Mycosphere 9(2): 271–430 (2018) www.mycosphere.org ISSN 2077 7019

Article

Doi 10.5943/mycosphere/9/2/8

Mycosphere notes 169–224

Hyde KD[1,2], Chaiwan N[2], Norphanphoun C[2,6], Boonmee S[2], Camporesi E[3,4], Chethana KWT[2,13], Dayarathne MC[1,2], de Silva NI[1,2,8], Dissanayake AJ[2], Ekanayaka AH[2], Hongsanan S[2], Huang SK[1,2,6], Jayasiri SC[1,2], Jayawardena RS[2], Jiang HB[1,2], Karunarathna A[1,2,12], Lin CG[2], Liu JK[7,16], Liu NG[2,15,16], Lu YZ[2,6], Luo ZL[2,11], Maharachchimbura SSN[14], Manawasinghe IS[2,13], Pem D[2], Perera RH[2,16], Phukhamsakda C[2], Samarakoon MC[2,8], Senwanna C[2,12], Shang QJ[2], Tennakoon DS[1,2,17], Thambugala KM[2], Tibpromma, S[2], Wanasinghe DN[1,2], Xiao YP[2,6], Yang J[2,16], Zeng XY[2,6], Zhang JF[2,15], Zhang SN[2,12,16], Bulgakov TS[18], Bhat DJ[20], Cheewangkoon R[12], Goh TK[17], Jones EBG[21], Kang JC[6], Jeewon R[19], Liu ZY[16], Lumyong S[8,9], Kuo CH[17], McKenzie EHC[10], Wen TC[6], Yan JY[13], Zhao Q[2]

[1] *Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, P.R. China*
[2] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3] *A.M.B. Gruppo Micologico Forlivese ''Antonio Cicognani'', Via Roma 18, Forlı`, Italy*
[4] *A.M.B. Circolo Micologico ''Giovanni Carini'', C.P. 314, Brescia, Italy*
[5] *Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, P.R. China*
[6] *Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of national education Ministry of Education, Guizhou University, Guiyang, Guizhou Province 550025, P.R. China*
[7] *Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand.*
[8] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand*
[9] *Center of Excellence in Bioresources for Agriculture, Industry and Medicine, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand*
[10] *Landcare Research Manaaki Whenua, Private Bag 92170, Auckland, New Zealand*
[11] *College of Agriculture & Biological Sciences, Dali University, Dali 671003, Yunnan, P.R. China*
[12] *Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand*
[13] *Beijing Municipal Key Laboratory of Environmental Friendly Management on Fruits Pests in North China, Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Sciences, Beijing 100097, PR China*
[14] *Department of Crop Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, P.O. Box 34, 123 Al-Khoud, Oman*
[15] *Faculty of Agriculture, Natural Resources and Environment, Naresuan University, Phitsanulok, 65000, Thailand*
[16] *Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang, 550006, P.R. China*
[17] *Department of Plant Medicine, National Chiayi University, 300 Syuefu Road, Chiayi City 60004, Taiwan*
[18] *Russian Research Institute of Floriculture and Subtropical Crops, 2/28 Yana Fabritsiusa Street, Sochi 354002, Krasnodar region, Russia*
[19] *Dept of Health Sciences, Faculty of Science, University of Mauritius, Reduit, Mauritius*
[20] *No. 128/1-J, Azad Housing Society, Curca, Goa Velha-403108, India*
[21] *No. 33 B St. Edwards Road Southsea Hants. PO5 3DH, UK*

Hyde KD, Chaiwan N, Norphanphoun C, Boonmee S, Camporesi E, Chethana KWT, Dayarathne MC, de Silva NI, Dissanayake AJ, Ekanayaka AH, Hongsanan S, Huang SK, Jayasiri SC,

---

Submitted 1 April 2018, Accepted 29 April 2018, Published 30 April 2018

Corresponding Author: K.D. Hyde – e-mail – kdhyde3@gmail.com

Jayawardena R, Jiang HB, Karunarathna A, Lin CG, Liu JK, Liu NG, Lu YZ, Luo ZL, Maharachchimbura SSN, Manawasinghe IS, Pem D, Perera RH, Phukhamsakda C, Samarakoon MC, Senwanna C, Shang QJ, Tennakoon DS, Thambugala KM, Tibpromma, S, Wanasinghe DN, Xiao YP, Yang J, Zeng XY, Zhang JF, Zhang SN, Bulgakov TS, Bhat DJ, Cheewangkoon R, Goh TK, Jones EBG, Kang JC, Jeewon R, Liu ZY, Lumyong S, Kuo CH, McKenzie EHC, Wen TC, Yan JY, Zhao Q 2018 – Mycosphere notes 169–224. Mycosphere 9(2), 271–430, Doi 10.5943/mycosphere/9/2/8

Abstract

This is the fourth in a series of *Mycosphere notes* wherein we provide notes on various fungal genera. In this set of notes, we introduce Phaeoseptaceae as a new family, *Pseudobyssosphaeria* (Melanommataceae) as a new genus, 40 new species, 11 new host or country records, one reference specimen, one new combination and provide a description of the holotype of *Uleodothis balansiana* (Dothideaceae). The new species are *Acrospermum longisporium* (Acrospermaceae), *Ascitendus aquaticus* (Annulatascaceae), *Ascochyta clinopodiicola* (Didymellaceae), *Asterina magnoliae* (Asterinaceae), *Barbatosphaeria aquatica* (Barbatosphaeriaceae), *Camarosporidiella populina* (Camarosporidiellaceae), *Chaetosphaeria mangrovei* (Chaetosphaeriaceae), *Cytospora predappioensis*, *Cytospora prunicola* (Cytosporaceae), *Dendryphiella phitsanulokensis* (Dictyosporiaceae), *Diaporthe subcylindrospora*, *Diaporthe subellipicola* (Diaporthaceae), *Diplodia arengae* (Botryosphaeriaceae), *Discosia querci* (Sporocadaceae), *Dyfrolomyces sinensis* (Pleurotremataceae), *Gliocladiopsis aquaticus* (Nectriaceae), *Hysterographium didymosporum* (Pleosporomycetidae genera, incertae sedis), *Kirschsteiniothelia phoenicis* (Kirschsteiniotheliaceae), *Leptogium thailandicum* (Collemataceae), *Lophodermium thailandicum* (Rhytismataceae), *Medicopsis chiangmaiensis* (Neohendersoniaceae), *Neocamarosporium phragmitis* (Neocamarosporiaceae), *Neodidymelliopsis negundinis* (Didymellaceae), *Neomassarina pandanicola* (Sporormiaceae), *Neoocultibambusa pandanicola* (Occultibambusaceae), *Neophaeosphaeria phragmiticola* (Neophaeosphaeriaceae), *Neosetophoma guiyangensis* (Phaeosphaeriaceae), *Neosetophoma shoemakeri* (Phaeosphaeriaceae), *Neosetophoma xingrensis* (Phaeosphaeriaceae), *Ophiocordyceps cylindrospora* (Ophiocordycipitaceae), *Otidea pseudoformicarum* (Otideaceae), *Periconia elaeidis* (Periconiaceae), *Phaeoisaria guttulata*, *Pleurotheciella krabiensis*, *Pleurotheciella tropica* (Pleurotheciaceae), *Pteridiospora bambusae* (Astrosphaeriellaceae), *Phaeoseptum terricola* (Phaeoseptaceae), *Poaceascoma taiwanense* (Lentitheciaceae), *Pseudobyssosphaeria bambusae* (Melanommataceae) and *Roussoella mangrovei* (Roussoellaceae). The new host records or new country records are provided for *Alfaria terrestris* (Stachybotryaceae), *Arthrinium phragmites* (Apiosporaceae), *Bertiella ellipsoidea* (Melanommataceae), *Brevicollum hyalosporum* (Neohendersoniaceae), *Byssosphaeria siamensis* (Melanommataceae), *Cerothallia subluteoalba* (Teloschistaceae), *Cryptophiale hamulata* (Chaetosphaeriaceae), *Didymella aliena* (Didymellaceae), *Epicoccum nigrum* (Didymellaceae), *Periconia pseudobyssoides* (Periconiaceae) and *Truncatella angustata* (Sporocadaceae). We provide new molecular data for 52 species and updated phylogenetic trees for 15 orders (Acrospermales, Amphisphaeriales, Annulatascales, Asterinales, Botryosphaeriales, Chaetosphaeriales, Diaporthales, Dyfrolomycetales, Hypocreales, Kirschsteiniotheliales, Peltigerales, Pleosporales, Pleurotheciales, Rhytismatales and Teloschistales) and 35 families (Acrospermaceae, Annulatascaceae, Apiosporaceae, Asterinaceae, Astrosphaeriellaceae, Barbatosphaeriaceae, Botryosphaeriaceae, Camarosporidiellaceae, Chaetosphaeriaceae, Collemataceae, Cytosporaceae, Diaporthaceae, Dictyosporiaceae, Didymellaceae, Kirschsteiniotheliaceae, Lentitheciaceae, Melanommataceae, Neocamarosporiaceae, Neohendersoniaceae, Neophaeosphaeriaceae, Nectriaceae, Occultibambusaceae, Ophiocordycipitaceae, Otideaceae, Periconiaceae, Phaeoseptaceae, Phaeosphaeriaceae, Pleurotheciaceae, Pleurotremataceae, Rhytismataceae, Roussoellaceae, Sporocadaceae, Sporormiaceae, Stachybotryaceae and Teloschistaceae) and 45 genera (*Acrospermum*, *Alfaria*, *Arthrinium*, *Ascitendus*, *Ascochyta*, *Asterina*, *Barbatosphaeria*, *Bertiella*, *Brevicollum*, *Byssosphaeria*, *Camarosporidiella*, *Cerothallia*, *Chaetosphaeria*, *Cryptophiale*, *Cytospora*, *Dendryphiella*, *Diaporthe*, *Didymella*, *Diplodia*, *Discosia*, *Dyfrolomyces*, *Epicoccum*, *Gliocladiopsis*, *Hysterographium*, *Kirschsteiniothelia*, *Leptogium*, *Lophodermium*, *Medicopsis*, *Neocamarosporium*, *Neodidymelliopsis*, *Neooccultibambusa*, *Neomassarina*, *Neophaeosphaeria*, *Neosetophoma*, *Ophiocordyceps*, *Otidea*, *Periconia*, *Phaeoisaria*, *Phaeoseptum*, *Pleurotheciella*, *Poaceascoma*, *Pseudobyssosphaeria*, *Pteridiospora*, *Roussoella* and *Truncatella*). A reference specimen is provided for *Periconia cookei* (Periconiaceae). A new combination is proposed for *Seimatosporium ciliata* (Sporocadaceae).

Key words – 42 new taxa – Ascomycota – Description of type species of genus – Dothideomycetes– Lecanoromycetes – Leotiomycetes – Molecular phylogeny – New combinations – New family – New records – New species – Pezizomycetes – Phylogenetic – Reference specimens – Sordariomycetes – Taxonomy

Table of Contents

The numbers of taxa in this study are a continuation from previous papers (Thambugala et al. 2017, 1–50, Boonmee et al. 2017, 51–101, Jayawardena et al. 2018, 102–168) and organized as in the “Outline of Ascomycetes” (Wijayawardene et al. 2018).

Phylum Ascomycota
Class Dothideomycetes

For recent treatments of Dothideomycetes we follow Liu et al. (2017a) and Wijayawardene et al. (2018).

Subclass Dothideomycetidae
Dothideales Lindau
Dothideaceae Chevall.

169. ***Uleodothis balansiana*** (Sacc., Roum. & Berl.) Theiss. & Syd., Annls mycol. 13(3/4): 305 (1915), ***description of type species of genus***

Subclass Pleosporomycetidae
Pleosporales Luttrell ex M.E. Barr
Astrosphaeriellaceae Phook. et al.

170. ***Pteridiospora bambusae*** Tennakoon, C.H. Kuo & K.D. Hyde, in Mycosphere 9(2): 281 (2018), ***new species***

Camarosporidiellaceae Wanas. et al.

171. ***Camarosporidiella populina*** Chethana, Bulgakov & K.D. Hyde, in Mycosphere 9(2): 284 (2018), ***new species***

Dictyosporiaceae Boonmee & K.D. Hyde

172. ***Dendryphiella phitsanulokensis*** N.G. Liu & K.D. Hyde, in Mycosphere 9(2): 287 (2018), ***new species***

Didymellaceae Gruyter et al.

173. ***Ascochyta clinopodiicola*** Pem, Camporesi & K.D. Hyde, in Mycosphere 9(2): 289 (2018), ***new species***
174. ***Didymella aliena*** (Fr.) Q. Chen & L. Cai, Stud. Mycol. 82: 173 (2015), ***new record***
175. ***Epicoccum nigrum*** Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816), ***new record***
176. ***Neodidymelliopsis negundinis*** Manawasinghe, Bulgakov & K.D. Hyde, in Mycosphere 9(2): 293 (2018), ***new species***

Lentitheciaceae Yin. Zhang et al.

177. ***Poaceascoma taiwanense*** Tennakoon, C.H Kuo & K.D. Hyde, in Mycosphere 9(2): 297 (2018), ***new species***

Melanommataceae G. Winter

178. ***Bertiella ellipsoidea*** Ekanayaka, Q. Zhao & K.D. Hyde, Fungal Diversity 80: 79 (2016), ***new record***
179. ***Byssosphaeria siamensis*** Boonmee, Q. Tian & K.D. Hyde, Fungal Diversity 74: 283 (2015), ***new record***
180. ***Pseudobyssosphaeria*** H.B. Jiang & K.D. Hyde, in Mycosphere 9(2): 303 (2018), ***new genera***
181. ***Pseudobyssosphaeria bambusae*** H.B. Jiang & K.D. Hyde, in Mycosphere 9(2): 306 (2018), ***new species***

Neocamarosporiaceae Wanas. et al.

182. ***Neocamarosporium phragmitis*** Wanas., E.B.G. Jones & K.D. Hyde, in Mycosphere 9(2): 306 (2018), ***new species***

Neohendersoniaceae Giraldo & Crous

183. ***Brevicollum hyalosporum*** Kaz. Tanaka & Toy. Sato, Mycologia 109: 4 (2017), ***new host record***
184. ***Medicopsis chiangmaiensis*** Q.J. Shang & K.D. Hyde, in Mycosphere 9(2): 313 (2018), ***new species***

Neophaeosphaeriaceae Ariyaw. & K.D. Hyde

185. ***Neophaeosphaeria phragmiticola*** A. Karunarathna & K.D. Hyde, in Mycosphere 9(2): 316 (2018), ***new species***

Occultibambusaceae D.Q. Dai & K.D. Hyde

186. ***Neooccultibambusa pandanicola*** Tibpromma, D.J. Bhat & K.D. Hyde, in Mycosphere 9(2): 317 (2018), ***new species***

Periconiaceae Nann.

187. ***Periconia cookei*** E.W. Mason & M.B. Ellis, Mycol. Pap. 56: 72 (1953), ***reference specimen***
188. ***Periconia elaeidis*** T. Sunpapao & K.D. Hyde, in Mycosphere 9(2): 323 (2018), ***new species***
189. ***Periconia pseudobyssoides*** S. Markovskaja & A. Kačergius, Mycological Progress 13 (2): 293 (2014), ***new record***

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

190. **Phaeoseptaceae** S. Boonmee, Thambugala & K.D. Hyde, in Mycosphere 9(2): 323 (2018), ***new family***
191. ***Phaeoseptum terricola*** S. Boonmee & K.D. Hyde, in Mycosphere 9(2): 326 (2018), ***new species***

Phaeosphaeriaceae M.E. Barr

192. ***Neosetophoma guiyangensis*** J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, in Mycosphere 9(2): 331 (2018), ***new species***
193. ***Neosetophoma shoemakeri*** Senwanna, Wanas., Bulgakov, E.B.G. Jones & K.D. Hyde, in Mycosphere 9(2): 332 (2018), ***new species***
194. ***Neosetophoma xingrensis*** J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, in Mycosphere 9(2): 335 (2018), ***new species***

Sporormiaceae Munk

195. ***Neomassarina pandanicola*** Tibpromma & K.D. Hyde, in Mycosphere 9(2): 336 (2018), ***new species***

Roussoellaceae J.K. Liu et al.

196. ***Roussoella mangrovei*** C. Phukhamsakda & K.D. Hyde, in Mycosphere 9(2): 339 (2018), ***new species***

Pleosporomycetidae genera, *incertae sedis*

197. ***Hysterographium didymosporum*** S. Boonmee & K.D. Hyde, in Mycosphere 9(2): 342 (2018), ***new species***

Dothideomycetes orders, *incertae sedis*
Acrospermales Minter et al.
Acrospermaceae Fuckel

198. ***Acrospermum longisporium*** Jayasiri, E.B.G. Jones & K.D. Hyde, in Mycosphere 9(2): 347 (2018), ***new species***

Asterinales M.E. Barr ex D. Hawksw. & O.E. Erikss.
Asterinaceae Hansf. (= Lembosiaceae Hosag.)

199. ***Asterina magnoliae*** X.Y. Zeng, T.C. Wen & K.D. Hyde, in Mycosphere 9(2): 349 (2018), ***new species***

Botryosphaeriales C.L. Schoch et al.
Botryosphaeriaceae Theiss. & H. Syd.

200. ***Diplodia arengae*** R.H. Perera, Wanas. & K.D. Hyde, in Mycosphere 9(2): 352 (2018), ***new species***

Dyfrolomycetales K.L. Pang et al.
Pleurotremataceae Walt. Watson

201. ***Dyfrolomyces sinensis*** Samarak., Tennakoon & K.D. Hyde, in Mycosphere 9(2): 354 (2018), ***new species***

Kirschsteiniotheliales Hern.-Restr. et al.
Kirschsteiniotheliaceae Boonmee & K.D. Hyde

202. ***Kirschsteiniothelia phoenicis*** S.N. Zhang & K.D. Hyde, in Mycosphere 9(2): 357 (2018), ***new species***

Class Lecanoromycetes O.E. Erikss. & Winka
Subclass Acarosporomycetidae Reeb et al.
Teloschistales D. Hawksw. & O.E. Erikss.
Teloschistaceae Zahlbr.

203. ***Cerothallia subluteoalba*** (S.Y. Kondr. & Kärnefelt) Arup, Frödén & Søchting, Nordic Jl Bot. 31(1): 40 (2013), ***new record***

Subclass Lecanoromycetidae P.M. Kirk et al. ex Miadl. et al.
Peltigerales W. Watson
Collemataceae Zenker

204. ***Leptogium thailandicum*** Ekanayaka, Zhao & K.D. Hyde, in Mycosphere 9(2): 361 (2018), ***new species***

Class Pezizomycetes O.E. Erikss. & Winka
Pezizales J. Schröt.
Otideaceae Eckblad
205. ***Otidea pseudoformicarum*** Ekanayaka, Q. Zhao and K.D. Hyde, in Mycosphere 9(2): 364 (2018), ***new species***

Class Leotiomycetes O.E. Erikss. & Winka
Rhytismatales M.E. Barr ex Minter
Rhytismataceae Chevall.
206. ***Lophodermium thailandicum*** N.I. de Silva & K.D. Hyde, in Mycosphere 9(2): 369 (2018), ***new species***

Class Sordariomycetes O.E. Erikss. & Winka
Subclass Diaporthomycetidae Senan. et al.
Annulatascales D'souza et al.
Annulatascaceae S.W. Wong et al.
207. ***Ascitendus aquaticus*** Dayarathne, Fryar, K.D. Hyde, in Mycosphere 9(2): 372 (2018), ***new species***

Diaporthales Nannf.
Cytosporaceae Fr.
208. ***Cytospora predappioensis*** Q.J. Shang, Norphanph., E. Camporesi & K.D. Hyde, in Mycosphere 9(2): 376 (2018), ***new species***
209. ***Cytospora prunicola*** Norphanph., Camporesi, T.C. Wen & K.D. Hyde, in Mycosphere 9(2): 378 (2018), ***new species***

Diaporthaceae Höhn. ex Wehm.
210. ***Diaporthe subellipicola*** S.K. Huang, T.C. Wen & K.D. Hyde, in Mycosphere 9(2): 381 (2018), ***new species***
211. ***Diaporthe subcylindrospora*** S.K. Huang, T.C. Wen & K.D. Hyde, in Mycosphere 9(2): 381 (2018), ***new species***

Diaporthomycetidae families, *incertae sedis*
Barbatosphaeriaceae H. Zhang et al.
212. ***Barbatosphaeria aquatica*** N.G. Liu & K.D. Hyde, in Mycosphere 9(2): 384 (2018), ***new species***

Subclass Hypocreomycetidae O.E. Erikss. & Winka
Hypocreales Lindau
Nectriaceae Tul. & C. Tul.
213. ***Gliocladiopsis aquaticus*** Y.Z. Lu, R.H. Perera & K.D. Hyde, in Mycosphere 9(2): 387 (2018), ***new species***

Ophiocordycipitaceae G.H. Sung et al.
214. ***Ophiocordyceps cylindrospora*** Y.P. Xiao, T.C. Wen & K.D. Hyde, in Mycosphere 9(2): 391 (2018), ***new species***

Stachybotryaceae L. Lombard & Crous
215. ***Alfaria terrestris*** L. Lombard & Crous, in Lombard, Houbraken, Decock, Samson, Meijer, Réblová, Groenewald & Crous, Persoonia 36: 181 (2016), ***new record***

Subclass Sordariomycetidae O.E. Erikss & Winka
Chaetosphaeriales Huhndorf et al.
Chaetosphaeriaceae

216. ***Chaetosphaeria mangrovei*** Dayarathne, E.B.G. Jones & K.D. Hyde, in Mycosphere 9(2): 395 (2018), ***new species***
217. ***Cryptophiale hamulata*** Whitton, K.D. Hyde & McKenzie, in Whitton, McKenzie & Hyde, Fungal Diversity Res. Ser. 21: 174 (2012), ***new record***

Subclass Savoryellomycetidae Hongsanan et al.
Pleurotheciales Réblová & Seifert
Pleurotheciaceae Réblová & Seifert

218. ***Phaeoisaria guttulata*** J. Yang & K.D. Hyde, in Mycosphere 9(2): 401 (2018), ***new species***
219. ***Pleurotheciella krabiensis*** J. Yang & K.D. Hyde, in Mycosphere 9(2): 403 (2018), ***new species***
220. ***Pleurotheciella tropica*** J. Yang & K.D. Hyde, in Mycosphere 9(2): 407 (2018), ***new species***

Subclass Xylariomycetidae O.E. Erikss & Winka
Amphisphaeriales D. Hawksw. & O.E. Erikss.
Apiosporaceae K.D. Hyde et al.

221. ***Arthrinium phragmites*** Crous, ***new host record***

Sporocadaceae Corda

222. ***Discosia querci*** Jayasiri, E.B.G. Jones & K.D. Hyde, in Mycosphere 9(2): 410 (2018), ***new species***
223. ***Seimatosporium ciliata*** (Petr.) Hongsanan & K.D. Hyde, ***new combination***
224. ***Truncatella angustata*** (Pers.) S. Hughes, Can. J. Bot. 36: 822 (1958), ***new host record***

Taxonomic treatment

Phylum Ascomycota

Class Dothideomycetes

For recent arrangements of Dothideomycetes we follow Liu et al. (2017a) and Wijayawardene et al. (2018).

Subclass Dothideomycetidae P.M. Kirk et al.
Dothideales Lindau
Dothideaceae Chevall.

The family is characterized by immersed to erumpent or superficial, uni to multiloculate ascostromata, 8- or poly-spored, bitunicate asci and hyaline or brown ascospores, with transversely septate, or muriform ascospores (Thambugala et al. 2014). The family was recently revised by Thambugala et al. (2014). In this paper, *Uleodothis* is accommodated within Dothideaceae as a sister genus to *Plowrightia* based on the type material of *Uleodothis balansiana*.

Uleodothis Theiss. & Syd.

Plowrightia was introduced in the family Dothideaceae to accommodate twelve species, with *P. ribesia* as the type species (Saccardo 1883). Theissen and Sydow (1915) synonymized *P. balansiana* Sacc. et al., *P. rhynchosporae* (Rehm) Höhn and *Polystomella aphanes* Rehm under a new genus *Uleodothis* in Dothideales based on morphological characters. *Uleodothis* was originally placed in Dothioraceae Theiss. & Syd. (Dothideales) by Stevens (1920), while Müller and von Arx (1962) accepted this genus in Mycosphaerellaceae Lindau (Pseudosphaeriales). Subsequently, the genus was referred to Venturiaceae E. Müll. et al. (Venturiales) by Luttrell (1973). However, Zhang et al. (2011) excluded *Uleodothis* from Venturiales and treated it as genus in

Dothideomycetes *incertae sedis* based on its immersed ascomata in ascostromata, persistent pseudoparaphyses, cylindrical asci, with 1-septate ascospores and this scheme was followed by Wijayawardene et al. (2014, 2017a, 2018). *Uleodothis* is somewhat similar to *Plowrightia* in having semi-immersed, pulvinate, multi-loculate, dark brown to black ascostromata and 1-septate ascospores. However, *Plowrightia* has thick-walled locules developing in the upper part of stroma, lacks pseudoparaphyses and ascospores are constricted at the septum (Barr 1987, Thambugala et al. 2014), while *Uleodothis* has thin-walled locules developing in the middle of stroma, persistent pseudoparaphyses and ascospores not or slightly constricted at the septum (Theissen & Sydow 1915). *Uleodothis* is also similar to *Aplosporella* Speg. (Aplosporellaceae, Botryosphaeriales), however, *Aplosporella* has a wide and irregular opening, thick-walled locules, lacks pseudoparaphyses, usually clavate asci with short pedicels and hyaline to dark brown, uniseptate ascospores (Liu et al. 2012, Thambugala et al. 2014, Ekanayaka et al. 2016).

Morphological similarity and the relationships between *Plowrightia*, *Uleodothis* and other relatives are unresolved due to lack of molecular data. No DNA sequence data is available for *Uleodothis*. Recent phylogenetic studies indicate that *Plowrightia* is a member of Dothideaceae (Winton et al. 2007, Thambugala et al. 2014). Therefore, we place *Uleodothis* in Dothideaceae as a sister genus to *Plowrightia* based on morphological evidence. Fresh collections and sequence data of *Plowrightia* and Uleodothis-like taxa are needed to further clarify their phylogenetic placement and relationships.

Uleodothis balansiana (Sacc., Roum. & Berl.) Theiss. & Syd., Annls mycol. 13(3/4): 305 (1915)
Fig. 1

Index Fungorum number: IF153174; Facesoffungi number: FoF04463

Epiphytes on the lower surface of leaves of *Bignonia* sp. Sexual morph *Ascostromata* 0.33−0.47 mm high × 1−2.6 mm diameter ($\bar{x}$ = 3.6 × 2.2 mm, n = 3), scattered, semi-immersed in host tissue, pulvinate, subglobose to globose, dark brown to black, with branched, projected-ostiole, surface verrucose. *Locules* 177−197 µm high × 114−162 µm diameter ($\bar{x}$ = 182 × 145 µm, n = 10), completely immersed in the middle of the ascostromata, composed of thin, flattened cells of *textura angularis*, pale brown to hyaline. *Hamathecium* of 2−2.5 µm wide, hyaline, aseptate, pseudoparaphyses, embedded in a gelatinous matrix. *Peridium* 40−50 µm, comprising two-layers, outer layer: yellowish-brown to dark brown, cells of *textura angularis*, inner layer: thin, hyaline, flattened cells of *textura angularis*. *Asci* 92−98 × 12−15 µm ($\bar{x}$ = 96 × 13 µm, n = 10), 8-spored, bitunicate, cylindrical to oblong, with slightly long pedicel. *Ascospores* 11−13 × 4−5 µm ($\bar{x}$ = 12 × 4.5 µm, n = 20), uni to biseriate in ascus, uniseptate or swollen at the center, oval to ellipsoid, generally straight, rounded at both ends, not constricted, hyaline, verrucose, embedded in gelatinous matrix. Asexual morph Undetermined.

Material examined – BRAZIL, Santos, on lower surface of leaves of *Bignonia* (Bignoniaceae), June 1884, J. Roumeguère no. BT8164 (BR 5020077187720, holotype).

Notes – *Uleodothis balansiana* was described as having uniseptate ascospores (Saccardo & Berlese 1885). However, we re-examined the type specimen of this species and found that ascospores are generally swollen in the middle of the ascospores, which makes them appear as 2-septate. The ascospore septation of *U. balansiana* is unclear, thus, more specimens are needed to check its septation and other characters (Fig. 1).

Order Pleosporales Luttrell ex M.E. Barr

Astrosphaeriellaceae Phookamsak & K.D. Hyde

The family Astrosphaeriellaceae was introduced by Phookamsak et al. (2015b) to accommodate two genera viz. *Astrosphaeriella* and *Pteridiospora*, which have distinct trabeculae (*sensu* Liew et al. 2001). Members of Astrosphaeriellaceae are characterized by large, conical, carbonaceous ascostromata, with ruptured, reflexed, stellate, host remnants, fusiform or obclavate ascospores and a coelomycetous asexual morph (Phookamsak et al. 2015b).

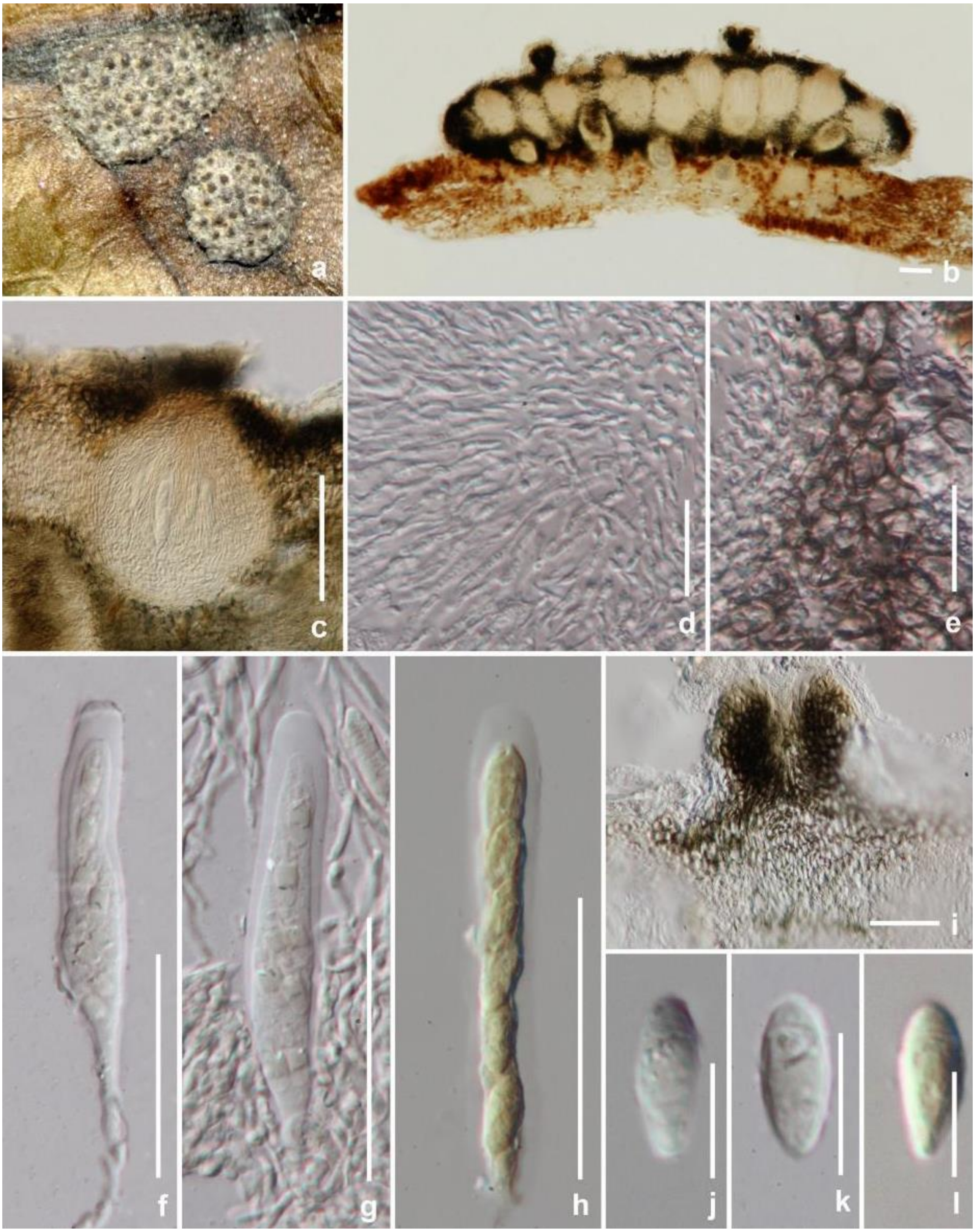


Figure 1 – *Uleodothis balansiana* (BR 5020077187720, holotype). a Habit and ascostromata on substrate. b Section through ascostroma. c Locule. d Pseudoparaphyses. e Peridium of locules. f–g Asci. h Ascus in Melzer's reagent. i Projecting ostiole. j–k Ascospores. l Ascospore in Melzer's reagent. Scale bars: b, c = 100 µm, d, e = 20 µm, f–i = 50 µm, j–l = 10 µm.

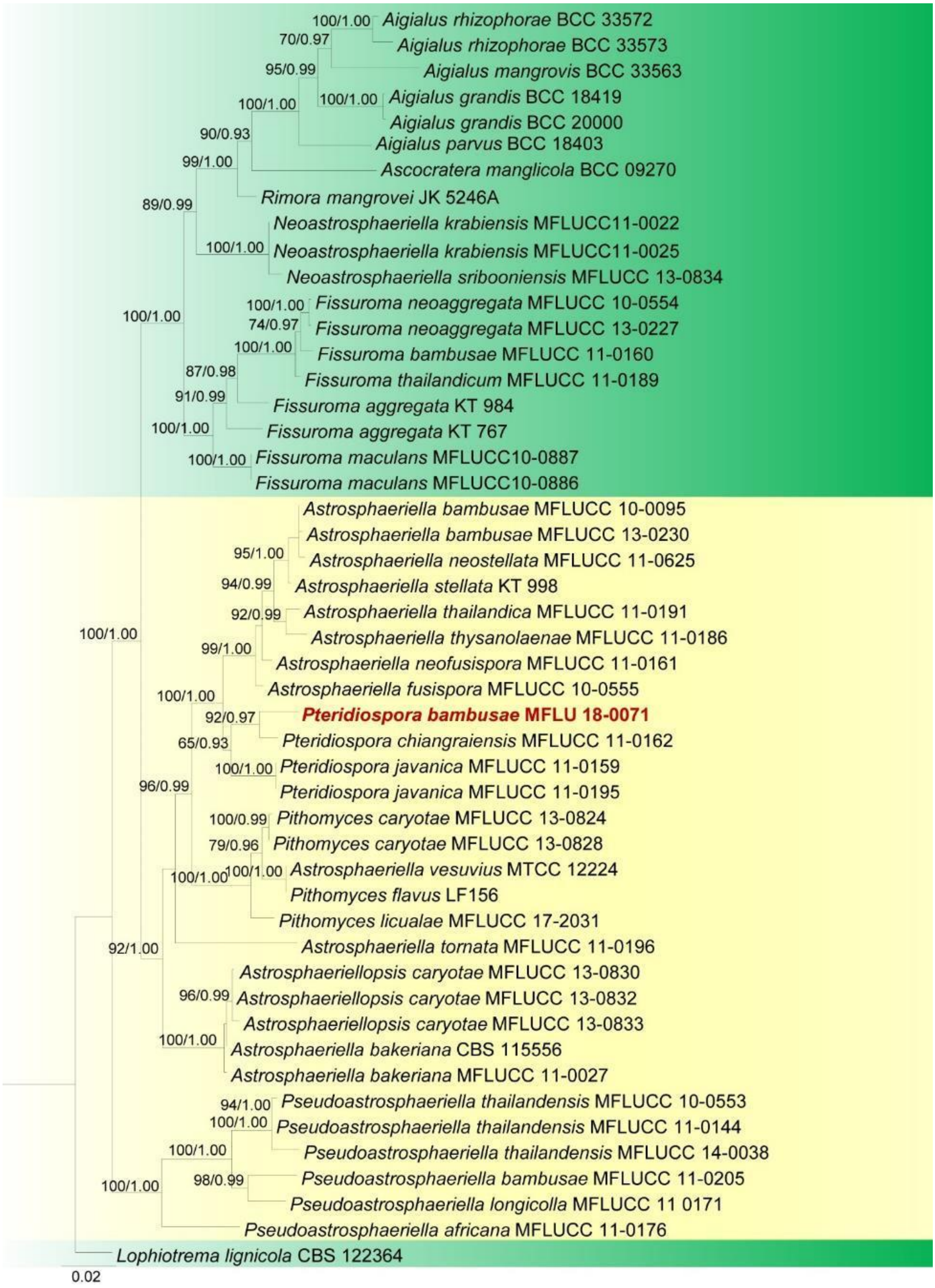


Figure 2 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, and TEF sequenced data of Astrosphaeriellaceae. Related sequences were obtained from Phookamsak et al. (2015b) and Wanasinghe et al. (2017a). Forty-nine strains are included in the combined sequence analyses, which comprise 2935 characters with gaps. *Lophiotrema lignicola*

(CBS 122364) is used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -13717.595943 is presented. The matrix had 912 distinct alignment patterns, with 22.65% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245984, C = 0.246474, G= 0.282945, T = 0.224598; substitution rates AC = 0.896188, AG = 2.815720, AT = 0.826212, CG = 1.104916, CT = 8.845426, GT = 1.000000; gamma distribution shape parameter α = 0.769779. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes respectively. Newly generated sequences are in red.

Pteridiospora Penz. & Sacc.

Pteridiospora was established by Penzig and Saccardo (1897) to accommodate species having mammiform, carbonaceous ascostromata with obclavate to ellipsoidal, or subfusoid ascospores, with a thick, distinct, mucilaginous sheath (Penzig & Saccardo 1897, Phookamsak et al. 2014a, 2015b). Currently, seven *Pteridiospora* species have been recorded viz. *P. chiangraiensis* Phook. & K.D. Hyde, *P. chochrjakovii* Hüseyın, *P. curreyi* (Tul. & C. Tul.) E. Müll., *P. javanica* Penz. & Sacc. (Type species), *P. munkii* Subhedar & V.G. Rao, *P. scoriadea* (Fr.) Dennis and *P. spinosispora* Filer (Index Fungorum 2018). In this study, we illustrate *Pteridiospora bambusae* as a new species from Taiwan.

Pteridiospora bambusae Tennakoon, C.H Kuo & K.D. Hyde, sp. nov. Fig. 3

Index Fungorum number: IF554199; Facesoffungi number: FoF04083

Etymology – the specific epithet *bambusae* was given after the host bamboo on which the fungus was collected.

Holotype – MFLU 18-0071

Saprobic on *Bamboo*. Sexual morph *Ascostromata* 270–350 µm high, 380–530 µm diameter, dark opaque, black, cone-like, gregarious, erumpent to superficial, stellate, host remnants around the base, uni-loculate, glabrous, brittle, carbonaceous, ostiolate. *Ostiole* central, with pore-like opening. *Peridium* 25–50 µm wide, of unequal thickness, poorly developed at the base, composed of small dark, dark brown to black, pseudoparenchymatous cells of *textura angularis*, base and corners comprising a mixture of host and fungal cells. *Hamathecium* composed of 1.5–2 µm wide, filiform, trabeculate pseudoparaphyses, anastomosing at the apex, embedded in a gelatinous matrix. *Asci* (140–)145–180(–190) × (13–)14–17(–18) µm ($\bar{x}$ = 168.6 × 15.5 µm, n = 25), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with short obtuse pedicel, apically rounded with well-developed ocular chamber. *Ascospores* (31–)32–36(–38)×6–8 µm ($\bar{x}$ = 34.5 × 7.5 µm, n = 25), overlapping, uni-to bi-seriate, initially hyaline, becoming brown when mature, subfusoid, with rounded to acute ends, narrow towards the apex, 1-septate, constricted at the septum, upper cell shorter than lower cell, surrounded by an irregular, distinct mucilaginous sheath, with wing-like appendage extending from the lower cell. Asexual morph Undetermined.

Material examined – TAIWAN, Chiayi, Shihnong Forest, dead stems of *Bamboo* sp. (Poaceae), 25 June 2017, D.S. Tennakoon, DTW 020 (MFLU 18-0071, holotype).

GenBank numbers – LSU: MG831565, SSU: MG831566, TEF1: MG833012.

Notes – The morphological characters of *Pteridiospora bambusae* fit in to the generic concept of *Pteridiospora* in having mammiform, carbonaceous ascostromata with obclavate to ellipsoidal, or subfusoid ascospores with a thick, distinct mucilaginous sheath (Penzig & Saccardo 1897, Phookamsak et al. 2015b). Phylogenetic analysis of combined LSU, SSU and TEF sequence data indicates that *P. bambusae* is closely related to *P. chiangraiensis* with high bootstrap support (92% ML, 0.97 BYPP) (Fig. 2). *Pteridiospora bambusae* shares some similar characters with *P. chiangraiensis* and *P. javanica* in having erumpent to superficial, carbonaceous ascomata, short pedicellate, cylindrical-clavate asci and sub-fusoid ascospores, with a thick, distinct mucilaginous sheath and wing-like appendage extending from lower cell (Phookamsak et al. 2015b). *Pteridiospora bambusae* differs from *P. javanica*, in having brown ascospores (initially hyaline), while *P. javanica* has distinct hyaline ascospores. In particular, *P. bambusae* can be distinguished from *P*. *chiangraiensis* by using ascospores characters. Ascospores of *Pteridiospora bambusae* have wing-like appendages which extend from lower long cell, whereas *P*. *chiangraiensis* appendages extend from lower, short cell. Additionally, *P*. *bambusae* has a broad mucilaginous sheath around the upper cell (clearly visible with Indian ink), whereas *P*. *chiangraiensis* lacks a broad mucilaginous sheath. A comparison of the 871 nucleotides across the TEF gene region of *P*. *bambusae* and *P*. *chiangraiensis* (MFLU 11-0198) reveals 29 base pair differences (a difference of 3.3% which supports our establishment of the new taxon as recommended by Jeewon & Hyde (2016)).

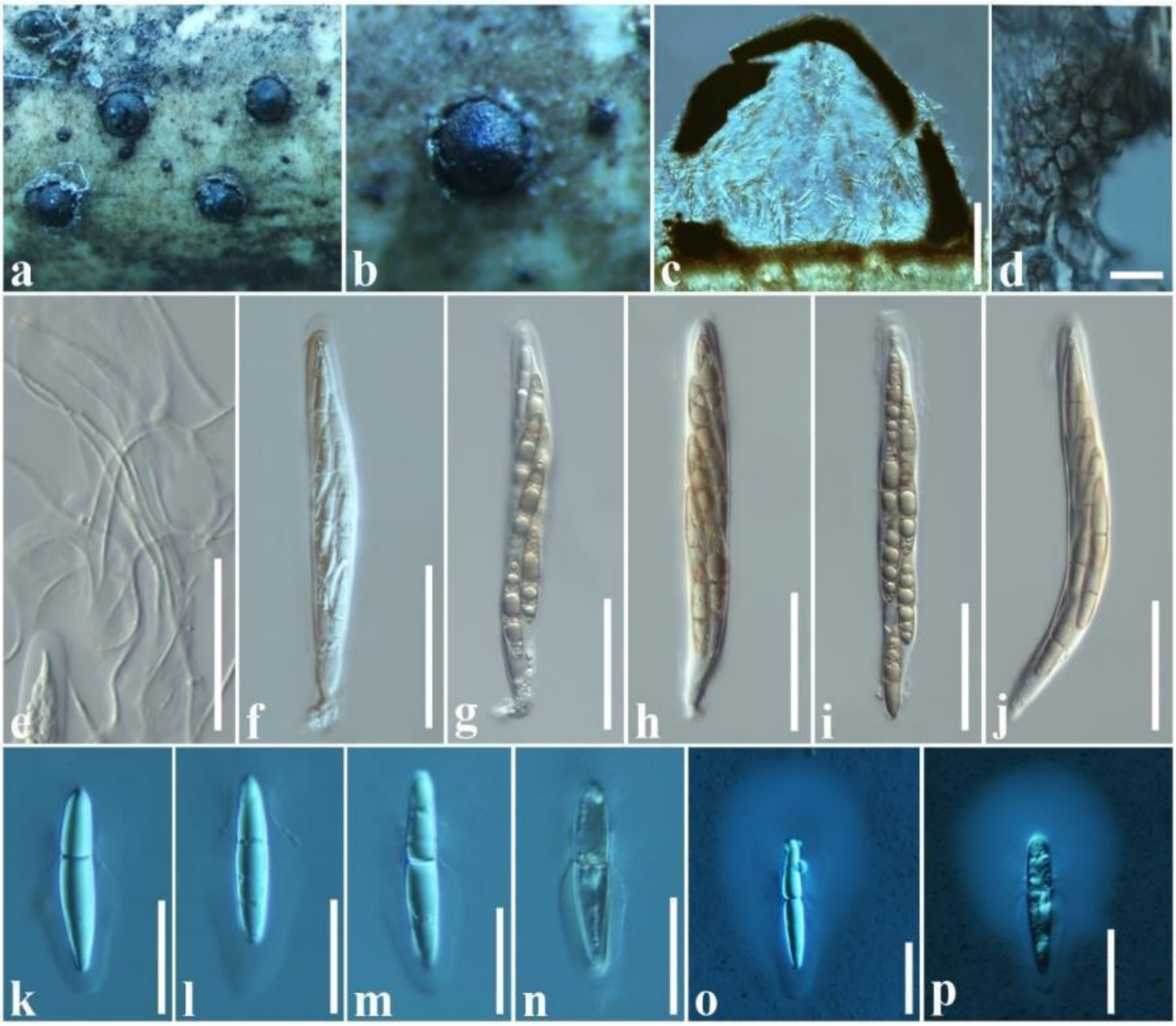


Figure 3 – *Pteridiospora bambusae* (MFLU 18-0071 holotype). a Ascostromata on host. b Close-up of ascostroma. c Vertical section of ascostroma. d Section of peridium. e Pseudoparaphyses. f–j Asci. k–n Ascospores. o, p Ascospores stained in Indian ink. Scale bars: c = 75 µm, d = 50 µm, e–j = 50 µm, k–p = 20 µm.

Camarosporidiellaceae Wanas. et al.

Camarosporidiellaceae was introduced by Wanasinghe et al. (2017b) to accommodate species with conidial morphology resembling *Camarosporium sensu stricto* and other camarosporium-like genera. The family includes a single genus *Camarosporidiella*. The family comprises endophytes, plant pathogens and saprobes (Wanasinghe et al. 2017b). An updated phylogenetic tree for the family is presented in Fig. 4 and we introduce a new species in the genus *Camarosporidiella*.

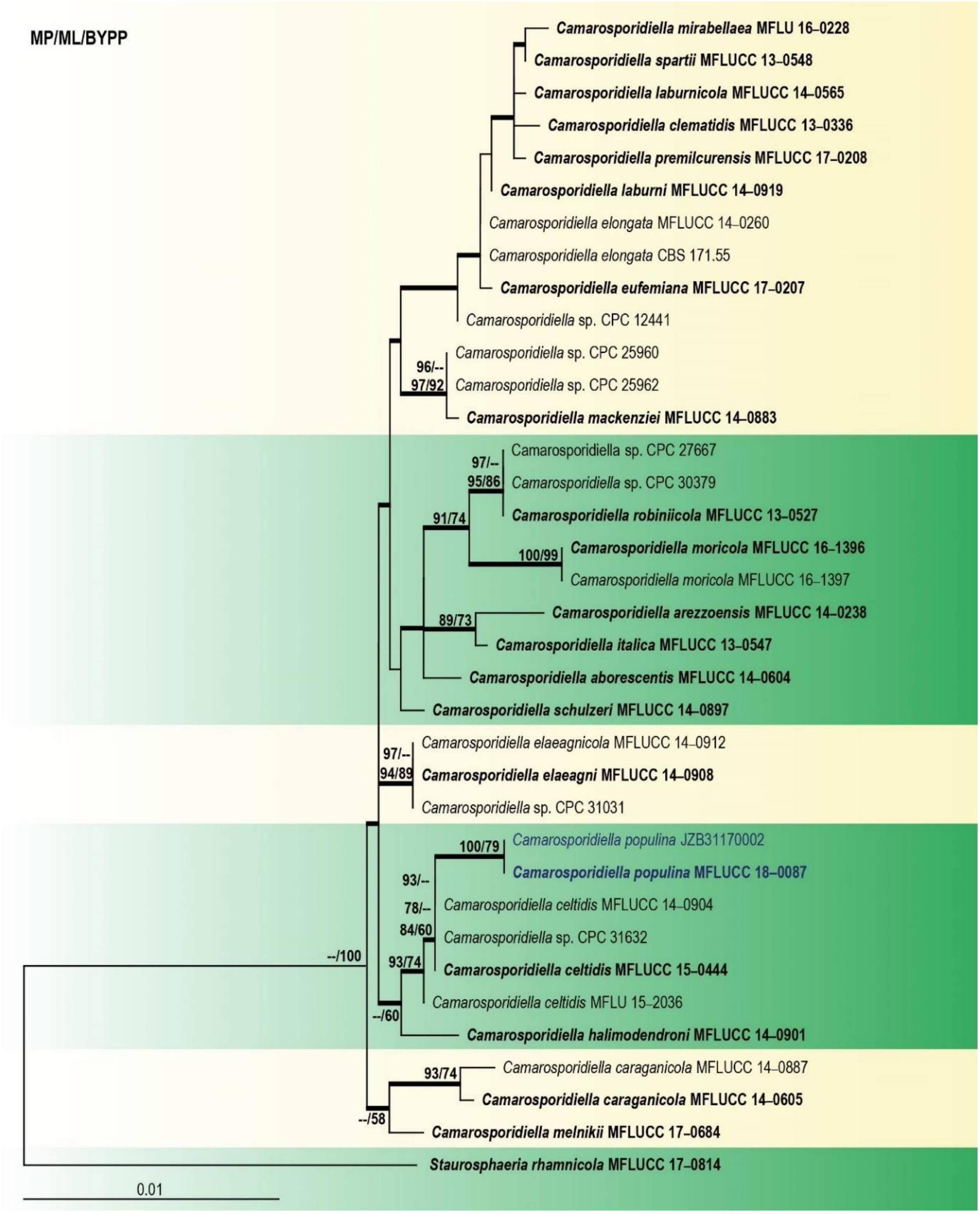


Figure 4 – Phylogenetic tree generated by maximum likelihood analysis of combined LSU, SSU and ITS sequence data of *Camarosporidiella* species. Related sequences were obtained from GenBank. Thirty-six strains are included in the analyses, which comprise 2403 characters including gaps. Tree was rooted with *Staurosphaeria rhamnicola* (MFLUCC 17-0814). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of -4430.059713 is presented. The matrix had 223 distinct alignment patterns, with 12.01% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.251012, C = 0.214068, G = 0.274213, T = 0.260707, substitution rates AC = 1.402990, AG = 3.311951, AT = 1.880669, CG = 0.441830, CT = 4.042681, GT = 1.000000; gamma distribution shape parameter α =

0.020013. The maximum parsimonious dataset consisted of constant 2283, 50 parsimony-informative and 70 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted two equally most parsimonious trees with a tree length of 166 steps (CI = 0.783, RI = 0.829, RC = 0.649, HI = 0.217) in the first tree. RAxML and maximum parsimony bootstrap support values ≥ 50% are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.95 (PP) indicated as thickened black branches. The scale bar indicates 0.01 changes. The ex-type strains are in bold and new isolates in blue.

Camarosporidiella Wanas. et al.

Camarosporidiella was introduced by Wanasinghe et al. (2017b) with *Camarosporidiella caraganicola* (Phukhams. et al.) Phukhams. et al. as the type species (Wanasinghe et al. 2017b). This genus includes camarosporium-like asexual morph and cucurbitaria-like sexual morph.

Camarosporidiella populina Chethana, Bulgakov & K.D. Hyde, sp. nov. Fig. 5

Index Fungorum number: IF553974; Facesoffungi number: FoF03871

Etymology – the specific epithet '*populina'* was given after the host genus *Populus*, from which the fungus was collected.

Holotype – MFLU 16-1722

Necrotrophic or *saprobic* on dead and dying branches of *Populus nigra* L. var. *italica* Münchh. Sexual morph Undetermined. Asexual morph *Conidiomata* 0.2–0.36 mm ($\bar{x}$ = 0.27 mm, n = 10) diameter, pycnidial, solitary, scattered, superficial to semi-immersed, unilocular, globose, black. *Pycnidial wall* multi-layered, 25 µm wide at the base, 16–20 µm wide in sides, outer layer composed of 3–5 layers of thick, brown cells, inner 4–5 layers of hyaline cells of *textura angularis*, cells towards inner layer becomes lighter. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–16 × 2–4 µm ($\bar{x}$ = 10.2 × 3.6 µm, n = 20), enteroblastic, phialidic, doliiform, hyaline, smooth-walled, formed from the inner most layer of pycnidial wall. *Conidia* 11–17 × 4–7 µm ($\bar{x}$ = 13.9 × 5.2 µm, n = 30), oblong, rarely allantoid, straight or slightly curved, initially aseptate, hyaline, becoming 1–3 transverse septate, pale to dark brown at maturity, rarely a longitudinal septum in the middle cell, smooth-walled, rounded at both ends.

Culture characteristics – Colonies on PDA, circular, fimbriate, rough margin, with both surfaces grayish-white in the margin and grey olivaceous towards the center, slow growing, reach 3 cm diameter after 7 days at 20 °C.

Material examined – RUSSIA, Rostov region, Krasnosulinsky District, Donskoye forestry, bottomland shrubbery near Kundryuchya River, on dead and dying branches of *Populus nigra* L. var. *italica* Münchh. (Salicaceae), 6 April 2016, Timur S. Bulgakov TB(F) 1428 (MFLU 16-1722, holotype), ex-type living culture, JZB31170001, JZB31170002, MFLUCC 18-0087, KUMCC 17-0324; *ibid.* (HKAS 101462, isotype).

GenBank numbers – MFLUCC 18-0087 – ITS: MG571222, LSU: MG571224, SSU: MG571226; JZB31170002 – LSU: ITS: MG571223, MG571225, SSU: MG571227.

Notes – Morphological characters indicate that our species belongs to Camarosporidiellaceae and phylogenetic analysis reveal that *C. populina* constitutes a strongly supported independent lineage (93% MLBT /1.00 PP) in Pleosporinae, Pleosporales. In our phylogenetic analyses of combined LSU, SSU and ITS sequence data of *Camarosporidiella* (Fig. 4), *C. populina* strains cluster together sister to *C. celtidis* (MFLUCC 15-0444) and an unidentified *Camarosporidiella* species. *Camarosporidiella populina* is distinct in having superficial to semi-immersed, smaller conidiomata (0.2–0.36 mm), phialidic, conidiogenous cells and 1–3 transversely septate, larger conidia (11–17 × 4–7 µm), in contrast to immersed, large conidiomata (0.35−0.45 mm), annellidic, integrated, conidiogenous cells, smaller conidia (15−20 × 6−8 µm) with 2−3-transverse septa and a longitudinal septum in *C. celtidis* (Wanasinghe et al. 2017b). Our species also shares some morphological characters with *C. populinum* Maubl. Since, this species was introduced in 1923, DNA sequences are unavailable in databases. Our species exhibits conidial characters similar to *C. populinum*, while all other morphological characters were found to be different (Henkel 1923).

Figure 5 – *Camarosporidiella populina* (MFLUCC 18-0087, holotype). a Appearance of conidiomata on dead branch of *Populus nigra* var. *italica*. b Horizontal section of a conidioma. c Longitudinal section of a conidioma. d–e Longitudinal section of conidioma wall showing cell organization. f–g Conidiogenous cells with developing conidia. h–i Different septation patterns on conidia. j–k Upper view (j) and the reverse view (k) of the colony on PDA. Scale bars: a = 1 mm, b = 10 µm, c = 50 µm, d–e = 20 µm, f– i = 10 µm.

Dictyosporiaceae Boonmee & K.D. Hyde

The family Dictyosporiaceae was first mentioned in Liu et al. (2015) which was referred as Dictyosporiaceae. Tanaka et al. (2015) included Dictyosporiaceae in the order Pleosporales within the suborder Massarineae. Boonmee et al. (2016) validated this family typified by the genus *Dictyosporium* Corda, along with nine genera named *Aquaticheirospora*, *Cheirosporium*, *Dendryphiella*, *Dictyocheirospora*, *Digitodesmium*, *Gregarithecium*, *Jalapriya*, *Pseudocoleophoma*, *Pseudodictyosporium* and an undetermined genus based on both morphology and phylogeny. In this paper, we introduce a new species of *Dendryphiella* and provide an updated backbone tree for the family.

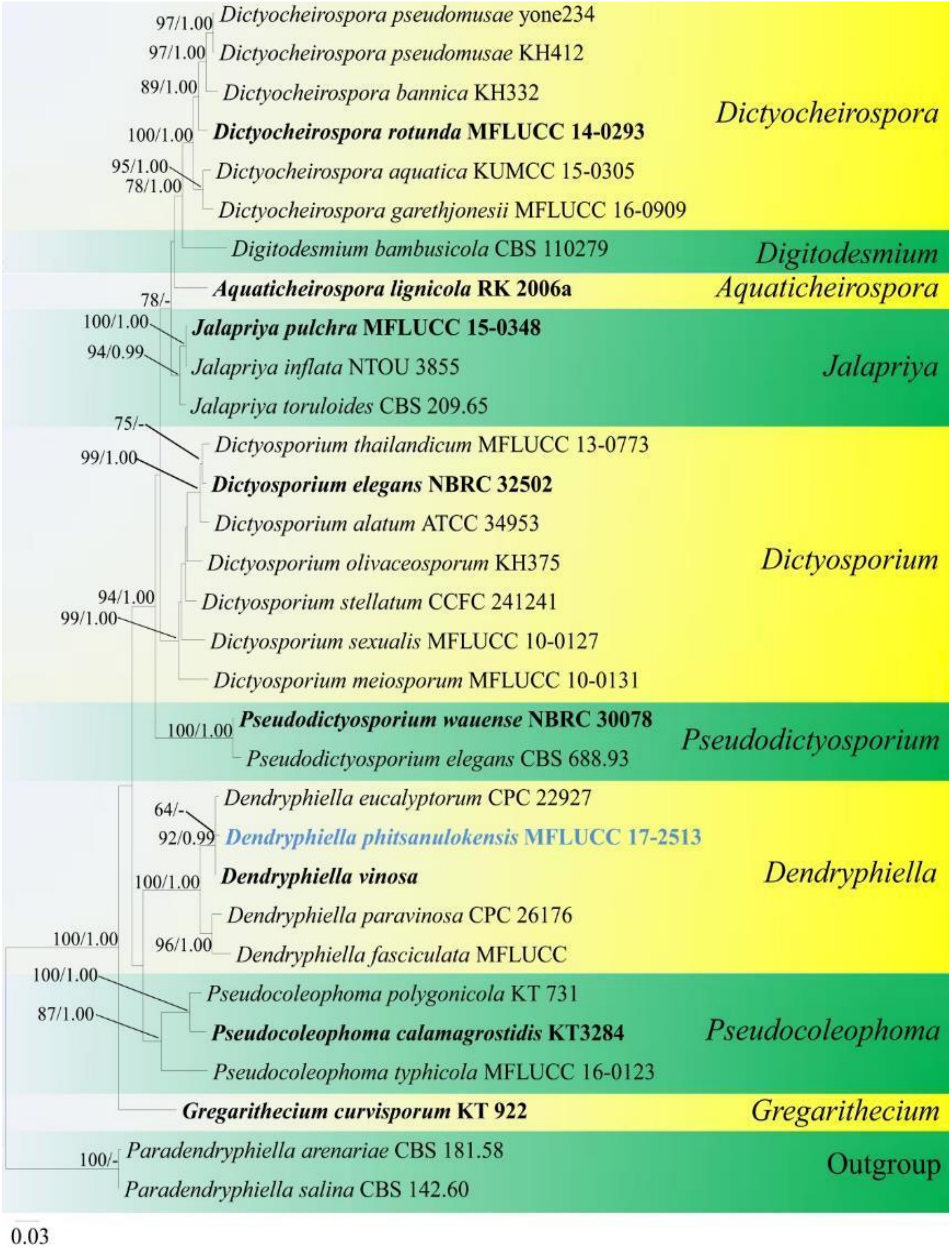


Figure 6 – Maximum likelihood (RAxML) tree based on analysis of a combined dataset of ITS and LSU sequence data representing Dictyosporiaceae. Related sequences are obtained from GenBank. Thirty-one stains are included in the analyses, which comprise 1892 characters including gaps. Tree topologies are similar between ML and BI analyses. The tree is rooted with *Paradendryphiella arenariae* (CBS 181.58) and *P. salina* (CBS 142.60). The best scoring RAxML tree with a final likelihood value of -8400.855146 is presented. The matrix had 527 distinct alignment patterns, with 23.99% of undetermined characters or gaps. Estimated base frequencies were as follows; A =

0.244437, C = 0.231831, G = 0.277299, T = 0.246433; substitution rates AC = 1.481839, AG = 2.484138, AT = 2.286573, CG = 0.384699, CT = 6.114449, GT = 1.000000; gamma distribution shape parameter α = 0.145556. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The scale bar indicates 0.03 changes. The genetic types are indicated in bold and new isolate in bold and blue.

Dendryphiella Bubák & Ranoj.

The genus *Dendryphiella* was established by Ranojevic (1914), with the type species *D. interseminata* (Berk. & Ravenel) Bubák. The genus is characterized by macronematous conidiophores with polytretic, integrated conidiogenous cells at the swollen apices and intercalary swellings and catenate or solitary conidia (Ellis 1971, Matsushima 1971, Rai & Kamal 1986, Guo & Zhang 1999, Crous et al. 2014, Crous et al. 2016, Liu et al. 2017b). Conidiogenesis in *Dendryphiella* is distinct from other genera residing in Dictyosporiaceae. Historically, *Dendryphiella* was transferred to *Dendryphion* and *Scolecobasidium* based on morphology. Liu et al. (2017b) updated the taxonomy of this genus with twelve species and a key.

Dendryphiella phitsanulokensis N.G. Liu & K.D. Hyde, sp. nov. Fig. 7

Index Fungorum number: IF554049; Facesoffungi number: FoF03897

Etymology – name reflects the location where the specimen was collected.

Holotype – MFLU 17-2651

Saprobic on decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* on natural substrate superficial, effuse, greyish-brown. *Mycelium* partly immersed, composed of septate, branched, brown, guttulate, 1.5−3 μm wide hyphae. *Conidiophores* 130−260 μm long, macronematous, mononematous, occasionally fasciculate, dark brown at base, paler towards the apex, thick-walled, erect, straight or slightly flexuous, minutely verruculose, septate, unbranched, wider at the sub-section. *Conidiogenous cells* 15−28 μm long ($\bar{x}$ = 22.35 μm, n = 15), polytretic, terminal and intercalary, proliferating asymmetrically, integrated, brown, minutely verrucose, enlarged at vertex. *Conidia* 16−26 × 2.5−4.4 μm ($\bar{x}$ = 12.09 × 3.59 μm, n = 25), solitary to catenate, when catenate in acropetal chains, fusiform to ellipsoidal, rounded at apex, truncate at the base, pale brown, aseptate when young, brown or dark brown, 3(4)-septate when mature, slightly constricted at septa, thick-walled, verrucose.

Culture characteristics – Conidia germinated on WA (Water Agar) within 24 hours. One or two germ tubes produced from both ends. Colonies reached about 5 cm diameter after 2 weeks on PDA at 25°C. Mycelia are superficial, with entire edge, floccose at the center, white to light brown from above and light brown from below.

Material examined – THAILAND, Phitsanulok Province, on decaying wood, 10 October 2016, Ningguo Liu, J4 (MFLU 17-2651, holotype); ex-type living culture, MFLUCC 17-2513.

GenBank numbers – ITS: MG754400, LSU: MG754401, SSU: MG754402.

Notes – *Dendryphiella phitsanulokensis* and *D. fasciculata* share similar conidial characters (pale brown, aseptate when young, brown, 3-septate when mature). The appearance of most solitary conidiophores makes *D. phitsanulokensis* different from *D. broussonetiae*, *D. fasciculata* and *D. lycopersicifolia* which have fasciculate conidiophores. *Dendryphiella phitsanulokensis* resembles *D. aspera* in occasionally having fasciculate conidiophores. However, *D. phitsanulokensis* has shorter conidiophores and smaller conidia than those of *D. aspera* (100−150 vs. up to 136−544 μm and 9−14 × 2.5−4.4 vs. 10−22 × 4−6 μm). Moreover, *D. phitsanulokensis* differs from *D. eucalypti* in having rough conidia, while the latter have smooth conidia. Phylogenetic analysis indicates a close affinity of *D. phitsanulokensis* to *D. vinosa* and *D. eucalyptorum* without much resolution (Fig. 6). This could be an artifact of taxon sampling (e.g Huang et al 2017) and problems associated with only the rDNA sequence data analysed (Liu et al. 2017b). However, *D. phitsanulokensis* differs from *D. vinosa* and *D. eucalyptorum* in terms of shorter and unbranched conidiophores. Moreover, examination of the 500 nucleotides across the ITS regions reveals 12 bp (2.4%) differences between *D. phitsanulokensis* and *D. eucalyptorum* (KJ869139).

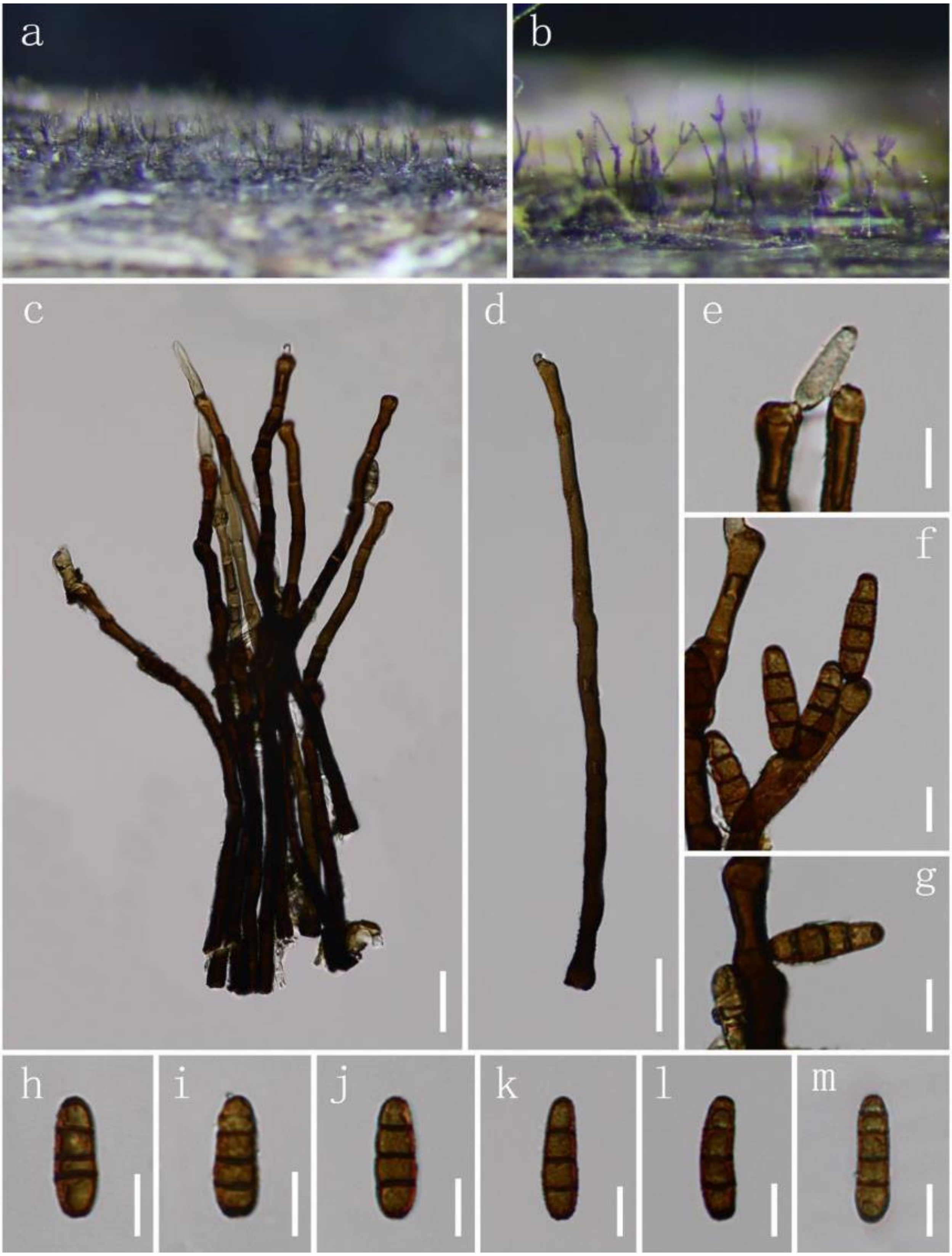


Figure 7 – *Dendryphiella phitsanulokensis* (MFLU 17-2651, holotype). a, b Colonies on host. c, d Conidiophores. e–g Conidiogenous cells and conidia. h–m Conidia. Scale bars: c, d = 25 µm, e–m = 10 µm.

Didymellaceae Gruyter et al.

Didymellaceae was introduced by de Gruyter et al. (2009) to accommodate *Ascochyta*, *Didymella*, *Phoma* and phoma-like genera. The family comprises numerous endophytic, pathogenic and saprobic species associated with a wide range of hosts worldwide (Chen et al. 2015, Hyde et al. 2016). In this paper, we provide an updated phylogeny for selected genera (*Ascochyta*, *Didymella*, *Epicoccum* and *Neodidymelliopsis*) in Didymellaceae (Fig. 8). We also introduce the new species, *Ascochyta nepetigena* and *Neodidymelliopsis negundinis* and provide new host records for *Didymella aliena* and *Epicoccum nigrum*.

Ascochyta Lib.

The genus *Ascochyta* was described and introduced by Libert in 1830 typified by *A. pisi* (=*Didymella pisi* Chilvers, J.D. Rogers & Peever 2009). *Ascochyta* is characterized by globose locules with perithecial protuberances immersed in the stroma. Most species in *Ascochyta* are endophytic, pathogenic and saprobic and associated with a number of hosts worldwide (Wijayawardene et al. 2017a). *Ascochyta* was accepted as a genus in Didymellaceae (Hyde et al. 2013, Kirk et al. 2013). The asexual morph of *Ascochyta* is coelomycetous (Chen et al. 2015). Currently, around 400 species are accomodated in this genus (Wijayawardene et al. 2017a), however, the genus *Ascochyta* needs generic revision as more than 1000 records are available. In this paper, we introduce a new species in the genus *Ascochyta* which was isolated from the stem of *Clinopodium nepeta* in Italy.

Ascochyta clinopodiicola D. Pem, Camporesi & K.D. Hyde, sp. nov. Fig. 9

Index Fungorum number: IF554300; Facesoffungi number: FoF04374

Etymology – referring to the host from which the specimen was isolated.

Holotype – MFLU 17-1034

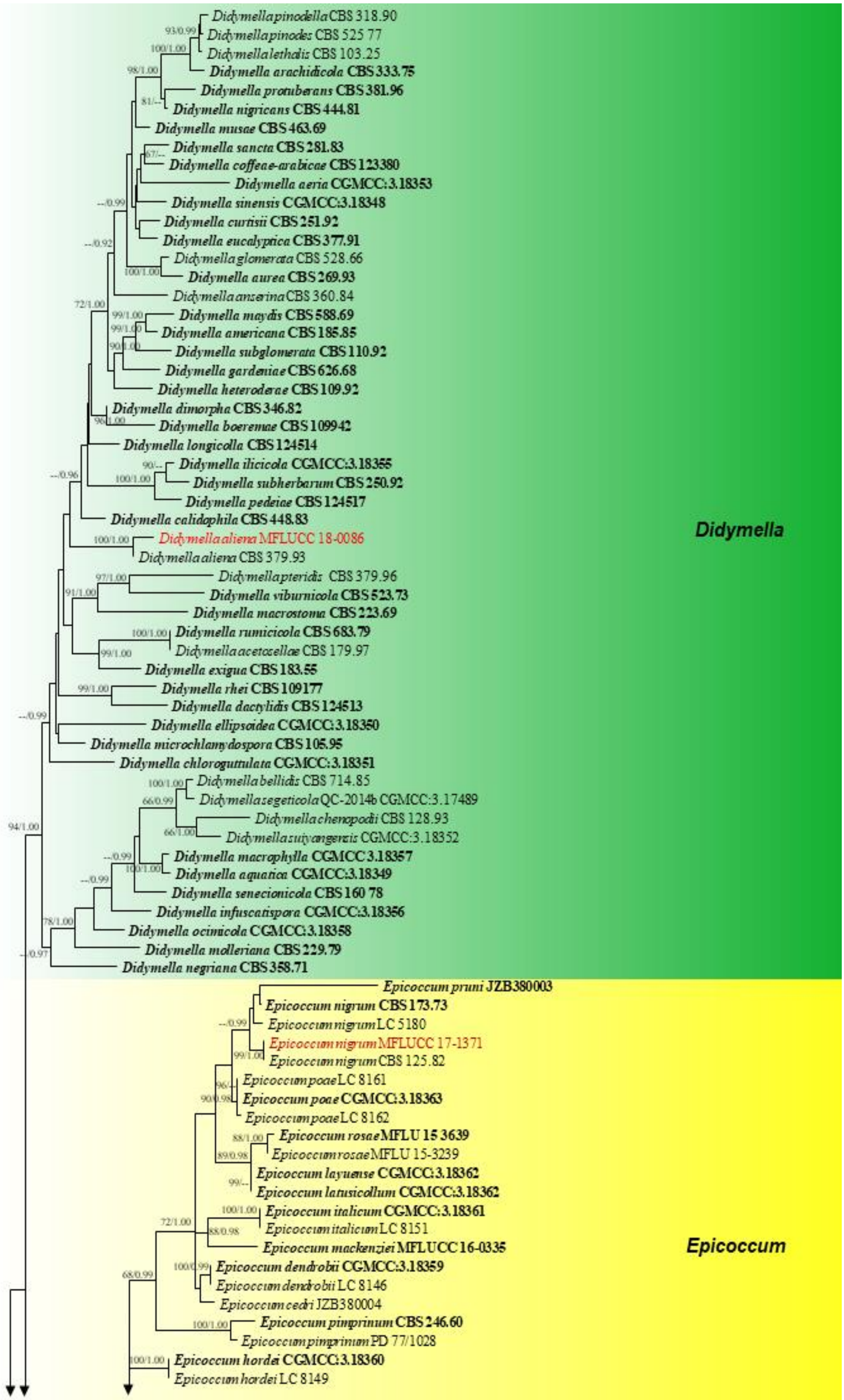
Saprobic on *Clinopodium nepeta*. Sexual morph *Ascomata* 16−33 µm diameter, 15−33 µm high ($\bar{x}$ = 19.3 × 25.4 µm, n = 20), pseudothecia, solitary or gregarious, semi-immersed to erumpent, or rarely superficial, black, papillate, ostiole filled with hyaline cells. *Peridium* 8–9 µm wide at the base, 15–20 µm wide at the sides, comprising two layers cells of *textura angularis*, innermost layer pale brown to darker brown at outer surface, thin-walled. *Hamathecium* lacking pseudoparaphyses. *Asci* 25−34 × 5−7 µm ($\bar{x}$ = 28.6 × 6.5 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, short-pedicellate, apically rounded, with an ocular chamber. *Ascospores* 8−11 × 2−3 µm ($\bar{x}$ = 9.5 × 2.5 µm, n = 10), overlapping uniseriate or biseriate, hyaline, ovoid to ellipsoidal, asymmetrical, upper cell wider than lower cell, 1-septate, slightly constricted at the septum, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours. *Colonies* growing on MEA, reaching 2 cm diameter in 1 week at 16°C. *Mycelium* superficial, surface smooth, irregular, slightly raised, edge crenate, velutinous, from above white to pale yellow, reverse yellow-brown to orange-brown.

Material examined – ITALY, Province of Forlì-Cesena [FC], Spinello - Santa Sofia, on dead aerial stem of *Clinopodium nepeta* (L.) Kuntze (Lamiaceae), 18 May 2017, Erio Camporesi IT 3353 (MFLU 17-1034, holotype); ex-type living culture, MFLUCC 18-0344, ICMP; *ibid.* (HKAS 97475, isotype).

GenBank numbers – ITS: MH017431, LSU: MH017429, SSU: MH017430.

Notes – During our investigation on the diversity of microfungi in Italy, a fungal isolate was collected from a dead stem of *Clinopodium nepeta* in the Province of Forlì-Cesena. Morphological characters, namely erumpent, papillate ascomata, bitunicate, subcylindrical to subclavate, somewhat curved, slightly pedicellate asci and ovoid to ellipsoidal, hyaline, 1-septate ascospores (Fig. 9), fit well within the species concept of *Ascochyta* (Kaiser et al. 1997, Chilvers et al. 2009). DNA sequence analyses from the ribosomal genes confirm that our new taxon belongs to the genus *Ascochyta* and is closely related to *A. medicaginicola* and *A. premilcurensis* (Fig. 8). However, our new taxon *A. clinopodiicola* differs from *A. medicaginicola* by its smaller ascomata (16−33 µm diameter, 15−33 µm high vs. 165−190 µm high, 170−210 µm wide), shorter asci (25−34 × 5−7 µm vs. 50−84 × 8−14 µm) and narrower ascospores (8−11 × 2−3 µm vs. 12−16 × 3−5 µm) (Jayasiri et al. 2017).


Didymella pinodella CBS 318.90
93/0.99
Didymella pinodes CBS 525 77
100/1.00
Didymella lethalis CBS 103.25
98/1.00
Didymella arachidicola CBS 333.75
Didymella protuberans CBS 381.96
81/--
Didymella nigricans CBS 444.81
Didymella musae CBS 463.69
Didymella sancta CBS 281.83
67/--
Didymella coffeae-arabicae CBS 123380
Didymella aeria CGMCC:3.18353
--/0.99
Didymella sinensis CGMCC:3.18348
Didymella curtisii CBS 251.92
--/0.92
Didymella eucalyptica CBS 377.91
Didymella glomerata CBS 528.66
100/1.00
Didymella aurea CBS 269.93
Didymella anserina CBS 360.84
72/1.00
99/1.00
Didymella maydis CBS 588.69
99/1.00
Didymella americana CBS 185.85
90/1.00
Didymella subglomerata CBS 110.92
Didymella gardeniae CBS 626.68
Didymella heteroderae CBS 109.92
Didymella dimorpha CBS 346.82
96/1.00
Didymella boeremae CBS 109942
Didymella longicolla CBS 124514
90/--
Didymella ilicicola CGMCC:3.18355
--/0.96
100/1.00
Didymella subherbarum CBS 250.92
Didymella pedeiae CBS 124517
Didymella calidophila CBS 448.83
100/1.00
Didymella aliena MFLUCC 18-0086
Didymella aliena CBS 379.93
97/1.00
Didymella pteridis CBS 379.96
91/1.00
Didymella viburnicola CBS 523.73
Didymella macrostoma CBS 223.69
100/1.00
Didymella rumicicola CBS 683.79
Didymella acetosellae CBS 179.97
99/1.00
Didymella exigua CBS 183.55
99/1.00
Didymella rhei CBS 109177
Didymella dactylidis CBS 124513
--/0.99
Didymella ellipsoidea CGMCC:3.18350
Didymella microchlamydospora CBS 105.95
Didymella chloroguttulata CGMCC:3.18351
100/1.00
Didymella bellidis CBS 714.85
66/0.99
Didymella segeticola QC-2014b CGMCC:3.17489
94/1.00
Didymella chenopodii CBS 128.93
66/1.00
Didymella suiyangensis CGMCC:3.18352
--/0.99
Didymella macrophylla CGMCC 3.18357
100/1.00
Didymella aquatica CGMCC:3.18349
--/0.99
Didymella senecionicola CBS 160 78
Didymella infuscatispora CGMCC:3.18356
78/1.00
Didymella ocimicola CGMCC:3.18358
Didymella molleriana CBS 229.79
--/0.97
Didymella negriana CBS 358.71
Didymella
Epicoccum pruni JZB380003
Epicoccum nigrum CBS 173.73
--/0.99
Epicoccum nigrum LC 5180
Epicoccum nigrum MFLUCC 17-1371
99/1.00
Epicoccum nigrum CBS 125.82
Epicoccum poae LC 8161
96/--
90/0.98
Epicoccum poae CGMCC:3.18363
Epicoccum poae LC 8162
88/1.00
Epicoccum rosae MFLU 15 3639
89/0.98
Epicoccum rosae MFLU 15-3239
Epicoccum layuense CGMCC:3.18362
99/--
Epicoccum latusicollum CGMCC:3.18362
100/1.00
Epicoccum italicum CGMCC:3.18361
72/1.00
88/0.98
Epicoccum italicum LC 8151
Epicoccum mackenziei MFLUCC 16-0335
Epicoccum
100/0.99
Epicoccum dendrobii CGMCC:3.18359
68/0.99
Epicoccum dendrobii LC 8146
Epicoccum cedri JZB380004
100/1.00
Epicoccum pimprinum CBS 246.60
Epicoccum pimprinum PD 77/1028
100/1.00
Epicoccum hordei CGMCC:3.18360
Epicoccum hordei LC 8149

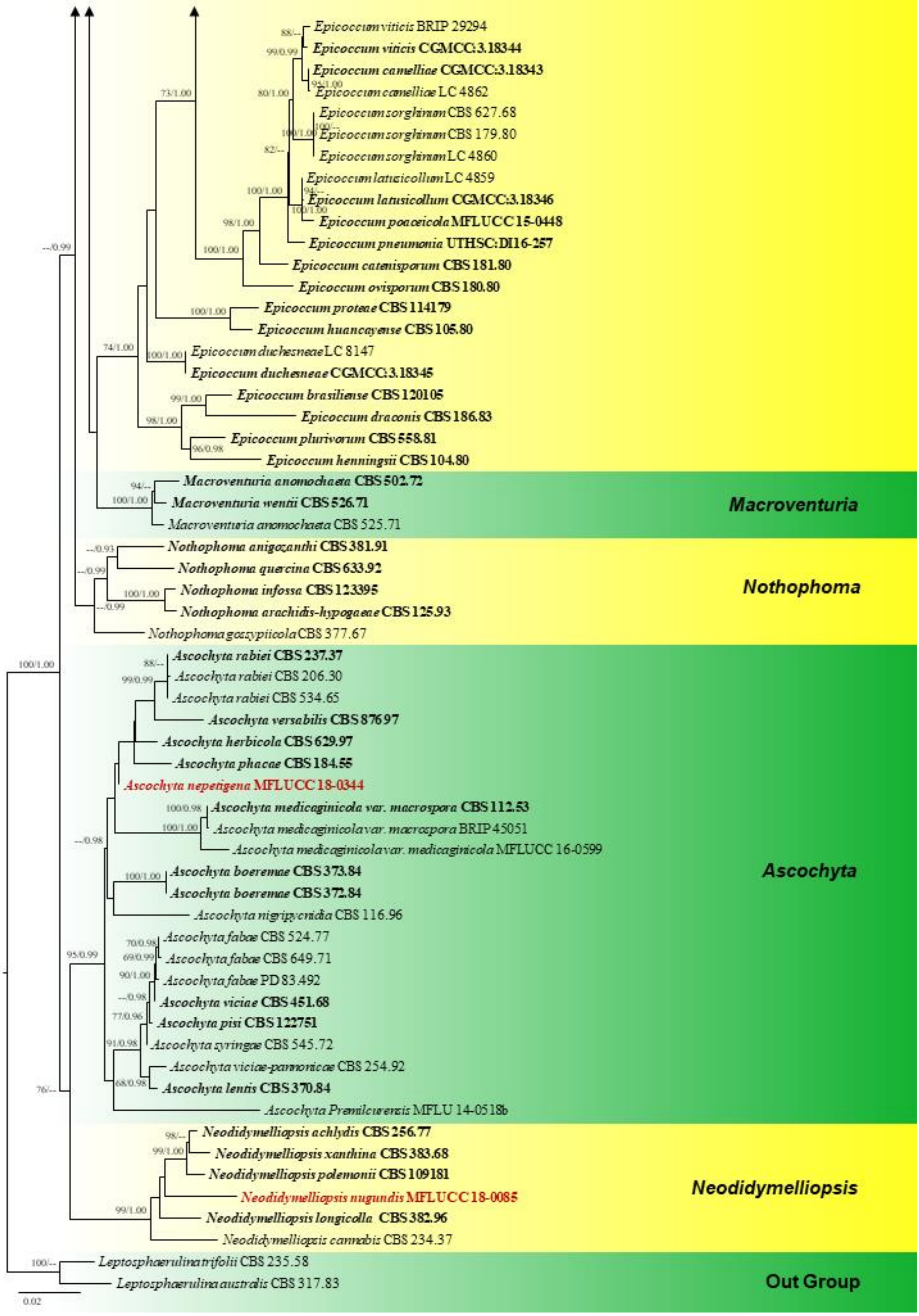


Figure 8 – Phylogram generated from maximum likelihood analysis of a combined LSU, ITS, RPB2 and β-tubulin DNA sequence data of Didymellaceae. Related sequences were obtained from Hyde et al. (2017a, b) and Chen et al. (2017). One hundred and thirty-three strains are included in the combined dataset, which comprise 2863 characters with gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability.

