grammothele brasiliensis Ryvarden [as 'brasiliensis'], Syn. Fung. (Oslo) 33: 38 (2015)

Facesoffungi number: FoF05976; Fig. 155

Description: Ryvarden (2015).

Material examined: BRAZIL, Amapá: Serra do Navio, on dead wood, October 2014, W. Xavier, WX2014-87 (MG232006), WX2014-132 (MG232007), WX2014-100 (MG232008), WX2014-28 (MG232009), WX2014-101 (MG232010); WX2014-148 (MG232011). *Grammothele subargentea* – BRAZIL, Amapá: Serra do Navio, on dead wood, October 2014, W. Xavier, WX2014-26 (MG232013), WX2014-155 (MG232014). *Grammothele lineata* – BRAZIL, Amapá: Serra do Navio, on dead wood, October 2014, W. Xavier, WX2014-208 (MG232015), WX2014-40 (MG232016).

GenBank numbers: ITS: MH844864, MH844550, MH844679, MH844866, MH844553, MH844563, MH842150, LSU: MH844863, MH844887, MH844583, MH844865, MH844553, MH842149.

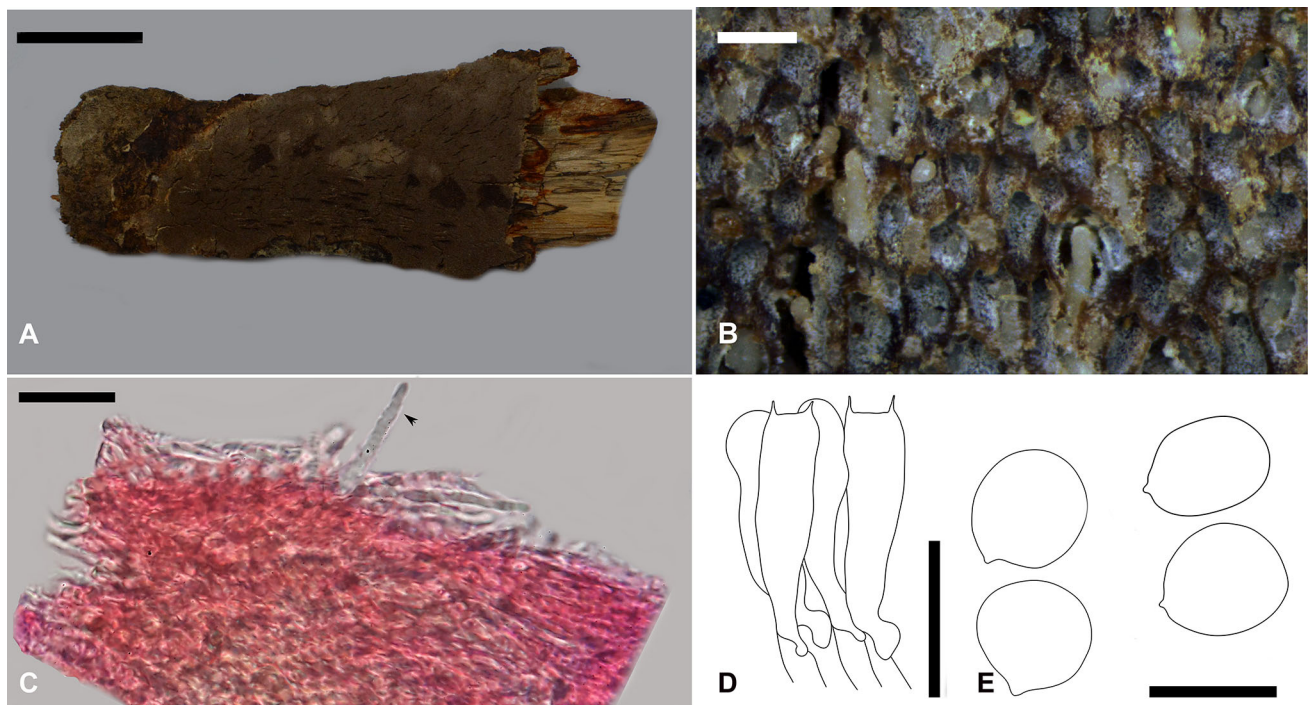


Fig. 155 *Grammothele brasiliensis* (MG 232007, new record). **a** Basidioma. **b** Pores. **c** Encrusted hyphae from the sub-hymenium. **d** Basidia. **e** Basidiospores. Photos: A.M.S. Soares; Drawings: R.L. Alvarenga. Scale bars: **a** = 2 cm, **b** = 0.2 mm, **c** = 10 μm , **d**, **e** = 5 μm

Notes: This species is characterized by the dark grey basidiomata, round and entire pores (5–6 per mm), dimitic hyphal system, clamped generative hyphae, skeletal hyphae strongly agglutinated with numerous crystals and cylindrical basidiospores ($5\text{--}6 \times 2.5\text{--}3 \mu\text{m}$) (Ryvarden 2015). Dendrohyphidia were easily identified on the studied material, which were not found by Ryvarden (2015). He, however, presumed their presence in the dissepiments. This species may be confused with *Tinctoporellus epimiltinus* (Berk. & Br.) Ryvarden, which has similar colour (bluish white and light beige), pores (angular to round, 7–9 per mm), and dimitic hyphal system. However, the ellipsoid to subglobose basidiospores [$4\text{--}5 (5.5) \times 2.5\text{--}3 \mu\text{m}$], absence of dendrohyphidia and cystidioles separate it from *G. brasiliensis* (Ryvarden 1979). Besides, *G. brasiliensis* did not group in the *Tinctoporellus* clade (1.00/95%), but formed a monophyletic lineage with strong support (1.00/100%) within the *Grammothele* clade (Fig. 156). This is the first time this species is sequenced, the second record of this species for Brazil and the first to the Brazilian Amazonia.

