Fungal Diversity – March (2016)

Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa

Guo Jie Li[1] ● Kevin D. Hyde[2,3,4] ● Rui Lin Zhao[1] ● Hongsanan Sinang[2,3] ● Faten Awad Abdel-Aziz[5] ● Mohamed A. Abdel-Wahab[4,5] ● Pablo Alvarado[6] ● Genivaldo Alves-Silva[7] ● Joseph F. Ammirati[8] ● Hiran A. Ariyawansa[9] ● Abhishek Baghela[10] ● Ali Hassan Bahkali[4] ● Michael Beug[11]·● D. Jayaram Bhat[2] ● Dimitar Bojantchev[12] ● Thitiya Boonpratuang[13] ● Timur S. Bulgakov[14] ● Erio Camporesi[15,16,17] ● Marcela C. Boro[18] ● Oldriska Ceska[19] ● Dyutiparna Chakraborty[20] ● Jia Jia Chen[21] ● K. W. Thilini Chethana[2,22] ● Putarak Chomnunti[2] ● Giovanni Consiglio[23] ● Bao Kai Cui[21] ● Dong Qin Dai[2]● Yu Cheng Dai[21] ● Dinushani A. Daranagama[1,2] ● Kanad Das[20] ● Monika C. Dayarathne[2,3,24] ● Eske De Crop[25] ● Rafael J. V. De Oliveira[26] ● Carlos Alberto Fragoso de Souza[26] ● José I. de Souza[18] ● Bryn T.M. Dentinger[27,28] ● Asha J. Dissanayake[2,22] ● Mingkwan Doilom[2,3] ● E. Ricardo Drechsler-Santos[7] ● Masoomeh Ghobad-Nejhad[29] ● Sean P. Gilmore[30] ● Aristóteles Góes-Neto[31] ● Michał Gorczak[32] ● Charles H. Haitjema[30] ● Kalani Kanchana Hapuarachchi[2,33] ● Akira Hashimoto[34,35] ● Mao Qiang He[1,36] ●John K. Henske[30] ● Kazuyuki Hirayama[37] Maria J. Iribarren[38] ● Subashini C. Jayasiri[2] ● Timothy Y. James[39] ● Ruvishika S. Jayawardena[2,22] ● Sun Jeong Jeon[40] ● Gustavo H. Jerônimo[18] ● Ana L. Jesus[18] ● E. B. Gareth Jones[4] ● Ji Chuan Kang[33] ● Samantha C. Karunarathna[2,3,24] ● Paul M. Kirk[41] ● Sirinapa Konta[2,3] ● Eric Kuhnert[42,43] ● Ewald Langer[44] ● Haeng Sub Lee[40] ● Hyang Burm Lee[40] ● Wen Jing Li[2,3] ● Xing Hong Li[22] ● Kare Liimatainen[45] ● Diogo Xavier Lima[26] ● Chuan Gen Lin[2,46] ● Jian Kui Liu[9] ● Xings Zhong Liu[1] ● Zuo Yi Liu[9] ● J. Jennifer Luangsa-ard[13] ● Robert Lücking[47] ● H. Thorsten Lumbsch[48] ● Saisamorn Lumyong[49] ● Eduardo M. Leaño[50] ● Agostina V. Marano[18] ● Misato Matsumura[34,35] ● Eric H. C. McKenzie[51] ● Suchada Mongkolsamrit[13] ● Peter Mortimer[3,24] ● Thi Thuong Thuong Nguyen[40] ● Tuula Niskanen[27] ● Chada Norphanphoun[2,3] ● Michelle A. O'Malley[30] ● Sittiporn Parnmen[52] ● Julia Pawłowska[32] ● Rekhani H. Perera[2,3] ● ● Rungtiwa Phookamsak[2,3] ● Chayanard Phukhamsakda[2,3] ● Carmen L. A. Pires-Zottarelli[18] ● Olivier Raspé[53,54] ● Mateus A. Reck[7] ● Sarah C. O. Rocha[18] ● André L. C. M. de A. Santiago[26] ● Indunil C Senanayake[2] ● Ledo Setti[55] ● Qiu Ju Shang[2] ● Sanjay K. Singh[10] ● Esteban B. Sir[56, 57] ● Kevin V. Solomon[30] ● Jie Song[21] ● Prasert Srikitikulchai[13] ● Marc Stadler[42,43] ● Satinee Suetrong[58] ● Hayato Takahashi[35] ● Takumasa Takahashi[35] ● Kazuaki Tanaka[35] ● Li Ping Tang[59] ● Kasun M. Thambugala[2,9] ● Donnaya Thanakitpipattana[13] ● Michael K. Theodorou[60] ● Benjarong Thongbai[2] ● Tuksaporn Thummarukcharoen[13] ● Qing Tian[2,3] ● Saowaluck Tibpromma[2,3] ● Annemieke Verbeken[25] ● Alfredo Vizzini[61] ● Josef Vlasák[62] ● Kerstin Voigt[63] ● Dhanushka N. Wanasinghe[2,3] ● Yong Wang[46] ● Gothamie Weerakoon[48] ● Hua An Wen[1] ● Ting Chi Wen[33] ● Nalin N. Wijayawardene[2] ● Sarunyou Wongkanoun[13] ● Marta Wrzosek[32] ● Yuan Pin Xiao[2,33] ● Jian Chu Xu[3] ● Ji Ye Yan[22] ● Jing Yang[2,9] ● Shu Da Yang[59] ● Yu Hu

[59] ● Jin Feng Zhang[2,9] ● Jie Zhao[30] ● Li Wei Zhou[64] ● Derek Peršoh[65] ● Alan J. L. Phillips [66]● Sajeewa S. N. Maharachchikumbura[67]
[1] R. L. Zhao, G. J. Li, D. A. Daranagama, M. Q. He, H. A. Wen, X. Z. Liu
State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No 3 1st West Beichen Road, Chaoyang District, Beijing 100101, P. R. China
*Corresponding author: Rui Lin Zhao (zhaorl@im.ac.cn)

[2]K. D. Hyde, S. Hongsanan, D. Q. Dai, D. A. Daranagama, M. C. Dayarathne, K. W. T. Chethana, A. J. Dissanayake, M. Doilom, K. K. Hapuarachchi, C. S. Jayasiri, R. S. Jayawardena, S. C. Karunarathna, S. Konta, W. J. Li, C. G. Lin, Q. J. Shang, C. Norphanphoun, R. H. Perera, R. Phookamsak, C. Phukhamsakda, I. C Senanayake, B. Thongbai, K. M. Thambugala, Q. Tian, S. Tibpromma, D. N. Wanasinghe, N. Wijayawardene, Y. P. Xiao, J. Yang, J. F. Zhang
Centre of Excellence in Fungal Research and School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand

[3]K. D. Hyde, S. Hongsanan, D. Q. Dai, M. C. Dayarathne, S. C. Karunarathna, M. Doilom, S. Konta, W. J. Li, P. Mortimer, C. Norphanphoun, R. H. Perera, R. Phookamsak, C. Phukhamsakda, Q. Tian, S. Tibpromma, D. N. Wanasinghe, J.C. Xu
Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, P. R. China

[4]K. D. Hyde, M. A. Abdel-Wahab, A. H. Bahkali, E. B. G. Jones
Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box: 2455, Riyadh 1145, Saudi Arabia

[5]F. A. Abdel-Aziz, M. A. Abdel-Wahab
Department of Botany and Microbiology, Faculty of Science, Sohag University, Sohag 82524, Egypt

[6]P. Alvarado
ALVALAB, C/ La Rochela nº 47, E-39012, Santander, Spain

[7]G. Alves-Silva, M. A. Reck, E. R. Drechsler-Santos
Micolab, Programa de Pós-Graduação em Biologia de Fungos, Algas e Plantas, Departamento de Botânica, Universidade Federal de Santa Catarina, Campus Universitário Trindade, CEP: 88040-900, Florianópolis, Santa Catarina, Brazil

[8]J. Ammirati
Department of Biology, University of Washington, Box 351800, Seattle, Washington 98195–1800, U.S.A.