Leptosphaerulina australis (CBS 317.83) and *Leptosphaerulina trifolii* (CBS 235.58) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -22539.886013 is presented. The matrix had 748 distinct alignment patterns, with 17.94% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 1.000000, C = 0.242053, G= 0.239955, T = 0.274733; substitution rates AC = 1.818252, AG = 1.330539, AT = 5.943005, CG = 1.868178, CT = 0.883503, GT = 11.631688; gamma distribution shape parameter α = 0.788126. Bootstrap support values for ML equal to or greater than 65% and BYPP equal to or greater than 0.90 are given above the nodes respectively. Ex-type strains and reference strains are in bold. Newly generated sequences are in red.

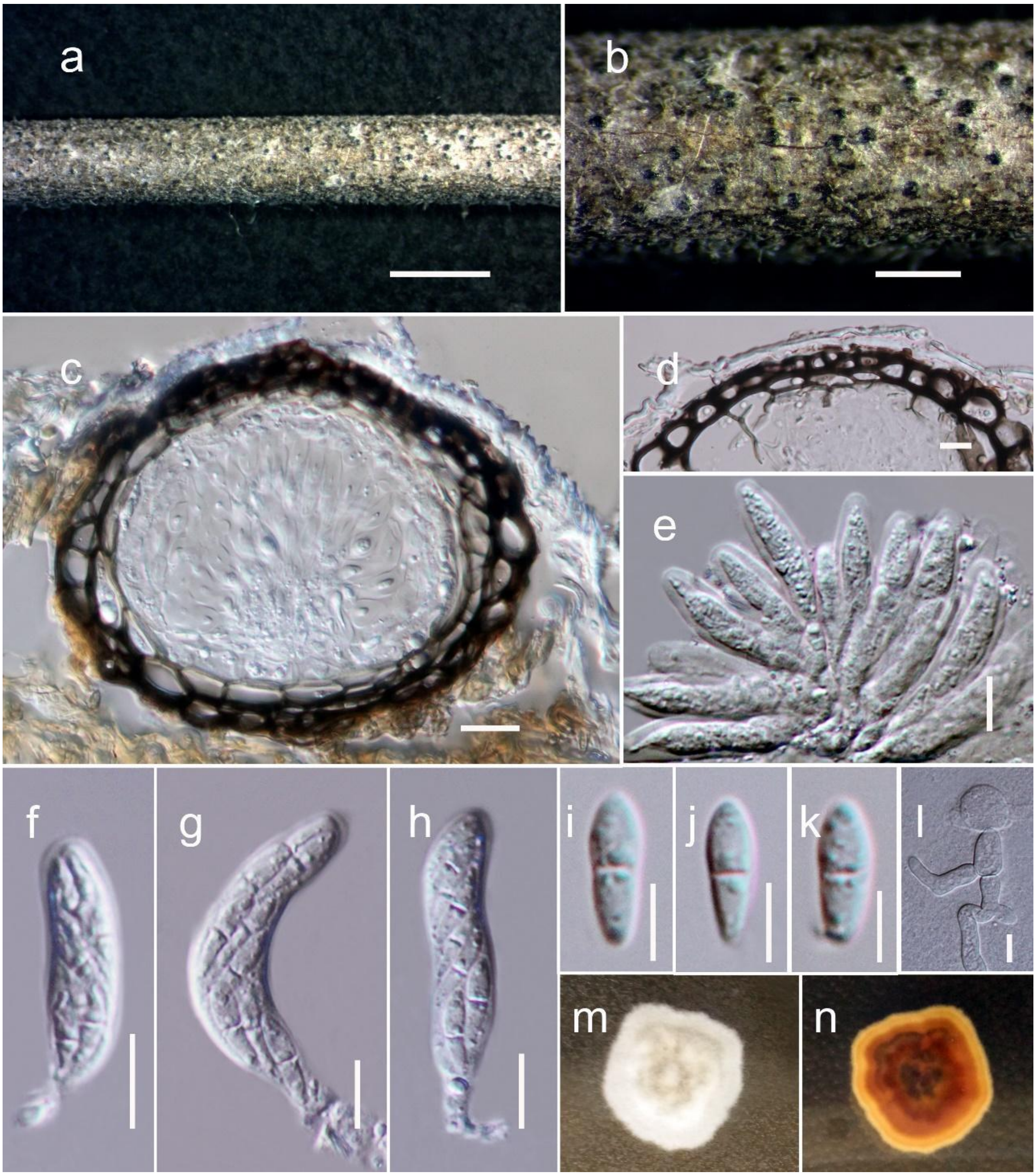


Figure 9 – *Ascochyta clinopodiicola* (MFLU 17-1034, holotype) a, b Ascomata on host surface. c Section of ascoma. d Peridium. e Asci. f–h Developmental stages of Asci. i–k Ascospores. l Germinated Ascospores. m, n Culture characters on MEA (m: above view, n: reverse view). Scale bars: a, b = 500 µm, c = 15 µm, d–h = 10 µm, i–k = 5 µm, l = 10 µm.

Didymella Sacc.

Didymella was described by Saccardo in 1880 with the description of *Didymella exigua* (Niessl) Sacc. (Corlett 1981, Chen et al. 2015). This genus has received much attention in recent studies and several new species has been introduced (Wijayawardene et al. 2017a, Thambugala et al. 2017, Chen et al. 2017, Valenzuela-Lopez et al. 2018).

Didymella aliena (Fr.) Q. Chen & L. Cai, Stud. Mycol. 82: 173 (2015) Fig. 10

Facesoffungi number: FoF03870

Basionym – *Sphaeria aliena* Fr., Syst. Mycol. 2(2): 502 (1823).

Opportunistic pathogenic on dead and dying branch of *Malus domestica* Borkh. Sexual morph Undetermined. Asexual morph Coelomycetous. *Conidiomata* on host 0.17–0.33 mm ($\bar{x}$ = 0.23 mm, n = 10) diameter, pycnidial, solitary, scattered, semi-immersed, unilocular, globose, black; in culture: 0.12–0.25 mm ($\bar{x}$ = 0.17 mm, n = 10) diameter, pycnidial, solitary, scattered, superficial, globose, black. *Pycnidial wall* 9–17 µm, multi-layered, outer layer composed of 3–4 layers of thick, dark brown cells, inner 2–3 layers of hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* on host 4–8 × 1–3 µm ($\bar{x}$ = 5.6 × 2.1 µm, n = 20), enteroblastic, phialidic, globose to bottle-shaped, hyaline, smooth-walled, formed from the inner most layer of pycnidial wall. *Conidia* on host 6–10 × 3–5 µm ($\bar{x}$ = 8.2 × 4.2 µm, n = 30), ellipsoid, straight, initially aseptate, hyaline, becoming 1-septate, pale brown at maturity, smooth-walled, acutely-rounded apex; in culture: 3–7.5 × 2–4 µm ($\bar{x}$ = 5.8 × 3.1 µm, n = 30), ellipsoid to slightly ovoid, initially hyaline, becoming light brown at maturity, aseptate, smooth-walled, with acutely-rounded ends, with or without some small guttules at the ends.

Culture characteristics – *Colonies* on PDA reach 45 mm diameter, after 3 days at 25°C, floccose to woolly, white to grey olivaceous aerial mycelium, reverse olivaceous grey to dark iron grey, with vinaceous buff margin.

Material examined – RUSSIA, Rostov region, Shakhty City, on dead and dying branch of *Malus domestica* Borkh. (Rosaceae), 1 March 2016, Timur S. Bulgakov T-1235 (MFLU 16-1529); living cultures, JZB380010, MFLUCC 18-0086, KUMCC 17-0323.

GenBank numbers – β-tubulin: MG571228, ITS: MG571229, LSU: MG571230, RPB2: MG571231.

Notes – *Didymella aliena* has been reported from France, Italy, Netherlands and Poland on several hosts including *Berberis* sp., *Buxus* sp., *Cotoneaster* sp., *Euonymus europaeus*, *Mahonia aquifolium* and *Pyrus calleryana* (Boerema et al. 2004, Chen et al. 2015, Farr & Rossman 2017). Based on our phylogenetic analysis of combined LSU, ITS, RPB2, and β-tubulin sequence data of Didymellaceae species (Fig. 8), our strain (MFLUCC 18-0086) clusters with the ex-type strain of *Didymella aliena* (CBS 379.93) with high bootstrap support (100% MP/1.00 PP respectively). The holotype of the *Sphaeria aliena* (basionym of *Didymella aliena*) is not known to exist. Therefore, a neotype was designated for the species (de Gruyter et al. 1998). Our isolate is similar to the neotype of *D. aliena* (CBS 379.93). However, the description only includes several morphological characters on different kinds of agar. In this paper we provide a full description of the species on the host, as well as on media.

Epicoccum Link

The genus *Epicoccum* has an estimated over 30 species (Hyde et al. 2017b, Wijayawardene et al. 2017a, Wanasinghe et al. 2018). *Epicoccum* has a hyphomycetous asexual morph and the sexual morph is presently unknown. *Epicoccum* has a cosmopolitan distribution and comprises saprobes in terrestrial habitats (Wijayawardene et al. 2017a).

Epicoccum nigrum Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815] Fig. 11

Facesoffungi number: FoF02685

Saprobic on dead leaves of *Sasa nipponica*. Sexual morph Undetermined. Asexual morph

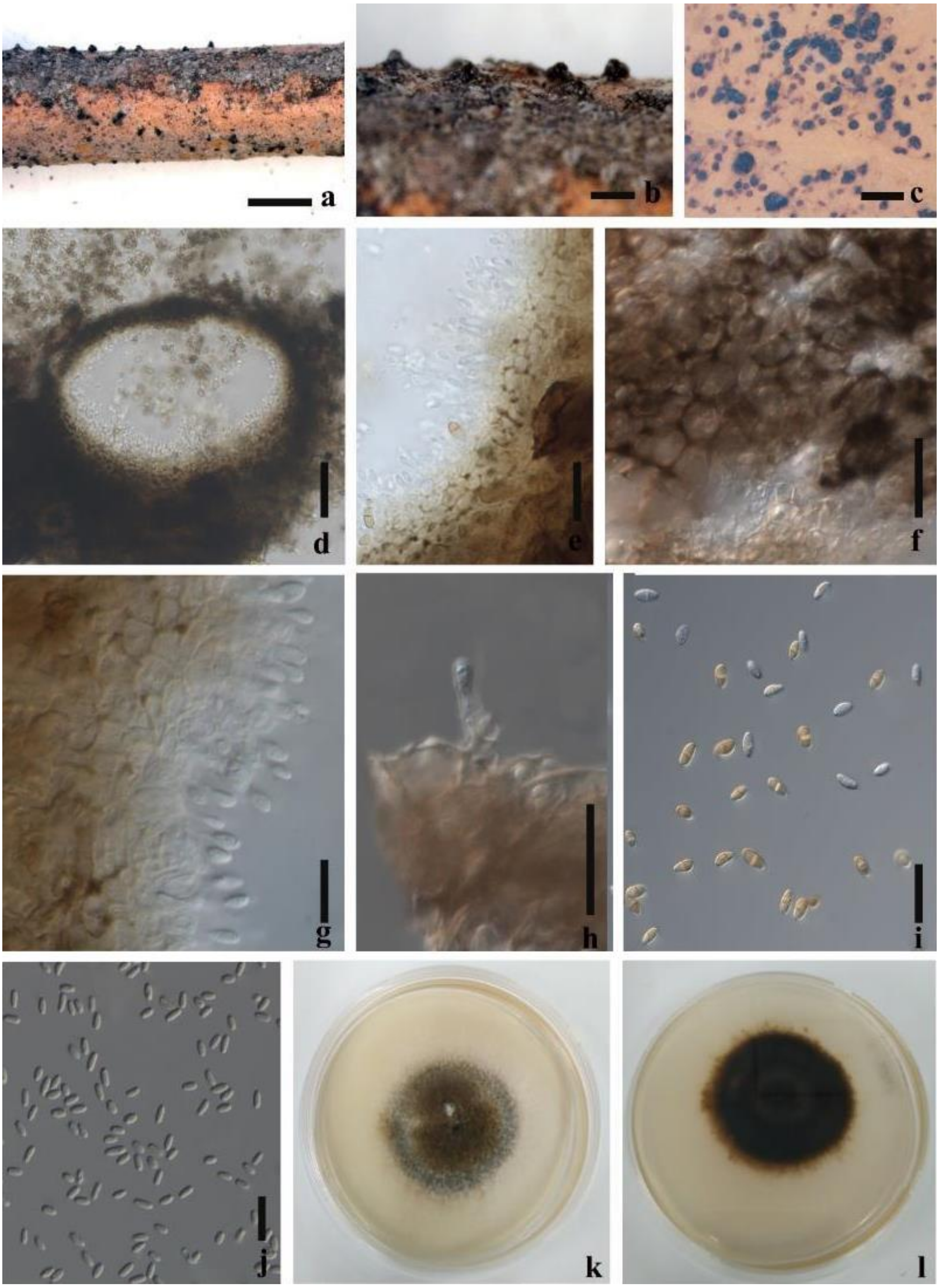


Figure 10 – *Didymella aliena* (MFLUCC 18-0086). a, b Semi-immersed conidiomata on the host surface. c Superficial pycnidia in agar. d Longitudinal section of a conidioma. e Conidioma wall showing cell organization in host. f Sections of the pycnidial wall from culture. g Conidiogenous cells from host. h Conidiogenous cells from culture. i Conidia from host. j Conidia from culture. k–l Upper view (k) and the reverse view (l) of the colony on PDA. Scale bars: a = 2 mm, b, c = 500 µm, d = 50 µm, e, f = 20 µm, g = 10 µm, h = 20 µm, i–j = 20 µm.

Colonies effuse, dark brown to black with occasional bright orange anterior margins. Mycelium mostly immersed, with dematiaceous hyphae. *Conidiophores* 3–6 × 3–4 µm ($\bar{x}$ = 5 × 3 µm, n = 10), micronematous, mononemous, closely packed, hyaline, thin-walled, aseptate, smooth. *Conidiogenous cells* 3–4 × 4–7 µm ($\bar{x}$ = 3 × 5 µm, n = 10) integrated. *Conidia* 10–21 × 8–21 µm ($\bar{x}$ = 15 × 15 µm, n = 40), solitary, sphaerical or pyriform, dark golden brown, verrucose, muriform, slightly constricted at septa, sometimes with septa obscured at maturity by rough wall, sometimes remaining attached with a pale protuberant basal stalk cell.

Culture characteristics – Conidia germinating on PDA, within 12 hours. Colonies growing on PDA, cottony, bright yellow to bright orange reaching 5 mm in 10 days at 25°C, mycelium superficial, effuse, with regular edge, hyphae pale to bright orange, producing orange pigments in PDA

Material examined – CHINA, Yunnan Province, Kunming Institute of Botany, Botanical Garden, on dead leaves of *Sasa nipponica*, 5 October 2016, A. Karunarathna, AKKIB 10 (MFLU 17-0359, HKAS 97353); living culture MFLUCC 17-1371, KUMCC 16-0221.

GenBank numbers – ITS: MG822858, LSU: MG822859.

Notes – Pairwise comparison of DNA sequences of ITS regions between our strain KUMCC 16-0221 and the type strain CBS 173.73 revealed very minor differences. Based on Jeewon & Hyde (2016) and morphological similarities, we treat both as the same species. Phylogeny (Fig 8) also supports this identification. Thus, this fresh collection is identified as *Epicoccum nigrum*. Description and illustrations are provided which will facilitate identification of *Epicoccum nigrum* on *Sasa nipponica* (Poaceae) as the first report from China.

Neodidymelliopsis Q. Chen & L. Cai.

Neodidymelliopsis was introduced by Chen et al. (2015), with *Neodidymelliopsis cannabis* (G. Winter) Q. Chen & L. Cai as the type species (Chen et al. 2015, Hyde et al. 2016, Thambugala et al. 2016a).

Neodidymelliopsis negundinis Manawasinghe, Bulgakov & K.D. Hyde, sp. nov. Fig. 12

Index Fungorum number: IF554044; Facesoffungi number: FoF03891

Etymology – name reflects the host genus.

Holotype – MFLU 16-1733

Saprobic or *necrotrophic* on dead and dying twigs and branches of *Acer negundo* L. Sexual morph Undetermined. Asexual morph Coelomycetous. *Conidiomata* on host 255–559 µm diameter ($\bar{x}$ = 395.4 µm, n = 10), pycnidial, solitary, scattered, globose to subglobose, black, semi-immersed to immersed, sometimes erumpent; *Conidiophores* not observed. *Conidiogenous cells* not observed. *Conidia* on host 4–10 × 1.5–2 µm diameter ($\bar{x}$ = 5.5 × 1.8 µm, n = 40), oblong to ellipsoid, hyaline, aseptate, smooth-walled; in culture, 4.6–6.7 × 1.6–2.4 µm diameter ($\bar{x}$ = 5.5 × 2 µm, n = 40), straight. Conidial exudates not observed.

Culture characteristics – Colonies on PDA reach 80 mm diameter after 7 days at 25 °C, with undulate edge, with grey olivaceous aerial mycelium, surface floccose to woolly

Material examined – RUSSIA, Rostov region, Shakhty City, urban artificial forest, on dead and dying twigs and branches of *Acer negundo* (Sapindaceae), 6 April 2016, Timur S. Bulgakov (MFLU 16-1733, holotype), ex-type living culture, MFLUCC 18-0083, KUMCC 18-0006.

GenBank numbers – β-tubulin: MG564164, ITS: MG564165, LSU: MG564163, RPB2 MG564166.

Notes – *Neodidymelliopsis negundinis* was collected from *Acer negundo* in the Rostov region (European part of Russia). Morphological characters such as spores and colony characters (Fig. 12), fit well within the species concept of *Neodidymelliopsis* (Chen et al. 2015). DNA sequence analyses from the ITS, LSU, RPB2 and β-tubulin genes confirm that our new taxon belongs in *Neodidymelliopsis* (Fig. 8). *Neodidymelliopsis negundinis* has a particular neighbour relationship with *N. longicolla* and *N. polemonii*, but this was not supported in our phylogeny analyses (Fig. 8). *Neodidymelliopsis negundinis* differs by developing smaller-sized (4–10 × 1.5–2.45 conidia in both culture and on the host compared to other species in this genus (7.5–10(–18) × 2–3.5(–5) (Chen et al. 2015, Hyde et al. 2017b). In addition, this is the first report of *Neodidymelliopsis* reported on *Acer* species (Farr & Rossman 2018).

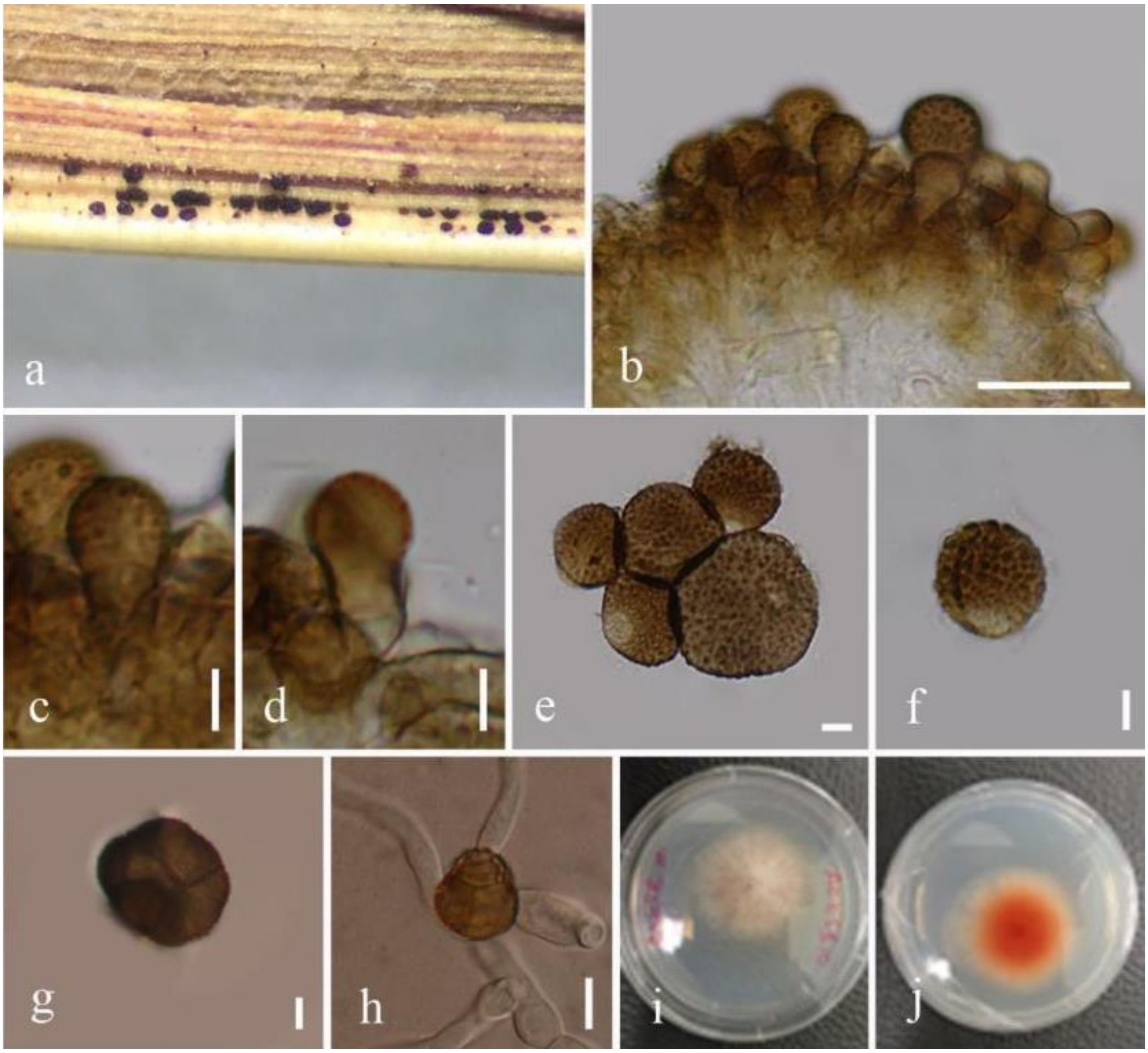


Figure 11 – *Epicoccum nigrum* (MFLU 17-0359). a Appearance of synnemata on host substrate. b Longitudinal section of synnema. c–d Attachment of conidia to the conidiophores. e–g Conidia. h Germinated conidium. i–j Culture characteristics on PDA (i = from above, j = from below). Scale bars: b = 50 µm, c–f = 10 µm, g–j = 10 µm.

Lentitheciaceae Yin. Zhang et al.

The family Lentitheciaceae was established by Zhang et al. (2012) to accommodate massarina-like species in the suborder Massarineae and is typified by *Lentithecium fluviatile* (Aptroot & Van Ryck.) K.D. Hyde et al. (Zhang et al. 2009, 2012, Hyde et al. 2013, 2016, Tibpromma et al. 2017). Ten genera have been reported in the family, viz. *Darksidea* (Knapp et al. 2015), *Katumota*, *Keissleriella*, *Lentithecium*, *Murilentithecium* (Wanasinghe et al. 2014), *Neoophiosphaerella* (Tanaka et al. 2015), *Phragmocamarosporium* (Wijayawardene et al. 2015), *Poaceascoma* (Phookamsak et al. 2015a), *Setoseptoria* (Tanaka et al. 2015) and *Tingoldiago* (Hyde et al. 2013, Knapp et al. 2015, Phookamsak et al. 2015a, Tanaka et al. 2015, Wanasinghe et al. 2018). In this paper, we introduce *Poaceascoma taiwanense* as a new species form Taiwan.

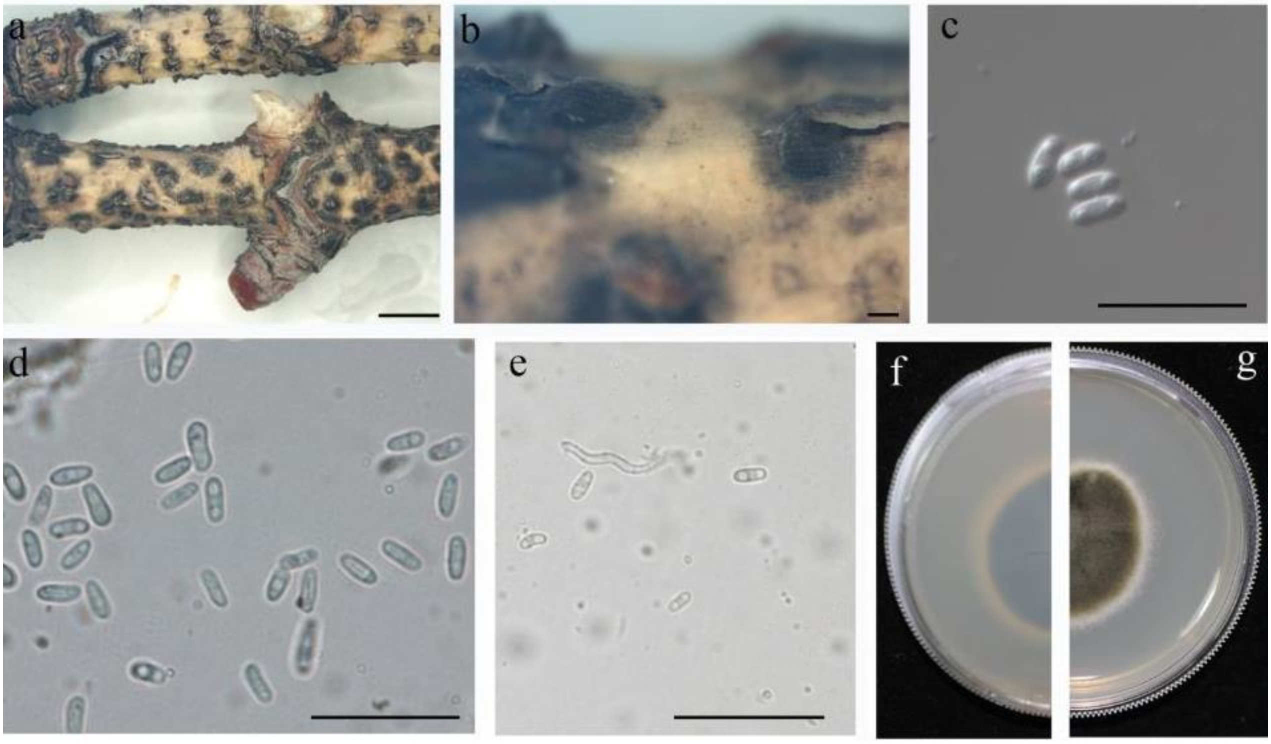


Figure 12 – *Neodidymelliopsis negundinis* (MFLU 16-1733, holotype) a Appearance of conidia on dead branch of *Acer negundo*. b Submerged conidiomata on the host surface. c Conidia on host. d, e Conidia on host in agar. e Upper view of 7 days old culture on PDA. f Reverse view of 7 days old culture on PDA. f Upper side of colony on PDA. Scale bars: a = 2000 µm, b = 200 µm, c, d, e = 20 µm.

Poaceascoma Phookamsak & K.D. Hyde

Poaceascoma was introduced by Phookamsak et al. (2015a) to accommodate a dothideomycete species associated with Poaceae which forms setose ascoma with filiform ascospores and is typified by *Poaceascoma helicoides* Phookamsak & K.D. Hyde. Currently, three species have been recognized in the genus viz. *Poaceascoma aquaticum* Z.L. Luo & K.D. Hyde, *P. halophila* Dayarathne & K.D. Hyde and *P. helicoides* Phook. & K.D. Hyde (Index Fungorum 2018)

Poaceascoma taiwanense Tennakoon, C.H. Kuo & K.D. Hyde, sp. nov. Fig. 14

Index Fungorum number: IF554200; Facesoffungi number: FoF04084

Etymology – named after the country where this fungus was collected, Taiwan.

Holotype – MFLU 18-0083

Saprobic on dead stem of *Panicum virgatum* L. Sexual morph *Ascomata* 140–180 µm high, 150–220 µm diameter, semi-immersed to erumpent, solitary, scattered or sometimes grouped beneath the host tissues, globose, dark brown to black, coriaceous, ostiolate, papillate. *Peridium* 40–50 µm wide, with thick walls, composed of several layers of pseudoparenchymatous cells, outer layer comprising several layers of dark brown cells, arranged in a *textura angularis*, inner layer comprising several layers of hyaline, flattened cells, arranged in *a textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 2−3.5 µm wide, filamentous, broad, cellular pseudoparaphyses, with distinct septa, embedded in a mucilaginous matrix. *Asci* (63–)65–80(–82) × 6–8(–8.6) µm ($\bar{x}$ = 73 × 7.2 µm, n = 30), 4-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 50–60 × 2–3 µm ($\bar{x}$ = 55.6 × 2.6 µm, n = 30), fasciculate, scolecosporous, hyaline, elongate, filiform, tapering towards the rounded ends, slightly curved, 15–17-septate, slightly constricted at septa, smooth-walled. Asexual morph Undetermined.

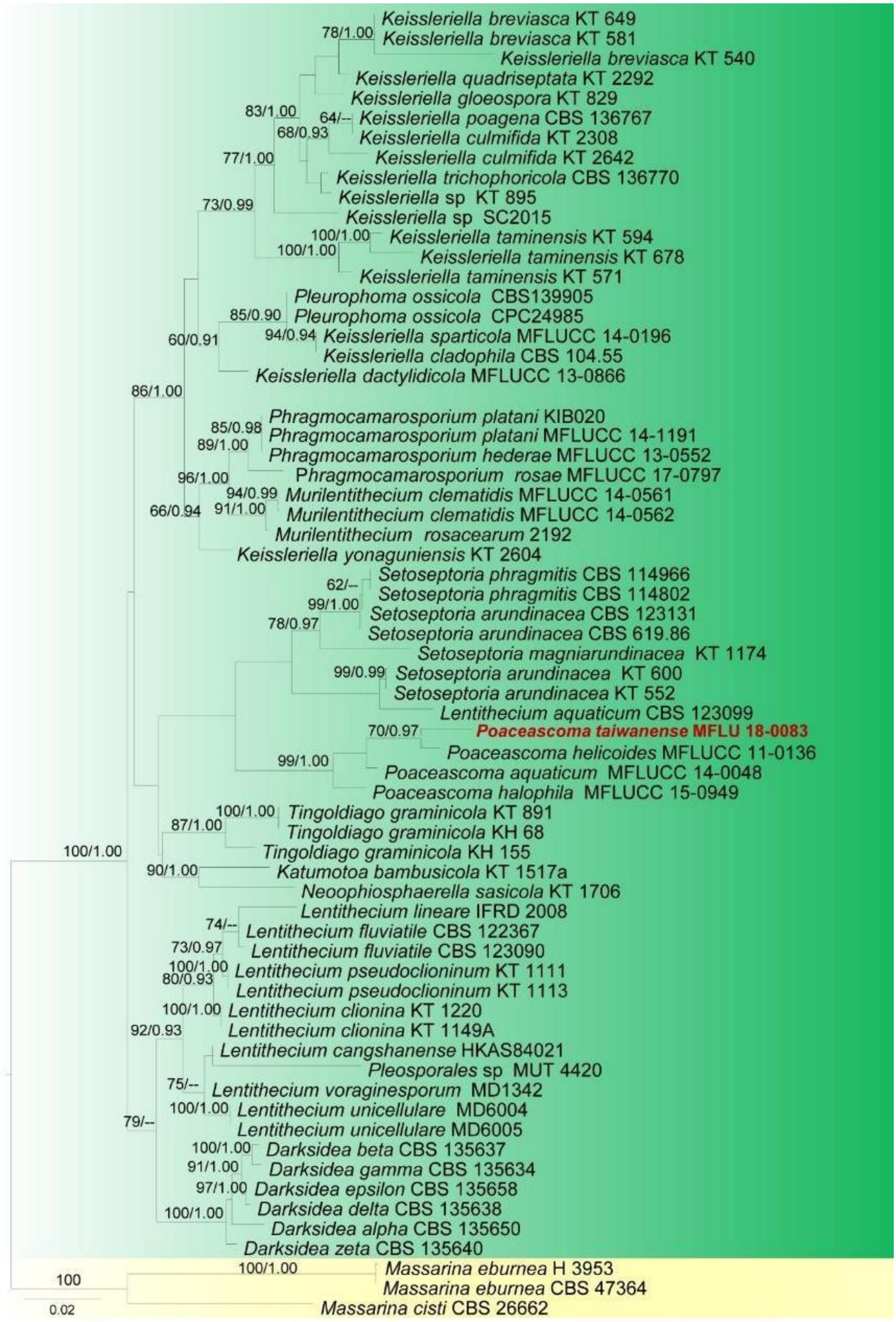


Figure 13 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF sequenced data of Lentitheciaceae. Related sequences were obtained from Luo

et al. (2016) and Hyde et al. (2017b). Sixty-six strains are included in the combined sequence analyses, which comprise 3421 characters with gaps. *Massarina eburnea* (H 3953, CBS 47364) and *Massarina cisti* (CBS 26662) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -15553.519520 is presented. The matrix had 847 distinct alignment patterns, with 22.85% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239923, C = 0.248830, G= 0.272362, T = 0.238884; substitution rates AC = 1.408036, AG = 2.598862, AT = 1.789820, CG = 1.645928, CT = 8.851789, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.497322$. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes respectively. Newly generated sequences are in red.

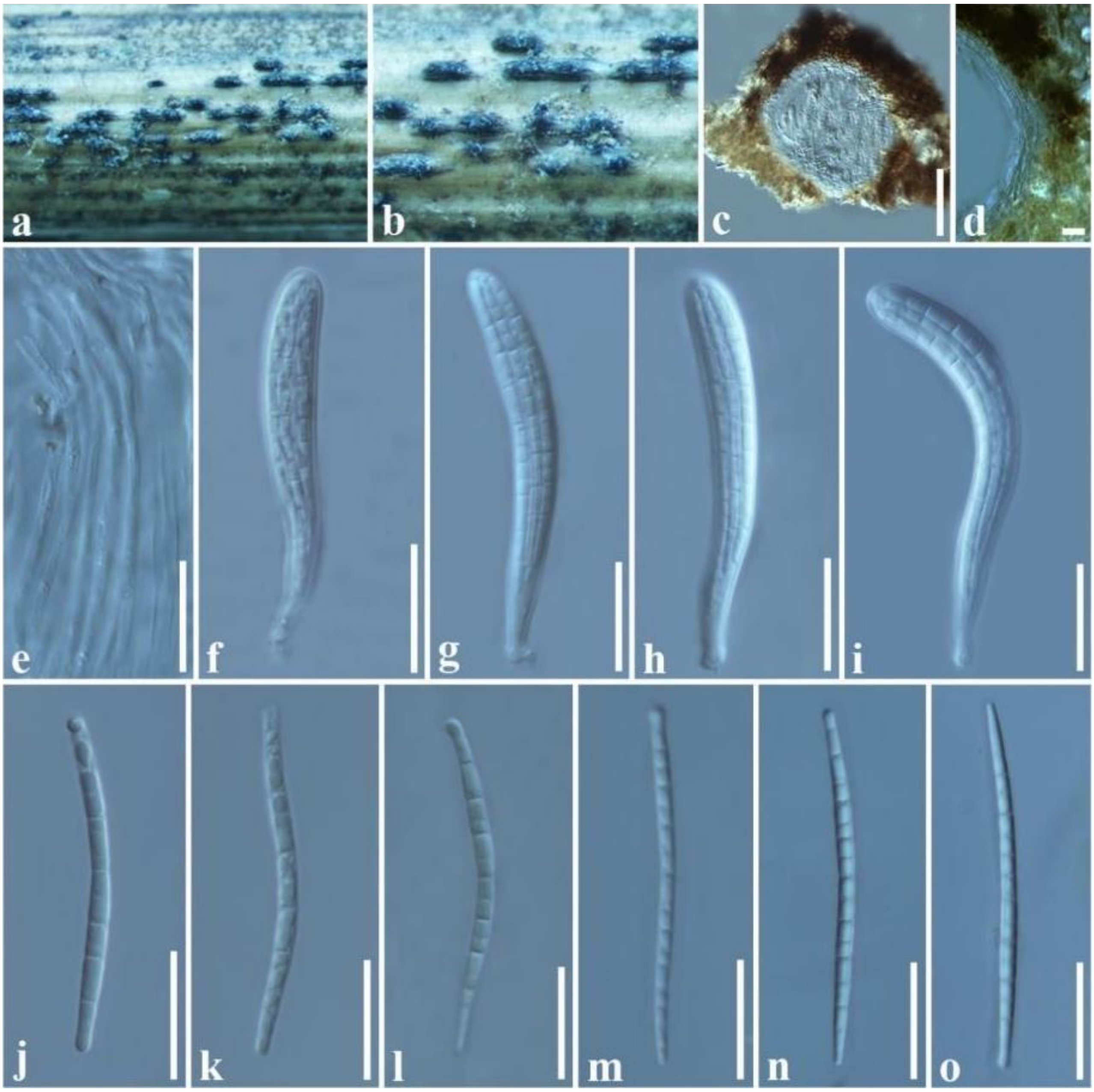


Figure 14 – *Poaceascoma taiwanense* (MFLU 18-0083, holotype) a Ascomata on host. b Close-up of ascomata. c Vertical section of ascoma. d Section of peridium. e Pseudoparaphyses. f–i Asci. j–o Ascospores. Scale bars: c = 50 µm, d–i = 20 µm, j–o = 18 µm.

Material examined – TAIWAN, Chiayi, Shihnong Forest, dead stems of *Panicum virgatum* L. (Poaceae), 25 June 2017, D.S. Tennakoon, DTW 030 (MFLU 18-0083, holotype).

GenBank numbers – ITS: MG831569, LSU: MG831567, SSU: MG831568.

Notes – Morphological characters of *Poaceascoma taiwanense* fit into the generic concept of *Poaceascoma* in having filiform, multi-septate ascospores (Phookamsak et al. 2015a, Luo et al. 2016, Hyde et al. 2017b). *Poaceascoma taiwanense* differs from other *Poaceascoma* species in having unique morphological characters, such as 4-spored asci and 15–17-septate ascospores. The main morphological differences across similar species are shown in Table 1.

Table 1 Synopsis of morphological similarities and differences among *Poaceascoma* species.

***Poaceascoma* species**	**Size (µm)**			**Ascospores**		**References**
	Ascomata	**Asci**	**Ascospores**	**Septation**	**Colour**	
P. aquaticum	280–380 × 310–500	184.5–210.5 × 12–16	214–231 × 4.2–5.2	21–36	Pale brown to brown	Luo et al. 2016
P. halophila	260–315 × 270–350	248.5–300 × 11–14	191–230 × 2.5–3	20–25	Hyaline	Hyde et al. 2017b
P. helicoides	270–360 × 320–450	160–185 × 8.5–10	150–185 × 2–2.5	29–33	Hyaline	Phookamsak et al. 2015a
P. taiwanense	140–180× 150–220	65–80× 6–8	50–60 × 2–3	15–17	Hyaline	This study

Melanommataceae G. Winter

The family Melanommataceae was established by Winter (1885), which is typified by *Melanomma pulvis-pyrius*. Tian et al. (2015) accepted 20 genera in Melanommataceae based on morphological and phylogenetic evidence. Recent taxonomic surveys have also revealed the family to be highly diverse with many new species (Hyde et al. 2016, Li et al. 2016b, 2017, Almeida et al. 2017, Jaklitsch & Voglmayr 2017). Hashimoto et al. (2017) reported that Melanommataceae should be restricted to the type genus *Melanomma*. In addition, they have introduced Pseudodidymellaceae to accommodate four genera viz. *Mycodidymella*, *Petrakia*, *Pseudodidymella*, and *Xenostigmina*. However, in a recent study, Wanasinghe et al. (2018) considered that the new family Pseudodidymellaceae was untenable as it resulted in more intergeneric taxonomic confusion and the family Melanommataceae was already a well established family with strong phylogenetic support. Besides, they introduced five new genera in the family Melanommataceae, viz. *Melanocucurbitaria*, *Marjia*, *Melanodiplodia*, *Monoseptella*, *Uzbekistanica*. In this paper, we introduce *Pseudobyssosphaeria* gen. nov with *Pseudobyssosphaeria bambusae* sp. nov, two new records, *Bertiella ellipsoidea* and *Byssosphaeria siamensis*, our conclusions based on multi-gene analyses and morphological characters (Fig. 15).

Bertiella (Sacc.) Sacc. & P. Syd.

The genus *Bertiella* was introduced by Saccardo and Sydow (1899) and it is typified by *Bertiella macrospora* (Sacc.) Sacc. & Traverso. Recent phylogenetic studies support its placement within Melanommataceae close to *Byssosphaeria* (Mugambi & Huhndorf 2009, Tian et al. 2015, Hyde et al. 2016, Li et al. 2016b, 2017). Previously, *Bertiella* was characterized by black, superficial, subglobose ascomata with a carbonaceous peridium. However, we considered that a carbonaceous peridium is not an absolute characteristic to identify this genus. In this paper, we introduce a new collection of *Bertiella ellipsoidea* from submerged wood in a freshwater stream in northern Thailand.

Bertiella ellipsoidea Ekanayaka, Q. Zhao & K.D. Hyde, Fungal Diversity 80: 79 (2016) Fig. 16

Index Fungorum number: IF552201; Facesoffungi number: FoF03894

Saprobic on woody substrata in a freshwater stream. Sexual morph *Ascomata* 170–375 high × 165–345 µm diameter ($\bar{x}$ = 285 × 214 µm, n = 15), superficial, solitary or scattered, sessile,

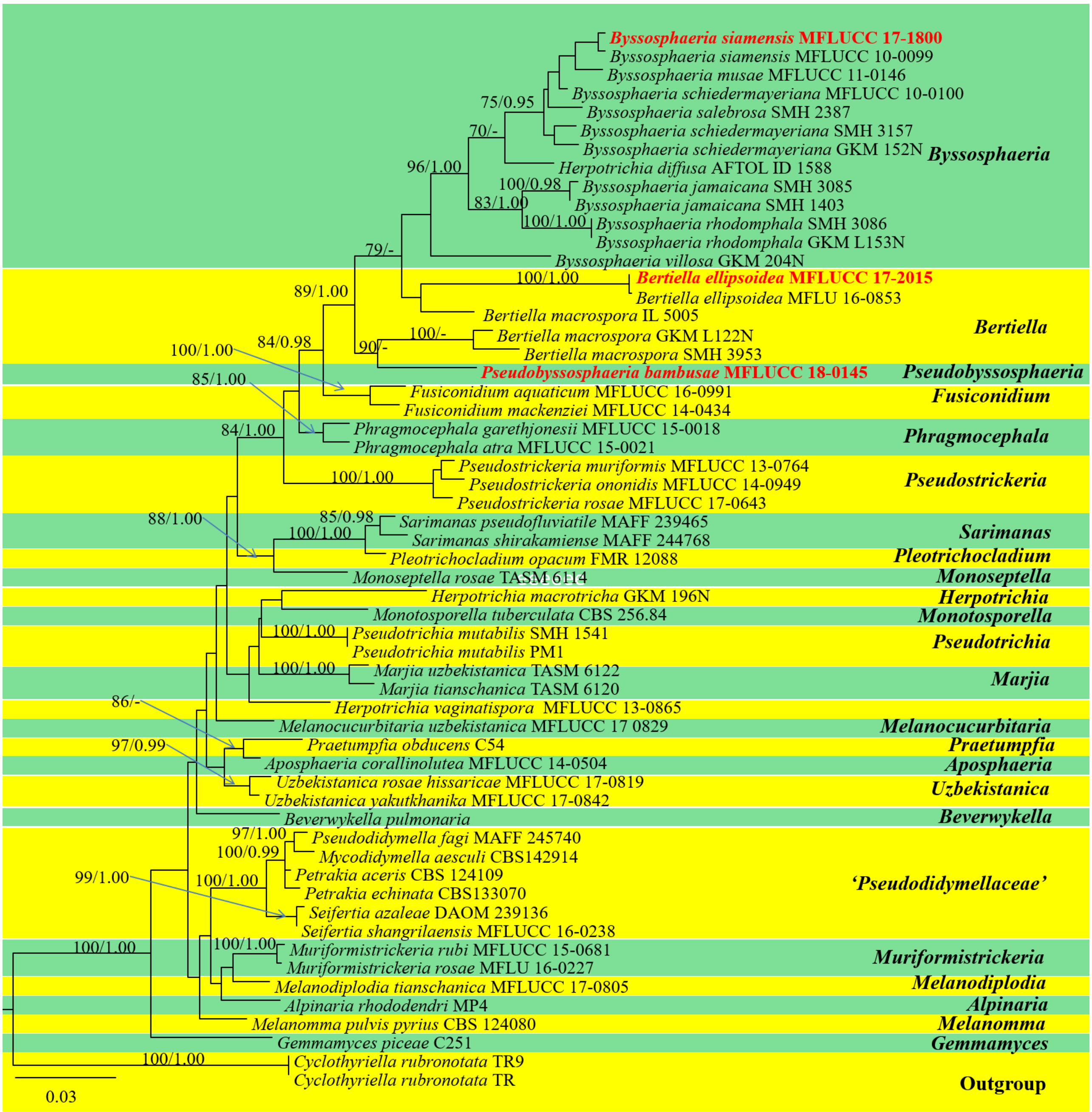


Figure 15 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and TEF1α sequence data for species of Melanommataceae. The newly generated nucleotide sequences were compared against the GenBank database using the Mega BLAST program. Sequences that relate were obtained from GenBank (http://www.ncbi.nlm.nih.gov/). Fifty-five strains are included in the combined sequence analyses which comprise 3,894 characters with gaps (539 characters for ITS, 1308 for LSU, 1061 for SSU and 986 for TEF1α). *Cyclothyriella rubronotata* TR9 and *Cyclothyriella rubronotata* TR (Cyclothyriellaceae) are used as the outgroup taxa. Tree topology of the maximum-likelihood analysis is similar to the maximum parsimony analysis and the Bayesian analysis. The best scoring RAxML tree with a final likelihood value of -16110.950054 is presented. RAxML bootstrap support values equal to or greater than 70% are given before the forward slash. Bayesian posterior probabilities equal to or higher than 0.95 are given after the forward slash. Hyphen ("–") indicates a value lower than 70% for RAxML and a posterior probabilities lower than 0.95 for Bayesian analysis. Newly generated sequences are in red.

globose to subglobose, dark brown, setose, coriaceous. *Ostiole* single, central. *Setae* 160–330(–398) × 3–4 µm, covering the whole ascoma, brown to dark brown, unbranched, apically rounded, thick-walled. *Peridium* 27–40 µm thick, 2-layered, outer layer comprising pale brown to dark brown cells of *textura angularis*, inner layer comprising hyaline cells of *textura angularis*. *Hamathecium* comprising numerous, 1.5–2.5 µm wide, hyaline, long, filiform, aseptate, branched pseudoparaphyses, anastomosing between and above the asci. *Asci* 100–150 × 8–12 µm ($\bar{x}$ = 120 × 10 µm, n = 20), 8-spored, bitunicate, cylindrical to clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 16–21 × 6–8 µm ($\bar{x}$ = 18 × 7 µm, n = 50), 1–2-seriate, ellipsoid to fusiform, hyaline to pale brown, 1-septate, constricted at septum, acute at the apex, smooth and thick-walled, with 2–4 globules. Asexual morph Undetermined.

Culture characteristics – *Ascospores* germinating on water agar (WA) within 48 hours and germ tubes produced from ascospores. *Colonies* growing slowly on malt extract agar (MEA), circular, with flat surface, edge undulate, reaching 6 mm in 2 weeks at 28°C, white to brown in MEA media. *Mycelium* superficial and partially immersed, branched, septate, hyaline to pale brown (Figs 16t, 16u).

Material examined – THAILAND, Chiang Rai, Muang, Ban Nang Lae Nai, on submerged decaying wood in a freshwater stream, 31 December 2016, Yong-Zhong Lu, CR10 (MFLU 17-1092, HKAS 100762); living culture, MFLUCC 17-2015, TBRC.

GenBank numbers – ITS: MG543922, LSU: MG543913, RPB2: MG547224, TEF1: MG547226.

Notes – A new collection of *Bertiella ellipsoidea* (MFLU 17-1092) was found on submerged wood in a freshwater stream from northern Thailand and it is the first report of *B. ellipsoidea* from aquatic habitats. Phylogenetic analyses placed our new strain in a clade with *B. ellipsoidea* (MFLU 16-0583) (Fig. 15). We compared our new taxon with *B. ellipsoidea* based on base pair differences of ribosomal and protein loci. There was only one base pair difference in LSU, and there were no differences in SSU and TEF1α, which provide further evidence to support our new strain as *Bertiella ellipsoidea*. Morphologically there are two different features between our new collection and the holotype of *B. ellipsoidea* (MFLU 16-0583) (Hyde et al. 2016): viz. i) there are abundantly long setae covering the whole ascoma and ii) coriaceous ascomata (carbonaceous in the holotype). Thus, we name our strain as *B. ellipsoidea* (MFLUCC 17-2015) as the first record from aquatic habitats. Moreover, we also provide their culture characteristics which were obtained from single spore isolations.

Byssosphaeria Cooke

Byssosphaeria was introduced by Cooke & Plowright (1879) and is typified by *B. keithii* based on its superficial ascomata seated on a "tomentose subiculum of interwoven threads" (Cooke & Plowright 1879). Tian et al. (2015) introduced a new *Byssosphaeria* species and reported that *Byssosphaeria* belongs to Melanommataceae based on multigene phylogenetic analyses. Index Fungorum (2018) lists 44 species epithets under *Byssosphaeria*, but only seven species have been confirmed by molecular data, viz. *B. jamaicana* (Sivan.) M.E. Barr, *B. musae* Phook. & K.D. Hyde, *B. rhodomphala* (Berk.) Cooke, *B. salebrosa* (Sacc.) M.E. Barr, *B. schiedermayeriana* (Fuckel) M.E. Barr, *Byssosphaeria siamensis* Boonmee, Q. Tian & K.D. Hyde, *Byssosphaeria villosa* (Samuels & E. Müll.) Boise. In this study, we report *Byssosphaeria siamensis* with new morphological data.

Byssosphaeria siamensis Boonmee, Q. Tian & K.D. Hyde, Fungal Diversity 74: 283 (2015)

Fig. 17

Index Fungorum number: IF551430; Facesoffungi number: FoF03895

Saprobic on woody substrata in a freshwater stream. Sexual morph *Ascomata* 445–475 µm high × 430–555 µm diameter ($\bar{x}$ = 460 × 490 µm, n = 5), superficial, globose to subglobose, solitary to gregarious, dark brown to black, setose, coriaceous, apically ostiolate. *Ostiole* single, central, with a pore-like opening, orange to yellow around pore, apapillate. *Setae* 325–400 × 4.5–6 µm, covering the whole ascoma, dark brown to black, unbranched, thick-walled. *Peridium* 50–70 µm wide, thickest at the apex, 2-layered, outer layer comprising pale brown to dark brown cells of *textura angularis*, inner layer comprising hyaline to pale brown cells of *textura prismatica*. *Hamathecium* 1–2 µm wide, comprising hyaline, dense, filiform, septate pseudoparaphyses, anastomosing and branching between and above the asci. *Asci* 110–150 × 12–14 µm ($\bar{x}$ = 131 × 13 µm, n = 20), 8-spored, bitunicate, cylindrical to clavate or saccate, pedicellate, with a 29–45 µm long pedicel, apically rounded with an ocular chamber. *Ascospores* 28–33 × 5–7 µm ($\bar{x}$ = 30 × 6 µm, n = 50), 1–2-seriate, hyaline to pale brown, ellipsoid to fusiform, 1-septate, constricted at septum, slightly curved, with 1–2 globules, acute at the apex, smooth and thick-walled. Asexual morph undetermined.

Culture characteristics – *Ascospores* germinating on water agar within 12 hours and germ tubes produced from ascospores. *Colonies* growing slowly on MEA, circular, with flat surface, edge undulate, reaching 31 mm in 3 weeks at 28°C, pale brown to yellow in MEA media. *Mycelium* superficial and partially immersed, branched, septate, hyaline to pale brown.

Material examined – THAILAND, Chiang Rai, Muang, Ban Nang Lae Nai, on submerged decaying wood in a freshwater stream, 31 December 2016, Yong-Zhong Lu, CR25 (MFLU 17-1104, HKAS 100774); living culture, MFLUCC 17-1800.

GenBank numbers – ITS: MG543923, LSU: MG543914, SSU: MG543917, RPB2: MG547225.

Notes – Our new collection shares a sister relationship to *Byssosphaeria siamensis* (MFLUCC 10-1099). We compared our new taxon with *B. siamensis* based on base pair differences. There were 3, 2, 1 and 3 base pair differences in ITS, LSU, SSU and RPB2 respectively, which confirmed they should belong to same species (Jeewon & Hyde 2016). Morphologically there are four different features between our new collection and the holotype of *B. siamensis* (MFLU 10-0029) (Tian et al. 2015): 1), smaller ascomata (445–475 × 430–555 µm vs. 501–692 × 561–720 µm); 2) longer pedicel (29–45 µm vs. 14.5–24 µm); 3) smaller ascospores (28–33 × 5–7 µm vs. 40.5–50 × 7–11 µm); 4) ascospores surrounded by a gelatinous and fusiform sheath in the holotype, but our new collection lacks these.

Pseudobyssosphaeria H.B. Jiang & K.D. Hyde, gen. nov.

Index Fungorum number – IF554471

Etymology – refers to the morphologically being similar to *Byssosphaeria*.

Saprobic on dead bamboo culms. Sexual morph *Ascomata* superficial, solitary, scattered or gregarious, subglobose, blackened, with a central ostiole, ascomata covered with outwardly brown, septate, branched hyphae. *Setae* covering the whole ascoma, dark brown, unbranched, septate. *Peridium* multi-layered, outer layer composed of thick-walled, dark brown cells of *textura angularis*; inner layer composed of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* comprising septate, branched, anastomosing pseudoparaphyses embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, cylindrical to clavate, short pedicellate with furcate ends, apically rounded. *Ascospores* overlapping bi-seriate, fusiform, 1-septate, constricted at the septum, hyaline. Asexual morph Undetermined.

Type species – *Pseudobyssosphaeria bambusae* H.B. Jiang & K.D. Hyde

Notes – Although *Pseudobyssosphaeria* grouped with *Bertiella macrospora* (strains GKM L122N and SMH 3953) and three collections of *B. macrospora* (IL 5005, GKM L122N and SMH 3953), they clustered into two groups in our multi-gene phylogenetic tree. *Bertiella macrospora* strain IL 5005 has LSU sequence data only and strains GKM L122N and SMH 3953 have TEF1-alpha sequences only. *Pseudobyssosphaeria* however, forms a basal clade to *Bertiella* and is morphologically distinct.

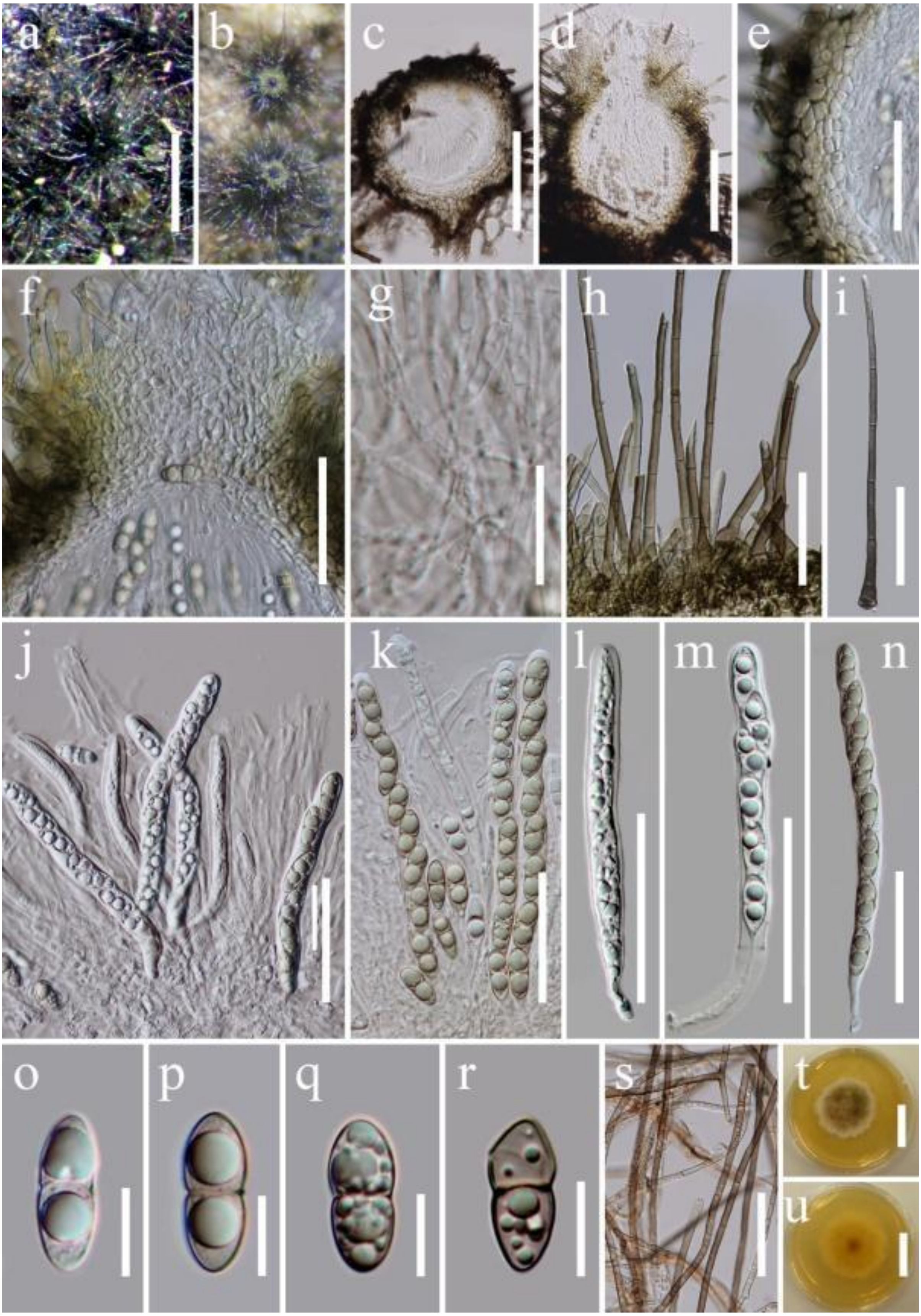


Figure 16 – *Bertiella ellipsoidea* (MFLU 17-1092). a, b Superficial ascomata on substrate. Note ascomata surrounded by brown setae. c, d Vertical section of ascoma. e Peridium. f Ostiole g Hamathecium. h, i Setae. j–n Asci. o–r Ascospore. s Hyphae in culture. t, u Colony on PDA from above and below. Scale bars: a = 500 µm, c, d = 100 µm, e, f, h–n = 50 µm, g = 20 µm, o–r = 10 µm, s = 50 µm, t, u = 20 mm.

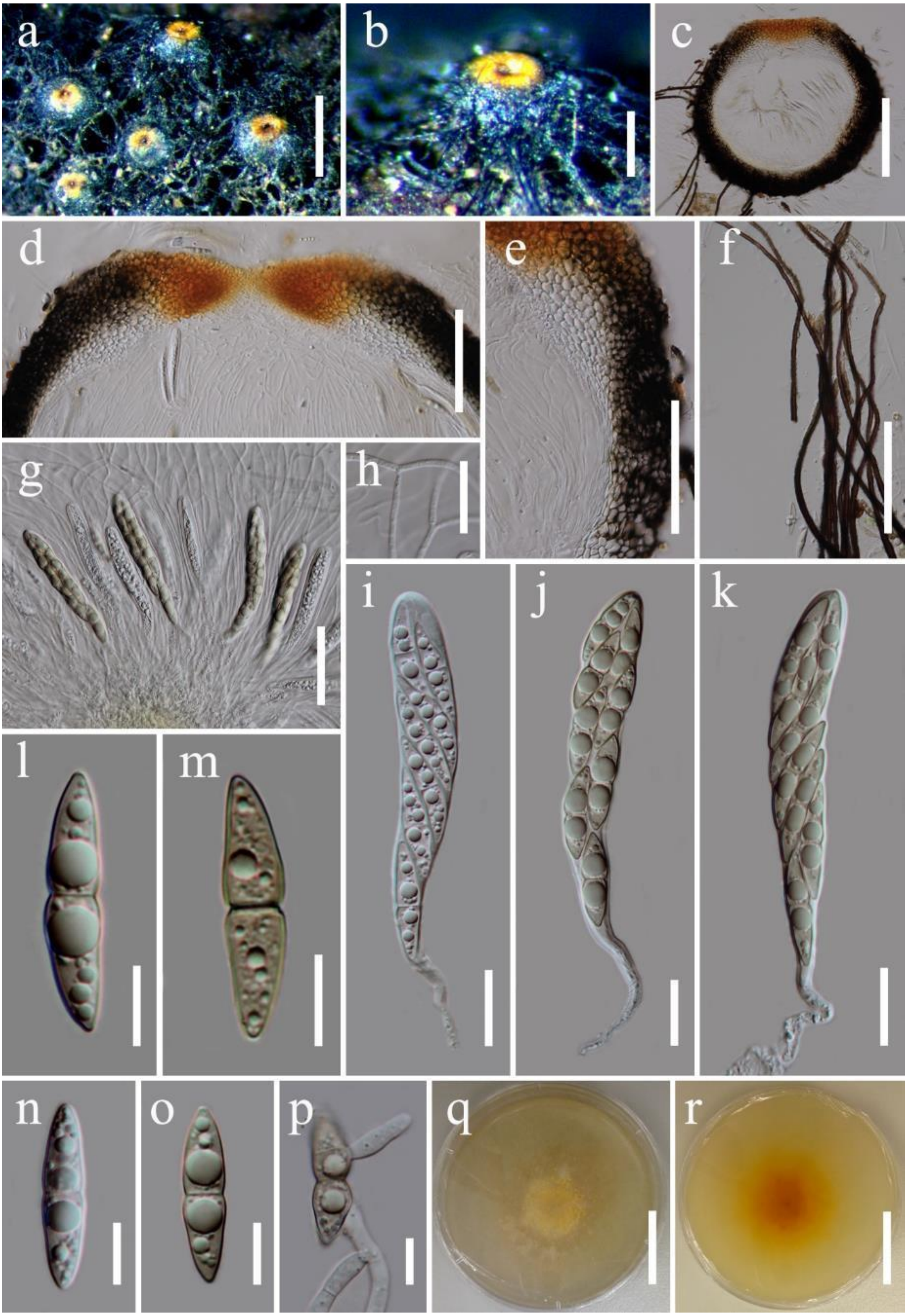


Figure 17 – *Byssosphaeria siamensis* (MFLU 17-1104). a, b Superficial ascomata on substrate. Note ascomata surrounded by dark brown setae. c Ascoma. d Ostiole. e Peridium. f Setae. g Asci with hamathecium. h Hamathecium. i–k Ascus. l–o Ascospore. p Germinating ascospore. q, r Colony on PDA from above and below. Scale bars: a = 500 µm, b, c = 200 µm, d–f = 100 µm, g = 50 µm, h–k = 20 µm, l–p = 10 µm, q, r = 20 mm.

Pseudobyssosphaeria bambusae H.B. Jiang & K.D. Hyde, sp. nov. Fig. 18

Index Fungorum Number: IF554470; Facesoffungi number: FoF 03921

Etymology – in reference to the host genus.

Holotype – MFLU 18-0151

Saprobic on rotting bamboo culms in terrestrial habitats. Sexual morph *Ascomata* 530–570 µm high, 470–525 µm diam. ($\bar{x}$ = 550 × 497 µm, n = 10), superficial, solitary, scattered or gregarious, subglobose, black, with a central ostiole, ascomata covered with outwardly brown, septate, branched hyphae. *Setae* 100–260 × 4.5–6 µm, dense, covering the whole ascoma, dark brown, unbranched, septate. *Peridium* 65–85 µm wide, multi-layered, outer layer composed of thick-walled, dark brown cells of *textura angularis*; inner layer composed of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* composed of 1–2 µm wide, septate, branched, anastomosing pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 125–160 × 8–11 µm ($\bar{x}$ = 143.5 × 9.5 µm, n = 20), 8-spored, unitunicate, cylindrical to clavate, short pedicellate, with furcate to obtuse ends, apically rounded. *Ascospores* 29.5–32.7 × 4.6–5.6 µm ($\bar{x}$ = 31.1 × 5.1 µm, n = 20), overlapping bi-seriate, fusiform with obtuse ends, 1-septate, constricted at the septum, hyaline, normally 4-guttulate, straight, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 hours and germ tubes developing from one end. Colonies slowly growing on PDA, reaching 20 mm in 4 weeks at 23 °C, under 12 h light/12 h dark, flocculent, brown from above and below.

Material examined – THAILAND, Chiang Rai, near Fathai market, on dead bamboo culms, 11 March 2017, Hong-Bo Jiang, Fathai005 (MFLU 18-0151, holotype), ex-type living cultures, MFLUCC 18-0145, KUMCC 17-0327; *ibid*. (HKAS 101463, isotype).

GenBank numbers – ITS: MG737555, LSU: MG737556, TEF: MG737557.

Notes – Although a LSU NCBI blast search places *Pseudobyssosphaeria bambusae* close to *Bertiella macrospora* (IL 5005), the former differs from *Bertiella* species in having hyaline ascospores. *Pseudobyssosphaeria bambusae* also has setose ascomata and forms a basal clade to *Bertiella sensu stricto* and is thus cosidered a new genus and species.

Neocamarosporiaceae Wanas. et al.

Neocamarosporiaceae was introduced by Wanasinghe et al. (2017b) to accommodate *Dimorphosporicola* and *Neocamarosporium*. We followed the classification of Wanasinghe et al. (2017b) for species delineations. In this paper we introduce *Neocamarosporium phragmitis* as a new species which was collected from the UK.

Neocamarosporium Crous & M.J. Wingf.

The genus *Neocamarosporium* was introduced based on *Neocamarosporium goegapense* from South Africa, which is morphologically similar to the genus *Camarosporium* (Wanasinghe et al. 2017b). In a recent study, Wanasinghe et al. (2017b) amended this genus to accommodate its sexual morphs. Currently there are 14 accepted species in *Neocamarosporium* and we introduce the fifteenth species herein.

Neocamarosporium phragmitis Wanas., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 20

Index Fungorum number: IF554240; Facesoffungi number: FoF04099

Etymology − name reflect the host genus, *Phragmites*.

Saprobic on culms of *Phragmites australis*. Sexual morph *Ascomata* 150−200 µm high, 120−180 µm diameter ($\bar{x}$ = 180.6 × 147.6 µm, n = 10), black, semi-immersed, confluent, gregarious, cupulate when dry, globose, uniloculate, with an apapillate ostiole. *Ostiole* central, short, slightly sunken, minute and inconspicuous at the surface, smooth, ostiolar canal filled with brown to hyaline cells. *Peridium* 10–25 µm wide at the base, 30–40 µm wide in sides, comprising 4–5 layers of reddish-brown to brown, cells, lighter and flattened towards the inside, of thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 2–3 µm (n = 40) wide,

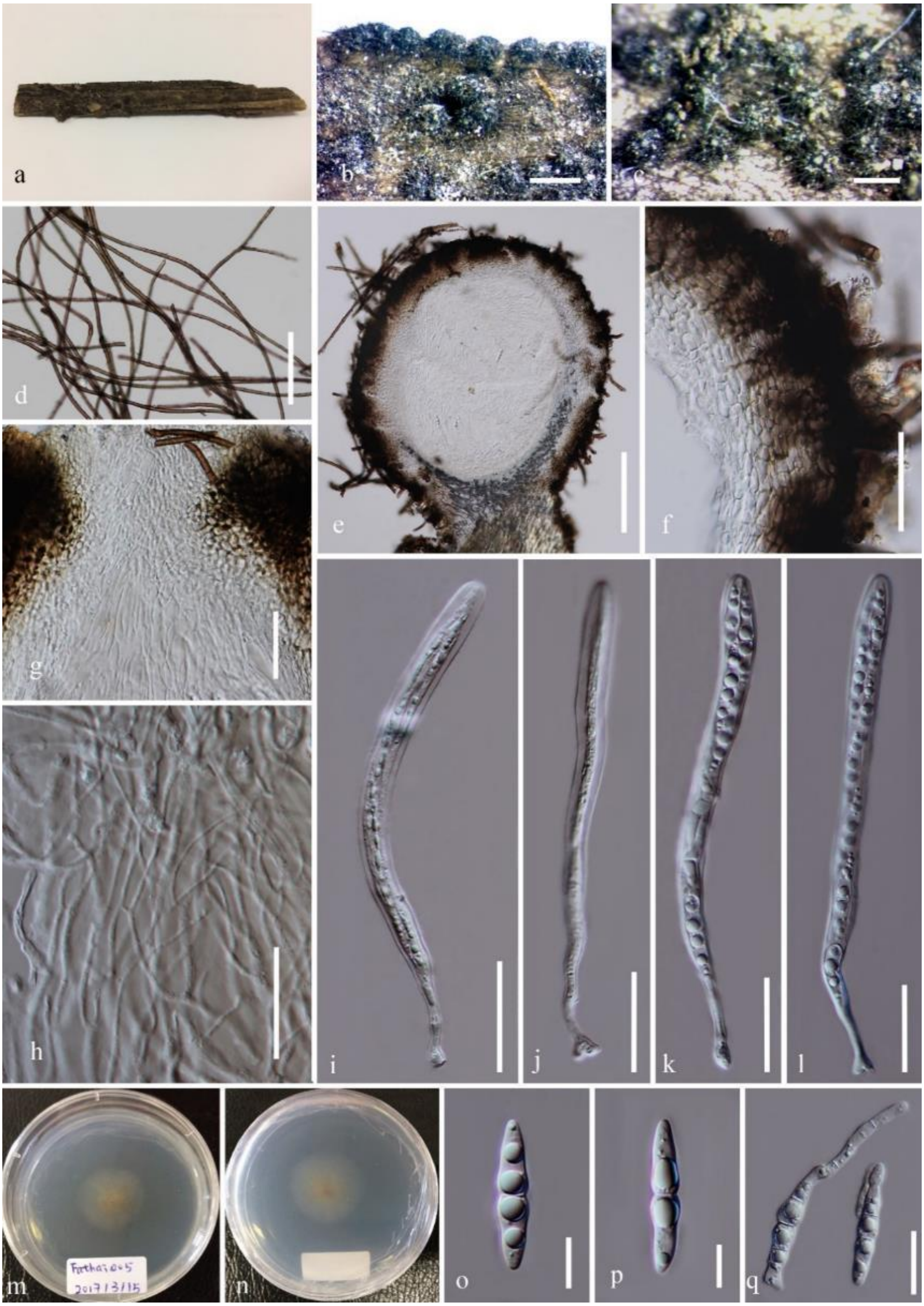


Figure 18 – *Pseudobyssosphaeria bambusae* (MFLU 18-0151, holotype). a–c Ascomata on bamboo host. d Brown mycelium (surrounding ascomata). e Ascomata. f Peridium. g Ostiole. h Pseudoparaphyses. i–k Asci. m, n Culture characters on PDA (note n reverse). o, p Ascospores. q Germinating ascospores. Scale bars: b = 1000 µm, c = 500 µm, e = 150 µm, d, f, g = 50 µm, h–l = 30 µm, q = 20 µm, o, p = 10 µm.

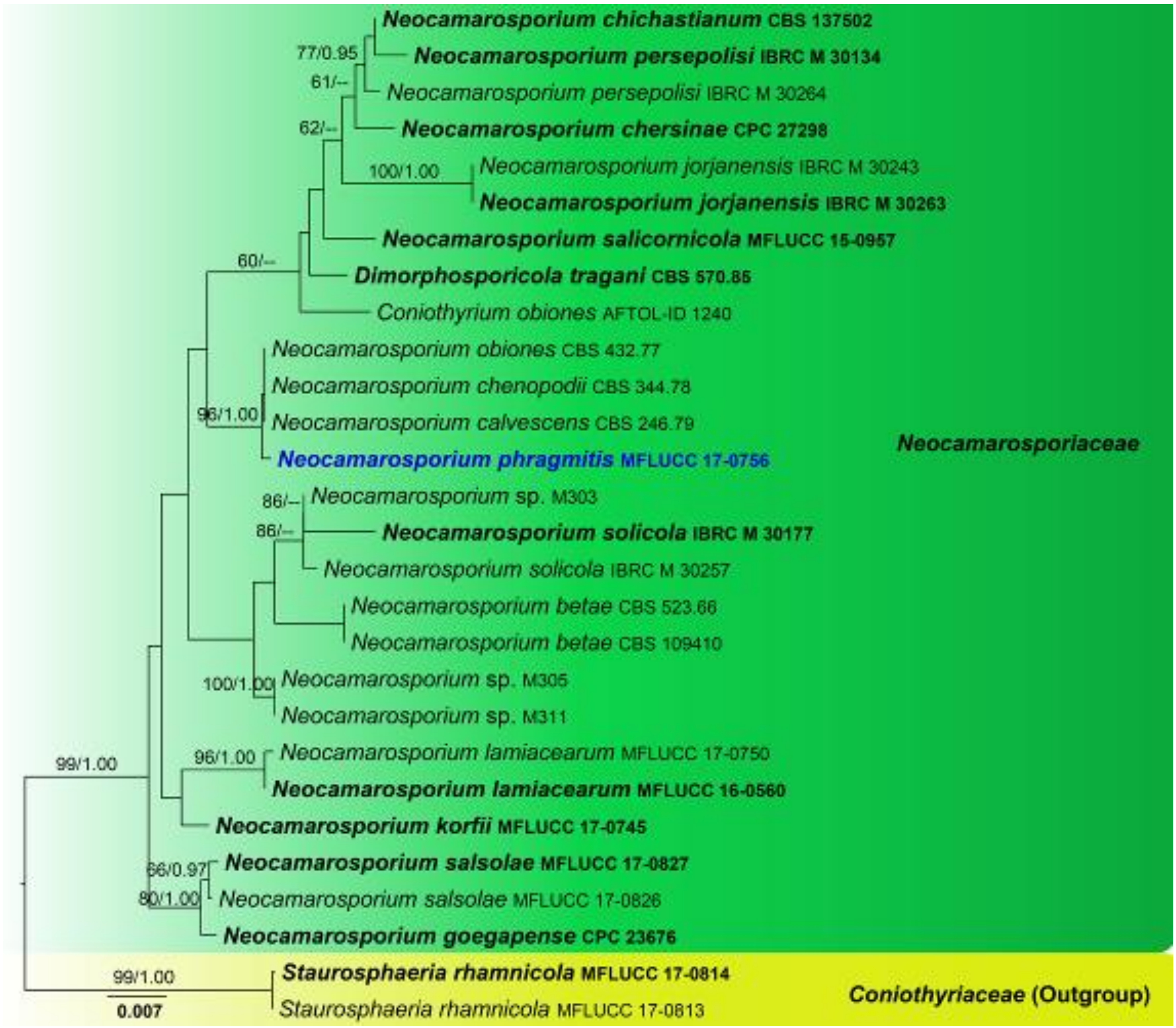


Figure 19 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF partial sequence data. Related sequences were obtained from Wanasinghe et al. (2017b). Twenty-eight strains are included in the combined LSU, SSU, ITS and TEF sequence analyses, which comprise 3,382 characters with gaps (857 for LSU, 982 for SSU, 572 for ITS and 953 for TEF). Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. *Staurosphaeria rhamnicola* (Coniothyriaceae) is used as the outgroup taxon. Tree topology of the maximum-likelihood analysis was similar to the Bayesian analysis. The best scoring RAxML tree with a final likelihood value of -7076.920933 is presented. The matrix had 327 distinct alignment patterns, with 39.76% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244371, C = 0.240432, G = 0.267282, T = 0.247915; substitution rates AC = 1.075762, AG = 2.163702, AT = 1.116814, CG = 0.758517, CT = 5.979769, GT = 1.000000; gamma distribution shape parameter α = 0.756726. Bootstrap support values for ML (first set) and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in blue.

filamentous, branched, septate, pseudoparaphyses. *Asci* 60–90 × 14–17 µm ($\bar{x}$ = 75.9 × 15.4 µm, n = 40), 8-spored, bitunicate, fissitunicate, cylindrical-clavate to cylindrical, short pedicellate (8–12 µm long), apex rounded with a minute ocular chamber. *Ascospores* 12–16 × 6–8 µm ($\bar{x}$ = 14.9 × 7.2 µm, n = 50), overlapping biseriate, muriform, mostly ellipsoidal, with 3 transverse septa and one longitudinal septum, deeply constricted at the middle septum, slightly constricted at remaining septa, initially hyaline, becoming pale brown at maturity, upper part wider than lower part, slightly paler, rounded at both ends, conical at the lower end. Asexual morph Undetermined.

Culture characteristics − Colonies on PDA reaching 2 cm diameter after 4 weeks at 16 °C, later with dense mycelium, circular, rough margin, white, reverse cream-grey, flat on the surface, without aerial mycelium. Hyphae septate, branched, hyaline, thin-walled.

Material examined − UK, Hampshire, Southsea, Eastney shore, on a washed-up culm of *Phragmites australis* (Poaceae), 9 November 2015, EBG Jones GJ212 (MFLU 17-0585, holotype), ex-type living culture MFLUCC 17-0756.

GenBank numbers − ITS: MG844345, LSU: MG844347, SSU: MG844349, TEF: MG844351.

Notes − *Neocamarosporium phragmitis* is similar to *N. lamiacearum* in having globose ascomata with an apapillate ostiole, cylindrical-clavate asci and muriform, ellipsoidal, with 3-transversely septate, ascospores with one longitudinal septum, which are rounded at upper end and conical at lower end. However, *N. lamiacearum* has thin peridium and larger asci comparatively to *N. phragmitis*. To further support the establishment of the new taxon as proposed by Jeewon & Hyde (2016) a comparison of the 522 ITS (+5.8S) nucleotides reveals 32 (6.13%) differences that justify they are different taxa. We therefore identify our isolate (MFLUCC 17-0756) as *Neocamarosporium phragmitis* sp. nov.

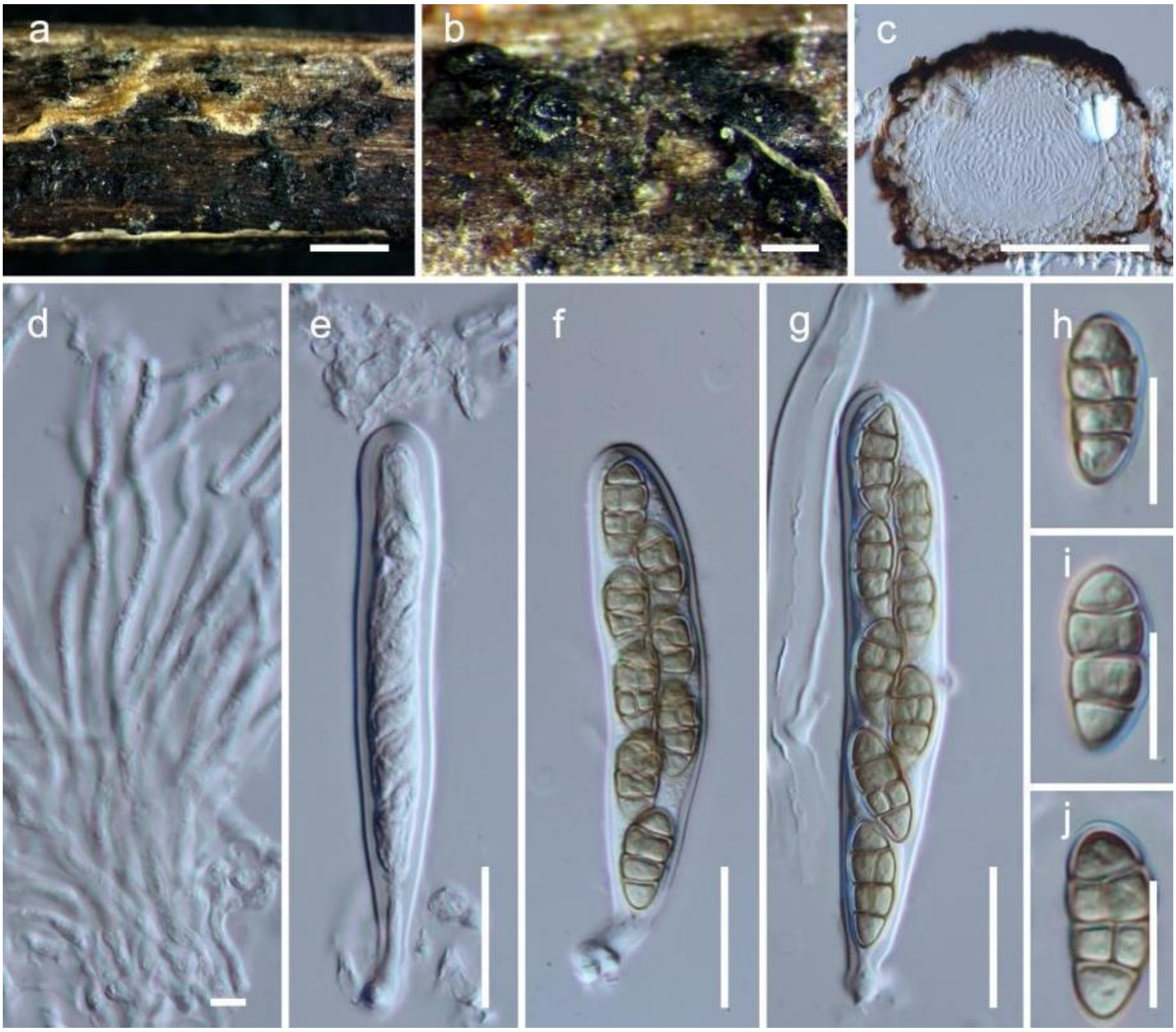


Figure 20 – *Neocamarosporium phragmitis* (MFLU 17-0585, holotype). a, b Ascomata on host substrate. c Section of ascoma. d Pseudoparaphyses. e–g Asci. h–j Ascospores. Scale bars: a = 1 mm, b = 200 µm, c = 100 µm, d = 5 µm, e–g = 20 µm, h–i = 10 µm.

Neohendersoniaceae Giraldo & Crous

The family Neohendersoniaceae was introduced by Giraldo et al. (2017) with *Neohendersonia* as the type genus. Tanaka et al. (2017) listed *Brevicollum*, *Crassiparies*, *Medicopsis* and *Neohendersonia* as members in this family based on multi-gene phylogenetic analysis. In this paper, a new host and country record for *Brevicollum hyalosporum* and a new taxon, *Medicopsis chiangmaiensis*, are described, illustrated and compared with related taxa, based on the evidence from morphology and phylogenetic analyses of combined LSU, RPB2, SSU and TEF1 sequence data.