The colour of *G. subargentea* (Speg.) Rajchenb. resembles *G. brasiliensis*, but the former has larger pores and longer basidiospores [$(2\text{--}3 \text{ per mm}; \text{cylindrical } (6\text{--}6.5\text{--}8.5 \times (2.5) 3\text{--}4 \mu\text{m})$]. The type species of *G. subargentea* is from Paraguay, and the morphological characters of the specimens analyzed in this study are very similar to the original description (Ryvarden 2015). Although there is no sequence of the type locality, our phylogenetic analyses confirm this species in the *Grammothele* clade (0.91/69%). Another species registered in Brazil, *G. lineata* Berk. & M.A. Curtis, has also white to greyish basidiomata, later pinkish, and might be mistaken for *G. brasiliensis*; however, the former has trimitic hyphal system and a partly hydroid surface with dots of numerous dark bundles of skeletal hyphae (Ryvarden 2015). In addition, the specimens collected in the Brazilian Amazonia sistered with *G. lineata* from China and Malaysia, and *Grammothele* sp. and *G. denticulata* Y.C. Dai & L.W. Zhou (1.00/99%) from China, in the *Grammothele* clade. *Grammothele lineata* was originally collected in Cuba and there is no sequence from the type locality. The new sequences generated from Brazilian material may represent *G. lineata* due the closeness to the type locality, since both are in the Neotropics. Thus, the Asian collections should be re-evaluated.

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David

Notes: The concept of Russulales was gradually developed in morphological analyses for several groups of macro-fungi. Singer and Smith (1960) have noticed the close morphological relationship between agaricoid and

gasteroid homobasidiomycetes taxa. The amyloid basidiospore ornamentations and gloeoplerous hyphae system reminded the Dutch mycologist Marinus Anton Donk of some families (e.g. Hericiaceae) may be members of an unknown order (Donk 1971). Oberwinkler (1977) regarded this order as Russulales which include agaricoid, discoid, fused-reflexed, gasteroid, hydroid, and resupinate taxa. The order Russulales was officially acknowledged in the Dictionary of Fungi (Kirk et al. 2001; Miller et al. 2006). The independence of this order has been supported by some recent phylogenetic analyses (Hibbett et al. 2007; Zhao et al. 2017).

Russulaceae Lotsy

Notes: The family Russulaceae was established by Dutch botanist Johannes Paulus Lotsy to accommodate species with granular flesh, thick gills, spiny spores, and milky hyphae and rounded cells (sphaerocytes). This family includes gasteroid and agaricoid genera, *Lactarius* Pers., *Lactifluus* (Pers.) Roussel, *Multifurca* Buyck & V. Hofst. and *Russula* Pers., together with the crust-like genera *Boidinia* Stalpers & Hjortstam, *Gloeopeniophorella* Rick, and *Pseudoxenasma* K.H. Larss. & Hjortstam (Lotsy 1907; Larsson and Larsson 2003; Miller et al. 2006; Larsson 2007; Buyck et al. 2008, 2010; Verbeken and Nuytinck 2013). The family comprises ectomycorrhizal (Tedersoo and Nara 2010), arbutoid mycorrhizal (Smith and Read 2008), monotropoid mycorrhizal (Bidartondo 2005), orchid mycorrhizal (Dearnaley 2007), and saprotrophic, wood-degrading species (Larsson and Larsson 2003).

Russula Pers.

Notes: The genus *Russula* was introduced by Persoon (1796) with the type species *R. emetica* (Schaeff.) Pers. This genus is characterized by fairly large basidiocarps, brightly colored pileus, white to dark yellow basidiospore print, attached lamellae, absence of volva and milky latex, amyloid basidiospore ornamentations, and numerous spherocysts in context (Sarnari 1998). Over 800 species are accommodated in this genus (Li 2014; Li et al. 2015, 2018c). Most recent new *Russula* species were described based on specimens from Asia (Li et al. 2016, 2018a, b; Sang et al. 2016; Das et al. 2017a, b, 2018b; Hyde et al. 2016, 2017b; Jiang et al. 2017; Zhang et al. 2017). In this paper, we introduce a new species in the genus *Russula* which was collected in coniferous and broad-leaved intermixed forests from Guangxi of South China.