[9]H. A. Ariyawansa, J. K. Liu, Z. Y. Liu, S. S. N. Maharachchikumbura, K. M. Thambugala, J. Yang, J. F. Zhang
Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang 550006, Guizhou, P. R. China

[10]A. Baghela, S.K. Singh
National Fungal Culture Collection of India (NFCCI), Biodiversity and Palaeobiology Group, MACS'Agharkar Research Institute, G.G. Agarkar Road, Pune 411004, India

[11]M. Beug
PO Box 116 Husum, WA 98623–0116, U.S.A.

[12]D. Bojantchev
MushroomHobby.com, 345 Shipwatch Lane, Hercules, CA 94547 U.S.A.

[13]T. Boonpratuang, J. J. Luangsa-ard, S. Mongkolsamrit, P. Srikitikulchai, D. Thanakitpipattana, T. Thummarukcharoen, S. Wongkanoun
Microbe Interaction Laboratory (BMIT), BIOTEC, National Science and Technology Development Agency (NSTDA), 113 Thailand Science Park, Thanon Phahonyothin, Tombon Khlong Nueng, Amphoe Khlong Luang, Pathum Thani 12120, Thailand

[14]T. S. Bulgakov
Academy of Biology and Biotechnology, Southern Federal University, Rostov-on-Don 344090, Rostov region, Russia

[15]E. Camporesi
A.M.B. Gruppo Micologico Forlivese “Antonio Cicognani”, Via Roma 18, Forlì, Italy

[16]E. Camporesi
A.M.B. Circolo Micologico “Giovanni Carini”, C.P.314, Brescia, Italy

[17]E. Camporesi
Società per gli Studi Naturalistici della Romagna, C.P. 144, Bagnacavallo (RA), Italy

[18]M. C. Boro, G. H. Jerônimo, A. L. Jesus, J. I. de Souza, A. V. Marano, S. C. O. Rocha, C. L. A. Pires-Zottarelli
Núcleo de Pesquisa em Micologia, Instituto de Botânica, Av. Miguel Stéfano 3687, 04301-912, São Paulo, SP, Brazil

[19]O. Ceska
1809 Penshurst Rd., Victoria, British Columbia, V8N 2N6 Canada

[20]D. Chakraborty, K. Das,
Cryptogamic Unit, Botanical Survey of India, Botanic Garden, Howrah 711103, India

[21]J. J. Chen, B. K. Cui, Y. C. Dai, J. Song
Institute of Microbiology, Beijing Forestry University, PO Box 61, Beijing 100083, P. R. China

[22]K. W. T. Chethana, A. J. Dissanayake, R. S. Jayawardena, X. H. Li, J. Y. Yan
Institute of Plant and Environment Protection, Beijing Academy of Agriculture and Forestry Sciences, No. 9 of ShuGuangHuaYuanZhongLu, Haidian District, Beijing 100097, P. R. China

[23]G. Consiglio
Via C. Ronzani 61, I-40033, Casalecchio di Reno (BO), Italy

[24] M. C. Dayarathne, S. C. Karunarathna, D. N. Wanasinghe
Soil Biology Group, World Agro forestry Centre East and Central Asia Office, Lanhei Road, Heilongtan, Kunming 650201, Yunnan, P. R. China

[25]E. De Crop, A. Verbeken
Research Group Mycology, Department of Biology, Ghent University, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium

[26]R. J. V. de Oliveira, D. X. Lima, C. A. F. de Souza, A. L. C. M. A. Santiago
PostGraduate Program in Biology of Fungi, Department of Mycology, Federal University of Pernambuco, Av. Nelson Chaves, s/n, 50670-420, Recife, PE, Brazil

[27]B. T. M. Dentinger, T. Niskanen
Jodrell Laboratory, Royal Botanic Gardens, Kew, Surrey TW9 3DS, UK

[28]B. T. M. Dentinger
Institute of Biological, Environmental and Rural Sciences, Cledwyn Building, Aberystwyth University, Penglais, Aberystwyth, Ceredigion SY23 3DD, UK

[29]M. Ghobad-Nejhad
Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), P. O. Box 3353-5111, Tehran 3353136846, Iran

[30]S. P. Gilmore, C. H. Haitjema, J. K. Henske, M. A. O’Malley, K. V. Solomon
Department of Chemical Engineering, University of California Santa Barbara, Santa Barbara, CA, 93106, USA

[31]A. Góes-Neto
Laboratório de Pesquisa em Microbiologia (LAPEM), Departamento de Ciências Biológicas, Programa de Pós-Graduação em Botânica, Feira de Santana, CEP: 44036-900, Bahia, Brazil

[32]M. Gorczak, J. Pawłowska, M. Wrzosek
Department of Molecular Phylogenetics and Evolution, Institute of Botany, Faculty of Biology, University of Warsaw, Al. Ujazdowskie 4, 00-478 Warsaw, Poland

[33]K. K. Hapuarachchi, J. C. Kang, T. C. Wen, Y. P. Xiao
The Engineering and Research Center for Southwest Bio-Pharmaceutical Resources, Ministry of Education, Guizhou University, Huaxi District, Guiyang 550025, P.R. China

[34]A. Hashimoto, M. Matsumura
The United Graduate School of Agricultural Sciences, Iwate University, 18-8 Ueda 3 chome, Morioka 020-8550, Japan

[35]A. Hashimoto, M. Matsumura, K. Tanaka, H. Takahashi, T. Takahashi
Faculty of Agriculture and Life Sciences, Hirosaki University, 3 Bunkyo-cho, Hirosaki, Aomori 036-8561, Japan

[36]M. Q. He
Key Laboratory of Forest Disaster Warning and Control in Yunnan Province, Faculty of Biology Conservation, Southwest Forestry University, Kunming 650224, P. R. China

[37]K. Hirayama
Apple Experiment Station, Aomori Prefectural Agriculture and Forestry Research Center, 24 Fukutami, Botandaira, Kuroishi, Aomori 036-0332, Japan

[38]M. J. Iribarren
Universidad Nacional de Luján (UNLu), Ruta 5 y Avenida Constitución, 6700, Luján, Buenos Aires, Argentina

[39]T. Y. James
Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109, USA

[40]S. J. Jeon, H. S. Lee, H. B. Lee, T. T. T. Nguyen
Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 61186, R.O. Korea

[41]P. M. Kirk
Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS, UK

[42]E. Kuhnert, M. Stadler

Department of Microbial Drugs, Helmholtz-Zentrum für Infektionsforschung GmbH, Inhoffenstrasse 7, 38124 Braunschweig, Germany

[43]E. Kuhnert, M. Stadler
Partner site Hannover-Braunschweig, German Centre for Infection Research (DZIF), 38124 Braunschweig, Germany

[44]E. Langer
Department of Ecology, University of Kassel, Heinrich-Plett-Str. 40, D-34132 Kassel, Germany

[45]K. Liimatainen
Department of Biosciences, Plant Biology, University of Helsinki, P.O. Box 65, FI–00014 University of Helsinki, Finland

[46]C. G. Lin, Y. Wang
Department of Plant Pathology, College of Agriculture, Guizhou University, Guiyang, Guizhou 550025, P.R. China

[47]R. Lücking
Botanischer Garten & Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Straße 6–8, 14195 Berlin, Germany

[48]H. T. Lumbsch, G. Weerakoon
Science & Education, The Field Museum, 1400 South Lake Shore, Drive, Chicago, IL 60605-2496, U.S.A

[49]S. Lumyong
Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai, 50200, Thailand

[50]E. M. Leaño
Network of Aquaculture Centres in Asia-Pacific, Suraswadi Building, Kasetsart University Campus, Jatujak, Ladyao, Bangkok 10900, Thailand

[51]E. H. C. McKenzie
Landcare Research, Private Bag 92170, Auckland Mail Centre, Auckland 1142, New Zealand

[52]S. Parnmen
Toxicology Center, National Institute of Health, Department of Medical Sciences, Ministry of Public Health, Nonthaburi 11000, Thailand

[53]O. Raspé

Botanic Garden Meise, Nieuwelaan 38, 1860 Meise, Belgium

[54]O. Raspé
Fédération Wallonie-Bruxelles, Service général de l'Enseignement Universitaire et de la Recherche Scientifique, Rue A. Lavallée 1, 1080 Bruxelles, Belgium

[55]L. Setti
Via C. Pavese, 1, I-46029, Suzzara (MN), Italy

[56]E. B. Sir
Fundación Miguel Lillo, Laboratory of Mycology, Miguel Lillo 251, San Miguel de Tucumán 4000, Tucumán, Argentina

[57]E. B. Sir
Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET).