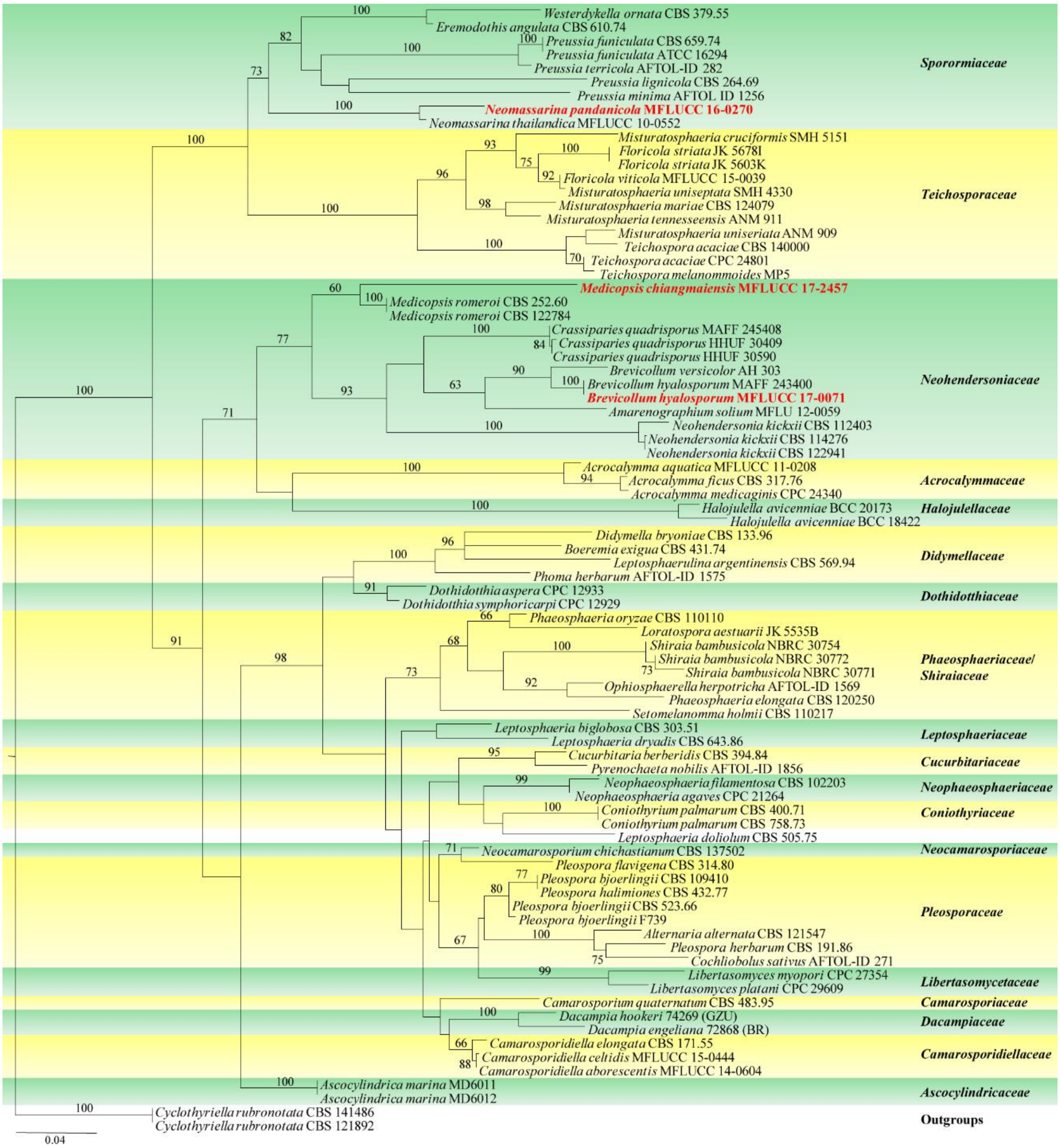


Figure 21 – Phylogram generated from maximum likelihood analysis based on combined LSU, RPB2, SSU and TEF1 partial sequence data. Related sequences were obtained from Hyde et al. (2016). Fifty-four strains are included in the combined LSU, RPB2, SSU and TEF1 sequence analyses, which comprise 3,769 characters with gaps (986 for LSU, 973 for SSU, 907 for TEF and

903 for RPB2). *Cyclothyriella rubronotata* is used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -31102.781686 is presented. The matrix had 1716 distinct alignment patterns, with 43.56% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250598, C = 0.237272, G= 0.273530, T = 0.238600; substitution rates AC = 1.408199, AG = 4.058254, AT = 1.480490, CG = 1.063567, CT = 7.536065, GT = 1.000000; gamma distribution shape parameter α = 0.204321. Bootstrap support values for ML (first set) equal to or greater than 60% are given above/below the nodes. The newly generated sequences are in red.

Brevicollum Kaz. Tanaka et al.

Tanaka et al. (2017) introduced *Brevicollum* to accommodate *B. hyalosporum*, characterized by immersed ascomata with short ostiolar necks, a thin ascomatal wall, clavate asci with a shallow ocular chamber and broadly fusiform, 3–5-septate ascospores. Currently, two species have been reported, viz. *Brevicollum hyalosporum* and *B. versicolor* (Tanaka et al. 2017). *Brevicollum* is morphologically similar to *Crassiparies* in ascospore characteristics. They are however, different, as *Brevicollum* has 8-spored asci, while *Crassiparies* has 4-spored asci. They are also phylogenetically apart (Tanaka et al. 2017). The ML tree generated based on analysis of the combined LSU, RPB2, SSU and TEF1 sequence data indicates that our isolate of *Brevicollum hyalosporum*, *B. hyalosporum* type (MAFF 243400) and *B. versicolor* group as a monophyletic subclade sister to *Amarenographium solium* with moderate support (63% ML) and nested in between *Crassiparies* and *Neohendersonia* (Fig. 21). Unfortunately, no sexual morph has been reported for *A. solium* (Hodhod et al. 2012).

Brevicollum hyalosporum Kaz. Tanaka & Toy. Sato, Mycologia 109: 4 (2017) Fig. 22

Facesoffungi number: FoF 03899

Saprobic branch of *Hevea brasiliensis* Müll.Arg. Sexual morph Ascomata 200–300 µm diameter, 100–250 µm high, scattered, sometimes clustered, immersed, globose to subglobose, ostiole central. *Peridium* 13–45 µm wide, composed of two type of cell layers, outer layer comprising 2–4 layers of thick-walled, dark brown to black cells of *textura angularis*, inner layer comprising 2–3 layers of thin-walled, hyaline cells of *textura angularis*. *Hamathecium* 2–3 µm wide, comprising dense, hyaline, septate, branched, filamentous pseudoparaphyses, slightly constricted at septa. *Asci* (90–)92–120(–155) × 17–22(–25) µm ($\bar{x}$ = 110 × 21 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, subsessile to short pedicellate,apically rounded, with indistinct ocular chamber. *Ascospores* (23–)29–43(–44) × (3–)7–12(–13) µm ($\bar{x}$ = 38.4 × 10.5 µm, n = 30), uniseriate at the lower part and overlapping biseriate at the upper part of the ascus, hyaline to sub-hyaline, broadly fusiform, thick-walled, straight to straightly curved, initially aseptate with small guttules, becoming 3–5-septate, deeply constricted at the middle septum, slightly constricted at the remaining septa, median cell slightly broader, each cell containing distinct large guttule, smooth-walled, with a mucilaginous sheath. Asexual morph Undetermined.

Culture characteristics – Ascospores germinated on MEA within 24 hours and germ-tube produced from one or both sides of the ascospore. Colonies on MEA reaching 2 cm diameter after 21 days at 25°C, colonies circular, medium dense, surface smooth with edge entire, velvety to woolly, colony from above white at the margin, with white-greyish to grey in the centre; from below: white brown to light brown at the margin, white-greyish to grey in the middle, dark grey to blackish at the centre; not producing pigmentation in agar.

Material examined – THAILAND, Chiang Rai Province, Wiang Chiang Rung District, on branch of *Hevea brasiliensis* (Euphorbiaceae), 1 November 2016, Chanokned Senwanna, RBCR012 (MFLU 17-1978), living culture, MFLUCC 17-0071.

GenBank numbers – ITS: MG602204, LSU: MG602200, SSU: MG602202, TEF1: MG739516.

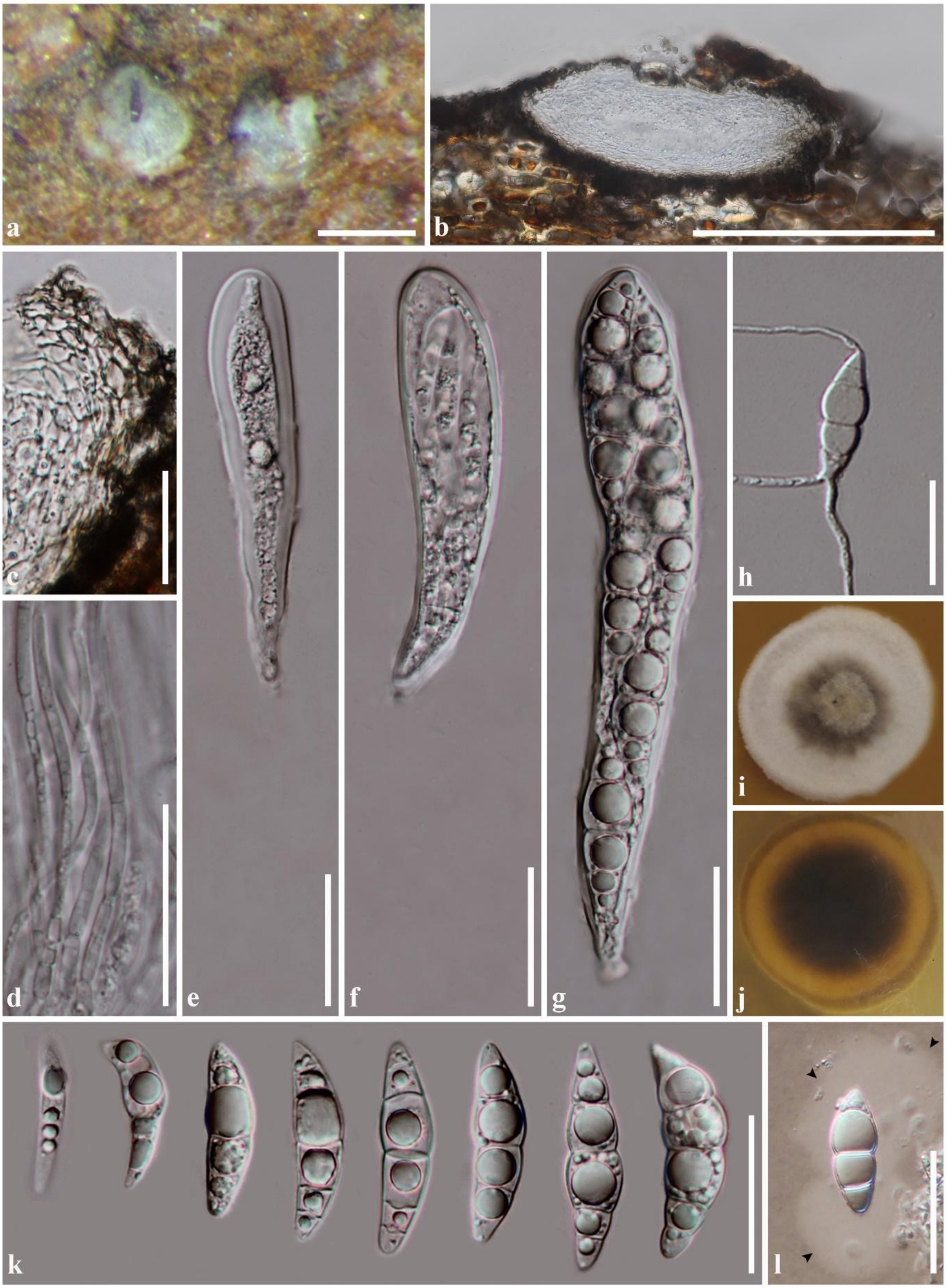


Figure 22 – *Brevicollum hyalosporum* (MFLU 17-1978, new host record). a, b Longitudinal sections through ascomata. c Peridium. d Paraphyses. e–g Asci. h Germinated ascospore. i, j Culture characteristic on MEA after 21 days (i = colony from above, j = colony from below). k Ascospores. l Arrowheads indicate gelatinous sheath surrounding ascospores after treating with India ink. Scale bars: a, b = 200, c–h, k, l = 30 µm.

Notes – During our investigation on diversity of microfungi in Thailand, an isolate (MFLUCC 17-0071) was recovered from *Hevea brasiliensis* in Chiang Rai Province. The phylogeny inferred using analysis of LSU, RPB2, SSU and TEF1 sequence data showed that our isolate clustered with *Brevicollum hyalosporum* with strong bootstrap support (100% ML, Fig. 21). The comparisons of ITS sequence data show 100% similarity with *Brevicollum hyalosporum* (Tanaka et al. 2017). Morphological characters of our collection (Fig. 22) also resembles those in Tanaka et al. (2017). *Brevicollum hyalosporum* was introduced from Japan on dead twigs of *Syzygium samarangense* (Myrtaceae) (Tanaka et al. 2017). Therefore, we consider the new collection as a new host record and new record for Thailand.

Medicopsis Gruyter

Medicopsis is a monotypic genus introduced to accommodate *Pyrenochaeta romeroi* by de Gruyter et al. (2013), although it was originally established for a coelomycetous taxon. Multigene phylogeny from Tanaka et al. (2017) indicates that *Medicopsis* belongs to Neohendersoniaceae in Pleosporales. Only one species *Medicopsis romeroi* is included in *Medicopsis* (Index Fungorum 2018). Members of this genus can be found as a pathogen of humans and also can occur on plants (Badali et al. 2010, Khan et al. 2011, de Gruyter et al. 2013, Ahmed et al. 2014).

Medicopsis chiangmaiensis Q.J. Shang & K.D. Hyde, sp. nov. Fig. 23

Index Fungorum number: IF553978; Facesoffungi number: FoF 03875

Etymology – the specific epithet "*chiangmaina*'' refers to the province in Thailand from which the holotype was collected.

Holotype –MFLU 17-1960

Saprobic on bark. Sexual morph *Stromata* with poorly developed interior, scattered or in groups, immersed to erumpent from the bark by ostiolar canal, circular to irregular in shape. *Ascomata* 295–530 µm high, 410–770 µm diameter ($\bar{x}$ = 410 × 590 µm, n = 25), perithecial, immersed in a stroma, solitary or gregarious, dark brown to black, globose to subglobose, ostiolate, with cylindrical necks, periphysate. *Peridium* 30–55 µm wide, composed of two section layers, outer section comprising 5–10 layers of relatively small, dark brown to black, thick-walled cells, arranged in *textura globulosa* to *textura angularis*, inner part comprising 5–8 layers of hyaline cells of *textura angularis*. *Hamathecium* of 1–2 µm wide, dense, filamentous, septate, hyaline, pseudoparaphyses which branch and anastomose frequently between and above asci. *Asci* (59–)90–137(–178) × (10.5–)12–16(–20) µm ($\bar{x}$ = 115 × 14 µm, n = 50), 8-spored, bitunicate, fissitunicate, clavate, with long pedicel and indistinct ocular chamber. *Ascospores* (16–)18–21(–23.5) × (6–)7.5–9.5(–10) µm ($\bar{x}$ = 20 × 8.5 µm, n = 145), obliquely uniseriate and partially overlapping to biseriate, fusoid to fusoid-ellipsoidal, with narrowly rounded ends, brown when mature, some lightly curved, 1- to 3-septate, with dark bands at the septa, constricted at the median septum, the upper cell often broader than the lower one, minutely verrucose, guttulate, smooth-walled, without a mucilaginous sheath. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 hours. Germ tubes produced from all sides. Colonies on PDA reaching 5–6.5 cm diameter after 7 days at room temperature, colonies circular to irregular, medium dense, flat or effuse, slightly raised, with edge fimbriate, fluffy to fairy fluffy, white from above and below; not producing pigments in agar.

Material examined – THAILAND, Chiang Mai Province, on undetermined dead wood, 27 January 2017, Qiuju Shang, M7P4-15 (MFLU 17-1960, holotype), ex-type living culture, MFLUCC 17-2457, KUMCC 17-0327; *ibid.* (HKAS 100867, isotype).

GenBank numbers – ITS: MG873485, LSU: MG873481, SSU: MG873483.

Notes – *Medicopsis chiangmaiensis* fits well with the classical description of Pleosporales and is characterized by pseudoparaphyses, ostiolate ascomata with bitunicate asci and single-celled ascospores (Zhang et al. 2012). We cannot compare our sexual morphs with other species of *Medicopsis* as this genus lacks a known sexual morph (de Gruyter et al. 2013). However,

Figure 23 – *Medicopsis chiangmaiensis* (MFLU 17-1960, holotype). a Host. b Stroma on host surface. c Section of stroma. d Section of ostiole. e Section of peridium. f–i Asci. j Pseudoparaphyses. k–q Ascospores. r Germinating ascospore. Scale bars: c = 200 µm, d = 50 µm, e, l–r = 10 µm, f–k = 20 µm.

phylogenetic analyses based on the combined LSU, SSU, TEF1 and RPB2 sequence data (Fig. 21) show that *M. chiangmaiensis* (MFLUCC 17-2457) forms a distinct lineage from *M. romeroi* with moderate support (60% in ML).

Neophaeosphaeriaceae Ariyaw. & K.D. Hyde

Neophaeosphaeriaceae was introduced by Ariyawansa et al. (2015) to accommodate *Neophaeosphaeria* and its allied species in the suborder Pleosporineae, order Pleosporales, Dothideomycetes (Ariyawansa et al. 2015). Currently, *Neophaeosphaeria* is the only genus accommodated in this family (Wijayawardene et al. 2018). Detailed taxonomic notes and revisions are provided in Ariyawansa et al. (2015) for this family. Herein, an updated tree for the family is provided (Fig. 24) and a new species, *Neophaeosphaeria phragmiticola*, is introduced.

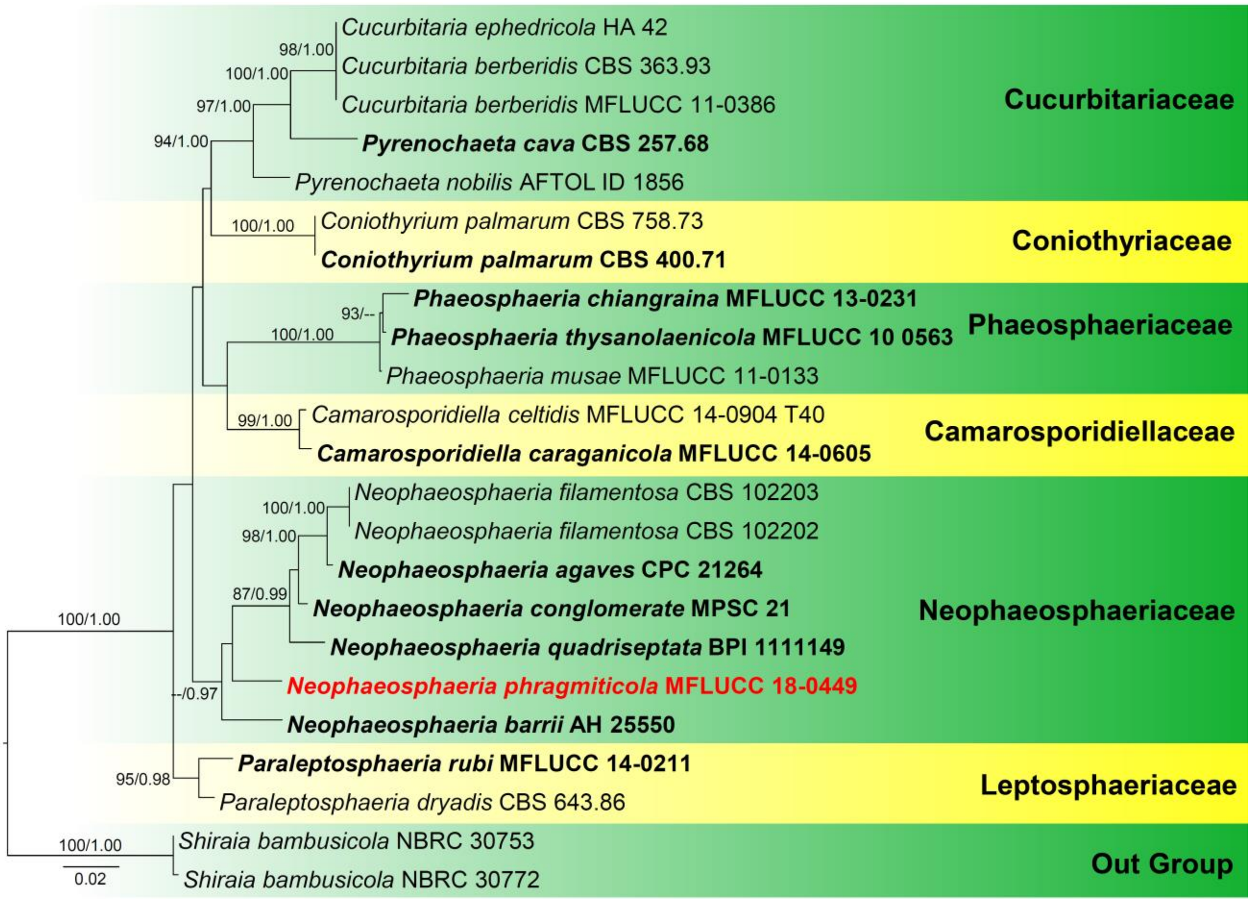


Figure 24 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF sequenced data of Neophaeosphaeriaceae. Related sequences were obtained from Ariyawansa et al. (2015). 23 strains are included in the combined sequence analyses, which comprise 3256 characters with gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. *Shiraia bambusicola* (NBRC 30753) and *Shiraia bambusicola* (NBRC 30772) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -8537.368649 is presented. The matrix had 490 distinct alignment patterns, with 32.23% undetermined characters or gaps. Estimated base frequencies were as follows; A = 1.000000, C = 0.244434, G= 0.235548, T = 0.267643; substitution rates AC = 0.503206, AG = 1.237779, AT = 2.388948, CG = 2.835816, CT = 0.417870, GT = 9.060268; gamma distribution shape parameter α = 0.512703. Bootstrap support values for ML equal to or greater than 65% and BYPP equal to or greater than 0.90 are given above the nodes respectively. Ex-type strains and reference strains are in bold, newly generated sequences are in red.

Neophaeosphaeria M.P.S. Câmara et al.

Neophaeosphaeria was introduced by Câmara et al. (2003) to accommodate *N. filamentosa, N. barrii*, *N. conglomerata* and *N. quadriseptata*. Currently, five species are known (Wijayawardene et al. 2017a). The asexual morphs are coelomycetous and species are pathogenic or saprobic in terrestrial habitats (Wijayawardene et al. 2017a).

Neophaeosphaeria phragmiticola A. Karunarathna & K.D. Hyde, sp. nov. Fig. 25

Index Fungorum number: IF554111; Facesoffungi number: FoF 03942

Etymology – named after *Phragmites*, the host genus from which it was collected.

Holotype – HKAS 97353

Saprobic on dead stems of *Phragmites australis* (Cav.) Trin. ex Steud. Sexual morph Undetermined. Asexual morph Coelomycetous, *Conidiomata* 69–76 µm high × 74–79 µm diameter ($\bar{x}$ = 73.3 × 76.4 µm, n = 5), solitary, immersed to slightly erumpent, dark brown to black, globose to subglobose, slightly depressed, unilocular, lacking ostiole. *Conidiomatal wall* 12–14 µm wide, composed of 3–4 cell layers of thin-walled, brown to dark brown pseudoparenchymatous cells of *textura angularis*, hyaline towards the inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 15–13 µm high × 1–1.6 µm wide ($\bar{x}$ = 14 × 1.3 µm, n = 10), enteroblastic, phialidic, integrated to discrete, branched, doliiform, lageniform or cylindrical, smooth, hyaline, thin-walled, arising from the basal cavity. *Conidia* 32–37 × 17–20 µm ($\bar{x}$ = 34 × 18 µm, n = 40), ellipsoidal to obovoid, truncate at the base, obtuse at the apex, muriform at maturity, hyaline when immature and brown to dark brown at maturity, with 4 transverse septa and 1 longitudinal septum between 1–2 and 2–3, continuous or constricted at the septa, rough-walled.

Culture characteristics – Conidia germinating on PDA, within 14 hours. Colonies growing on PDA, cottony, white to gray reaching 5 mm in 20 days at 25ºC, mycelium superficial, effuse, with regular edge, hyphae pale yellow to white.

Material examined – CHINA, Yunnan Province, Erhai Lake, on dead stems of *Phragmites australis* (Cav.) Trin. ex Steud, 5 October 2016, K.D Hyde, AKDF 05 (HKAS 97353, holotype), ex-type living culture, MFLUCC 18-0449, KUMCC 16–0216.

GenBank numbers – LSU: MG837009, RPB2: MG838021, SSU: MG837008, TEF1: MG838020.

Notes – The phylogenetic affinities of *Neophaeosphaeria phragmiticola* to other species is not well-resolved. A close relationship to *N. quadriseptata* and *N. barrii* is observed but without support (Fig. 24). However, this is the first time muriform spores are reported in *Neophaeosphaeria* and hence we describe our taxon as a new species.

Occultibambusaceae D.Q. Dai & K.D. Hyde

The family Occultibambusaceae was introduced by Dai et al. (2016) with *Occultibambusa* as the type genus. The family is characterized by immersed, solitary to gregarious ascomata, with black ostioles, broadly cylindrical to clavate, bitunicate asci, and broad-fusiform, hyaline to dark brown ascospores (sexual morph) and asexual morphs are morphologically diverse (Dai et al. 2017). This family comprises four genera including *Seriascoma, Occultibambusa* (Dai et al. 2017), *Versicolorisporium* (Hatakeyama et al. 2008) and *Neooccultibambusa* (Doilom et al. 2017). In this paper, we introduce a new *Neooccultibambusa* species from Pandanaceae habitats with support from combined multi-loci phylogenetic analyses (Fig. 26).

Neooccultibambusa Doilom & K.D. Hyde

The genus *Neooccultibambusa* is typified by *N. chiangraiensis* which is characterized by sexual morphs having cylindrical to subcylindrical asci, and ascospores with 1–3 transverse septa. The asexual morph of this genus produces chlamydospores in culture (Doilom et al. 2017) and it has circular, floccose, dark brown to black colonies, with subglobose to globose, dark brown conidia (Jayasiri et al. 2016). In this study, we introduce a new species *Neooccultibambusa pandanicola* which is the hyphomycetous asexual morph.

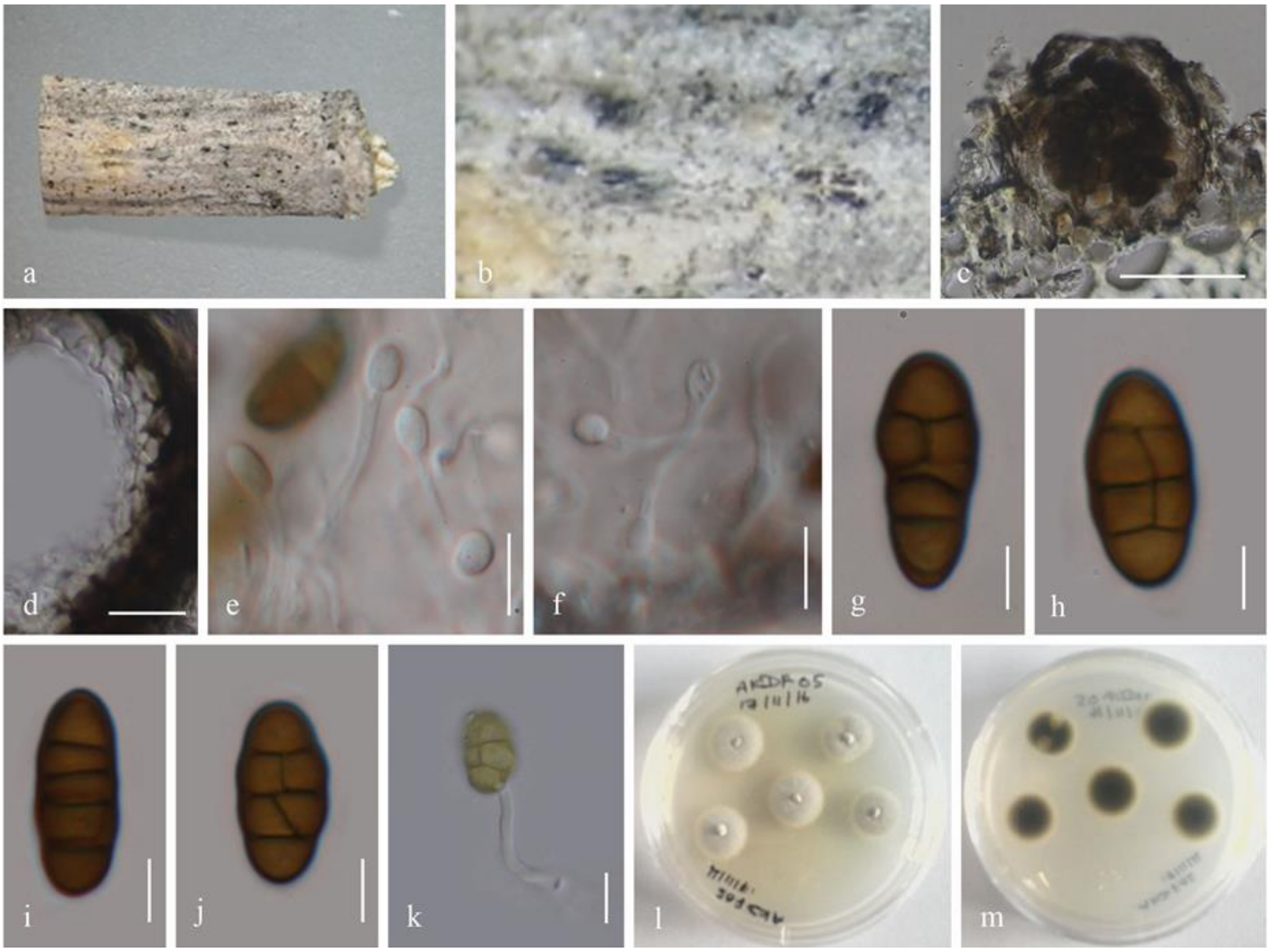


Figure 25 – *Neophaeosphaeria phragmiticola* (HKAS 97353, holotype). a, b Appearance of conidiomata on host. c Longitudinal section of conidioma. d Conidioma wall. e–f Conidiogenous cells and developing conidia. g–j Conidia. k Germinated conidium. l–m Culture characteristics on PDA (l = from above, m = from below). Scale bars: c = 50 µm, d = 10 µm, e–f = 10 µm, g–k = 5 µm.

Neooccultibambusa pandanicola Tibpromma, D.J. Bhat & K.D. Hyde, sp. nov. Fig. 27

Index Fungorum number: IF553942; Facesoffungi number: FoF03814

Etymology – refers to the name of the host plant which the fungus was collected.

Holotype – HKAS 99623

Saprobic on dead leaves of *Pandanus utilis* Bory. *Colonies* dark olive-green, erumpent. *Mycelium* comprising hyaline to pale brown, branched, septate, thin-walled hyphae. Sexual morph Undetermined. Asexual morph Hyphomycetous. *Conidiophores* 13–71 µm high × 3.5–7 wide µm ($\bar{x}$ = 36.8 × 5.4 µm, n = 10) diameter, macronematous, mononematous, solitary, pale-brown to brown, cylindrical, 3–5-septate, straight or slightly flexuous, erect, guttulate, smooth-walled. *Conidiogenous cells* 2.5–5.5 × 4–5.5 µm ($\bar{x}$ = 3.1 × 3.6 µm, n = 10), holoblastic, monoblastic, integrated, terminal, brown, determinate, cylindrical. *Conidia* 28–150 × 7–21 µm ($\bar{x}$ = 86.2 × 12.8 µm, n = 10), acrogenous, solitary, olivaceous brown to mid-brown, obclavate, rostrate at apex, straight or curved, 7–17-euseptate, wide at broadest middle part, truncate at the base, some with basal scar, without with a mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 24 hours. Germ tubes produced from both ends. Colonies on PDA reaching 9 cm diameter after 2 weeks at room temperature, greyish-green on the surface, with dense, fluffy mycelium, circular colony with entire, raised on the surface, dark green in reverse, with smooth margin.

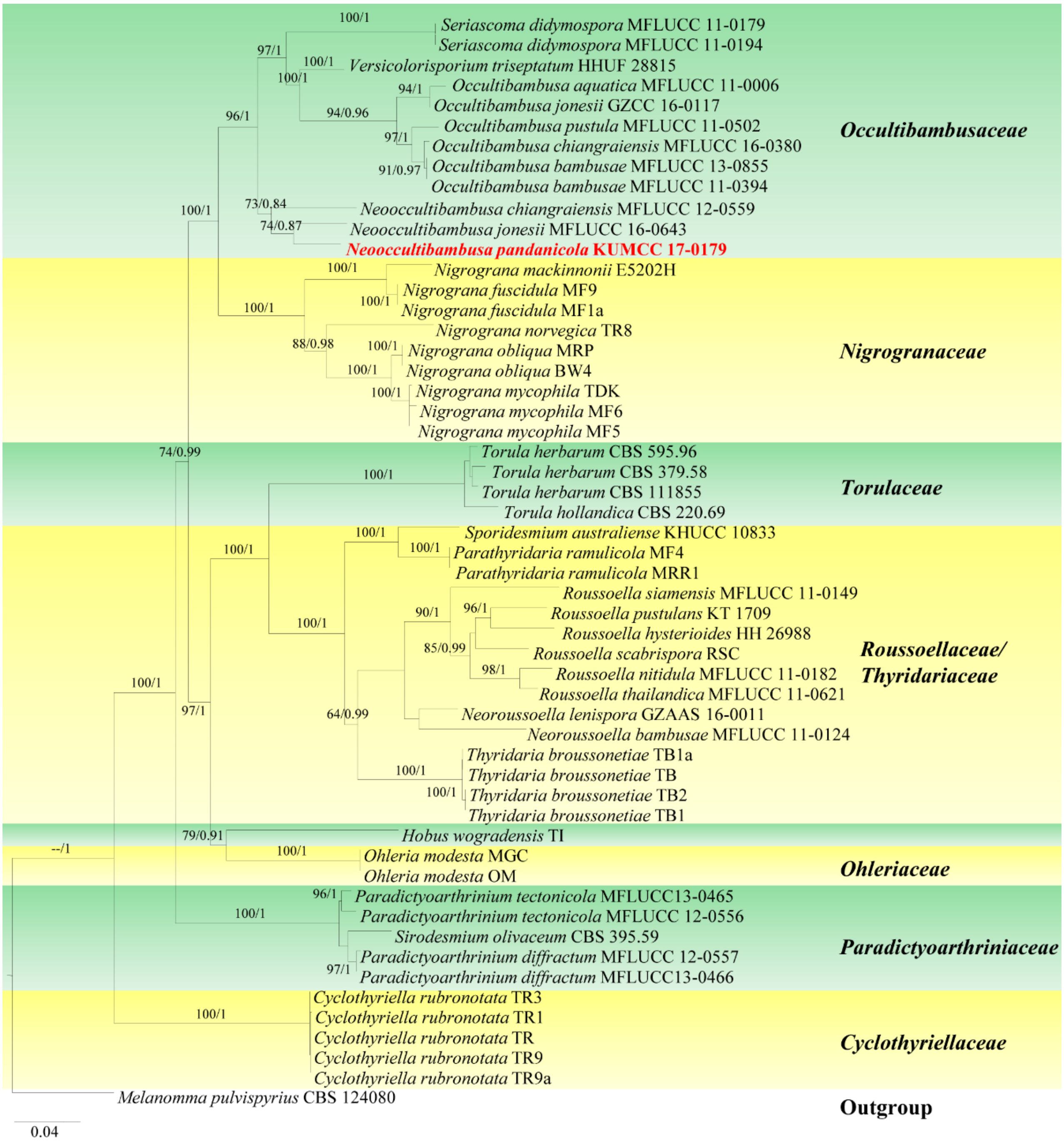


Figure 26 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1 and RPB2 partial sequence data. Related sequences were obtained from Zhang et al. (2017a). Fifty-four strains are included in the combined LSU, SSU, TEF1 and RPB2 sequence analyses, which comprise 3,808 characters with gaps (848 for LSU, 1019 for SSU, 935 for TEF and 1006 for RPB2). Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. *Melanomma pulvis-pyrius* is used as the outgroup taxon. Tree topology of the maximum-likelihood analysis was similar to the Bayesian analysis. The best scoring RAxML tree with a final likelihood value of -21677.689087 is presented. The matrix had 1126 distinct alignment patterns, with 35.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.251517, C = 0.243434, G= 0.276276, T = 0.228772; substitution rates AC = 1.477547, AG = 5.073666, AT = 1.504758, CG = 1.082277, CT = 9.409453, GT = 1.000000; gamma distribution shape parameter α = 0.159759. Bootstrap support values for ML (first set) and BYPP equal to or greater than 0.80 are given above the nodes. The newly generated sequence is in red.

Figure 27 – *Neooccultibambusa pandanicola* (HKAS99623, holotype). a Colonies on the substratum. b, c Conidiophores and conidia. d–f Conidia. g Germinating conidium. h, i Cultures on PDA, h from above, i from below. Scale bars: b–g = 10 µm.

Material examined – CHINA, Yunnan, Xishuangbanna Tropical Botanical Garden, on fallen dead and decaying leaves of *Pandanus utilis* Bory. (Pandanaceae), 28 April 2017, Rungtiwa Phookamsak and Nimali Indeewari de Silva, XTBG15 (HKAS 99623, holotype), extype living culture, KMUCC 17-0179, MFLUCC 17-2265; *ibid.* (MFLU, isotype).

GenBank numbers – ITS: MG298941, LSU: MG298940, RPB2: MG298944, SSU: MG298942, TEF1: MG298943.

Notes – The new species, *Neooccultibambusa pandanicola*, is introduced based on multigene analysis of LSU, SSU, TEF1 and RPB2 sequence data. The new species is phylogenetically closely related to *N. jonesii* Jayasiri et al. with moderate support (74% in ML, 0.87 in PP) (Fig. 26). We also compared the morphology of the asexual morph of our new taxon with *N. jonesii* which has subglobose to globose, unicellular, dark brown conidia (Jayasiri et al. 2016).Our new taxon is different in having obclavate, olivaceous brown to mid-brown, 3–17-euseptate conidia, which are widest at the middle part.

Periconiaceae (Sacc.) Nann.

The family Periconiaceae was introduced by Nannizzi (1934) with *Periconia* as the type genus. Periconiaceae has long been ignored in modern fungal systematics and Tanaka et al. (2015) reinstated Periconiaceae in the suborder Massarineae based on phylogenetic analyses. In this paper, we introduce one new species, *Periconia elaeidis*, designate a reference specimen for *Periconia cookei* E.W. Mason & M.B. Ellis and report *Periconia pseudobyssoides* S. Markovskaja & A. Kačergius from China for the first time.

Periconia Tode

The genus *Periconia* was introduced by Tode (1791) with *P. lichenoides* Tode as the type species. There are 187 species epithets in Index Fungorum (2018) with more than 20 transferred to other genera, but currently only ca. 50 species are recognized as genuinely belonging to *Periconia* (Carmarán & Novas 2003, Kirk et al. 2008, Seifert et al. 2011, Markovskaja & Kačergius 2014, Tanaka et al. 2015, Chuaseeharonnachai et al. 2016, Hyde et al. 2017b, Liu et al. 2017a, Thambugala et al. 2017).

Periconia cookei E.W. Mason & M.B. Ellis, Mycol. Pap. 56: 72 (1953) Fig. 29

Facesoffungi number: FoF 03856

Saprobic on submerged decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* on natural substrate effuse, scattered, hairy, brown to dark brown. *Mycelium* mostly immersed, branched, septate, smooth, brown. *Conidiophores* mononematous, macronematous, cylindrical, erect, straight or flexuous, septate, dark brown at the base and gradually paler towards the apex, unbranched, 240–372 µm ($\bar{x}$ = 306 µm, SD = 66, n = 10) long, 15.5–19.5 µm ($\bar{x}$ = 17.5 µm, SD = 2, n = 10) wide. *Conidiogenous cells* polyblastic, discrete, sphaerical, terminal, brown. *Conidia* catenate, verrucose, brown, mostly sphaerical, dry, thin-walled, 12–15 µm ($\bar{x}$ = 13.5 µm, SD = 1.5, n = 35) diameter.

Material examined – CHINA, Yunnan Province, saprobic on decaying wood submerged in stream in Cangshan Mountain, July 2016, S.M. Tang, S-835 (MFLU 17-1969, reference specimen designated here); living culture, MFLUCC 17-1679, ICMP; S-812 (MFLU 17-1972); living culture, MFLUCC 17-1399, ICMP.

GenBank numbers – MFLUCC 17-1679 – LSU: MG333492, TEF1: MG438278; MFLUCC 17-1399 – ITS: MG333490, LSU: MG333493, TEF1: MG438279.

Notes – *Periconia cookei* was introduced by Mason & Ellis (1953) and is characterized by unbranched, septate, pale brown to dark brown, polyblastic, conidiophores, catenate, verrucose, brown, mostly sphaerical conidia, mostly 13–16 µm diameter (Mason & Ellis 1953). Two fresh isolates were obtained from submerged wood in a stream in Cangshan Mountain during our study of lignicolous freshwater fungi in Yunnan Province, China. The morphological characters of our fresh collection especially the shape and diameter of conidia fit well with the description of *P.*

cookei. Thus, we identified our fresh isolate as *P. cookei* and provided sequence data for this species. Ariyawansa et al. (2014) suggested that if some of morphological characters of the fungus being studied differ from those in the original description, the original material exists but cannot be examined, or its location is different, or the host differs from the holotype, or if no sequences can be obtained from an otherwise satisfactory existing type material, we can designate a reference specimen (RefSpec) in order to clarify the placement of the species using morphology coupled with molecular data. The morphological characters of our new collections fit well with the holotype of *Periconia cookei* Mason & Ellis (1953), and since we could not obtain material from the same host or location, a reference specimen is designated here.

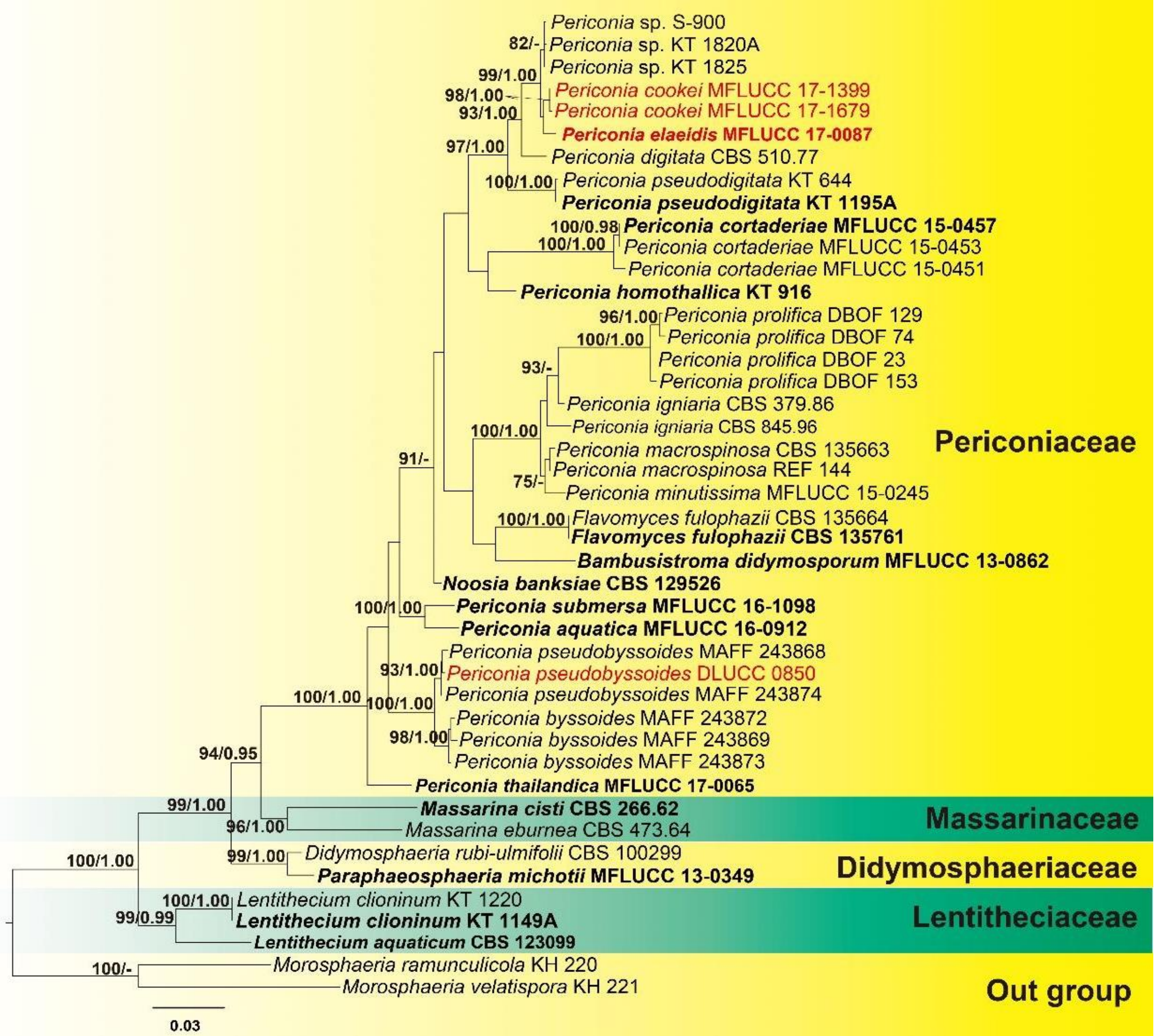


Figure 28 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and TEF sequence data from selected species of Periconiaceae, Massarinaceae, Didymosphaeriaceae and Lentitheciaceae. Maximum likelihood and maximum parsimony bootstrap support values greater than 75% are shown in above and below and branches, while Bayesian posterior probabilities greater than 0.95 are in bold. The new isolates are in red. The tree is rooted with *Morosphaeria ramunculicola* (KH 220) and *M. velatispora* (KH 221). Type, ex-type, epitype and reference strains are in bold.

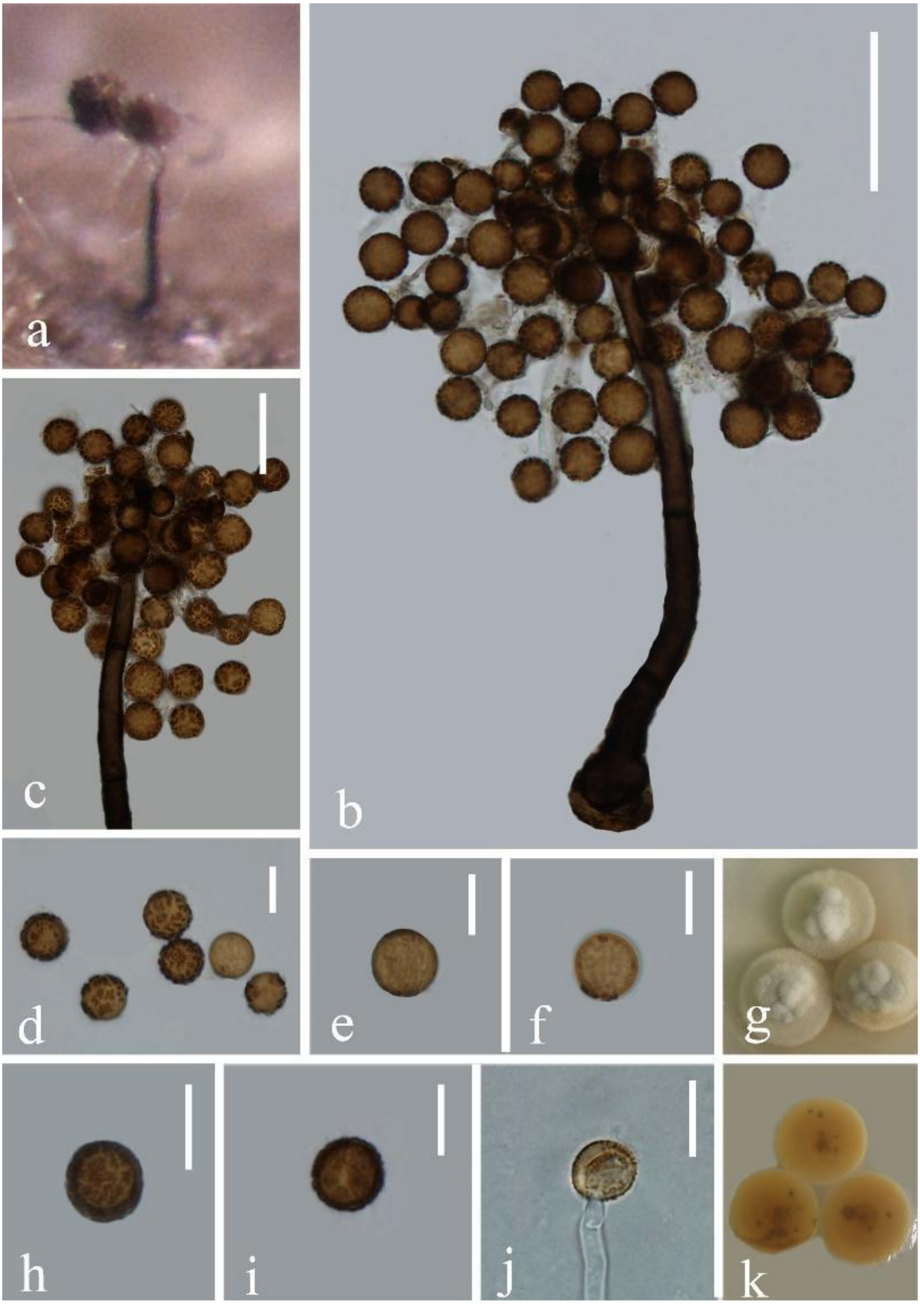


Figure 29 – *Periconia cookei* (MFLU 17-1969, reference specimen) a Colonies on wood. b Conidiophore with conidia. c Conidiogenesis cells and conidia. d–i Conidia. j Germinating conidium. g, k Culture on PDA, g from above, k from below. Scale bars: b = 100 µm, c = 30 µm, d–j = 15 µm.

Periconia elaeidis T. Sunpapao & K.D. Hyde, sp. nov. Fig. 30

Index Fungorum number: IF554399; Facesoffungi number: FoF04473

Etymology – name reflects the host genus *Elaeis*.

Holotype – MFLU 18−0626

Saprobic on dead oil palm leaves. Asexual morph *Colonies* on substrate numerous, effuse, dark brown to black. *Conidiophores* 200−400 μm long × 8−10 μm wide, macronematous, mononematous, unbranched, erect, straight or slightly flexuous, single, grayish-brown to dark brown, 4−7-septate, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* polyblastic, proliferating, terminal, integrated or discrete, ovoid to globose, pale brown, smooth, collapsing when old. *Conidia* 4.5−6.5 μm diameter ($\bar{x}$ = 5.5 μm, n = 30), solitary, subglobose to globose, subhyaline to pale brown, verruculose, aseptate. Sexual morph Undetermined.

Culture characters – Conidia germinating on PDA within 24 hours. Colonies reaching about 6 cm diameter in 5 days on PDA with sparse white mycelia on the surface. The reverse of colony with a dark in the center with a white margin.

Material examined – THAILAND, Phrae, on decaying oil palm, 28 January 2017, Thanawat Sunpapao ESL-1 (MFLU 18−0626, holotype), ex-type living culture MFLUCC 17−0087.

GenBank number – ITS: MG742713, LSU: MH108552, SSU: MH108551.

Notes – *Periconia elaeidis* resembles *P. cookei* in having macronematous, mononematous, unbranched, erect conidiophores, polyblastic, terminal conidiogenous cells and verruculose conidia. However, *Periconia elaeidis* differs from *P. cookei* in having thinner conidiophores (8−10 μm vs 15.5−19.5 μm) and smaller conidia (4.5−6.5 μm vs 12−15 μm). The phylogenetic analysis based on combined ITS, LSU and TEF1 sequence data also indicate that they are distinct species.

Periconia pseudobyssoides S. Markovskaja & A. Kačergius, Mycological Progress 13 (2): 293 (2014) Fig. 31

Facesoffungi number: FoF 03857

Saprobic on submerged decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* effuse, scattered, hairy, dark brown to black. *Mycelium* mostly immersed but sometimes partly superficial, septate. *Conidiophores* mononematous, macronematous, straight or flexuous, solitary, unbranched, often verruculose, cylindrical, brown, 277–411 μm ($\bar{x}$ = 344 μm, SD = 67, n = 10) long, 9–13 μm ($\bar{x}$ = 11 μm, SD = 2, n = 10) wide. *Conidiogenous cells* polyblastic, holoblastic, determinate, integrated, brown, cylindrical. *Conidia* sphaerical or subsphaerical, golden yellow to golden brown, verruculose, 5.5–7.5 μm ($\bar{x}$ = 6.5 μm, SD = 1, n = 35) diameter

Material examined – CHINA, Yunnan Province, saprobic on decaying wood submerged in stream in Cangshan Mountain, September 2016, S.M. Tang, S-850 (MFLU 17-1970); living culture, DLUCC 0850.

GenBank numbers – ITS: MG333491, LSU: MG333494, TEF1: MG438280.

Notes – *Periconia pseudobyssoides* was introduced by Markovskaja and Kačergius (2014) and is characterized by macronematous, often verruculose, brown to reddish-brown conidiophores, sphaerical, golden yellow to golden brown or reddish-brown conidia (Markovskaja & Kačergius 2014). A fresh isolate was obtained from submerged wood in a stream in Cangshan Mountain during our study of lignicolous freshwater fungi in Yunnan Province, China. The morphological characters of our fresh collection fit well with the description of *P. pseudobyssoides*. Phylogenetic analysis also indictes that our strain clusters with *P. pseudobyssoides* (MAFF 243868, MAFF 243874) with strong support (93 ML/1.00 PP). Thus, we identified our fresh isolate as *P. pseudobyssoides* and provide sequence data for this species. This is the first record of this fungus for China.

Phaeoseptaceae S. Boonmee, Thambugala & K.D. Hyde, fam. nov.

Index Fungorum number: IF 554385; Facesoffungi number: FoF04462

Saprobic on dead or decaying wood in terrestrial and freshwater habitats. Sexual morph

Figure 30 – *Periconia elaeidis* (MFLU 18−0626, holotype). a Substrate. b Conidiophores on substrate. c–e Conidiophores. f–i Conidia. j Germinated conidia. k Colony on MEA. Scale bars: b = 100 µm, c–e = 50 µm, f–i = 5 µm, j = 10 µm.

Ascomata immersed in host tissues, erumpent when mature, visible as black spots, solitary, scattered, globose to subglobose, dark brown, with or without a pseudoclypeus, short papillate, with an apical ostiole. *Peridium* comprising several layers, outer layers dark brown to black, of somewhat flattened cells of *textura angularis*; inner layers hyaline to lightly pigmented cells of *textura angularis*. *Hamathecium* comprising cylindrical, branched, septate, anastomosed,

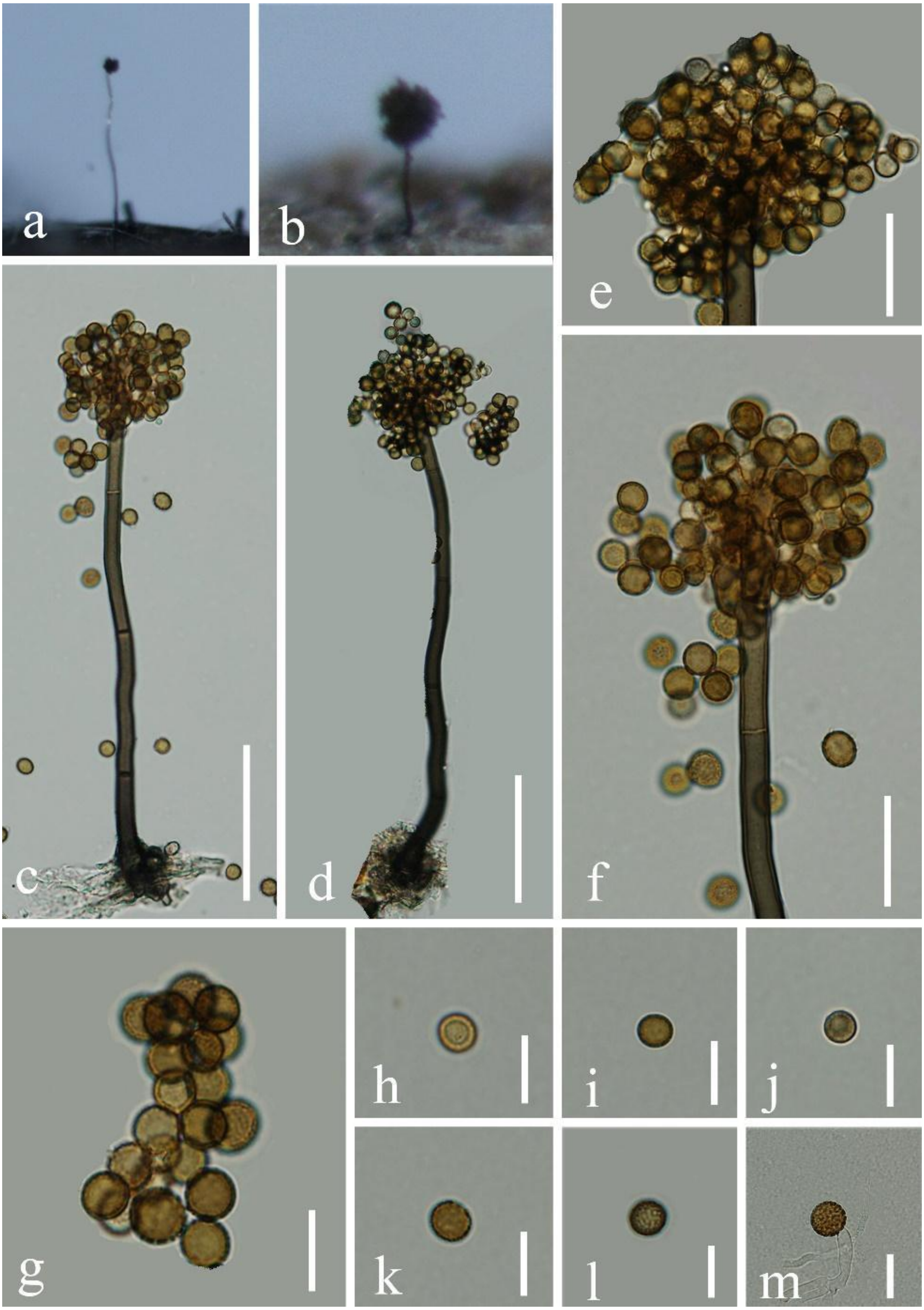


Figure 31 – *Periconia pseudobyssoides* (MFLU 17-1970). a, b Colonies on wood. c, d Conidiophore with conidia. e, f Conidiogenous cells and conidia. g–i Conidia. j Germinating conidium. Scale bars: c, d = 100 µm, e–f = 30 µm, g–m = 15 µm.

pseudoparaphyses. *Asci* 8-spored, bitunicate, cylindrical-clavate, long pedicellate, with a small ocular chamber. *Ascospores* 2–(-3)-seriate, light brown, muriform, allantoid, cylindrical, broadly fusoid to broadly tapering towards the rounded ends, slightly curved, ends asymmetrical, slightly wider at median part, rounded at both ends, with multi-transverse septa, and 1 longitudinal septum in each cell, sometimes with 2 longitudinal septa, constricted and darkened at the septa, smooth-walled. Asexual morph Undetermined.

Family type – *Phaeoseptum* Ying Zhang, J. Fourn. & K.D. Hyde

Notes – The new family Phaeoseptaceae is introduced to accommodate the genera *Phaeoseptum*, *Lignosphaeria* Boonmee et al. and *Neolophiostoma* Boonmee & K.D. Hyde. In the present phylogenetic analysis of LSU, SSU, RPB2 and TEF1α sequence data *Phaeoseptum*, *Lignosphaeria* and *Neolophiostoma* form a well-supported clade (Fig. 32) together with putatively named strains of *Decaisnella formosa* (BCC 25616 and BCC 25617) and *Thyridaria macrostomoides* (GKM 1033 and GKM 1159), sister to the family Halotthiaceae (Fig. 32). However, *Decaisnella formosa* and *Thyridaria macrostomoides* need to be recollected and epitypified with DNA sequence data in order to ensure correct placement (Abdel-Wahab and Jones, 2003, Mugambi and Huhndorf 2009). *Lignosphaeria* and *Neolophiostoma* are characterized by phragmosporous, elongate, cylindrical to fusiform and hyaline ascospores and *Phaeoseptum* mainly differs from *Lignosphaeria* and *Neolophiostoma* in having muriform, allantoid, cylindrical, pigmented ascospores. All of the species of these genera are wood inhabiting taxa collected in Thailand (Zhang et al. 2013, Ariyawansa et al. 2015, Thambugala et al. 2015).

Phaeoseptum Ying Zhang et al.

Phaeoseptum was introduced by Zhang et al. (2013) to accommodate a single species *P. aquaticum* Ying Zhang et al. Zhang et al. (2013) placed this genus in *Halotthiaceae* based on analysis of LSU sequence data. The genus is characterized immersed ascomata with a black pseudoclypeus, bitunicate, broadly fusoid asci with broadly rounded ends and multi-transversally septate, brown ascospores, which are darkly pigmented at the septa. In this study, we provide an updated phylogenetic tree for the new family Phaeoseptaceae and introduce a new species of *Phaeoseptum* (Fig. 32).

Phaeoseptum terricola S. Boonmee & K.D. Hyde, sp. nov. Figs 33, 34

Index Fungorum number – IF554376, Facesoffungi number: FoF 04384

Etymology – the epithet *terricola* (Latin) means living on terrestrial ecosystems.

Holotype – MFLU 10-0032

Saprobic on dead wood. Sexual morph *Ascomata* 137–214 µm high × 155–224 µm diameter ($\bar{x}$ = 172 × 183.5 µm, n = 5), initially immersed and erumpent when mature, visible as black spots, solitary, scattered, globose to subglobose, dark brown, short papillate, with an apical ostiole. *Peridium* 14–24 µm wide, comprising several layers, outer layers dark brown to black, somewhat flattened cells of *textura angularis*; inner layers hyaline to lightly pigmented cells of *textura angularis*. *Hamathecium* comprising 0.5–1 µm wide, cylindrical, branched, septate, anastomosed, pseudoparaphyses. *Asci* 64–90 × 13–17.5 µm ($\bar{x}$ = 79 × 16 µm, n = 15), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, long pedicellate, with a small ocular chamber. *Ascospores* 19–25 × 5–7 µm ($\bar{x}$ = 22 × 6 µm, n = 20), 2-seriate, light brown, muriform, allantoid, cylindrical, tapering towards the ends, slightly curved, ends asymmetrical, slightly wider at median part, rounded at both ends, with 9–10(–11) transverse septa, and 1 longitudinal septum in each cell, sometimes with 2 longitudinal septa, constricted and darkened at the septa, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on MEA within 12 hours and germ tubes produced from each cell. Colonies slow growing on MEA, reaching less than 8 mm in 7 days at 28°C, slightly convex, undulating to raised, dentate, with slightly radial striations and lobate edges, brown.

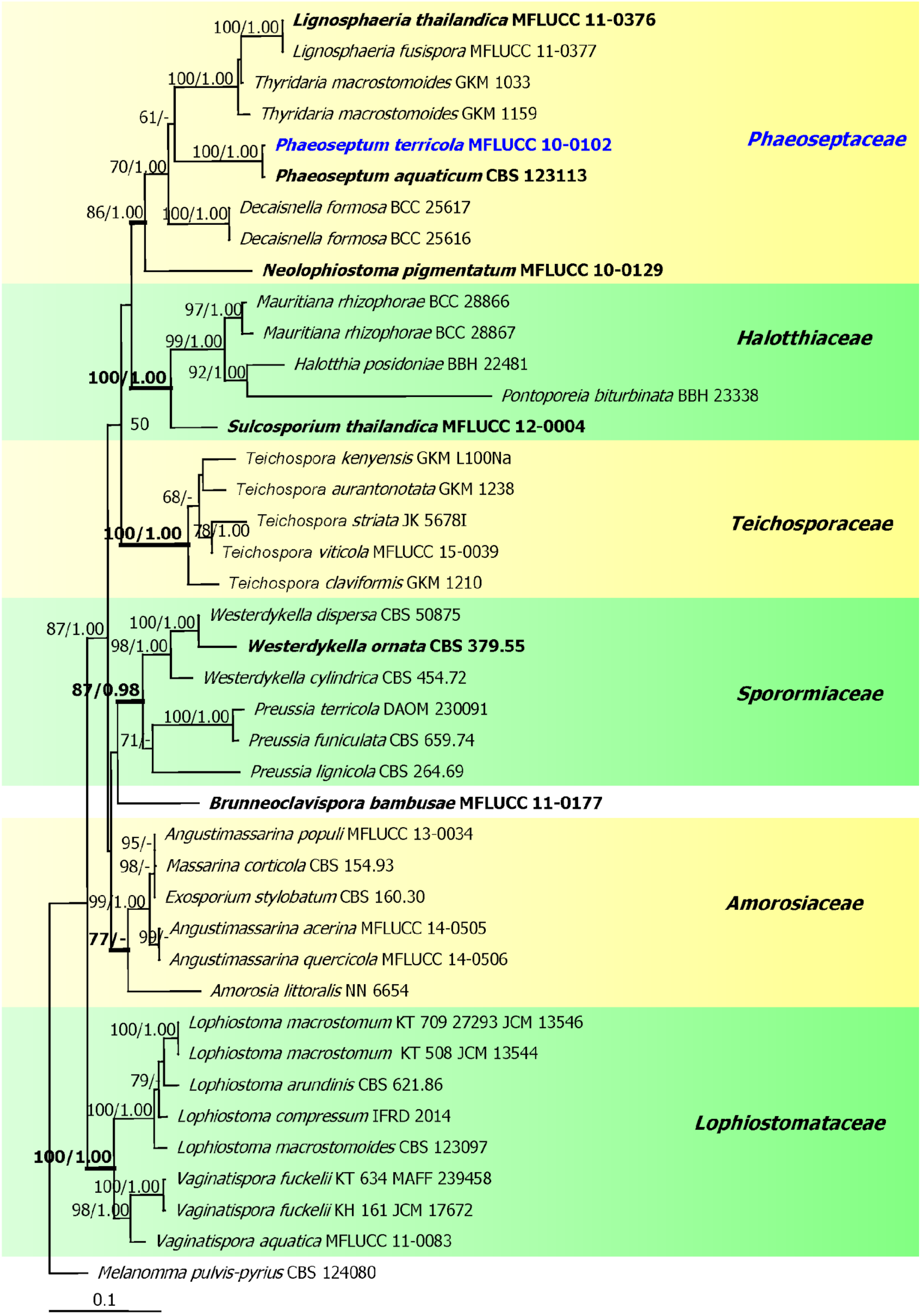


Figure 32 – RAxML phylogenetic tree generated from LSU, SSU and TEF1 sequence data of *Phaeoseptum terricola* (strain MFLUCC 10–0102) and related genera of *Pleosporales*. The tree is rooted with *Melanomma pulvis-pyrius* CBS 124080 (*Melanommataceae*, Pleosporales). RAxML bootstrap support values ≥ 50% (BT) and Bayesian posterior probabilities ≥ 95% (PP) are given above the nodes. The ex-type strains are in bold and new strain in blue.

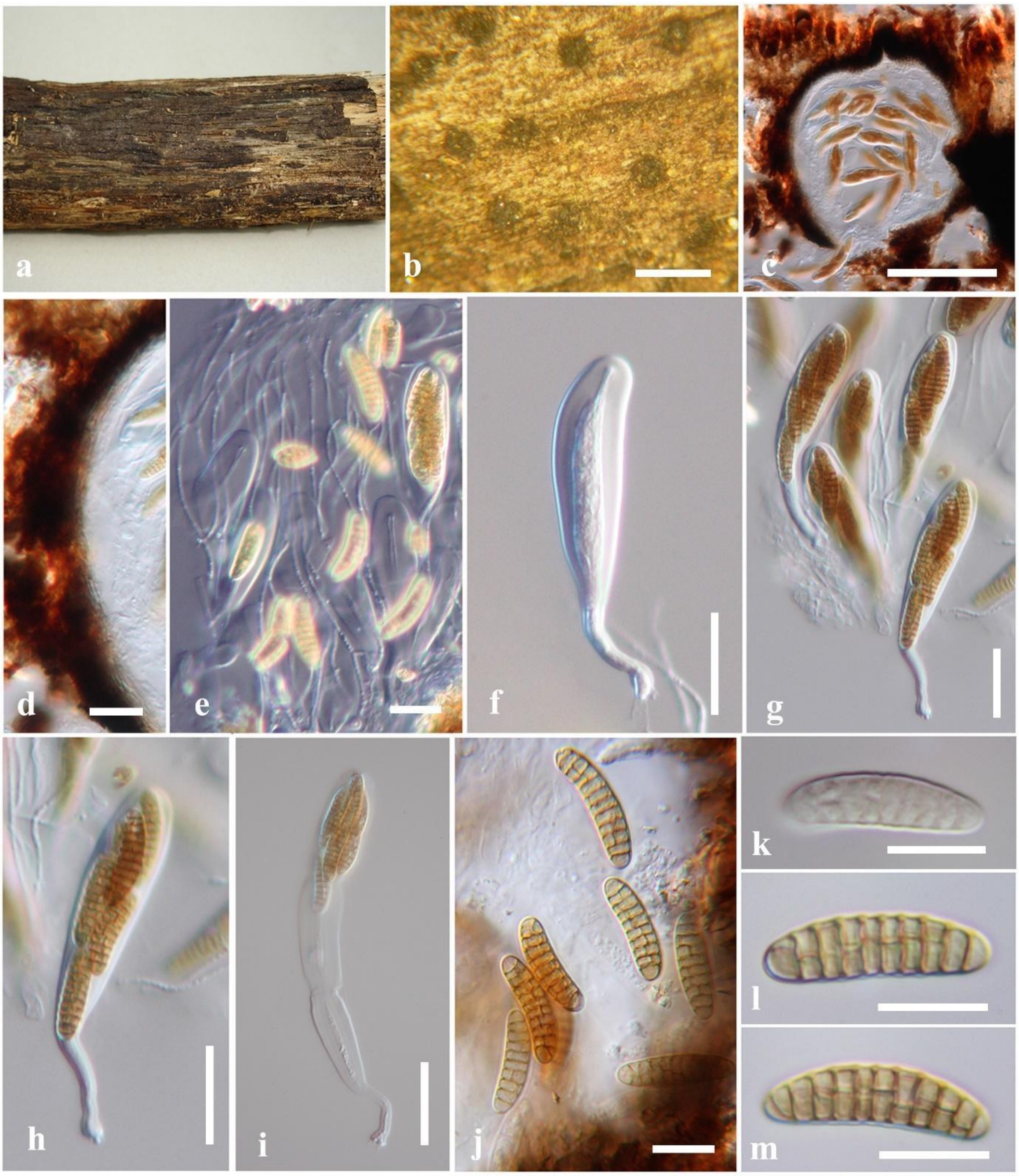


Figure 33 – *Phaeoseptum terricola* (MFLU 10–0032, holotype). a Herbarium material. b Appearance of ascomata on host. c Section of ascoma. d Peridium. e Pseudoparaphyses. f–i Immature and mature asci. j–m Ascospores. Scale bars: a = Material, b = 500 µm, c = 100 µm, d–i = 20 µm, j–m = 10 µm.

Material examined – THAILAND, Chiang Mai, Doi Inthanon, Jom Thong, elev. 800–1000 msl., N18°31.576' E 98°29.790', on dead wood, 5 September 2009, S. Boonmee, ITN01 (MFLU10–0032, holotype), ex-type living culture: MFLUCC 10–0102, IFRDCC 2183, BCC 52150.

GenBank numbers – ITS – MH105778, LSU – MH105779, RPB2 – MH105782, SSU – MH105780, TEF1 – MH105781.

Notes – *Phaeoseptum terricola* is introduced as a new species in the genus *Phaeoseptum* based on morphology and phylogenetic evidence. In the present multi-gene phylogenetic analysis

(LSU, SSU and TEF1 sequence data), *Phaeoseptum terricola* clusters with the ex-type strain of *P. aquaticum* with strong support (100% MLBT and 1.00 BYPP, Fig. 32). *Phaeoseptum terricola* shares common features of the genus, such as dark pigmented and immersed ascomata, cylindrical-clavate, pedicellate asci and muriform, brown ascospores. However, *Phaeoseptum aquaticum* differs from *P. terricola* in having elongate, immersed ascomata with a pseudoclypeus, clearly fissitunicate asci and allantoid, cylindrical ascospores, with multi-transverse septa and a single longitudinal septum in each cell.

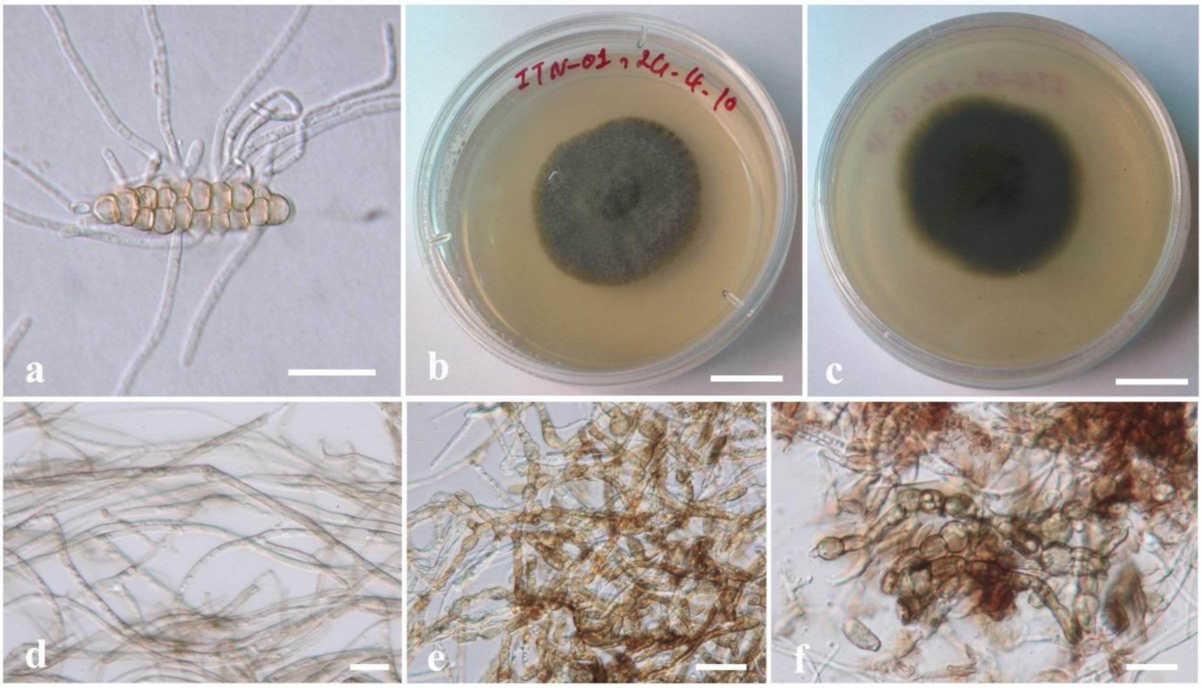


Figure 34 – *Phaeoseptum terricola* (MFLUCC 10-0102, ex-type culture). a Germinating spore. b, c Colonies cultures on MEA from surface and reverse. d Aerial hyphae in culture. e, f The formation of chlamydospore-like structures. Scale bars: a = 10 µm, b, c = 10 mm, d–f = 20 µm.

Phaeosphaeriaceae M.E. Barr.

The family Phaeosphaeriaceae was introduced by Barr (1979) with the type species *Phaeosphaeria oryzae*. Members of this family are characterized by immersed to superficial, globose to subglobose ascomata, bitunicate asci and hyaline, yellowish or brown, fusiform to ellipsoidal, muriform, 1 to multi-septate ascospores, and holoblastic or enteroblastic conidiogenesis with aseptate or septate conidia (Barr 1979, Zhang et al. 2012, Hyde et al. 2013, Phookamsak et al. 2014b, Tennakoon et al. 2016, Tibpromma et al. 2017). Phaeosphaeriaceae is recognized as a heterogeneous group, comprising plant pathogens, saprobes and endophytes associated with a wide range of host plants (Zhang et al. 2012, Hyde et al. 2013, Phookamsak et al. 2014b, 2017, Tibpromma et al. 2017). According to recent publications, 52 genera are accepted within this family (Phookamsak et al. 2014b, 2017, Hyde et al. 2016, Tibpromma et al. 2017, Wijayawardene et al. 2018). In the present study, three novel species are assigned to this family and placed in the genus *Neosetophoma* on account of their morphological and phylogenetic relationships. Descriptions of new taxa and the comparisons with reported species are also provided.

Neosetophoma Gruyter et al.

Neosetophoma, is characterized by globose to irregular conidiomata, with papillate ostioles, and with yellowish conidia that are attenuate at one end (de Gruyter et al. 2010, Liu et al. 2015, Wijayawardene et al. 2016), which has been often reported as a pathogen causing leaf spots of various hosts (Phookamsak et al. 2014b). In recent studies, Tibpromma et al. (2017) introduced *N.*

garethjonesii as the first report of the sexual morph of *Neosetophoma* and Wanasinghe et al. (2018) introduced another three taxa to *Neosetophoma viz. N. rosae, N. rosarum* and *N. rosigena*. In this study, we introduce another new species *Neosetophoma shoemakeri*, with both its sexual and asexual morphs.

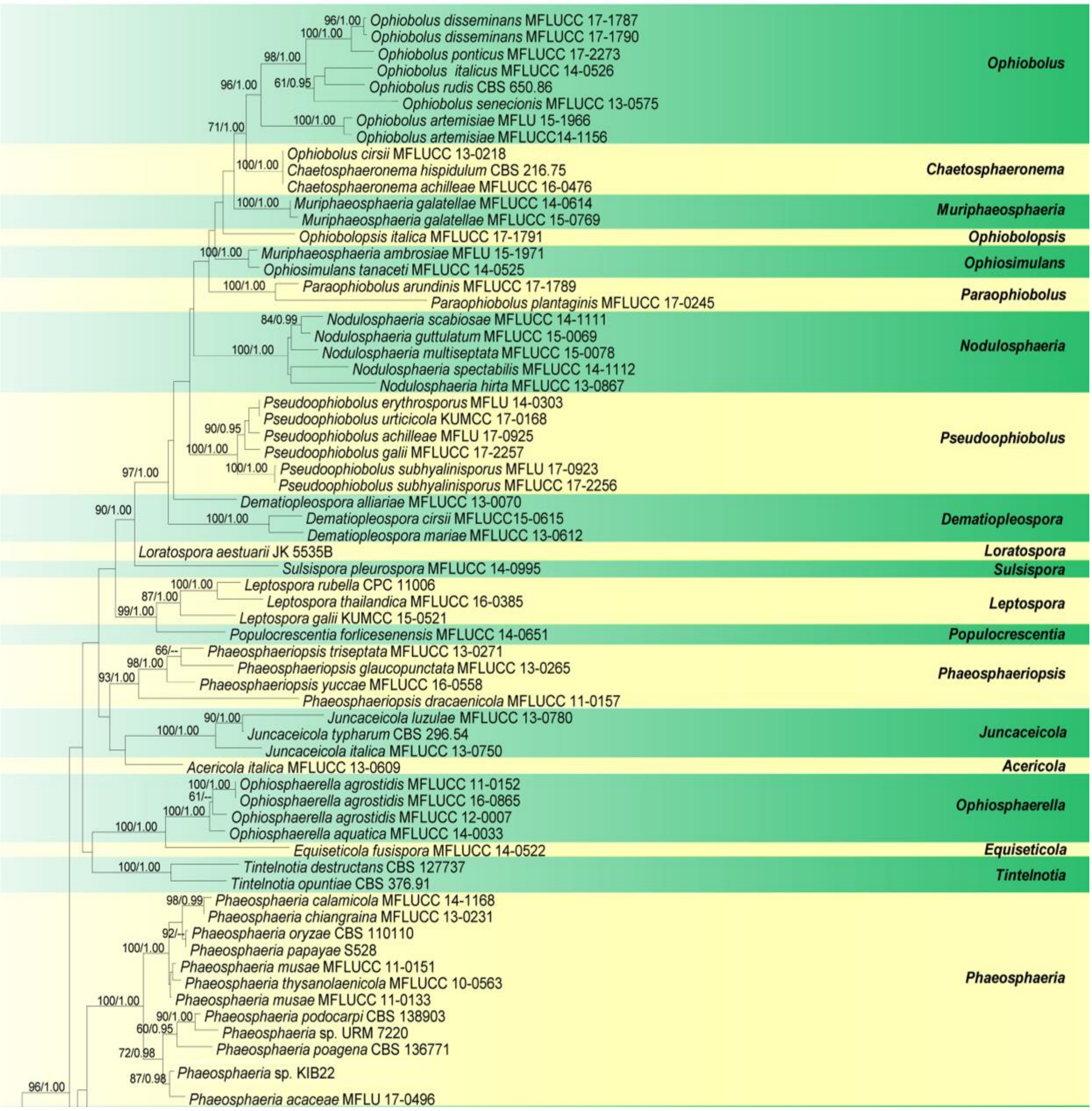


Figure 35 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF sequence data of Phaeosphaeriaceae. Related sequences were obtained from Hyde et al. (2017b) and Phookamsak et al. (2017). 132 strains are included in the combined sequence analyses, which comprise 3510 characters with gaps. *Leptosphaeria doliolum* (CBS 505.75) and *Paraleptosphaeria dryadis* (CBS 643.86) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -29771.43732 is presented. The matrix had 1473 distinct alignment patterns, with 26.99% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246460, C = 0.234850, G = 0.265591, T = 0.253100; substitution rates AC = 1.126918, AG = 2.548533, AT = 1.959684, CG = 0.714174, CT = 5.985048, GT = 1.000000; gamma distribution shape parameter α = 0.478992. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes respectively. Newly generated sequences are in red.

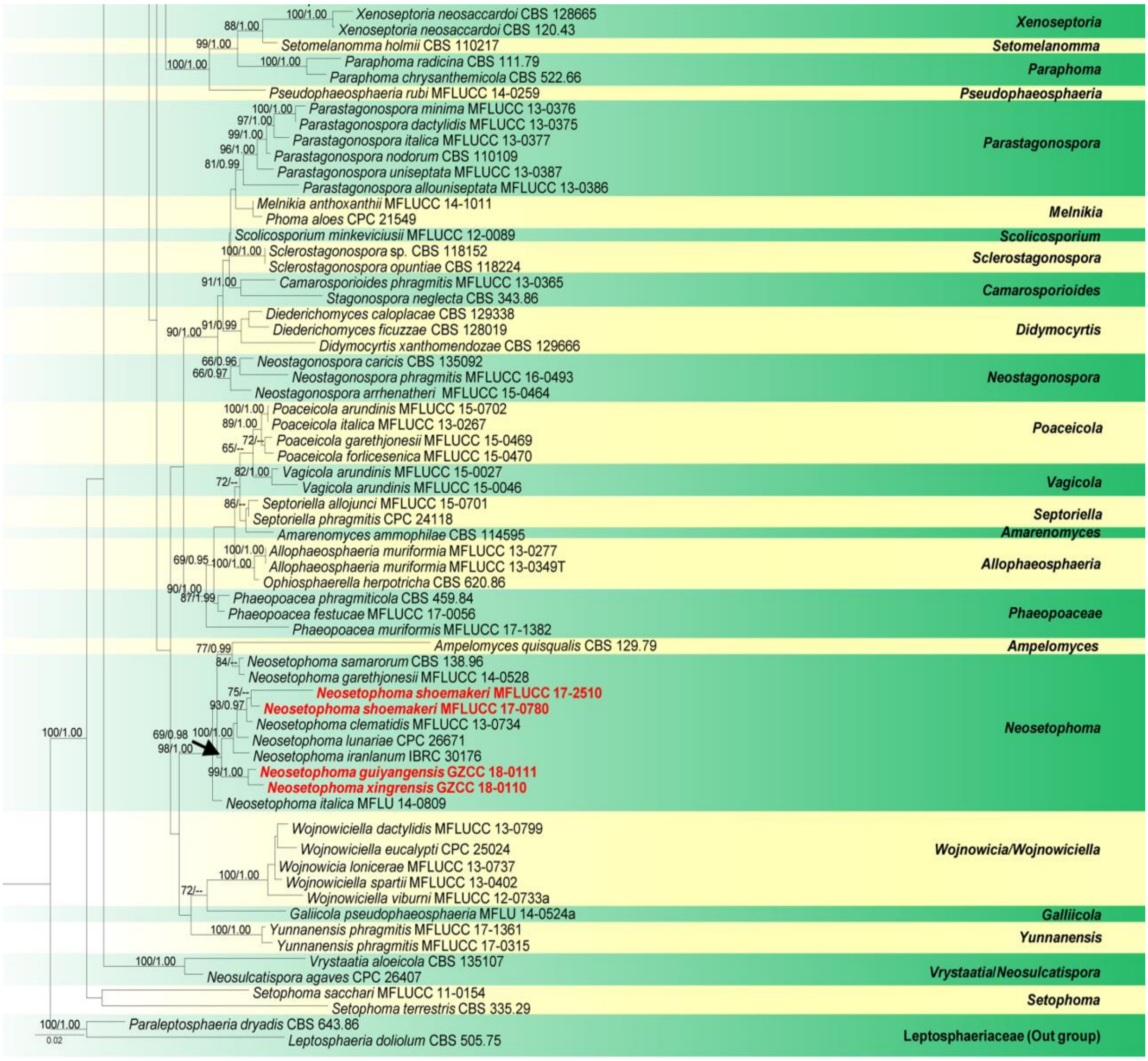


Figure 35 – Continued.

Neosetophoma guiyangensis J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, sp. nov. Fig. 36

Index Fungorum number: IF554080; Facesoffungi number: FoF 04378

Etymology – in reference to the collection site where the holotype was collected, Guiyang City, China.

Holotype – GZAAS 18–0101

Saprobic on unidentified dead branch, visible as raised, black, globular structures on host surface. Sexual morph *Ascomata* immersed under epidermis to superficial, globose to subglobose, dark brown to black, solitary to gregarious, coriaceous, ostiolate. *Peridium* up to 13–18.5 µm wide, comprising two strata, the outer stratum composed of thick-walled, black, pseudoparenchymatous cells, fusing at the outside with the host tissue, inner stratum composed of slightly pigmented, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, cellular pseudoparaphyses, anastomosing among and above the asci, embedded in a gelatinous matrix. *Asci* (52–)55–69.5(–75.5) × 8–11.5 µm ($\bar{x}$ = 64.5 × 9 µm, n = 25), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate with a furcate pedicel, apically rounded, with a minute ocular chamber. *Ascospores* (17–)20–25.5(–28) × 3.5–4.5 µm ($\bar{x}$ = 22 × 3.9 µm, n = 25), overlapping 1–2-seriate, fusiform, slightly curved, with acute ends, 1–3(–5)-septate, hyaline when young, becoming pale brown at maturity, not constricted at the septum, smooth-walled, without any appendages. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on WA within 12 hours. Colony reaching up to 23 mm on PDA after 10 days at 25°C, circular, surface flat or effuse, slightly raised at center, fluffy, greenish-grey from above, and yellowish-grey from below.