Russula prasina G.J. Li & R.L. Zhao, *sp. nov.*

Index Fungorum number: IF570591; **Facesoffungi number:** FoF05086; Fig. 157

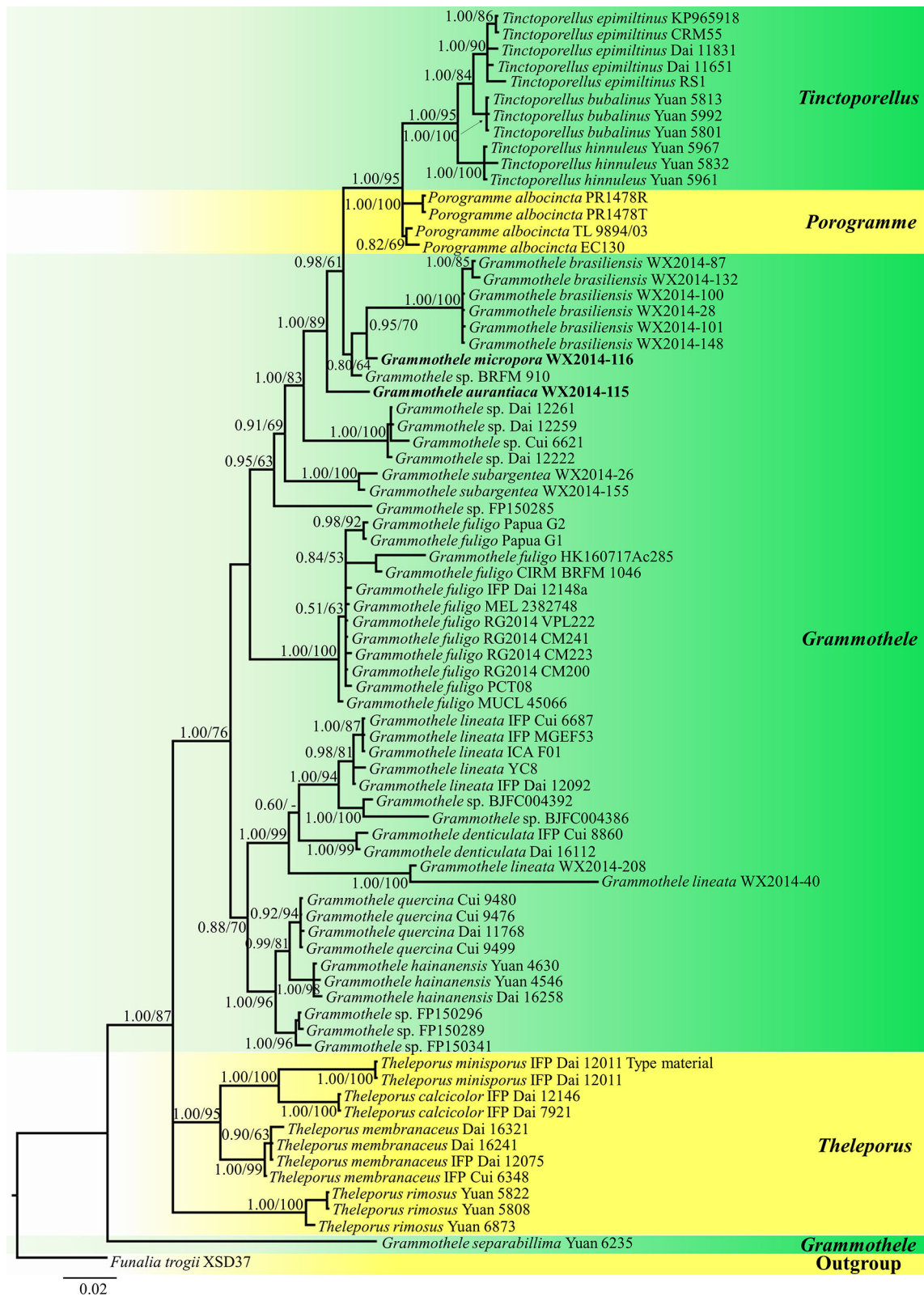


Fig. 156 Maximum likelihood consensus phylogenetic tree of the concatenated ITS1, 5.8S, ITS2 and partial 28S rDNA sequences. Bootstrap supporting values (1000 replicates) and posterior probabilities (PP) from Bayesian analysis to each node are shown from left to

right. Only bootstrap values above 50% and BYPP above 0.75 are provided. The newly generated sequences are indicated in bold and black. The tree was rooted with *Funalia trogii* (XSD37)