[58]S. Suetrong
Fungal Biodiversity Laboratory (BFBD), BIOTEC, National Science and Technology Development Agency (NSTDA), 113 Thailand Science Park, Thanon Phahonyothin, Tombon Khlong Nueng, Amphoe Khlong Luang, Pathum Thani 12120, Thailand

[59]L. P. Tang, J. Zhao, S. D. Yang, H. Yu
School of Pharmaceutical Sciences and Yunnan Key Laboratory of Pharmacology for Natural Products, Kunming Medical University, 1168 West Chunrong Road, Yuhua Avenue, Chenggong District, Kunming 650500, P. R. China

[60]M. K. Theodorou
Animal Production, Welfare and Veterinary Sciences, Harper Adams University, Newport, Shropshire, TF10 8NB, United Kingdom

[61]A. Vizzini
Department of Life Sciences and Systems Biology, Università di Torino, Viale P.A. Mattioli 25, I-10125, Torino, Italy

[62]J. Vlasák
Biology Centre of the Academy of Sciences of the Czech Republic, Institute of Plant Molecular Biology, Branišovská 1160/31, CZ – 370 05 České Budějovice, Czech Republic

[63]K. Voigt
Jena Microbial Resource Collection, Leibniz Institute for Natural Product Research and Infection Biology, Adolf-Reichwein-Strasse 23, 07745 Jena, Germany

[64]L. W. Zhou

Institute of Applied Ecology, Chinese Academy of Sciences, 72 Wenhua Road, Shenyang 110016, P. R. China

[65]D. Peršoh
Geobotany, Ruhr-Universität Bochum, Universitätsstraße 150, 44780 Bochum, Germany

[66]A. J. L. Phillips
University of Lisbon, Faculty of Sciences, Biosystems and Integrative Sciences Institute (BioISI), Campo Grande, 1749-016 Lisbon, Portugal

[67]S. S. N. Maharachchikumbura
Department of Crop Sciences, Sultan Qaboos University, Box 34, Al Khod 123, Oman

Abstract Notes on 113 fungal taxa are compiled in this paper, including 11 new genera, 89 new species, one new subspecies, three new combinations and xx reference specimens. A wide geographic and taxonomic range of fungal taxa are detailed. In the Ascomycota the new genera *Angustospora* (*Testudinaceae*), *Camporesia* (*Xylariaceae*), *Clematidis*, *Crassiparies* (*Pleosporales* genera *incertae sedis*), *Farasanispora*, *Longiostiolum* (*Pleosporales* genera *incertae sedis*), *Multilocularia* (*Parabambusicolaceae*), *Neophaeocryptopus* (*Dothideaceae*), *Parameliola* (*Pleosporales* genera *incertae sedis*), and *Towyspora* (*Lentitheciaceae*) are introduced. Newly introduced species are *Angustospora nilensis*, *Aniptodera aquibella*, *Annulohypoxylon albidiscum*, *Astrocystis thailandica*, *Camporesia sambuci*, *Clematidis italica*, *Colletotrichum menispermi*, *C. quinquefoliae*, *Comoclathris pimpinellae*, *Crassiparies quadrisporus*, *Cytospora salicicola*, *Diatrype thailandica*, *Dothiorella rhamni*, *Durotheca macrostroma*, *Farasanispora avicenniae*, *Halorosellinia rhizophorae*, *Humicola koreana*, *Hypoxylon lilloi*, *Kirschsteiniothelia tectonae*, *Lindgomyces okinawaensis*, *Longiostiolum tectonae*, *Lophiostoma pseudoarmatisporum*, *Moelleriella phukhiaoensis*, *M. pongdueatensis*, *Mucoharknessia anthoxanthi*, *Multilocularia bambusae*, *Multiseptospora thysanolaenae*, *Neophaeocryptopus cytisi*, *Ocellularia arachchigei*, *O. ratnapurensis*, *Ochronectria thailandica*, *Ophiocordyceps karstii*, *Parameliola acaciae*, *P. dimocarpi*, *Parastagonospora cumpignensis*, *Pseudodidymosphaeria phlei*, *Polyplosphaeria thailandica*, *Pseudolachnella brevifusiformis*, *Psiloglonium macrosporum*, *Rhabdodiscus albodenticulatus*, *Rosellinia chiangmaiensis*, *Saccothecium rubi*, *Seimatosporium pseudocornii*, *S. pseudorosae*, *Sigarispora ononidis* and *Towyspora aestuari*. New combinations are provided for *Eutiarosporella dactylidis* (sexual morph described and illustrated) and *Pseudocamarosporium pini*. Descriptions, illustrations and / or reference specimens are designated for *Aposphaeria corallinolutea*, *Cryptovalsa ampelina*, *Dothiorella* *vidmadera*, *Ophiocordyceps formosana*, *Petrakia echinata*, *Phragmoporthe conformis* and *Pseudocamarosporium pini*. The new species of *Basidiomycota* are *Agaricus coccyginus, A. luteofibrillosus, Amanita atrobrunnea, A. digitosa, A. gleocystidiosa, A. pyriformis, A. strobilipes, Bondarzewia tibetica, Cortinarius albosericeus, C. badioflavidus*, *C. dentigratus*, *C. duboisensis, C. fragrantissimus*, *C. roseobasilis, C. vinaceobrunneus*, *C. vinaceogrisescens*, *C. wahkiacus*, *Cyanoboletus hymenoglutinosus*, *Fomitiporia atlantica*, *F. subtilissima*, *Ganoderma wuzhishanensis*, *Inonotus shoreicola*, *Lactifluus armeniacus*, *L. ramipilosus*, *Leccinum indoaurantiacum, Musumecia alpinaare*, *M. sardoa*, *Russula amethystin*a subp. *tengii* and *R. wangii* are introduced. Descriptions, illustrations, notes and / or reference specimens are designated for *Clarkeinda trachodes*, *Dentocorticium ussuricum*, *Galzinia longibasidia*, *Lentinus stuppeus* and *Leptocorticium tenellum*. The other new genera, species new combinations are *Anaeromyces robustus*, *Neocallimastix californiae* and *Piromyces finnis* from *Neocallimastigomycota*, *Phytophthora estuarina*, *P. rhizophorae*, *Salispina*, *S. intermedia*, *S. lobata* and *S. spinosa* from *Oomycota*, and *Absidia stercoraria*, *Gongronella orasabula*, *Mortierella calciphila*, *Mucor caatinguensis*, *M. koreanus*, *M. merdicola* and *Rhizopus koreanus* in Zygomycota.