Material examined – CHINA, Guizhou Province, Guiyang City, on dead branch of undetermined host, 12 May 2016, J.F. Zhang, GZ-13 (GZAAS 18-0101, holotype), ex-type living culture, GZCC 18-0111.

GenBank numbers – ITS: MH018134, LSU: MH018132, SSU: MH018136.

Notes – *Neosetophoma guiyangensis* is phylogenetically close to *N. xingrensis* with high bootstrap support (99% BP and 1.00 PP) (Fig. 35). However, it can be distinguished from the latter in its longer asci (52–75.5 µm vs. 40–64 µm). The most conspicuous difference between these two taxa, is that *N. guiyangensis* has a furcate pedicel, while the pedicel in *N. xingrensis* is sessile.

Neosetophoma shoemakeri Senwanna, Wanas., Bulgakov, E.B.G. Jones & K.D. Hyde, sp. nov.

Figs 37, 38

Index Fungorum number: IF554067; Facesoffungi number: FoF03920

Etymology – in honour of Shoemaker R.A., for his immense contribution to mycology.

Holotype – MFLU 16-1606

Saprobic on *Cirsium* sp. (Asteraceae) and *Malva* sp. (Malvaceae) in terrestrial habitats. Sexual morph *Ascomata* 170–230 µm high, 170–200 µm diameter, solitary, sometimes clustered, immersed to slightly erumpent, visible as slightly raised, small, black dots on the host surface, uniloculate, globose to subglobose, dark brown to black, ostiolate. *Peridium* 15–40 µm wide, thick at the apex, thinner at the base and side, composed of 2–4 layers of dark brown to black cells of *textual angularis* to *textura prismatica*. *Hamathecium* comprising 1.5–3 µm wide, numerous, filamentous, septate, pseudoparaphyses. *Asci* 60–100 × 6–11 µm ($\bar{x}$ = 83.7 × 9.4 µm, n = 40), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded with an indistinct ocular chamber. *Ascospores* 15–27 × 3–6 µm ($\bar{x}$ = 20.4 × 4.6 µm, n = 70), 1–2 seriate, partially overlapping, fusiform, initially hyaline to subhyaline with small guttules, becoming yellowish-brown to brown at maturity, 3-septate, enlarged at the second cell below the apex, slightly curved, constricted at the septa, smooth-walled. Asexual morph coelomycetous. *Conidiomata* 120–180 µm high, 120–160 µm diameter ($\bar{x}$ = 164.7 × 142.9 µm, n = 5), pycnidial, separate, dark brown, globose, subepidermal, unilocular, thin-walled, papillate. *Conidiomatal wall* 5–15 µm wide, composed of 2–4 layers, lightly pigmented to brown, thick-walled, cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 µm long × 2.5–4 µm wide, enteroblastic, phialidic, doliiform to ampulliform, determinate, hyaline, smooth-walled. *Conidia* 7.5–10.5 × 2.5–3 µm ($\bar{x}$ = 9.1 × 2.6 µm, n = 30), subcylindrical, fusiform, or ellipsoid to fusiform, individually hyaline, olivaceous-brown at maturity as a mass, smooth-walled, 1-septate, usually attenuate at one end, thin and smooth-walled, with minute granules.

Culture characteristics – Colonies on *PDA* reaching 2 cm diameter after 21 days at 16 °C, colonies medium dense, irregular, flat or effuse, slightly raised, margin filiform, fluffy, white from above, yellowish in media from below, not produced pigmentation on PDA media. Mycelium immersed in and superficial on the media.

Material examined – RUSSIA, Rostov region, Shakhty City, Alexandrovsky (Central) Park, on dead stem of *Cirsium arvense* (L.) Scop. (Asteraceae), 14 March 2016, Timur S. Bulgakov, T-1312 (MFLU 16-1606, holotype); ex-type living culture, MFLUCC 17-2510; United Kingdom, Hampshire, Southsea, Eastney shore, on stems of *Malva* sp., (Malvaceae), 17 April 2016, EBG Jones GJ268 (MFLU 17-0607); living culture, MFLUCC 17-0780, ICMP.

GenBank numbers – MFLUCC 17-2510 – ITS: MG602203, LSU: MG602199, SSU: MG602201, TEF: MG739515; MFLUCC 17-0780 – ITS: MG844346, LSU: MG844348, SSU: MG844350, TEF: MG844352.

Notes – During our investigations on diversity of microfungi in Russia and UK, two fresh collections (MFLU 16-1606 and MFLU 17-0607) were made from *Cirsium arvense* and *Malva* sp.

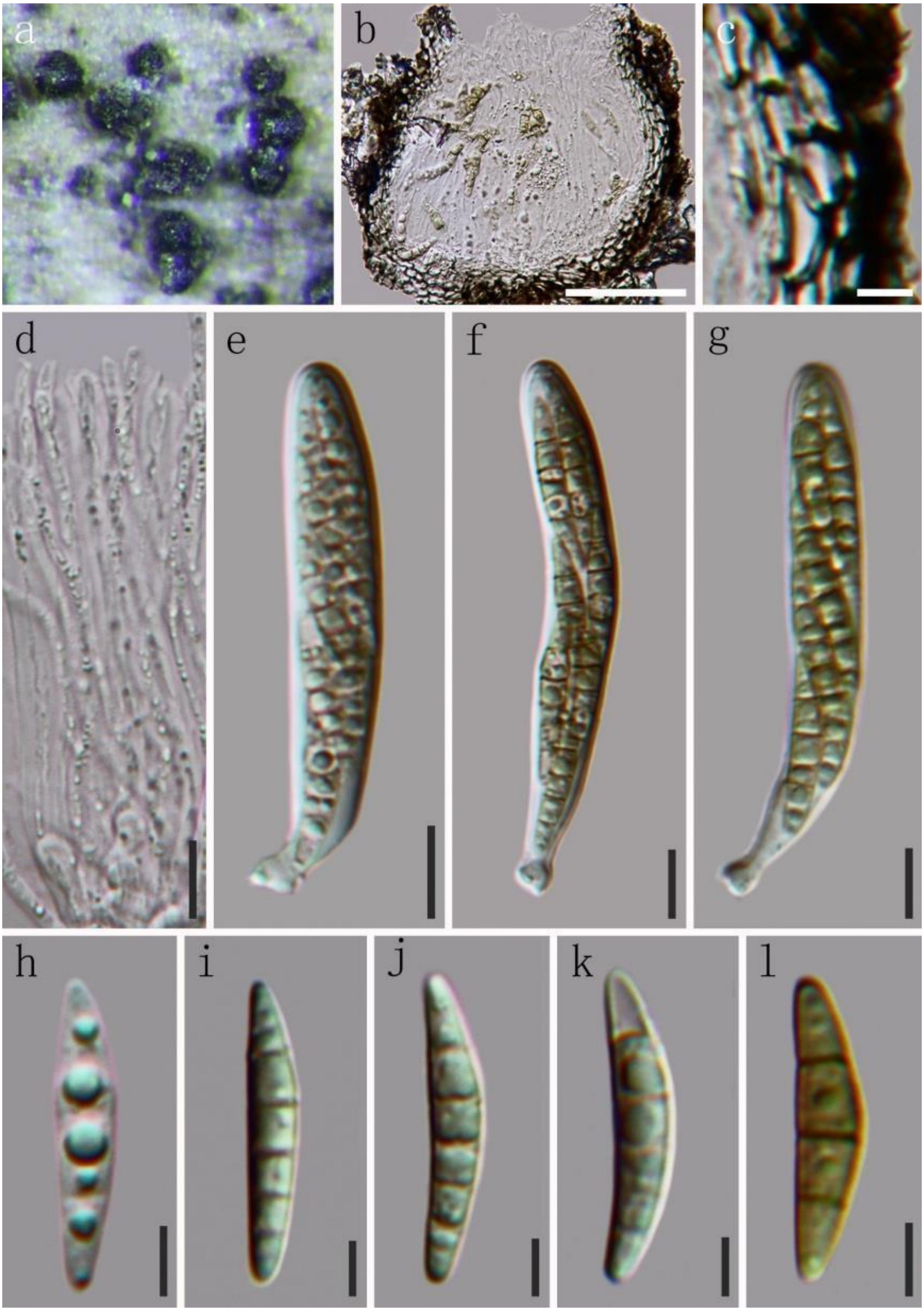


Figure 36 – *Neosetophoma guiyangensis* (GZAAS 18-0101, holotype) a Appearance of ascomata on host surface. b Vertical section through ascoma. c Section of peridium. d Pseudoparaphyses. e–g Asci. h–l Immature and mature ascospores. Scale bars: b = 50 µm, c, h–l = 5 µm, d = 20 µm, e–g = 10 µm.

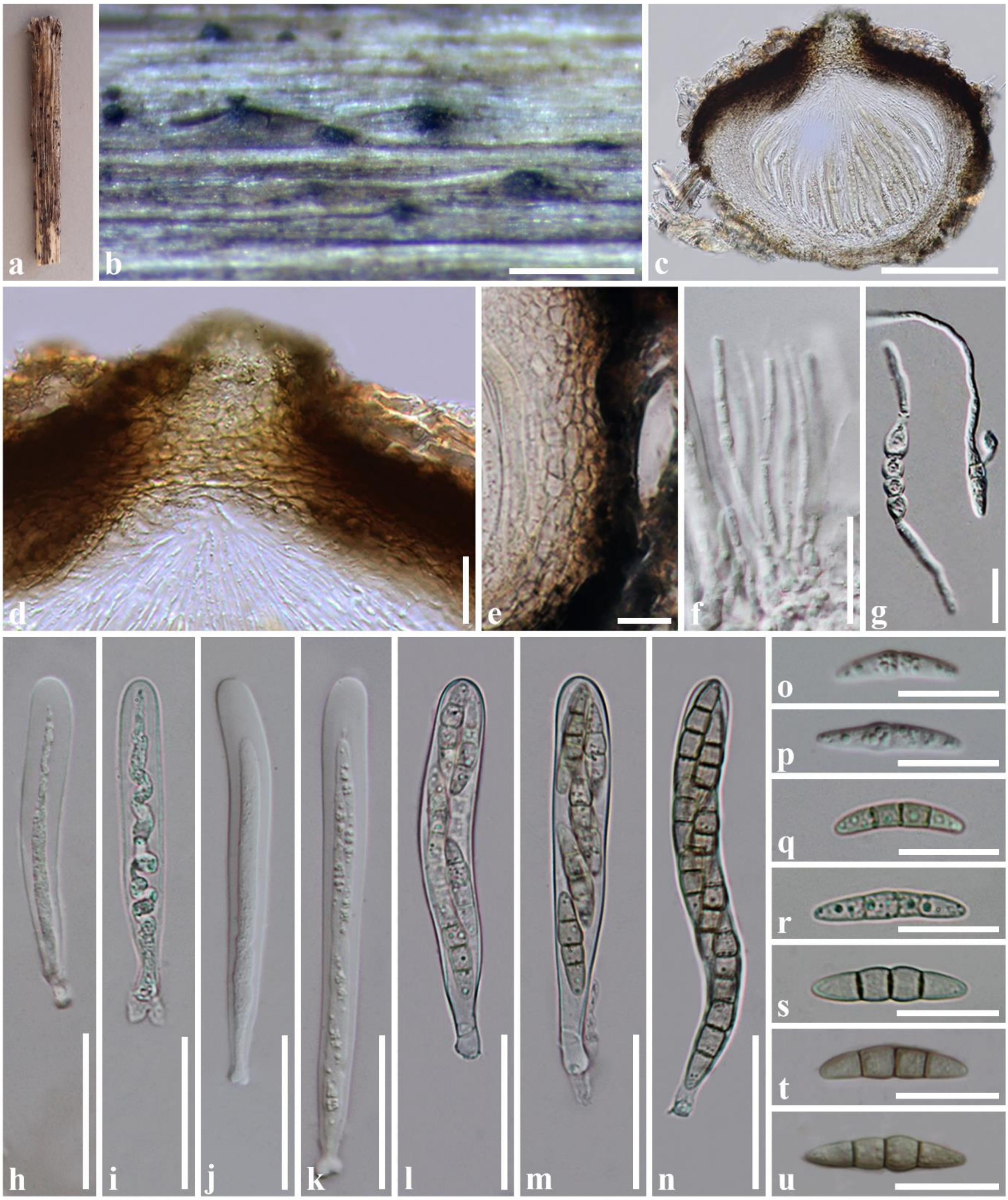


Figure 37 – Sexual morph of *Neosetophoma shoemakeri* (MFLU 16-1606, holotype). a, b Appearance of ascomata on host surface. c Section through ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g Germinated spores. h–n Immature and mature asci. o–u Immature and mature ascospores. Scale bars: b = 500 µm, c = 100 µm, d–g = 20 µm, h–n = 30 µm, o–u = 15 µm.

in the Rostov region of European Russia and Eastney shore of Hampshire in the United Kingdom, respectively. MFLUCC 17-2510 was derived from the Russian collection (ascomycetous fungal species), while MFLUCC 17-0780 was obtained from the UK collection (coelomycetous asexual morph). In our combined LSU, SSU, ITS and TEF sequenced data analyses, these two new isolates share a monophyletic relationship within *Neosetophoma* in Phaeosphaeriaceae. A comparison of the 574 ITS (+5.8S) nucleotides with these two new strains reveals only two base-pair differences and a comparison of the 898 TEF nucleotides were identical within both of these strains. This justifies both strains as the sexual and asexual morphs of the same taxon. The asexual morph morphologically fits well within the generic concept of *Neosetophoma* in having hyaline, phialidic conidiogenous cells and slightly yellowish, ellipsoidal to cylindrical, conidia which are usually attenuate at one end (de Gruyter et al. 2010). There are no previously published literature records of the sexual morph in this genus. The sexual morph of our new isolate is morphologically similar to *Phaeosphaeria oryzae* in having phragmosporous, narrowly fusiform, pale brown to brown or yellowish-brown, straight or slightly curved, 3-septate ascospores. However, they are phylogenetically not closely related (Fig. 35).

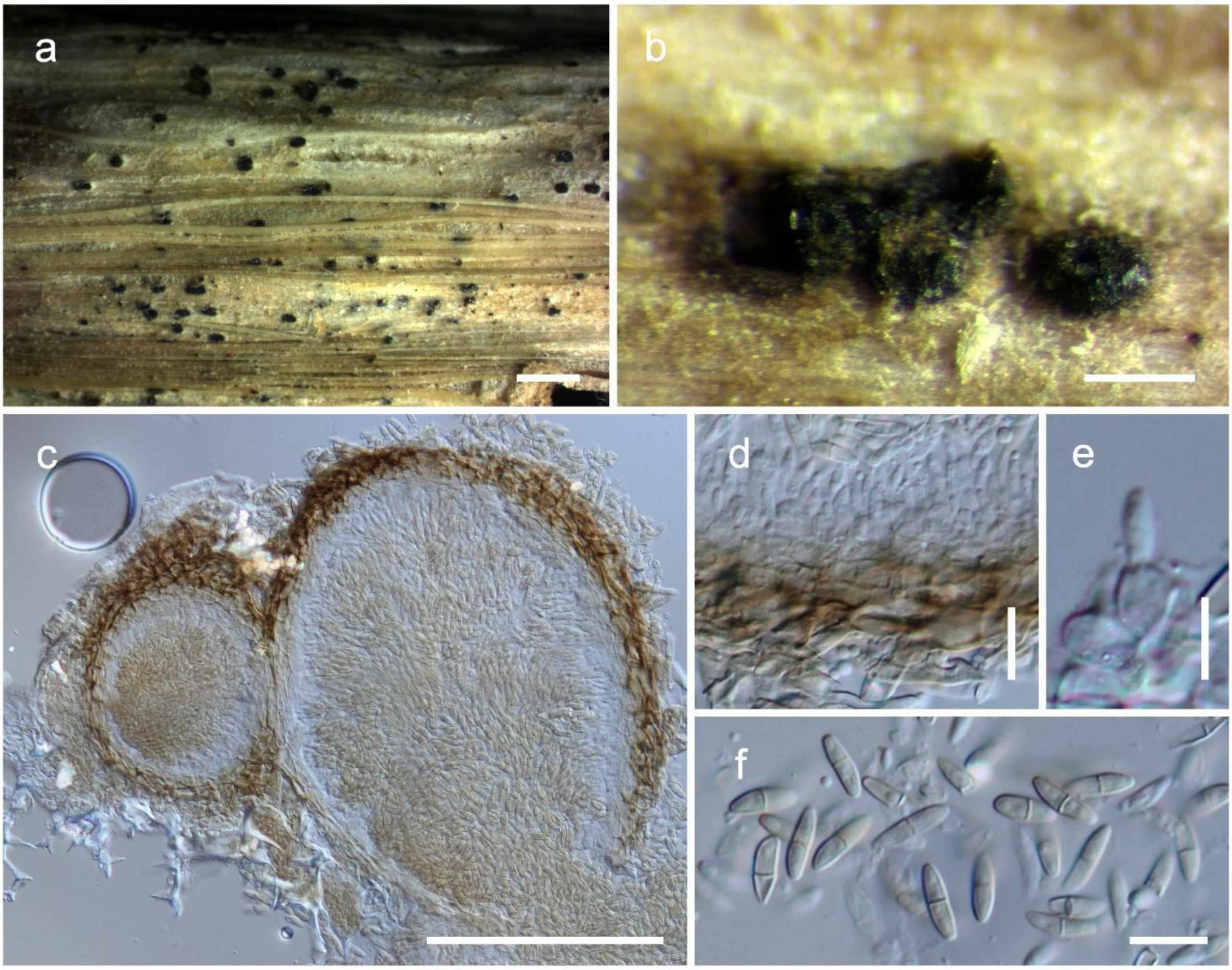


Figure 38 – Asexual morph of *Neosetophoma shoemakeri* (MFLU 17-0607). a, b Conidiomata on host substrate. c Vertical section through conidioma. d, e Conidia attached to conidiogenous cells. f Conidia. Scale bars: a = 1 mm, b = 200 µm, c = 100 µm, d, f = 10 µm, e = 5 µm.

Neosetophoma xingrensis J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, sp. nov. Fig. 39

Index Fungorum number: IF554079; Facesoffungi number: FoF04379

Etymology – in reference to the collection site where the fungus was collected, Xingren County, China.

Holotype – GZAAS 18–0100

Saprobic on decaying wood, visible as raised, shiny-black spots on host surface. Sexual morph *Ascomata* 112–195 µm high, 120–193 µm diameter, globose to subglobose, dark brown to black, solitary to gregarious, immersed to erumpent through the host surface, coriaceous, ostiolate. *Peridium* 11.5–21 µm wide, composed of two strata, an outer stratum comprising dark brown to black, thick-walled, pseudoparenchymatous cells, and an inner stratum composed of hyaline to slightly pigmented, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 2–3 µm wide, cellular pseudoparaphyses, anastomosing among and above asci, embedded in a gelatinous matrix. *Asci* (40–)51–59(–64) × 8–11 µm ($\bar{x}$ = 52 × 9 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a very short pedicel, apically rounded with an ocular chamber. *Ascospores* (15–)21–28 × 3–6 µm ($\bar{x}$ = 22 × 5 µm, n = 30), 1–3-seriate, fusiform, straight to slightly curved, hyaline when young, and becoming pale brown at maturity, normally 3-septate, not constricted at the septum, smooth-walled, guttulate, without any mucilaginous sheath and appendages. Asexual morph Undetermined.

Material examined – CHINA, Guizhou Province, Xingren County, on decaying wood, 2 June 2015, J.F. Zhang, XY 5–7 (GZAAS 18–0100, holotype), ex-type living culture, GZCC 18–0110.

GenBank numbers – ITS: MH018135, LSU: MH018133.

Culture characteristics – Ascospores germinating on WA within 12 hours and germ tubes produced from one or both ends. Colonies growing on PDA, reaching a diameter of 31 mm after 15 days at 25°C, flat, circular, with entire edge, grey-greenish from above, moderately dense, and slightly yellowish from below.

Notes – In the present analysis (Fig. 35), the new taxon is placed in *Neosetophoma* and clusters with *N. guiyangensis* with high bootstrap support. However, it differs from other *Neosetophoma* species by its sessile asci.

Sporormiaceae Munk

The family Sporormiaceae was introduced by Munk (1957) with *Sporormia* as the type genus and *S. fimetaria* (Rabenh.) De Not as the type species. Species of this family occur worldwide, mostly as saprobes on various substrates, including dung, plant debris, soil and wood (Cain 1961, Dissing 1992, Kruys et al. 2006, Sue et al. 2014). Sexual morphs of this family are dark brown ascospores which are strongly constricted at septa and often fragment into part-spores at maturity (Barr 2000) and asexual morphs are coelomycetous or hyphomycetous (Phukhamsakda et al. 2016). In this study, we introduce a new species of *Neomassarina* based on morphological and molecular data and include this genus in Sporormiaceae.

Neomassarina Phook. et al.

Neomassarina was introduced by Hyde et al. (2016) with *N. thailandica* as the type species. Earlier this monospecific genus did not cluster with members of the main families of Dothideomycetes in phylogenetic analyses. Therefore, it was placed in Pleosporales genera *incertae sedis*. The morphological features of the species in this genus are massarina-like and according to our multi-gene phylogenetic analyses in this study, *Neomassarina* clusters in Sporormiaceae with high bootstrap support (Fig. 21). In this study, we introduce a second species of *Neomassarina* on a dead leaf of *Pandanus* sp. from Thailand.

Neomassarina pandanicola Tibpromma & K.D. Hyde, sp. nov. Fig. 40

Index Fungorum number: IF553941; Facesoffungi number: FoF03813

Etymology – refers to the name of the host plant which the fungus was collected.

Holotype – MFLU 16-0554

Saprobic on dead leaf of *Pandanus* sp. Sexual morph *Ascomata* 140–160 µm high × 130–180 µm diameter ($\bar{x}$ = 152 × 156.4 µm, n = 5), semi-immersed to erumpent through host surface, globose to subglobose, as small black dots on the host surface, solitary, without papilla, ostiole central, black, smooth-walled. *Peridium* 16–18.5 µm, thin-walled, composed two layers, the outer layer composed of thick-walled, dark brown to black cells of *textura angularis*; the inner layer composed of hyaline to light brown cells of *textura angularis*. *Hamathecium* comprising 1.5–2.5 µm wide, hyaline, septate, cylindrical pseudoparaphyses. *Asci* 50–80 × 6.5–10 µm ($\bar{x}$ = 67.7 × 8.9 µm, n = 20), 6–8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with short, club-

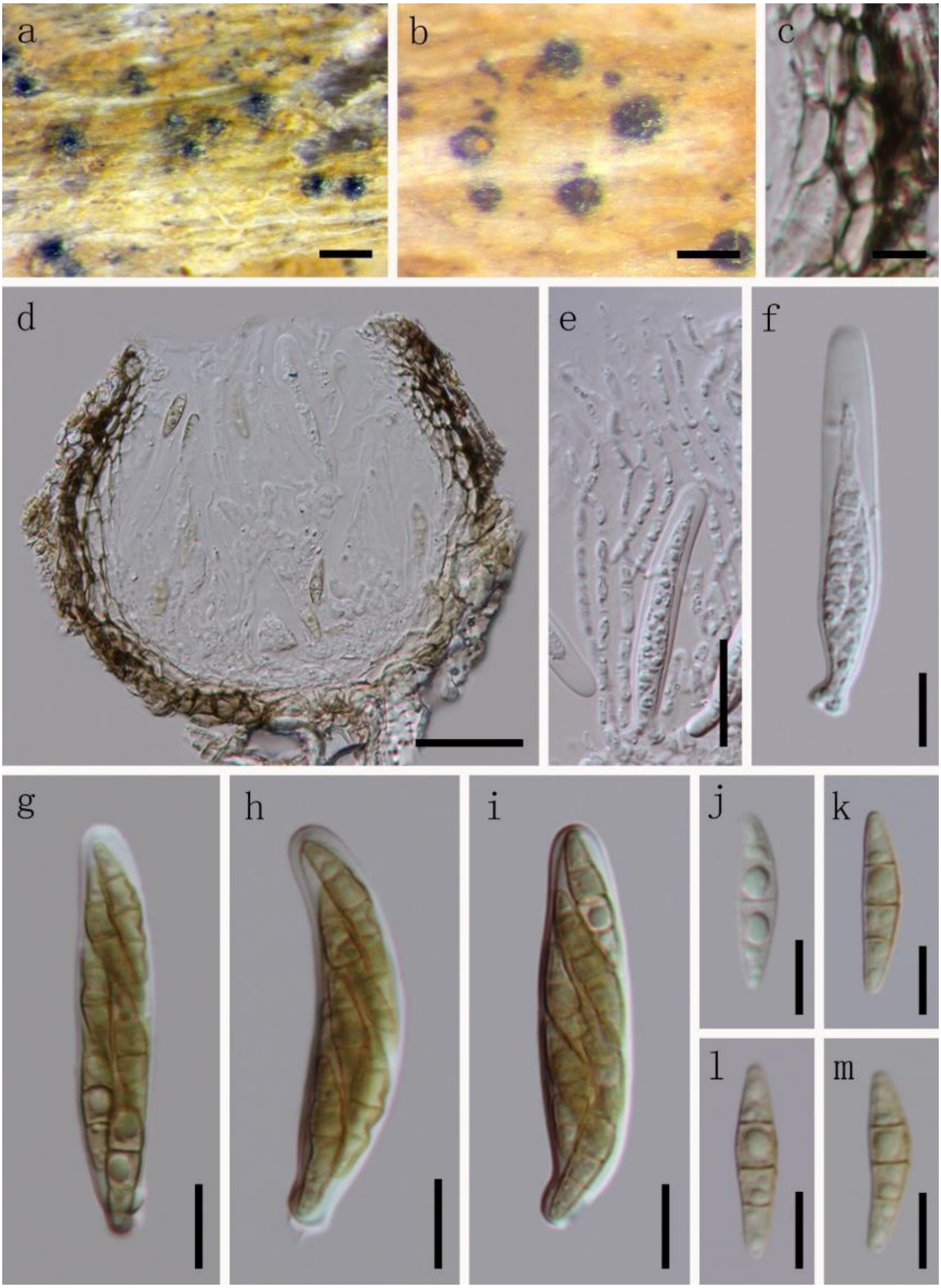


Figure 39 – *Neosetophoma xingrensis* (GZAAS 18-0100, holotype). a, b Appearance of ascomata on host surface. c Section of peridium. d Vertical section through ascoma. e Pseudoparaphyses. f–i Immature and mature asci. j–m Immature and mature ascospores. Scale bars: a = 200 µm, b = 100 µm, c = 5 µm, d = 30 µm, e = 20 µm, f–m = 10 µm.

Figure 40 – *Neomassarina pandanicola* (holotype). a Colony on dead leaves of *Pandanus* sp. b Section of ascoma. c Peridium. d Hamathecium. e–g Asci. h, i Ascospores. j Ascospore stained with India ink. k Germinating ascospore. l, m Culture characters on MEA (note m reverse). Scale bars: a = 200 µm, b = 50 µm, c = 10 µm, d = 5 µm, e–g = 20 µm, h–k = 5 µm.

shaped pedicel, apically rounded with an ocular chamber. *Ascospores* 11–20 × 3–5 µm ($\bar{x}$ = 15.2 × 3.8 µm, n = 20), overlapping uni- to bi-seriate, hyaline, fusiform, 1-septate, constricted at the septum, narrowly rounded both end, ends cone-shaped, smooth-walled, guttulate, with appendages at both ends (3.5–6 µm long). Asexual morph Undetermined.

Culture characteristics – Colonies on MEA reaching 9 cm diameter after 4 weeks at room temperature, colony from above, white to yellow-white; from below, white to yellow-white at the margin, dark-brown at the centre; circular, with entire edge, raised on media surface, flossy, velvety.

Material examined – THAILAND, Prachuap Khiri Khan Province, Sai Khu Waterfall, Bang Saphan District, on dead leaf of *Pandanus* sp. (Pandanaceae), 30 July 2015, Saowaluck Tibpromma, SF15-032 (MFLU 16-0554, holotype); ex-type living culture, MFLUCC 16-0270, KUMCC; *ibid*. (HKAS100837bis, paratypes).

GenBank numbers – ITS: MG298946, LSU: MG298945, SSU: MG298947.

Notes – *Neomassarina pandanicola* was collected on dead leaves of a *Pandanus* sp. from southern Thailand. Based on phylogenetic analysis, *N. pandanicola* clusters with *N. thailandica* with strong bootstrap support (100% in ML, Fig. 21). Moreover, we compared the culture and morphological characteristics of *N. pandanicola* with *N. thailandica* and found that *N. thailandica* differs from *N. pandanicola* (Hyde et al. 2016) in having ascospores with a distinct mucilaginous sheath and being pale brown at maturity, whereas *N. pandanicola* has ascospores with appendages at both ends of the ascospores and are not pale brown at maturity. We also compared the DNA sequences of *N. pandanicola* and *N. thailandica* and found that there are nine base pair differences in ITS and eleven base pair differences in both LSU and SSU regions. Thus, based on both morphological and phylogenetic support (Jeewon & Hyde 2016), *Neomassarina pandanicola* is introduced here as a new species.

Roussoellaceae J.K. Liu et al.

Although Jaklisch et al. (2016) consider Roussoellaceae to be a synonym of Thyridariaceae, this has not been followed by numerous subsequent authors (Liu et al. 2017a, Tibpromma et al. 2017, Wanasinghe et al. 2018, Wijayawardene et al. 2017a, 2018). Thus, we accept Roussoellaceae as a distinct family. A new species of *Roussoella*, *R. mangrovei* is described here based on morphological characters and phylogenetic analysis.

Roussoella Sacc.

The genus *Roussoella* was described by Saccardo & Paoletti (1888) with *R. nitidula* as the type species. A distinctive character of this genus is the trabeculate pseudoparaphyses, although Liew et al. (2001) has shown this characters occurs across the Dothideomycetes (e.g. also in some genera of Melanommataceae, Tian et al. 2015). *Roussoella* occurs mostly on monocotyledons except *Roussoella mexicana* Crous & Yáñez-Moral. and *R. solani* Crous & M.J. Wingf. (Crous et al. 2016). Currently, 33 species epithets are listed in Index Fungorum (2018).

Roussoella mangrovei Phukhamsakda & K.D. Hyde, sp. nov. Fig. 42

Index Fungorum number: IF554073; Facesoffungi number: FoF 03923

Holotype – MFLU 17-1542

Saprobic on dead branches of *Rhizophora* L., forming raised, dark brown areas with black dots on the host surface. Sexual morph *Ascomata* 352–476 µm high × 290–400 µm wide ($\bar{x}$ = 434 × 340 µm, n = 10) diameter, on the surface of the host, solitary, gregarious, erumpent through host surface by papilla, globose to subglobose, coriaceous, ostioles central, black to dark brown, smooth to papillate, ostiolate with periphysoids. *Peridium* 12–43(–58 at apex) µm wide, multi-layered, outer layer composed of 7–12 layers of dark, brown to light brown cells of *textura angularis*, the inner layer comprising hyaline thin-walled cells. *Hamathecium* of dense, 1–1.6 µm ($\bar{x}$ = 1.3 µm, n = 20), filiform, branches, anastomosing, transverse septate, trabeculate psedoparaphyses. Asci

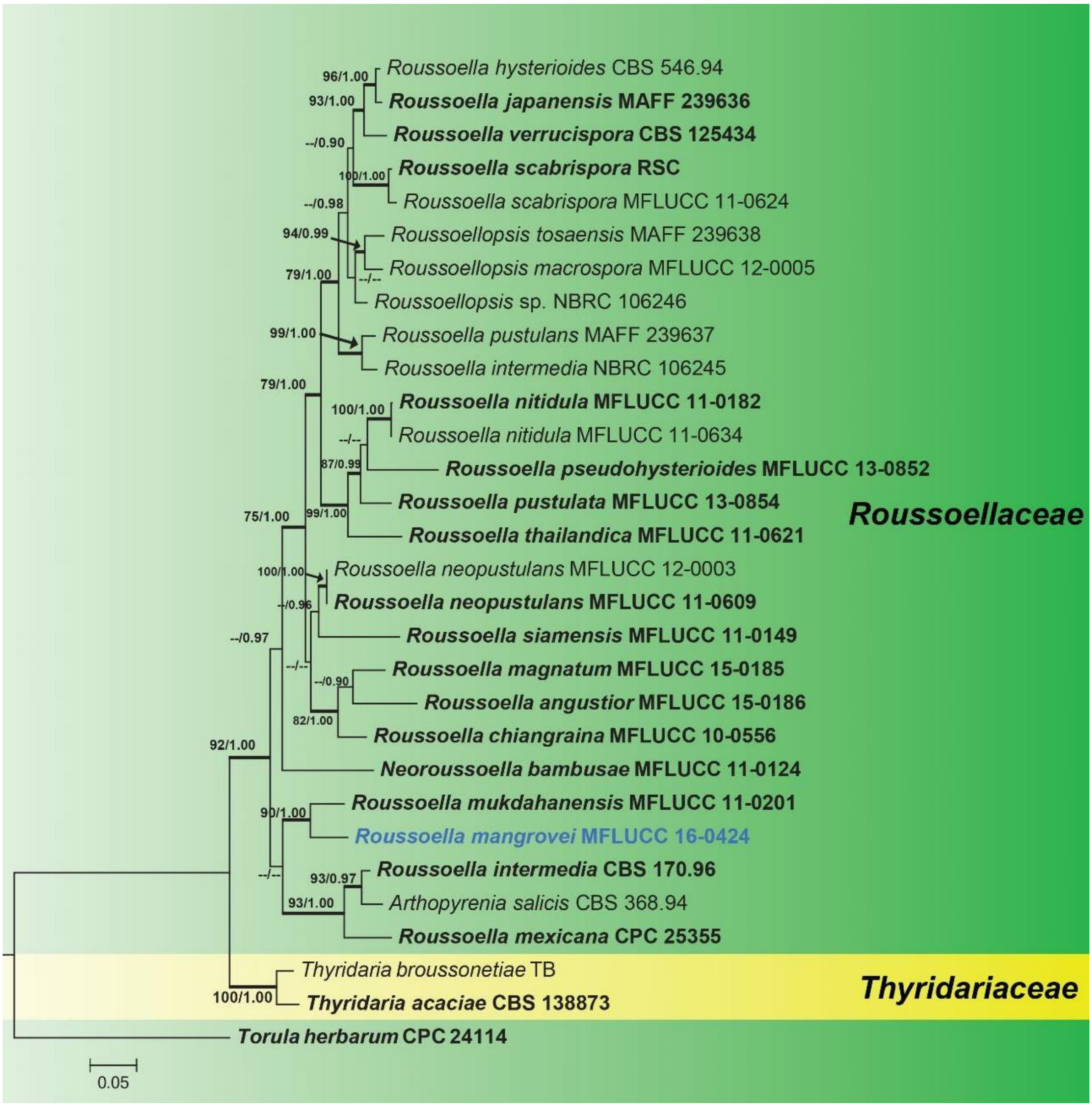


Figure 41 – The best scoring RAxML tree based on combined partial LSU, SSU, ITS, and TEF1-α gene datasets. Bootstrap values ≥70% from the maximum likelihood analysis are followed by Bayesian posterior probabilities (PP) values ≥ 0.90 at the nodes. The tree is rooted with *Torula herbarum* (CPC 24114). The species determined in this study indicated in blue. The ex-type and references strains are indicated in black bold. Hyphen (-) represents support values ≤ 70%/0.90.

82–115 × 12–19 µm ($\bar{x}$ = 117 × 15 µm, n = 20), 8-spored, bitunicate, fisitunicate, broad-cylindrical to clavate, apically round with an ocular chamber. *Ascospores* 15–20 × 7–11 µm ($\bar{x}$ = 16 × 9 µm, n = 50), uni-seriate to partial overlapping, oval with round ends, pale-brown to brown, uni-septate, constricted at septum, granulate in each cell well visible when young, rough-walled, surrounded with mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics – Colonies on MEA, with dense mycelium, flat on the surface circular, umbonate, upper part white, become cream after 4 weeks, without aerial mycelium. Reverse brown in the middle, mycelia radiating outwards with cream, hyphae septate branched.

Figure 42 – *Roussoella mangrovei* (MFLU 17-1542, holotype) a Substrate. b Ascomata on *Rhizophora* sp. c Vertical section of ascoma. d Ostiole filled with periphysoids. e Partial part of peridium. The peridium comprising *textura angularis*. f Hyaline pseudoparaphyses. g–i Developing stages of asci. j–n Developing ascospores. Scale bars: b = 500 µm, c = 200 µm.

Material examined – THAILAND, Krabi Province, on dead branches of *Rhizophora* sp. (Rhizophoraceae), 16 December 2015, C. Phukhamsakda (MFLU 17-1542, holotype), ex-type living culture, MFLUCC 16-0424, ICMP.

GenBank numbers – ITS: MH025951, LSU: MH023318, RPB2: MH028250, TEF1: MH028246.

Notes – *Roussoella mangrovei* (MFLUCC 16-0424) is described herein as a novel species in *Roussoella* occurring on an intertidal mangrove branch in Thailand. The strain shares a close relationship with *Roussoella mukdahanensis* Phook. et al. (90% ML/1.00 PP), which was reported from bamboo (Dai et al. 2016b). *Roussoella mangrovei* can be distinguished by its relatively larger solitary ascomata, a thick peridium, cylindrical to clavate asci and pale-brown to brown, 1-septate ascospores, with clearly visible granules.

Pleosporomycetidae genera, *incertae sedis*

The class Dothideomycetes comprises two subclasses which are Dothideomycetidae and Pleosporomycetidae (Hyde et al 2013, Liu et al. 2017). Pleosporomycetidae includes the orders Pleosporales, Mytilinidiales and Hysteriales (Boehm et al. 2009, Hyde et al. 2013; Wijayawardene et al. 2014, Liu et al. 2017). In this study, we provide an updated phylogenetic tree for the subclass Pleosporomycetidae and introduce a new species of *Hysterographium*, Pleosporomycetidae genera, *incertae sedis*.

Hysterographium Corda

Hysterographium is a genus in the subclass Pleosporomycetidae, and is typified by *H. fraxini* (Pers.) De Not (Boehm et al. 2009a, b). Currently, there are 142 epithets listed under this genus (Index Fungorum 2018). However, only one species has molecular data and other species are synonymised under different genera. In this study, we describe and introduce a new species *Hysterographium didymosporum* based on morphology and phylogenetic support.

Hysterographium didymosporum S. Boonmee & K.D. Hyde, sp. nov. Figs 44, 45

Index Fungorum number: IF554386; Facesoffungi number: FoF04107

Etymology – the epithet “didymosporum” refers to two celled ascospores.

Holotype – MFLU 10–0031

Saprobic on dead branches of dicotyledonous plans. Sexual morph *Ascomata* 179–242 µm high × 145–167 µm diameter ($\bar{x}$ = 216 × 155 µm), hysterothecial, completely immersed, becoming erumpent at maturity, with longitudinal slit, dark brown, grouped to scattered, straight to slightly curved, subglobose to obovoid in vertical section. *Peridium* 27–30 µm wide, composing several layers of dark brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1–2(–2.5) µm wide, cylindrical, septate, branched, anastomosed, pseudoparaphyses, embedded within a gelatinous matrix. *Asci* 60–99 × 10–14 µm ($\bar{x}$ = 85 × 12 µm, n = 15), 8-spored, bitunicate, cylindrical-clavate, sessile or with short pedicel, with a small ocular chamber. *Ascospores* 13–16 × 6–8 µm ($\bar{x}$ = 15 × 7 µm, n = 20), biseriate, conglobate, ellipsoid, upper cell wider, ends rounded, 1-septate, constricted at the septum, hyaline, smooth-walled. Asexual morph coelomycetous. *Conidiomata* 28–42 × 28–52 µm, pycnidial, clustered, globose-subglobose, dark brown, invisible conidiophores and conidiogenous cells, surrounded by aerial hyphae, septate, branched, white when viewed with the unaided eye, and under microscopic hyaline. *Conidia* 7–11 × 2–4 µm ($\bar{x}$ = 8 × 3 µm, n = 20), oblong, slightly curved, aseptate, with or without guttules, hyaline, smooth-walled.

Cultural characteristics – Ascospores germinating on MEA within 12 hours and germ tubes produced at both ends. Colonies slow growing on MEA, reaching less than 5 mm in 7 days at 28 C, slightly convex, undulating to raised, dentate, with slightly radial striations and lobate edges, brown. Asexual morph produced in culture.

Material examined – THAILAND, Lam Pang, Wang Neua, Wat Pa Putta Sri, elev. *ca*. 800–900 msl., on dead branches of an unidentified host, 7 January 2011, S. Boonmee, LP01 (MFLU 10–0031, holotype), ex-type culture: MFLUCC 10–0101, IFRDCC 2187, BCC 52329.

Figure 43 – RAxML phylogenetic tree generated from LSU, RPB2, SSU and TEF1 sequence data of *Hysterographium didymosporum* MFLUCC 10–0101 with related orders of subclass Pleosporomycetidae. RAxML bootstrap support values ≥ 50% (BT) and Bayesian posterior probabilities ≥ 95% (PP) are given above the nodes. The ex-type strains are in bold and new strain in blue.

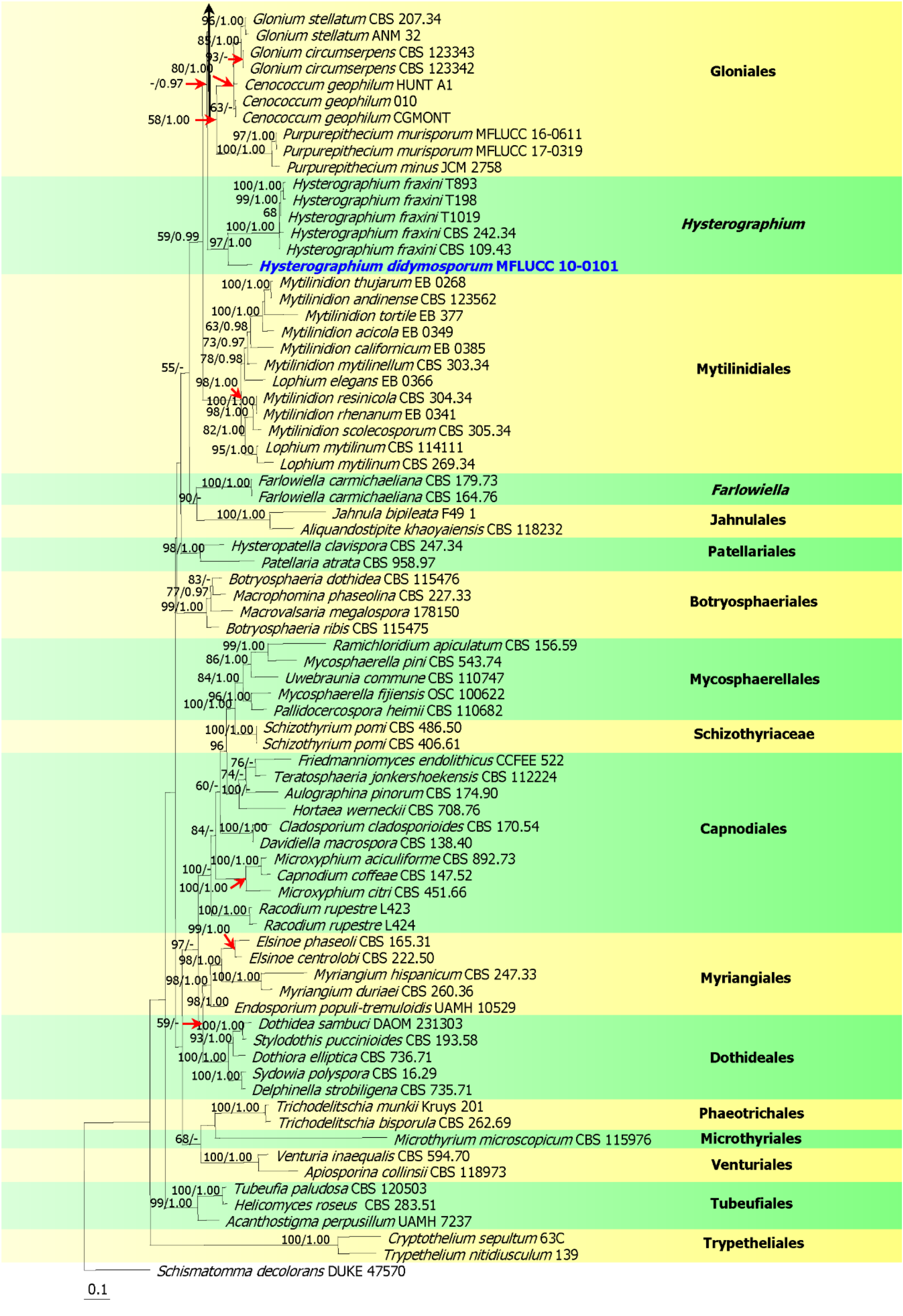


Figure 43 – Continued.

GenBank numbers – LSU – MH105775, RPB2 – MH105777, SSU – MH105776.

Notes – *Hysterographium didymosporum* is introduced as a new species with both sexual and asexual morphs. The asexual morph developed in culture grown on MEA (Fig. 45). In our phylogenetic analysis of combined LSU, RPB2, SSU and TEF1 sequence data, *Hysterographium didymosporum* constitutes an independent lineage with high statistical support (97% MLBT and 1.00 BYPP, Fig. 43) and appears to be phylogenetically distinct from *H. fraxini* (type species). *Hysterographium didymosporum* shares common features of dark brown, hysterothecial, immersed to erumpent ascomata, with a longitudinal slit, but differs from taxa in *Hysterographium* in ascomata lacking carbonaceous wall and having 1-septate and hyaline ascospores.

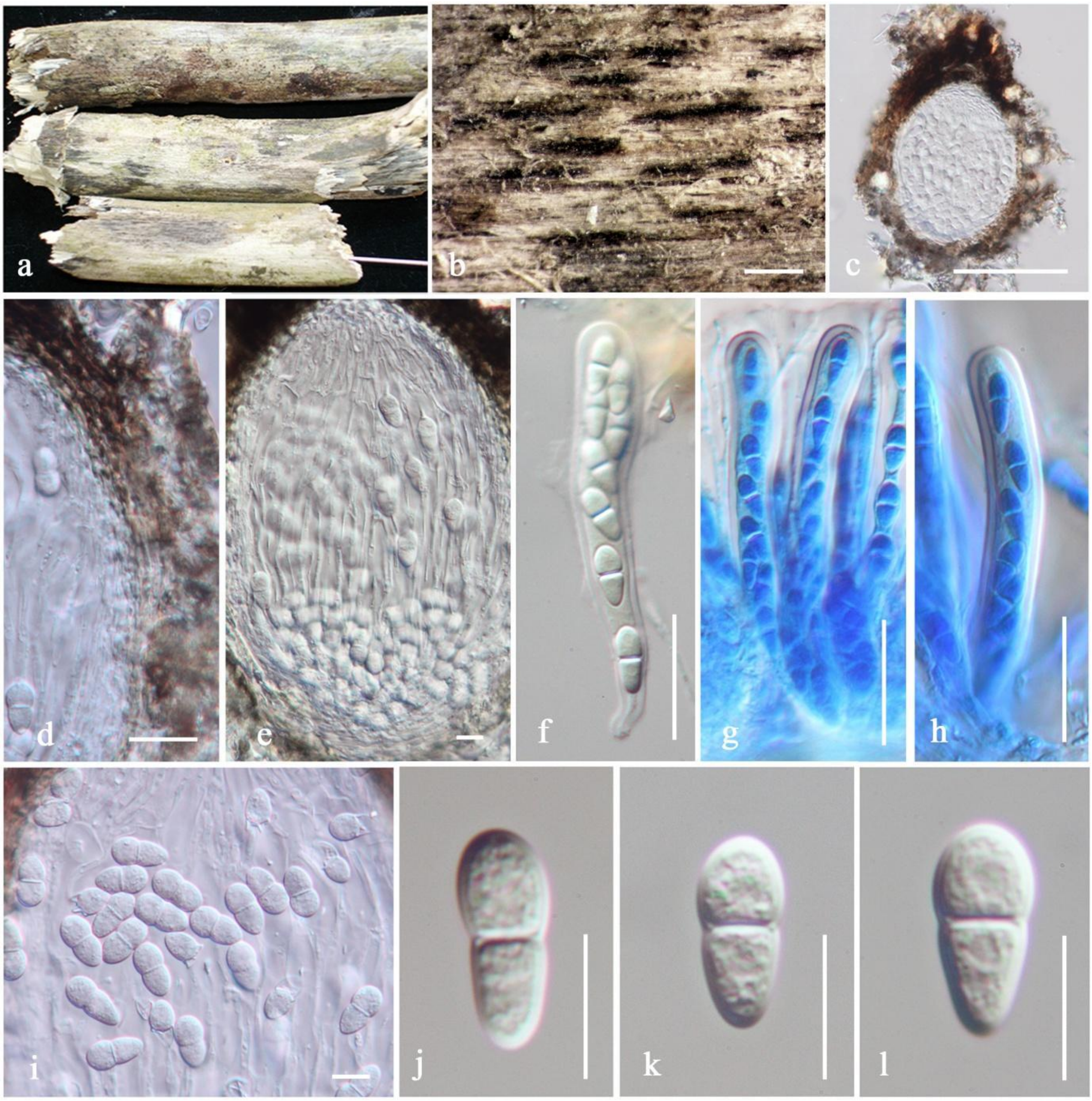


Figure 44 – *Hysterographium didymosporum* (MFLU 10–0031, holotype). a, b Appearance of ascomata on dead branches of an unidentified host. c Section of ascoma. d Peridium. e Pseudoparaphyses. f–h Asci (Figs. g, h stained in cotton blue reagent). i–l Ascospores. Scale bars: b = 500 µm, c = 100 µm, d = 50 µm, e = 5 µm, f–h = 20 µm, i–l = 10 µm.

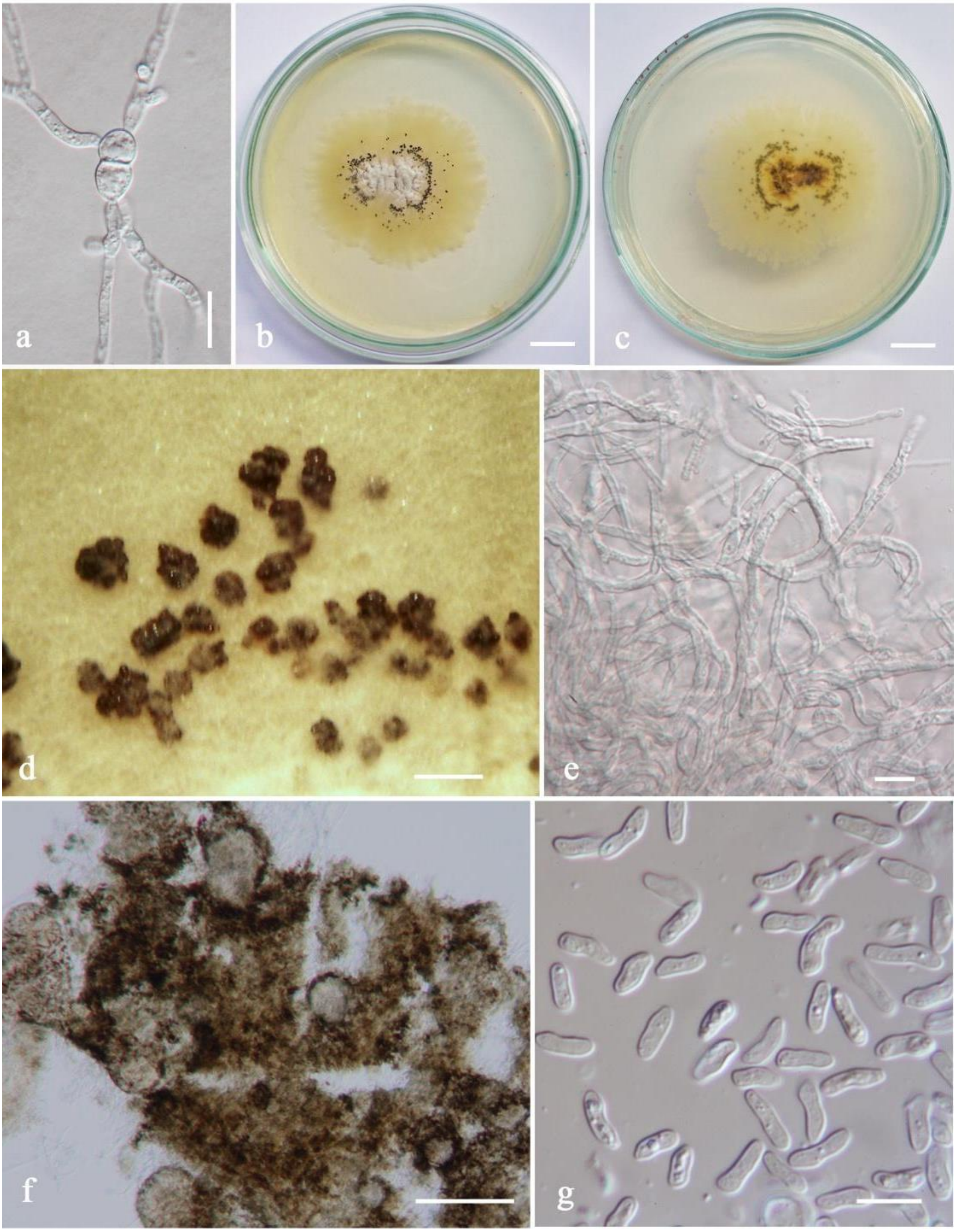


Figure 45 – *Hysterographium didymosporum* (MFLU 10–0031, ex-type culture). a Germinating spore. b, c Colonies on MEA from surface and reverse. d Developing conidiomata. e Aerial hyphae in culture. f Squash mount of conidiomata. g Conidia. Scale bars: a, g = 10 µm, b–c = 10 mm, d = 100 µm, e = 5 µm, f = 50 µm.

Dothideomycetes orders, *incertae sedis*

Acrospermales Minter et al.

Acrospermaceae Fuckel

Minter et al. (2007) introduced the order Acrospermales to accommodate the family Acrospermaceae, which is typified by *Acrospermum compressum* Tode. Lumbsch & Huhndorf (2010) placed the Acrospermales in Dothideomycetes, order *incertae sedis*. The family Acrospermaceae presently includes two genera *Acrospermum* and *Oomyces* (Wijayawardene et al. 2018). The asexual morphs of this family include members of *Dactylaria* and *Gonatophragmium* which are linked to asexual *Acrospermum* (Wijayawardene et al. 2012, 2017b).

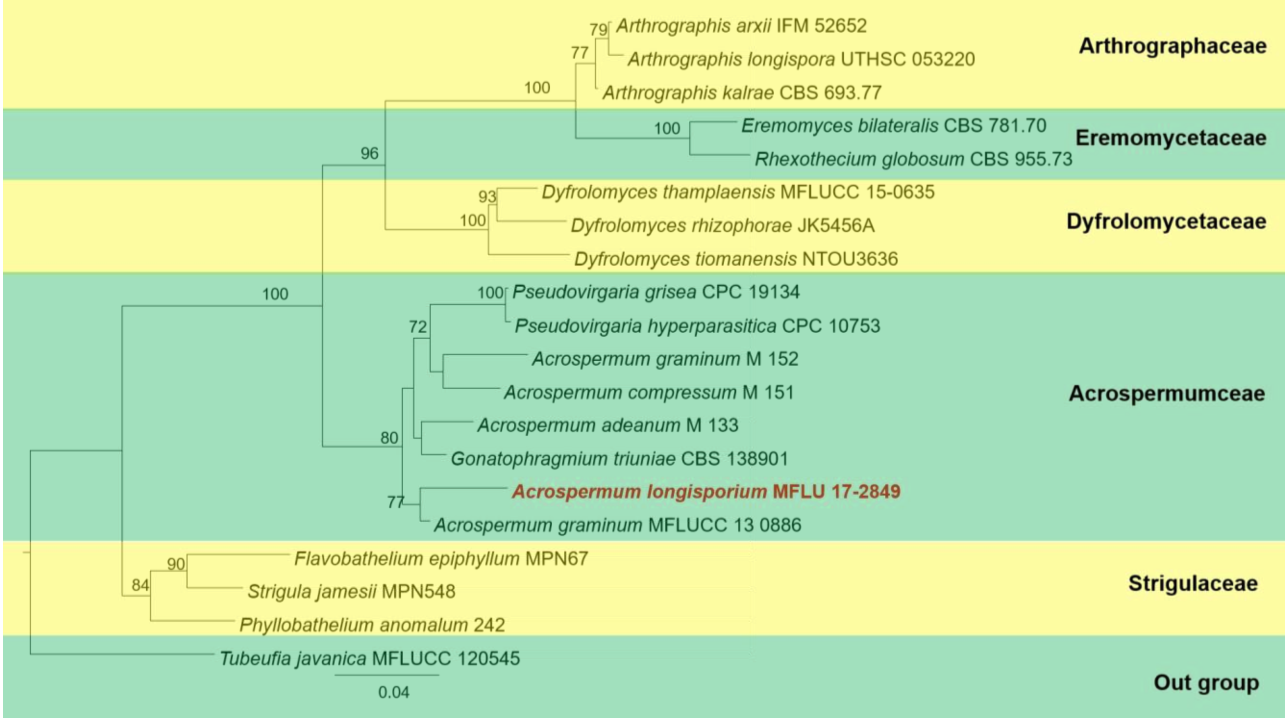


Figure 46 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from a combined multigene (LSU and SSU) matrix including species in Acrospermaceae and related families. Related sequences were obtained from GenBank. Twenty strains are included in the combined sequence analyses, which comprise 2774 characters with gaps. The best scoring RAxML tree with a final likelihood value of -9380.272776 is presented. The matrix had 611 distinct alignment patterns, with 48.85% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.248348, C = 0.230480, G = 0.299990, T = 0.221182. ML values above 70% are given at each branch. MLBS values above 70% are given at each branch. The tree is rooted with *Tubeufia javanica* (MFLUCC 120545) (Tubeufiaceae). New isolates are in bold and red.

Acrospermum longisporium Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 47

Index Fungorum number: IF554046; Facesoffungi number: FoF03887

Etymology – with reference to the long ascospores

Holotype – MFLU 17-2849

Saprobic on *Urtica dioica* (Urticaceae). Sexual morph *Ascomata* 1.5–2 mm high × 0.4–0.5 mm diameter ($\bar{x}$ = 1.8 × 0.45 mm), solitary or in groups, superficial, club-shaped to conoid, erect, uni-locular, brown to blackish when dry, with a short pedicel or sessile, flattened when dry, swelling when moist, ostiole large, apex rounded. *Peridium* in horizontal section comprising three layers, an outer layer comprising dark brown cells of *textura angularis*, a central thick layer, comprising pale brown tissue of gelatinized hyphae with elongated cells, and an inner layer comprising dense tissue of small, light brown cells. *Hamathecium* of narrow, long, pseudoparaphyses. *Asci* 300–370 × 3–5 µm ($\bar{x}$ = 350 × 4 µm), 8-spored, bitunicate, narrowly cylindrical, pedicellate, with an ocular chamber. *Ascospores* 150–170 × 0.5–1 µm ($\bar{x}$ = 160 × 0.75 µm), fasciculate, filiform, hyaline, multi-septate, almost long as the asci, smooth-walled. Asexual morph Undetermined.

Material examined – United Kingdom, England, Hampshire, Botley wood, decaying branch of *Urtica dioica* (Urticaceae), 25 May 2016, E.B.G. Jones GJ 293 (MFLU 17-2849, holotype); *ibid.*, (PDD, isotype).

GenBank numbers – LSU: MG815827, SSU: MG815828.

Notes – *Acrospermum longisporium* fits well with the generic concept of *Acrospermum* in having club-shaped, brown, uni-locular ascomata and narrow, long paraphyses which resemble ascospores (Hyde et al. 2013). *Acrospermum longisporium* is related to *Acrospermum graminum* (77% ML support). However the latter differs from *Acrospermum longisporium* in having platted ascoma and unequally thick peridia.

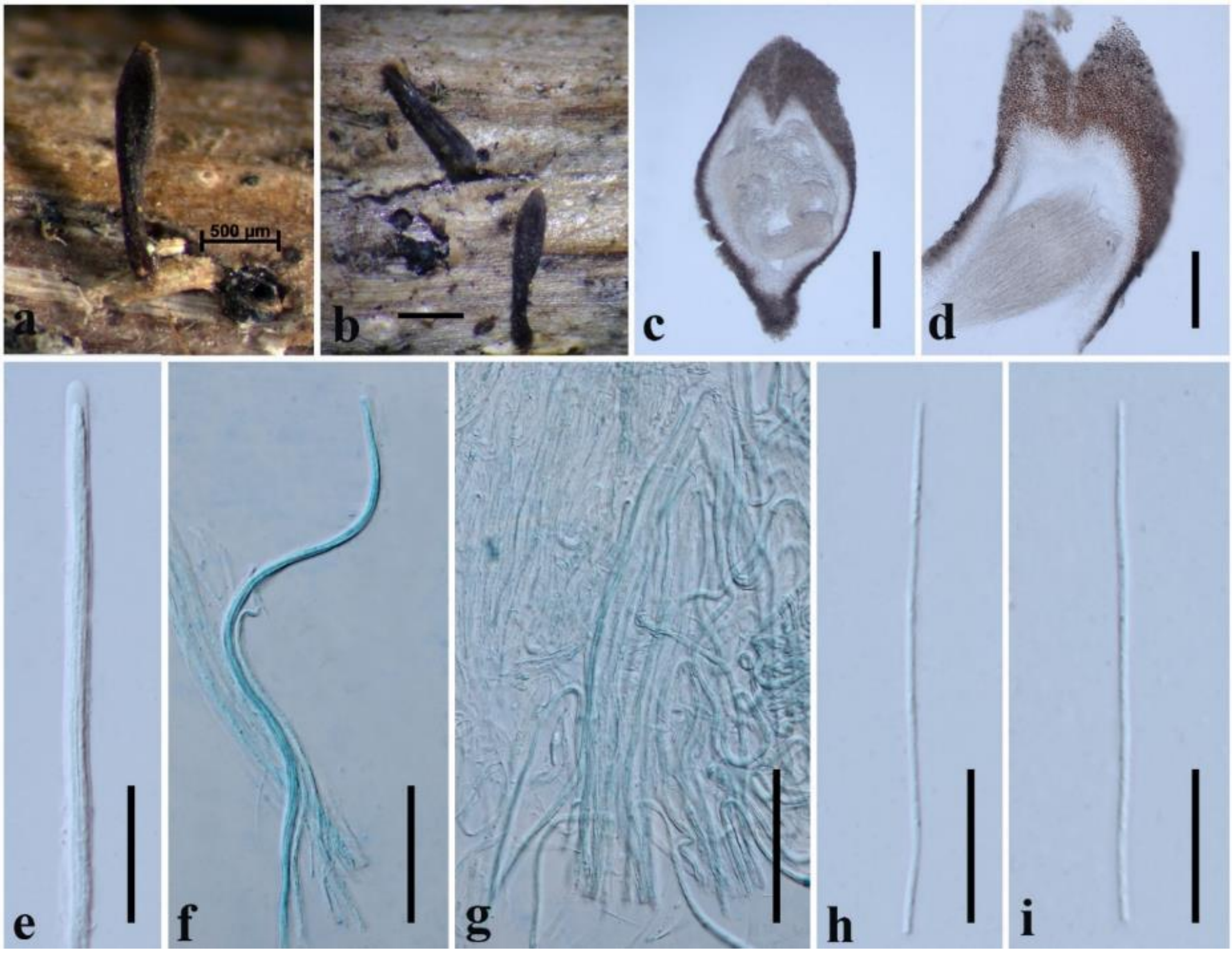


Figure 47 – *Acrospermum longisporium*. a, b Ascomata. c, d Sections through ascomata. e–g Asci. h, i Ascospores. Scale bars: a, b = 500 µm, c = 200 µm, d = 100 µm, e–i = 50 µm.

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

Asterinaceae Hansf.

Asterinaceae was established as a member of Myriangiales by Hansford (1946). Species of Asterinaceae are characterized by dark brown hyphae with hyphopodia, dark brown thyriotheciawith stellate dehiscence, and dark brown ascospores with a single septum. Phylogenetic studies have resulted in several different interpretations of this family (Hongsanan et al. 2014, Guatimosim et al. 2015, Liu et al. 2017). In this study, we introduce a new species of *Asterina* based on morphological and molecular data.

Asterina Lév.

Asterina is the type genus of the family Asterinaceae, which was introduced by Léveillé in 1845. *Asterina* is the largest genus in Asterinaceae and has a cosmopolitan distribution in tropical and subtropical regions (Hongsanan et al. 2014).

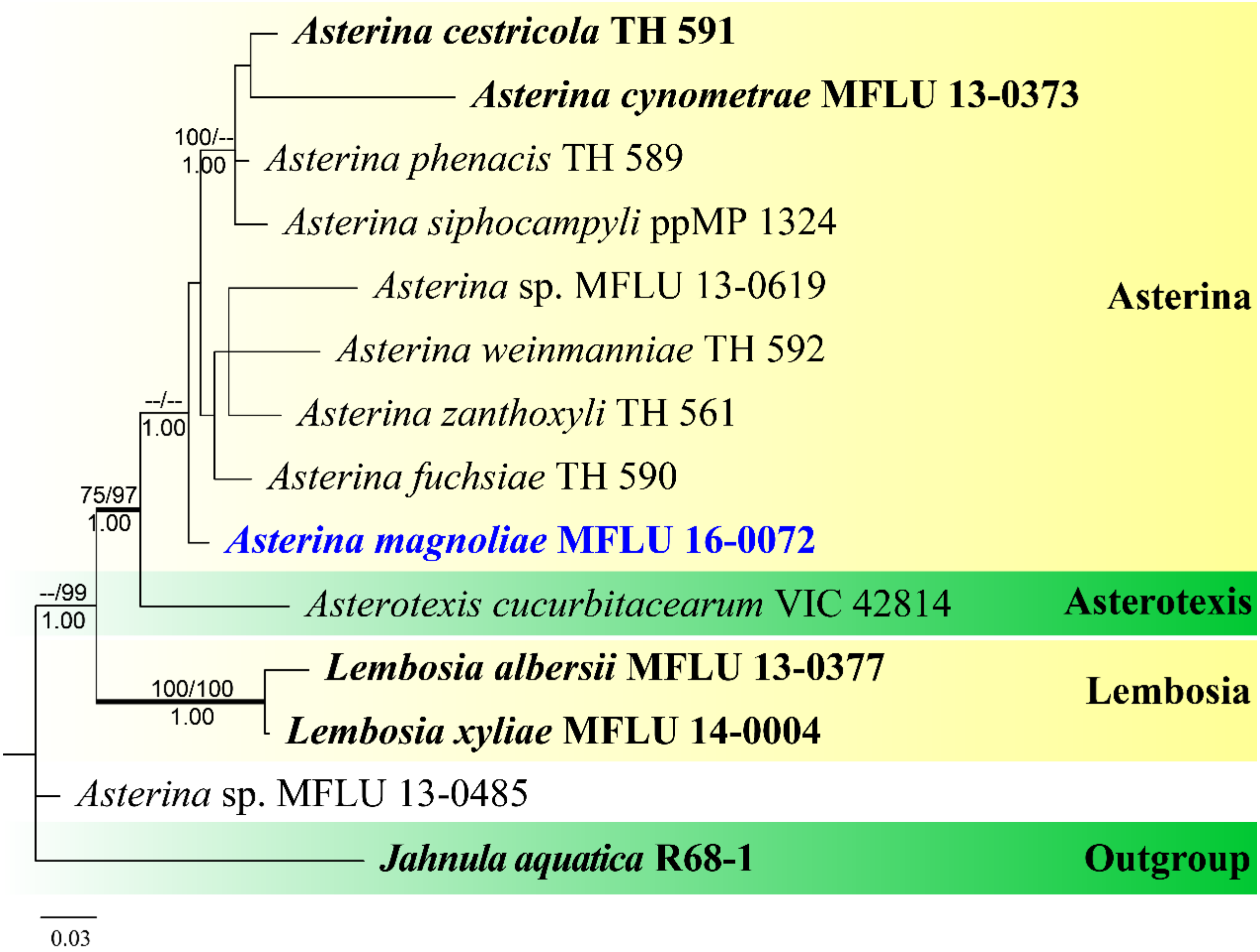


Figure 48 – Phylogram generated from Bayesian analysis based on LSU sequence data from species of Asterinales. Maximum parsimony/likelihood bootstrap support values greater than 50%/70% are shown above the nodes, while Bayesian posterior probabilities greater than 0.9 are displayed below the nodes. Sequences from type specimens are in bold and new sequences are in blue bold.

Asterina magnoliae X.Y. Zeng, T.C. Wen & K.D. Hyde, sp. nov. Fig. 49

Index Fungorum number: IF554238; Facesoffungi number: FoF04089

Etymology – referring to the host genus *Magnolia*.

Holotype – MFLU 16-0072

Colonies epiphyllous or hypophyllous, scattered. *Hyphae* superficial, brown, septate, reticulate, with hyphopodia. *Hyphopodia* subglobose, unicellular, alternate. Sexual morph *Thyriothecia* 88–144(-152) µm ($\bar{x}$ = 115 µm, n = 20) in diameter, dense, circular, flattened, dark brown, with stellate dehiscence. *Upper wall* brown, comprising radial arrangement of septate cells of *textura prismatica*. *Asci* 40–48 µm ($\bar{x}$ = 45 µm, n = 20) in diameter, 8-spored, bitunicate, globose to subglobose. *Ascospores* 25–28 × 11–12 µm ($\bar{x}$ = 26.5 × 11.5 µm, n = 20), cylindrical, 1-septate, slightly constricted at the septum, hyaline when young, becoming brown when mature, with a darkened band and a large guttule in the middle of each cell. Asexual morph *Conidia* ovoid, aseptate, hyaline when young, become brown when mature, with two-layered cell wall.

Material examined – THAILAND, Chiang Mai, Mae Taeng, Pa Pae, Bahn Pa Deng, 128 Moo 3, Mushroom Research Centre, on living leaves of *Magnolia odora* (Magnoliaceae), 8 July 2015, Xiang-Yu Zeng (MFLU 16-0072, holotype).

GenBank numbers – LSU: MG844186.

Notes – There was no report of *Asterina* species found on *Magnolia* (Zeng et al. 2017) and our new taxon is different from other *Asterina* species in having a coloured band at center of each cell of the ascospores. The phylogeny herein also positions *A. magnolia* in an independent lineage basal to other *Asterina* species analysed (Fig 48).

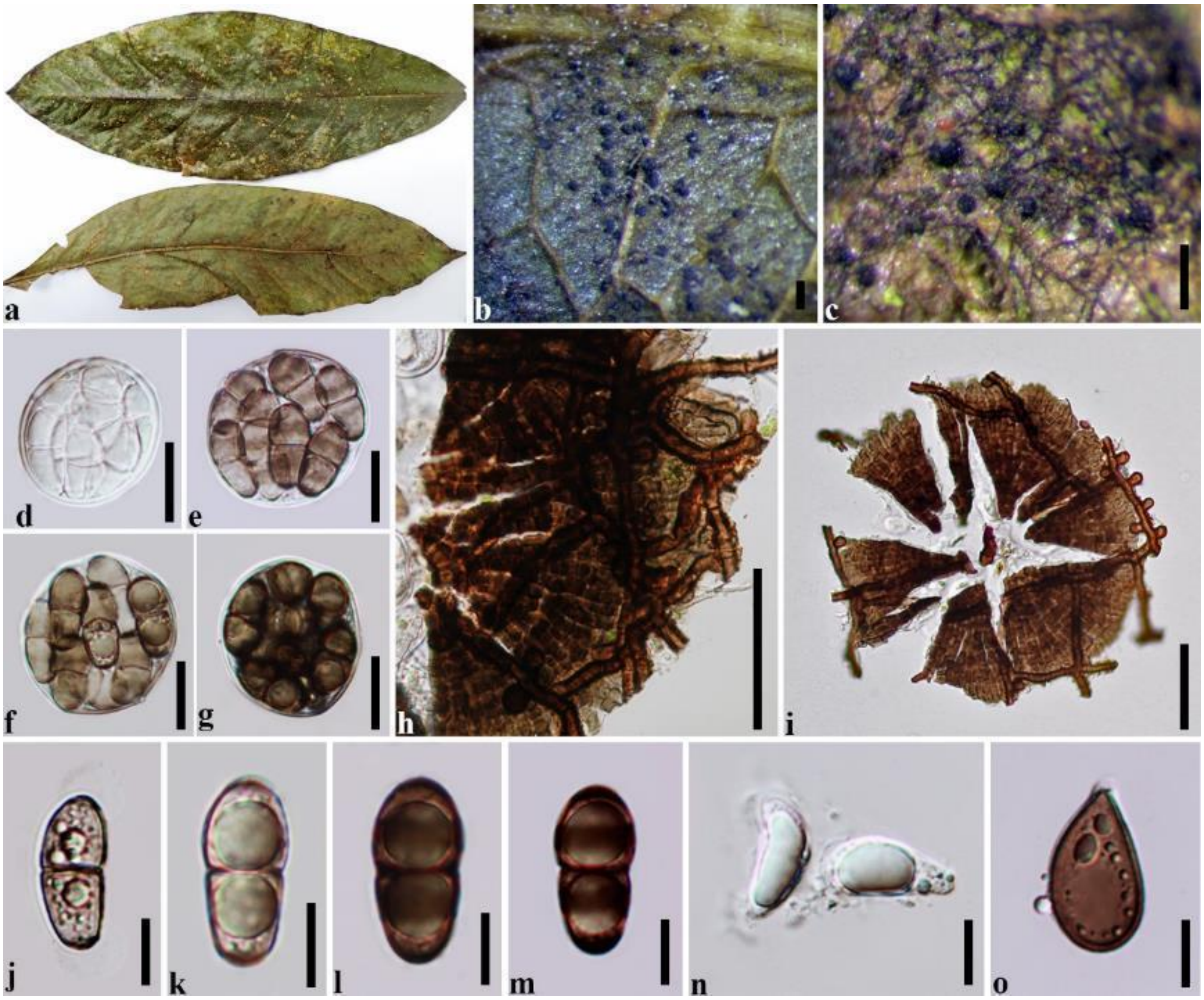


Figure 49 – *Asterina magnoliae*. a Host leaves. b, c Colony on host surface. d–g Ascus from young state to mature state. h Upper wall of thyriothecium. i Squash mount of thyriothecium. j–m Ascospore from young state to mature state. n–o Conidia. Scale bars: b–c = 200 µm, d–g = 20 µm, h–I = 50 µm, j–o = 10 µm.

Botryosphaeriales C.L. Schoch et al.
Botryosphaeriaceae Theiss. & H. Syd.

Taxa of the family Botryosphaeriaceae are endophytes, plant pathogens and saprobes (Phillips et al. 2008, 2013, Liu et al. 2012, Dissanayake et al. 2016). Currently the family comprises 23 accepted genera (Dissanayake et al. 2016). Morphological characters alone are inadequate to define genera or identify species in the family (Phillips et al. 2013). Hence SSU, ITS, LSU, EF1-α and β-tubulin sequence data are needed when defining a new species and genus level identifications (Phillips et al. 2013). In this study, we introduce a new *Diplodia* species based on molecular and morphological evidence.

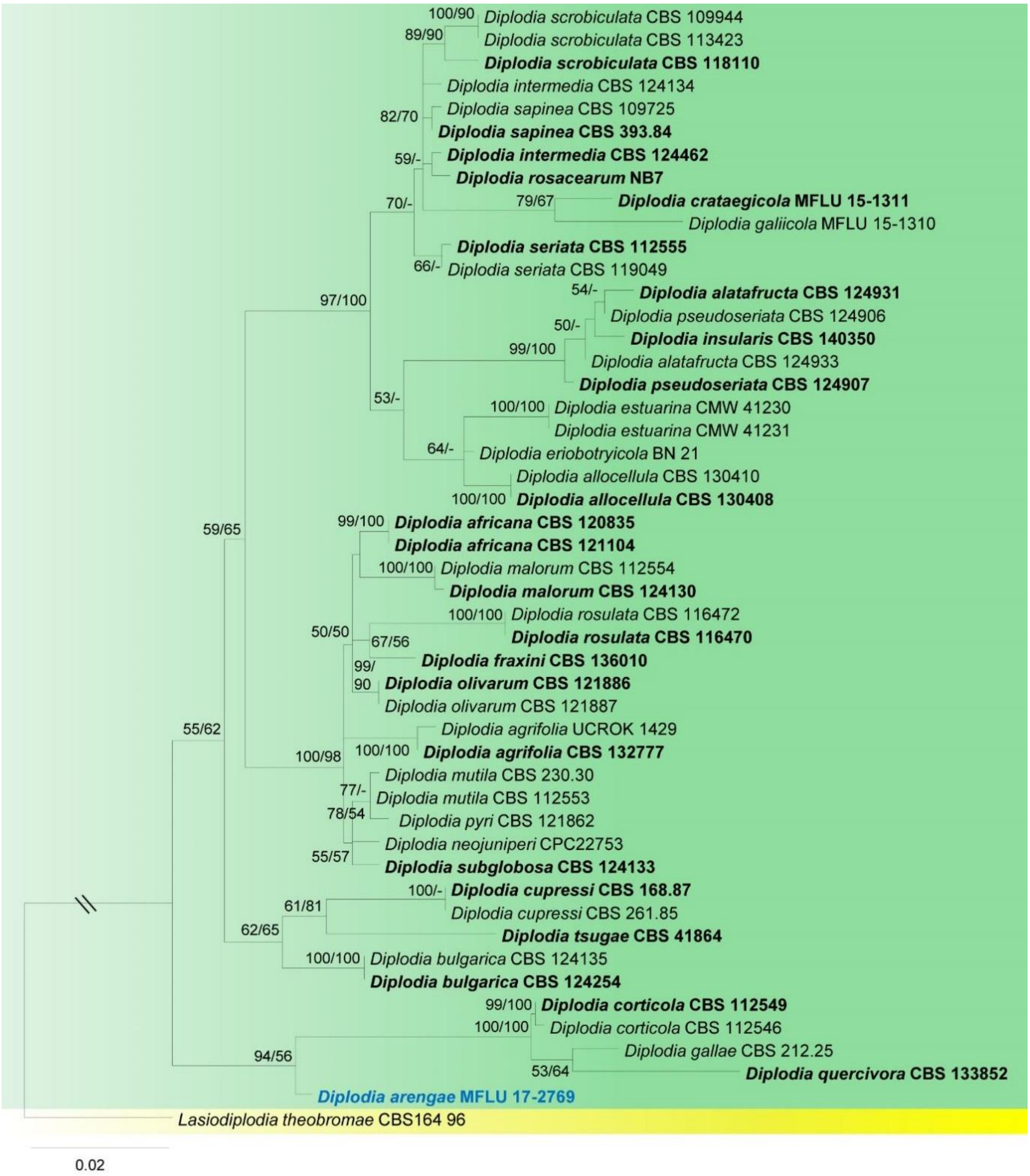


Figure 50 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS and TEF-α sequence data of *Diplodia* species. Related sequences were obtained from GenBank. Forty-six strains are included in the analyses, which comprise 820 characters including gaps. The tree is rooted with *Lasiodiplodia theobromae* (CBS 164.96). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of -3144.936756 is presented. The matrix had 49 isolates, 254 distinct alignment patterns, with 4.02% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.208206, C = 0.208206, G = 0.261341, T = 0.233093; substitution rates AC = 1.031688, AG = 3.931659, AT = 0.914981, CG = 1.704693, CT = 5.063628, GT = 1.000000; gamma distribution shape parameter α = 0.662619. The maximum parsimonious dataset consisted of constant 634, 138 parsimony-informative and 48 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the

maximum of two equally most parsimonious trees with a length of 361 steps (CI = 0.657, RI = 0.857, RC = 0.563, HI = 0.343) in the first tree. RAxML and maximum parsimony bootstrap support values ≥ 50% (BT) are shown respectively near the nodes. The scale bar indicates 0.04 changes. The ex-type strains are in bold and new isolates in blue.

Diplodia Fr.

The genus *Diplodia* was introduced based on *D. mutila* (Fr.) Mont. by Montagne (1834). The genus comprises 31 species with sequence data (Dissanayake et al. 2016). Species of *Diplodia*, are pathogens, endophytes or saprobes on a wide range of woody hosts (Crous et al. 2006, Slippers & Wingfield 2007, Phillips et al. 2012). Two types of conidia can be observed in *Diplodia* species (Phillips et al. 2005, 2012). Conidia remain hyaline for a long time before they become brown and 1-septate, but in some species, conidia become pigmented before discharge from the conidiomata and mostly remain aseptate (Phillips et al. 2005, 2012).

Diplodia arengae R.H. Perera, Wanas. & K.D. Hyde, sp. nov. Fig. 51

Index Fungorum number: IF554057; Facesoffungi number: FoF03908

Etymology – name reflects the host genus *Arenga*.

Holotype – MFLU 17-2769

Saprobic on dead leaves of *Arenga hookeriana* (Becc.) Whitmore. Sexual morph *Ascomata* 240–280 µm high, 250–300 µm diameter ($\bar{x}$ = 262.9 × 271.3 µm, n = 5), scattered, immersed, globose to subglobose, glabrous, brown to dark brown, ostiolate. *Ostiole* 60–90 µm long 55–75 µm diameter, short papillate, black, smooth, filled with hyaline cells. *Peridium* 30–40 µm wide at the base, 35–60 µm wide at the sides, comprising 4–5 layers, outer layer pigmented, comprising reddish-brown to dark brown, thin-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 3.5–4.5 µm wide, filamentous, branched, septate, pseudoparaphyses. *Asci* 130–160 × 25–35 µm ($\bar{x}$ = 144.6 × 30.5 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, with a pedicel 20–30 µm long, apically rounded, with broad ocular chamber. *Ascospores* 25–35 × 10–12 µm ($\bar{x}$ = 30.8 × 11.3 µm, n = 40), overlapping biseriate to triseriate, ellipsoidal, hyaline, aseptate, smooth-walled, guttulate, ends remaining cone-shaped, with pointed ends, not surrounded by a mucilaginous sheath. Asexual morph Undetermined.

Culture characteristics – Colonies on PDA reaching 3 cm diameter after 30 days at 25°C, circular, smooth margin white at first, dark coffee after 4 weeks, flat on the surface, without aerial mycelium, reverse black. Hyphae septate branched, hyaline, thin, smooth-walled. We could not manage to maintain a living culture as subsequent attempts to subculture failed and hence a living culture is unavailable.

Material examined – CHINA, Mengla, Menglun, Xishuangbanna Tropical Botanical Garden, on dead leaf of *Arenga hookeriana* (Arecaceae), 21 December 2013, D.N. Wanasinghe, XTBG28 (MFLU 17-2769, holotype).

GenBank numbers – β-tubulin: MG783039, ITS: MG762771, LSU: MG762772, SSU: MG762773, TEF: MG762774.

Notes – *Diplodia arengae* forms a well-supported independent lineage sister to *D. corticola*, *D. gallae* and *D. quercivora*. *Diplodia arengae* differs from *D. corticola* by possessing unilocular, smaller ascomata (vs. multiloculate, 1 mm diameter), longer asci (vs. 160–250 µm) and narrower ascospores (vs. 14.6–15.3 µm) (Alves et al. 2004). There is no sexual morph reported for *D. quercivora* for morphological comparison with *D. arengae* (Linaldeddu et al. 2013, Phillips et al. 2013). However, those two species are phylogenetically distant in our analysis (Fig. 50).