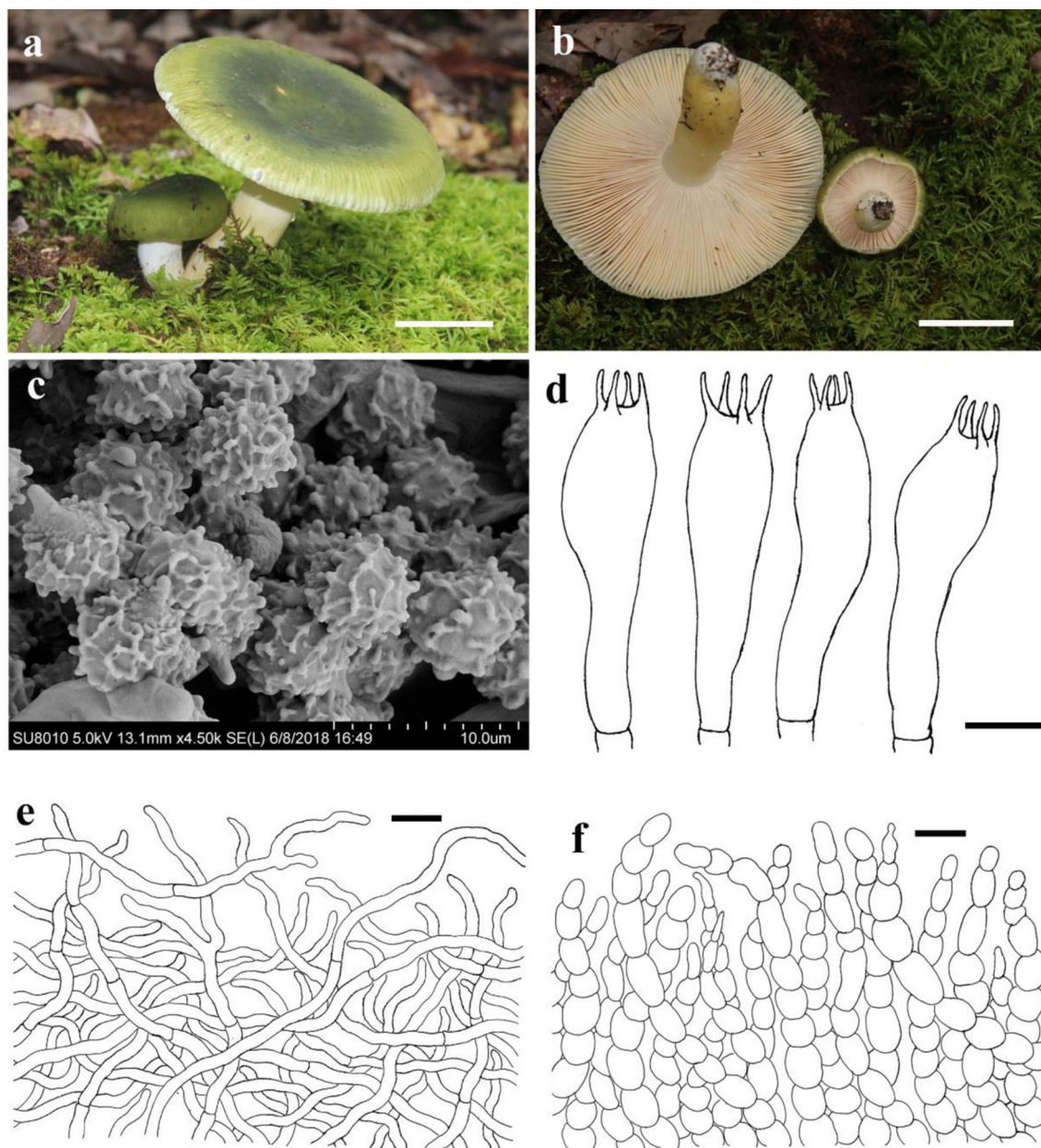


Fig. 157 *Russula prasina* (HMAS 281232, holotype). **a, b** Basidiocarps. **c** Basidiospores. **d** Basidia. **e** Subpellis. **f** Epipellis. Scale bars: **a, b** = 5 cm, **f** = 20 μ m, **d, e** = 10 μ m

Etymology: Refers to the grass green tinged pileus of this species.

Holotype: HMAS 281232

Basidiocarps small to large sized. **Pileus** 43–130 mm in diam., first hemispheric, then plane to depressed at centre when mature, slightly striate 25–30 mm towards the edge when mature, not cracked, slightly viscid when wet, dull, peeling 1/5–1/4 from the edge, grass green tinge of Winter Green (XVIII33'i), Motmot Green (XX43'i) to Courge Green (XVII25'i) at centre, pale yellowish green tinge of Oil Yellow (V27 k), Javel Green (V27i) to Calliste Green

(VI31i) towards margin. **Lamellae** adnate, 3–5 mm in height, 8–13 pieces per centimeter at edge, rarely forked near stipe, often interveined, pale ocher tinge of Ochraceous-Buff (XV15'b), unchanging when bruised, lamellulae absent. **Stipes** central to subcentral, 4.1–7.7 \times 2.4–3.6 cm, subcylindrical to cylindrical, surface dry, rugulose longitudinally, dull, without annulus, slightly attenuate downward, White (LIII) at upper part, ochraceous yellow tinge of Light Ochraceous Salmon (XV13'b) to Salmon Buff (XIV11'd) towards the base, stuffed at first, becoming hollow when old. Context up to 3–5 mm at