Keywords: *Ascomycota*, *Basidiomycota*, *Neocallimastigomycota*, *Oomycota*, *Zygomycota*, Phylogeny, Taxonomy, new genus, new species

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279. ***Clematidis*** Tibpromma, Camporesi & K.D. Hyde, in Fungal Diversity 78: xx (2016)
280. ***Clematidis italica*** Tibpromma, Camporesi & K.D. Hyde, in Fungal Diversity 78: xx (2016)
281. ***Crassiparies*** Matsumura, K. Hiray. & Kaz. Tanaka, in Fungal Diversity 78: xx (2016)
282. ***Crassiparies quadrisporus*** Matsumura, K. Hiray. & Kaz. Tanaka, in Fungal Diversity 78: xx (2016)
283. ***Farasanispora*** Abdel-Wahab, Bahkali & E.B.G. Jones, ***gen. nov.***
284. ***Farasanispora avicenniae*** Abdel-Wahab, Bahkali & E.B.G. Jones, in Fungal Diversity 78: xx (2016)
285. ***Parameliola*** Hongsanan, Peršoh & K.D. Hyde, in Fungal Diversity 78: xx (2016)
286. ***Parameliola dimocarpi*** Hongsanan & K.D. Hyde, in Fungal Diversity 78: xx (2016)
287. ***Parameliola acaciae*** Hongsanan & K.D. Hyde, in Fungal Diversity 78: xx (2016)

***Dothideomycetes* family, incertae sedis**

Kirschsteiniotheliaceae

288. ***Kirschsteiniothelia tectonae*** Doilom, D.J. Bhat & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Lecanoromycetes

Ostropales

Graphidaceae

289. ***Ocellularia arachchigei*** Weerakoon, Lücking & Lumbsch, in Fungal Diversity 78: xx (2016)
290. ***Ocellularia ratnapurensis*** Weerakoon, Lücking & Lumbsch, in Fungal Diversity 78: xx (2016)
291. ***Rhabdodiscus albodenticulatus*** Weerakoon, Lücking & Lumbsch, in Fungal Diversity 78: xx (2016)

Sordariomycetes

Chaetosphaeriales

Chaetosphaeriaceae

292. ***Pseudolachnella brevifusiformis*** A. Hashim. & Kaz. Tanaka, in Fungal Diversity 78: xx (2016)

Diaporthales

Gnomoniaceae

293. ***Phragmoporthe conformis*** R.H. Perera & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Valsaceae

294. ***Cytospora salicicola*** C. Norphanphoun, Bulgakov & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Glomerellales

Glomerellaceae

295. ***Colletotrichum menispermi*** Chethana, Jayawardena, Bulgakov & K.D. Hyde, in Fungal Diversity 78: xx (2016)
296. ***Colletotrichum quinquefoliae*** Jayawardena, Bulgakov & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Hypocreales

Bionectriaceae

297. ***Ochronectria thailandica*** Q.J. Shang & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Clavicipitaceae

298. ***Moelleriella phukhiaoensis*** Mongkol., Thanakitp. & Luangsa-ard, in Fungal Diversity 78: xx (2016)
299. ***Moelleriella pongdueatensis*** Mongkol., Thanakitp. & Luangsa-ard, in Fungal Diversity 78: xx (2016)

Ophiocordycipitaceae

300. ***Ophiocordyceps formosana*** Y.W. Wang et al.

301. ***Ophiocordyceps karstii*** T.C. Wen, Y.P. Xiao & K.D. Hyde, ***sp. nov.***, in Fungal Diversity 78: xx (2016)

Microascales

Halosphaeriaceae

302. ***Aniptodera aquibella*** J. Yang & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Sordariales

Chaetomiaceae

303. ***Humicola koreana*** Hyang B. Lee & T.T.T. Nguyen, in Fungal Diversity 78: xx (2016)

Amphisphaeriales

Amphisphaeriaceae

304. ***Seimatosporium pseudocornii*** Wijayaw., Camporesi & K.D. Hyde, in Fungal Diversity 78: xx (2016)
305. ***Seimatosporium pseudorosae*** Wijayaw., Camporesi & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Xylariales

Diatrypaceae

306. ***Cryptovalsa ampelina*** (Nitschke) Fuckel
307. ***Diatrype thailandica*** R.H. Perera, J.K. Liu & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Xylariaceae

308. ***Annulohypoxylon albidiscum*** J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, in Fungal Diversity 78: xx (2016)
309. ***Astrocystis thailandica*** Daranagama and K.D. Hyde, in Fungal Diversity 78: xx (2016)
310. ***Camporesia*** W.J. Li & K.D. Hyde, in Fungal Diversity 78: xx (2016)
311. ***Camporesia sambuci*** W.J. Li & K.D. Hyde, in Fungal Diversity 78: xx (2016)
312. ***Durotheca macrostroma*** Srikitik., Wongkanoun & Luangsa-ard, in Fungal Diversity 78: xx (2016)

313. ***Halorosellinia rhizophorae*** Dayarathne, E.B.G. Jones & K.D. Hyde, in Fungal Diversity 78: xx (2016)

314. ***Hypoxylon lilloi*** Sir, Lambert & Kuhnert, in Fungal Diversity 78: xx (2016)

315. ***Rosellinia chiangmaiensis*** Daranagama and K. D. Hyde, in Fungal Diversity 78: xx (2016)

Ascomycota*, genera *incertae sedis

316. ***Petrakia echinata*** (Peglion) Syd. & P. Syd.

Basidiomycota

Agaricomycetes

Agaricales

Agaricaceae

317. ***Agaricus coccyginus*** M.Q. He & R.L. Zhao, in Fungal Diversity 78: xx (2016)

318. ***Agaricus luteofibrillosus*** M.Q. He, L.J. Chen & R.L. Zhao, in Fungal Diversity 78: xx (2016)

319. ***Clarkeinda trachodes*** (Berk.) Singer

Amanitaceae

320. ***Amanita atrobrunnea*** Thongbai, Raspé & K.D. Hyde, in Fungal Diversity 78: xx (2016)

321. ***Amanita digitosa*** Boonprat. & Parnmen, in Fungal Diversity 78: xx (2016)

322. ***Amanita gleocystidiosa*** Boonprat. & Parnmen, in Fungal Diversity 78: xx (2016)

323. ***Amanita pyriformis*** Boonprat. & Parnmen, in Fungal Diversity 78: xx (2016)

324. ***Amanita strobilipes*** Thongbai, Raspé & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Cortinariaceae

325. ***Cortinarius albosericeus*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, in Fungal Diversity 78: xx (2016)

326. ***Cortinarius badioflavidus*** Ammirati, Beug, Niskanen, Liimat. & Bojantchev, in Fungal Diversity 78: xx (2016)

327. ***Cortinarius denigratus*** Ammirati, Beug, Niskanen, Liimat. & O. Ceska, in Fungal Diversity 78: xx (2016)

328. ***Cortinarius duboisensis*** Ammirati, Beug, Niskanen & Liimat., in Fungal Diversity 78: xx (2016)

329. ***Cortinarius fragrantissimus*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, in Fungal Diversity 78: xx (2016)

330. ***Cortinarius roseobasilis*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, in Fungal Diversity 78: xx (2016)

331. ***Cortinarius vinaceobrunneus*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, in Fungal Diversity 78: xx (2016)

332. ***Cortinarius vinaceogrisescens*** Ammirati, Beug, Liimat. & Niskanen, in Fungal Diversity 78: xx (2016)

333. ***Cortinarius wahkiacus*** Ammirati, Beug, Liimat. & Niskan, in Fungal Diversity 78: xx (2016)

Tricholomataceae

334. ***Musumecia alpina*** L.P. Tang, J Zhao & S.D. Yang, in Fungal Diversity 78: xx (2016)

335. ***Musumecia sardoa*** G. Consiglio, A. Vizzini & L. Setti, in Fungal Diversity 78: xx (2016)

Boletales

Boletaceae

336. ***Cyanoboletus hymenoglutinosus*** D. Chakr., K. Das, A. Baghela, S.K. Singh & Dentinger, in Fungal Diversity 78: xx (2016)

337. ***Leccinellum indoaurantiacum*** D. Chakr., K. Das, A. Baghela, S.K. Singh & Dentinger, in Fungal Diversity 78: xx (2016)

Polyporales* genus, *incertae sedis

338. ***Galzinia longibasidia*** Hallenb.