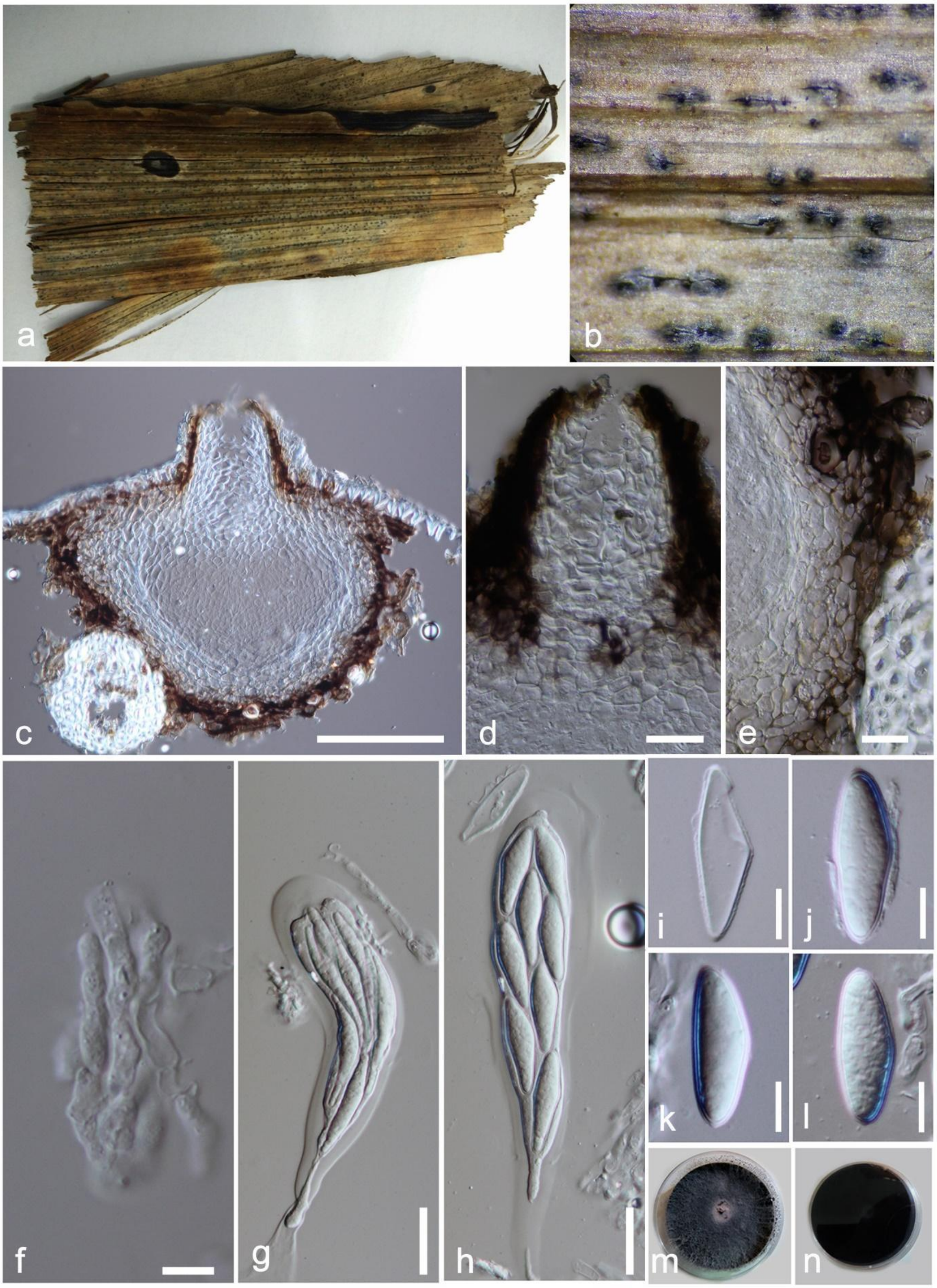


Figure 51 – *Diplodia arengae* (MFLU 17-2769, holotype). a, b Appearance of ascomata on dead leaf of *Arenga hookeriana*. c Section of ascoma. d Close up of ostiole. e Peridium. f Pseudoparaphyses. g, h Asci. i–l Ascospores. Scale bars: c = 100 µm, d, e, g, h = 20 µm, f, i–l = 10 µm.

Dyfrolomycetales K.L. Pang et al.

Pleurotremataceae Walt. Watson

The family Pleurotremataceae was re-established after several contradictions with re-examination of the isotype of *Pleurotrema polysemum*, and exclusion of Dyfrolomycetaceae from the class Sordariomycetes. However, sequence data for the type of *Pleurotrema* is still lacking (Maharachchikumbura et al. 2016a). Recently, studies have revealed that the family Pleurotremataceae is phylogenetically close to Acrospermaceae (Dothideomycetes), and comprises *Dyfrolomyces*, *Melomastia* and *Pleurotrema* (Pang et al. 2013, Norphanphoun et al. 2017b, Zhang et al. 2017b). In this study, a new *Dyfrolomyces* species collected from *Camellia sinensis* is introduced with detailed morphological information and support from combined multi-loci phylogenetic analysis.

Dyfrolomyces K.D. Hyde et al.

Pang et al. (2013) introduced *Dyfrolomyces*, with species characterized by a clypeus on the substrate, immersed ascomata and multi-septate ascospores with/without a sheath in bitunicate/fissitunicate asci, to accommodate *D. tiomanensis*. Currently, the genus consists of eight species, which have mostly been collected from marine habitats on mangrove wood (Hyde 1992, Pang et al. 2013, Hyde et al. 2017b, Norphanphoun et al. 2017b, Zhang et al. 2017b).

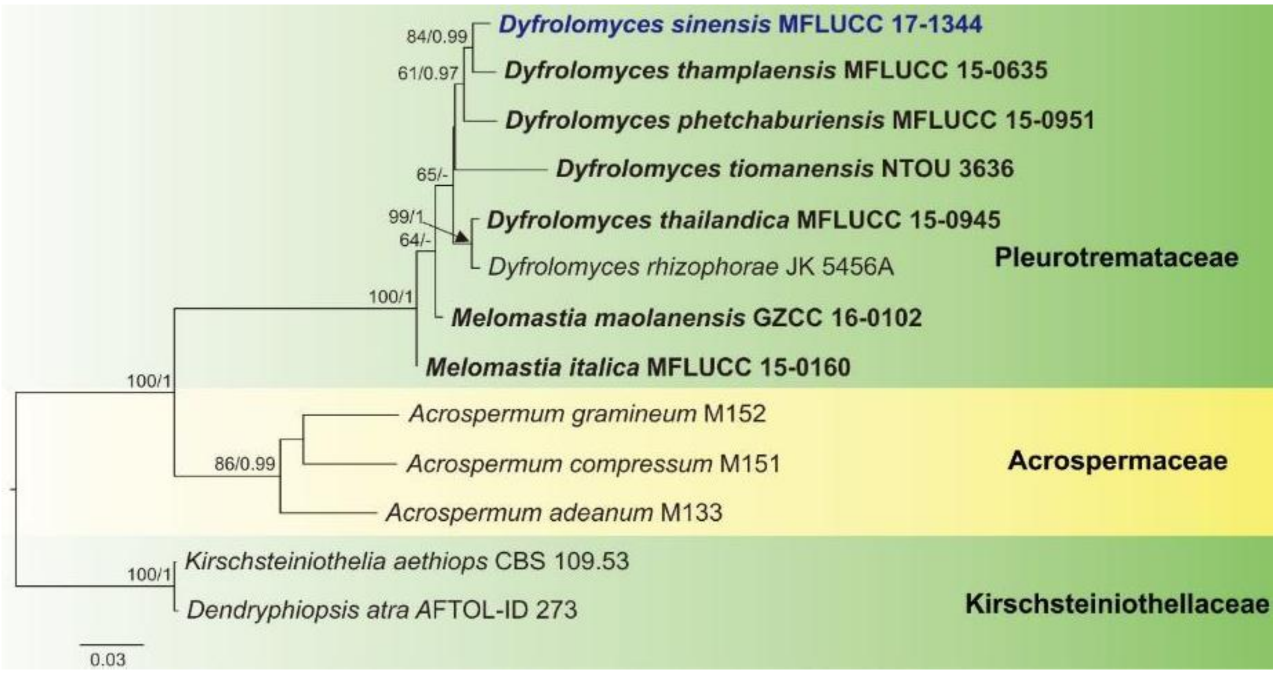


Figure 52 – Phylogram generated from maximum likelihood (RAxML) analysis of combined SSU and LSU partial sequence data. The best scoring RAxML tree with a final likelihood value of -4848.762798 is presented with *Dendryphiopsis atra* and *Kirschsteiniothelia aethiops* (Kirschsteiniotheliaceae) as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -4848.762798 is presented. The matrix had 222 distinct alignment patterns, with 0% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240566, C = 0.238552, G = 0.309758, T = 0.211124; substitution rates AC = 1.010469, AG = 3.557274, AT = 1.030465, CG = 1.606891, CT = 10.067712, GT = 1.000000; gamma distribution shape parameter α = 0.292895. Bootstrap values for ML (≥60) and Bayesian posterior probabilities (≥0.95) are shown near the nodes. The newly generated sequence is in blue, and the ex-type strains are in bold. The scale bar represents the expected number of nucleotide substitutions per site.

Dyfrolomyces sinensis Samarak., Tennakoon & K.D. Hyde, sp. nov. Fig. 53

Index Fungorum number: IF554110; Facesoffungi number: FoF03935

Etymology – named *sinensis*, after the host species from which it was collected.

Holotype – MFLU 17-0777

Saprobic on *Camellia sinensis* (L.) Kuntze (Theaceae). Sexual morph *Ascomata* 450–600 µm diameter × 350–450 µm high ($\bar{x}$ = 510 × 397 µm, n = 10), solitary, superficial, clypeate, globose to subglobose, dark brown to black, ostiolate. *Ostiole* centric to eccentric, apapillate. *Peridium* 55–75 µm wide ($\bar{x}$ = 65.1 µm, n = 10), 10–35 µm wide at base ($\bar{x}$ = 21.8 µm, n = 10), comprising an outer layer of dark brown cells of *textura angularis*, becoming lighter inwardly. *Hamathecium* comprising numerous, 2.4–5 µm wide ($\bar{x}$ = 3.5 µm, n = 20), septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 160–220 × 8–10 µm ($\bar{x}$ = 187.5 × 8.5 µm, n = 12), 8-spored, bitunicate, cylindrical, short-pedicellate, with a thickened apex. *Ascospores* 18–30 × 5– 8 µm ($\bar{x}$ = 23.1 × 6.2 µm, n = 25), L/W ratio 3.7, uniseriate, hyaline, cylindrical, mostly 6–7-septate, often similar width of cells with several small guttules, slightly constricted at the septum. Asexual morph Undetermined.

Culture characteristics – Colonies on PDA at 25–28°C, reaching 33–35 mm in 8 days, surface smooth, effuse, undulate to slightly with radially striated lobate edges. Colonies from above site are greyish to dirty white at the margin, whitish sparse mycelia in the centre; reverse yellowish-brown to light yellow at the margin. Odour not pronounced.

Material examined – THAILAND, Chiang Rai, Mae Fah Luang University, on stems of *Camellia sinensis* (Theaceae), 25 March 2017, Danushka S. Tennakoon, MFLU 001 (MFLU 17-0777, holotype), ex-type living culture, MFLUCC 17-1344.

GenBank numbers – LSU: MG836699, SSU: MG836700.

Notes – The new taxon, *Dyfrolomyces sinensis*, shares similar morphological characters with other *Dyfrolomyces* species (Pang et al. 2013, Norphanphoun et al. 2017b, Zhang et al. 2017b). However, it differs from otherspecies (viz. *D. aquatica*, *D. mangrovei*, *D. marinospora*, *D. rhizophorae* and *D. thailandica*) by lacking a gelatinous sheath around the ascospores (Hyde 1992, Tsui et al. 1998, Pang et al. 2013). *Dyfrolomyces phetchaburiensis* and *D. thamplaensis* also have similar characters and lack a gelatinous sheath and cluster with *D. sinensis* in the multi-loci phylogenetic analyses. However, *D. sinensis* differs from *D. thamplaensis* based on number of septa (6–7, 3) and L/W ratio (3.7, 4) of the ascospores. In addition, both *D. phetchaburiensis* has been reported on submerged wood of *Rhizophora apiculata* in marine habitats and *D. thamplaensis* on corticated dead branch in Karst habitats (Hyde et al. 2017b, Zhang et al. 2017b). Therefore *D. sinensis* is introduced as a new species on dead stem of *Camellia sinensis* from terrestrial habitats (Fig. 52).

Kirschsteiniotheliales Hern.-Restr. et al.

Kirschsteiniotheliaceae Boonmee & K.D. Hyde

The family Kirschsteiniotheliaceae Boonmee & K.D. Hyde was proposed by Boonmee et al. (2012), to accommodate the genus *Kirschsteiniothelia* D. Hawksw. (Hawksworth 1985), and its asexual morph *Dendryphiopsis* S. Hughes (1953). Members of Kirschsteiniotheliaceae are distinguished by superficial, globose to subglobose ascomata, ellipsoidal, septate, coloured ascospores and a *Dendryphiopsis* asexual morph (Boonmee et al. 2012, Hyde et al. 2013, 2017b, Li et al. 2016a, Mehrabi et al. 2017). However, *Kirschsteiniothelia arasbaranica* and *K. thujina* (Hawksworth 1985), as well as *K. phoenicis*, which we introduce here, lacks any asexual morph, but groups within this family supported by molecular data. Based on phylogenetic analysis, Kirschsteiniotheliaceae was assigned to the order Kirschsteiniotheliales (Hernández-Restrepo et al. 2017, Wijayawardene et al. 2018). In the study, we provide an updated phylogenetic tree (Fig. 54) and introduce a new species, *Kirschsteiniothelia phoenicis*.

Kirschsteiniothelia D. Hawksw.

Kirschsteiniothelia was introduced by Hawksworth (1985) and typified by *K. aethiops* (Sacc.) D. Hawksw based on *Sphaeria aethiops* Berk. & M.A. Curtis. The ascomycetous genus comprises 21 species according to Index Fungorum (2018) and is characterized by superficial, erumpent, globose to subglobose, dark brown to black, membranaceous, scattered or loosely aggregated ascomata with or without a central papilla; a thick pseudoparenchymatous peridium consisting of thick-walled cells arranged in a pallisadic configuration at the base angles (*textura angularis*); a hamathecium comprising numerous, filiform, hyaline, pseudoparaphyses; bitunicate, fissitunicate, cylindrical-clavate, 8-spored asci with a long pedicel and an ocular apical chamber and bi- or tri-seriate ascospores, ellipsoidal, slightly curved, smooth-walled, olive brown to dark brown, 1-2-septate with a median or submedian septum, with or without a mucilaginous sheath (Boonmee et al. 2012, Hawksworth 1985, Hyde et al. 2013, Mehrabi et al. 2017).

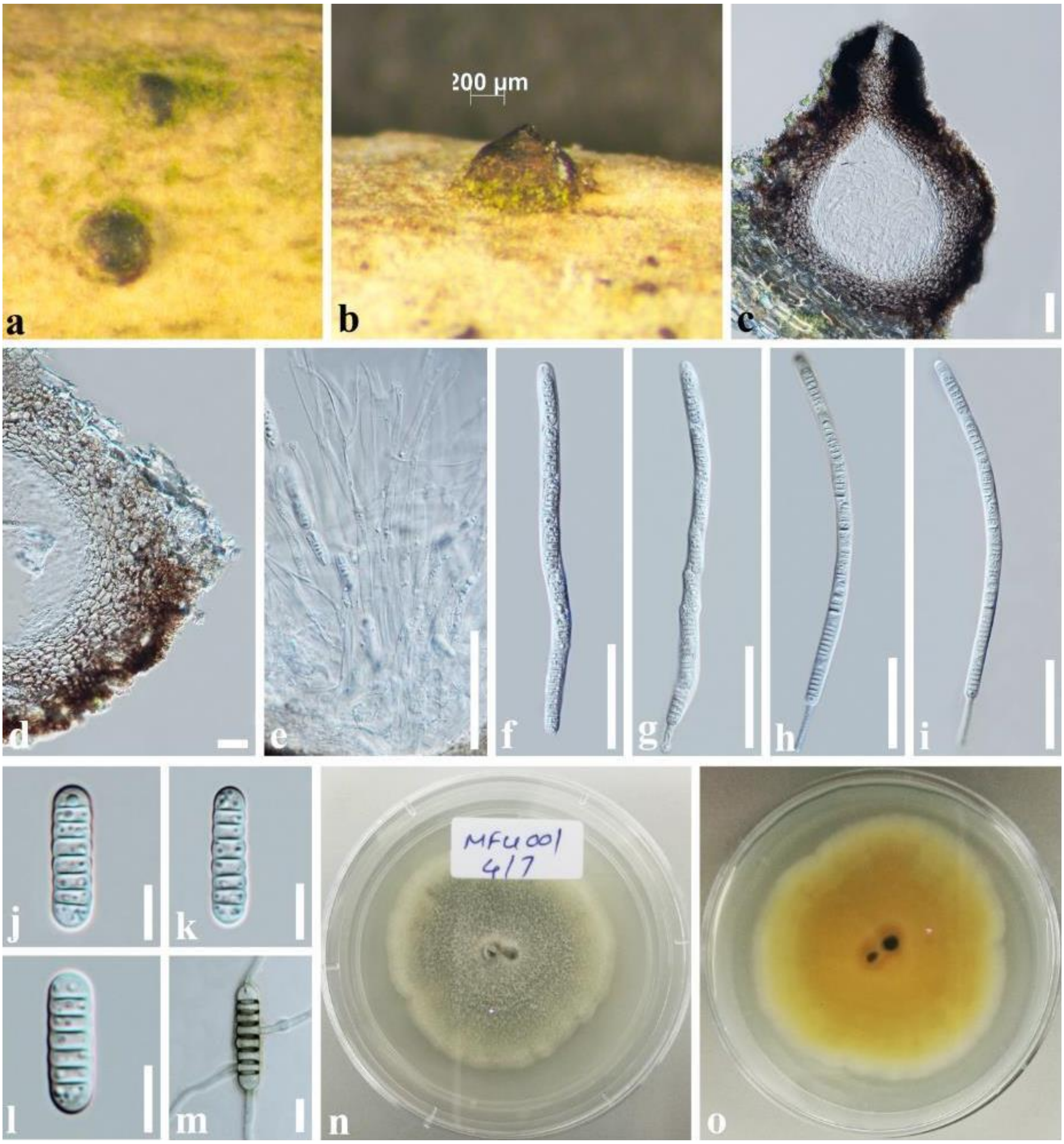


Figure 53 – *Dyfrolomyces sinensis* (MFLU 17-0777, holotype). a, b Appearance of ascomata on host surface. c Vertical section through ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–l Ascospores. m Germinating ascospore. n, o Culture on PDA (n. upper, o. lower). Scale bars: c, e–i = 50 µm, d = 20 µm, j–l = 10 µm.

The asexual morph of *Kirschsteiniothelia* is *Dendryphiopsis* (Wijayawardene et al. 2017b), which is supported by molecular data (Boonmee et al. 2012, Hawksworth 1985, Hyde et al. 2013, Schoch et al. 2006). Wijayawardene et al. (2014) proposed to use *Kirschsteiniothelia* over *Dendryphiopsis* and corrected the name *D. atra* as *Kirschsteiniothelia atra* (Corda) D. Hawksw. The asexual morph is macronematous, mononematous, erect, branched or unbranched, septate, brown to dark brown, smooth-walled conidiophores; monoblastic, terminal, with delimited conidiogenous cells, constricted at the septa and apically produced, broadly ellipsoid-obovoid, 1–2(–3)-septate, light brown, red brown to dark brown and smooth-walled conidia (Hawksworth 1985, Hyde et al. 2013, Su et al. 2016).

The genus *Kirschsteiniothelia* was originally assigned in Pleosporaceae (Hawksworth 1985, Barr 1987), but later Barr (1993) reported that *Kirschsteiniothelia* belongs to the Pleomassariaceae based on host, morphology and anamorph characters. With the support of molecular data, Schoch et al. (2006) showed that the type species, *K. aethiops*, was not phylogenetically related to the Pleosporaceae, and suggested that *Kirschsteiniothelia* should be transferred to a separate family. In further phylogenetic analysis, *K. elaterascus* Shearer grouped within Morosphaeriaceae, while *K. maritima* (Linder) D. Hawksw. clustered with *Mytilinidion spp*. in the Mytilinidiaceae clade (Schoch et al. 2009, Shearer et al. 2009, Suetrong et al. 2009). The taxa which are related to *K. aethiops* are included in Kirschsteiniotheliaceae (Boonmee et al. 2012).

Kirschsteiniothelia phoenicis S.N. Zhang & K.D. Hyde, sp.nov. Fig. 55

Index Fungorum number: IF554239; Facesoffungi number: FoF04093

Etymology – name reflects the host genus *Phoenix*.

Holotype: MFLU 18-0153.

Saprobic on *Phoenix paludosa* Roxb. Sexual morph *Ascomata* 135–160 µm high, 183–235 µm diameter ($\bar{x}$ = 143.8 × 201.7 µm, n = 10), black, scattered, subglobose to globose or slightly conical in appearance, superficial with apical papilla or plane, base remaining immersed, usually flattened. *Peridium* laterally 24–34 µm wide, composed of 5-6 layers of *textura angularis*, with dark brown outer layer cells and inner layers pale brown, cells around the ostiole with small lumina, reduced at the base, of 1–2 layers of cells. *Pseudoparaphyses* 0.8–1.5 µm wide, branched, embedded in a gelatinous matrix. *Asci* 70–112 × 14–24 µm ($\bar{x}$ = 84.7 × 19.4 µm, n = 15), 8-spored, bi-or tri- seriate in the middle of the ascus, cylindrical-clavate, straight or slightly curved, apically rounded, with a short pedicellate up to 5 µm long. *Ascospores* 18–27 × 5–7.5 µm ($\bar{x}$ = 21.3 × 6.6 µm, n = 36), brown, ellipsoid, rounded or slightly pointed at the ends, 1-septate, septum submedian and constricted, upper cell broader than the lower cell, each cell containing a distinct large guttule, smooth-walled, with a mucilaginous sheath. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 hours. Colonies growing on PDA and MEA dense, reaching 1–1.5 cm diameter after two weeks growing on PDA at 25°C, the surface covered with a white mat of aerial hyphae in first week, then becoming grayish-blue and dark bluish, composed of brown to dark brown, septate, smooth or verrucose hyphae 1.5–2.5 µm wide and up to 5 µm wide.

Material examined – THAILAND, Ranong, Ranong Mangrove Forest Research Center, on rachis of *Phoenix paludosa* (Arecaceae), that was probably intertidal as it was immersed in mangrove mud with water, 7 December 2016, S.N. Zhang, SNT76 (MFLU 18-0153, holotype); ex-type living culture, MFLUCC 18-0216, TBRC; *ibid*. (BBH 43493, isotype).

GenBank numbers – ITS: MG859978, LSU: MG860484, SSU: MG859979 (RPB2: MG994912, TEF1: MG994911, are submitted but not included in this analysis).

Notes – *Kirschsteiniothelia phoenicis* is morphologically simiar to the type species *K. aethiops* and *K. reticulata* C.Y. Chen et al. in ascospore width. However, *K. phoenicis* differs from *K. aethiops* as it has smaller ascospores, and a mucilaginous sheath. The asexucal morph was not determined. *Kirschsteiniothelia phoenicis* can easily be distinguished from *K. reticulata* as the ascospores lack any reticulate ornamentation. The phylogeny based on multigene analysis herein, also indicates that *K. phoenicis* is distinct from other species, given that it constitutes a strongly supported independent lineage, basal to other *Kirschsteiniothelia* species (Fig. 54).

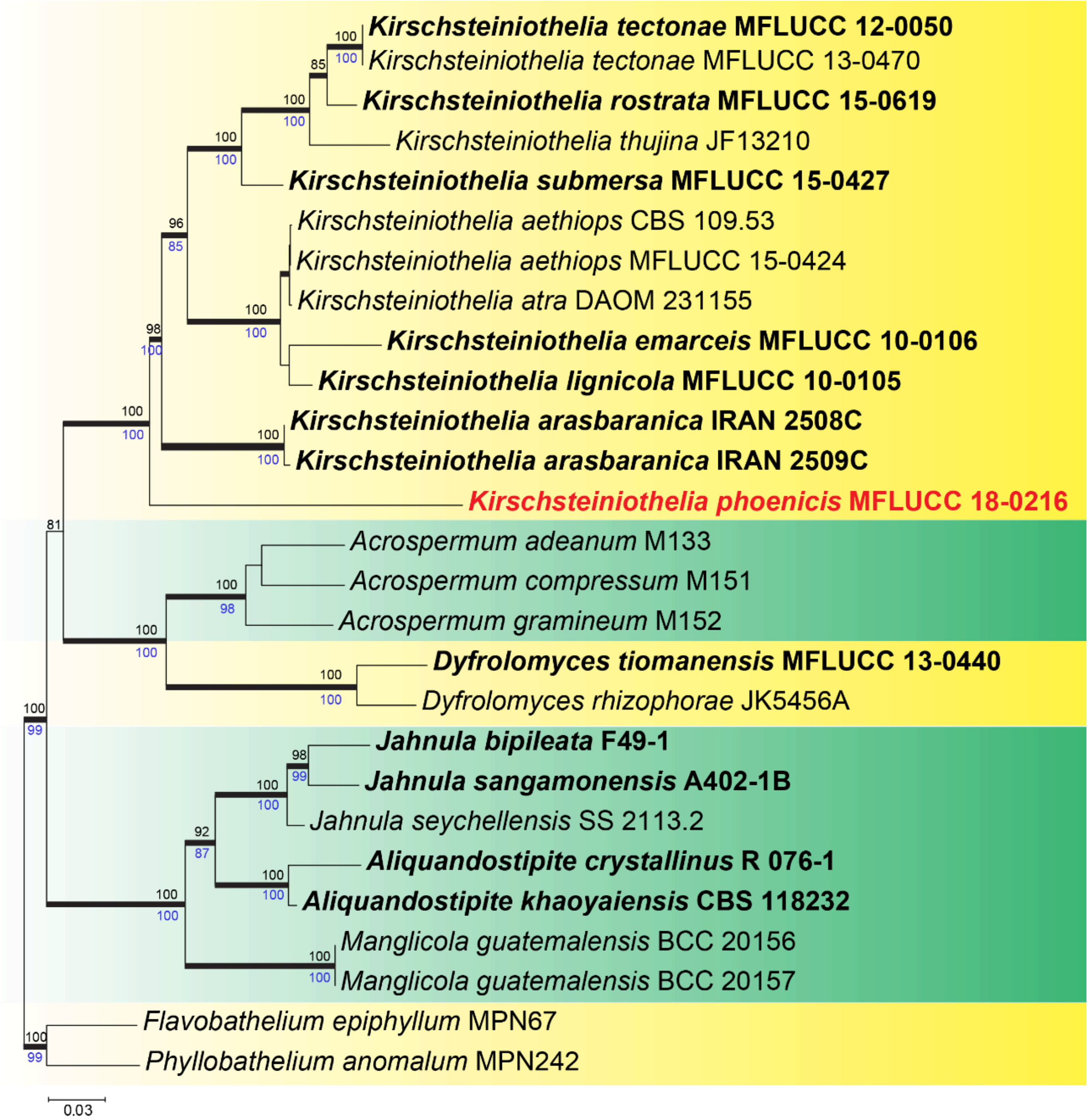


Figure 54 – RAxML tree based on analysis of combined ITS, LSU and SSU rDNA sequence data. Bootstrap values for ML and MP equal to or greater than 75% are placed above and below the branches respectively. Branches with Bayesian posterior probabilities (PP) from MCMC analysis equal or greater than 0.95 are in bold. The ex-type strains are in bold and newly generated sequences are indicated in red. The tree is rooted with *Phyllobathelium anomalum* and *Flavobathelium epiphyllum*. The final dataset consisted of 27 taxa (25 ingroup) with a total 2726 characters after alignment. 1673 characters were constant and 741 characters were parsimony informative, while 312 variable characters were parsimony uninformative. After a heuristic search using PAUP, one equally most parsimonious tree was obtained (tree length = 2195 steps, CI = 0.678, RI = 0.767, RC = 0.520, HI = 0.322).

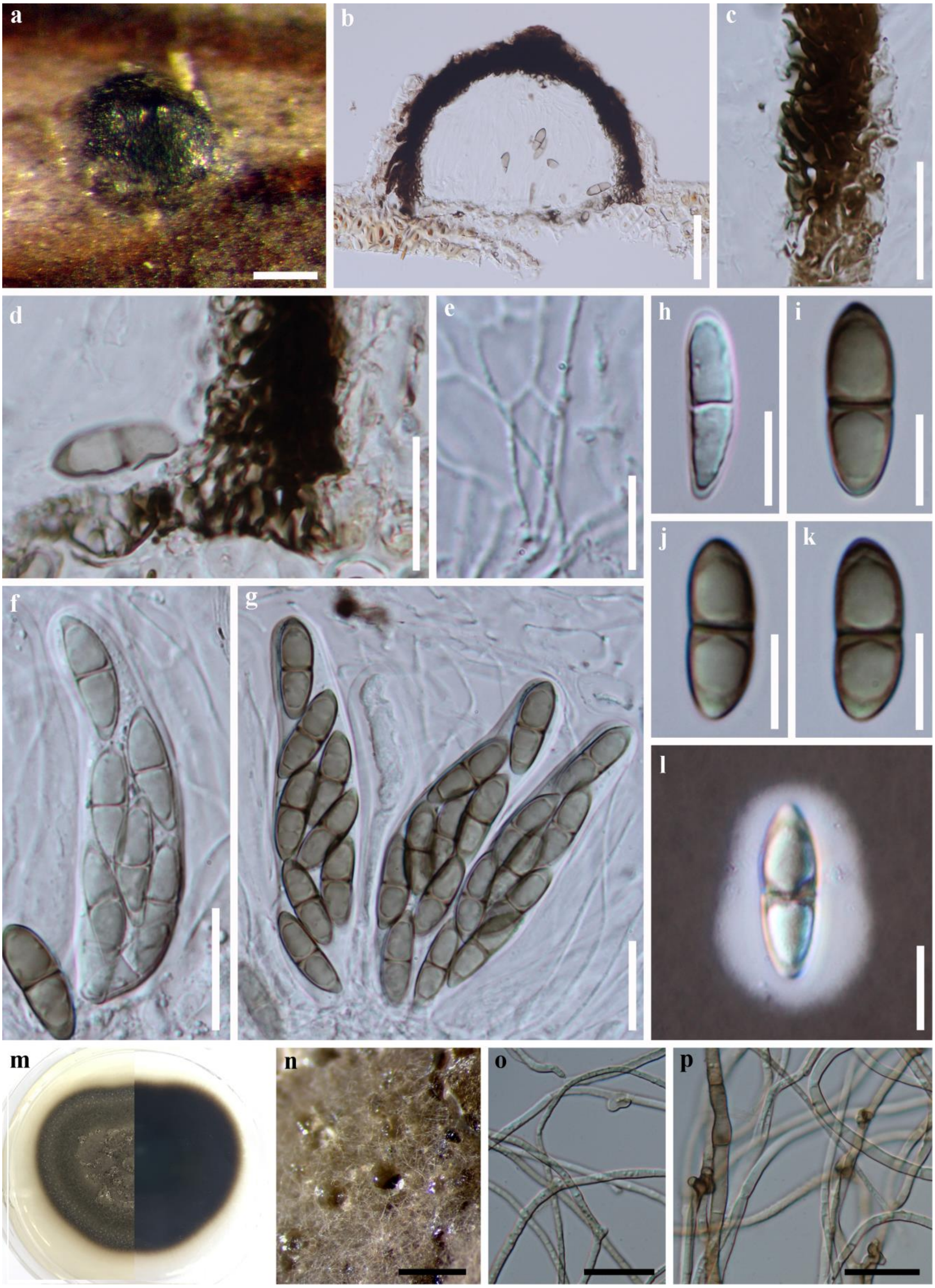


Figure 55 – *Kirschsteiniothelia phoenicis* (MFLU 18-0153, holotype). a Appearance of ascomata on host surface with ostiole. b Vertical section through the ascoma. c, d Structure of peridium. e Pseudoparaphyses. f, g Asci. h–k Ascospores. l Ascospore in India ink showing sheath. m–p Colony and mycelia growing on PDA. Scale bars: a = 100 μm, b = 50 μm, c, d, f, g, o, p = 20 μm, e, h–l = 10 μm, n = 1 mm.

Class Lecanoromycetes O.E. Erikss. & Winka
Subclass Acarosporomycetidae Reeb et al.
Teloschistales D. Hawksw. & O.E. Erikss.
Teloschistaceae Zahlbr.

Taxa are lichenized with photobiont member *Trebouxia*. Ascomata are apothecial with well-developed thallin margins (Gaya et al. 2008). Most Teloschistaceae species produce anthraquinone pigments in the cortex which provide yellow to orange colours to their apothecia (Arup et al. 2013). Paraphyses are unbranched to slightly branched and usually slightly capitate. Asci are semifissitunicate, with apical tholus and distinct ocular chamber. Ascospores are mostly 1–3-septate and ellipsoid. The asexual morph is pycnidial (Jaklitsch et al. 2016a). In this study, we illustrate *Cerothallia subluteoalba* collected from Australia.

Cerothallia Arup et al.

Cerothallia is a small genus in the family Teloschistaceae with four species (Lücking et al. 2016). They form crustose lichenized thalli with trebouxia-like photobionts. This genus is geographically restricted in temperate regions (Nimis & Martellos 2017).

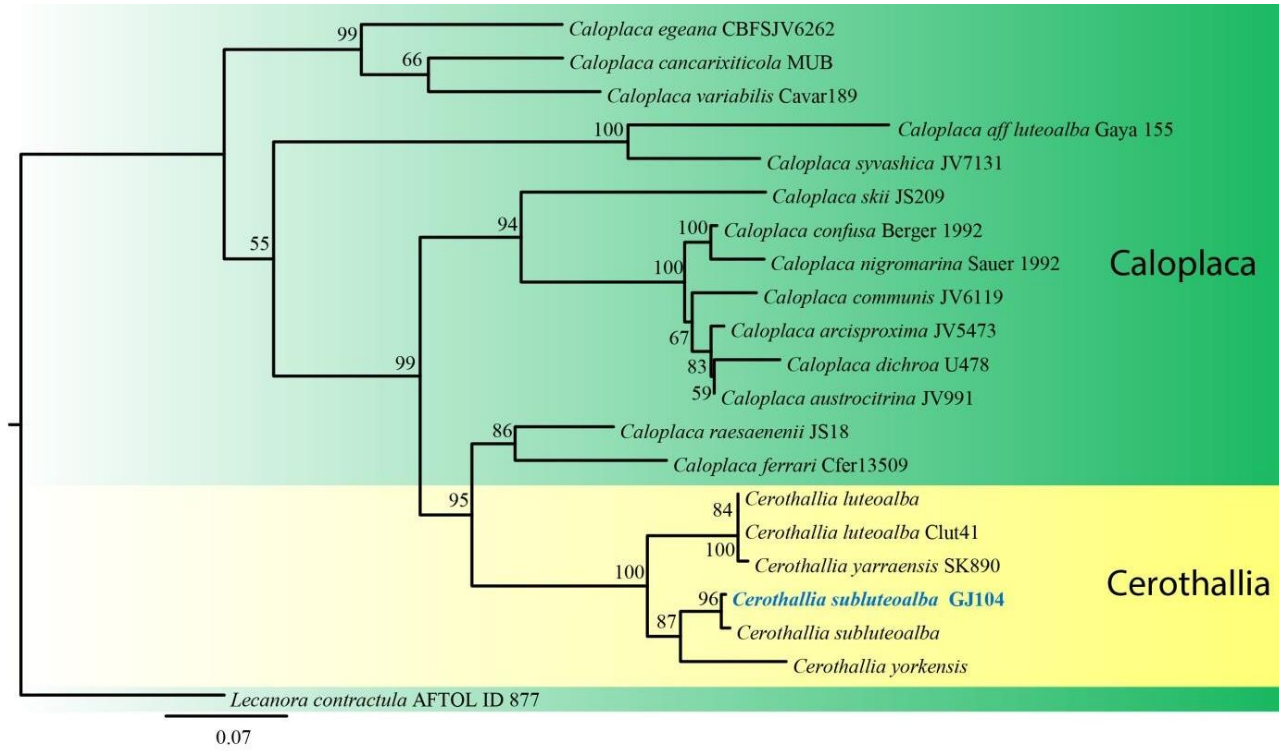


Figure 56 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS sequence data of *Caloplaca* and *Cerothallia* species. Related sequences were obtained from GenBank. Twenty-one strains are included in the analyses, which comprise 605 characters including gaps. The tree is rooted with *Lecanora contractuala* (AFTOL ID 877). The best scoring RAxML tree with a final likelihood value of -4428.138068 is presented. The matrix had 344 distinct alignment patterns, with 9.93% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.200210, C = 0.293629, G= 0.276064, T = 0.230097; substitution rates AC = 1.227023, AG = 3.402371, AT = 1.963531, CG = 1.415528, CT = 6.016852, GT = 1.000000; gamma distribution shape parameter α = 1.734937. RAxML bootstrap support values ≥ 50% (BT) are shown respectively near the nodes. The scale bar indicates 0.07 changes. The new isolates are in blue.

Cerothallia subluteoalba (S.Y. Kondr. & Kärnefelt) Arup, Frödén & Søchting (2013) Fig. 57

Facesoffungi number: FoF04096

Lichenized on dead stem. Sexual morph 350–400 × 134–178 µm ($\bar{x}$ = 373.5 × 152 µm, n = 10). *Apothecia* scattered on the host thallus, sessile, erumpent from the substrate, yellow when both dry and moist conditions. *Hypothecium* pulvinate, disc convex, margins slightly elevated, disc and the margins yellow. *Exciple* 26–42 µm ($\bar{x}$ = 34.3 µm, n = 10), yellowish-brown in water, becoming reddish in KOH, laterally consisting of thick-walled, isodiametric cells (mainly in the upper part), basally of conglutinated, thick-walled, hyaline, more or less isodiametric cells. *Hymenium* upper part yellowish-brown and lower part is hyaline, in KOH upper part becoming reddish, embedded in a thick gelatinous matrix. *Paraphyses* 0.5–1 µm wide ($\bar{x}$ = 0.8 µm, n = 20), numerous, filiform, aseptate, capitate or enlarged and pigmented at the apex, exceeding asci in length, apices are glued together to develop epithecium. *Asci* 28–35 × 8–12 µm ($\bar{x}$ = 33.6 × 10 µm, n = 30), 8-spored, sessile, arising from croziers, cylindric–clavate, rounded at the apex, amyloid ring absent at the ascus apex. *Ascospores* 8–10 × 4–6 µm ($\bar{x}$ = 9.6 × 5.3 µm, n = 40), multiseriate, 1-celled, ovoid, hyaline to reddish, smooth, thick-walled. Asexual morph Undetermined.

Material examined – AUSTRALIA, Peninsula, Mornington, on the dead stem, 10 March 2015, E.B. Gareth Jones, GJ103 (MFLU 16-0561).

GenBank number –ITS: MG820705, LSU: MH216681.

Notes – *Cerothallia subluteoalba* is characterized by pulvinate apothecia, a yellowish-brown excipulum which turns red in KOH, filiform paraphyses swollen at the apex, short sessile asci and ellipsoid ascospores (Kantvilas 2016).

Subclass Lecanoromycetidae P.M. Kirk et al. ex Miadl. et al.

Peltigerales W. Watson

Collemataceae Zenker

Taxa form gelatinous lichen thalli with cyanobacteria of the genus *Nostoc* (Otálora et al. 2014). Thalli lobes are small to large, leathery to papery when dry and swell to becomes extremely gelatinous when wet, lower side glabrous or tomentose. They are mostly epiphytic on bark, on rocks, soil and between bryophytes (Otálora et al. 2013, 2014). Ascomata are apothecial. The hamathecium comprises amyloid, unbranched paraphyses and asci are mostly 8-spored or rarely 4-spored, semi-fissitunicate, clavate to cylindrical and amyloid. Ascospores are transversely septate to muriform, fusiform to ellipsoid and hyaline. Asexual morphs are pycnidial (Otálora et al. 2013, 2014, Jaklitsch et al. 2016a). In the study, we introduce *Leptogium thailandicum* sp. nov. from Thailand.

Leptogium (Ach.) Gray

Leptogium is a widely distributed genus which includes around 250 species (Aragón et al. 2005). More studies are required on this genus as there are many species complexes and groups which need to be resolved (Otálora et al. 2008).

Leptogium thailandicum Ekanayaka & K.D. Hyde, sp. nov. Fig. 59

Index Fungorum number: IF554068; Facesoffungi number: FoF04094

Etymology – with reference to the country where the holotype was collected.

Holotype – MFLU 16-0586

Lichenized on dead stems. Sexual morph *Apothecia* 1125–1828 × 251–655 µm ($\bar{x}$ = 1525.5 × 425.7 µm, n = 10), arising in small groups, sessile to sub-stipitate on the thallus. *Hypothecium* cupulate, external surface greenish. *Disc* flat to slightly concave, light brown to dark brown when fresh. *Margins* light green. *Hymenium* hyaline, enclosed in a thick gelatinous matrix. *Ectal excipulum* 17.7–37.5 µm ($\bar{x}$ = 25.4 µm, n = 10), composed of small, thin-walled, hyaline cells of *textura angularis*. *Medullary excipulum* composed of hyaline cells of *textura intricata*. *Paraphyses* 1.4–2.4 µm wide ($\bar{x}$ = 1.9 µm, n = 20), numerous, filiform, obtuse at the apex, aseptate, unbranched. *Asci* 98.6–123.4 × 14.9–26.9 µm ($\bar{x}$ = 112.9 × 18 µm, n = 30), 8-spored, medium to long pedicellate, cylindric–clavate, rounded at the apex, amyloid ring absent at the ascus

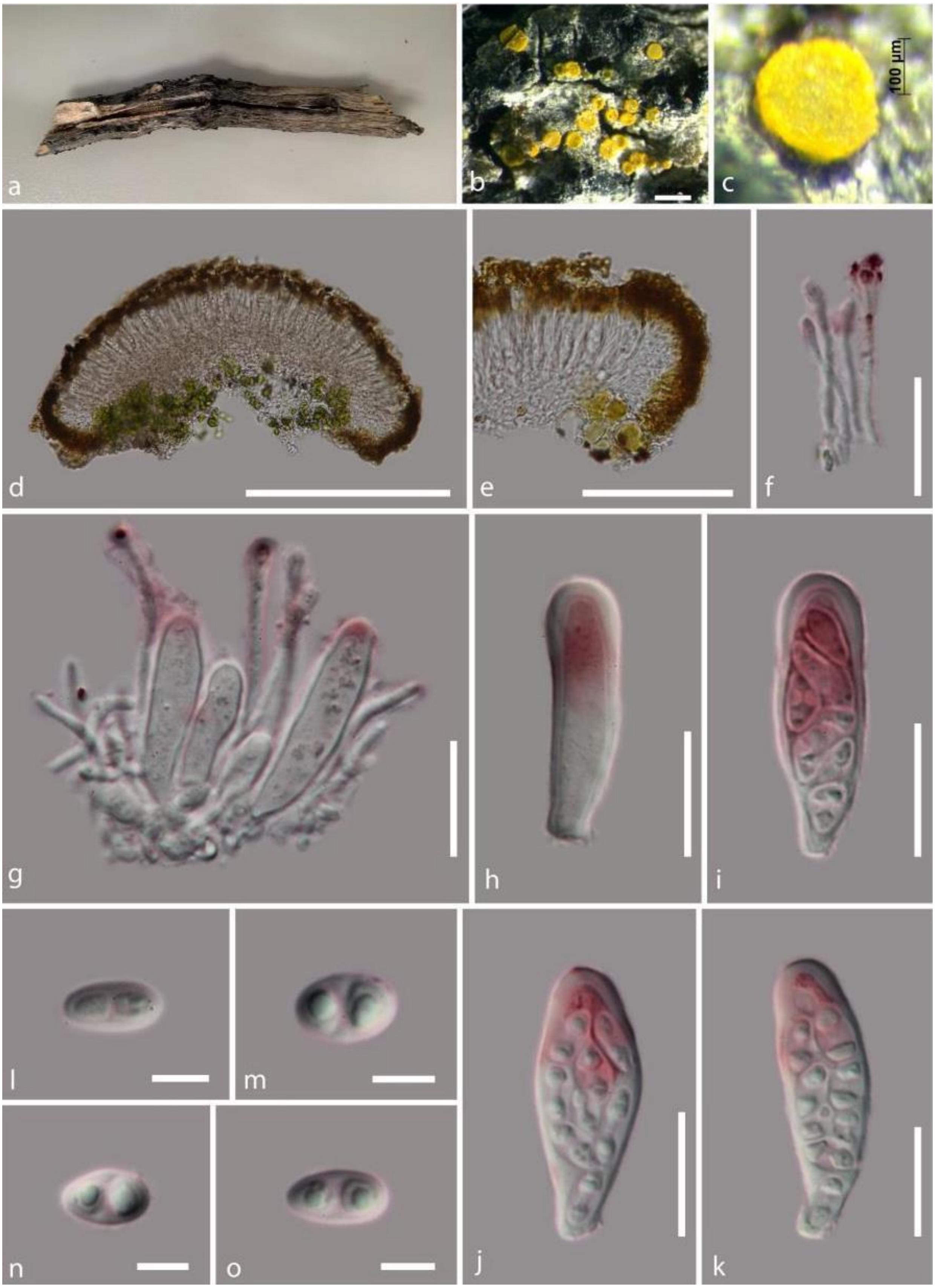


Figure 57 – *Cerothallia subluteoalba* (MFLU 16-0561). a Substrate. b Ascomata on wood. c Ascoma on wood. d Cross section of an ascoma. e Close up of a vertical section of the ascoma at the margin. f Aseptate paraphyses. g Arrangement of asci and paraphyses in the hymenium layer. h–k Short sessile asci (f–k mounted in KOH). l–o Ovoid ascospores. Scale bars: b = 500 µm, d = 200 µm, c = 100 µm, e = 40 µm, f = 20 µm, g–k = 15 µm, l–o = 5 µm.

Figure 58 – Phylogenetic tree generated by maximum likelihood analysis of LSU sequence data of *Leptogium* species. Related sequences were obtained from GenBank. Seventy-four strains are included in the analyses, which comprise 1243 characters including gaps. The tree is rooted with

Lecanora contractula (AFTOL ID 877). The best scoring RAxML tree with a final likelihood value of -6512.383381 is presented. The matrix had 499 distinct alignment patterns, with 26.01% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239, C = 0.252, G= 0.323, T = 0.185; substitution rates AC = 1.384799, AG = 2.394283, AT = 0.793732, CG = 1.334471, CT = 8.586646, GT = 1.000000; gamma distribution shape parameter α = 0.198923. Maximum likelihood bootstrap values ≥50% are given near the nodes. The scale bar indicates 0.06 changes. Strain/culture numbers are given after the taxon names. Newly generated sequences are in blue bold.

apex. *Ascospores* 18.6–24.2× 6.5–11.6 µm ($\bar{x}$ = 20.1 × 8.7 *µm*, n = 40), partially biseriate, lower spores are uniseriate, hyaline, smooth, muriform, 3–5-transverse septate, with 1-longitudinal septa, ellipsoid to subfusiform with pointed apices in mature spores. Asexual morph Undetermined.

Material examined – THAILAND, Chiang Rai Province, Doi Mae Salong, on dead stems, 22 June 2015, A.H. Ekanayaka, HD025 (MFLU 17-2769, holotype); *ibid.* (HKAS, isotype).

GenBank number – LSU: MG820706, ITS: MH216041.

Notes – *Leptogium thailandicum* is phylogenetically close to *L. phyllocarpum*. They however, differ by 22 base pairs in the LSU region. Moreover, *L. phyllocarpum* has highly wrinkled margins, while *L. thailandicum* has smooth margins and ascospores with pointed apices (Nash et al. 2004). *Leptogium corticola* is morphologically similar to *L. thailandicum,* but differs in having larger ascospores (30–56 × 10–20 µm) (Sierk 1964, Brodo et al. 2001).

Class Pezizomycetes O.E. Erikss. & Winka
Pezizales J. Schröt.
Otideaceae Eckblad

This family contains eight genera and around 70 species (Jaklitsch et al. 2016a, Ekanayaka et al. 2018). Most Otideaceae taxa are characterized by cupulate to ear-shaped, brownish, and sessile to sub-stipitate apothecia. Some form cleistothecia (Ekanayaka et al. 2018). The ectal excipulum is composed of *textura angularis* and medullary excipulum of *textura intricata*. Paraphyses are straight or apically curved and asci are 8-spored, cylindric-clavate with ellipsoid ascospores (Liu & Zhuang 2006, Leuchtmann & Clémençon 2012, Hansen et al. 2013). In this study, we introduce *Otidea pseudoformicarum* sp. nov. from China.

Otidea (Pers.) Bonord.

The genus *Otidea* was established by Bonorden (1851). The recent comprehensive study on this genus is by Olariaga et al. (2015). The species of this are restricted to the Northern Hemisphere (Olariaga et al. 2015).

Otidea pseudoformicarum Ekanayaka, Q. Zhao and K.D. Hyde, sp. nov. Fig. 61

Index Fungorum number: IF554071; Facesoffungi number: FoF04095

Etymology – the specific epithet *pseudoformicarum* refers to the morphological similarity of this species to *O. formicarum*.

Holotype – HKAS 101386

Saprobic on soil. Sexual morph *Apothecia* 2–5 cm high, 2–7 cm in diameter, broadly ear-shaped to cupulate or flattened, sub-stipitate, split, hymenium surface yellowish-brown when dry. *Receptacle* concave, yellowish-brown dry, with pruinose outer surface. *Disc* concolorous to receptacle. *Ectal excipulum* composed of smooth, thin-walled hyaline cells of *textura angularis* to *globulosa* with yellowish to brownish exudates. *Medullary excipulum* composed of loosely arranged, hyaline, non-gelatinized, septate, smooth, thin-walled hyphae of *textura intricata*. *Paraphyses* 1.5–2.3 µm ($\bar{x}$ = 1.9 µm, n = 20) wide at the middle, filiform, smooth and thin-walled, septate, hyaline. *Asci* 115–150 × 7–10 µm ($\bar{x}$ = 131.4 × 9 µm, n = 15), 8-spored, unitunicate, subcylindrical, short pedicellate, arising from croziers, non-amyloid, ascospores released from an eccentric split at the apical apex. *Ascospores* 8–10 × 5–7 µm ($\bar{x}$ = 9 × 5.8 µm, Q_m= 1.6–1.4, n =

25), ellipsoid, with 2 guttules, sometimes multi-guttulate, smooth-walled, uniseriate. Asexual morph Undetermined.

Material examined – CHINA, Yunnan Province, Lijiang, Yushuizhai, 7 September 2014, Qi Zhao N243 (HKAS 101386, holotype).

GenBank numbers – ITS: KY498601, LSU: KY498606.

Notes – *Otidea pseudoformicarum* is phylogenetically close to *O*. *formicarum* and *O*. *subformicarum*. However, *O*. *pseudoformicarum* separates from them in a single lineage with 100% bootstrap support (Fig. 60). *Otidea pseudoformicarum* is morphologically similar to *O*. *formicarum* in having broadly ear-shaped apothecia, an ectal excipulum with exudates, however, *O*. *pseudoformicarum* differs in having shorter asci arising from croziers and smaller ascospores (Olariaga et al. 2015).

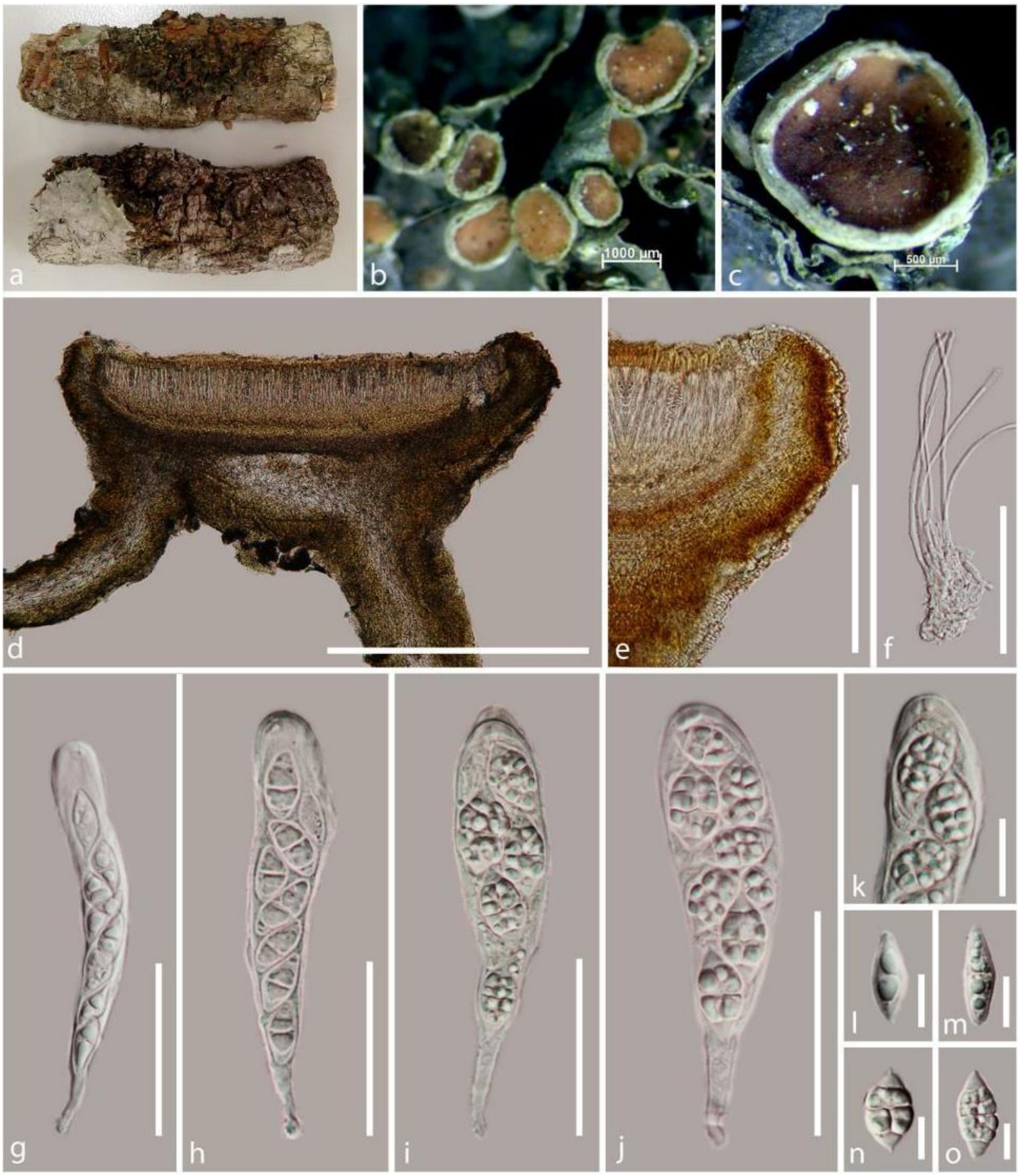


Figure 59 – *Leptogium thailandicum* (MFLU 16-0586, holotype). a Substrate. b Apothecia on wood. c Apothecium on wood. d Cross section of an apothecium. e Close up of a vertical section of the apothecium at the margin. f Septate paraphyses. g–j Long pedicellate asci. k Non-amyloid apical apex. l–o Ovoid ascospores. Scale bars: b = 1000 µm, d = 800 µm, c = 500 µm, e = 200 µm, f = 70 µm, g–j = 50 µm, k = 20 µm, l–o = 10 µm.

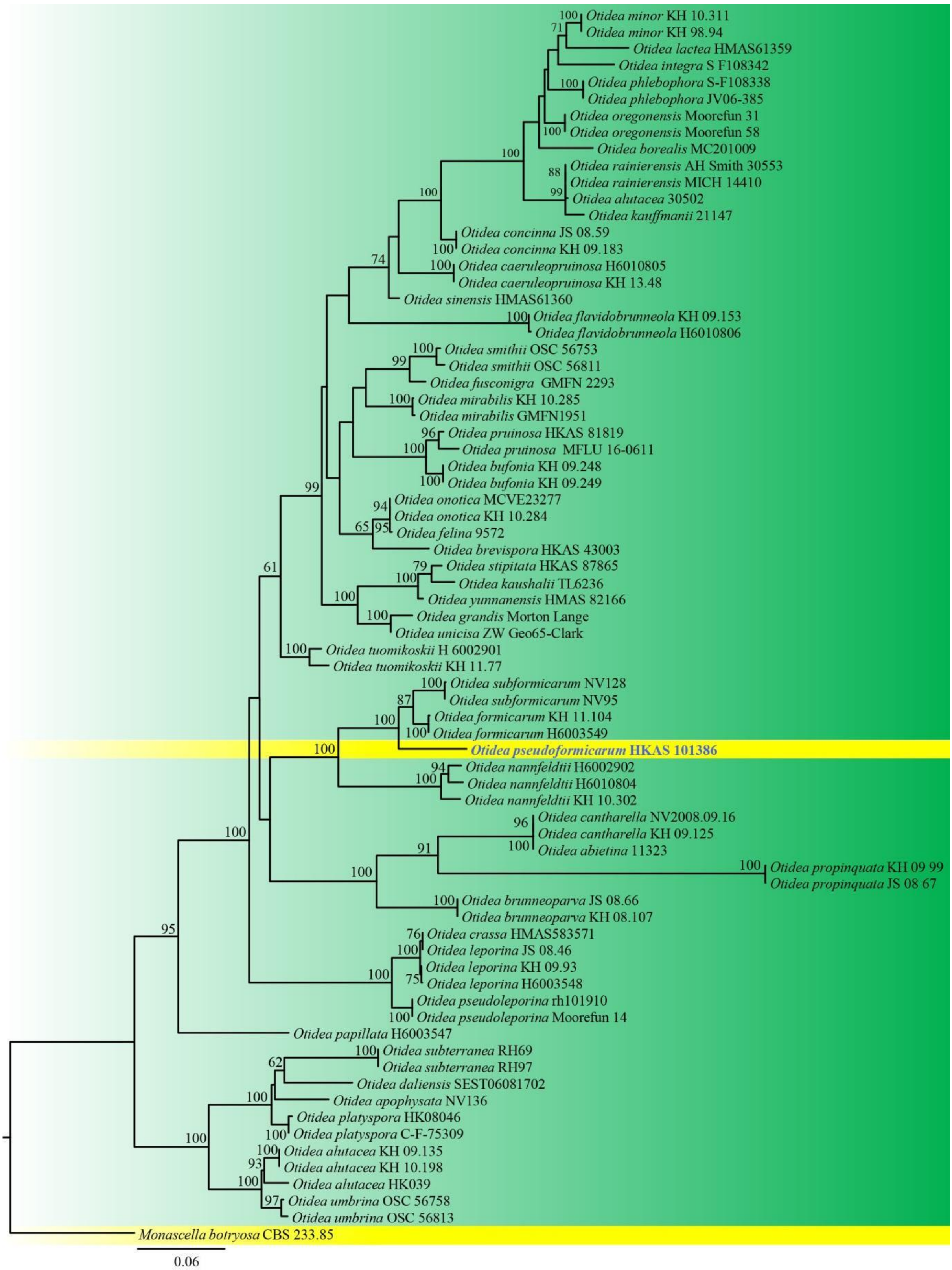


Figure 60 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS and LSU sequence data of *Otidea* species. Related sequences were obtained from GenBank. Seventy-four strains are included in the analyses, which comprise 1598 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree is rooted with *Monascella botryosa* (CBS 233.85). The best scoring RAxML tree with a final likelihood value of -15790.294971 is presented. The matrix had 895 distinct alignment patterns, with 22.64% of undetermined characters or gaps. Estimated base

frequencies were as follows; A = 0.248, C = 0.206, G= 0.275, T = 0.270; substitution rates AC = 1.117181, AG = 2.684224, AT = 1.368399, CG = 0.761371, CT = 5.232977, GT = 1.000000; gamma distribution shape parameter α = 0.366724. RAxML bootstrap support values ≥ 50% (BT) are shown respectively near the nodes. The scale bar indicates 0.06 changes. The new isolates are in blue bold.

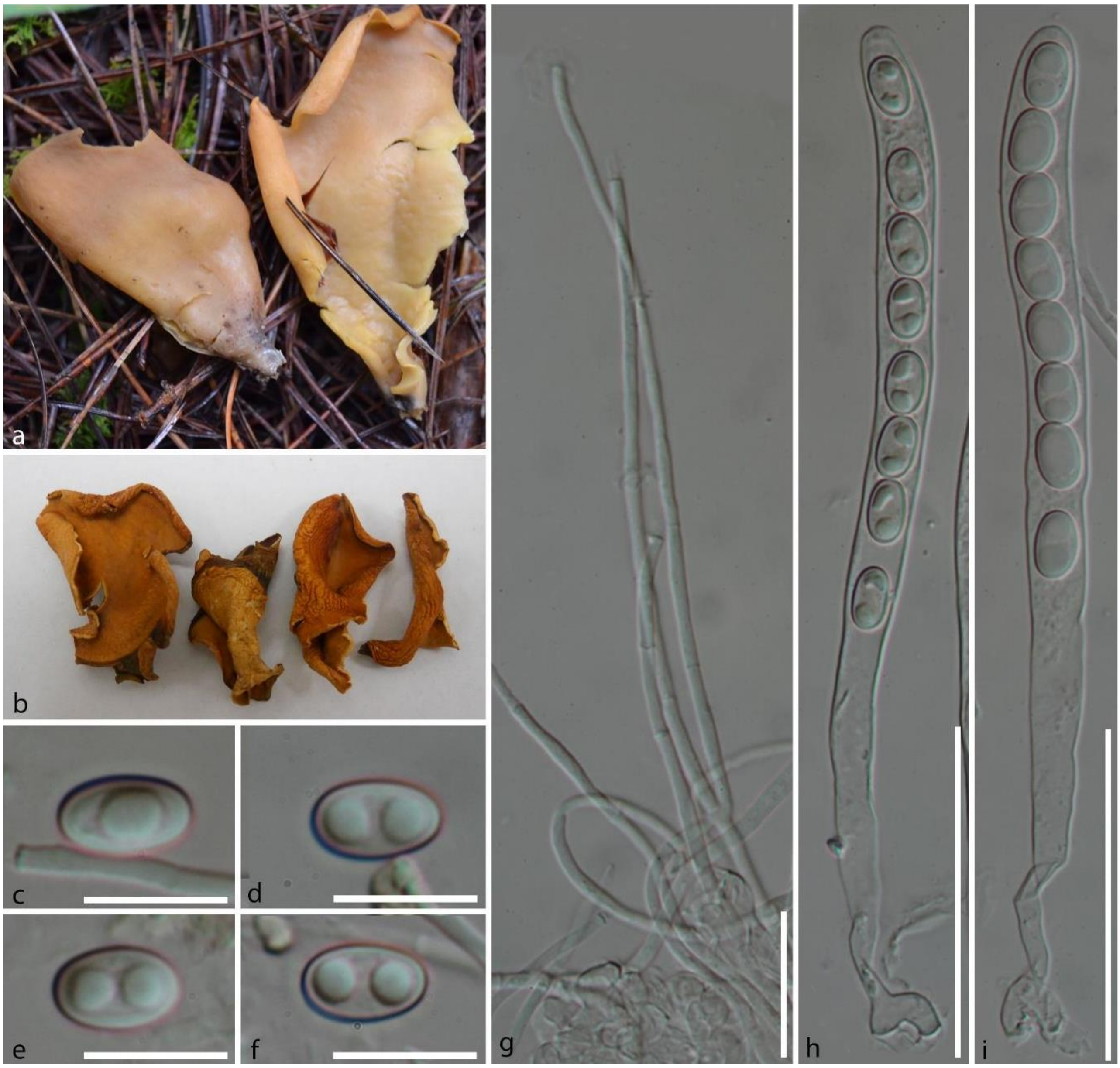


Figure 61 – *Otidea pseudoformicarum* (HKAS 101386, holotype). a Habit of fresh apothecia. b Habit of dried apothecia. c–f Ellipsoid ascospores. g Cylindrical paraphyses. h, i Cylindrical asci. Scale bars: h, i = 50 µm, g = 25 µm, c–f = 10 µm.

Class Leotiomycetes O.E. Erikss. & Winka
Rhytismatales M.E. Barr ex Minter
Rhytismataceae Chevall.

Rhytismataceae is a large family in Rhytismatales (Leotiomycetidae, Leotiomycetes, Pezizomycotina, Ascomycota) and includes 44 genera and 400 species (Lumbsch & Huhndorf 2010, Lantz et al. 2011, Hyde et al. 2016). Taxa in Rhytismataceae can be endophytes, pathogens and saprobes (Lantz et al. 2011, Hyde et al. 2016).

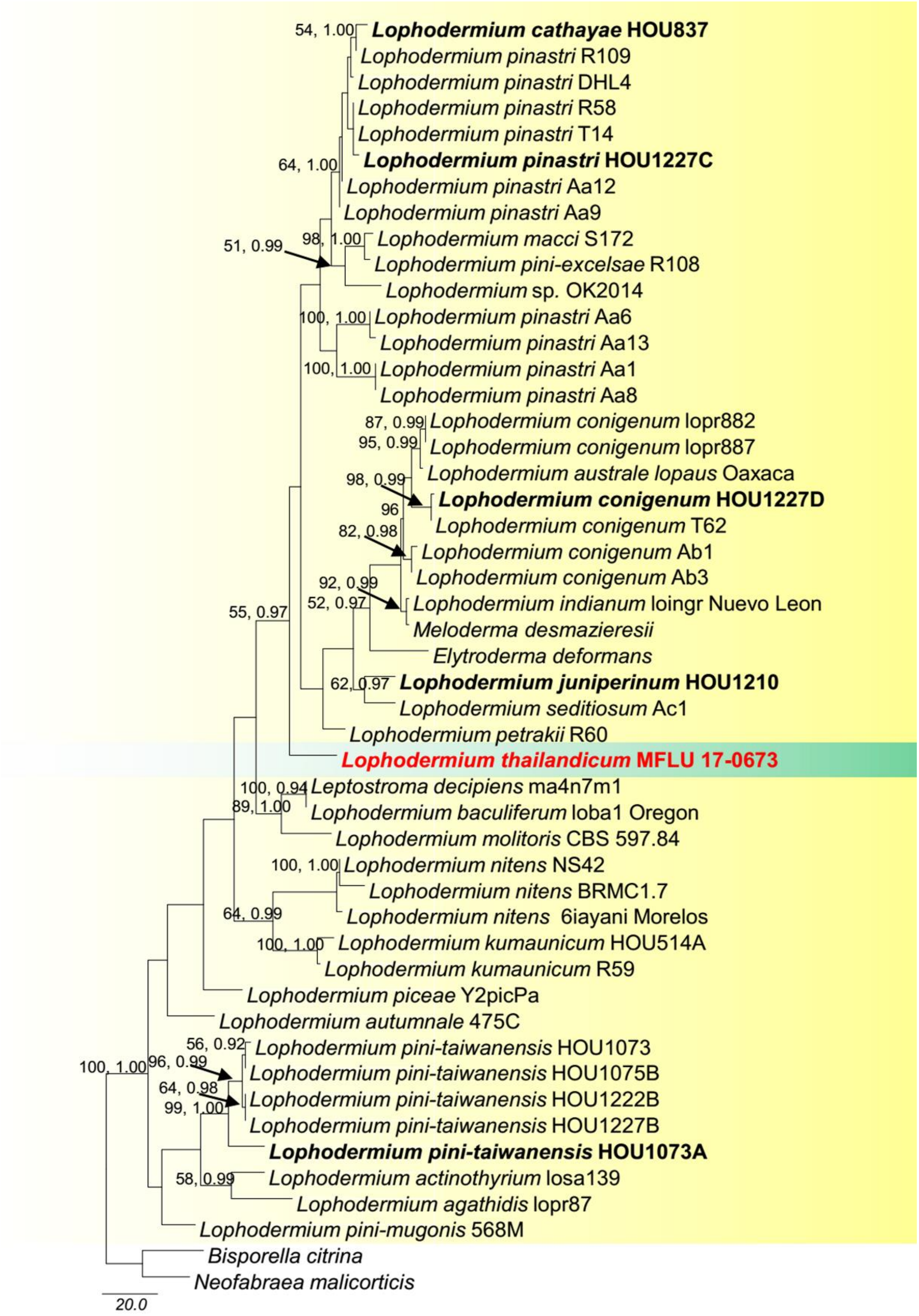


Figure 62 – The maximum parsimony (MP) tree based on analysis of ITS sequences of *Lophodermium* species. Related sequences were obtained from Li et al. (2016c). Forty-nine strains

are included in the combined sequence analyses, which comprise 1773 characters with gaps. *Bisporella citrina* and *Neofabraea malicorticis* are used as the outgroup taxa. The matrix had 1089 distinct alignment patterns, with 35% of undetermined characters or gaps. Bootstrap support values higher than 50% and Bayesian posterior probabilities ≥ 0.95 (PP) are defined above the nodes respectively. Newly generated sequences are in red bold. Ex-type strains are shown in black bold.

Lophodermium Chevall.

Lophodermium is the largest genus in family Rhytismataceae with more than 100 species (Lantz et al. 2011, Hyde et al. 2016). They are economically important parasites, particularly on conifers (Lantz et al. 2011).

Lophodermium thailandicum N.I. de Silva & K.D. Hyde, sp. nov. Fig. 63

Index Fungorum number: IF554201; Facesoffungi number: FoF04081

Etymology – specific epithet refers to the country that specimen collected.

Holotype – MFLU 17-0673

Saprobic on dead leaf of unknown host species. Sexual morph *Apothecia* 350–420 µm high × 750–1000 µm diameter ($\bar{x}$ = 400 × 880 µm, n = 10), rounded, scattered, sessile, erumpent, discoid. *Receptacle* concave, dark brown to black. *Margins* concolorous to receptacle. *Disc* olive green, concave. *Ectal excipulum* 26–33 µm, composed of cells of *textura globulosa* to *angularis*. *Medullary excipulum* 35–40 µm, composed of cells of *textura porrecta*. *Paraphyses* 2–3 µm wide, cylindrical, hyaline, embedded in common gelatinous matrix with asci. *Asci* 120–200 × 4–8 µm ($\bar{x}$ = 180 × 7 µm, n = 25), 8-spored, cylindrical, with a short pedicel. *Ascospores* 80–160 × 1–2 µm ($\bar{x}$ = 130 × 1.5 µm, n = 25), hyaline, elongated, filiform, sometimes curved and semi-circular. Asexual morph Undetermined.

Material examined – THAILAND, Chiang Mai Province, Muang District, on dead leaf of unknown host species, 27 September 2016, N. I de Silva, NI101 (MFLU 17-0673, holotype).

GenBank number – ITS: MG818852.

Notes – The phylogenetic analysis of ITS data indicates that our taxon belongs to *Lophodermium*. We tried to isolate this taxon, unfortunately its ascospores failed to germinate. Therefore, we obtained sequence data directly from the fruiting bodies. The phylogeny depicts an interesting finding to support establishment of our new taxon. *Lophodermium thailandicum* is positioned in a moderately supported independent lineage and nested inbetween other *Lophodermium* species analysed but with poor support (Fig 62). The new taxon differs from *Lophodermium seditiosum* in having rounded apothecia. Apothecia of *Lophodermium seditiosum* are oval to elliptical and open by a split in the middle (Minter et al. 1978). Both *Lophodermium seditiosum* and our strain have similar ascus morphology and ascospore length and width range (Minter et al. 1978). *Lophodermium seditiosum* was found on pine needles in the USA (Minter et al. 1978), but our strain was found on dead leaves of unknown host plant in Thailand. Therefore, we introduce a new species, *Lophodermium thailandicum*, considering its phylogeny, morphology and biogeography.

Class Sordariomycetes O.E. Erikss. & Winka

Subclass Diaporthomycetidae Senan. et al.

Annulatascales D'souza et al.

Annulatascaceae S.W. Wong et al.

Annulatascaceae comprises the genera *Annulatascus*, *Annulusmagnus*, *Ascitendus* and *Submersisphaeria*, which are freshwater ascomycetes growing on submerged wood (Zhang et al. 2017a). Based on molecular data, Campbell and Shearer (2004) considered that taxa assigned to Annulatascaceae were polyphyletic, and this was subsequently confirmed by various researchers.

(Abdel-Wahab et al. 2011, Boonyuen et al. 2012, Dayarathne et al. 2016) However, the recent study of Zhang et al. (2017a) resolved taxonomic relationships among members of this family by excluding several genera from Annulatascaceae based on analyses of a combined analysis of LSU, SSU, ITS and RPB2 sequence data. In this study, we introduce a novel *Ascitendus* species from a decaying wood submerged in the Mulgrave River, Australia.

Ascitendus J. Campb. & Shearer

The genus *Ascitendus* was established for *Ascolacicola austriacus*, by Campbell & Shearer (2004) as a monotypic genus. *Ascitendus* comprises saprobic, freshwater or terrestrial ascomycetes found from Austria and its sexual morph is unknown (Campbell & Shearer 2004, Wijayawardene at al. 2017a).

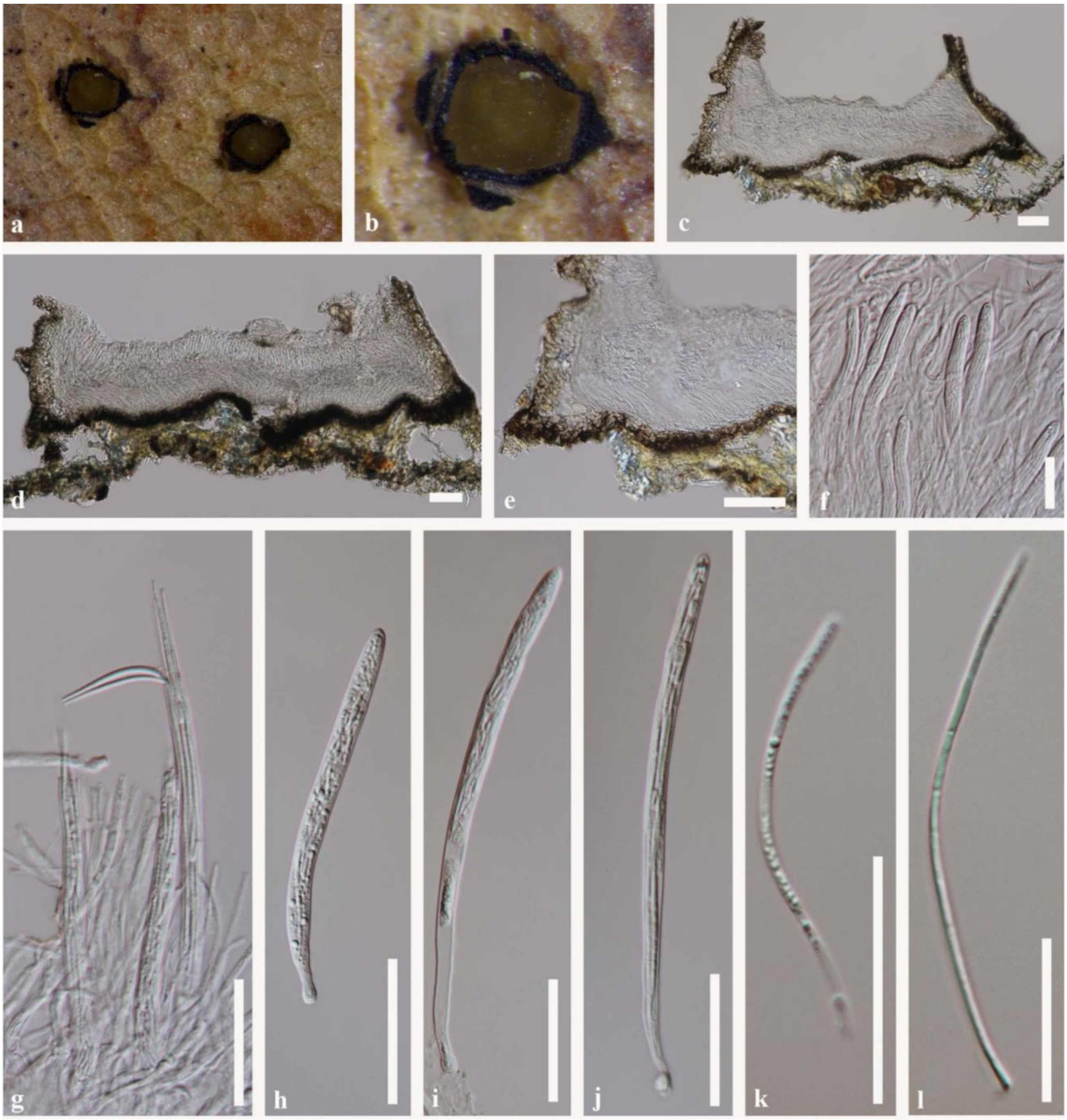


Figure 63 – *Lophodermium thailandicum* (MFLU 17-0673, holotype). a, b Appearance of ascomata on host. c, d Vertical section of ascoma. e Peridium. f, g Paraphyses. h–j Asci. k, l Ascospores. Scale bars c–e = 80 µm, f = 30 µm, g–k = 50 µm, l = 30 µm.

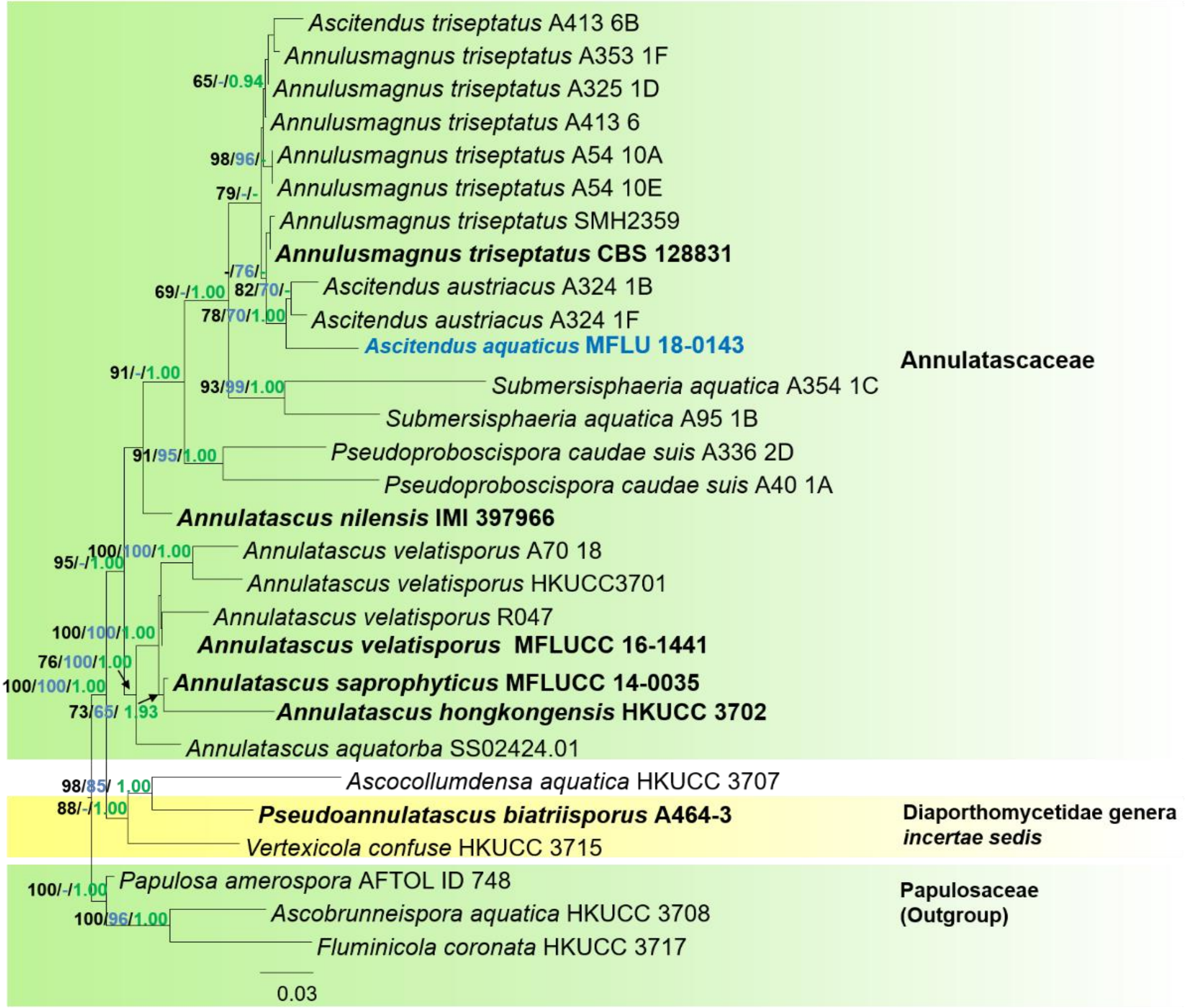


Figure 64 – Phylogram generated from maximum likelihood analysis based on combined LSU and SSU sequence data of selected taxa. Related sequences were obtained from GenBank. Twenty-nine strains are included in the analyses, which comprise 1785 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree is rooted with *Papulosa amerospora* (AFTOL ID 748), *Ascobrunneispora aquatica* (HKUCC 3708) and *Fluminicola coronata* (HKUCC 3717). The tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of -7506.256928 is presented. The matrix had 483 distinct alignment patterns, with 47.67% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.253321, C = 0.232540, G = 0.300821, T = 0.213318; substitution rates AC = 0.627195, AG = 1.154324, AT = 0.764306, CG = 0.897430, CT = 3.282253, GT = 1.000000; gamma distribution shape parameter α = 0.910487. The maximum parsimonious dataset consisted of constant 1204, 200 parsimony-informative and 381 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 1002 steps (CI = 0.736, RI = 0.625, RC = 0.459, HI = 0.264) in the first tree Maximum parsimony bootstrap (MPBT, black) values > 60%, Bayesian posterior probabilities (PP, blue) > 0.80% and maximum likelihood bootstrap (ML, green) values > 60%) are given above the nodes. The scale bar indicates 0.04 changes. The ex-type strains are in bold and new isolates in blue bold.

Ascitendus aquaticus Dayar, Fryar & K.D. Hyde, sp. nov. Fig. 65

Index Fungorum number: IF554115; Facesoffungi number: FoF03926

Etymology – name reflects the host habitat aquatic environment.

Holotype – MFLU 18-0143

Saprobic on decaying wood submerged in freshwater. Sexual morph *Ascomata* 160–280 µm high, 135–190 µm diameter, solitary to gregarious, semi-immersed to superficial, black, coriaceous, globose to subglobose, ostiolate with a prominent neck, venter 150–230 × 195–240 µm. *Peridium* 25–45 µm wide, comprised of three layers: outer layer of pseudoparenchyma cells incorporated with dark brown amorphous material; middle layer of brown, thin-walled, laterally compressed, elongated cells; inner layer of hyaline, laterally compressed, elongated, hyaline cells. *Neck* 85–300 × 50–140 µm, central, cylindrical, periphysate, black at wall 2-layered, outer layer of dark brown, laterally compressed thin-walled cells incorporated with brown amorphous material, inner layer of laterally compressed thin-walled hyaline cells. *Hamathecium* paraphysate; paraphyses longer than asci, 160–210 µm long, 4–10 µm broad at base, septate. *Asci* 150–200 × 5–12 µm ($\bar{x}$ = 175.5 × 8 µm, n = 20), 8-spored, unitunicate, cylindrical, long pedicellate, with a prominent cylindrical to flaring apical ring, 2.5–3 × 3–3.5 µm wide at apex, 1–3 µm wide at the base, J$^-$. *Ascospores* 15–25 × 4–8 µm ($\bar{x}$ = 20 × 6 µm, n = 20), uniseriate, hyaline when immature, becoming brown, fusoid, straight to curved, 3-septate when mature, each cell with a single large guttule, slightly/not constricted at septa; septa prominent, smooth-walled, without appendages or a sheath. Asexual morph Undetermined.

Material examined – AUSTRALIA, North Queensland, Mulgrave River, S 17.17724, E 145.72374, on decaying wood submerged in a river, 14 April 2015, Sally Fryar and Ben Cawson, MR150 (MFLU 18-0143, holotype); *ibid.* (AD279865, isotype).

GenBank numbers – LSU: MG813820, SSU: MG813821.

Notes – The new species, *Ascitendus aquaticus*, best fits the genus *Ascitendus* in both morphology and receives phylogenetic support. It resembles *Ascitendus* by having globose to subglobose, ostiolate ascomata with a prominent neck, cylindrical to flaring apical ring and brown ascospores, with 3-prominent septa and each cell having a single large guttule. Our phylogenetic analysis indicates that *A. aquaticus* is closely related to *A. austriacus*, but with moderate support (78% ML, 70% MP, 1.00 PP) forming a separate lineage basal to *A. austriacus*. *Ascitendus aquaticus* can be clearly distinguished from *A. austriacus* by having smooth-walled ascospores, where the ascospore wall of *A. austriacus* are roughened in a striated pattern and ascospore end cells have small refractive dots at the ends. *Annulatascus velatisporus*, *Annulusmagnus triseptatus*, and *Ascolacicola aquatica* are also morphologically similar to *Ascitendus aquaticus*. However, *A. aquaticus* can be clearly distinguished from all these species by asci, ascospore nature and measurements as listed in Table 2.

Diaporthales Nannf.

For treatment of Diaporthales we follow Senanayake et al. (2017).

Cytosporaceae Fr.

Cytosporaceae was introduced by Fries (1823) as a family in Diaporthales (Wehmeyer 1975, Barr 1978, Eriksson 2001, Castlebury et al. 2002). Maharachchikumbura et al. (2015, 2016a) listed 13 genera under Cytosporaceae. Recently, Senanayake et al. (2017) excluded seven genera and accepted only five genera in Cytosporaceae as *Cytospora*, *Paravalsa*, *Pachytrype*, *Waydora* and *Xenotypa* based on morphological characteristics. In the study, we provide an updated tree and introduced two new species of Cytospora (Fig. 66).