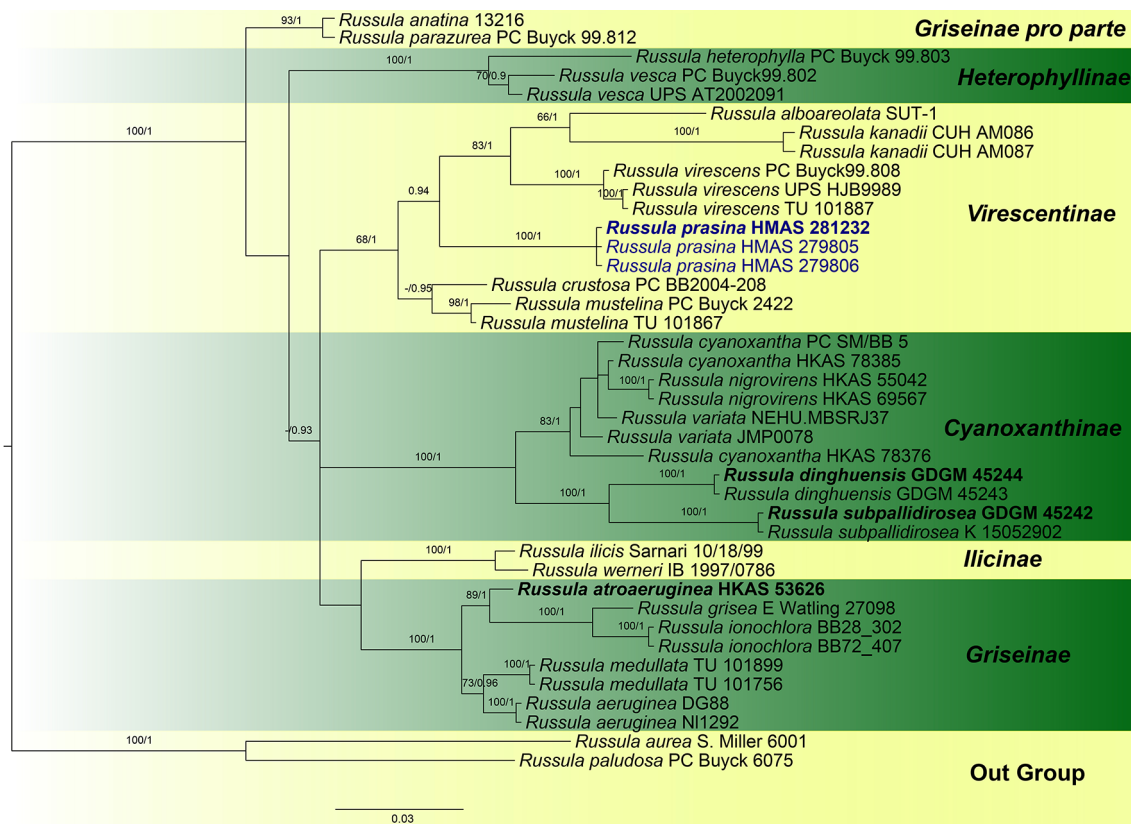


Fig. 158 Phylogram generated from Bayesian analysis of ITS sequence data of *Russula* subgenus *Heterophyllidia*. Related sequences were obtained from Miller and Buyck (2002), Abarenkov et al. (2010), Li et al. (2013), Guo et al. (2014), Dutta et al. (2015), Zhao et al. (2015) and Zhang et al. (2017). *Russula aurea* and *R. paludosa* are used as the outgroup taxa. Bootstrap (BS) support values

for ML equal to or greater than 65% and Bayesian posterior probability (BYPP) values equal to or greater than 0.90 are given above the nodes respectively as (BS/BYPP). Phylogenetic topology of the ML analysis was similar to that of the BI. The type specimens are in bold and black. The newly generated sequences are in blue

centre of pileus, White (LIII) first, unchanging when bruised, fragile, no distinct odor; taste mild. *Spore print* Ocher (Romagnesi III b–c).

Basidiospores [300/3/3] (5.9–) 6.2–7.3 (–7.6) × (5–) 5.4–6.5 (–7) μm, Q = 1.01–1.21 (–1.25) (Q = 1.12 ± 0.07), hyaline, globose to subglobose, rarely broadly ellipsoid; ornamentation composed of amyloid obtuse warts and short crests that are mostly interconnected as short crests and ridges, forming a complete network, warts 0.3–0.6 μm high; suprahilar area nonamyloid to rarely weakly amyloid. *Basidia* 35–53 × 8–11 μm, projecting 10–20 μm beyond hymenium, four-spored, sterigmata 4–6 μm long, hyaline, unchanging in KOH, subclavate to clavate, rarely cylindrical. *Pleurocystidia* and *cheilocystidia* not observed. *Subhymenium* cellular layer 15–30 μm thick composed of voluminous cells 10–20 μm in diam., hyaline, rarely pale yellowish in KOH. *Pileipellis* is composed of epipellis and subpellis; epipellis pseudo-parenchymatous, 100–250 μm thick, composed of thin-walled, unbranched and inflated cells 10–20 μm wide, narrowing to 5–7 μm towards the terminal cells;

pileocystidia absent; subpellis slightly gelified, a cutis 150–250 μm thick, composed of parallel to interweaved, rarely branched and septate, hyaline hyphae 2–4 μm wide. *Stipitipellis* cutis, upper layer composed of parallel filamentous hyphae 3–6 μm in diam., inner layer hyaline filamentous hyphae interweaved with sphaerocytes 15–25 μm in diam., some filamentous hyphae pale yellow in KOH; caulocystidia not observed. *Trama* composed of sphaerocytes 15–40 μm in diam. and scattered by filamentous and cystidioid hyphae. *Clamp connections and laticiferous hyphae* absent in all tissues.