Russulales* genus, *incertae sedis

339. ***Leptocorticium tenellum*** Nakasone

Hymenochaetales

Hymenochaetaceae

340. ***Fomitiporia atlantica*** Alves-Silva, Reck & Drechsler-Santos, in Fungal Diversity 78: xx (2016)

341. ***Fomitiporia subtilissima*** Alves-Silva, Reck, & Drechsler-Santos, in Fungal Diversity 78: xx (2016)

342. ***Inonotus shoreicola*** L.W. Zhou, Y.C. Dai & Vlasák, in Fungal Diversity 78: xx (2016)

Polyporales

Ganodermataceae

343. ***Ganoderma wuzhishanensis*** T.C. Wen, K. Hapuarachchi & K.D. Hyde, in Fungal Diversity 78: xx (2016)

Polyporales* genus, *incertae sedis

344. ***Dentocorticium ussuricum*** (Parmasto) M.J. Larsen & Gilb.

Polyporaceae

345. ***Lentinus stuppeus*** Klotzsch

Russulales

Bondarzewiaceae

346. ***Bondarzewia tibetica*** B.K. Cui, J. Song & Jia J. Chen, in Fungal Diversity X78: XX (2016)

Russulaceae

347. ***Lactifluus armeniacus*** De Crop & Verbeken, in Fungal Diversity 78: xx (2016)

348. ***Lactifluus ramipilosus*** Verbeken & De Crop, in Fungal Diversity 78: xx (2016)

349. ***Russula amethystina* subsp. *tengii*** G.J. Li, H.A. Wen & R.L. Zhao, in Fungal Diversity 78: xx (2016)

350. ***Russula wangii*** G.J. Li, H.A. Wen & R.L. Zhao, in Fungal Diversity 78: xx (2016)

Neocallimastigomycota

Neocallimastigomycetes

Neocallimastigales

Neocallimastigaceae

351. ***Anaeromyces robustus*** O'Malley, Theodorou & Henske, in Fungal Diversity 78: xx (2016)
352. ***Neocallimastix californiae*** O'Malley, Theodorou & Solomon, in Fungal Diversity 78: xx (2016)
353. ***Piromyces finnis*** O'Malley, Haitjema & Gilmore, in Fungal Diversity 78: xx (2016)

Oomycota

Peronosporales

Pythiaceae

354. ***Phytophthora estuarina*** Marano, A.L. Jesus & Pires-Zottar., in Fungal Diversity 78: xx (2016)
355. ***Phytophthora rhizophorae*** Pires-Zottar., A.L. Jesus & Marano, in Fungal Diversity 78: xx (2016)

Oomycota, incertae sedis

356. ***Salispina*** Marano, A.L. Jesus & Pires-Zottar., in Fungal Diversity 78: xx (2016)
357. ***Salispina intermedia*** A.L. Jesus, Pires-Zottar. & Marano, in Fungal Diversity 78: xx (2016)
358. ***Salispina lobata*** (Fell & Master) A.L. Jesus, Marano & Pires-Zottar. , in Fungal Diversity 78: xx (2016)
359. ***Salispina spinosa*** (Fell & Master) Marano, A.L. Jesus & Pires-Zottar. , in Fungal Diversity 78: xx (2016)

Zygomycota

Mucorales

Mortierellaceae

360. ***Mortierella calciphila*** Wrzosek, in Fungal Diversity 78: xx (2016)

Cunninghamellaceae

361. ***Absidia stercoraria*** Hyang B. Lee, H.S. Lee & T.T.T. Nguyen, in Fungal Diversity 78: xx (2016)

362. ***Gongronella orasabula*** Hyang B. Lee, K. Voigt, P.M. Kirk & T.T.T. Nguyen, in Fungal Diversity 78: xx (2016)

Mucoraceae

363. ***Mucor caatinguensis*** A.L. Santiago, C.A. de Souza & D.X. Lima, in Fungal Diversity 78: xx (2016)
364. ***Mucor koreanus*** Hyang B. Lee, S.J. Jeon & T.T.T. Nguyen, in Fungal Diversity 78: xx (2016)
365. ***Mucor merdicola*** C.A. de Souza & A.L. Santiago, in Fungal Diversity 78: xx (2016)
366. ***Rhizopus koreanus*** Hyang B. Lee & T.T.T. Nguyen, in Fungal Diversity 78: xx (2016)

Introduction

This is the third paper in a series of complied notes on new fungal taxa, reference specimens, new data, and other taxonomic changes.

Materials and methods

Specimens and cultures were photographed under daylight in the field or lamplight in the laboratory. Macro- and microscopic characteristics were measured and recorded. Codes of colours are cited from those of Kornerup and Wanscher (1978), Maerz and Paul (1950), Ridgway (1912) and Seguy (1936). Fungal Names/Index Fungorum/MycoBank accession numbers and Facesoffungi numbers were obtained as detailed in Fungal Names (2016), Index Fungorum (2016), MycoBank (2016), and Jayasiri et al. (2015).

Phylogenetic analyses were carried out based on holotypes, ex-types, and sequence data available from GenBank. Genomic DNA samples were extracted from growing mycelium, ascomata or basidiomata. Genetic markers applied for each genus and family were based on historic references and have commonly been used in corresponding families and genera. Multiple sequences were aligned in ClustalX v. 2.1 (Larkin et al. 2007), Maffet v. 7.215 (http://mafft.cbrc.jp/alignment/software/) or Bioedit 7.0 (Hall 2004). The alignments were reviewed visually and adjusted manually where necessary. All introns were deleted or aligned separately. Leading or trailing regions containing many gaps were removed from the alignments prior to tree building. Different single alignments were linked in needed of multi-gene backbone tree constructions. The phylogenetic analyses were carried out for maximum parsimony in PAUP v. 4.0b10 (Swofford 2002), maximum likelihood in RAxML v. 7.2.7 -HPC2, RAxML 7.4.2 Black Box (Stamatakis 2006; Stamatakis et al. 2008), RAxML GUI (Stamatakis 2006; Silvestro and Michalak 2011), or PhyML 3.0 (Guindon et al. 2010), and Bayesian inferences in MrBayes v. 3.2 (Ronquist et al. 2012) as indicated in the legend of each phylogenetic tree. Data of the newly generated sequences are listed in Table 1. The phylogenetic trees were constructed and analyzed by authors of corresponding new taxa based on the selection of genes in given publications.

Table 1 Newly generated sequence data from this study

Taxon Name	Strain/Specimen No.	ITS	nrLSU	nrSSU	TEF-1α	ACT	β-tubulin	CHS	GADPH	RPB1	RPB2	COI
Absidia stercoraria	EML-DG8-1	KU168828	KT921998	KT921996	KT922002	KT922000						
Absidia stercoraria	EML-DG8-2	KU168829	KT921999	KT921997	KT922003	KT922001						
Agaricus coccyginus	HMAS275416	KU245979										
Agaricus coccyginus	HMAS275413	KU245984										
Agaricus coccyginus	HMAS275412	KU245981										
Agaricus coccyginus	HMAS275420	KU245983										
Agaricus coccyginus	HMAS254484	KU245980										
Agaricus luteofibrillosus	HMAS 254487	KU245972										
Agaricus luteofibrillosus	HMAS275419	KU245978										
Agaricus luteofibrillosus	HMAS 254486	KU245977										
Agaricus luteofibrillosus	HMAS 275415	KU245973										

Amanita atrobrunnea	MFLU 15–1415		KT934314		
Amanita digitosa	BBH 32154	KT213722			
Amanita gleocystidiosa	BBH 31901	KT213717			
Amanita gleocystidiosa	BBH 31902	KT213718			
Amanita gleocystidiosa	BBH 31903	KT213719			
Amanita pyriformis	BBH 38643	KT213723			
Amanita strobilipes	MFLU 12–2246		KT934313		
Anaeromyces robustus	S4	KU057354			
Angustospora nilensis	MFLU 15–1511		KT944072	KT944071	
Aniptodera aquibella	MFLU 15–1140		KU556854	KU556853	
Annulohypoxylon albidiscum	MFLU 15–3883	KU852741			
Annulohypoxylon annulatum	CBS 140775				KU159523
Annulohypoxylon moriforme	STMA 14065				KU159525
Annulohypoxylon nitens	MFLUCC 14-1232				KU159521