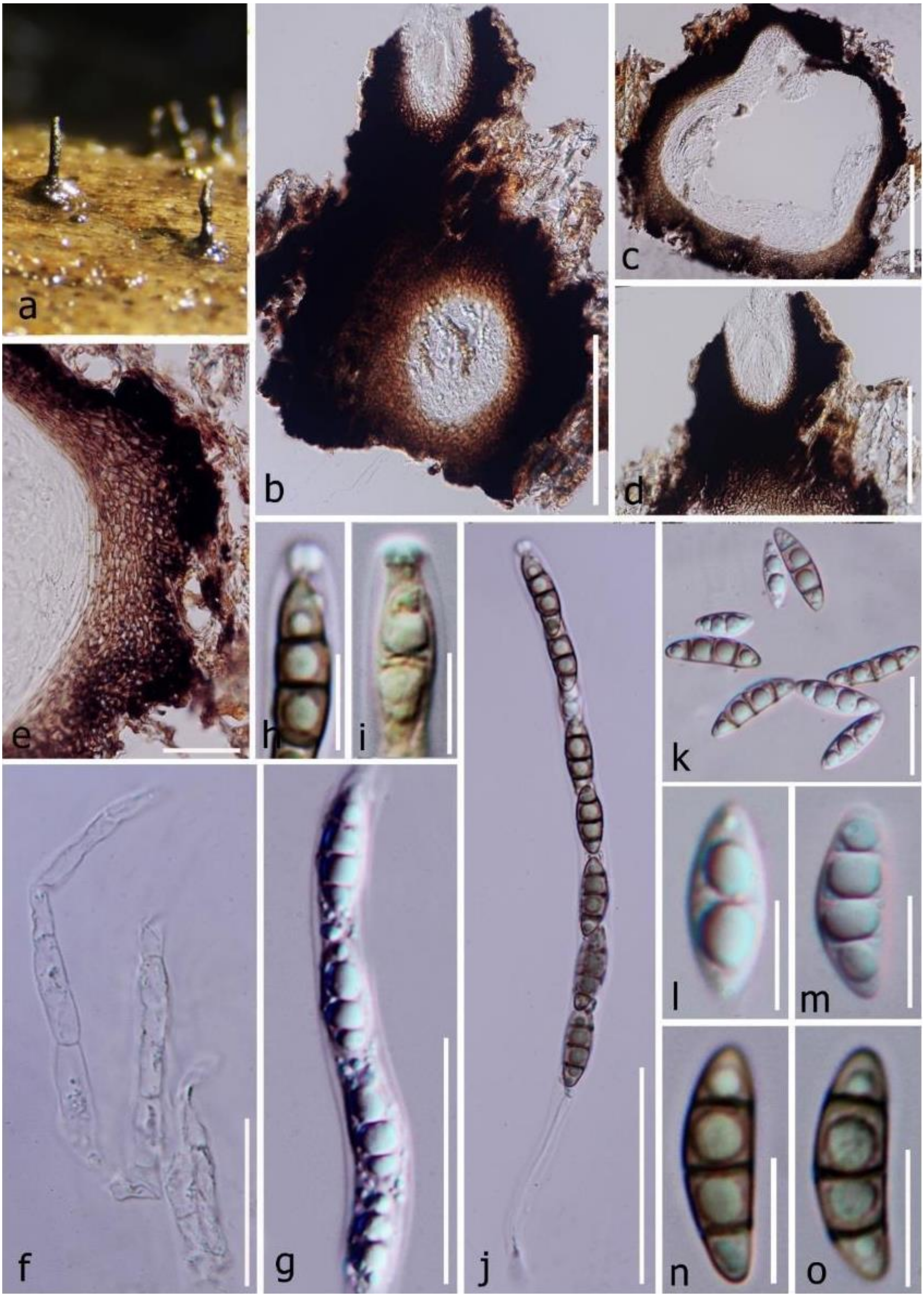


Figure 65 – *Ascitendus aquaticus* (MFLU 18-0143, holotype). a Ascomata on submerged wood. b, c Sections of ascomata. d Section through neck region. e Section through peridium. f Paraphyses g Part of an immature ascus. h Apical ring. i Apical ring in Melzer's reagent. J Mature ascus. k–o Ascospores. Scale bars: b, c = 50 µm, c–d, f, g, j, k = 20 µm, e, h, i, l–o = 10 µm.

Table 2 – Synopsis of the characteristics of *Ascitendus aquatica* and other related species.

Taxon	**Ascomata**	**Asci**	**Apical ring**	**Ascospores**	**Nature of end cells**	**Reference**
Annulatascus velatisporus	Globose to subglobose, 445–500 × 280–450 µm	Unitunicate, cylindrical, apically rounded, 224 –300 300 × 10.5 10.5–14 µm	J^{-}, 6–8 × 2–5 µm	Aseptate, fusiform, hyaline, thick, 19.5–28 × 8–12 µm	-	Dayarathne et al. (2016)
Annulusmagnus triseptatus	Oblate to suboblate to globose, venter 375–660 × 400–700 µm	Cylindrical, 138–283 × 7–14 µm	J^{-}, 2–4 × 3–5 µm, tapering 1–2 µm from top to bottom	3 septate, hyaline, multiguttulate, becoming pale straw-colored or pale brown with age, 16–37 × 5–10 µm	-	Campbell & Shearer, (2004)
Ascitendus austriacus	Globose to subglobose, venter 350–585 × 295–505 µm	Cylindrical, 100–160 × 4–6 µm	J^{-}, cylindrical to flaring, 2.5–3.5 µm long, 3.0–3.8 µm	3-septate, middle cells darker than outer cells, each cell with a single large guttule, wall roughened in a striated pattern, 4–27 × 4–9 µm	With small refractive dots at ends	Campbell & Shearer, (2004)
Ascitendus aquaticus	Globose to subglobose, 160–280 × 135–190 µm	Cylindrical, 150–200 × 5–12 µm	J-, cylindrical	Hyaline when immature becoming 3-septate at maturity, each cell with a single large guttule, smooth walled, 15–25 × 4–8 µm	Without small refractive dots at ends	In this study
Ascolacicola aquatica	Subglobose, 250–375 µm high, 225–275 µm	Cylindrical, 125–163 × 10–12.5 µm	J-, discoid, apical ring, 2.5–3.7 µm high, 6.2 µm	3-septate, brown 12.5–16. 4–7.5 µm	With hyaline to pale brown end cells	Ranghoo & Hyde (1998)

Cytospora Ehrenb.

Cytospora was introduced by Ehrenberg (1818), which causes canker and dieback disease on branches of a wide range of host and has a worldwide distribution (Adams et al. 2005, 2006, Norphanphoun et al. 2017a). Currently, there are 611 epithets for *Cytospora* (Index Fungorum 2018, 16 April 2018) with an estimated 110 species in Kirk et al. (2008). Norphanphoun et al. (2017a), Tibpromma et al. (2017), Senanayake et al. (2017) and Hyde et al. (2016, 2017b) provided a recent account of the genus with several new taxa.

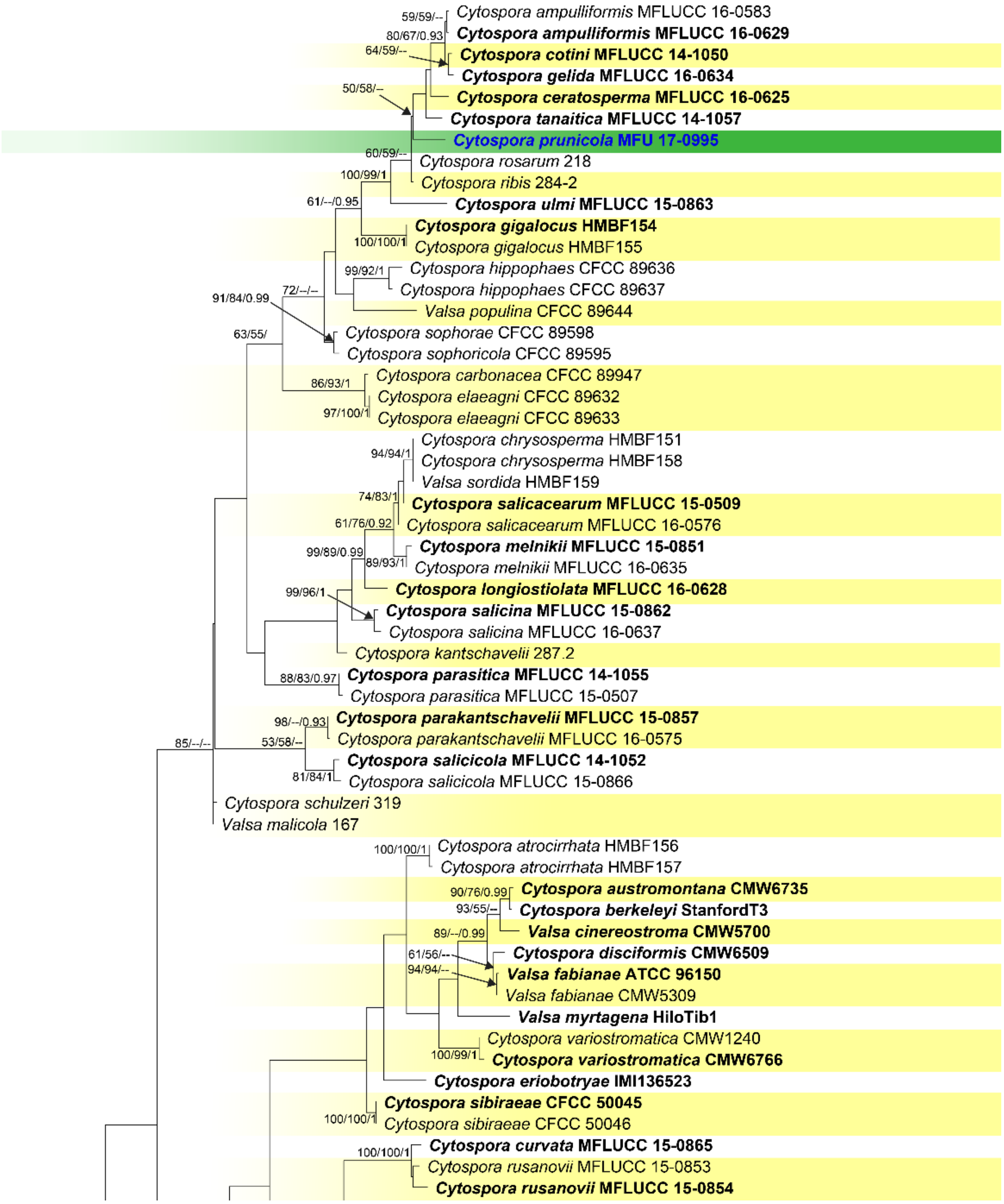


Figure 66 – Phylogram generated from maximum parsimony analysis based on combined ITS, LSU, RPB2 and ACT sequence data of *Cytospora* isolates with *Phomopsis vaccinii* (ATCC 18451) as the outgroup taxon. The newly generated nucleotide sequences were compared against the GenBank database using the Mega BLAST program. Related sequences were obtained from GenBank (http://www.ncbi.nlm.nih.gov/). Taxa selection was based on Norphanphoun et al. (2017a). Maximum parsimony and maximum likelihood bootstrap values ≥50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PP) are given at the nodes. The species obtained in this study are in blue and ex-types from the study are in blue bold. Ex-type taxa from other studies are in black bold.

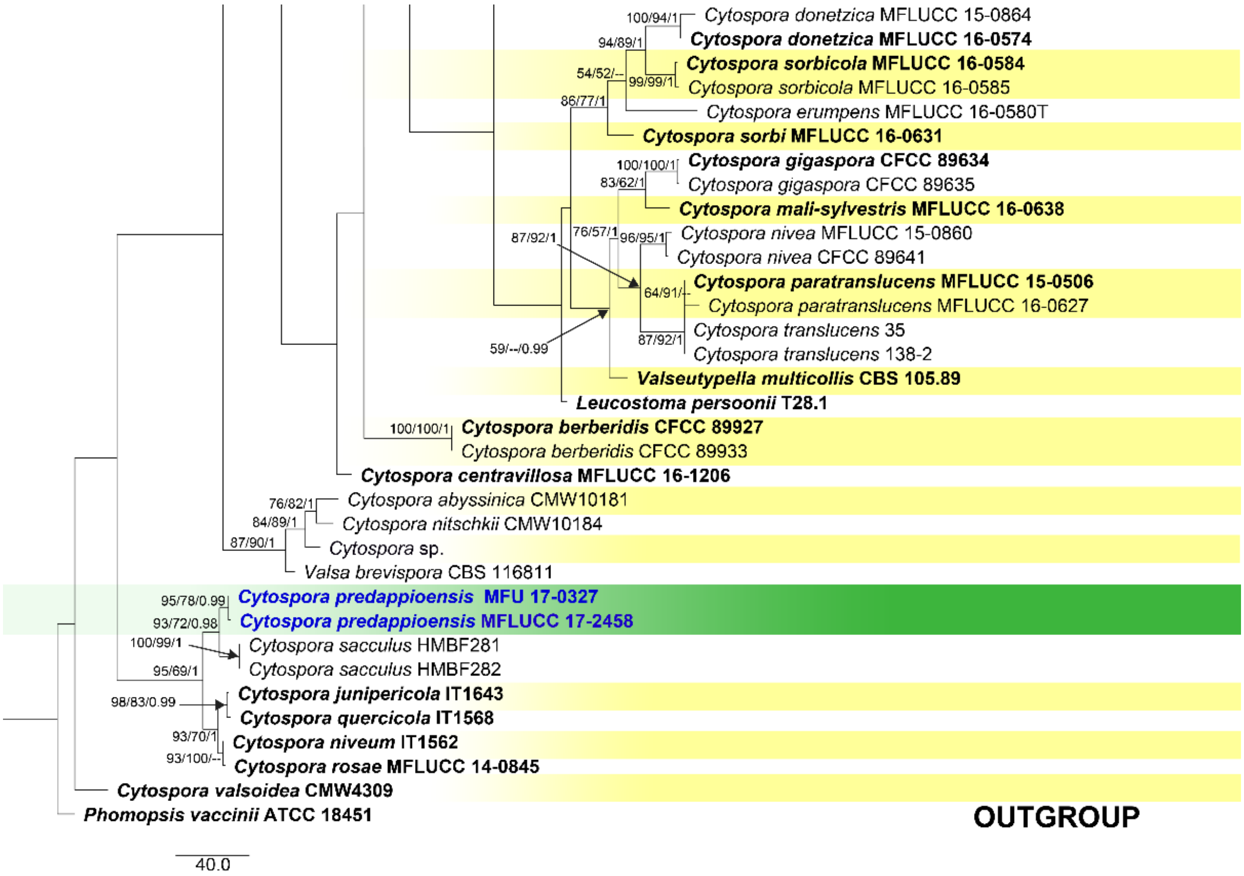


Figure 66 – Continued.

Cytospora predappioensis Q.J. Shang, Norphanph., Camporesi & K.D. Hyde, sp. nov. Fig. 67

Index Fungorum number: IF554083; Facesoffungi number: FoF03936

Etymology – the specific epithet "*predappioensis*'' refers to the town of *Predappio* in Italy from which the holotype was collected.

Holotype – MFLU 17-0323

Saprobic on dead branch of *Platanus hybrida*. Sexual morph *Stromata* 875–2685 µm wide, with poorly developed interior, solitary to gregarious, immersed, becoming raised to erumpent by ostiolar canal, dark brown to black, glabrous, circular to irregular in shape, arranged with conspicuous, clustered, roundish to cylindrical prominent ostioles in the centre. *Ascomata* (excluding necks) 240–480 µm high, 450–680 µm diameter ($\bar{x}$ = 365×567 µm, n = 10), perithecial, immersed in a stroma, dark brown to black, globose to subglobose, glabrous, with individual ostiolar neck. *Ostiole* 70–520 µm high, 100–150 µm diameter ($\bar{x}$ = 444 × 124 µm, n = 6), cylindrical, sulcate, periphysate. *Peridium* 25–45 µm wide, composed of two section layers, outer section comprising 5–7 layers, of relatively small, brown to dark brown, thick-walled cells, arranged in *textura angularis*, inner part comprising 3–5 layers of hyaline cells of *textura angularis*. *Hamathecium* 2.5–4 µm wide, dense, cylindrical, septate, hyaline, paraphyses. *Asci* (25–)32–42(–54) × (4.5–)5.5–8(–9.8) µm ($\bar{x}$ = 37 × 7.7 µm, n = 50), 8-spored, unitunicate, clavate, without stalks, apically rounded to truncate, with a J- apical ring. *Ascospores* (6.5–)8–10(–11) × (1–)1.5–3(–3.5) µm ($\bar{x}$ = 9 × 2 µm, n = 110), biseriate, hyaline, fusiform to oblong, aseptate, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Ascospores germinating on PDA within 12 hours. Germ tubes produced from all sides. Colonies on PDA reaching 2–2.5 cm diameter after 3 days at room temperature, colonies circular to irregular, medium dense, flat or effuse, slightly raised, with edge fimbriate, fluffy to fairy fluffy, white to gray from above, light yellow to green from below; not producing pigments in agar.

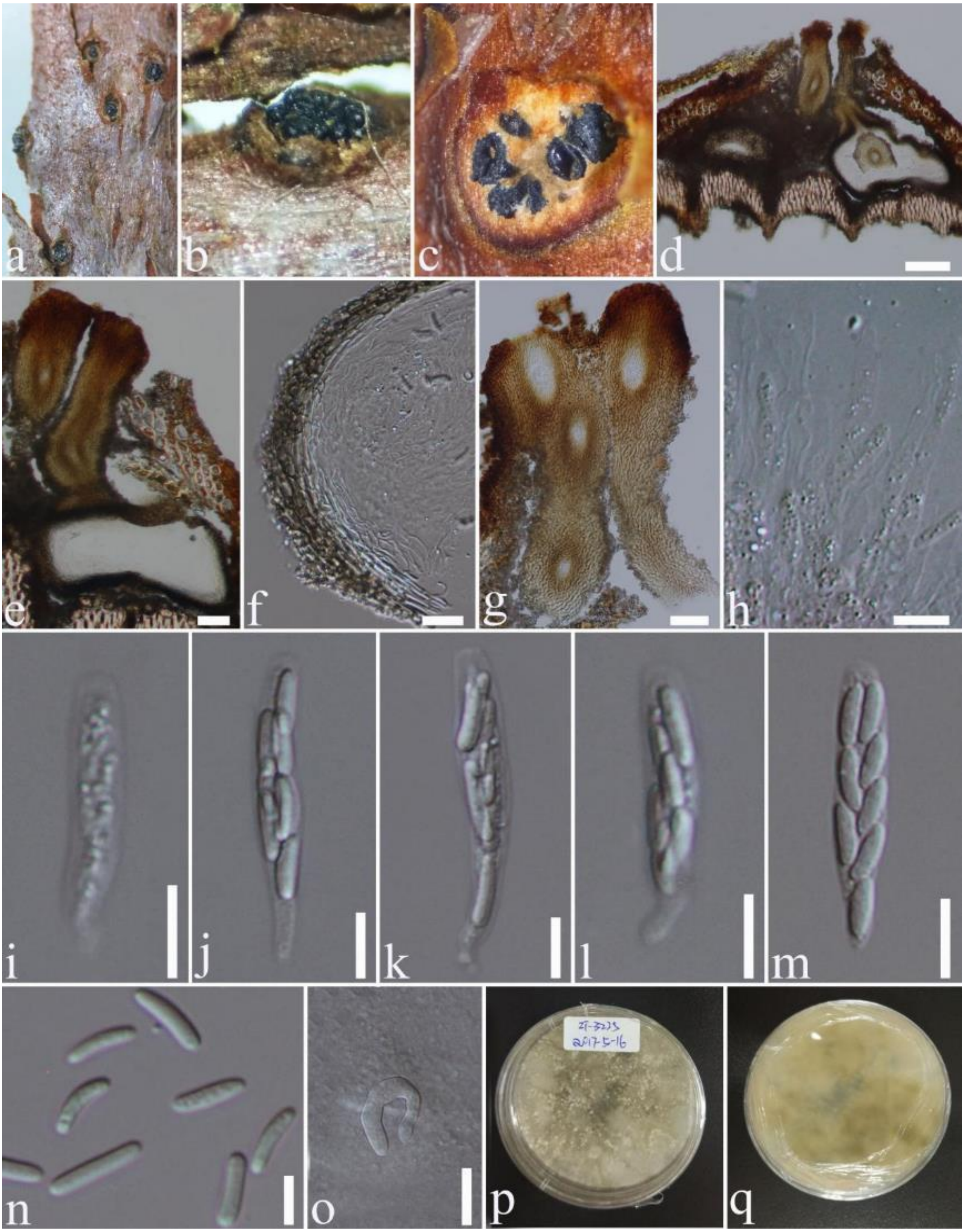


Figure 67 – *Cytospora predappioensis* (MFLU 17-0323, holotype). a Stromata on substrate. b Surface of fruiting bodies showing the black ostioles. c Transverse sections through stroma to show distribution of locules. d, e Longitudinal sections through stroma to show distribution of locules and ostiolar canal. f Peridium. g Ostiolar neck. h Paraphyses. i–m Asci. n Ascospores. o Germinating ascospore. p, q Culture characteristic on PDA after 7 days (p = colony from above, q = colony from below). Scale bars: d, g = 50 µm, e, f, o = 20 µm, h–m = 10 µm, n = 5 µm.

Material examined – ITALY, Province of Forlì-Cesena [FC], Massera, Predappio, on dead aerial branch of *Platanus hybrida*, 27 January 2017, E. Camporesi, IT 3225 (MFLU 17-0323, holotype), ex-type living culture, MFLUCC 17-2458, KUMCC 17-0328; *ibid.* (KUN-HKAS 100896, isotype).

GenBank numbers – MFLUCC 17-2458, ITS: MG873484, LSU: MG873480, SSU: MG873482.

Notes – Based on phylogenetic analyses and morphological comparison, our isolates belong to Cytosporaceae. Phylogenetic analyses of a combined sequence data, show that our taxon, *Cytospora predappioensis* (MFLUCC 17-2458 and MFLUCC 17-0327), forms a distinct lineage and shares a close relationship to *Cytospora sacculus* (Schwein.) Gvrit. (HMBF281 and HMBF282), with good-support (ML 93%, MP 73% and 0.98 PP) (Fig. 66). The morphology of stromata, ascomata, asci and ascospores of our isolate (Fig. 67), fits well with the description of the sexual morph of *Cytospora* (Adams et al. 2005, Fan et al. 2015, Norphanphoun et al. 2017a). Compared with *C. ceratosperma*, the sexual morph of *Cytospora sacculus*, the morphological characters of *C. predappioensis* are similar except for the ascospores sizes (Spielman 1985, 3–12 × 1–3 µm versus (6.5–)8–10(–11) × (1–)1.5–3(–3.5) µm, this study). However, given that our two isolates cluster together in a highly supported subclade and segregated from *C. sacculus*, there is ample evidence to justify a new species.

Cytospora prunicola Norphanph., Camporesi, T.C. Wen & K.D. Hyde, sp. nov. Fig. 68

Index Fungorum number: IF554078; Facesoffungi number: FoF04097

Etymology – named after the host, *Prunus* from which it was isolated.

Holotype – MFLU 17-0995

Associated with twigs and branches of *Prunus* sp. Sexual morph Undetermined. Asexual morph *Conidiomata* 500–1000 × 450–500 µm diameter, immersed in host tissue, scattered, erumpent, discoid, circular, with 2–4 locules, ostiolate. *Ostioles* 170–180 µm diameter, at the same level, with flattened top. *Peridium* comprising a few to several layers of cells of *textura angularis*, inner layer thick, brown, outer later dark brown. *Conidiophores* branched, reduced to conidiogenous cells. *Conidiogenous cells* blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. *Conidia* (4–)5.2–6.6 × 1.1–1.3(–1.6) µm ($\bar{x}$ = 5.5 × 1.3 µm, n = 30), unicellular, allantoid, slightly curved ends, hyaline, smooth-walled.

Material examined – ITALY, Province of Forlì-Cesena [FC]), Pieve di Rivoschio - Bagno di Romagna, on dead land branch of *Prunus* sp., 30 April 2017, E. Camporesi, IT3337 (MFLU 17-0995, holotype); *ibid.* (PDD, isotype).

GenBank numbers – ACT: MG742353, ITS: MG742350, LSU: MG742351, RPB2: MG742352, TEF1: MG742354.

Notes – *Cytospora* species are important plant pathogens causing dieback and canker diseases on a wide range of hosts, such as *Prunus* sp. Norphanphoun et al. (2017a) found eleven species of *Cytospora* on *Prunus* sp. with species identifications confirmed with molecular data. In this study, the new species has immersed, 2–4-loculate conidiomata with ostioles and unicellular conidia. *Cytospora prunicola* is most similar to *C. sorbicola* Norphanph. et al. and *C. ulmi* Norphanph. et al. in conidial size (5.6 × 1.5, 5.4 × 1.4 respectively) (Norphanphoun et al. 2017a). However, *C. sorbicola* differs from C. *prunicola* in having 1–2 loculate conidiomata with unbranched conidiophores (Norphanphoun et al. 2017a). Phylogenetic analyses using a combined ITS, LSU, RPB2 and ACT sequence dataset indicate that *C. prunicola* constitutes a moderately supported independent lineage (Fig 66) and hence can be distinguished from *C. sorbicola* and *C. ulmi* and other species. Therefore, we introduce *C. prunicola* as a new species from *Prunus* in Italy.

Diaporthaceae Höhn. ex Wehm.

Diaporthaceae was established by Wehmeyer (1926). This family is characterized by globose or compressed, coriaceous, black ascomata with 0–1-septate, ellipsoid to fusoid ascospores and

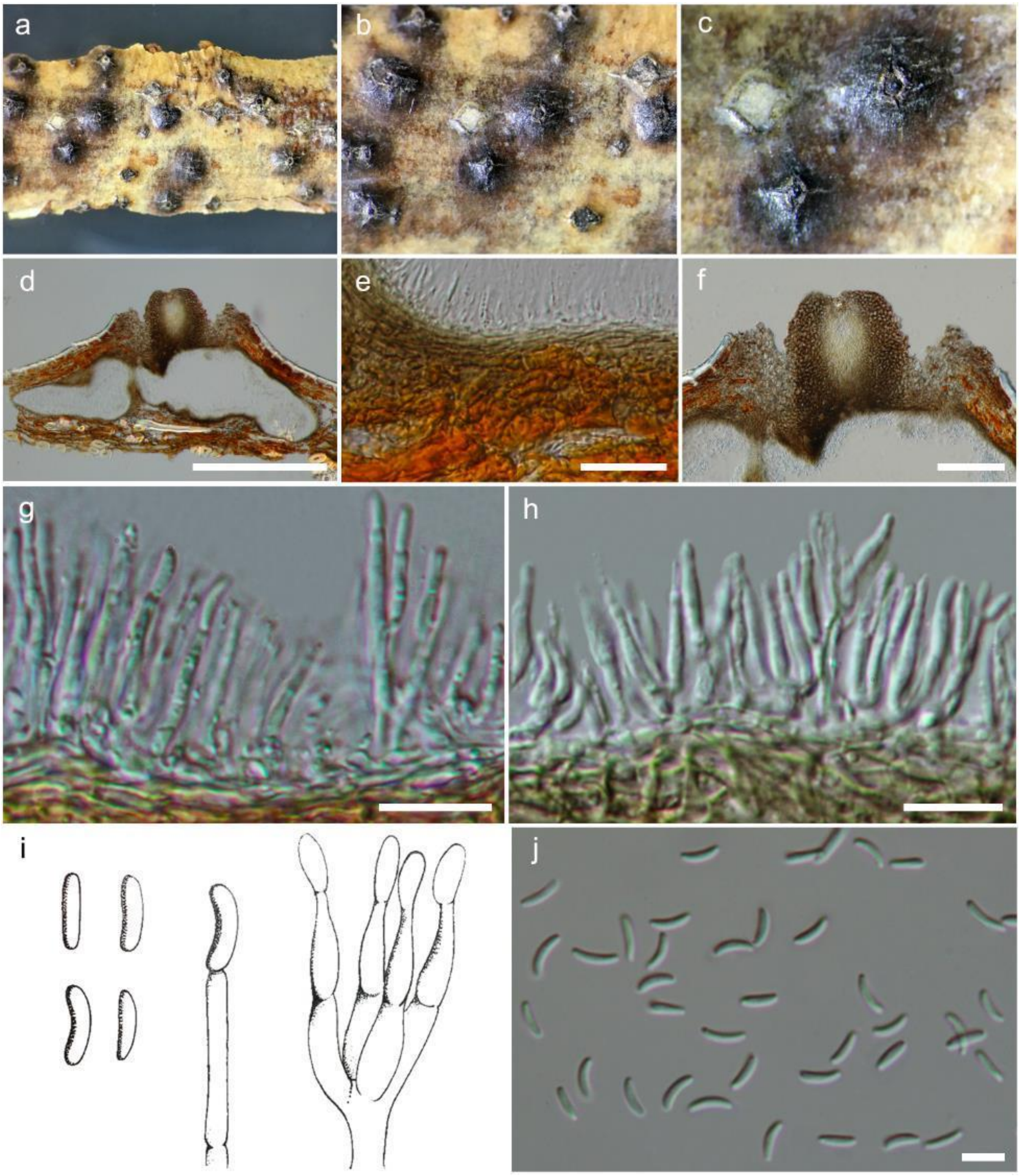


Figure 68 – *Cytospora prunicola* (MFLU 17-0995, holotype). a Stromatal habit in wood. b Fruiting bodies on host surface. c Surface of fruiting bodies showing the black ostioles. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–h Conidia attached to conidiogenous cells. i Morphology drawing. j Conidia. Scale bars: d = 400 µm, f = 100 µm, e, g–h = 10 µm, j = 5 µm.

aseptate, variously coloured conidia (Maharachchikumbura et al. 2016a, Gao et al. 2017). Diaporthaceae was transferred to Valsaceae as a synonym (Barr 1978). However, Castlebury et al. (2002) showed that Diaporthaceae taxa could be distinguished from others in Diaporthales based on phylogenetic (2002) showed that Diaporthaceae taxa could be distinguished from others in Diaporthales based on phylogenetic analyses of rDNA LSU sequence data. Senanayake et al. (2017) listed *Allantoporthe*,*Apioporthella*, *Chaetoconis*, *Chiangraiomyces*, *Diaporthe*, *Hyaliappendispora*, *Leucodiaporthe*, *Mazzantia*, *Ophiodiaporthe*, *Paradiaporthe*, *Phaeocytostroma*, *Phaeodiaporthe*, *Pustulomyces* and *Stenocarpella* as members in this family based on multi-gene analysis and morphology. In this study, we introduce two new species, *Diaporthe subellipicola* and *D. subcylindrospora*, collected in China. The novel species are described morphologically and selected phylogenetic datasets from Dissanayake et al. (2017) and Gao et al. (2017) are used to determine its phylogenetic affinity with other species.

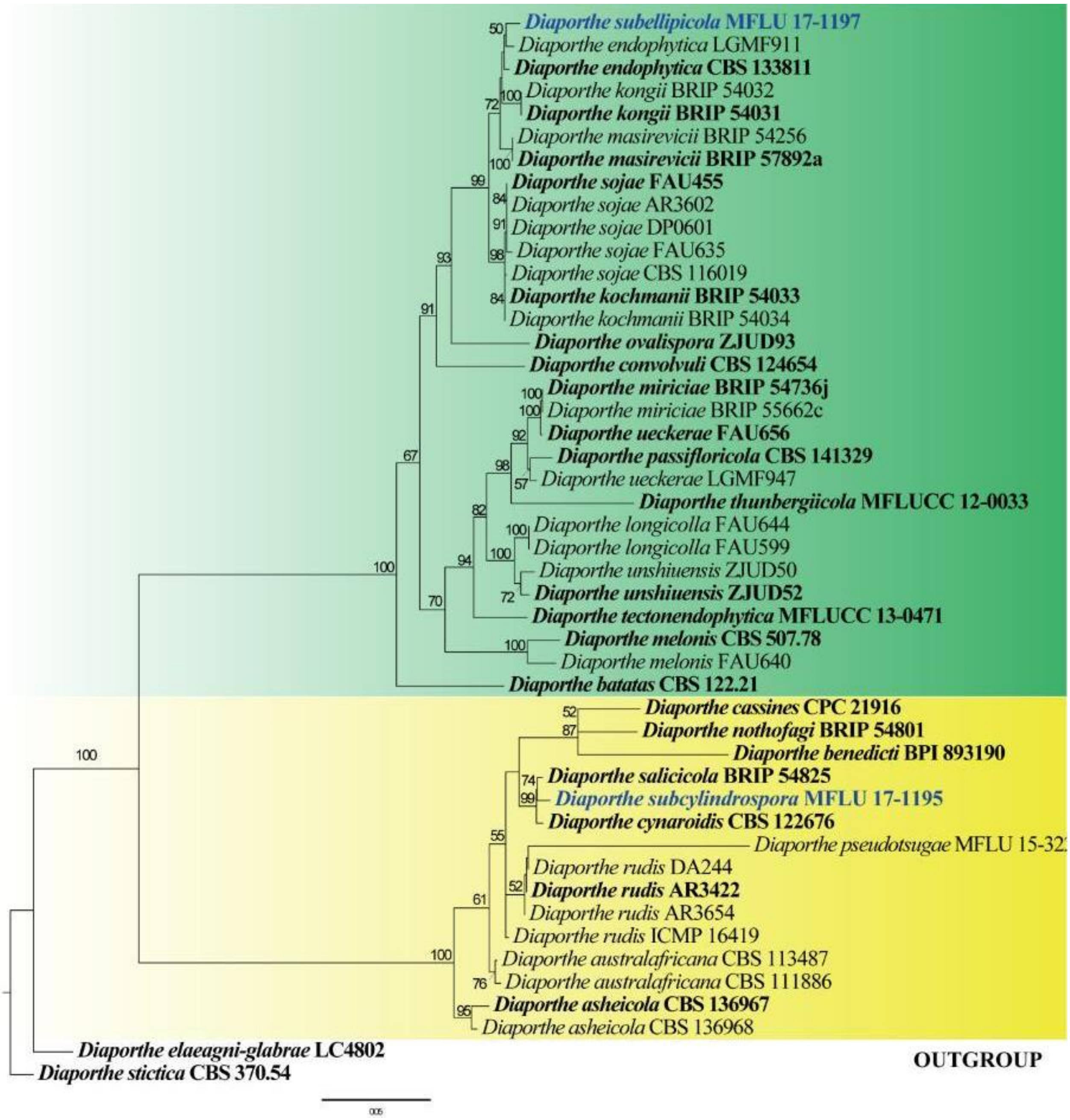


Figure 69 – Maximum likelihood phylogenetic tree generated from analysis of a combined ITS, TEF and TUB sequences dataset for 47 taxa of *Diaporthe* with *Diaporthe elaeagni-glabrae* and *D. stictica* as the outgroup taxa. ML support values greater than 50% and a best scoring tree with a final optimization likelihood value of -7531.270123 is indicated above the nodes. The strain numbers are noted after the species names. Ex-type strains are indicated in bold.

Diaporthe Nitschke

Diaporthe was introduced by Nitschke (1870) with *Diaporthe eres* as the type species. Species of *Diaporthe* are well-known as pathogens, endophytes or saprobes on a diverse range of host plants (Uecker 1988, Santos et al. 2011, Hyde et al. 2014, Udayanga et al. 2014a, b, 2015). The genus is characterized by black to brown ascomata with hyaline to brown, ovoid to ellipsoid ascospores and hyaline conidia (Dissanayake et al. 2017, Gao et al. 2017, Senanayake et al. 2017).

Diaporthe subellipicola S.K. Huang, T.C. Wen & K.D. Hyde, sp. nov. Fig. 70

Index Fungorum number: IF554076; Facesoffungi number: FoF03855

Etymology – the name *subellipicola* refers to the ellipsoid spores.

Holotype – MFLU 17-1197

Saprobic on dead straw. Sexual morph *Ascomata* 245–280 µm diameter, scattered, immersed, eventually the neck erumpent, unilocular, globose to subglobose, black. *Neck* about 2 mm long, central, lined with periphyses. *Peridium* 15–25 *µm* diameter, membranaceous, composed of brown to hyaline cells of *textura angularis*. *Asci* 48–65 × 10–15 µm ($\bar{x}$ = 57 × 13 µm, n = 20), 8-spored, unitunicate, clavate, without pedicel, rounded at the apex, with a conspicuous refractive apical ring. *Ascospores* 10–18 × 2–6 µm ($\bar{x}$ = 13 × 4 µm, n = 50), ellipsoid, hyaline, 0–1-septate, the apical cell swellom, slightly constricted at the septum at maturity, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diameter after 7 days at room temperature (~ 25 °C), circular, brown from above and reverse, with filamentous mycelium, filiform at the margin, with rough surface and raised elevation.

Material examined – CHINA, Yunnan Province, Songming City, on dead wood, 21 December 2016, S.K. Huang (MFLU 17-1197, holotype), ex-type living culture, KUMCC 17-0153; *ibid.* (HKAS99560, isotype).

GenBank numbers – β-tubulin: MG746634, ITS: MG746632, TEF1: MG746633.

Notes – Phylogenetic analysis of ITS, *TEF* and *TUB* sequence dataset indicates that *Diaporthe subellipicola* belongs to *Diaporthe* (Fig. 69). *Diaporthe subellipicola* is closely related to *D. endophytica*, an asexual species (Thompson et al. 2011, Gomes et al. 2013), but with weak bootstrap support. Unfortunately, we could not obtain the asexual morph of *D. subellipicola* for any further morphological comparison. The endophytic lifestyle of *D. endophytica* from *Maytenus* spp. and *Schinus* spp., distributed in Brazil (Gomes et al. 2013) is different from our species, which is a saprobe. Futher, comparison of the 544 bp across the ITS1-5.8S-ITS2 regions also reveals that there are 5 bp (1%) differences when compared to *D. endophytica* (LGMF911). In the same way, comparison of 712 bp of *TUB* region reveals 8 bp (1.2%) difference compared to *D. endophytica* (LGMF911).

Diaporthe subcylindrospora S.K. Huang, T.C. Wen & K.D. Hyde, sp. nov. Fig. 71

Index Fungorum number: IF554077; Facesoffungi number: FoF03854

Etymology – the name *subfusispora* refers to the subcylindrospora spores.

Holotype – MFLU 17-1195

Saprobic on dead branch of *Salix*. Sexual morph *Ascomata* 390–395 µm diameter, scattered to gregarious, immersed, eventually the neck erumpent, unilocular, globose to subglobose, black. *Neck* about 1 mm long, central, lined with periphyses. *Peridium* 45–65 *µm* diameter, membranaceous, composed of brown to hyaline cells of *textura angularis*. *Asci* 52–55 × 7–10 µm ($\bar{x}$ = 55 × 9 µm, n = 20), 8-spored, unitunicate, cylindrical, without pedicellate, rounded at the apex, with a conspicuous refractive apical ring. *Ascospores* 10–15 × 2–4 µm ($\bar{x}$ = 12 × 3 µm, n = 50), fusiform, hyaline, 0–1-septate, slightly constricted at the septum at maturity, smooth-walled. Asexual morph Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diameter after 7 days at room temperature (25 °C), circular, pale brown from above and reverse, with filamentous mycelium, filiform at margin, with rough surface and raised elevation.

Material examined – China, Yunnan Province, Dali City, on dead branch of *Salix*, 21 December 2016, S.K. Huang (MFLU 17-1195, holotype), ex-type living culture KUMCC 17-0151; *ibid.* (HKAS 99547, isotype).

GenBank numbers – β-tubulin: MG746631, ITS: MG746629, TEF: MG746630.

Figure 70 – *Diaporthe subellipicola* (MFLU 17-1197, holotype). a Material. b Ascomata on host. c Appearance of ascomata on host. d Ascoma in vertical section. e Squashed neck with light brown apex. f Peridium. g–j Asci. k–n Ascospores. Scale bars: d–e = 100 µm, f = 50 µm, g–j = 20 µm, k–n = 10 µm.

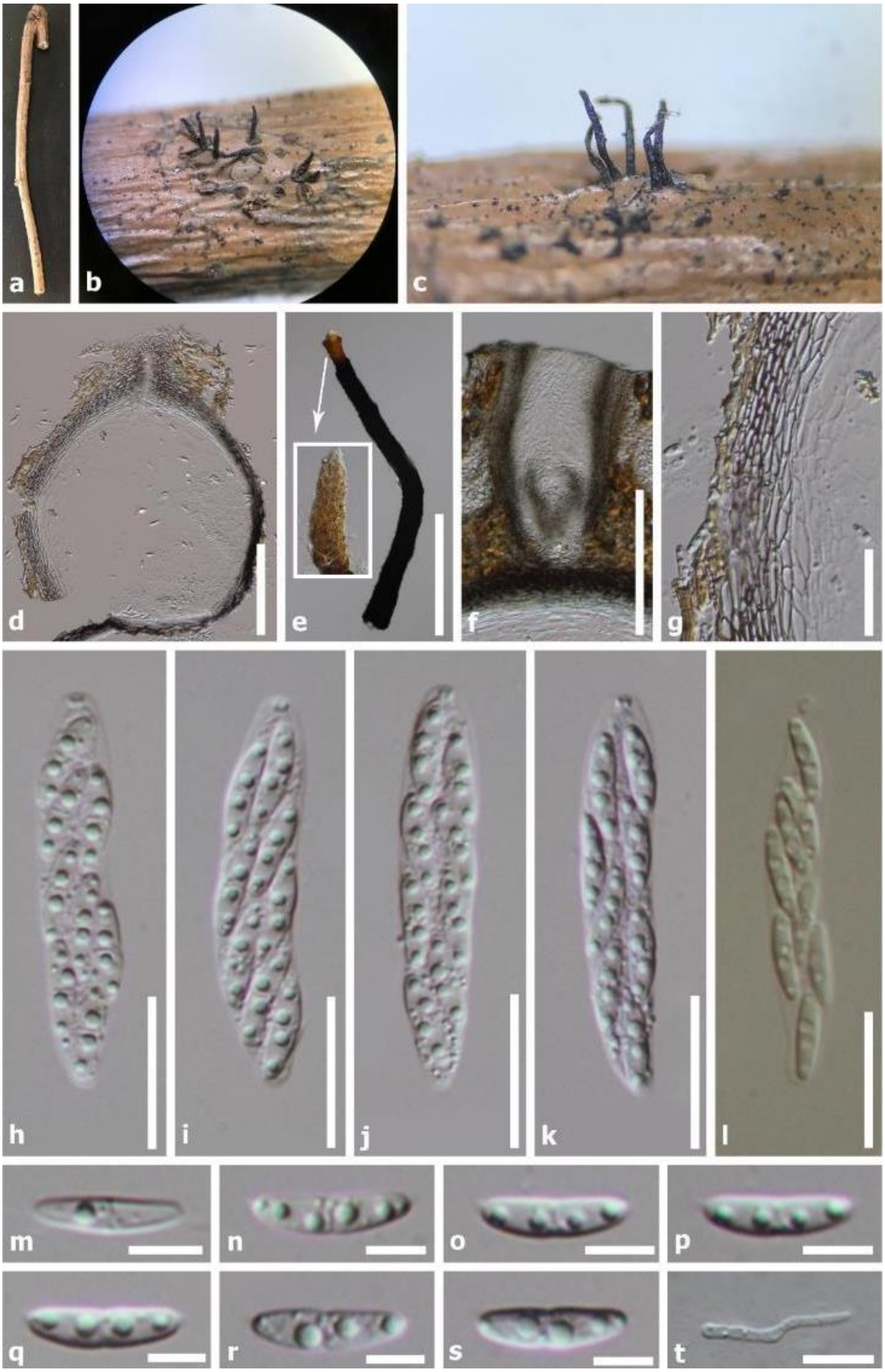


Figure 71 – *Diaporthe subcylindrospora* (MFLU 17-1195, holotype). a Herbarium material. b Ascomata on host. c Appearance of ascomata on host. d Ascoma in vertical section. e Squashed neck with light brown apex. f Peridium of neck with periphyses. g Peridium. h–l Asci (l: stained in Melzer's reagent). m–s Ascospores. t Germinating ascospores. Scale bars: e = 500 µm, d, f = 100 µm, g–l, t = 20 µm, m–s = 5 µm.

Notes – Phylogeny positions our new taxon in a moderately supported subclade (74%) with *D. salicicola*, an asexual species (Fig. 69). A close phylogenetic affinity to *D. cynaroidis* is also noted. The asexual morph of *D. cynaroidis* was isolated from *Protea* in South Africa (Gomes et al. 2013) and *D. salicicola* was isolated from *Salix* in Australia (Tan et al. 2013). However, the sexual morph of *Diaporthe subcylindrospora* was found from *Salix* in China. We noted a 6 bp (1.1%) difference across the 560 bp nucleotides of the ITS regions and 8 bp (1.7%) difference across the 484 bp of *TUB* region compared to *D. salicicola*. *Diaporthe subcylindrospora* is introduced as a new species.

Diaporthomycetidae families incertae sedis

Barbatosphaeriaceae H. Zhang et al.

The family was established by Zhang et al. (2017a) with the type genus *Barbatosphaeria* Réblová. It currently comprises three genera, namely *Barbatosphaeria*, *Ceratostomella* and *Xylomelasma*, which share similar characters in having dark, long-necked, astromatic ascomata, mostly surrounded by sparse mycelia, clavate asci, arising from ascogenous hyphae and mostly ellipsoidal ascospores (Zhang et al. 2017a). Based on phylogenetic analysis, Zhang et al. (2017a) placed this family in Diaporthomycetidae families *incertae sedis*. In the study, we provide an updated tree for the family and introduce a new species, *Barbatosphaeria aquatica*, characterised by different asexual form.

Barbatosphaeria Réblová

The genus *Barbatosphaeria* was introduced by Réblová (2007) for *Calosphaeria barbirostris* (Fr.) Ellis & Everh. based on cultivation experiments, revision of the herbarium material and phylogenetic analysis. It is characterized by dark ascomata with long decumbent necks and ellipsoid to oblong, hyaline, septate ascospores in unitunicate, clavate asci with a non-amyloid apical ring (Réblová 2007, Réblová et al. 2015, Zhang et al. 2017a). Réblová (2007) placed the genus in the Sordariomycetes *incertae sedis* based on LSU sequence data. Réblová et al. (2015) revised taxonomy of the genus and expanded it to include nine species. Zhang et al. (2017a) studied Annulatascaceae-like taxa. *Barbatosphaeria* was accommodated in a new family Barbatosphaeriaceae, along with *Ceratostomella* and *Xylomelasma*. The known asexual morphs are Ramichloridium- and Sporothrix-like taxa (Réblová 2007, Réblová et al. 2015, Zhang et al. 2017a).

Barbatosphaeria aquatica N.G. Liu & K.D. Hyde, sp. nov. Fig. 73

Index Fungorum number: IF554085; Facesoffungi number: FoF 03937

Etymology – with reference to the habitat of this fungus.

Holotype – MFLU 18-0040

Saprobic on decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* on natural substrate superficial, effuse, dark brown to black, velvety. *Mycelium* immersed, composed of septate, branched, medium brown, 1.5–3 µm wide hyphae. *Conidiophores* 70–100 µm long, 4–6 µm wide at base, 1.5–2.2 µm wide at apex, mononematous, erect, straight or broadly curved, greenish-brown to brown, smooth-walled, 4–6-septate, thick-walled, unbranched. *Conidiogenous cells* 10–15 µm long, monoblastic, terminal, integrated, medium brown, smooth-walled. *Conidia* 20–27 × 10–17 µm ($\bar{x}$ = 22.22 × 13.29 µm, n = 13), solitary, dry, clavate, green to greenish-brown, with 3–4 transverse septa, deeply constricted at the septa, distinctly verruculose, with 1–2 basal cells subhyaline to pale brown, smooth-walled and appressed at the upper half.

Culture characteristics – Conidia germinated on WA (Water Agar) within 24 hours. One germ tube produced from the basal cell. Colonies reaching about 5 cm diameter after 10 days on PDA at 25 °C. Mycelia superficial, initially white, later becoming brown to dark brown, hairy, effuse with the entire edge; reverse dark brown at center, light brown towards margin.

Material examined – THAILAND, Chiang Rai Province, Muang, Ban Nang Lae Nai, on decaying wood submerged in a freshwater stream, 31 December 2016, Ningguo Liu, CR004 (MFLU 18-0040, holotype); ex-type living culture MFLUCC 18-0356.

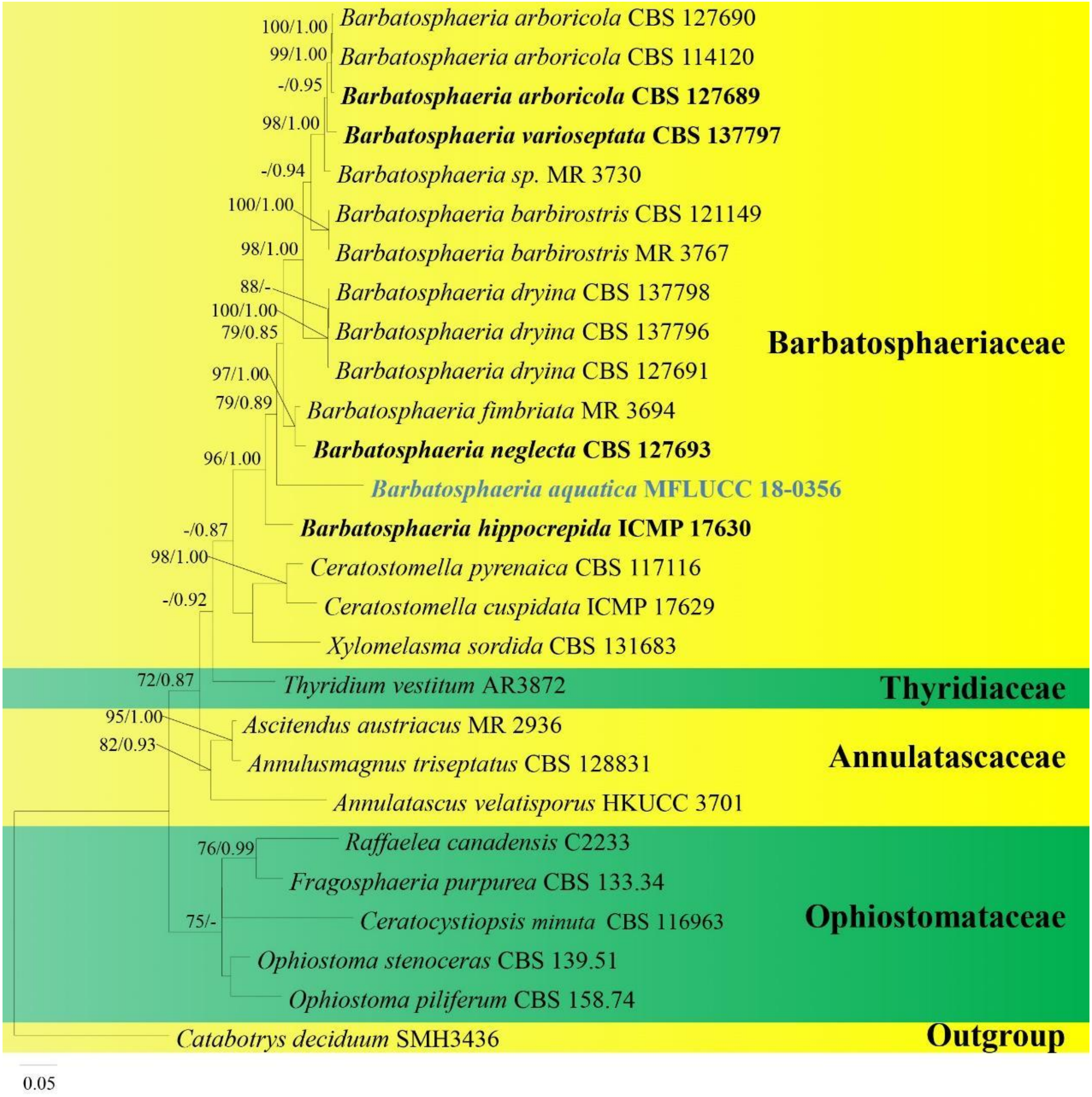


Figure 72 – Maximum likelihood (RAxML) tree based on analysis of a combined dataset of ITS and LSU sequence data representing four families in Sordariomycetes. Related sequences were obtained from GenBank. Twenty-seven stains are included in the analyses, which comprise 1526 characters including gaps. Tree topologies are similar between ML and BI analyses. The tree is rooted with *Catabotrys deciduum* SMH3436. The best scoring RAxML tree with a final likelihood value of -7652.009089 is presented. The matrix had 565 distinct alignment patterns, with 24.34% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244210, C = 0.246103, G = 0.294155, T = 0.215533; substitution rates AC = 0.912854, AG = 1.825402, AT = 1.503492, CG = 1.089820, CT = 5.670850, GT = 1.000000; gamma distribution shape parameter α = 0.470150. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.80 are given near nodes. The scale bar indicates 0.05 changes. The ex-type strains are indicated in bold and the new isolate is in bold and blue.

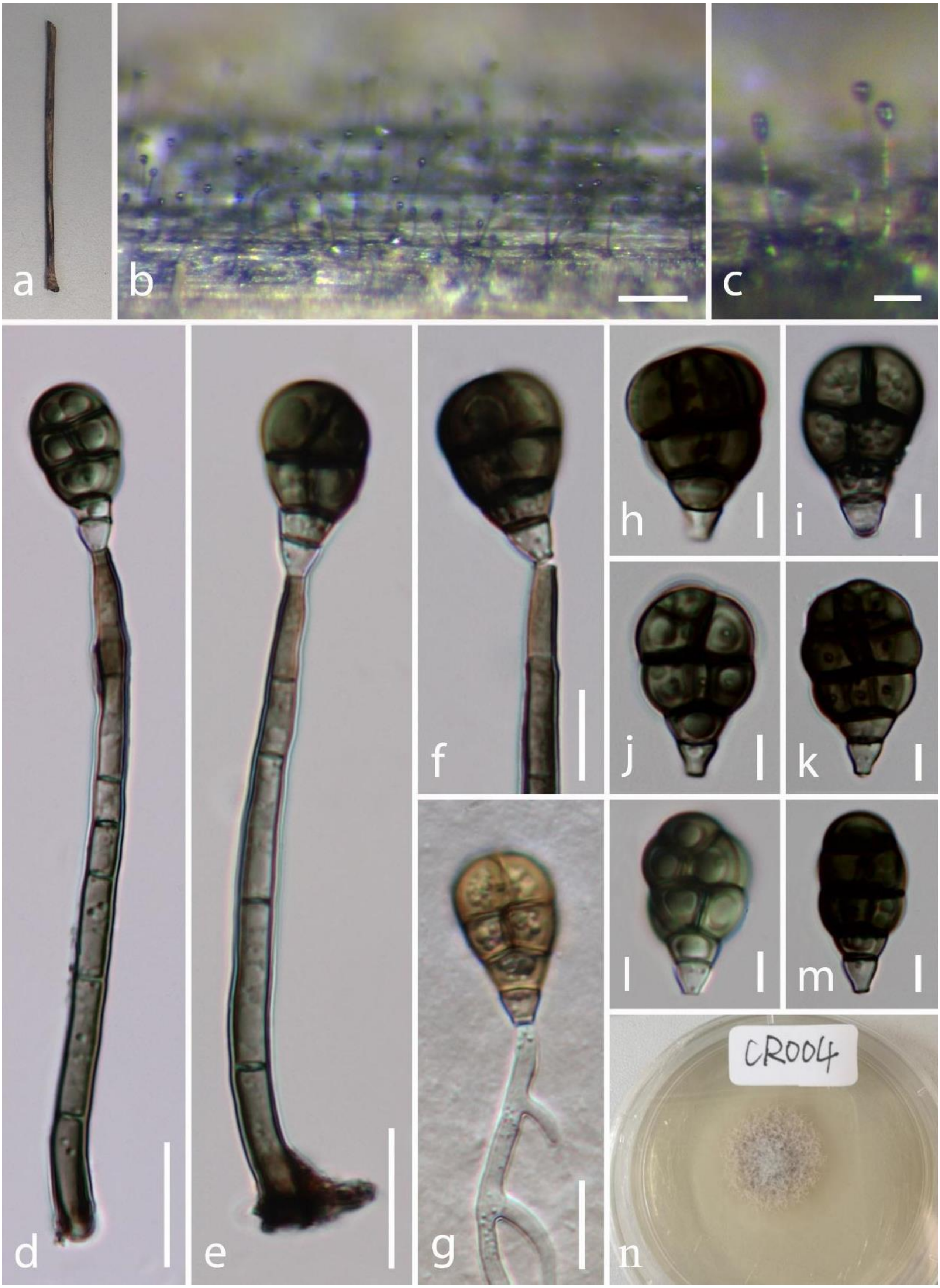


Figure 73 – *Barbatosphaeria aquatica* (MFLU 18-0040, holotype). a Specimen. b, c Colonies on substrate. d, e Conidiophores and conidia. f Conidiogenous cell and conidium. g Germinated spore. h–m Conidia. n Colony on PDA media. Scale bars: b = 100 µm, c–e = 15 µm, f, g = 10 µm, h–m = 5 µm.

GenBank numbers – ITS: MG835711, LSU: MG835712.

Notes – The asexual morphs of this genus are dematiaceous hyphomycetes with blastic denticulate conidiogenesis and resemble *Ramichloridium* and *Sporothrix* (Réblová 2007). In this study, a new asexual morph is accommodated in this genus. Unlike the other morphs, which have ellipsoidal conidia with a hilum in *Ramichloridium* (Arzanlou et al. 2007) and tear-shaped conidia on small, clustered denticles in *Sporothrix* (Zhou et al. 2014), the present asexual morph has clavate, green to greenish-brown conidia with several transverse and longitudinal septa. Despite the differences in morphology, the new strain formed a distinct clade in the genus *Barbatosphaeria* with 79% ML bootstrap and 0.89 Bayesian PP support. Thus, a new species is introduced based on both morphology and phylogenetic studies.

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

The family Nectriaceae is characterized by uniloculate ascomata that are white, yellow, orange-red or purple. They are associated with phialidic asexual morphs producing amerosporous to phragmosporous conidia (Rossman et al. 1999, Rossman 2000). Nectriaceae includes 55 genera and approximately 900 species (Index Fungorum 2018, Wijayawardene et al. 2018). The majority of these species are soil-borne saprobes or weak to virulent, facultative or obligate plant pathogens, while some are facultatively fungicolous or insecticolous (Rossman et al. 1999, Rossman 2000, Schroers et al. 2011). Several species have been reported as important opportunistic pathogens of humans (Chang et al. 2006, Guarro 2013), while others produce mycotoxins of medical concern (Rossman 1996). In this study, we introduce a new *Gliocladiopsis* species based on phylogenetic and morphological evidence.

Gliocladiopsis S.B. Saksena

The genus *Gliocladiopsis* was introduced by Saksena (1954) based on the type species *G. sagariensis* S.B. Saksena that had penicillate conidiophores resembling *Penicillium* and *Gliocladium*. Crous & Wingfield (1993) resurrected *Gliocladiopsis* to accommodate species characterized by dense, penicillate conidiophores, which unlike *Cylindrocladiella* and *Calonectria*, lacked sterile stipe extensions. The taxonomic status of *Gliocladiopsis* was re-evaluated by Lombard & Crous (2012) based on multi-gene phylogeny. Liu & Cai (2013) introduced a new *Gliocladiopsis* species, *G. guangdongensis*, which was the first isolation from a freshwater habitat. Species of *Gliocladiopsis* are difficult to distinguish morphologically as the branching structure of conidiophores as well as the size and shape of conidia, are similar between species (Liu & Cai 2013, Parkinson et al. 2017). Currently *Gliocladiopsis* contains 13 species, namely, *G. curvata*, *G. elghollii*, *G. forsbergii*, *G. guangdongensis*, *G. indonesiensis*, *G. irregularis*, *G. mexicana*, *G. peggii*, *G. pseudotenuis*, *G. sagariensis*, *G. sumatrensis*, *G. tenuis* and *G. whileyi* (Lombard & Crous 2012, Liu & Cai 2013, Parkinson et al. 2017). In this paper, we introduce a new *Gliocladiopsis* species, *G. aquaticus*, based on multi-gene phylogenetic analyses, which is the second taxon from freshwater habitat.

Gliocladiopsis aquaticus Y.Z. Lu, R.H. Perera & K.D. Hyde, sp. nov. Fig. 75

Index Fungorum number: IF554048; Facesoffungi number: FoF03893

Etymology – '*aquaticus*' referring to aquatic habitat of this fungus.

Holotype – MFLU 17-1976

Saprobic on submerged decaying wood in a lake. Sexual morph Undetermined. Asexual morph appearing as white masses on the substrate, becoming yellowish with age. *Conidiophores* penicillate, 100–140 × 4–6.5 µm, without stipe extensions and terminal vesicles. *Conidiogenous apparatus* with several series of hyaline branches: primary branches 19–26 × 3.5–4.5 µm, aseptate; secondary branches 15–25 × 3–4 µm, aseptate; tertiary branches 8–15 × 2–3.5 µm, aseptate; phialides doliiform to cymbiform to cylindrical, 11–19 × 2–3 µm, arranged in terminal whorls of 2–

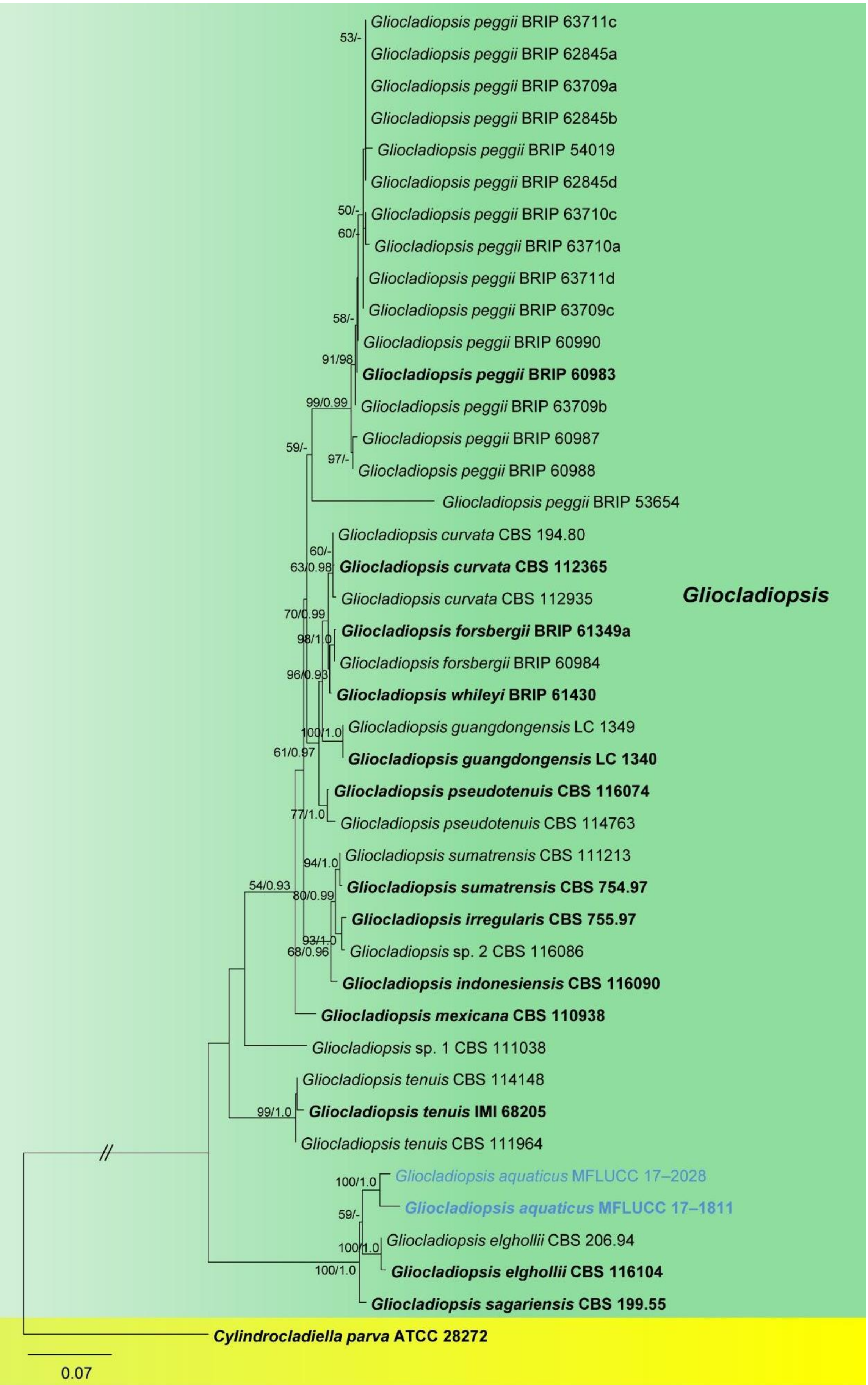


Figure 74 – Phylogenetic tree generated by maximum likelihood analysis of the combined ITS, β-tub and H3 dataset of *Gliocladiopsis* species. Related sequences were obtained from GenBank.

Fourty-two strains are included in the analyses, which comprises 1697 characters including gaps. The tree is rooted with *Cylindrocladiella parva* (ATCC 28272). Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of - 5668.766010 is presented. The matrix had 381 distinct alignment patterns, with 5.77% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.219613, C = 0.322518, G= 0.235367, T = 0.222502; substitution rates AC = 0.926729, AG = 1.749796, AT = 0.794257, CG = 0.329025, CT = 3.846114, GT = 1.000000; gamma distribution shape parameter α = 0.177707. RAxML bootstrap support values greater than 50% (BT) (before the forward slash) and Bayesian posterior probabilities greater than 0.90 (PP) (after the forward slash) are shown near the nodes. The ex-type strains are in bold and new isolates in blue.

6 per branch, with minute collarettes, central phialide frequently extending above the rest. *Conidia* cylindrical, 16.5–21 × 2–3 µm ($\bar{x}$ = 19 × 2.5 µm, n = 50), hyaline, smooth with rounded ends, straight, aseptate to 1-septate.

Culture characteristics – Conidia germinating on water agar (WA) within 8 hours. Colonies growing on PDA, circular, with flat surface, edge entire, reaching 36 mm within 2 weeks at 28 °C, white to pale brown, mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth-walled.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on submerged decaying wood in a freshwater lake, 19 February 2017, Yong-Zhong Lu, MFU07 (MFLU 17-1976, holotype); ex-type living culture, MFLUCC 17-1811, TBRC; MFU08 (MFLU 17-1977, paratype); living culture, MFLUCC 17-2028.

GenBank numbers – MFLUCC 17-1811 – β-tubulin: MG574421, Histone3: MG734182, ITS: MG543924, LSU: MG543915, SSU: MG543918; MFLUCC 17-2028 – β-tubulin: MG574422, Histone3: MG734183, ITS: MG543925, LSU: MG543916, SSU: MG543919.

Notes – *Gliocladiopsis aquaticus* is morphologically similar to *Gliocladiopsis elghollii* in conidiophores and conidia but can be distinguished from *G. elghollii* by its smaller conidia (16.5–21 × 2–3 vs. 19–23 × 2–4 µm) and different series of conidiogenous apparatus branches (3–4 branches vs. 5 branches). Phylogenetically, two isolates of *G. aquaticus* formed one subclade with good support (1.00 PP, 100% ML) and shares a sister relationship to *G. elghollii.*

Ophiocordycipitaceae G.H. Sung et al.

The family Ophiocordycipitaceae (order: Hypocreales) was introduced by Sung et al. (2007) based on phylogenetic analyses and later listed by Kirk et al. (2013) and Quandt et al. (2014). Kirk et al. (2013) accepted eleven genera in Ophiocordycipitaceae, but Quandt et al. (2014) refined and proposed six genera, *Drechmeria, Harposporium, Ophiocordyceps, Polycephalomyces, Purpureocillium* and *Tolypocladium* to comprise the family. Matočec et al. (2014) introduced *Perennicordyceps* under Ophiocordycipitaceae. Maharachchikumbura et al. (2015) confirmed this system and Spatafora et al. (2015) introduced some necessary species combinations based on this classification. Simmons et al. (2015) refined the genus *Hirsutella* under Ophiocordycipitaceae. Most species of Ophiocordycipitaceae produce darkly pigmented, tough to pliant stromata that often possess aperithecial apices (Sung et al. 2007). The main distinguishing characters of this genus are that the ascospores do usually not break into part-spores at maturity and asci have thin apical caps (Petch 1931, 1932). In the study, we introduce one new species *Ophiocordyceps cylindrospora* based on phylogeny and morphology.

Ophiocordyceps Petch

Ophiocordyceps was introduced by Petch (1931) and revised as the type genus under the family Ophiocordycipitaceae by Sung et al. (2007), with the type species *Ophiocordyceps blattae* (Petch) Petch, which was a cockroach pathogen. This genus includes most of the species in the family and some of the species are host-specific insect pathogens (Quandt et al. 2014).

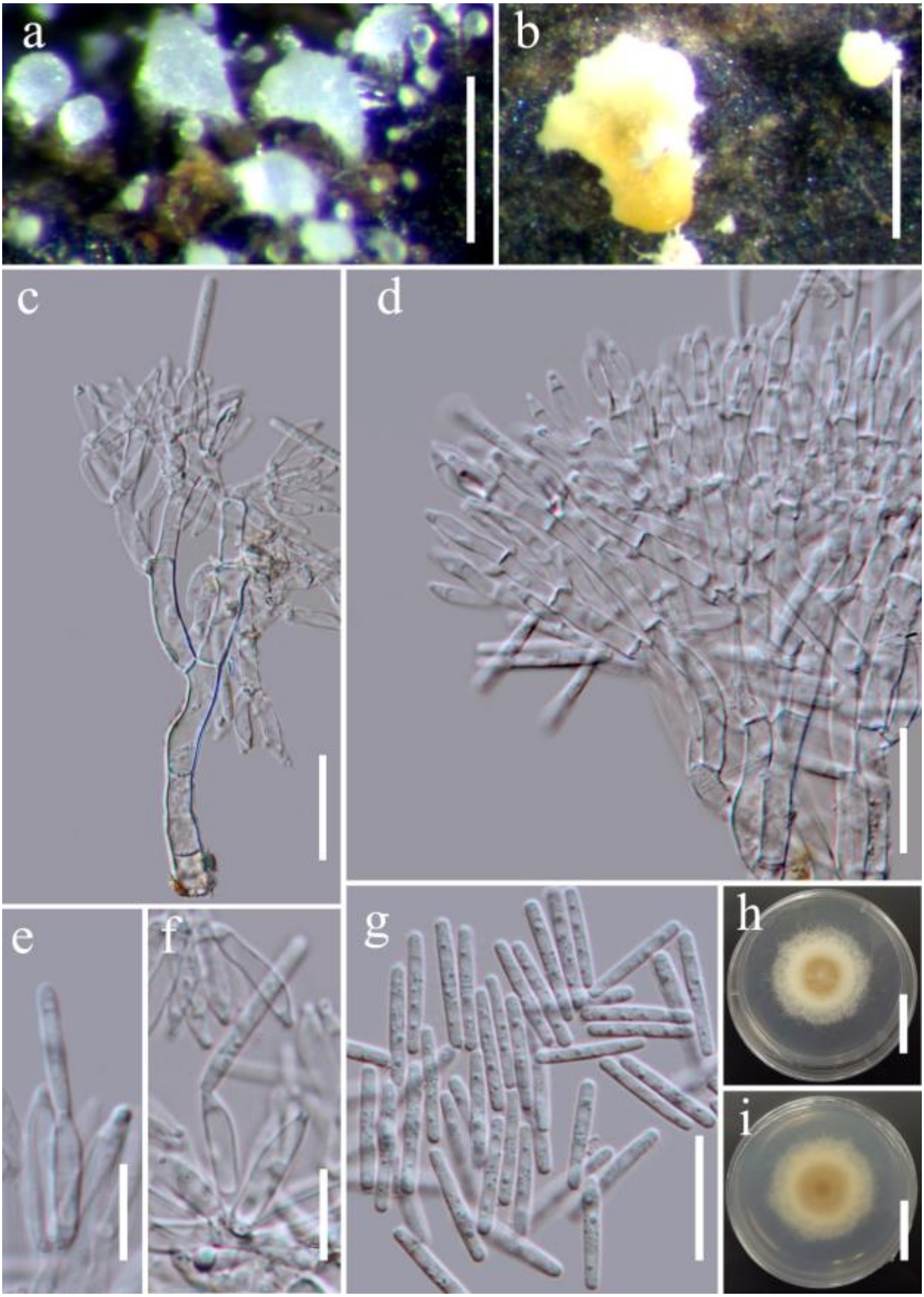


Figure 75 – *Gliocladiopsis aquaticus* (MFLU 17-1976, holotype). a, b Colonies on substrate. c, d Conidiophores. e, f Conidiogenous cells with attached conidia. g Conidia. h, i Colony on PDA from above and below. Scale bars: a = 200 µm, b = 500 µm, c, d, g = 20 µm, e, f = 10 µm, h, i = 20 mm.

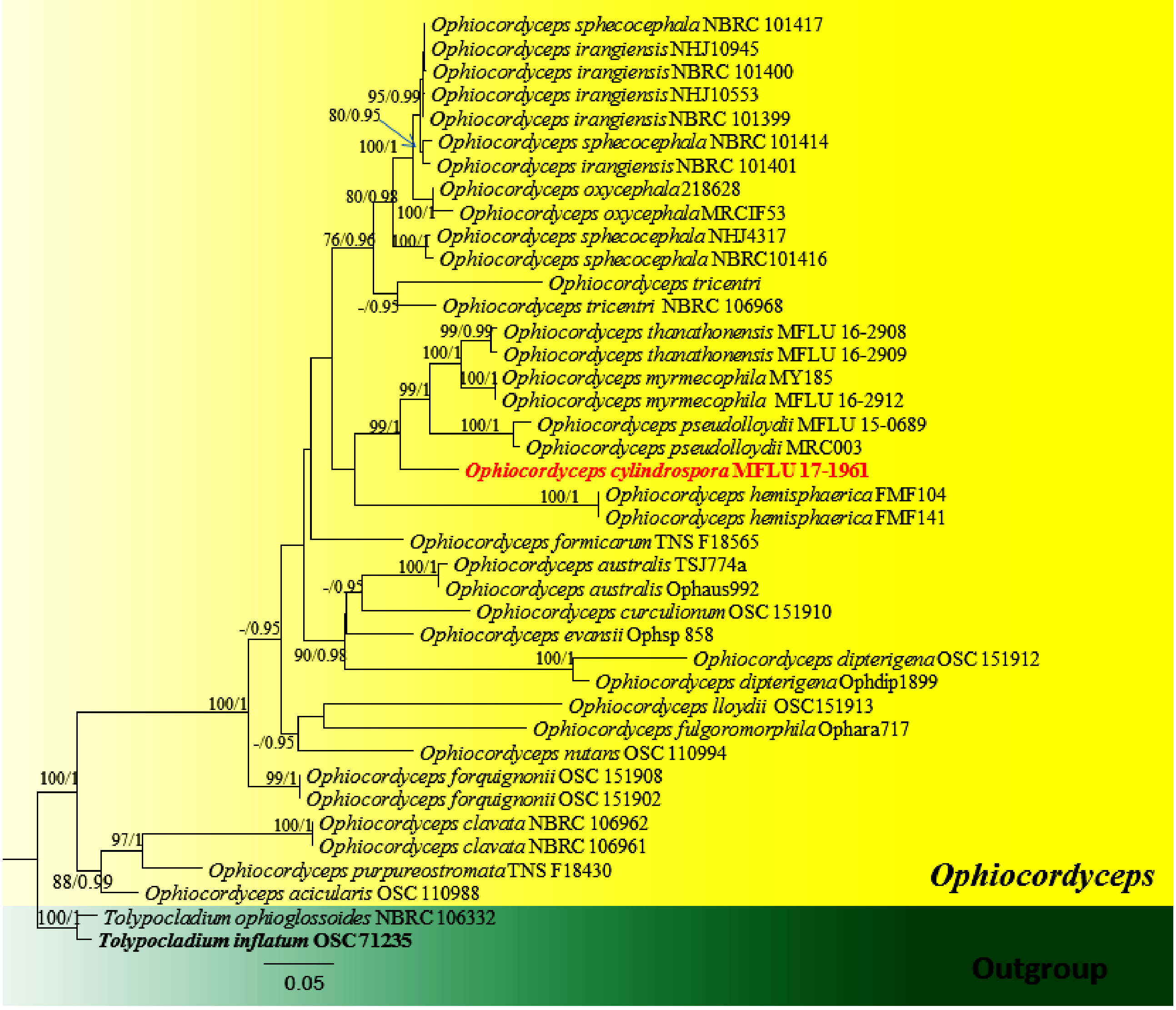


Figure 76 – Phylogram of *Ophiocordyceps cylindrospora* generated from maximum likelihood analysis of ITS, SSU, LSU and RPB2 sequence data. *Tolypocladium inflatum* (OSC 71235) and *Tolypocladium ophioglossoides* (NBRC 106332) were used as outgroup taxa. The tree topology of the ML was similar to the ML and BI analysis. The best scoring RAxML tree with a final likelihood value of -22779.351826 is presented. The matrix had 1558 distinct alignment patterns, with 45.49% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.259547, C = 0.235029, G = 0.269944, T = 0.235480; substitution rates AC = 1.192392, AG = 3.825106, AT = 1.220677, CG = 0.895628, CT = 6.933089, GT = 1.000000; gamma distribution shape parameter α = 0.202843. Maximum likelihood bootstrap values greater than 75% and Bayesian posterior probabilities over 0.95 are indicated above the nodes. The scale bar indicates 0.04 changes. The new species was in red.

Ophiocordyceps cylindrospora Y.P. Xiao, T.C. Wen & K.D. Hyde, sp. nov. Fig. 77

Index Fungorum number: IF553983; Facesoffungi number: FoF03878

Etymology – the specific epithet refers to Thanathon in north Thailand, the collection location.

Holotype – MFLU 17-1961

Parasitic on wasps (Hymenoptera), collected from the underside of leaf litter. Sexual morph *Host* 11 mm long, 3–5 mm wide, black wasp without hyphae on the surface. *Stromata* 50–90 mm long, 0.5–1.5 mm diameter, mostly single, stipitate, rarely double, arising from between the head and thorax of adult wasps, pale yellow to yellow. *Stipe* 25–27 mm long, 0.5–2 mm diameter, clavate, with a fertile apex, becoming pale to yellow. *Fertile head* 3–3.2 mm wide, 1–1.2 mm diameter, fusiform, yellow, upper surface roughened, lateral surface, ridged and furrowed. *Ascomata* 551–638 × 261–327 µm ($\bar{x}$ = 594 × 294 µm, n = 30), immersed, oblique flask-shaped, thin-walled. *Peridium* 20–25 mm ($\bar{x}$ = 23 µm, n = 60) wide. *Asci* 248–313 × 5–7 µm ($\bar{x}$ = 480 × 6 µm, n = 60), 8-spored, hyaline, narrow cylindrical, with a thickened apex. *Apical cap* 5–12.5 × 8.5–10.4 µm ($\bar{x}$ = 8.7 × 9.5 µm, n = 60), with a small channel in the center. *Ascospores* easily breaking into part-spores, filiform. *Secondary ascospores* 3.1–3.9 × 1.6–2 µm ($\bar{x}$ = 3.5 × 1.8 µm, n = 90) cylindrical, truncated at both ends, straight, hyaline, smooth. Asexual morph Undetermined.

Material examined – THAILAND, Chiang Mai Province, Mushroom Research Centre, on dead wasp, 19 July 2015, YuanPin Xiao, MSCM15071905 (MFLU 17-1961, holotype); *ibid.* (MFLU 17-1962, MFLU 17-1963 isotypes).

GenBank numbers – ITS: MG553635, LSU: MG553652, RPB2: MG647029, SSU: MG553651.

Notes – *Ophiocordyceps cylindrospora* is a pathogen of wasps and was collected from Chiang Mai, Thailand. The morphology of the new species is similar to *Ophiocordyceps sphecocephala*, *O. myrmecophila*, *O. pseudolloydii*, *O. hemisphaerica*, *O. irangiensi*, which are shown in Table 3. The morphology of *Ophiocordyceps cylindrospora* differs from other species in the genus *Ophiocordyceps* in having cylindrical and shorter secondary ascospores. Phylogenetic analyses of combined SSU, LSU, ITS, RPB1 and RPB2 sequence data also support it as a new species in the genus (Fig. 76).

Table 3 Synopsis of *Ophiocordyceps* species discussed in the paper.

Species	Host	Stromata (mm)	Ascomata (µm)	Asci (µm)	Ascospores (µm)	Secondary ascospores (µm)	Reference
O. cylindrospora	Wasp	50–90 × 0.5–1.5	551–638 × 261–327	248–313 × 5–7	As long as asci	3.1–3.9 × 1.6–2	This study
O. myrmecophila	Ant	10–40 × 0.2–0.5	600–890 × 180–275	460–630 × 4–6,5	310–390 × 1–2	8–10 × 1.5–2.3 cylindrical	Mains 1940, Luangsa-Ard et al. 2008
O. sphecocephala	Wasp	45 × 1.4–1.8	880–1000 × 200–260	700 ×7	As long as asci	10–14 × 1.5–2.5	Hywel-Jones 1995
O. irangiensi	Ant	25–60 × 0.2–0.7	1000 × 150–200	900 × 6–8	700 × 1.3–2.3	8.5–12.5 × 1.3–2.3 fusoid	Hywel-Jones1996
O. hemisphaerica	Fly	12–20 ×0.8–1	780–860 × 220–290	500–640 × 5–6	-	-	Hyde et al. 2016
O. pseudolloydii	Ant	2–6 × 0.5–2	380–550 × 140–240	240–485 × 12–16	160–470 × 5–6	4.5–6.3 × 1–2.5 cylindrical	Evans & Samson 1984

Stachybotryaceae Crous

The family Stachybotryaceae was introduced by Crous et al. (2014) within the order Hypocreales (Hypocreomycetidae, Sordariomycetes). Thirty-four genera are accepted in Stachybotryaceae based on morphology and multi-gene phylogeny and the family is typified by *Stachybotrys* Corda (Crous et al. 2014, Lombard et al. 2016, Gordillo & Decock 2017, Wijayawardene et al. 2016, 2018). The species are saprobes or pathogens and some may cause risk to human health (Lombard et al. 2016). In the study, we introduce a saprobic *Alfaria terrestris* as a new record in Thailand from dead grass leaves.

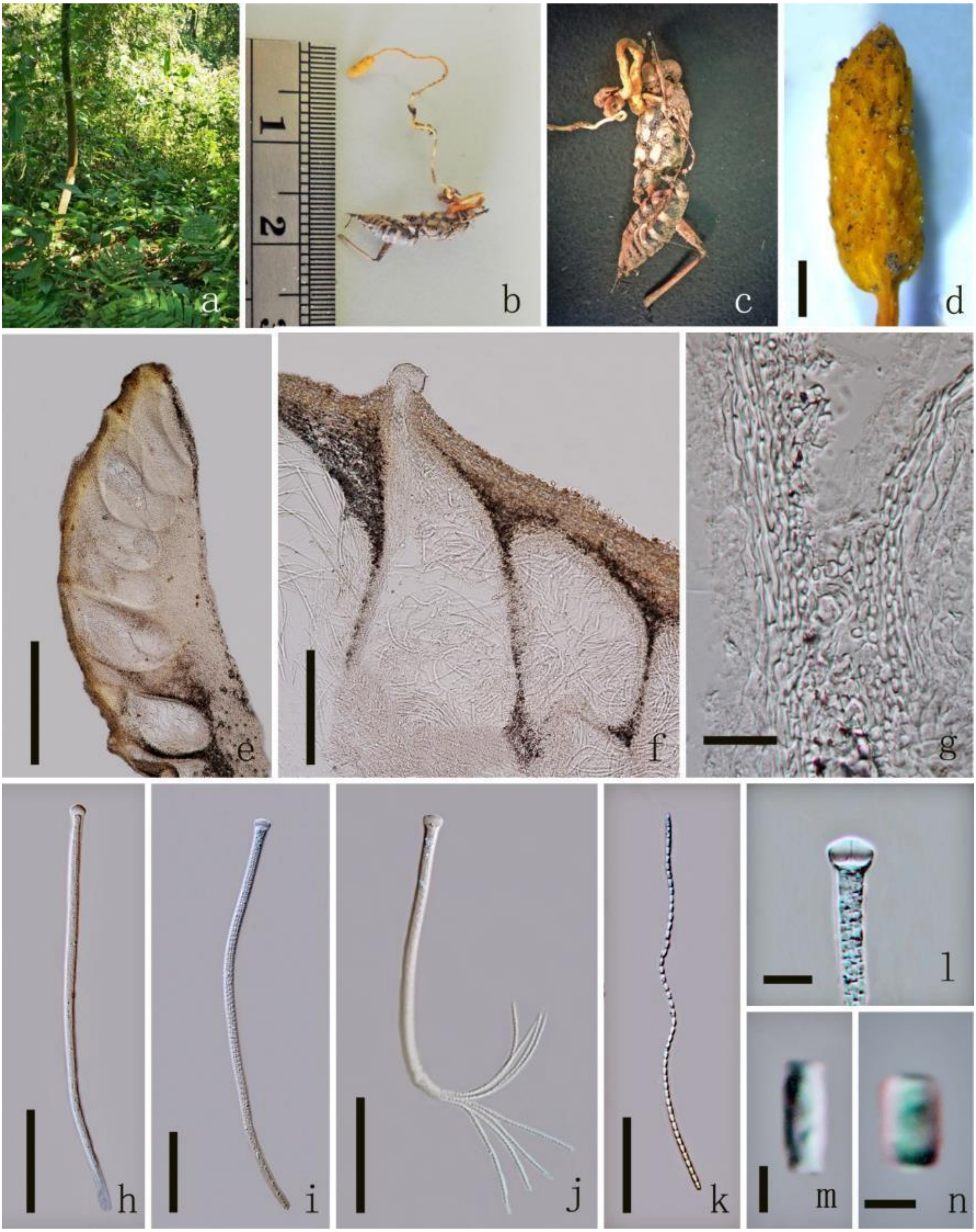


Figure 77 – *Ophiocordyceps cylindrospora* (MFLU 17-1961, holotype). a Habitat of *Ophiocordyceps cylindrospora*. b Ascostroma emerging from infected wasps. c Overview of host. d Fertile head of ascostroma. e, f Perithecia. g Peridium. h–j Immature to mature asci. k Part of the ascospores. l Apical cap of asci. m, n Secondary ascospores. Scale Bars: d, e = 500 µm, f = 200 µm, g = 20 µm, h–k = 100 µm, l = 10 µm, m, n = 2 µm.