Material examined: CHINA, Guangxi Zhuang Autonomous Region, Baise City, Leye County, Huangjingdong National Forest Park, N 24°74'E 106°32', elev. 378 m., 6 August 2017, Hui-Jun Wang GX20170580 (HMAS 281232, **holotype**); *ibid.* elev. 464 m., GX20170846 (HMAS 279805); *ibid.* elev. 395 m., GX20170937 (HMAS 279806).

Habit and habitat: Scattered or single in coniferous and broad-leaved intermixed forests (dominated by e.g. *Pinus*

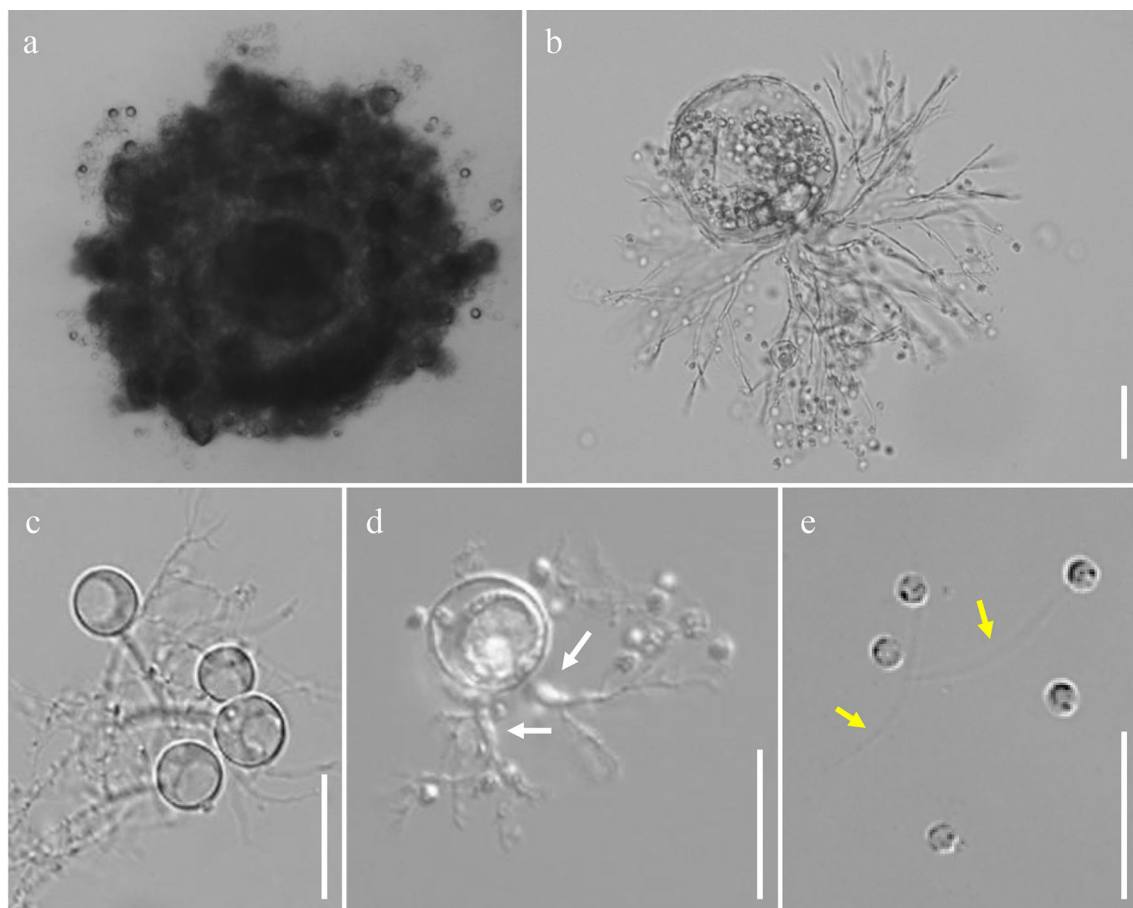


Fig. 159 *Rhizophydium koreanum* (CNUFC-17CPW1-1, **holotype**). **a** Colony on PmTG agar. **b** Developing zoosporangium with branched rhizoids. **c** Resting spores. **d** Developing thallus with two rhizoidal

axes (white arrows). **e** Uniflagellate zoospores (yellow arrows). Scale bars: **b–e** = 20 μ m

crassicornicea, *P. yunnanensis* var. *tenuifolia*, *Quercus acutissima*, and *Q. variabilis*) at 300–500 m altitude.

Distribution: CHINA (Guangxi Zhuang Autonomous Region). Season. August.