Annulohypoxylon stygium var. annulatum	STMA 14066						KU159526					
Annulohypoxylon truncatum	CBS 140777						KU159524					
Aposphaeria corallinolutea	MFLU 15–3203		KU243051	KU243052	KU243050							
Astrocystis thailandica	MFLU 15–3525	KU246224	KU246225									
Bondarzewia tibetica	BJFC Cui 12078	KT693202	KT693204									
Bondarzewia tibetica	BJFC Yu 56	KT603203	KT693205									
Camporesia sambuci	MFLU 15–3905	KU746392	KU746394	KU746396								KU746390
Clarkeinda trachodes	MFLU10–0139	HM897839										
Clematidis italica	MFLU 14–0669	KU842380	KU842381	KU842382								
Colletotrichum menispermi	MFLU 14–0625	KU242357				KU242353	KU242354	KU242355	KU242356			
Colletotrichum quinquefoliae	MFLU 14–0626	KU236391				KU236389	KU236392		KU236390			
Comoclathris pimpinellae	MFLU 15–0010	*****										
Cortinarius albosericeus	K(M):200657	KU041721										

Cortinarius albosericeus	K(M):200658	KU041722
Cortinarius badioflavidus	K(M): 200672	KU041723
Cortinarius badioflavidus	DBB28196	KU041724
Cortinarius badioflavidus	DBB13504	KU041725
Cortinarius badioflavidus	K(M) 200689	KU041726
Cortinarius badioflavidus	K(M): 200673	KU041727
Cortinarius badioflavidus	K(M): 200686	KU041728
Cortinarius badioflavidus	01MWB032411	KU041729
Cortinarius badioflavidus	03MWB120308	KU041730
Cortinarius badioflavidus	K(M): 200690	KU041731
Cortinarius badioflavidus	02MWB043009	KU041732
Cortinarius badioflavidus	K(M): 200688	KU041733
Cortinarius denigratus	K(M): 200659	KU041734
Cortinarius duboisensis	K(M): 200660	KU041735

Cortinarius duboisensis	K(M): 200661	KU041736					
Cortinarius duboisensis	K(M): 200662	KU041737					
Cortinarius duboisensis	K(M): 200663	KU041738					
Cortinarius fragrantissimus	K(M): 200664	KU041739					
Cortinarius roseobasilis	K(M): 200665	KU041740					
Cortinarius roseobasilis	K(M): 200666	KU041741					
Cortinarius vinaceobrunneus	K(M): 200667	KU041742					
Cortinarius vinaceogrisescens	K(M): 200668	KU041743					
Cortinarius vinaceogrisescens	K(M): 200669	KU041744					
Cortinarius wahkiacus	K(M): 200670	KU041745					
Cortinarius wahkiacus	K(M): 200671	KU041746					
Crassiparies quadrisporus	HHUF30409	LC100020	LC100025	LC100017			
Creosphaeria sassafras	STMA 14088						KU159533
Cryptovalsa ampelina	MFLU 16–0007	KU550094	KU550096	KU550095			

Cyanoboletus hymenoglutinosus	DC 14-010	KT907355	KT860060					
Cytospora salicicola	MFLU 14–0785							
Dentocorticium ussuricum	TAA 42424	KU183718						
Diatrype thailandica	MFLU 15–3662	KU315392						
Dothiorella rhamni	MFLU 15–3541	KU246381	KU246382					
Dothiorella vidmadera	MFLU 15–3483	KU234792			KU234806			
Durotheca macrostroma	BBH39917					KT883901	KT883903	
Durotheca macrostroma	BCC78380					KT883902	KT883904	
Eutiarosporella dactylidis	MFLU 15–3502	KU246378	KU246380					
Farasanispora avicenniae	MFLU		KT950962	KT950961				
Fomitiporia atlantica	FLOR 58554	KU557528	KU557526					
Fomitiporia atlantica	FURB 47591	KU557529						
Fomitiporia subtilissima	FURB 47557	KU557531	KU557527		KU557532			KU557533
Fomitiporia subtilissima	FURB 47437	KU557530						KU557534

Galzinia longibasidia	GB NH2417	KU183721	KU183722				
Ganoderma wuzhishanensis	GZUH14081638						
Gongronella orasabula	EML-QF12-1	KT936269	KT936263	KT936261	KT936267	KT936265	
Gongronella orasabula	EML-QF12-2	KT936270	KT936264	KT936262	KT936268	KT936266	
Halorosellinia rhizophorae	MFLU 15–0183	KU516688	KU516689	KU516690			
Humicola koreana	EML-UD33-1	KU058192	KU058190				
Humicola koreana	EML-UD33-2	KU058193	KU058191				
Hypoxylon flavoargillaceum	STMA 14062						KU159532
Hypoxylon griseobrunneum	STMA 14052						KU159535
Hypoxylon haematostroma	STMA 14043						KU159527
Hypoxylon investiens	STMA 14058						KU159528
Hypoxylon lienhwacheense	MFLUCC 14-1231						KU159522
Hypoxylon lilloi	STMA 14142						KU159537
Hypoxylon lilloi	STMA 14143						KU159538

Hypoxylon lividipigmentum	STMA 14044			KU159529
Hypoxylon monticulosum	STMA14080			KU159534
Hypoxylon perforatum	STMA 14051			KU159531
Hypoxylon polyporus	STMA 14090			KU159530
Hypoxylon umbilicatum	STMA 15276			KU159536
Inonotus shoreicola	IFP LWZ 20140728-10		KT749418	
Inonotus shoreicola	IFP LWZ 20140728-23		KT749419	
Inonotus shoreicola	BJFC Dai13615		KT749417	
Inonotus shoreicola	IFP LWZ 20140729-1		KT749420	
Inonotus shoreicola	BJFC Dai13614		KT749416	
Kirschsteiniothelia tectonae	MFLU 15–1883	KU144916	KU764707	
Kirschsteiniothelia tectonae	MFLU 15–1884	KU144924	KU764708	
Lactifluus armeniacus	EDC 14-501	KR364127		

Lactifluus ramipilosus	EDC 14-503	KR364128				
Leccinellum indoaurantiacum	DC 14-019	KT907354	KT860059			
Lentinus stuppeus	MFLU10-0145	HM897840				
Leptocorticium tenellum	GB NH16311	KU183719	KU183720			
Lindgomyces okinawaensis	HHUF30498	LC100022	LC100027	LC100019		
Longiostiolum tectonae	MFLU 15–3532	KU712447	KU764700	KU712459	KU872759	
Lophiostoma pseudoarmatisporum	HHUF 30497	LC100021	LC100026	LC100018	LC100030	
Moelleriella phukhiaoensis	BCC19769		KT880502			KT880506
Moelleriella phukhiaoensis	BCC19773		KT880503			KT880507
Moelleriella pongdueatensis	BCC31787		KT880500			KT880504
Moelleriella pongdueatensis	BCC31788		KT880501			KT880505
Mortierella calciphila	WA18944	KT964845	KT964846	KT964847		
Mucoharknessia anthoxanthi	MFLU 15–3477	KU246377	KU246379			
Mucor caatinguensis	URM 7322	KT960377	KT960369			

Mucor caatinguensis	URM 7322	KT960376	KT960370			
Mucor caatinguensis	URM 7322	KT960375	KT96037			
Mucor koreanus	EML-QT1	KT936259	KT936253	KT936251	KT936257	KT936255
Mucor koreanus	EML-QT2	KT936260	KT936254	KT936252	KT936258	KT936256
Mucor merdicola	URM 7223	KT960373				
Mucor merdicola	URM 7223	KT960374	KT960372			
Multilocularia bambusae	MFLU 11–0216	KU693446	KU693438	KU693442	KU705656	
Multiseptospora thysanolaenae	MFLU 11–0238		KU693439	KU693443	KU705658	
Musumecia alpina	MHKMU 182	KR909102	KR909099		KR909096	
Musumecia alpina	MHKMU 346	KR909100	KR909097			
Musumecia alpina	MHKMU 347	KR909101	KR909098		KR909095	
Musumecia sardoa	AMB17139	KT122794	KT122795			
Neocallimastix californiae	G1	KU057353				
Neophaeocryptopus cytisi	MFLU 15–3542	KU248848	KU248849	KU248850		