Alfaria Crous et al.

The genus *Alfaria* belongs in the family Stachybotryaceae (Crous et al. 2014, Maharachchikumbura et al. 2015, 2016a, Wijayawardene et al. 2016, 2017a). *Alfaria* was introduced to accommodate pathogenic *A. cyperi-esculenti* Crous, N.J. Montaño-Mata & García-Jim (Crous et al. 2014). Nine species are currently accepted in *Alfaria* (Lin et al. 2017).

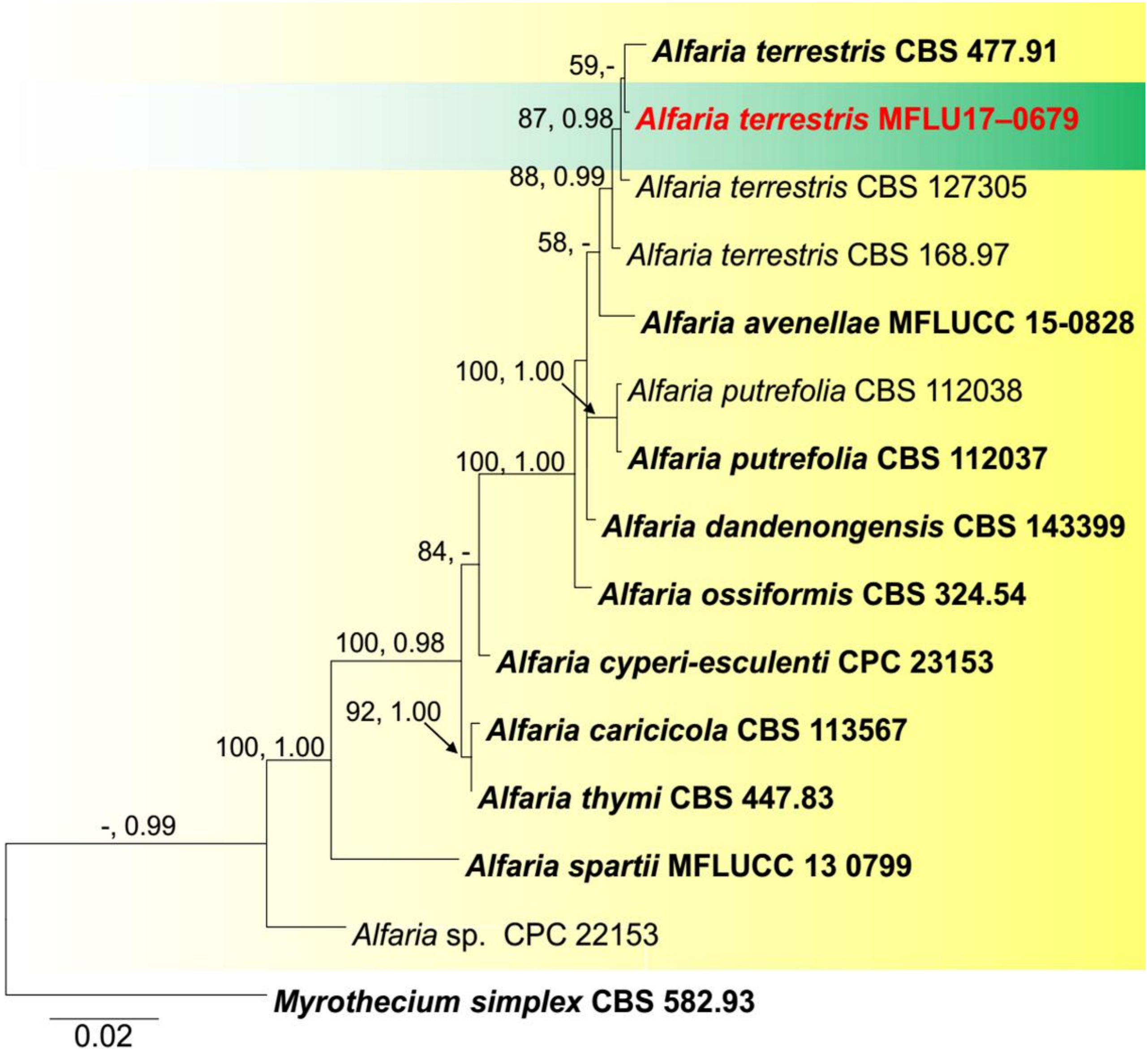


Figure 78 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequenced data of *Alfaria* species. Related sequences were obtained from Lin et al. (2017). Fifteen strains were included in the combined sequence analyses, which comprise 1424 characters with gaps. *Myrothecium simplex* (CBS 582.93) was used as the outgroup taxa. Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -3363.437417 is presented. The matrix had 290 distinct alignment patterns, with 20% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242693, C = 0.256230, G= 0.288945, T = 0.212132; substitution rates AC = 1.096356, AG = 0.714721, AT = 0.772509, CG = 0.707572, CT = 2.464121, GT = 1.000000; gamma distribution shape parameter α = 0.451441. Bootstrap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.90 are given above the nodes respectively. Newly generated sequences are in red bold. The ex-type strains are in black bold.

Alfaria terrestris L. Lombard & Crous, Persoonia 36:181 (2016) Fig. 79

Facesoffungi number: FoF04082

Saprobic on dead leaves of Grass (Poaceae) species. Sexual morph Undetermined. Asexual morph *Conidiomata* 250–400 µm ($\bar{x}$ = 310 µm, n = 10) diameter, superficial, solitary, black, oval to elongate or irregular and a green agglutinated mass of conidia surrounded by setae. Setae straight or bent, dark brown, arising from the basal of conidiomata. *Conidiophores* unbranched, green, smooth, up to 11 µm long. *Conidiogenous cells* 4–7 × 1–2 µm ($\bar{x}$ = 5.1 × 1.2 µm, n = 15), phialidic, cylindrical, hyaline, smooth-walled, cylindrical. *Conidia* 11–14 × 2–3 µm ($\bar{x}$ = 12 × 2 µm), smooth, light green to green, ellipsoidal and straight.

Material examined – THAILAND, Chiang Rai Province, Amphur Muang, on leaves of dead grass species, 23 September 2016, N. I de Silva, NI113 (MFLU 17-0679).

GenBank numbers – ITS: MG818852, LSU: MG821635.

Notes – Our strain clusters with the type *Alfaria terrestris* (CBS 477.91) in the combined LSU and ITS phylogenetic analysis. We were unable to get the culture from conidia. Therefore, we obtain sequence data directly from fruiting bodies. *Alfaria terrestris* has been isolated from soil in Turkey and the USA and leaf litter in Spain. The current collection of *A. terrestris* was from leaves of dead grass species in Chiang Rai, Thailand. Our strain has aseptate, smooth-walled, ellipsoidal conidia that are similar to type collection. However, our strain has light green to green, 11–14 × 2–3 µm (x = 12 × 2 µm) conidia and the type specimen had hyaline (4–)5–7 × 2–3 µm (av. 6 × 2 µm) conidia (Lombard et al. 2016), which suggests this may be a species complex. Our strain produces setae that arise from the base of conidiomata that has previously not been observed in the type.

Subclass Sordariomycetidae O.E. Erikss & Winka

Chaetosphaeriales Huhndorf et al.

Chaetosphaeriaceae Réblová et al.

The family Chaetosphaeriaceae was introduced by Locquin (1984) to accommodate *Chaetosphaeria* Tul. & C. Tul., *Loramyces* W. Weston, *Niesslia* Auersw., *Rhagadostoma* Körb. and *Zignoëlla* Sacc., but it was not validly published (Réblová et al. 1999). Réblová et al. (1999) re-described and validated Chaetosphaeriaceae and accepted *Ascocodinaea*, *Chaetosphaeria*, *Melanochaeta*, *Melanopsammella*, *Porosphaerella*, *Porosphaerellopsis* and *Striatosphaeria*. Presently, 38 genera were accepted within the family Chaetosphaeriaceae (Maharachchikumbura et al. 2016a, Wijayawardene et al. 2018). This family comprises the asexual morph genera *Catenularia*, *Cylindrotrichum*, *Chalara*, *Chloridium*, *Custingophora*, *Dictyochaeta*, *Menispora*, *Phialophora* and *Zanclospora* (Réblová et al. 1999, Ho et al. 2001, Huhndorf et al. 2001, Fernández & Huhndorf 2005, Fernández et al. 2006, Atkinson et al. 2007, Liu et al. 2016, Perera et al. 2016, Wijayawardene et a. 2017a, 2018). In this study, we introduce *Chaetosphaeria mangrovei* sp. nov. from an intertidal mangrove host, based on both morphological and phylogenetic analyses and designate an epitype for *Cryptophiale hamulata*.

Chaetosphaeria Tul. & C. Tul.

Chaetosphaeria is placed in Chaetosphaeriaceae (Chaetosphaeriales) (Réblová et al. 1999, Huhndorf et al. 2004, Maharachchikumbura et al. 2015, 2016a) based on molecular data, although it previously placed in Lasiosphaeriaceae by Barr (1990). Morphological characters of the sexual morphs are simple and difficult to differentiate, while the asexual morphs characters are considered as distinguishable (Gams & Holubová-Jechová 1976, Huhndorf et al. 2004). Taxa that belong to this genus are reported from decayed plant material in terrestrial, freshwater and marine habitats, worldwide and comprise more than 100 species (Ho et al. 2001, Huhndorf et al. 2001, Fernández & Huhndorf 2005, Fernández et al. 2006, Atkinson et al. 2007, Liu et al. 2016, Perera et al. 2016, Wijayawardene et al. 2017a).

Chaetosphaeria mangrovei Dayar., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 81

Index Fungorum number: IF554116; Facesoffungi number: FoF03927

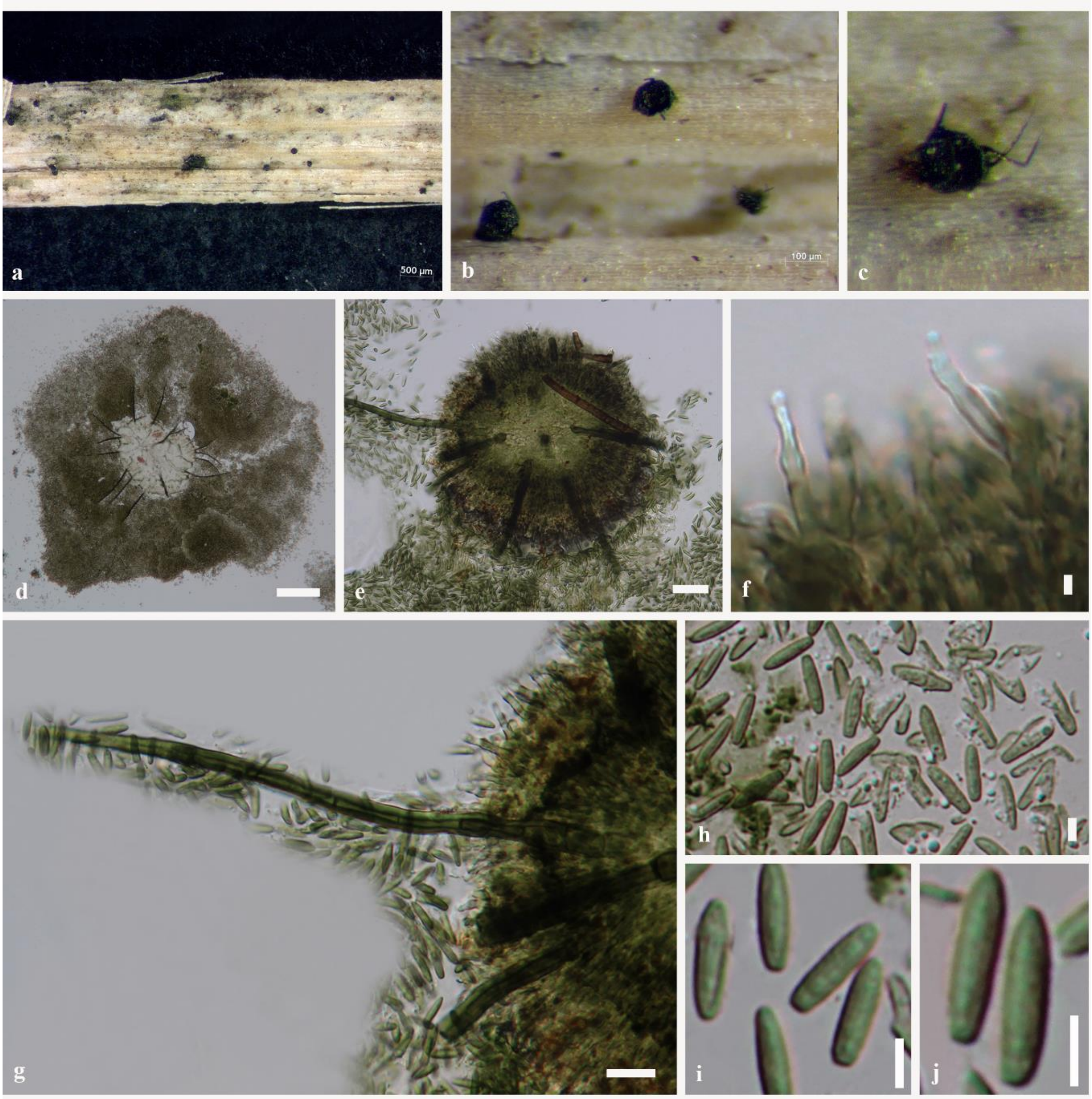


Figure 79 – *Alfaria terrestris* (MFLU 17-0679). a–c Appearance of conidiomata on host. d, e Squash mounts of conidiomata. f Conidiogenous cells. g Setae arising from base of conidiomata. h, i Conidia. Scale bars d, e = 50 µm, f = 5 µm, g = 20 µm h, i = 5 µm.

Etymology – name referring the host, of which the species was collected.

Holotype – MFLU 18-0146

Saprobic on wood. Sexual morph *Ascomata* 250–350 µm diameter, 300–450 µm high, superficial, arranged in clusters, ovoid, dark brown, surface rough, ostiolate. *Ostiole* periphysate. *Peridium* composed of dark brown cells of *textura angularis* in surface view, 15–20 µm thick in longitudinal section, 2-layered, inner layer 3–5 cells thick, composed of hyaline elongate cells of *textura angularis*, with outer layer 6–10 cells thick, composed of brown to dark brown, cell layers of *textura angularis*. *Paraphyses* 3–5 µm wide, sparse, simple, septate. *Asci* 75–80 × 8–10.5 ($\bar{x}$ = 82 × 10 µm, n = 20) µm, 8-spored, unitunicate, cylindrical-clavate, short-pedicellate, with a conspicuous, refractive, J-, apical ring. *Ascospores* 16–18.5 × 3–4.2 ($\bar{x}$ = 18 × 3.5 µm, n = 20) µm, overlapping biseriate, hyaline, ovoid-fusiform, 3–5-septate, straight, with small guttules. Asexual morph Undetermined.

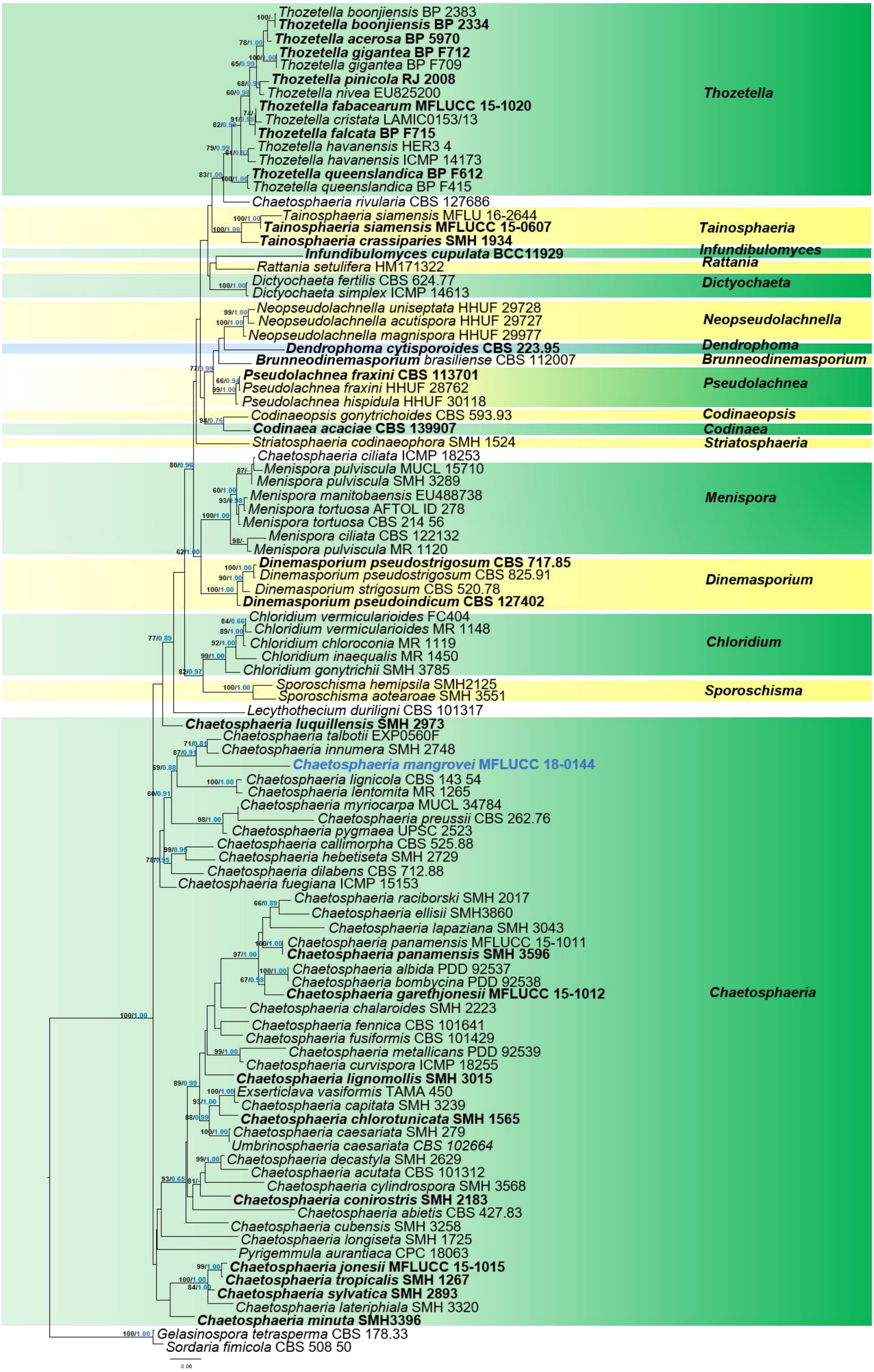

Thozetella boonjiensis BP 2383
Thozetella boonjiensis BP 2334
Thozetella acerosa BP 5970
Thozetella gigantea BP F712
Thozetella gigantea BP F709
Thozetella pinicola RJ 2008
Thozetella nivea EU825200
Thozetella fabacearum MFLUCC 15-1020
Thozetella cristata LAMIC0153/13
Thozetella falcata BP F715
Thozetella havanensis HER3 4
Thozetella havanensis ICMP 14173
Thozetella queenslandica BP F612
Thozetella queenslandica BP F415
Thozetella
Chaetosphaeria rivularia CBS 127686
Tainosphaeria siamensis MFLU 16-2644
Tainosphaeria siamensis MFLUCC 15-0607
Tainosphaeria crassiparies SMH 1934
Tainosphaeria
Infundibulomyces cupulata BCC11929
Infundibulomyces
Rattania setulifera HM171322
Rattania
Dictyochaeta fertilis CBS 624.77
Dictyochaeta simplex ICMP 14613
Dictyochaeta
Neopseudolachnella uniseptata HHUF 29728
Neopseudolachnella acutispora HHUF 29727
Neopseudolachnella magnispora HHUF 29977
Neopseudolachnella
Dendrophoma cytisporoides CBS 223.95
Dendrophoma
Brunneodinemasporium brasiliense CBS 112007
Brunneodinemasporium
Pseudolachnea fraxini CBS 113701
Pseudolachnea fraxini HHUF 28762
Pseudolachnea hispidula HHUF 30118
Pseudolachnea
Codinaeopsis gonytrichoides CBS 593.93
Codinaeopsis
Codinaea acaciae CBS 139907
Codinaea
Striatosphaeria codinaeophora SMH 1524
Striatosphaeria
Chaetosphaeria ciliata ICMP 18253
Menispora pulviscula MUCL 15710
Menispora pulviscula SMH 3289
Menispora manitobaensis EU488738
Menispora tortuosa AFTOL ID 278
Menispora tortuosa CBS 214 56
Menispora ciliata CBS 122132
Menispora pulviscula MR 1120
Menispora
Dinemasporium pseudostrigosum CBS 717.85
Dinemasporium pseudostrigosum CBS 825.91
Dinemasporium strigosum CBS 520.78
Dinemasporium pseudoindicum CBS 127402
Dinemasporium
Chloridium vermicularioides FC404
Chloridium vermicularioides MR 1148
Chloridium chloroconia MR 1119
Chloridium inaequalis MR 1450
Chloridium gonytrichii SMH 3785
Chloridium
Sporoschisma hemipsila SMH2125
Sporoschisma aotearoae SMH 3551
Sporoschisma
Lecythothecium duriligni CBS 101317
Chaetosphaeria luquillensis SMH 2973
Chaetosphaeria talbotii EXP0560F
Chaetosphaeria innumera SMH 2748
Chaetosphaeria mangrovei MFLUCC 18-0144
Chaetosphaeria lignicola CBS 143 54
Chaetosphaeria lentomita MR 1265
Chaetosphaeria myriocarpa MUCL 34784
Chaetosphaeria preussii CBS 262.76
Chaetosphaeria pygmaea UPSC 2523
Chaetosphaeria callimorpha CBS 525.88
Chaetosphaeria hebetiseta SMH 2729
Chaetosphaeria dilabens CBS 712.88
Chaetosphaeria fuegiana ICMP 15153
Chaetosphaeria raciborski SMH 2017
Chaetosphaeria ellisii SMH3860
Chaetosphaeria lapaziana SMH 3043
Chaetosphaeria panamensis MFLUCC 15-1011
Chaetosphaeria panamensis SMH 3596
Chaetosphaeria albida PDD 92537
Chaetosphaeria bombycina PDD 92538
Chaetosphaeria garethjonesii MFLUCC 15-1012
Chaetosphaeria chalaroides SMH 2223
Chaetosphaeria fennica CBS 101641
Chaetosphaeria fusiformis CBS 101429
Chaetosphaeria metallicans PDD 92539
Chaetosphaeria curvispora ICMP 18255
Chaetosphaeria lignomollis SMH 3015
Exserticlava vasiformis TAMA 450
Chaetosphaeria capitata SMH 3239
Chaetosphaeria chlorotunicata SMH 1565
Chaetosphaeria caesariata SMH 279
Umbrinosphaeria caesariata CBS 102664
Chaetosphaeria decastyla SMH 2629
Chaetosphaeria acutata CBS 101312
Chaetosphaeria cylindrospora SMH 3568
Chaetosphaeria conirostris SMH 2183
Chaetosphaeria abietis CBS 427.83
Chaetosphaeria cubensis SMH 3258
Chaetosphaeria longiseta SMH 1725
Pyrigemmula aurantiaca CPC 18063
Chaetosphaeria jonesii MFLUCC 15-1015
Chaetosphaeria tropicalis SMH 1267
Chaetosphaeria sylvatica SMH 2893
Chaetosphaeria lateriphiala SMH 3320
Chaetosphaeria minuta SMH3396
Chaetosphaeria
Gelasinospora tetrasperma CBS 178.33
Sordaria fimicola CBS 508 50
0.06

Figure 80 – Phylogram generated from maximum likelihood analysis based on combined LSU, and ITS sequenced data. One hundred strains are included in the analyses, which comprise 1470 characters including gaps. The tree is rooted to *Gelasinospora tetrasperma* (CBS 178.33) and *Sordaria fimicola* (CBS 508.50). Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of -17707.998520 is presented. The matrix had 792 distinct alignment patterns, with 36.43% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.233261, C = 0.262150, G = 0.300958, T = 0.203631; substitution rates AC = 1.405832, AG = 2.262138, AT = 2.187639, CG = 0.916401, CT = 7.644284, GT = 1.000000; gamma distribution shape parameter α = 0.264850. Maximum likelihood bootstrap (ML, black) values $\geq$ 60% and Bayesian posterior probabilities (PP, blue) $\geq$ 0.80% are given above the nodes.

Culture characteristics – *Colonies* on MDA reaching 10 mm diameter 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 – THAILAND, Ranong Province, Amphoe Muang, Mu 4 Tambol Ngao, Ranong Mangrove Research Center (GPS: 9°43' to 9°57'N; 98°29' to 98°39'E) on decaying wood of mangrove species, 7 December 2016, Monika C. Dayarathne, MCD 069 (MFLU 18-0146, holotype); ex-type living culture, MFLUCC 18-0144, TBRC.

GenBank numbers – LSU: MG813818, SSU: MG813819.

Notes – *Chaetosphaeria mangrovei*, the second *Chaetosphaeria* species reported from a marine based habitat is unique in having fusiform, 3–5-septate, straight ascospores with small guttules. However, Jones et al. (2014) reported that previously reported marine *Chaetosphaeria* species, *C. chaetosa* formed a monophyletic group with *Juncigena adarca*, *Moheitospora fruticosa* and two *Fulvocentrum* species, with high bootstrap support in a new family Juncigenaceae and this was followed in Jones et al. (2015). Hence, this the only record of marine *Chaetosphaeria* species at present. However, we did not observe the setae, enclosing the ascomata which is a characteristic feature of this genus (Fernández & Huhndorf 2005, Perera eta al. 2016). Maximum likelihood and Bayesian analyses of combined LSU and ITS sequence data indicate that *C. mangrovei* is a moderately supported lineage nested in between *C. innumera* Berk. & Broome ex Tul. & C. Tul. (SMH 2748), *C. lentomita* W. Gams & Hol.-Jech. (MR 1265), *C. lignicola* (Munk) Tomilin (CBS 143.54) and *C. talbotii* S. Hughes, W.B. Kendr. & Shoemaker (EXP0560F) (Fig. 80), which is suggestive of a new species status. *Chaetosphaeria innumera* is different from our species in having smaller ascospores (3.5–4.5 × 1.3–1.7 µm; Fernández & Huhndorf 2005). *Chaetosphaeria lentomita* is also morphologically similar to *C. mangrovei*, but *C. lentomita* possesses fairly long-stalked asci with an obtuse apex holding an inconspicuous apical ring and bi-seriately arranged, 1-septate ascospores with two guttules (Réblová et al. 1999).

Cryptophiale Piroz.

The genus *Cryptophiale* was established by Pirozynski (1968) to accommodate *C. kakombensis* Piroz. and *C. udagawae* Piroz. & Ichinoe. Presently, 20 species are accepted in the genus (Whitton et al. 2012). Each is characterized by having unbranched or apically dichotomous or verticillate, setiform conidiophores with a subapical or apical fertile region that produce hyaline, unicellular to multiseptate conidia (Seifert et al. 2011). The conidiogenous cells are in rows obscured by a shield of sterile cells (Seifert et al. 2011). The conidia are produced in slimy masses on one side of the conidiophore (Seifert et al. 2011).

Cryptophiale hamulata Whitton, K.D. Hyde & McKenzie, in Whitton, McKenzie & Hyde, Fungal Diversity Res. Ser. 21: 174 (2012) Fig. 83

Index Fungorum number: IF554379; Facesoffungi number: FoF04383

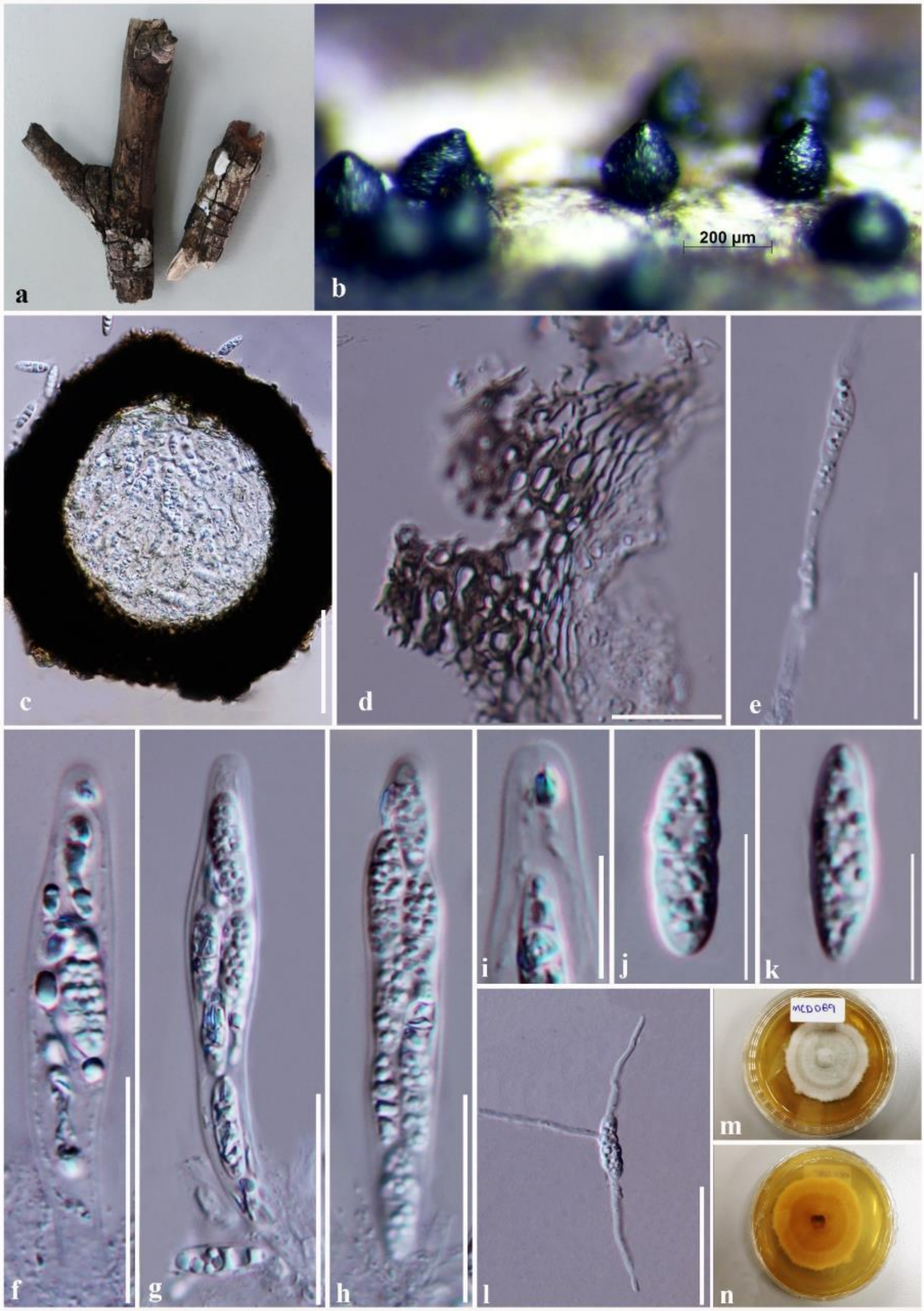


Figure 81 – *Chaetosphaeria mangrovei* (MFLU 18-0146, holotype). a Specimen. b Appearance of superficial ascomata on host surface. c Vertical section of an ascoma. d Section through peridium. e Paraphyses f–h Asci. i Close up of an apical ring of an asci. j–k Ascospores. l Germinating ascospore. m–n Culture on MEA (m-upper, n-lower). Scale bars: b = 200 µm, c = 100 µm, d–e = 20 µm, f–h = 50 µm, i–l = 10 µm.

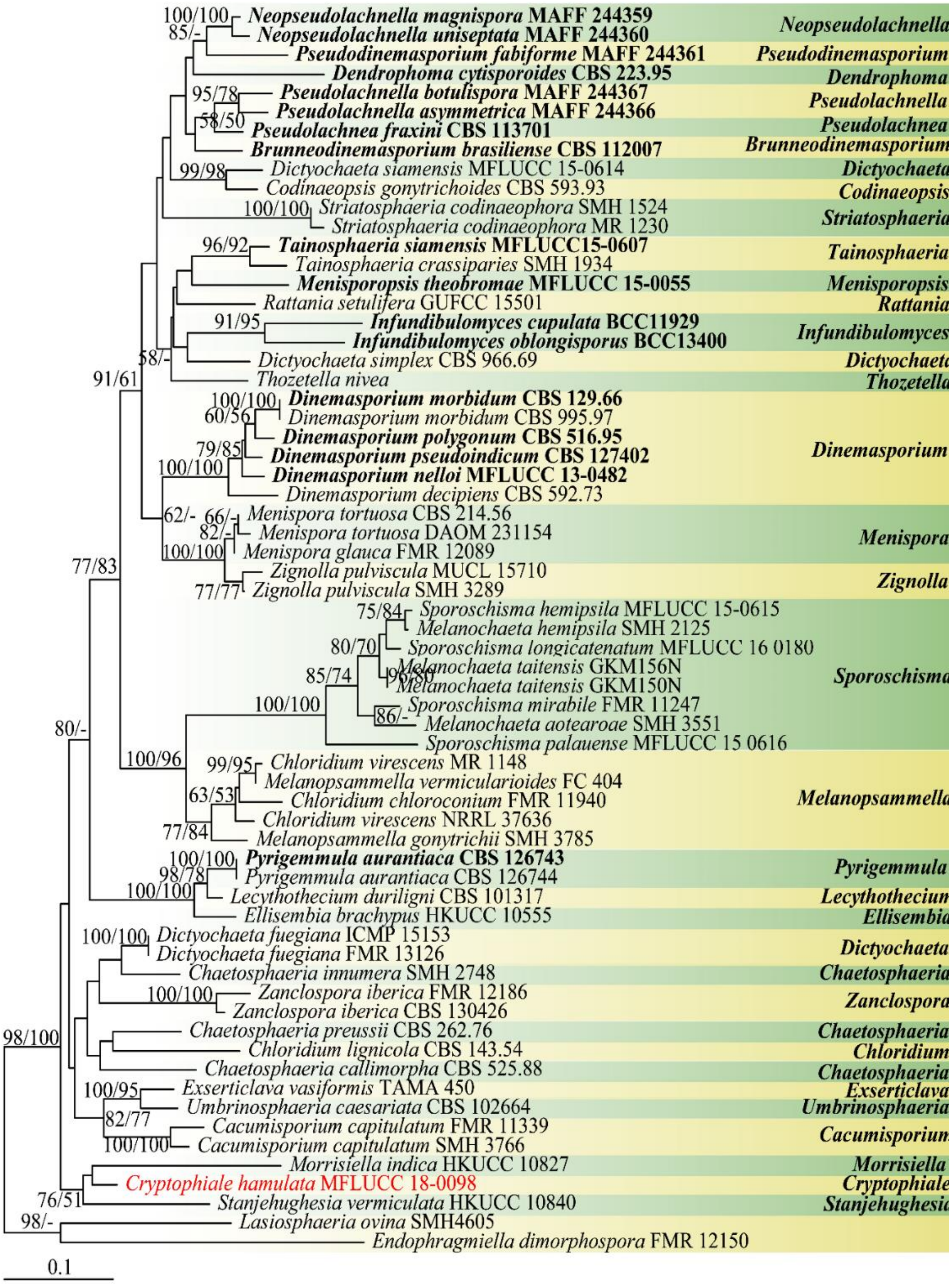


Figure 82 – Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU and ITS rDNA sequence data for selected genera within the family Chaetosphaeriaceae. Bootstrap support values for maximum likelihood and maximum parsimony greater than 50% are indicated above or below the nodes as ML/MP. Ex-type strains are in bold, the new isolate is in red. The tree is rooted with *Lasiosphaeria ovina* (SMH 4605) and *Endophragmiella dimorphospora* (FMR 12150).

Saprobic on decaying leaves. Asexual morph Colonies effuse, hairy, consisting of tall, scattered individual and fertile conidiophores. *Mycelium* predominantly immersed, partially superficial. Separate setae absent. *Conidiophores* macronematous, mononematous, solitary, scattered, erect, straight or flexuous, subulate, dark brown, smooth, thick-walled, multiseptate, base swollen, tapering to the apex, with the upper part sterile, setiform, simple, sometimes with a single dichotomously branching tip, 170–300 µm ($\bar{x}$ = 225 µm, n = 20) long, 5.5–10.5 µm ($\bar{x}$ = 8.2 µm, n = 20) wide just above the base, 4–6.5 µm ($\bar{x}$ = 5.4 µm, n = 20) wide below the fertile region. Fertile region on the sub-apex of conidiophores, septate, dark brown, cylindrical, 21.5–81.5 µm ($\bar{x}$ = 59.8 µm, n = 20) long, 9.5–15 µm ($\bar{x}$ = 12.6 µm, n = 20) wide. *Conidiogenous cells* monophialidic, discrete, in rows obscured by the shield of sterile cells, determinate, subsphaerical or lageniform. *Conidia* aggregated in slimy masses on one side of the conidiophore, simple, hyaline, smooth-walled, 0(–1)-septate, falcate, elongate to nearly filiform, lower end truncate to rounded, upper end appendiculate, 13–23 µm ($\bar{x}$ = 18.67 µm, n = 55) long, 1.6–3.4 µm ($\bar{x}$ = 2.42 µm, n = 55) wide. Sexual morph Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 hours. Colonies on PDA effuse, dark brown from above, dark from below, reaching a diameter of 3–5 cm in 10 days at 25°C.

Material examined – THAILAND, Chiang Mai Province, Mae Taeng, Ban Pa Deng, Mushroom Research Centre, on decaying leaf, 24 August 2016, Chuan-Gen Lin, MRC 11-1 (MFLU 17-1263, epitype designated here), ex-epitype living culture, MFLUCC 18-0098, KUMCC; *ibid.* (HKAS 101821)

GenBank numbers – LSU: MG386756, SSU: MG386757.

Notes – The combined LSU and ITS phylogenetic analysis showed that *Cryptophiale* clusters together with *Morrisiella* and *Stanjehughesia* (Fig. 82) but with weak support but these taxa are morphologically distinct. Keys and synopses to the genus *Cryptophiale* were provided by Whitton et al. (2012) and Goh & Hyde (1996). The specimen observed in this study agrees with the original description given in Whitton et al. (2012), except that sometimes conidia are 1-septate. This study is the first report of *C. hamulata* in Thailand which was previously known from the Philippines. We designate an epitype for the species (*sensu* Ariyawansa et al. 2014). This is the first study yielding DNA sequence data for the genus *Cryptophiale*.

Subclass Savoryellomycetidae Hongsanan et al.
Pleurotheciales Réblová & Seifert
Pleurotheciaceae Réblová & Seifert

Réblová et al. (2016) introduced the monotypic order Pleurotheciales based on morphological characters and phylogenetic analyses. Pleurotheciaceae was typified by *Pleurothecium* with an asexual species *Pleurothecium recurvatum* (Morgan) Höhn. as the type species. We introduce two new species of *Pleurotheciella* and a new species of *Phaeoisaria*. An updated tree for the order Pleurotheciales is provided in Fig. 84.

Phaeoisaria Höhn.

Phaeoisaria was established by Höhnel (1909) with *P. bambusae* Höhn. (now known as *P. clematidis* (Fuckel) S. Hughes) as the type species. The genus is characterized by indeterminate synnemata (except *P. fasciculata* Réblová & Seifert) with septate or aseptate ellipsoidal, obovoidal, fusiform-cylindrical or falcate conidia, formed on a sympodially extending rachis (Ruiz et al. 2002, Réblová et al. 2016). Presently, 23 species are accepted in the genus.

Phaeoisaria guttulata J. Yang & K.D. Hyde, sp. nov. Fig. 85

Index Fungorum number: IF554233; Facesoffungi number: FoF04086

Etymology – referring to the guttulate conidia.

Holotype – MFLU 18-0139

Figure 83 – *Cryptophiale hamulata* (MFLU 17-1263, epitype). a, b Host material. c, d Conidiophores on leaf surface. e, f Conidiophores, conidiogenous cells and conidia. g Conidiogenous cells. h–j Conidia. Scale bars: c, d = 100 µm, e, f = 50 µm, g–j = 10 µm.

Saprobic on submerged decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* effuse, scattered, brown, hairy, visible as solitary, dark brown conidiophores with white mass of conidia on the upper part. *Mycelium* partly immersed, partly superficial. *Conidiophores* macronematous, synnematous, erect, septate, smooth, mid brown to dark brown, 480–700 µm long, 2–5 µm wide. Synnemata erect, rigid, dark brown to black, velvety, smooth, composed of compact and parallel adpressed conidiophores, with flared conidiogenous cells in the above half. *Conidiogenous cells* integrated, terminal, polyblastic, pale brown to hyaline, sympodial, splaying out with one to several denticulate conidiogenous cells loci. *Conidia* globose to obovoid, hyaline, smooth-walled, guttulate, aseptate, 3.5–5.5 × 2.5–4.8 µm ($\bar{x}$ = 4.5 × 3.5 µm, n = 20).

Culture characteristics – Conidia germinating on PDA within 24 hours. Germ tubes produced from both ends. Colonies on PDA, reaching 5–10 mm diameter after two weeks at

25°C in natural light, with greyish-green aerial mycelium and brown mycelium on the surface, dark brown in reverse, margin filamentous.

Material examined – CHINA, Guizhou Province, Anshun City, Gaodang Village, 26°4′16″N, 105°41′53″E, on decaying wood submerged in Suoluo River, 19 October 2016, Jing Yang, GD 1-1 (MFLU 18-0139, holotype); ex-type living cultures, MFLUCC 17-1965, ICMP.

GenBank numbers – ITS: MG837021, LSU: MG837016, SSU: MG837026.

Notes – Phylogenetic analyses indicated *Phaeoisaria guttulata* belongs to *Phaeoisaria* and clusters with *P. aquatica* with little support (Fig. 84). *Phaeoisaria guttulata* can easily be distinguished from previously described species of *Phaeoisaria* by its morphology. Among the species sampled in our molecular dataset, *P. guttulata* is the only one which is characterized by globose to obovoid conidia, while others have clavate, narrowly ellipsoidal to obovoid conidia. *Phaeoisaria guttulata* is most similar to *P. clavulata* (Grove) E.W. Mason & S. Hughes in conidial shape, however, the conidia of *P. guttulata* (3.5–5.5 × 2.5–4.8 µm) are larger than *P. clavulata* (1–2 µm diam) (Révay 1985).

Pleurotheciella Réblová et al.

The holomorph genus *Pleurotheciella* was introduced by Réblová et al. (2012) with two species, *Pl. rivularia* Réblová et al. and *Pl. centenaria* Réblová et al., which have astromatic perithecia, unitunicate asci, persistent paraphyses and hyaline, septate ascospores and holoblastic, denticulate conidiogenous cells and hyaline, septate conidia. Based on morphological characters and phylogenetic analyses, *Dactylaria uniseptata* Matsush. was transferred to *Pleurotheciella* as *Pl. uniseptata* (Matsush.) Seifert (Réblová et al. 2016). Recently, Luo et al. (2017) introduced six new species from freshwater habitats. Thus, nine species from water-saturated decaying wood are accepted in *Pleurotheciella* with good descriptions and sequence data (Réblová et al. 2012, 2016, Luo et al. 2017).

Pleurotheciella krabiensis J. Yang & K.D. Hyde, sp. nov. Fig. 86

Index Fungorum number: IF554234; Facesoffungi number: FoF04087

Etymology – referring to the collection site.

Holotype – MFLU 18-0140

Saprobic on submerged decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* effuse, scattered, brown, hairy, upper part covered with bright white mass of conidia. *Mycelium* partly immersed, partly superficial. *Conidiophores* macronematous, synnematous, septate, smooth, brown, becoming paler towards the apex, straight or slightly curved, splaying out at the apex, 240–390 × 3.3–4.8 µm ($\bar{x}$ = 310 × 4.3 µm, n = 15). *Conidiogenous cells* integrated, terminal, polyblastic, sympodial, with cylindrical or tapering apex, pale brown or hyaline, denticulate, denticles conspicuously cylindrical. *Conidia* fusiform, subcylindrical to obovoid-subclavate, hyaline, smooth-walled, often guttulate, straight or slightly curved, with a single median septum, 19–25 × 4.5–6 µm ($\bar{x}$ = 22 × 5.3 µm, n = 20), obtuse at the apex, pointed at the base.

Culture characteristics – Conidia germinating on PDA within 24 hours. Germ tubes produced from both ends. Colonies on PDA slow growing, reaching 7–10 mm diameter after one month at 25 °C in natural light, circular, with yellowish-brown, dense aerial mycelium on the central surface and white, sparse mycelium on the entire margin, yellowish-brown in reverse.

Material examined – THAILAND, Krabi Province, on decaying wood submerged in a freshwater stream near Morakot Lake, 15 December 2015, S. Tibpromma, Site 6-6-3 (MFLU 18-0140, holotype); ex-type living cultures, MFLUCC 16-0852, ICMP.

GenBank numbers – ITS: MG837018, LSU: MG837013, SSU: MG837023.

Notes – The combined LSU, SSU and ITS phylogenetic analyses indicate that *Pleurotheciella krabiensis* nested within *Pleurotheciella* as a phylogenetically distinct species. *Pleurotheciella krabiensis* and *Pl. guttulata* Z.L. Luo et al. differ from other species in the genus by their synnematous conidiophores, and the brown conidiophores in *Pl. krabiensis* are distinguished from the hyaline conidiophores in *Pl. guttulata*. The occurrence of *Pl. krabiensis* on water saturated decayed wood is consistent with the ecology of the other nine species in the genus (Réblová et al. 2012, 2016, Luo et al. 2017).

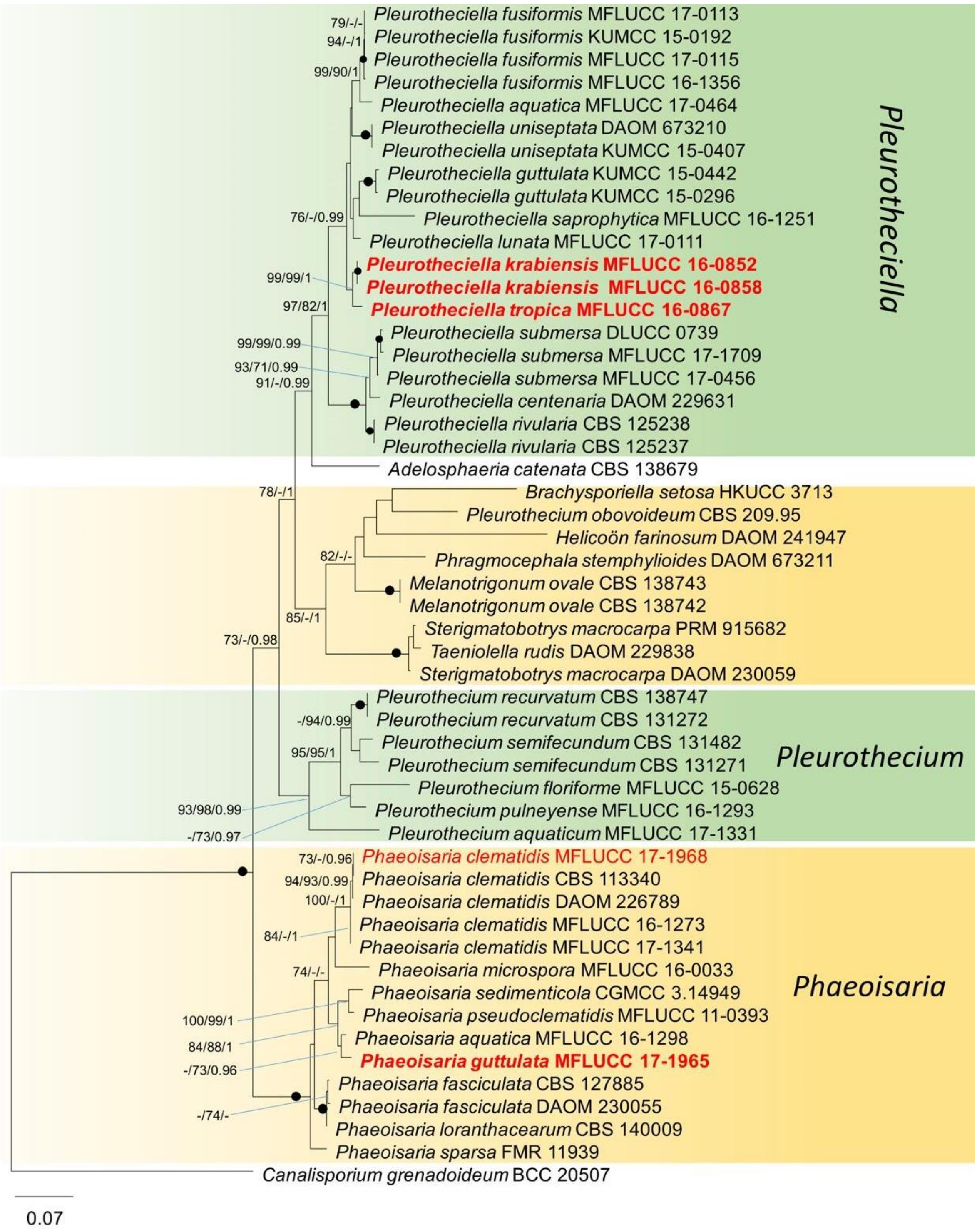


Figure 84 – Maximum likelihood majority rule consensus tree for the analyzed Hypocreomycetidae isolates based on a dataset of combined LSU, SSU and ITS sequence data. High branch support is shown at the nodes, maximum likelihood bootstrap support (ML BS) and maximum parsimony (MP BS) ≥ 70% and Bayesian posterior probability (PP) ≥ 0.95. The scale bar represents the expected number of changes per site. The tree is rooted with *Canalisporium grenadoideum*. The original isolate numbers are noted after the species names. The newly generated strains are in red, while new species are in red bold. Branches with 100% ML BS, 100% MP BS and 1.0 PP are noted with black node. Monotypic clades are indicated as coloured blocks.

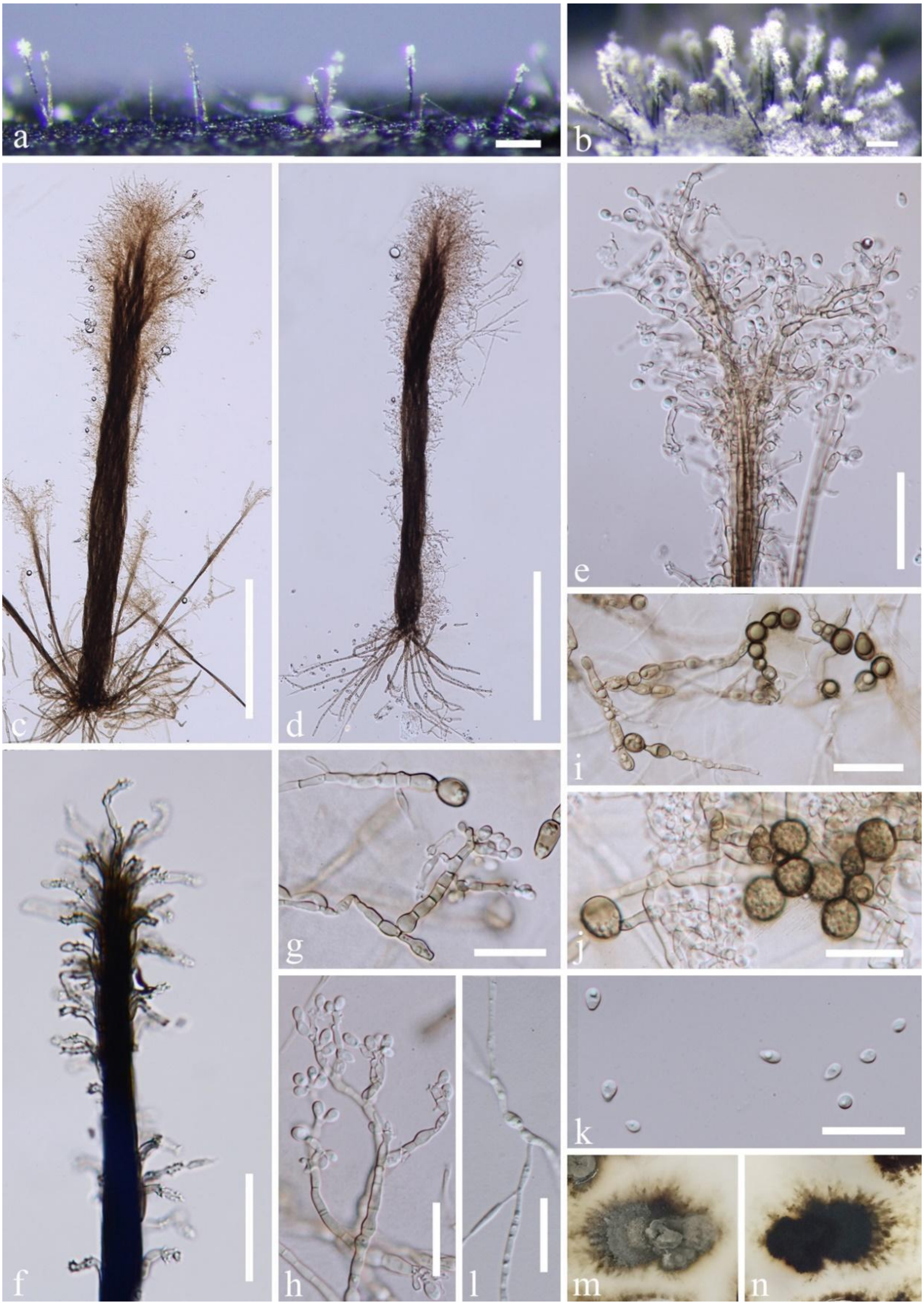


Figure 85 – *Phaeoisaria guttulata* (MFLU 18-0139, holotype) a Colonies on natural substrate. b Colonies on PDA medium. c, d Reproduced conidiophores with conidia. e, g, h Conidiogenous cells with conidia from culture. f Conidiogenous cells growing on natural substrate. i, j Brown globose cells from culture. k Germinated conidium on PDA medium. m, n Culture, m from above, n from below. Scale bars: a = 50 µm, b, f = 30 µm, c, j = 20 µm, d, e = 100 µm, g–i = 10 µm.

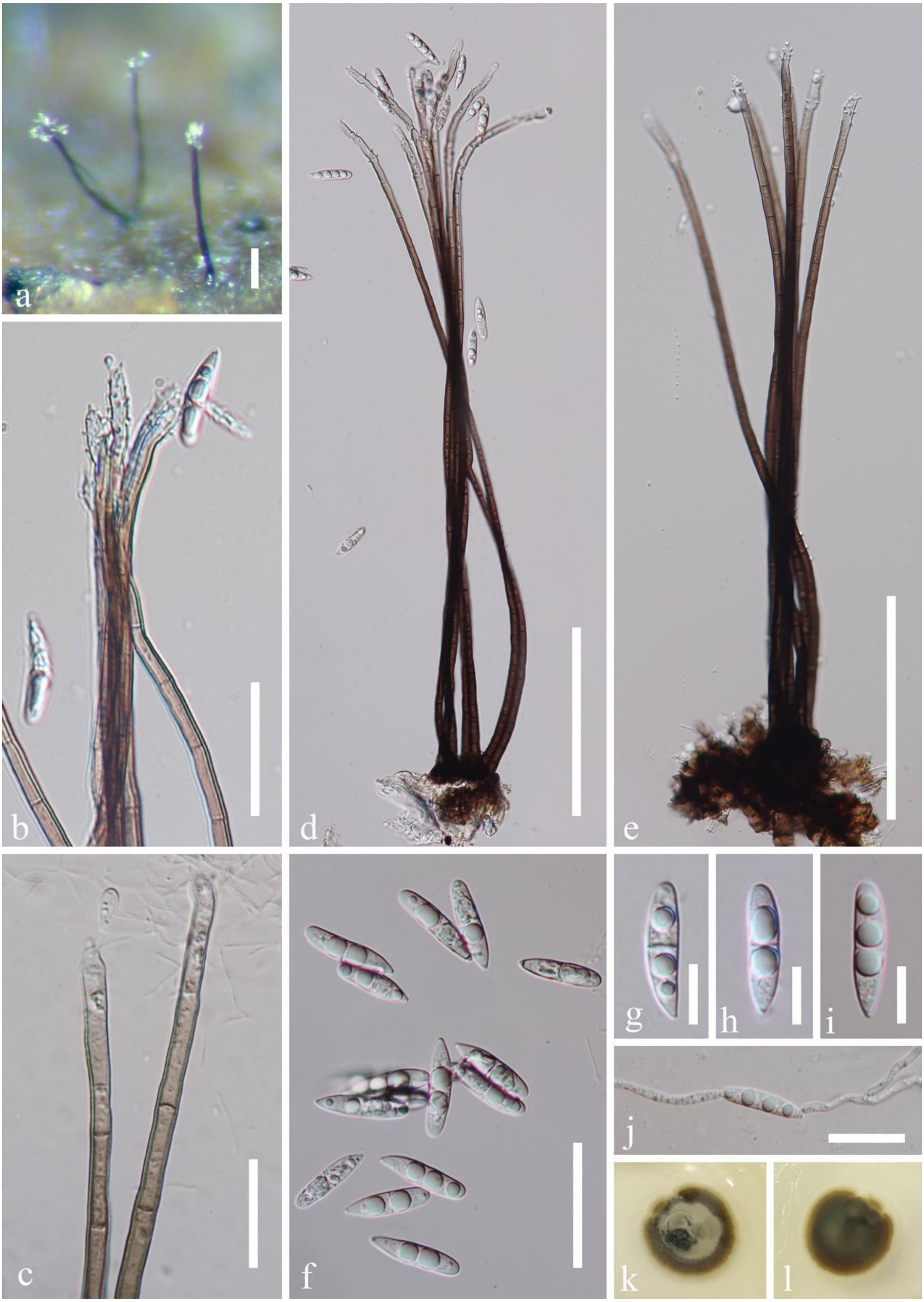


Figure 86 – *Pleurotheciella krabiensis* (MFLU 18-0140, holotype) a Colonies on natural substrate. b, c Conidiophores with conidia. d, e Conidiophores. f–i Conidia. j Germinated conidium on PDA medium. k, l Culture, k from above, l from below. Scale bars: a = 50 µm, b, f = 30 µm, c, j = 20 µm, d, e = 100 µm, g–i = 10 µm.

Pleurotheciella tropica J. Yang & K.D. Hyde, sp. nov. Fig. 87

Index Fungorum number: IF554235; Facesoffungi number: FoF04088

Etymology – referring to the collecting site in tropical country, Thailand.

Holotype – MFLU 18-0141

Saprobic on submerged decaying wood. Sexual morph Undetermined. Asexual morph *Colonies* effuse, scattered, brown, hairy, visible as solitary, dark brown conidiophores with bright white mass of conidia. *Mycelium* partly immersed, partly superficial. *Conidiophores* macronematous, mononematous, erect, septate, smooth, cylindrical, dark brown at the base, becoming paler towards the apex, straight or slightly curved, 100–250 µm long, 4–4.8 µm wide. *Conidiogenous cells* integrated, terminal, polyblastic, cylindrical, pale brown to hyaline, forming conidia sympodially on cylindrical denticles. *Conidia* narrowly obovoid or subclavate, hyaline, smooth-walled, guttulate, straight, uniseptate, 16–21 × 5.5–7 µm ($\bar{x}$ = 18.5 × 6.3 µm, n = 20), obtuse at the apex, pointed at the base.

Culture characteristics – Conidia germinating on PDA within 24 hours. Germ tubes produced from both ends. Colonies on PDA slow growing, reaching 7–10 mm diameter after one month at 25 °C in natural light, circular, wrinkled, with sparse aerial white mycelium in the center, yellowish-brown on the middle ring and sparse white mycelium at the entire margin, yellowish-brown in reverse.

Material examined – THAILAND, Phang Nga Province, Bann Tom Thong Khang, on decaying wood submerged in a freshwater stream, 17 December 2015, J Yang, Site 7-21-4 (MFLU 18-0141, holotype); ex-type living cultures, MFLUCC 16-0867, ICMP.

GenBank numbers – ITS: MG837020, LSU: MG837015, SSU: MG837025.

Notes – *Pleurotheciella tropica* is phylogenetically close to *Pl. krabiensis*, but its mononematous conidiophores differ from the synnematous conidiophores of *Pl. krabiensis*. Morphologically, *Pl. tropica* resembles *Pl. submersa* Z.L. Luo & K.D. Hyde and *Pl. uniseptata* (Matsush.) Seifert, in having brown, mononematous conidiophores, terminal conidiogenous cells and hyaline straight conidia. However, conidiophores of *Pl. tropica* (100–250 µm long) are longer than those in *Pl. submersa* (113–174 µm long) and *Pl. uniseptata* (100–150 µm long). Among them, *Pl. submersa* has larger conidia (25–28 × 5.5–6.5 µm) than in *Pl. tropica* (16–21 × 5.5–7 µm) and *Pl. uniseptata* (12.5–16.5 × 2–4 µm) (Réblová et al. 2016, Luo et al. 2017). In addition, the obovoid conidia with a pointed base in *Pl. tropica* are different from the subcylindrical conidia with rounded apex and tapering base in *Pl. submersa* and *Pl. uniseptata*.

Subclass Xylariomycetidae O.E. Erikss & Winka

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

Apiosporaceae K.D. Hyde et al.

The family Apiosporaceae was introduced by Hyde et al. (1998) with the type genus *Arthrinium* Kunze ex Fr. (sexual morph: *Apiospora* Sacc.). Currently, the family comprises *Appendicospora, Arthrinium, Dictyoarthrinium*, *Endocalyx*, *Scyphospora* and *Spegazzinia* (Lumbsch & Huhndorf 2010, Kirk et al. 2013, Maharachchikumbura et al. 2016a, Hongsanan et al. 2017, Wijayawardene et al. 2017a, 2018). In this study, we record *Arundo plinii* as a new host for *Arthrinium phragmites*.

Arthrinium Kunze

Arthrinium was established by Kunze & Schmidt in 1817 with *A. caricicola* Kunze & J.C. Schmidt as the type species (Wijayawardene et al. 2016). Currently the genus comprises 64 accepted species, with saprobic, pathogenic or endophytic nutritional modes (Wijayawardene et al. 2017a). Crous & Groenewald (2013) provided a phylogeny for this genus and the older name *Arthrinium* was conserved as it is a more commonly encountered name and more frequently used in the literature. Recently, Dai et al. (2016a) provided an updated phylogenetic analysis with two new *Arthrinium* species on bamboo from China.

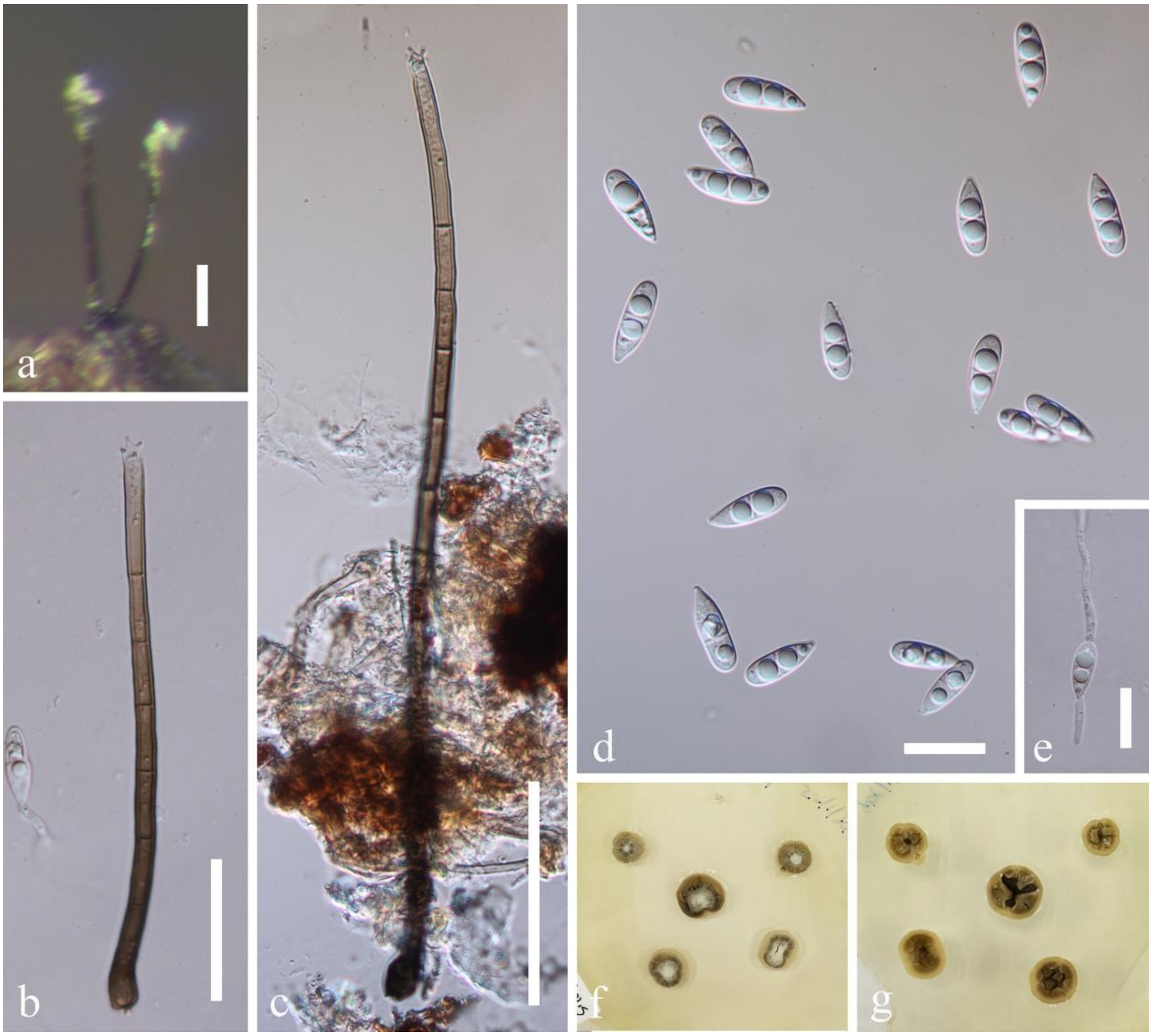


Figure 87 – *Pleurotheciella tropica* (MFLU 18-0141, holotype). a Colonies on natural substrate. b, c Conidiophores and conidiogenous cells. d Conidia. e Germinated conidium on PDA medium. f, g Culture, f from above, g from below. Scale bars: a, c = 50 µm, b = 30 µm, d, e = 20 µm.

Arthrinium phragmites Crous [as 'phragmites'], in Crous & Groenewald, IMA Fungus 4(1): 147 (2013) Fig. 89

Index Fungorum number: IF545031; Facesoffungi number: FoF03934

Saprobic on dead culms of *Arundo plinii* Turra. Sexual morph *Stromata* 1.8–3.2 mm long, 0.23–0.35 mm wide, 188–282 µm high, brown to black, scattered to gregarious, immersed, becoming erumpent, splitting along its length, revealing a row of separate, subglobose ascomata. *Ascomata* 170–210 µm high, 160–200 µm diameter, arranged in rows, clustered, gregarious, with 3–6 perithecia forming groups immersed in stromata, to erumpent through host surface, ellipsoidal to subglobose, dark brown, membranous, ostiolate. *Ostiole* raised from centre of ascomata, internally lined with periphyses. *Peridium* 6.5–12.5 µm ($\bar{x}$ = 9.6 µm, n = 15) wide, comprising 3–4 layers of dark brown or reddish-brown brown or reddish-brown to lightly pigmented cells, of *textura angularis*. *Hamathecium* composed of dense 3–5 µm ($\bar{x}$ = 3.9 µm, n = 25) wide, hyaline, filamentous, branched, septate paraphyses. *Asci* 90–130 × 15–20 µm ($\bar{x}$ = 107.5 × 16.9 µm, n = 15), 8-spored, unitunicate, clavate, with short basal pedicel, with obtusely rounded apex, lacking an apical ring. *Ascospores* 20–26 × 8–10 µm ($\bar{x}$ = 24.2 × 9.2 µm, n = 25), 2–3-seriate, 1-septate, hyaline, apiosporous, straight to curved, ellipsoid to reniform, with a gelatinous mucoid sheath. Asexual morph Undetermined.

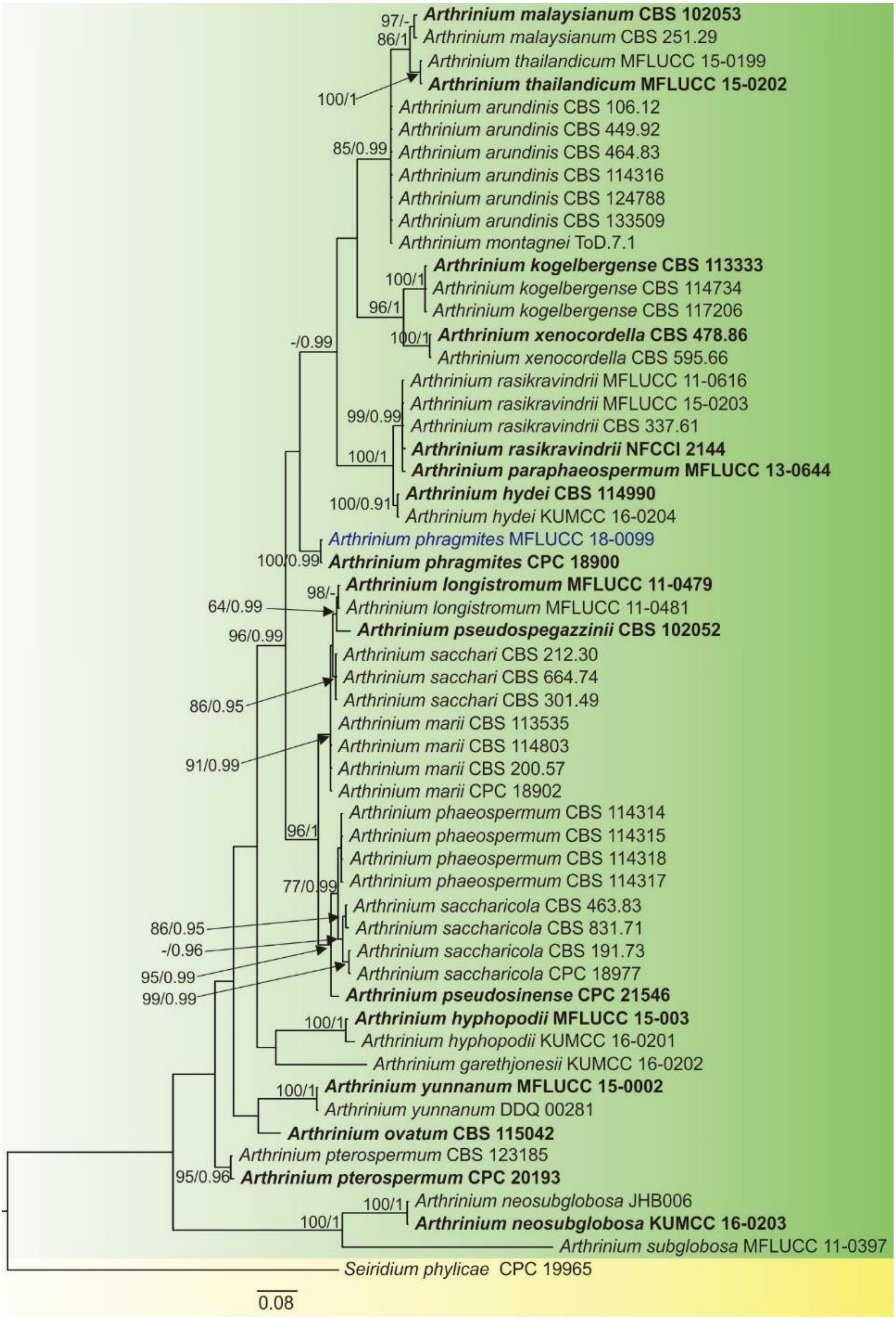

97/-
Arthrinium malaysianum CBS 102053
86/1
Arthrinium malaysianum CBS 251.29
Arthrinium thailandicum MFLUCC 15-0199
Arthrinium thailandicum MFLUCC 15-0202
100/1
Arthrinium arundinis CBS 106.12
Arthrinium arundinis CBS 449.92
85/0.99
Arthrinium arundinis CBS 464.83
Arthrinium arundinis CBS 114316
Arthrinium arundinis CBS 124788
Arthrinium arundinis CBS 133509
Arthrinium montagnei ToD.7.1
Arthrinium kogelbergense CBS 113333
100/1
Arthrinium kogelbergense CBS 114734
96/1
Arthrinium kogelbergense CBS 117206
-/0.99
100/1
Arthrinium xenocordella CBS 478.86
Arthrinium xenocordella CBS 595.66
Arthrinium rasikravindrii MFLUCC 11-0616
Arthrinium rasikravindrii MFLUCC 15-0203
99/0.99
Arthrinium rasikravindrii CBS 337.61
Arthrinium rasikravindrii NFCCI 2144
100/1
Arthrinium paraphaeospermum MFLUCC 13-0644
Arthrinium hydei CBS 114990
100/0.91
Arthrinium hydei KUMCC 16-0204
Arthrinium phragmites MFLUCC 18-0099
100/0.99
Arthrinium phragmites CPC 18900
Arthrinium longistromum MFLUCC 11-0479
98/-
64/0.99
Arthrinium longistromum MFLUCC 11-0481
Arthrinium pseudospegazzinii CBS 102052
96/0.99
Arthrinium sacchari CBS 212.30
Arthrinium sacchari CBS 664.74
86/0.95
Arthrinium sacchari CBS 301.49
Arthrinium marii CBS 113535
Arthrinium marii CBS 114803
91/0.99
Arthrinium marii CBS 200.57
Arthrinium marii CPC 18902
Arthrinium phaeospermum CBS 114314
96/1
Arthrinium phaeospermum CBS 114315
Arthrinium phaeospermum CBS 114318
Arthrinium phaeospermum CBS 114317
77/0.99
Arthrinium saccharicola CBS 463.83
86/0.95
Arthrinium saccharicola CBS 831.71
-/0.96
Arthrinium saccharicola CBS 191.73
95/0.99
Arthrinium saccharicola CPC 18977
99/0.99
Arthrinium pseudosinense CPC 21546
100/1
Arthrinium hyphopodii MFLUCC 15-003
Arthrinium hyphopodii KUMCC 16-0201
Arthrinium garethjonesii KUMCC 16-0202
100/1
Arthrinium yunnanum MFLUCC 15-0002
Arthrinium yunnanum DDQ 00281
Arthrinium ovatum CBS 115042
Arthrinium pterospermum CBS 123185
95/0.96
Arthrinium pterospermum CPC 20193
100/1
Arthrinium neosubglobosa JHB006
100/1
Arthrinium neosubglobosa KUMCC 16-0203
Arthrinium subglobosa MFLUCC 11-0397
Seiridium phylicae CPC 19965
0.08

Figure 88 – Phylogram generated from Bayesian analysis based on ITS sequence data. Related sequences were obtained from GenBank following Dai et al. (2016a). A total of 56 strains are included in the analyses. *Seiridium phylicae* (Sporocadaceae) is used as the outgroup taxon. Tree topology of the Bayesian analysis was similar to the maximum-likelihood analysis. The best scoring RAxML tree with a final likelihood value of -3843.7723 is presented. The matrix had 315 distinct alignment patterns, with 17.11% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.230383, C = 0.251582, G = 0.231302, T = 0.286733; substitution rates AC = 1.068770, AG = 2.218132, AT = 1.683025, CG = 0.944962, CT = 3.903708, GT = 1.000000; gamma distribution shape parameter α = 0.396682. Bootstrap values for ML (≥60) and Bayesian posterior probabilities (≥0.95) are given at the nodes. The newly generated sequence is in blue. The ex-type strains are in bold. The scale bar represents the expected number of nucleotide substitutions per site.

Culture characteristics – Colonies cottony, flat, spreading, with moderate aerial mycelium. On PDA surface dirty white, zonate, with patches of pale luteous, reverse luteous.

Material examined – ITALY, Province of Forlì-Cesena [FC], near Meldola, on dead aerial stem of *Arundo plinii* Turra (Poaceae), 16 January 2017, E. Camporesi, IT3211 (MFLU 17-0310); living culture MFLUCC 18-0099.

GenBank numbers – ITS: MG836697, LSU: MG836698.

Notes – *Arthrinium phragmites* Crous was introduced from Italy on culms of *Phragmites australis* (Crous & Groenewald 2013). The sexual morph and the culture characteristics of the taxon from a dead culm of *Arundo plinii* are similar to *Arthrinium phragmites*. Crous & Groenewald (2013) described some ascospores with remnants of mucoid sheath. The ascospores observed in this study clearly have a mucoid sheath seen following Indian ink treatment, while the asci and ascospore lengths and widths are slightly different (asci CBS H-21267: 70–110 × 17–25 µm, MFLU 17-0310: 90–130 × 15–20 µm; ascospores CBS H-21267: 22–25 × 7–9 µm, MFLU 17-0310: 20–26 × 8–10 µm). The ITS based phylogenetic analyses (100% ITS sequence similarity) also revealed a high support (100%/0.99PP) for this clade and this is a new host record as the *Arthrinium phragmites* on *Arundo plinii* from Italy (Fig. 88).

Sporocadaceae Corda

Jaklitsch et al. (2016a, b) treated Bartaliniaceae, Discosiaceae, Pestalotiopsidaceae and Robillardaceae as synonyms of Sporocadaceae and this is followed in Wijayawardene et al. (2018). This family comprises the genera *Annellolacinia*, *Bartalinia*, *Broomella*, *Ciliochorella*, *Discosia*, *Doliomyces*, *Dyrithiopsis*, *Hyalotiella*, *Immersidiscosia*, *Monochaetia*, *Morinia*, *Monochaetinula*, *Neopestalotiopsis*, *Neotruncatella*, *Pestalotiopsis*, *Pseudopestalotiopsis*, *Robillarda*, *Sarcostroma*, *Seimatosporium*, *Seiridium*, *Strickeria*, *Truncatella* and *Zetiasplozna* (Wijayawardene et al. 2018). In the present paper, we introduce a new species of genus *Discosia* and provide an updated tree for the genus.

Discosia Lib.

Libert (1837) introduced *Discosia* with *D. strobilina* as the type species. Wijayawardene et al. (2017a) treated *Adisciso* as a synonym of *Discosia* agreeing with the 'one fungus one name' concept (Hawksworth 2012). Senanayake et al. (2015) showed that *Discosia sensu stricto* groups with *Adisciso*, *Discostroma*, *Sarcostroma* and *Seimatosporium* as a distinct clade in Amphisphaeriales, and Senanayake et al. (2015) introduced Discosiaceae to accommodate these genera, which is now considered a synonym of Sporocadaceae.

Discosia querci Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 91

Index fungorum number: IF554075; Facesoffungi number: FoF03925

Holotype: MFLU 17-2848

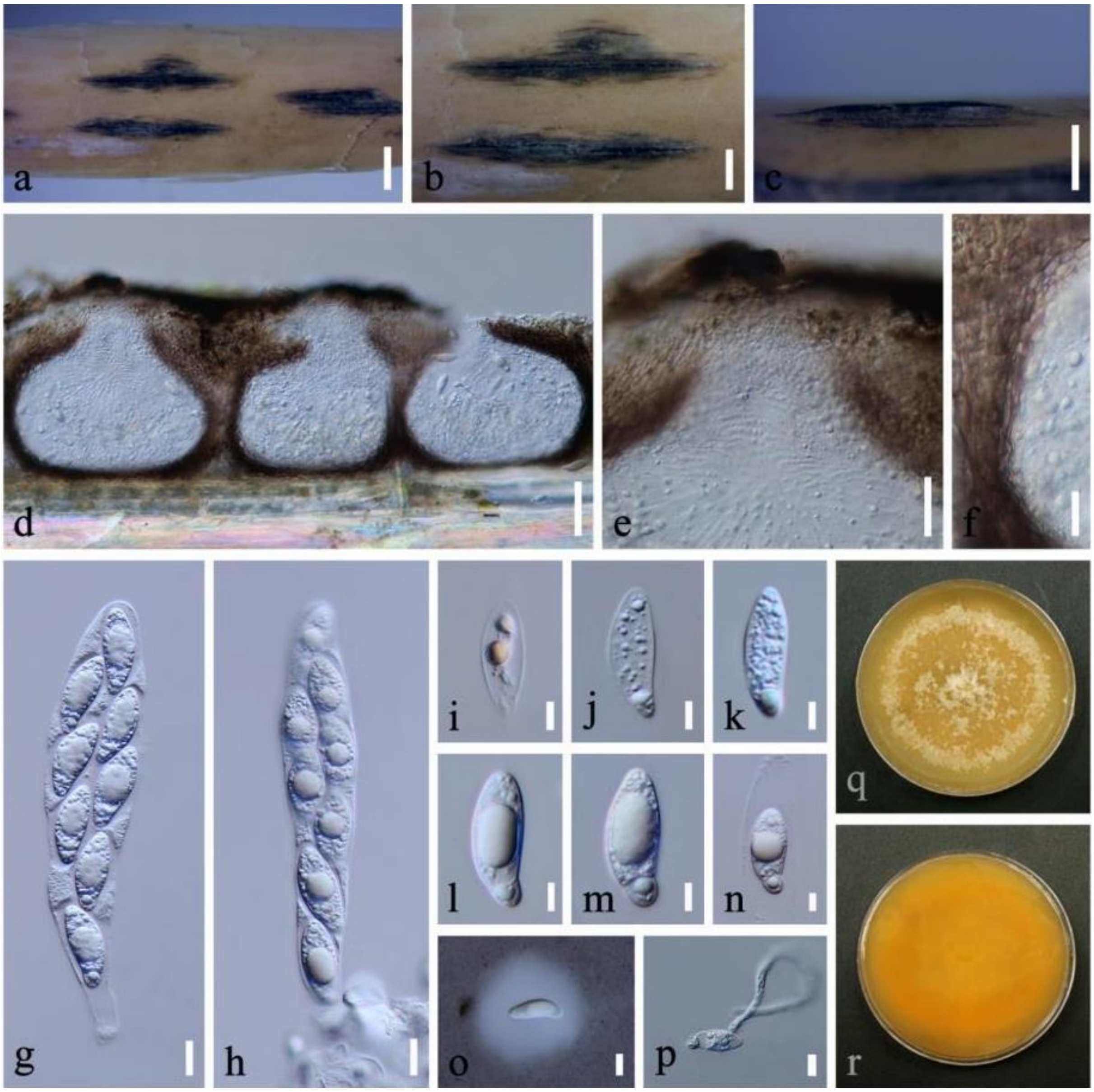


Figure 89 – *Arthrinium phragmites* (MFLU 17-0310). a–c Pseudostromata on the host surface. d Vertical section through pseudostroma. e Ostiole with periphyses. f Peridium. g, h Asci. i–n Ascospores. o Sheath surrounding ascospores after treatment in India ink. p Germinating ascospore. q Upper view of the colony. r Reverse view of the colony. Scale bars: a = 1000 µm, b, c = 500 µm, d = 50µm, e = 20 µm, f–h, o, p = 10 µm, i–n = 5 µm.