GenBank numbers: ITS: MH454351 (HMAS 281232), MH454352 (HMAS 279805), MH454353 (HMAS 279806).

Notes: *Russula prasina* is a member of subgenus *Heterophyllidia*, section *Virescentinae* because it has greenish tinged pileus, small basidiospores, spherocysts in epipellis, and absence of pileocystidia in pileipellis (Sarnari 1998). Unlike the furfuraceous and areolate pileus surfaces of the other *Virescentinae* members, that of *R. prasina* is relatively smooth. The hyphal cells in subpellis and epipellis of *R. prasina* are reminiscent of those of *R. parvovirescens* Buyck, D. Mitch. & Parrent, in contrast, *R. parvovirescens* has pileocystidia in pileipellis and hymenium with pleurocystidia and cheilocystidia (Buyck et al. 2006). This new species may be confused with some green-capped *Russula* in China and adjacent region, e.g. *R. atroaeruginea* G.J. Li, Q. Zhao & H.A. Wen, *R.*

dinghuensis J.B. Zhang & L.H. Qiu, *R. nigrovirens* Q. Zhao, Y.K. Li & J.F. Liang, *R. sikkimensis* K. Das, Atri & Buyck, *R. virescens* (Schaeff.) Fr., and *R. viridirubrolimbata* J.Z. Ying. These species can be distinguished from *R. prasina* by the following morphological characteristics: *R. atroaeruginea* differs in its radially yellowish-striped pileus, larger basidiospores (6.3–) 6.8–8.1 (–9.0) \times (5.9–) 6.1–7.4 (–7.8) μ m, and habitat of in alpine subtropical conifer forests dominated by *Picea* spp. (Li et al. 2013); *R. dinghuensis* has pileus surface cracking into small patches with rusty tinge, scattered lamellulae, white basidiospore print, and trichoderm epipellis (Zhang et al. 2017); *R. nigrovirens* can be differentiated by its longer basidia 45–75 \times 9–14 μ m, basidiospore ornamentation not forming a reticulum, and habitat of in alpine subtropical conifer forests dominated by *Picea* sp., *Rhododendron* sp., *Sorbus* sp. and *Abies* sp. (Zhao et al. 2015); *R. sikkimensis* has basidiospore ornamentation up to 0.9 μ m, cutis to trichoderm pileipellis and habitat of in alpine subtropical conifer forests dominated by *Abies* spp. (Das et al. 2013); *R. virescens* differs in its white to pale cream spore print,