Ochronectria thailandica	MFLU 16–0030	KU564071	KU564069	KU564070			
Ophiocordyceps formosana	MFLU 15–3888				KU854949	KU854947	
Ophiocordyceps formosana	MFLU 15–3889			KU854951	KU854950	KU854948	
Ophiocordyceps karstii	MFLU 15–3884			KU854952	KU854945	KU854943	
Ophiocordyceps karstii	MFLU 15–3885			KU854953	KU854946	KU854944	
Parameliola acaciae	MFLU 15–0378		KU285142				
Parameliola dimocarpi	MFLU 15–0045		KU285143				
Parastagonospora cumpignensis	MFLU 15–1480	KU842388	KU842389	KU842390			
Petrakia echinata	MFLU 15–7568	KU746391	KU746393	KU746395			
Phragmoporthe conformis	MFLU 15–2662	KU315388	KU315389	KU315390	KU315391		
Phytophthora estuarina	CCIBt 4157	KT886034	KT886030				KT886051
Phytophthora estuarina	CCIBt 4116	KT886033	KT886029				KT886050
Phytophthora rhizophorae	CCIBt 4152	KT886031	KT886028				KT886048
Phytophthora rhizophorae	CCIBt 4121	KT886032					KT886049

Piromyces finnis		KU057352				
Polyplosphaeria thailandica	MFLU 15–3273	KU248766	KU248767			
Pseudocamarosporium pini	MFLU 15−3290	KU764779	KU754540	KU754542		
Pseudodidymosphaeria phlei	MFLU 15–3281	KU764780	KU754541	KU754543		
Pseudolachnella brevifusiformis	HHUF 30495	LC100023	LC100028			
Pseudolachnella brevifusiformis	HHUF 30496	LC100024	LC100029			
Psiloglonium macrosporum	MFLU 14–0610	KU243048	KU243049			
Rhizopus koreanus	EML-HO95-1	KU058202	KU058196	KU058194	KU058200	KU058198
Rhizopus koreanus	EML-HO95-2	KU058203	KU058197	KU058195	KU058201	KU058199
Rosellinia chiangmaiensis	MFLU 15–3524	KU246226	KU246227			
Russula amethystina subsp. *tengii*	HMAS253336	KT949399				
Russula amethystina subsp. *tengii*	HMAS271033	KT949400				
Russula amethystina subsp. *tengii*	HMAS253216	KT949401				
Russula amethystina subsp. *tengii*	HMAS253241	KT949402				

Russula wangii	HMAS268809	KF851403			
Russula wangii	HMAS269106	KT949396			
Russula wangii	HMAS269308	KT949397			
Russula wangii	HMAS269580	KT949398			
Saccotheciumubi	MFLU 15–3400	KU290338	KU290336	KU290337	
Salispina intermedia	CCIBt 4155		KT920432	KT886044	KT886053
Salispina intermedia	CCIBt 4115				KT886055
Salispina intermedia	CCIBt 4153		KT920431	KT886042	KT886052
Salispina intermedia	CCIBt 4154			KT886043	
Salispina intermedia	CCIBt 4156		KT920433	KT886045	KT886054
Salispina lobata	CBS 588.85			KT886046	KT886056
Salispina spinosa	CBS 591.85		KT920434	KT886047	
Seimatosporium brunium	MFLU 14–0772				
Seimatosporium pseudocornii	MFLU 13−0529		KU359033	KU359034	

Seimatosporium pseudorosae	MFLU 14−0468		KU359035		
Sigarispora ononidis	MFLU 15–2667	KU243128	KU243125	KU243126	KU243127
Stagonospora russa	MFLU 15–0012				
Towyspora aestuari	MFLU 15–3543	KU248851	KU248852		

Results and discussion

The new taxa are described and illustrated in alphabetical order as following. A total of 74 genera in 44 families, 21 orders and five classes in the *Ascomycota*, *Basidiomycota*, *Oomycota*, *Neocallimastigomycota* and *Zygomycota* are introduced.

Contributions to *Ascomycota*

Dothideomycetes

We follow Hyde et al. (2013) and Wijayawardene et al. (2014) for classification of *Dothideomycetes*.

Botryosphaeriales

Members of the order *Botryosphaeriales* are commonly encountered as endophytes or pathogens of various plant hosts and comprise six ecologically diverse families; *Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Saccharataceae*, *Phyllostictaceae* and *Planistromellaceae* (Liu et al. 2012; Slippers et al. 2013).

Botryosphaeriaceae

The family *Botryosphaeriaceae* is found in all geographical and climatic areas of the world, encompassing a range of morphologically diverse fungi that are either pathogens, endophytes or saprobes (Phillips et al. 2013). Considerable interest in *Botryosphaeriaceae* has arisen due to their association with plant diseases (Yan et al. 2013; Pitt et al. 2013b; Linaldeddu et al. 2015). The phylogenetic tree for *Botryosphaeriaceae* is presented in Fig. 1.