Saprobic on dead seeds of *Quercus* sp. fruits. Sexual morph Undetermined. Asexual morph coelomycetous. *Conidiomata* 110–170 µm diameter, 50–80 µm high, ($\bar{x}$ = 150 × 70 µm) pycnidial, stromatic, solitary, scattered to gregarious or confluent, partly immersed or superficial, rounded in outline, glabrous, unilocular, *textura porrecta*, ostiole absence. *Peridium* 10–15 µm thick, composed of 5–6 layers of cells, with outer 5–6 layers dark brown, inner 1–2 layers colourless, comprising thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, arising from the upper cells of the basal stroma. *Conidiogenous cells* 4–8 × 1–3.5 ($\bar{x}$ = 6 × 2) µm, holoblastic, smooth, restricted to the basal conidiomata wall, each producing a single conidium, integrated, hyaline, smooth. *Conidia* 13–20 × 2.5–3 µm ($\bar{x}$= 17 × 2.8 µm, n = 50), hyaline, fusiform to cylindrical, thick-walled, smooth, straight or slightly curved, 3-septate, slightly constricted at one septum at apex, with cells of equal width, basal cell obconic, with a truncate base, apical cell subconical with a rounded apex, unbranched, filiform, flexuous or straight appendage; presence of both ends.

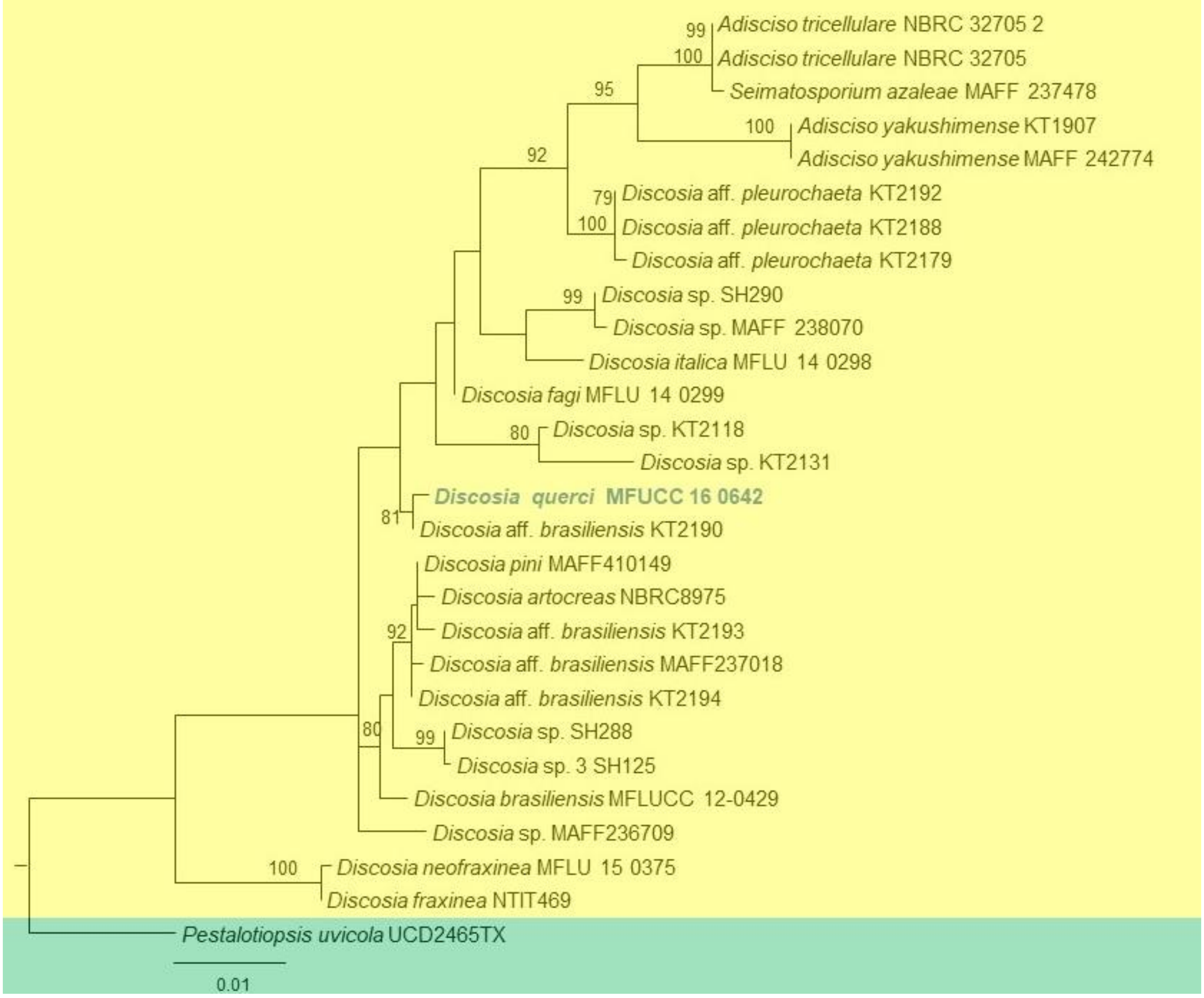


Figure 90 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined LSU and ITS matrix of species from the genus *Discosia*. Related sequences were obtained from GenBank (http://www.ncbi.nlm.nih.gov/). Twenty-eight strains are included in the combined sequence analyses, which comprise 1824 characters with gaps. The best scoring RAxML tree with a final likelihood value of -4959.075067 is presented. The matrix had 262 distinct alignment patterns, with 13.81% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.247425, C = 0.233400, G = 0.257560, T = 0.261614. MLBS above 70% are given at each branch. The tree is rooted with *Pestalotiopsis uvicola* (UCD2465TX). New isolates are in bold and green.

Material examined – UK, Hampshire, Swanick Lakes, on dead seed of *Quercus* sp. (Fagaceae) fruits, 28 September 2015, E.B. Gareth Jones, GJ 195 (MFLU 17-2848, holotype), ex-type living culture, MFUCC 16-0642, BCC; *ibid*. (PDD, isotype).

GenBank numbers – ITS: MG815829, LSU: MG815830, SSU: MG815831.

Notes – Tanaka et al. (2011) introduced four strains of *Discosia* aff. *brasiliensis* (KT2193, KT2190, KT2194 and MAFF237018) from Japan based on morphology and phylogenetic data. Our isolate, clusters with *Discosia* aff. *brasiliensis* (KT2190) with high statistical support (81 ML), but other strains of *Discosia brasiliensis* cluster separately from our isolate and KT 2190. Therefore, in this study, we introduce our strain as a new species of *Discosia*. *Discosia querci* shares similar conidiomata, conidiogenous cells and conidial morphology with *Discosia brasiliensis* (Nag Raj 1993, Tangthirasunun et al. 2015). However, *Discosia querci* differs from *Discosia brasiliensis* in having wider conidiomata (110–170 µm vs. 363–390 µm) and unilocular conidiomtaa. The type species of *Discosia brasiliensis* was identified from a Bignoniaceae host. However, *Discosia* aff. *brasiliensis* (KT2193, KT2190, KT2194 and MAFF237018) and *Discosia brasiliensis* (MFLUCC 12-0429) were isolated from decayed leaves of unknown hosts. *Discosia querci* was collected from seeds of *Quercus* sp. from the UK and in the USDA fungal database, *Discosia* sp. are listed from different *Quercus* sp. in different localities. *Discosia artocreas* has been reported from *Quercus* sp. in the UK, but in multigene phylogenetic analysis our isolate is in a distinct clade to *Discosia artocreas*. We were unable to loan the type of *Discosia quercicola* De Not. and even if we could it is unlikely we could obtain sequence data, and thus would be unable to use this name (Liu et al. 2016).

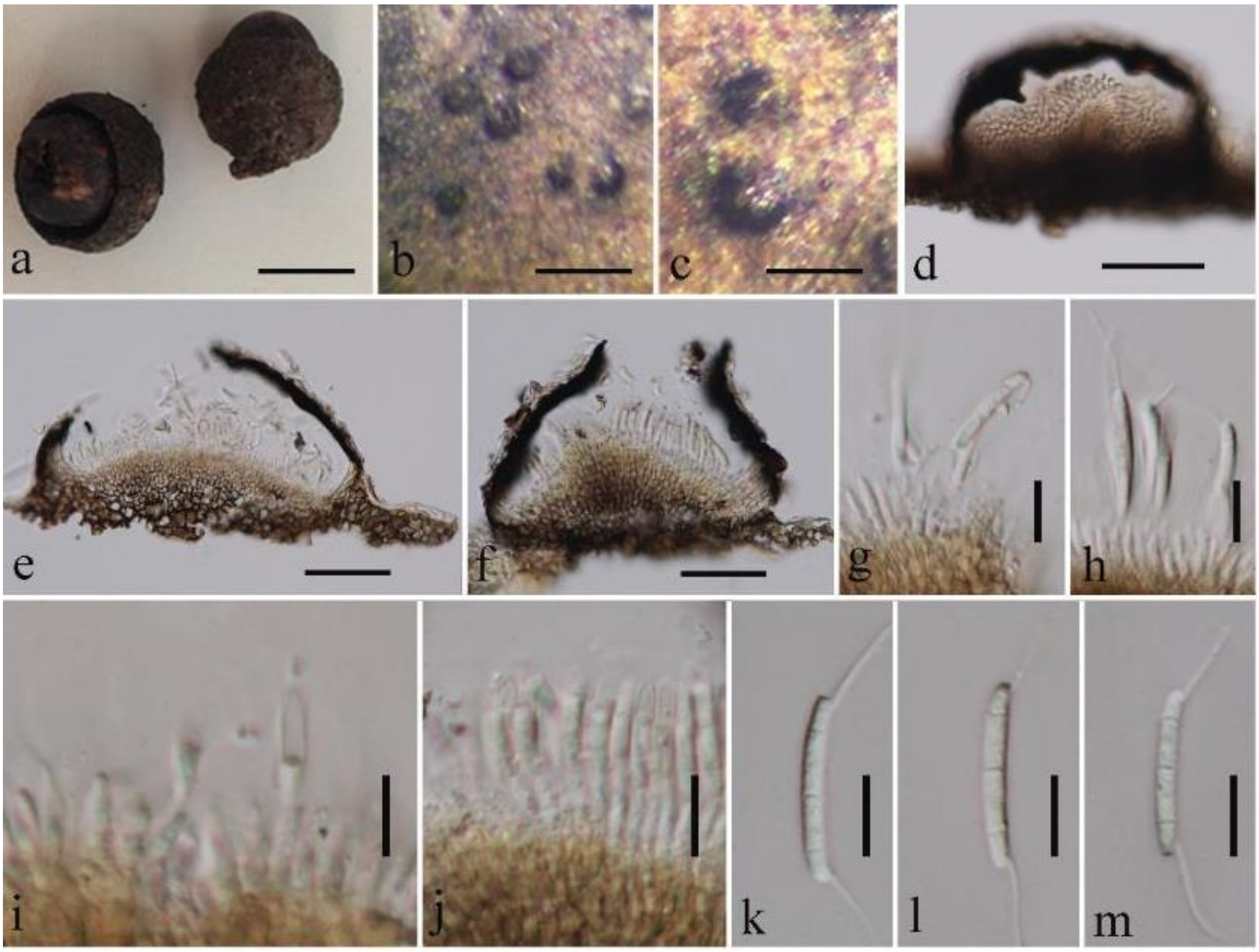


Figure 91 – *Discosia querci* (MFUCC 16-0642, holotype). a Seed samples. b, c Black conidiomata on the host surface. d Vertical section of conidioma. e, f, h Conidiogenous cells and developing conidia. g Section of peridium. i, j Conidia. Scale bars: a = 1 cm, b = 500 µm, c = 200 µm, d = 50 µm, e, f = 30 µm, g–m = 10 µm.

Seimatosporium Corda

The genus was introduced by Corda (1833), the type species is *S. rosae* Corda. Phylogenetic studies indicated that *Seimatosporium* should be placed in Discosiaceae, Amphisphaeriales (Senanayake et al. 2015, Norphanphoun et al. 2015, Wijayawardene et al. 2016). However, Discosiaceae was synonymized under Sporocadaceae with other families Bartaliniaceae, Pestalotiopsidaceae and Robillardaceae based on morphology and phylogeny (Jaklitsch et al. 2016). The asexual/sexual morph connection between *Discostroma* and *Seimatosporium* was confirmed by using a molecular approach (Jeewon et al. 2002, Norphanphoun et al. 2015). Rossman et al. (2016) concluded that the name *Seimatosporium* should be used as it is the oldest name and is most commonly used.

Seimatosporium ciliata (Petr.) Hongsanan & K.D. Hyde, comb. nov. Fig. 92

Index Fungorum number: IF554378; Facesoffungi number: FoF04465

≡ *Neobroomella ciliata* Petr., Sydowia 1(1-3): 5 (1947)

Epiphyte on surface of dead stems of *Phlomis brevilabris* Ehrenb. ex Boiss. Sexual morph *Ascomata* 197−220 µm high × 190−240 µm diameter ($\bar{x}$ = 210 × 200 µm, n = 5), scattered, semi-immersed in host tissue, subglobose to globose or ellipsoid, membranaceous, dark brown to black, with long papilla at the center. *Neck* 130 µm high × 95 µm diameter, papillate, composed of thin, flattened cells of *textura angularis*, hyaline to pale brown. *Peridium* 10−15 µm ($\bar{x}$ = 13 µm, n = 20), two-layered, comprising outer, dark brown to black, cells of *textura angularis* and inner, thin, hyaline, flattened cells of *textura angularis*. *Hamathecium* of 1 µm, pseudoparenchyma, aseptate, embedded in a gelatinous matrix. *Asci* 85−97 × 12−15 µm ($\bar{x}$ = 95 × 14 µm, n = 20), numerous, 8-spored, unitunicate, cylindrical to oblong, with a short pedicel. *Ascospores* 20−24 × 7−9 µm ($\bar{x}$ = 22 × 8 µm, n = 30), biseriate in ascus, 2-layered, 3-septate, oval to ellipsoid, generally straight, rounded at both ends, not constricted at the septum, hyaline, verrucose surface, embedded in gelatinous matrix. Asexual morph Undetermined.

Material examined – SYRIA, Lebanon, Jugi Sanin, in subalpine region, 1700-1900 m., on dead stems of *Phlomis brevilabris* (Lamiaceae), 21 July 1897, J. Bornmüller, (W no. 11029, holotype).

Notes – *Neobroomella* was introduced in Sphaeriales by Petrak (1947) with *N. ciliata* Petr. as the type species. The genus was accepted as Xylariomycetidae genera *incertae sedis* (Lumbsch & Huhndorf 2010, Kirk et al. 2013, Wijayawardene et al. 2017a). Senanayake et al. (2015) and Maharachchikumbura et al. (2015, 2016a) accepted *Neobroomella* in Phlogicylindriaceae, Amphisphaeriales. Sequence data is unavailable. Eriksson (1980) re-studied the herbarium specimen from W (no. 11029) and noted that *Neobroomella ciliata* was in good condition and we made same observation. *Neobroomella ciliata* is identical to species in *Discostroma* (current name *Seimatosporium*) in having semi-immersed ascomata, with a central papilla, unitunicate asci and uniseriate, ellipsoid, transversely septate, hyaline ascospores (Paulus et al. 2006). However, the subapical ring in the ascus apex was not J+ (Fig. 92). Culture and molecular data for *Neobroomella* are unavailable. Therefore, we synonymize *N. ciliata* under the genus *Seimatosporium* based on morphological characters (Fig. 92).

Truncatella Steyaert

The genus *Truncatella* was established by Steyaert (1949) to accommodate *T. truncata* which had distinct 3-septate, verruculose, pigmented conidia (Steyaert 1949, Maharachchikumbura et al. 2015). This genus was previously placed in Amphisphaeriaceae (Jeewon et al. 2002, 2003) and Bartaliniaceae (Senanayake et al. 2015). Jaklitsch et al. (2016a) placed this genus in the family Sporocadaceae. There are 22 species epithets in Index Fungorum (2018), however, there are only eleven estimated species (Wijayawardene et al. 2017a). Species of this genus are saprobes and have a wide terrestrial distribution (Wijayawardene et al. 2017a).

Truncatella angustata (Pers.) S. Hughes, Can. J. Bot. 36: 822 (1958) Fig. 94

≡ *Stilbospora angustata* Pers., Syn. meth. fung. (Göttingen) 1: 96 (1801)

Index Fungorum number: IF307155; Facesoffungi number: FoF04092

Saprobic on dead aerial branch of *Alnus glutinosa* (L.) Gaertn. Sexual morph not observed (after 5 weeks). Asexual morph *Conidiomata* 0.2–0.35 mm diameter ($\bar{x}$ = 0.24 mm, n = 10), pycnidial, semi-immersed to superficial, becoming erumpent at maturity, globose with a flattened base, solitary to aggregated, black. *Conidiomata wall* consisting of outer light brown to hyaline cells of *textura angularis* to *textura globulosa*. *Conidiophores* 23–26 × 2–4.5 µm ($\bar{x}$ = 23× 2 µm, n = 10), hyaline, cylindrical, simple or branched. *Conidiogenous cells* 6–9 µm long, hyaline, simple, cylindrical, integrated, smooth. *Conidia* 18–20 × 7–8 µm ($\bar{x}$ = 19 × 6 µm, n = 40), fusiform, straight, with 3 transverse septa, with a truncate base, age absent.

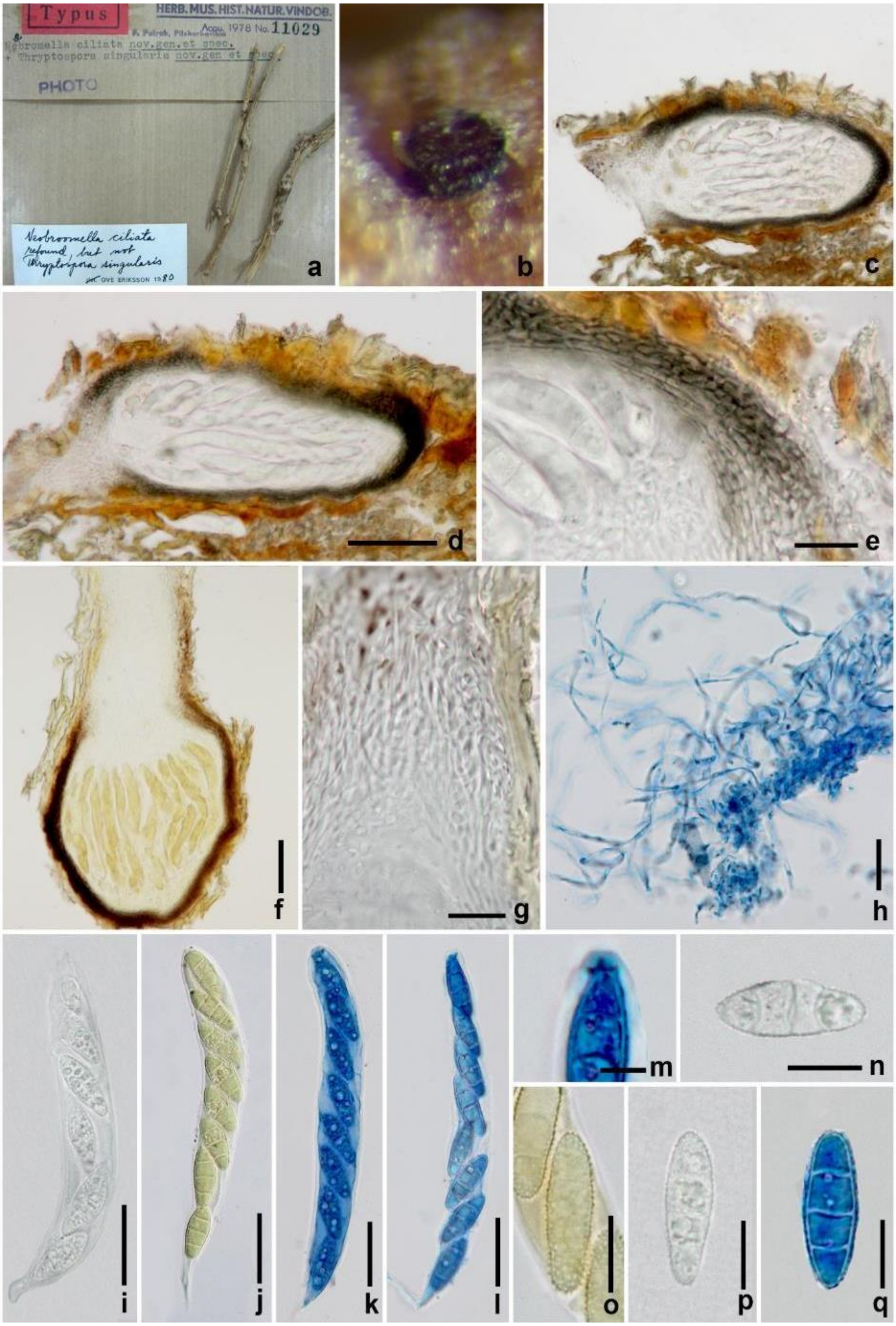


Figure 92 – *Seimatosporium ciliata* (W no. 11029, holotype). a, b Habit and ascoma on substrate. c, d, f Section of ascoma. e Peridium. g, h Pseudoparaphyses. i Ascus. j Ascus in Melzer's reagent. k, l Asci in cotton blue reagent. m Apex of ascus. n, p Ascospores. o Ascospores in Melzer's reagent. q Ascospore in cotton blue reagent. Scale bars: d, f = 50 µm, e, g, h, n−q = 10 µm, i–l = 20 µm, m = 5 µm.

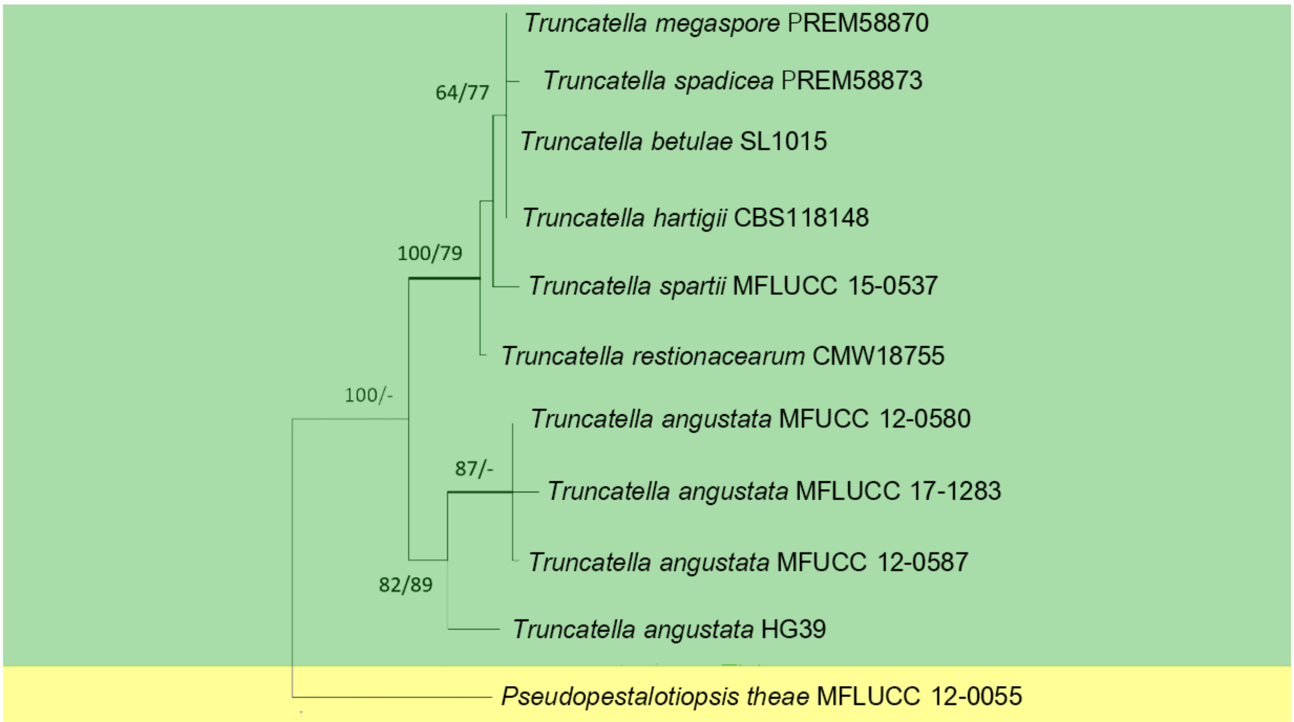


Figure 93 – Phylogenetic tree generated from maximum parsimony analysis based on ITS sequence data of *Truncatella* species. Related sequences were obtained from GenBank. Eleven strains are included in the analyses, which comprise 542 characters including gaps. Tree topology of the MP analysis was similar to the ML and BI. The maximum parsimonious dataset consisted of constant 456, 27 parsimony-informative and 59 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of three equally most parsimonious trees with a length of 102 steps (CI = 0.922, RI = 0.896, RC = 0.826, HI = 0.078) in the first tree. The best scoring RAxML tree with a final likelihood value of -1262.909320 is presented. The matrix had 76 distinct alignment patterns, with 5.32% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.261470, C = 0.234898, G= 0.200531, T = 0.303100; substitution rates AC = 1.928476, AG = 6.544930, AT = 1.879121, CG = 1.234597, CT = 6.560020, GT = 1.000000; gamma distribution shape parameter α = 0.188065. Maximum parsimony bootstrap, maximum likelihood support values higher than 70%, shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.95 (PP) indicated as thickened black branches. The scale bar indicates 0.04 changes. The ex-type strains are in bold and new isolates in blue. The new isolate is shown in blue bold and ex-type strains in black bold. The strain introduced in this study is in blue. The tree is rooted with *Pseudopestalotiopsis theae* (MFLUCC 12-0055).

Culture characteristics – On PDA, fast growing attaining 40 mm diameter after 7 days at 25 °C, serrate margin, white from above, reverse greyish-white. Black pycnidia were observed in the center after 7 days.

Material examined – ITALY, Province of Forli-Cesena [FC], San Benedetto in Alpe, on dead and aerial branch of *Alnus glutinosa* (Betulaceae), 18 April 2016, Erio Camporesi, IT2935 (MFLU 16-1271); living culture MFLUCC 17-1283.

GenBank number – ITS: MG835271.

Material examined – ITALY, Province of Forli-Cesena [FC], San Benedetto in Alpe, on dead and aerial branch of *Alnus glutinosa* (Betulaceae), 18 April 2016, Erio Camporesi, IT2935 (MFLU 16-1271); living culture MFLUCC 17-1283.

GenBank number – ITS: MG835271.

Notes – Phylogeny inferred using sequence data of ITS regions from the isolates obtained in this study with other known isolates of *T. angustata* and other *Truncatella* species in Tibpromma et al. (2017) clustered our isolates with *T. angustata* (100% bootstrap support value and 1.00

Bayesian posterior probability) (Fig. 93). The morphology of our isolates arein full agreement with the description for *T. angustata* (Sutton 1980). *Truncatella angustata* has a wide distribution and this is the first report of this species from *Alnus glutinosa* from Italy.

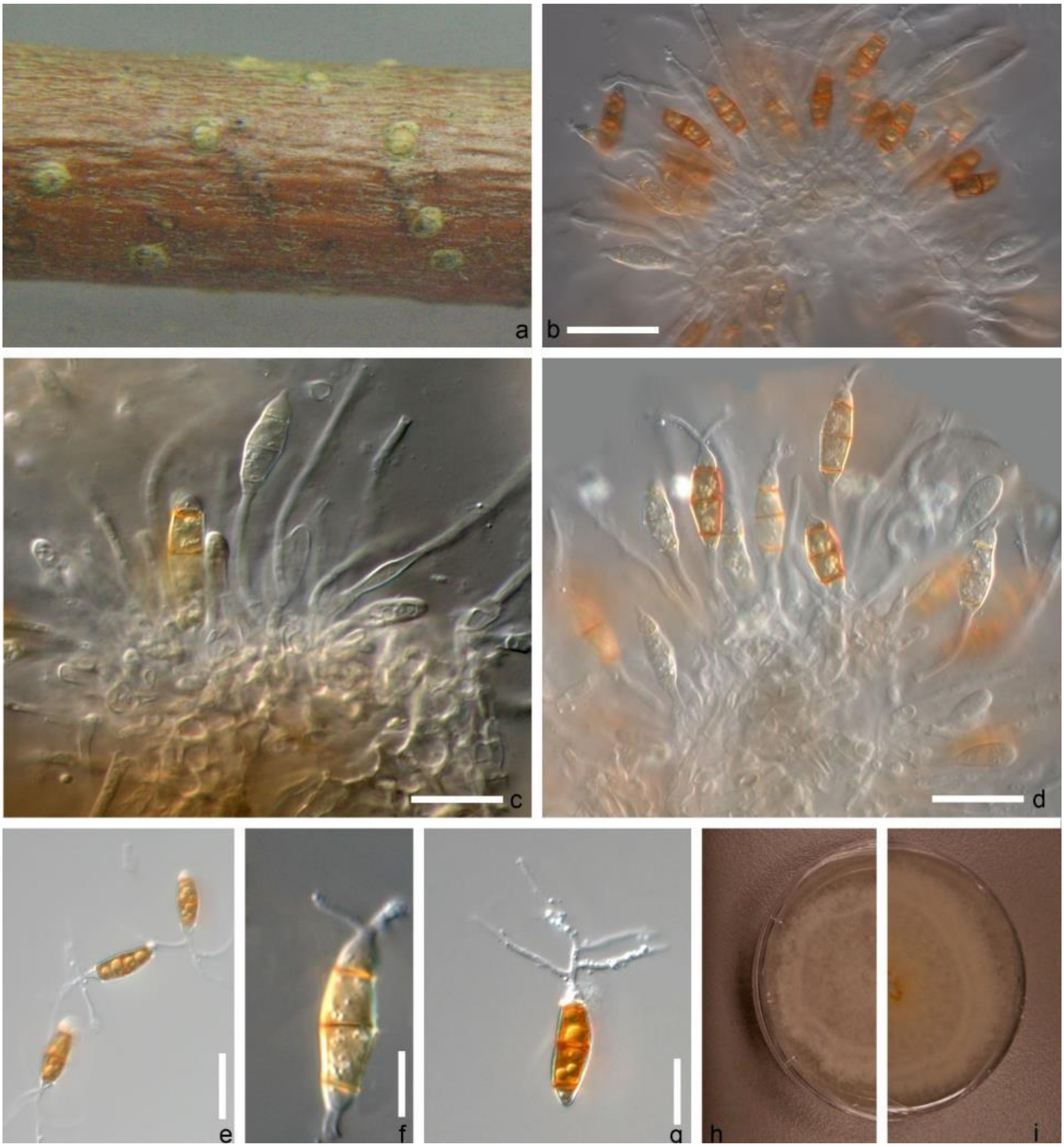


Figure 94 – Morphology of *Truncatella angustata*. a Conidiomata on host tissue. b–d Conidiophores and conidiogenous cells. e Conidia. f Immature conidia. g Branched apical appendages. h Above view of the culture after 7 days. i Reverse view of the culture after 7 days. Scale bars: b–d = 20 µm, e–g = 10 µm.

Acknowledgements

Kevin D. Hyde would like to thank the Thailand Research grants entitled Biodiversity, phylogeny and role of fungal endophytes on above parts of *Rhizophora apiculata* and *Nypa fruticans* (grant no: RSA5980068), the future of specialist fungi in a changing climate: baseline data for generalist and specialist fungi associated with ants, *Rhododendron* species and *Dracaena* species (grant no: DBG6080013), Impact of climate change on fungal diversity and biogeography in the Greater Mekong Subregion (grant no: RDG6130001), Mae Fah Luang University for the grant "Biodiversity, phylogeny and role of fungal endophytes of Pandanaceae" (grant number: 592010200112), ''Diseases of mangrove trees and maintenance of good forestry practice'' (grant number: 60201000201) and Taxonomy diversity, phylogeny and evolution of fungi in Capnodiales (grant no: 666713), for supporting this study. S. Boonmee would like to thank the National Research Council of Thailand (projects No. 61215320013 and No. 61215320023). This work was jointly supported by the National Natural Science Foundation of China (No. 31460012 & 31760014), the Science and Technology Foundation of Guizhou Province (No. [2016]2863). Shaun Pennycook is thanked for checking and suggesting corrections to the Latin names. R. Phookamsak expresses appreciation to The CAS President's International Fellowship for Postdoctoral Researchers, project number 2017PB0072, the Research Fund from China Postdoctoral Science Foundation (grant no. Y71B283261) and Chiang Mai University for financial support. We appreciate the staff at Ranong Mangrove Forest Research Center for giving us knowledge and granting us permission to study and collect specimens. Shi-Ke Huang is particularly grateful to Dr. Qi Zhao for his invaluable suggestions. The Department of Plant Medicine, National Chiayi University (NCYU), Taiwan is thanked for providing facilities for DNA molecular sequencing. Saowaluck Tibpromma thanks the Mushroom Research Foundation (MRF), Chiang Rai, Thailand for financial support. MC Dayarathne thanks the Thailand Research Fund grant no. MRG6080089. Rajesh Jeewon thanks Mae Fah Luang University and University of Mauritius for research support.

References

Abdel-Wahab MA, Abdel-Aziz FA, Mohamed SS, Abdel-Aziz AE. 2011 – *Annulatascus nilensis* sp. nov. a new freshwater ascomycete from the River Nile. Egypt. IMA Fungus 2, 1–6.

Adams GC, Wingfield MJ, Common R, Roux J. 2005 – Phylogenetic relationships and morphology of *Cytospora* species and related teleomorphs (*Ascomycota*, *Diaporthales*, *Valsaceae*) from *Eucalyptus*. Studies in Mycology 52, 1–144.

Adams GC, Roux J, Wingfield MJ. 2006 – *Cytospora* species (Ascomycota, Diaporthales, Valsaceae): introduced and native pathogens of trees in South Africa. Australasian Plant Pathology 35, 521–548.

Aragón G, Otálora MAG, Martínez I. 2005 – New data on the genus *Leptogium* (lichenized Ascomycetes) in the Iberian Peninsula. Nova Hedw 80, 199–226.

Ahmed SA, van de Sande WWJ, Stevens DA, Fahal A et al. 2014 – Revision of agents of black-grain eumycetoma in the order Pleosporales. Persoonia 33, 141–154.

Almeida DAC, Gusmão LFP, Miller AN. 2017 – A new species of *Bertiella* (Melanommataceae) from Brazil and a key to accepted species. Mycosphere 8, 392–396.

Alves A, Correia A, Luque J, Phillips A. 2004 – *Botryosphaeria corticola*, sp. nov. on *Quercus* species, with notes and description of *Botryosphaeria stevensii* and its anamorph, *Diplodia mutila*. Mycologia 96, 598–613.

Ariyawansa HA, Hawksworth DL, Hyde KD, Jones EBG et al. 2014 – Epitypification and neotypification: guidelines with appropriate and inappropriate examples. Fungal Diversity 69, 57–91.

Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B et al. 2015 – Fungal diversity notes 111–252 – Taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 75, 27–274.

Arup U, Søchting U, Frödén P. 2013 – A new taxonomy of the family Teloschistaceae. Nord Journal of Botany 31, 16–83.

Arzanlou M, Groenewald JZ, Gams W, Braun U et al. 2007 – Phylogenetic and morphotaxonomic revision of *Ramichloridium* and allied genera. Studies in Mycology 58, 57–93.

Atkinson TJ, Miller AN, Huhndorf SM, Orlovich DA. 2007 – Unusual new *Chaetosphaeria* species from New Zealand: Intrafamilial diversity and elucidations of the

Chaetosphaeriaceae-Lasiosphaeriaceae relationship (Sordariomycetes, Ascomycotina). New Zealand Journal of Botany 45, 685–706.

Badali H, Chander J, Gulati N, Attri A et al. 2010 – Subcutaneous phaeohyphomycotic cyst caused by *Pyrenochaeta romeroi*. Medical Mycology 48, 763–768.

Barr ME. 1978 – The *Diaporthales* in North America: with emphasis on *Gnomonia* and its segregates. Mycologia Memoirs 7, 1–232.

Barr ME. 1979 – A classification of Loculoascomycetes. Mycologia 71, 935–957.

Barr ME. 1987 – Prodomus to class Loculoascomycetes. Published by the author, Amherst.

Barr ME. 1990 – Prodomus to nonlichenized, pyrenomycetous members of class Hymenoascomycetes. Mycotaxon 39, 43–184.

Barr ME. 1993 – Notes on the Pleomassariaceae. Mycotaxon 49, 129–142.

Barr ME. 2000 – Notes on coprophilous bitunicate ascomycetes. Mycotaxon 76, 105–112.

Boehm EWA, Mugambi GK, Miller AN, Huhndorf SM et al. 2009a – A molecular phylogenetic reappraisal of the *Hysteriaceae*, *Mytilinidiaceae* and *Gloniaceae* (Pleosporomycetidae, Dothideomycetes) with keys to world species. Studies in Mycology 64, 49–83.

Boehm EWA, Schoch CL, Spatafora JW. 2009b – On the evolution of the *Hysteriaceae* and *Mytilinidiaceae* (Pleosporomycetidae, Dothideomycetes, Ascomycota) using four nuclear genes. Mycological Research 113, 461–479.

Boerema GH, de Gruyter J, Noordeloos ME, Hamers MEC. 2004 – *Phoma* identification manual. Differentiation of specific and infra-specific taxa in culture. Centre for Agriculture and Bioscience International. 1–448.

Boonmee S, Ko KTW, Chukeatirote E, Hyde KD. 2012 – Two new *Kirschsteiniothelia* species with a *Dendryphiopsis* anamorphs cluster in Kirschsteiniotheliaceae fam. nov. Mycologia 104, 698–714.

Boonmee S, D'souza MJ, Luo ZL, Pinruan U et al. 2016 – Dictyosporiaceae fam. nov. Fungal Diversity 80, 457–482.

Boonyuen N, Sri-Indrasutdhi V, Suetrong S, Sivichai S et al. 2012 – *Annulatascus aquatorba* sp. nov., a lignicolous freshwater ascomycete from Sirindhorn Peat Swamp Forest, Narathiwat. Thailand. Mycologia 104, 746–757.

Bonorden HF. 1851 – Handbuch der allgemeinen mykologie als anleitung zum studium derselben, nebst speciellen beiträgen zur vervolkommung dieses zweiges der naturkunde. Schweizerbart, Stuttgart, Germany.

Brodo IM, Duran SS, Sharnoff S. 2001 – Lichens of North America. Yale Univ. Press, New Haven.

Cain RF. 1961 – Studies of coprophilous ascomycetes VII. Preussia. Canadian Journal of Botany 39(7), 1633–1666.

Câmara MP, Ramaley AW, Castlebury LA, Palm ME. 2003 – Neophaeosphaeria and Phaeosphaeriopsis, segregates of Paraphaeosphaeria. Mycological Research 107, 516–522.

Carmarán CC, Novas MV. 2003 – A review of Spegazzini taxa of *Periconia* and *Sporocybe* after over 115 years. Fungal Diversity 14, 67–76.

Campbell J, Shearer CA. 2004 – Annulusmagnus and Ascitendus, two new genera in the Annulatascaceae. Mycologia 96, 822–833.

Castlebury LA, Rossman AY, Jaklitsch WJ, Vasilyeva LN. 2002 – A preliminary overview of *Diaporthales* based on large subunit nuclear ribosomal DNA sequences. Mycologia 94, 1017–1031.

Chang DC, Grant GB, O'Donnell K, Wannemuehler KA et al. 2006 – Multistate outbreak of *Fusarium keratitis* associated with use of a contact lens solution. Journal of the American Medical Association 296, 953–963.

Chen Q, Jiang JR, Zhang GZ, Cai L. 2015 – Resolving the *Phoma* Enigma. Studies in Mycology 82, 137–217.

Chen Q, Hou LW, Duan WJ, Crous PW. 2017 – Didymellaceae revisited. Studies in Mycology 87, 105–159. http://doi.org/10.1016/j.simyco.2017.06.002

Chilvers MI, Rogers JD, Dugan FM, Stewart JE et al. 2009 – *Didymella pisi* sp. nov., the teleomorph of *Ascochyta pisi*. Mycological Research 113, 391–400.

Chuaseeharonnachai C, Somrithipol S, Boonyuen N. 2016 – *Periconia notabilis* sp. nov. and a new record and notes on the genus in Thailand. Mycotaxon 131, 491–502.

Cooke MC, Plowright CB. 1879 – British Sphaeriacei. Grevillea 7, 77–89.

Corlett M. 1981 – A taxonomic survey of some species of *Didymella* and Didymella-like species. Canadian Journal of Botany 59, 2016–2042.

Crous PW, Slippers B,Wingfield MJ, Rheeder J et al. 2006 – Phylogenetic lineages in the Botryosphaeriaceae.Studies in Mycology 55, 235–253.

Crous PW, Wingfield MJ. 1993 – A re-evaluation of *Cylindrocladiella*, and a comparison with morphologically similar genera. Mycological Research 97, 433–448.

Crous PW, Groenewald JZ. 2013 – A phylogenetic re-evaluation of *Arthrinium*. IMA Fungus 4, 133–154.

Crous PW, Shivas RG, Quaedvlieg W, Van der Bank M et al. 2014 – Fungal Planet description sheets: 214–280. Persoonia 32, 184–306.

Crous PW, Wingfield MJ, Richardson DM, Le Roux JJ et al. 2016 – Fungal Planet description sheets: 400–468. Persoonia 36, 316–458.

Dai DQ, Jiang HB, Tang LZ, Bhat DJ. 2016a – Two new species of *Arthrinium* (Apiosporaceae, Xylariales) associated with bamboo from Yunnan, China. Mycosphere 7, 1332–1345.

Dai DQ, Phookamsak R, Wijayawardene NN, Li WJ et al. 2016b – Bambusicolous fungi. Fungal Diversity 82, 1–105.

Dayarathne MC, Maharachchikumbura SSN, Phookamsak R, Fryar S et al 2016 – Morpho-molecular characterization and epitypification of *Annulatascus velatisporus*. Mycosphere 7, 1389–1398.

de Almeida DAC, Gusmão LFP, Miller AN. 2014. – A new genus and three new species of hysteriaceous ascomycetes from the semiarid region of Brazil. Phytotaxa 176, 298–308.

de Gruyter J, Noordeloos ME, Boerema GH. 1998 – Contributions towards a monograph of Phoma (Coelomycetes)-I-3. Section Phoma: Taxa with conidia longer than 7 µm. Persoonia 16, 471–490.

de Gruyter JD, Aveskamp MM, Woudenberg JHC, Verkley GJM et al. 2009 – Molecular phylogeny of *Phoma* and allied anamorph genera: towards a reclassification of the Phoma complex. Mycological Research 113, 508–519.

de Gruyter J, Woudenberg JHC, Aveskamp MM, Verkley GJM et al. 2010 – Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. Mycologia 102, 1066–1081.

de Gruyter J, Woudebnerg JHC, Aveskamp MM, Verkley GJM. 2013 – Redisposition of phoma-like anamorphs in Pleosporales. Studies in Mycology 75, 1–36.

Dissanayake AJ, Phillips AJL, Hyde KD, Li XH. 2016 – Botryosphaeriaceae: Current status of genera and species. Mycosphere 7, 1001–1073.

Dissanayake AJ, Phillips AJL, Hyde KD, Yan JY et al. 2017 – The current status of species in *Diaporthe*. Mycosphere 8(5), 1106–1156.

Dissing H. 1992 – Notes on the coprophilous pyrenomycete *Sporormia fimetaria*. Persoonia-Molecular Phylogeny and Evolution of Fungi 14(4), 389–394.

Doilom M, Dissanayake AJ, Wanasinghe DN, Boonmee S et al. 2017 – Microfungi on *Tectona grandis* (teak) in Northern Thailand. Fungal Diversity 82, 107–182.

Durrieu B. 1957 – Deux Hypodermataceae nouvelles sur conifers. Sydowia 1, 356.

Ehrenberg CG. 1818 – Sylvae Mycologicae Berolinenses. Formis Theophili Bruschcke, Berlin, Germany. [In Latin]

Ekanayaka AH, Dissanayake AJ, Jayasiri SC, To-anun C et al. 2016 – *Aplosporella thailandica*; a novel species revealing the sexual-asexual connection in Aplosporellaceae (Botryosphaeriales). Mycosphere 7, 440–447.

Ekanayaka AH, Zhao Q, Hyde KD, Jones EBG. 2018 – Taxonomy and phylogeny of operculate discomycetes: Pezizomycetes. Fungal Diversity (inpress).

Ellis MB. 1971 – Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew, Surrey, England.

Eriksson O, Yue JZ. 1986 – *Bertiella* (Sacc.) Sacc. & Sydow a synonym of *Massarina* Sacc. Mycotaxon 27, 247–253.

Eriksson OE. 2001 – Outline of Ascomycota. Myconet 6, 1–27.

Evans HC, Samson RA. 1984 – *Cordyceps* species and their anamorphs pathogenic on ants (Formicidae) in tropical forest ecosystems II. The Camponotus (Formicinae) complex. Transactions of the British Mycological Society 82, 127–150.

Fan X, Hyde KD, Liu M, Liang Y. 2015 – *Cytospora* species associated with walnut canker disease in China, with description of a new species *C. gigalocus*. Fungal Biology 119, (5).

Farr DF, Rossman AY. 2018 – Fungal Databases, U.S. National Fungus Collections, Systematic Mycology and Microbiology Laboratory, ARS, USDA. https://nt.ars-grin.gov/fungaldatabases/

Fernández FA, Huhndorf SM. 2005 – New species of *Chaetosphaeria*, *Melanopsammella* and *Tainosphaeria* gen. nov. from the Americas. Fungal Diversity 18, 15–57.

Fernández FA, Miller AN, Huhndorf SM, Lutzoni FM et al. 2006 – Systematics of the genus *Chaetosphaeria* and its allied genera: morphological and phylogenetic diversity in north temperate and neotropical taxa. Mycologia 98, 121–130.

Fries EM. 1823 – Systema mycologicum vol 2. Greifswald, Germany. [In Latin]

Gams W, Holubová-Jechová V. 1976 – Chloridium and some other dematiaceous hyphomycetes growing on decaying wood. Studies in Mycology. 13, 1–99.

Gao YH, Liu F, Duan WJ, Crous PW. 2017 – *Diaporthe* is paraphyletic. IMA Fungus 8(1), 153–187.

Gaya E, Navarro-Rosines P, Llimona X, Hladun N. 2008 – Phylogenetic reassessment of the Teloschistaceae (lichen-forming Ascomycota, Lecanoromycetes). Mycological Research 112, 528–546.

Giraldo A, Crous PW, Schumacher RK, Cheewangkoon R et al. 2017 – The Genera of Fungi – G3: *Aleurocystis*, *Blastacervulus*, *Clypeophysalospora*, *Licrostroma*, *Neohendersonia* and *Spumatoria*. Mycological Progress 16, 325-348.

Goh TK, Hyde KD. 1996 – *Cryptophiale multiseptata*, sp. nov. from submerged wood in Australia, and keys to the genus. Mycological Research 100, 999–1004.

Gomes RR, Glienke C, Videira SIR, Lombard L et al. 2013 – *Diaporthe*: A genus of endophytic, saprobic and plant pathogenic fungi. Persoonia 31, 1–41.

Gordillo A, Decock C. 2017 – Myrothecium-like (Ascomycota, Hypocreales) species from tropical areas: Digitiseta gen. nov. and additions to Inaequalispora and Parvothecium. Mycological Progress. doi.org/10.1007/s11557– 017– 1302. 4, 1– 12.

Guarro J. 2013 – Fusariosis, a complex infection caused by a high diversity of fungal species refractory to treatment. European Journal of Clinical Microbiology & Infectious Diseases 32, 1491–1500.

Guatimosim E, Firmino AL, Bezerra JZ, Pereira OL et al. 2015 – Towards a phylogenetic reappraisal of Parmulariaceae and Asterinaceae (Dothideomycetes). Molecular Phylogeny and Evolution of Fungi. Persoonia 35, 230–241.

Guo YL, Zhang ZY. 1999 – A new species of *Dendryphiella*. Mycosystema 18, 236–237.

Hansen K, Perry BA, Dranginis AW, Pfister DH. 2013 – A phylogeny of the highly diverse cup-fungus family Pyronemataceae (Pezizomycetes, Ascomycota) clarifies relationships and evolution of selected life history traits. Mol Phyl Evol 67, 311–335.

Hansford CG. 1946 – The foliicolous Ascomycetes, their parasites and associated fungi. Mycological Papers. 15, 1–240.

Hashimoto A, Matsumura M, Hirayama K, Fujimoto R. 2017 – Pseudodidymellaceae fam. nov.: Phylogenetic affiliations of mycopappus-like genera in Dothideomycetes. Studies in Mycology 87, 187–206.

Hawksworth DL. 1985 – *Kirschsteiniothelia*, a new genus for the *Microthelia incrustans* group (Dothideales). Botanical Journal of the Linnean Society 91, 181–202.

Hawksworth DL. 2012 – Managing and coping with names of pleomorphic fungi in a period of transition. Mycosphere 3(2), 143–155.

Henkel A. 1923 – Neues und Bemerkenswertes der Pilzflora Thüringens. Annales Mycologici 21, 143–149.

Hernández-Restrepo M, Gené J, Castañeda-Ruiz R, Mena-Portales J. 2017 – Phylogeny of saprobic microfungi from Southern Europe. Studies in Mycology 86, 53–97.

Ho WH, Hyde KD, Hodgkiss IJ. 2001 – Fungal communities on submerged wood from streams in Brunei, Hong Kong, and Malaysia. Mycological Research 105, 1492–1501.

Hodhod MS, Abdel-Wahab MA, Bahkali AHA, Hyde KD. 2012 – *Amarenographium solium* sp. nov. from Yanbu Mangroves in the Kingdom of Saudi Arabia. Cryptogamie Mycologie 33, 285–294.

Höhnel Fv. 1909 – Fragmente zur Mykologie: VI. Mitteilung (Nr. 182 bis 288). Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Math-naturw Klasse Abt I 118, 275–452.

Hongsanan S, Chomnunti P, Crous PW, Chukeatirote E. 2014 – Introducing *Chaetothyriothecium*, a new genus of Microthyriales. Phytotaxa 161, 157–164.

Hongsanan S, Maharachchikumbura SS, Hyde KD, Samarakoon MC et al. 2017 – An updated phylogeny of Sordariomycetes based on phylogenetic and molecular clock evidence. Fungal Diversity 84, 25–41.

Huang SK, Jeewon R, Wanasinghe DN, Manawasinghe IS et al. 2017 – Phylogenetic taxonomy of *Dematiopleospora fusiformis* sp. nov. (Phaeosphaeriaceae) from Russia. Phytotaxa 316 (3), 239–349.

Huhndorf SM, Fernández FA, Taylor JE, Hyde KD. 2001 – Two pantropical Ascomycetes: *Chaetosphaeria cylindrospora* sp. nov. and a Rimaconus, a new genus for Lasiosphaeria jamaicensis. Mycologia 93, 1072–1080.

Huhndorf SM, Miller AN, Fernández FA. 2004 – Molecular systematics of the Sordariales: the order and the family Lasiosphaeriaceae redefined. Mycologia 96, 368–387.

Hyde KD. 1992 – The genus *Saccardoella* from intertidal mangrove wood. Mycologia 84, 803–810.

Hyde KD, Fröhlich J, Taylor JE. 1998 – Fungi from palms. XXXVI. Reflections on unitunicate ascomycetes with apiospores. Sydowia 50, 21–80.

Hyde KD, Jones EBG, Liu JK, Ariyawansa H et al. 2013 – Families of Dothideomycetes. Fungal Diversity 63, 1–313.

Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA et al. 2014 – One stop shop: backbones trees for important phytopathogenic genera: I. Fungal Diversity 67, 21–125.

Hyde KD, Hongsanan S, Jeewon R, Bhat DJ et al. 2016 – Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 80, 1–270.

Hyde KD, Maharachchikumbura SSN, Hongsanan S, Samarakoon MC et al. 2017a – The ranking of fungi—a tribute to David L. Hawksworth on his 70th birthday. Fungal Diversity 84, 1–23.

Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A et al. 2017b – Fungal diversity notes 603–708: Taxonomic and phylogenetic notes on genera and species. Fungal Diversity 87, 1–235.

Hywel-Jones N. 1995 – *Cordyceps sphecocephala* and a *Hymenostilbe sp*. infecting wasps. Mycological Research 99, 154–158.

Hywel-Jones NL. 1996 – *Cordyceps myrmecophila*-like fungi infecting ants in the leaf litter of tropical forest in Thailand. Microbiological Research 100, 613–619.

Index Fungorum. – 2018 http://www.indexfungorum.org/Names/Names.asp

Jaklitsch W, Baral HO, Lu¨cking R, Lumbsch HT. 2016a – Ascomycota. In: Frey W (ed) Syllabus of plant families—Adolf Engler’s syllabus der Pflanzenfamilien. Borntraeger, Stuttgart.

Jaklitsch WM, Gardiennet A, Voglmayr H. 2016b – Resolution of morphology-based taxonomic delusions: *Acrocordiella, Basiseptospora, Blogiascospora, Clypeosphaeria*, *Hymenopleella, Lepteutypa*, *Pseudapiospora*, *Requienella*, *Seiridium* and *Strickeria*. Persoonia 37, 82–105.

Jaklitsch WM, Voglmayr H. 2017 – Three former taxa of *Cucurbitaria* and considerations on *Petrakia* in the Melanommataceae. Sydowia 69, 81–95.

Jayasiri SC; Hyde KD; Jeewon R, Bhat JD. 2016 – *Neooccultibambusa jonesii*, a novel taxon within Occultibambusaceae. Mycosphere. 7(9), 1458–1472.

Jayasiri SC, Hyde KD, Jones EBG, Jeewon R. 2017 – Taxonomy and multigene phylogenetic evaluation of novel species in *Boeremia* and *Epicoccum* with new records of *Ascochyta* and *Didymella* (Didymellaceae). Mycosphere 8, 1080–1101.

Jeewon R, Hyde KD. 2016 – Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7, 1669–1677.

Jeewon R, Liew EC, Hyde KD. 2002 – Phylogenetic relationships of *Pestalotiopsis* and allied genera inferred from ribosomal DNA sequences and morphological characters. Molecular Phylogenetics and Evolution, 25(3), 378–392.

Jeewon R, Liew ECY, Hyde KD. 2003 – Molecular systematics of the Amphisphaeriaceae based on cladistic analyses of partial LSU rDNA gene sequences. Mycological Research 107(12), 1392–1402.

Jones EBG, Suetrong S, Cheng WH, Rungjindamai N et al. 2014 – An additional fungal lineage in the Hypocreomycetidae (*Falcocladium* species) and the taxonomic re-evaluation of *Chaetosphaeria chaetosa* and *Swampomyces species*, based onmorphology, ecology and phylogeny. Cryptog Mycol 35, 119–138.

Jones EBG, Suetrong S, Sakayaroj J, Bahkali AH et al. 2015 – Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. Fungal Diversity 73, 1–72.

Kaiser WJ, Wang BC, Rogers JD. 1997 – *Ascochyta fabae* and *A. lentis*: host specificity, teleomorphs (Didymella), hybrid analysis, and taxonomic status. Plant Disease 81, 809–816.

Kantvilas G. 2016 – A synopsis and key for the lichen genus Caloplaca (Teloschistaceae) on Kangaroo Island, with the description of two new species. Journal of the Adelaide Botanic Gardens 29, 53–69.

Khan Z, Ahmad S, Kapila K, Ramaswamy NV et al. 2011 – *Pyrenochaeta romeroi*: a causative agent of phaeohyphomycotic cyst. Journal of Medical Microbiology 60, 842–846.

Kirk MP, Cannon PF, Minter DW, Stalper JA. 2008 – Dictionary of the fungi (10th ed). CABI.

Kirk PM, Stalpers JA, Braun U, Crous PW et al. 2013 – A without prejudice list of generic names of fungi for protection under the International Code of Nomenclature for algae, fungi, and plants. IMA Fungus 4, 381–443.

Knapp DG, Kovács GM, Zajta E, Groenewald JZ et al. 2015 – Dark septate endophytic pleosporalean genera from semiarid areas. Persoonia 35, 87–100.

Kruys A, Eriksson OE, Wedin M. 2006 – Phylogenetic relationships of coprophilous Pleosporales (Dothideomycetes, Ascomycota), and the classification of some bitunicate taxa of unknown position. Mycological Research 110(5), 527–536.

Lantz H, Johnston PR, Park D, Minter DW. 2011 – Molecular phylogeny reveals a core clade of Rhytismatales. Mycologia 103, 57–74.

Leuchtmann A, Clémençon H. 2012 – The taxonomic position of the genus *Heydenia* (Pyronemataceae, Pezizales) based on molecular and morphological data. Mycological Progress 11, 699–710.

Li WJ, Liu JK., Bhat DJ, Camporesi E et al. 2015 – Molecular phylogenetic analysis reveals two new species of *Discosia* from Italy. Phytotaxa 203, 37–46.

Li GJ, Hyde KD, Zhao RL, Hongsanan S. 2016a – Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 78, 1–237.

Li J, Phookamsak R, Mapook A, Boonmee S et al. 2016b – *Seifertia shangrilaensis sp. nov*.(Melanommataceae), a new species from Southwest China. Phytotaxa 273, 34–42.

Li ZJ, Taylor JE, Hou CL. 2016c – An unusual *Lophodermium* species on needles of *Pinus taiwanensis* from China. Mycological Progress 15, 1229– 1237.

Li J, Jeewon R, Luo Z, Phookamsak R et al. 2017 – Morphological characterization and DNA based taxonomy of *Fusiconidium* gen. nov. with two novel taxa within Melanommataceae (Pleosporales). Phytotaxa 308, 206–218.

Libert MA. 1830 – Mémoire concernant les plantes cryptogames qui peuent être réunies sous le nom d' Ascoxytacei. Mem. Journal of the Science of Food and Agriculture. 1831, 174–176.

Libert MA. 1837 – Plantae Cryptogamae, quas in Arduenna collegit. Fasc 4, 301–400.

Liew ECY, Aptroot A, Hyde KD. 2001 – Phylogenetic significance of the pseudoparaphyses in Loculoascomycete taxonomy. Molecular Phylogeny and Evolution 16, 392-402.

Lin CG, Dai DQ, Bhat DJ, Hyde KD et al. 2017 – *Alfaria avenellae* sp. nov. from Italy. Phytotaxa 332, 67–74.

Linaldeddu BT, Franceschini A, Alves A, Phillips AJ. 2013 – *Diplodia quercivora* sp. nov.: a new species of *Diplodia* found on declining *Quercus canariensis* trees in Tunisia. Mycologia 105, 1266–1274.

Liu CY, Zhuang WY. 2006 – Relationships among some members of the genus *Otidea* (Pezizales, Pyronemataceae). Fungal Diversity 23, 181–192.

Liu F, Cai L. 2013 – A novel species of *Gliocladiopsis* from freshwater habitat in China. Cryptogamie, Mycologie 34, 233–241.

Liu JK, Phookamsak R, Doilom M, Wikee S. 2012 – Towards a natural classification of Botryosphaeriales. Fungal Diversity 57, 149–210.

Liu JK, Hyde KD, Jones EBG, Ariyawansa AA et al. 2015 – Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. Fungal Diversity 72, 1–197.

Liu JK, Yang J, Maharachchikumbura SSN, McKenzie EHC. 2016 – Novel chaetosphaeriaceous hyphomycetes from aquatic habitats. Mycological Progress 15, 1157– 1167.

Liu JK, Hyde KD, Jeewon R, Phillips AJL et al. 2017a – Ranking higher taxa using divergence times: a case study in Dothideomycetes. Fungal Diversity 84, 75−99.

Liu NG, Hongsanan S, Yang J, Lin CG et al. 2017b – *Dendryphiella fasciculata* sp. nov. and notes on other *Dendryphiella* species. Mycosphere 8, 1575–1586.

Locquin M. 1984 – Mycologie générale et structurale. Paris, French, Masson. p. 551.

Lombard L, Crous PW. 2012 – Phylogeny and taxonomy of the genus *Gliocladiopsis*. Persoonia 28, 25–33.

Lombard L, Houbraken J, Decock C, Samson RA et al. 2016 – Generic hyper-diversity in Stachybotriaceae. Persoonia 36, 156–246.

Luangsa-ard JJ, Tasanathai K, Mongkolsamrit S, Hywel-Jones NL. 2008 – Atlas of invertebrate-pathogenic fungi of Thailand. National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency.

Lücking R, Hodkinson BP, Leavitt SD. 2016 – The 2016 classification of lichenized fungi in the Ascomycota and Basidiomycota – Approaching one thousand genera. Bryologist 119, 361–416.

Lumbsch HT, Huhndorf SM. 2010 – Outline of Ascomycota 2009. Myconet 14, 1–64.

Luo ZL, Bahkali AH, Liu XY, Phookamsak R et al. 2016 – *Poaceascoma aquaticum* sp. nov. (Lentitheciaceae), a new species from submerged bamboo in freshwater. Phytotaxa 253, 71–80.

Luo ZL, Hyde KD, Bhat DJ, Jeewon R et al. 2017 – Morphological and molecular taxonomy of novel species Pleurotheciaceae from freshwater habitats in Yunnan, China. Mycological progress. https://doi.org/10.1007/s11557-018-1377-6

Luttrell ES. 1973 – Loculoascomycetes. In: Ainsworth GC, Sparrow FK, Sussman AS, editors. The fungi, an advanced treatise, vol. 4 A. A taxonomic review with keys: ascomycetes and fungi imperfecti. Academic; New York & London.

Maharachchikumbura SSN, Crous PW, Groenewald JZ, Xu J. 2014 – *Pestalotiopsis* revisited. Studies in Mycology 79, 121–186.

Maharachchikumbura SN, Hyde KD, Jones EBG, McKenzie EHC et al. 2015 – Towards a natural classification and backbone tree for *Sordariomycetes*. Fungal Diversity 72, 199–301

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016a – Families of Sordariomycetes. Fungal Diversity 79, 1–317.

Maharachchikumbura SSN, Larignon P, Hyde KD, Abdullah M. 2016b – Characterization of *Neopestalotiopsis*, *Pestalotiopsis* and *Truncatella* species associated with grapevine trunk diseases in France. Phytopathologia Mediterranea; Florence 55, 380–390.

Mains EB. 1940 – Species of *Cordyceps*. Mycologia 32, 310–320.

Markovskaja S, Kačergius A. 2014 – Morphological and molecular characterization of *Periconia pseudobyssoides* sp. nov. and closely related *P. byssoides*. Mycological Progress 13, 291–302.

Mason EW, Ellis MB. 1953 – British species of *Periconia*. Mycological Papers 56, 1–127.

Matsushima T. 1971 – Microfungi of the Solomon Islands and Papua-New Guinea. Published by the author, Kobe, Japan.

Matočec N, Kušan I, Ozimec R. 2014 – The genus Polycephalomyces (Hypocreales) in the frame of monitoring Veternica cave (Croatia) with a new segregate genus Perennicordyceps. Ascomycete.org 6, 125–133.

Mehrabi M, Hemmati R, Asgari B. 2017 – *Kirschsteiniothelia arasbaranica* sp. nov., and an emendation of the Kirschsteiniotheliaceae. Cryptogamie, Mycologie 38, 13–25.

Minter DW, Staley JM, Millar CS. 1978 – Four species of *Lophodermium* on *Pinus sylvestris*. Transactions of the British Mycological Society, 71, 295–301.

Minter DW, Peredo HL, Watson A. 2007 – Acrospermum chilense sp. nov. from Chile and the Acrospermales ord. nov. Boletín de la Sociedad Argentina de Botánica 42, 107–112.

Montagne JPFC. 1834 – Notice sur les plantes cryptogames récemment découvertes en France, contenant aussi l'indication précise des localités de quelques espèces les plus rares de la flore française. Annales des Sciences Naturelles Botanique. 1, 295–307.

Mugambi GK, Huhndorf SM. 2009 – Molecular phylogenetics of pleosporales: melanommataceae and lophiostomataceae re-circumscribed (pleosporomycetidae, dothideomycetes, Ascomycota). Studies in Mycology 64, 103–121.

Müller E, von Arx JA. 1962 – Die Gattungen der didymosporen pyrenomyceten. Beitr Krypt Fl Schweiz 11, 1–922.

Munk A. 1957 – Danish Pyrenomycetes. A preliminary flora. Dansk Botanisk Arkives 17(1), 1–491.

Nannizzi A. 1934 – Repertorio sistematico dei miceti dell' uomo e degli animali. Trattato di Micopatologia Umana 4, 1–557.

Nag Raj TR. 1993 – Coelomycetous anamorphs with appendage-bearing conidia, Waterloo, Ontario, Canada, Mycologue Publications, 1101 pp.

Nash TH, Ryan BD, Diederich P, Gries C. 2004 – Lichen Flora of the Greater Sonoran Desert Region. Vol. II. pp. 742. Lichen Unlimited: Arizona State University, Tempe.

Nimis PL, Martellos S. 2017 – ITALIC - The Information System on Italian Lichens. Version 5.0. University of Trieste, Dept. of Biology, (http://dryades.units.it/italic).

Nitschke TRJ. 1870 – Pyrenomycetes Germanici. Die Kernpilze Deutschlands Bearbeitet von Dr. Th. Nitschke 2, 161–320. Breslau, Eduard Trewent.

Norphanphoun C, Doilom M, Daranagama DA, Phookamsak R et al. 2017a – Revisiting the genus *Cytospora* and allied species. Mycosphere 8, 51–97.

Norphanphoun C, Jeewon R, Mckenzie EHC, Wen TC. 2017b – Taxonomic position of *Melomastia italica sp. nov.* and phylogenetic reappraisal of *Dyfrolomyces*. Cryptogamie Mycologie 38, 507–525.

Olariaga I, Van Vooren N, Carbone M, Hansen K. 2015 – A monograph of *Otidea* (Pyronemataceae, Pezizomycetes). Persoonia 35, 166–229.

Otálora MAG, Martínez I, Molina MC, Aragón G et al. 2008 – Phylogenetic relationships and taxonomy of the Leptogium lichenoides group (Collemataceae) in Europe. Taxon 57, 907–921.

Otálora MAG, Aragón G, Martínez I, Wedin M. 2013 – Cardinal characters on a slippery slope – A re-evaluation of phylogeny, character evolution, and evolutionary rates in the jelly lichens (Collemataceae s. str). Mol Phyl Evol 68, 185–198.

Otálora MAG, Jorgensen PM, Wedin M. 2014 – A revised generic classification of the jelly lichens, Collemataceae. Fung Divers 64, 275–293.

Pang KL, Hyde KD, Alias SA, Suetrong S. 2013 – *Dyfrolomycetaceae*, a new family in the Dothideomycetes, Ascomycota. Cryptogamie Mycologie 34, 223–232.

Parkinson LE, Shivas RG, Dann EK. 2017 – Novel species of *Gliocladiopsis* (Nectriaceae, Hypocreales, Ascomycota) from avocado roots (*Persea americana*) in Australia. Mycoscience 58, 95–102.

Paulus BC, Gadek PA, Hyde KD. 2006 – *Discostroma ficicola* sp. nov. (Amphisphaeriaceae) and a key to species of *Discostroma*. Sydowia 58, 76–90.

Penzig AGO, Saccardo PA. 1897 – Diagnoses fungorum novorum in insula Java collectorum. Ser Prim Malpighi 11, 387–409.

Perera RH, Maharachchikumbura SSN, Bhat JD, Al-Sadi AM et al. 2016 – New species of *Thozetella* and *Chaetosphaeria* and new records of *Chaetosphaeria* and *Tainosphaeria* from Thailand. Mycosphere 7, 1301–1321.

Petch T. 1931 – Notes on entomogenous fungi. Transactions of the British mycological Society 16, 55–75.

Petch T. 1932 – A list of the entomogenous fungi of Great Britain. Transactions of the British mycological Society 17, 170–178.

Petrak VF. 1947 – *Neobroomella* n. gen., eine neue Gattung der Sphaeriales. Sydowia 1, 5.

Phillips AJL, Alves A, Pennycook SR, Johnston PR et al. 2008 – Resolving the phylogenetic and taxonomic status of dark-spored teleomorph genera in the Botryosphaeriaceae. Persoonia 21, 29–55.

Phillips AJL, Lopes J, Abdollahzadeh J, Bobev S. 2012 – Resolving the *Diplodia* complex on apple and other Rosaceae hosts. Persoonia 29, 29–38.

Phillips AJ, Alves A, Abdollahzadeh J, Slippers B et al. 2013 – The Botryosphaeriaceae: genera and species known from culture. Studies in Mycology 76, 51–167.

Phillips AJL, Alves A, Correia A, Luque J. 2005 – Two new species of Botryosphaeria with brown, 1-septate ascospores and Dothiorella anamorphs. Mycologia 97, 513–529.

Phookamsak R, Liu JK, Manamgoda DS, Wanasinghe DN et al. 2014a – Epitypification of two bambusicolous fungi from Thailand. Cryptogamie Mycologie 35, 239–256.

Phookamsak R, Liu JK, McKenzie EHC, Manamgoda DS et al. 2014b – Revision of Phaeosphaeriaceae. Fungal Diversity 68, 159–238.

Phookamsak R, Manamgoda DS, Li WJ, Dai DQ et al. 2015a – *Poaceascoma helicoides* gen et sp. nov., a new genus with scolecospores in Lentitheciaceae. Cryptogamie Mycologie, 36, 225–236.

Phookamsak R, Norphanphoun C, Tanaka K, Dai DQ et al. 2015b – Towards a natural classification of Astrosphaeriella-like species; introducing Astrosphaeriellaceae and Pseudoastrosphaeriellaceae fam. nov. and *Astrosphaeriellopsis*, gen. nov. Fungal Diversity 74, 143–197.

Phookamsak R, Wanasinghe DN, Hongsanan S, Phukhamsakda C et al. 2017 – Towards a natural classification of *Ophiobolus* and ophiobolus-like taxa; introducing three novel genera *Ophiobolopsis*, *Paraophiobolus* and *Pseudoophiobolus* in Phaeosphaeriaceae (Pleosporales). Fungal Diversity 87, 299–339.

Phukhamsakda C, Ariyawansa HA, Phillips AJL, Wanasinghe DN et al. 2016 – Additions to Sporormiaceae: Introducing two novel genera, *Sparticola* and *Forliomyces*, from Spartium. Cryptogamie Mycologie 37, 75–97.

Pirozynski KA. 1968 – *Cryptophiale,* a new genus of Hyphomycetes. Canadian Journal of Botany 46(9), 1123–1127.

Quandt CA, Kepler RM, Gams W, Araújo JP et al. 2014 – Phylogenetic-based nomenclatural proposals for Ophiocordycipitaceae (Hypocreales) with new combinations in *Tolypocladium*. IMA Fungus 5, 121–134.

Rai AN, Kamal. 1986 – Fungi of Gorakhpur—XLII. Kavaka 14 (1–2), 31–36.

Ranojevic Nv. 1914 – Dritter beitrag zur pilzflora serbiens. Annales Mycologici 12(4), 393–421.

Réblová M, Barr ME, Samuels GJ. 1999 – *Chaetosphaeriaceae*, a new family for *Chaetosphaeria* and its relatives. Sydowia 51, 49–70.

Réblová M. 2007 – *Barbatosphaeria* gen. et comb. nov., a new genus for *Calosphaeria barbirostris*. Mycologia 99, 723–732.

Réblová M, Seifert KA, Fournier J, Štěpánek V. 2012 – Phylogenetic classification of Pleurothecium and Pleurotheciella gen. nov. and its dactylaria-like anamorph (Sordariomycetes) based on nuclear ribosomal and protein-coding genes. Mycologia 104(6), 1299–1314.

Réblová M, Réblová K, Štěpánek V. 2015 – Molecular systematics of *Barbatosphaeria* (Sordariomycetes): multigene phylogeny and secondary ITS structure. Persoonia 35, 21–38.

Réblová M, Seifert KA, Fournier J, Štěpánek V. 2016 – Newly recognised lineages of perithecial ascomycetes: the new orders Conioscyphales and Pleurotheciales. Persoonia 37, 57–81.

Révay Á. 1985 – Dematiaceous Hyphomycetes inhabiting forest debris in Hungary I. Studia Botanica Hungarica 18, 65–71.

Rossman AY. 1996 – Morphological and molecular perspectives on systematics of the Hypocreales. Mycologia 88, 1–19.

Rossman AY 2000 – Towards monophyletic genera in the holomorphic Hypocreales. Studies in Mycology 45, 27–34.

Rossman AY, Samuels GJ, Rogerson CT, Lowen R. 1999 – Genera of *Bionectriaceae*, *Hypocreaceae* and *Nectriaceae* (Hypocreales, Ascomycetes). Studies in Mycology 42, 1–248.

Ruiz RF, Velásquez S, Cano J, Saikawa M et al. 2002 – *Phaeoisaria aguileraeanam*. sp. nov. from submerged wood in Cuba with notes and reflections in the genus Phaeoisaria. Cryptogamie Mycologia 23(1), 9–18.

Saccardo PA. 1883 – Sylloge Pyrenomycetum, Vol. II. Sylloge Fungorum 2, 635.

Saccardo PA, Berlese AN. 1885 – Fungi Brasilienses a cl. B. Balansa lecti (3). Revue Mycologique Toulouse 7, 155–158.

Saccardo PA, Paoletti G. 1888 – Mycetes Malacenses. Funghi della penisola di Malacca raccolti nel 1885 dell. Ab. Benedetto Scortechini". Atti dell´Istituto Veneto Scienze. 6 (in Italian). 6, 387–428 (see p. 410).

Saccardo PA, Sydow P. 1899 – Sylloge Fungorum 14, 1–724.

Saksena SB. 1954 – A new genus of *Moniliaceae*. Mycologia 46, 660–666.

Santos JM, Vrandečić K, Ćosić J, Duvnjak T, Phillips AJL. 2011 – Resolving the *Diaporthe* species occurring on soybean in Croatia. Persoonia 27:9–19.

Schoch CL. Shoemaker RA, Seifert KA, Hambleton S. – 2006 A multigene phylogeny of the Dothideomycetes using four nuclear loci. Mycologia 98, 1041–1052.

Schoch CL. Crous PW, Groenewald JZ, Boehm EWA. 2009 – A class-wide phylogenetic assessment of Dothideomycetes. Studies in mycology. 64, 1–15.

Schroers HJ, Gräfenhan T, Nirenberg HI, Seifert KA. 2011 – A revision of *Cyanonectria* and *Geejayessia* gen. nov., and related species with Fusarium-like anamorphs. Studies in Mycology 68, 115–138.

Seifert KA, Morgan-Jones G, Gams W, Kendrick B. 2011 – The genera of hyphomycetes. Utrecht, The Netherlands, CBS-KNAW Fungal Biodiversity Centre.

Senanayake IC, Maharachchikumbura SSN, Hyde KD, Bhat JD et al. 2015 – Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). Fungal Diversity 73, 73–144.

Senanayake IC, Crous PW, Groenewald JC, Maharachchikumbura SSN et al. 2017 – Families of Diaporthales based on morphological and phylogenetic evidence. Studies in Mycology 86, 217–296.

Shearer CA, Raja HA, Miller AN, Nelson P et al. 2009 – The molecular phylogeny of freshwater Dothideomycetes. Studies in Mycology 64, 145–153.

Sierk HA. 1964 – The genus Leptogium in North America and North of Mexico. Bryologist 67: 245–317.

Simmons DR, Kepler RM, Rehner SA, Groden E. 2015 – Phylogeny of *Hirsutella* species (Ophiocordycipitaceae) from the USA: remedying the paucity of *Hirsutella* sequence data. IMA Fungus 6, 345–356.

Slippers B, Wingfield MJ. 2007 – Botryosphaeriaceae as endophytes and latent pathogens of woody plants: diversity, ecology and impact. Fungal Biology Reviews 21, 90–106.

Spatafora JW, Quandt CA, Kepler RM, Sung GH et al. 2015 – New 1F1N species combinations in Ophiocordycipitaceae (Hypocreales). IMA fungus 6, 357–62.

Spielman LJ. 1985 – A monograph of *Valsa* on hardwoods in North America. Canadian Journal of Botany 63, 1355–1378.

Stevens FL. 1920 – Dothidiaceous and Other Porto Rican Fungi. Botanical Gazette 69, 248–257.

Steyaert RL. 1949 – Contributions a´ le´ tude monographique de *Pestalotia* de Not. et Monochaetia Sacc. (*Truncatella* gen. nov. et *Pestalotiopsis* gen. nov.). Bulletin du Jardin botanique de l'E´ tat a Bruxelles 19, 285–354.

Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA et al. 2016 – The families Distoseptisporaceae fam. nov., Kirschsteiniotheliaceae, Sporormiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. Fungal Diversity 80, 375–409.

Sue PK, Gurda GT, Lee R, Watkins T et al. 2014 – First report of *Westerdykella dispersa* as a cause of an angioinvasive fungal infection in a neutropenic host. Journal of Clinical Microbiology 52(12), 4407–4411.

Suetrong S, Schoch CL, Spatafora JW, Kohlmeyer J. 2009 – Molecular systematics of the marine Dothideomycetes. Studies in Mycology 64, 155–173.

Sung GH, Hywel-Jones NL, Sung JM, Luangsa-ard JJ et al. 2007 – Phylogenetic classification of *Cordyceps* and the clavicipitaceous fungi. Studies in Mycology 57, 5–59.

Tanaka K, Endo M, Hirayama K, Okane I et al. 2011 – Phylogeny of *Discosia* and *Seimatosporium*, and introduction of *Adisciso* and *Immersidiscosia* genera nova. Persoonia 26, 85–98.

Tanaka K, Hirayama K, Yonezawa H, Sato G et al. 2015 – Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 82, 75–136.

Tanaka K, Hashimoto A, Matsumura M, Sato T. 2017 – *Brevicollum*, a new genus in Neohendersoniaceae, Pleosporales. Mycologia 109, 608-619.

Tangthirasunun N, Silar P, Bhat DJ, Maharachchikumbura SSN et al. 2015 – Morphology and phylogeny of appendaged genera of coelomycetes: *Ciliochorella* and *Discosia*. Sydowia 67, 217–226.

Thambugala KM, Ariyawansa HA, Li YM, Boonmee S et al. 2014 – Dothideales. Fungal Diversity 68, 105–158.

Thambugala KM, Hyde KD, Tanaka K, Tian Q et al. 2015 – Towards a natural classification and backbone tree for *Lophiostomataceae, Floricolaceae,* and *Amorosiaceae* fam. nov. Fungal Diversity 74, 199–266.

Thambugala KM, Daranagama DA, Phillips AJL, Bulgakov TS et al. 2016a– Microfungi on *Tamarix*. Fungal Diversity 82, 239–306.

Thambugala KM, Hyde KD, Eungwanichayapant PD, Romero AI et al. 2016b – Additions to the genus *Rhytidhysteron* in Hysteriaceae. Cryptogamie Mycologie 37, 99–116.

Thambugala KM, Wanasinghe DN, Phillips AJL, Camporesi E et al. 2017 – Mycosphere notes 1-50: Grass (Poaceae) inhabiting Dothideomycetes. Mycosphere 8, 697–796

Theissen F, Sydow H. 1915 – Die Dothideales. Kritisch-systematische original-untersuchungen. Annales Mycologici 13, 305–306.

Thompson SM, Tan YP, Young AJ, Neate SM et al. 2011 – Stem cankers on sunflower (*Helianthus annuus*) in Australia reveal a complex of pathogenic *Diaporthe* (*Phomopsis*) species. Persoonia 27, 80–89.

Tian Q, Liu JK, Hyde KD, Wanasinghe DN et al. 2015 – Phylogenetic relationships and morphological reappraisal of Melanommataceae (Pleosporales). Fungal Diversity 74, 267–324.

Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN et al. 2017 – Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 83, 1–261.

Tode HJ. 1791 – Fungi Mecklenburgenses selecti. Fasc. II, Generum novorum appendicem, Lüneburg.

Tsui KM, Hyde KD, Hodgkiss IJ, Goh TK. 1998 – A new freshwater species of *Saccardoella* from Hong Kong and South Africa. Mycologia 90, 701–704.

Udayanga D, Castlebury LA, Rossman AY, Chukeatirote E, Hyde KD. 2014a – Insights into the genus *Diaporthe*: phylogenetic species delimitation in the *D. eres* species complex. Fungal Diversity 67, 203–229.

Udayanga D, Castlebury LA, Rossman AY, Hyde KD. 2014b – Species limits in *Diaporthe*: molecular re-assessment of *D. citri, D. cytosporella, D. foeniculina* and *D. rudis*. Persoonia 32, 83–101.

Udayanga D, Castlebury LA, Rossman AY, Chukeatirote E et al. 2015 – The *Diaporthe sojae* species complex, phylogenetic re-assessment of pathogens associated with soybean, cucurbits and other field crops. Fungal Biology 119: 383–407.

Uecker FA. 1988 – A world list of *Phomopsis* names with notes on nomenclature, morphology and biology. Mycologia Memoir 13, 1–231.

Valenzuela-Lopez N, Cano-Lira JF, Guarro J, Sutton DA et al. 2018 – Coelomycetous Dothideomycetes with emphasis on the families *Cucurbitariaceae* and *Didymellaceae*. Studies in Mycology 90, 1–69.

Wanasinghe DN, Jones EBG, Camporesi E, Boonmee S et al. 2014 – An exciting novel member of Lentitheciaceae in Italy from *Clematis vitalba*. Cryptogamie Mycologie 35, 323–337.

Wanasinghe DN, Jeewon R, Jones EBG, Boonmee S et al. 2017a – Novel palmicolous taxa within Pleosporales: Multigene phylogeny and taxonomic circumscription. Mycological Progress (Online), 1–20.

Wanasinghe DN, Hyde KD, Jeewon R, Crous PW et al. 2017b – Phylogenetic revision of *Camarosporium* (*Pleosporineae*, *Dothideomycetes*) and allied genera. Studies in Mycology 87, 207–256.

Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R et al. 2018 – Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. Fungal Diversity 89, 1–236.

Wehmeyer LE. 1926 – A biologic and phylogenetic study of stromatic Sphaeriales. American Journal of Botany 13, 574–645.

Wehmeyer LE. 1975 – The pyrenomycetous fungi. Mycologia Memoir 6:1–250.

Whitton SR, McKenzie EHC, Hyde KD. 2012 – Fungi Associated with Pandanaceae. Springer Netherlands.

Wijayawardene NN, McKenzie EHC, Hyde KD. 2012 – Towards incorporating anamorphic fungi in a natural classification – checklist and notes for 2011. Mycosphere 3, 157–228.

Wijayawardene NN, Crous PW, Kirk PM, Hawksworth DL et al. 2014 – Naming and outline of Dothideomycetes 2014 – including proposals for the protection or suppression of generic names. Fungal Diversity 69, 1–55.

Wijayawardene NN, Hyde KD, Bhat DJ, Goonasekara ID et al. 2015 – Additions to brown spored coelomycetous taxa in *Massarinae*, *Pleosporales*: Introducing *Phragmocamarosporium* gen. nov. and *Suttonomyces* gen. nov. Cryptogamie Mycologie 36, 213–224.

Wijayawardene NN, Hyde KD, Wanasinghe DN, Papizadeh M et al. 2016 – Taxonomy and phylogeny of dematiaceous coelomycetes. Fungal Diversity 77, 1–316.

Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL et al. 2017a – Notes for genera: Ascomycota. Fungal Diversity 86, 1–594.

Wijayawardene NN, Hyde KD, Tibpromma S, Wanasinghe DN et al. 2017b – Towards incorporating asexual fungi in a natural classification: checklist and notes 2012–2016. Mycosphere 8, 1457–1554.

Wijayawardene NN, Hyde KD, Lumbsch HT, Liu JK et al. 2018 – Outline of *Ascomycota*: 2017. Fungal Diversity 88: 167–263.

Winter G. 1885 – Pilze–Ascomyceten. In GL Rabenhorst's Kryptogamen-Flora von Deutschland, Oesterreich und der Schweiz 1, 65–528.

Winton LM, Stone JK, Hansen EM, Shoemaker RA. 2007 – The systematic position of *Phaeocryptopus gaeumannii*. Mycologia 99, 240–252.

Zhang Y, Schoch CL, Fournier J, Crous PW et al. 2009 – Multi-locus phylogeny of the *Pleosporales*: a taxonomic, ecological and evolutionary re-evaluation. Studies in Mycology 64, 85–102.

Zhang Y, Crous PW, Schoch CL, Bahkali AH et al. 2011 – A molecular, morphological and ecological re-appraisal of Venturiales—a new order of Dothideomycetes. Fungal Diversity 51, 249–277.

Zhang Y, Crous PW, Schoch CL, Hyde KD. 2012 – Pleosporales. Fungal Diversity 53, 1–221.

Zhang Y, Fournier J, Phookamsak R, Bahkali AH et al. 2013 – *Halotthiaceae* fam. nov. (Pleosporales) accommodates the new genus *Phaeoseptum* and several other aquatic genera. Mycologia 105, 603–609.

Zhang H, Dong W, Hyde KD, Maharachchikumbura SSN et al. 2017a – Towards a natural classification of Annulatascaceae-like taxa: introducing Atractosporales ord. nov. and six new families. Fungal Diversity 85, 75–110.

Zhang JF, Liu JK, Hyde KD, Chen YY et al. 2017b – Two new species of *Dyfrolomyces* (*Dyfrolomycetaceae*, Dothideomycetes) from karst landforms. Phytotaxa 313, 267–277.

Zhou X, Rodrigues AM, Feng PY, de Hoog GS. 2014 – Global ITS diversity in the *Sporothrix schenckii* complex. Fungal Diversity 66, 153–165.