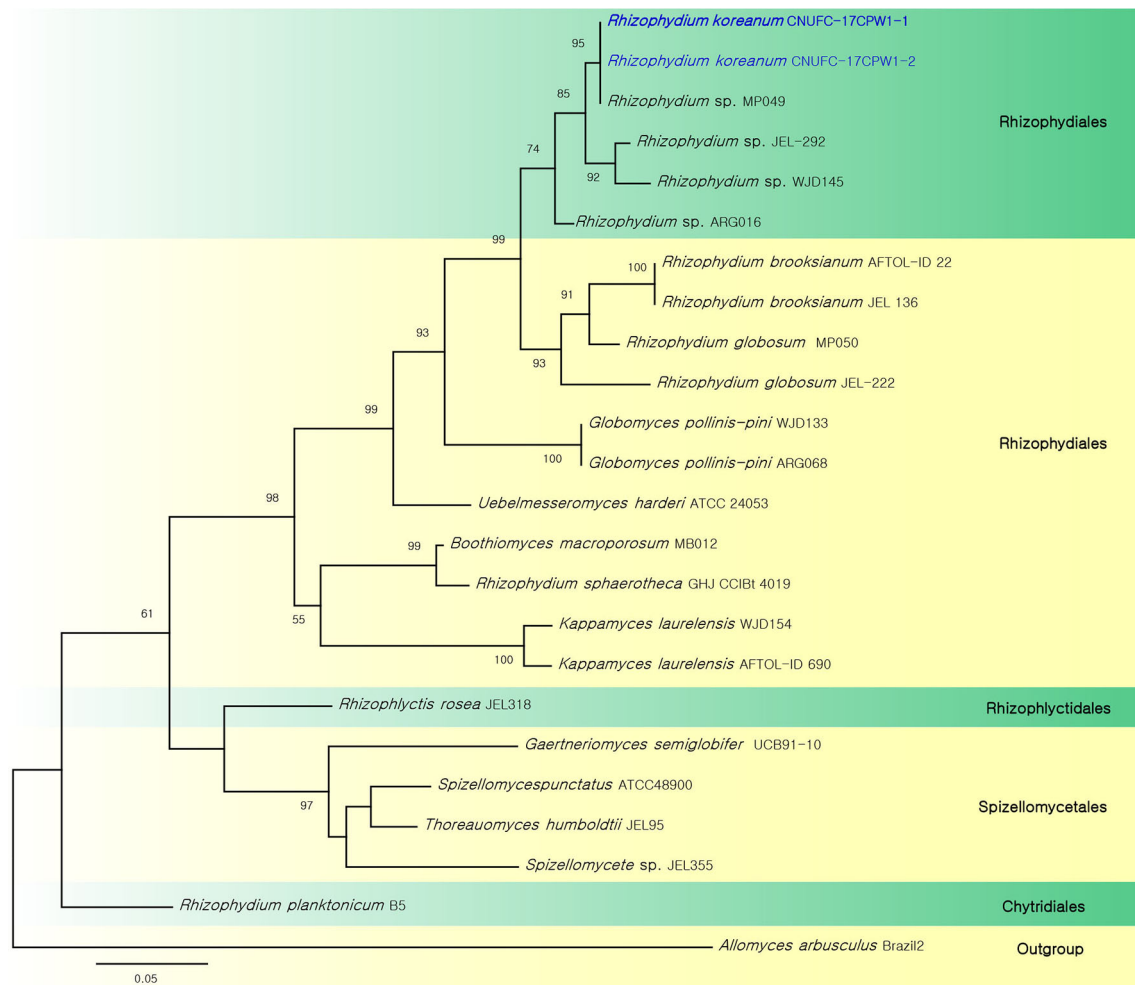


Fig. 160 Phylogenetic tree of *Rhizophydium koreanum* (CNUFC-17CPW1-1) and (CNUFC-17CPW1-2) and related species based on Maximum likelihood analysis of 28S. Sequence of *Allomyces arbusculus* was used as outgroup taxon. Numbers at the nodes

indicate the bootstrap values ($\geq 50\%$) from 1000 replications. The bar indicates the number of substitutions per position. The newly generated sequences are indicated in blue and ex-type strain in bold

elliptical to subglobose basidiospores, and frequently elongated and tapered terminal cells in pileipellis (Sarnari 1998, Li 2014); *R. viridirubrolimbata* can be differentiated by its red tinge in pileus, and acrid context (Ying 1983). Phylogenetic analysis showed that our strains formed a distinct clade from known *Russula* species (Fig. 158). Thus *Russula prasina* is introduced as a new species based on morphological and phylogenetic analyses.

Chytridiomycota Arx

Rhizophyidiomycetes Tedersoo, Koljalg et al.

Rhizophydiales Letcher

Notes: Currently, 17 families and 25 genera are placed in order Rhizophydiales based on molecular phylogeny and zoospore ultrastructure (Letcher et al. 2015; Van den Wyngaert et al. 2017; Seto and Degawa 2018; Wijayawardene et al. 2018b).

Rhizophydium Schenk

Notes: The genus *Rhizophydium* is the oldest genus within the order Rhizophydiales, proposed by Schenk (1858) and validated by Rabenhorst (1868). The species belonging to this genus are characterized by the formation of spherical zoosporangia with multiple, discharge pores, and branched rhizoids arising from the sporangium (Barr 1968; Letcher et al. 2006). Members of the genus occur in aquatic systems, primarily as parasites of algae, and from pollen, keratin, and soil as saprotrophs (Barr 1968; Longcore 1996; Letcher et al. 2004, 2006). In recent years, ultrastructural and molecular analyses have been used as a tool to delimit species in the genus, resulting in significant change in the taxonomy (Letcher et al. 2006; Seto et al. 2017). Many *Rhizophydium* species have been transferred to new genera (Letcher et al. 2006, 2015).

During a study of Rhizophydiales in water samples in Gwangju, Korea, a new species of *Rhizophydium* was

isolated and is described here, based on morphological characteristics and phylogenetic analyses.

Rhizophydium koreanum Hyang B. Lee, S.J. Jeon, T.T. T. Nguyen, *sp. nov.*

Index Fungorum number: IF554571; *Facesoffungi number:* FoF05792; Fig. 159

Etymology: *koreanum*, referring to the country from which the species was recorded.

Holotype: CNUFC-17CPW1-1

On PmTG (peptonized milk, tryptone and glucose) agar: *Zoosporangium* spherical, with many closely spaced and highly branched rhizoids, measured (100–)107.5–120.5(–131.5) µm diam. *Rhizoidal system* arising from a single point at the base of the sporangium. *Zoospores* abundantly produced, spherical, measured (3.0–)3.5(–4.0) µm diam., with a flagellum of (20–)23.5(–30) µm long. *Resting spore* spherical, measured (10–)12.5(–13.5) µm diam.

Culture characteristics: Colonies reaching 8.5 mm diam. on PmTG at 25 °C in 7 days, cream. Optimal growth was observed around 20 °C.

Material examined: REPUBLIC OF KOREA, from pond water collected at Chonnam National University Arboretum, Gwangju, Korea, 20 October 2017 (CNUFC-17CPW1-1, preserved as glycerol stock at – 80 °C in the Chonnam National University Fungal Collection; isotype in Culture Collection of Nakdonggang National Institute of Biological Resources [NNIBR], Sangju, Gyeongbuk Province).

Notes: Based on phylogenetic analyses and morphological comparison, our isolate belongs to *Rhizophydium*. *Rhizophydium koreanum* formed a distinct clade from other species in the phylogenetic tree (Fig. 160). It differs from the closely related species *R. globosum* and *R. brooksianum* by forming larger sporangia.

GenBank numbers: LSU: MH298649, MH298650.

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