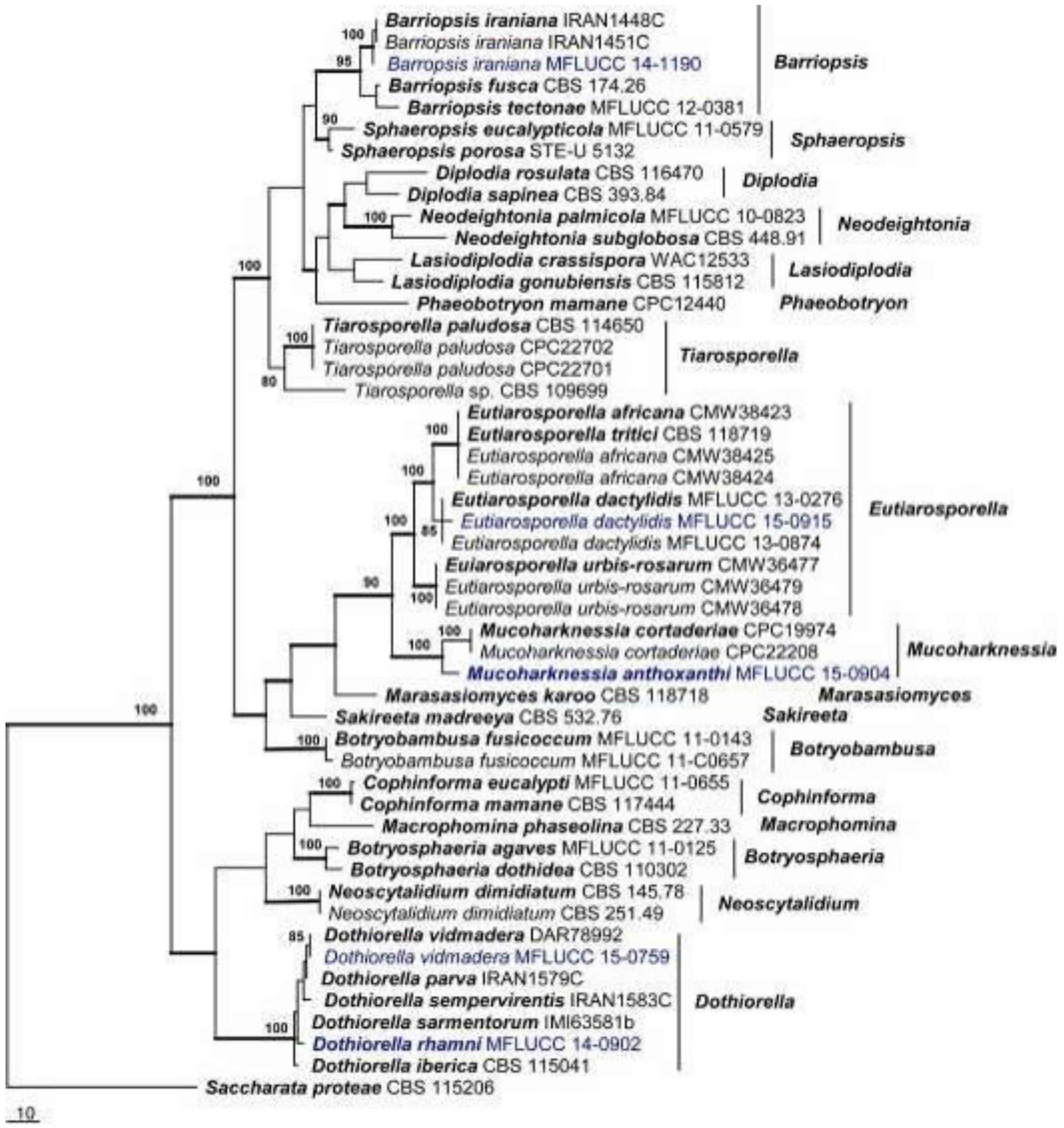


Fig. 1 Phylogram generated from Maximum Parsimony analysis based on combined ITS and LSU sequence data of species of *Botryosphaeriaceae*. Parsimony bootstrap support values for MP≥70 % are shown above the nodes and Bayesian posterior probabilities ≥95 % are indicated in bold branches. The tree is rooted with *Saccharata proteae*. All ex-types and reference strains are in bold and new isolates are in blue.

Dothiorella Sacc.

Based on morphology and molecular data, Phillips et al. (2005) revived *Dothiorella* for species with conidia that become brown and 1-septate, while they are still attached to the conidiogenous cells. Sexual morphs of *Dothiorella* have pigmented, 1-septate ascospores (Phillips et al. 2005, 2013). With the exception of *D. sarmentorum* and *D. iberica*, the sexual morphs of *Dothiorella* species are infrequently found in nature and have never been reported in culture (Phillips et al. 2013). Although there are 350 species records in *Dothiorella*, Phillips et al. (2013) revealed that cultures are available for only 17 species and of those four species have yet to be named. Abdollahzadeh et al. (2014) introduced three species names for these un-named taxa. Presently, 25 species are accepted in the genus (Abdollahzadeh et al.

2014; Crous et al. 2015a; Li et al. 2014; Phillips et al. 2013; Pitt et al. 2013b, 2015; Slippers et al. 2014). All species, except *D. sarmentorum*, have been introduced since 2005. A phylogenetic tree for *Dothiorella* is presented in Fig. 2.

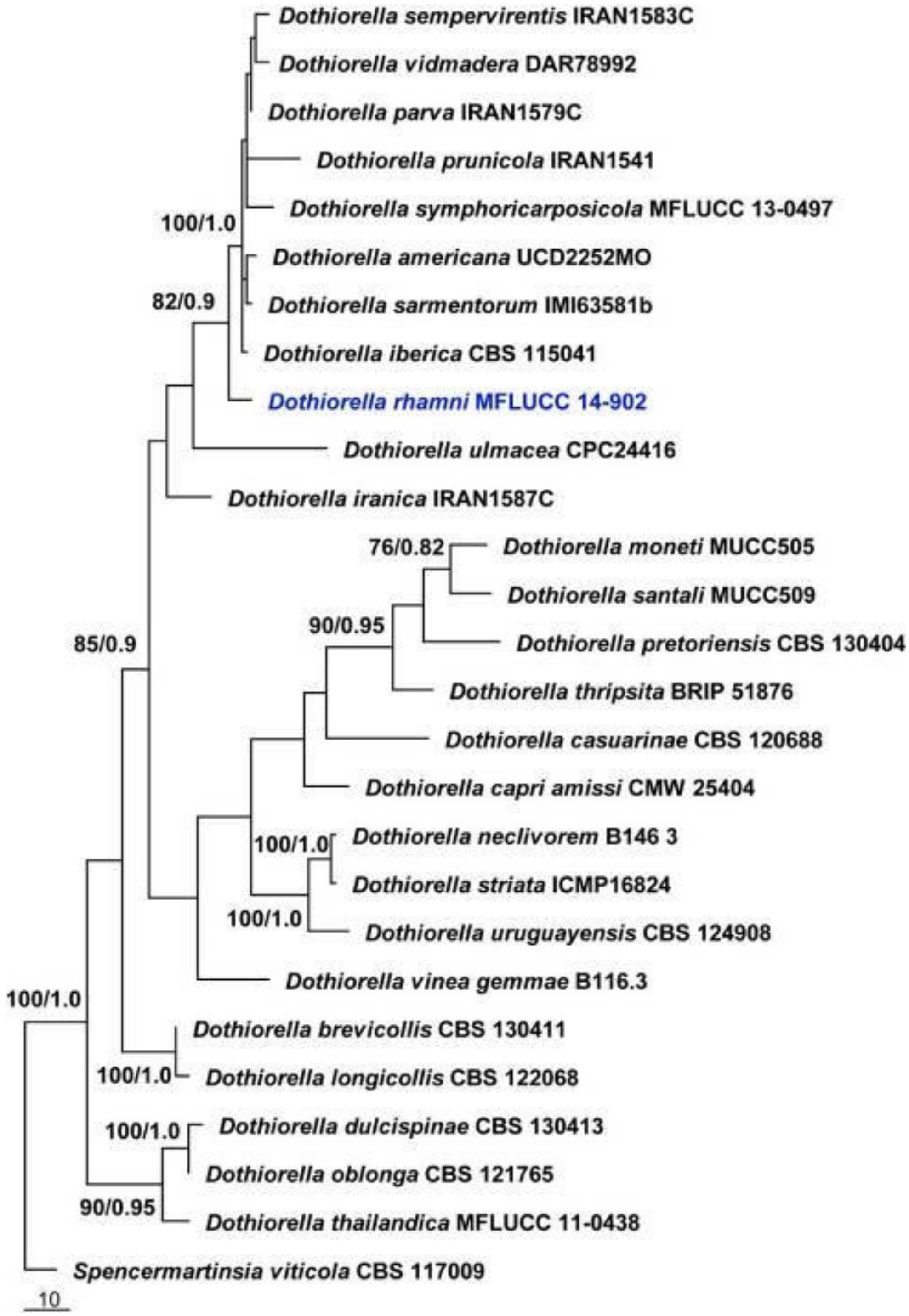


Fig. 2 Phylogram generated from Maximum Parsimony analysis based on combined ITS and EF sequence data for species of *Dothiorella*. Parsimony bootstrap support values for MP≥75 % and Bayesian posterior probabilities ≥0.9 % are shown above the nodes. The tree is rooted with *Spencermartinsia viticola* CBS 117009. All ex-types and reference strains are in bold and new isolates are in blue.

253. ***Dothiorella rhamni*** Wanasinghe, Bulgakov, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551784, *Facesoffungi number*: FoF 01668, Fig. 3

Etymology: Name reflects the host genus *Rhamnus*, from which the species was isolated.

Holotype: MFLU 15–3541

Saprobic or *weak pathogen* on dead twigs of *Rhamnus cathartica* L. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 420–460 *µm* high × 590–660 *µm* diam. ($\bar{x}$ = 443.3 × 623.2 *µm*, n = 10), pycnidial, stromatic, mostly solitary, semi-immersed to immersed in the host, dark brown to black, ostiolate, apapillate. *Peridium* 50–60 *µm* wide at the base, 70–90 *µm* wide in sides, comprising 8–10 layers, heavily pigmented, thick-walled, comprising blackish to dark brown, angular cells, becoming flattened towards the outer layers. *Conidiogenous cells* 8–12 *µm* high × 4–6 *µm* wide, holoblastic, cylindrical to subcylindrical, hyaline, the first conidium produced holoblastically and subsequent conidia enteroblastically, forming typical phialides with periclinal thickenings, swollen at the base, discrete, producing a single conidium at the apex. *Conidia* 17–24 × 9–12 *µm* ($\bar{x}$ = 20.7 × 10.4 *µm*, n = 50), initially hyaline, unicellular, becoming cinnamon to sepia and 1-septate, while still attached to conidiogenous cells; detached conidia, hyaline, sepia or dark brown, unicellular or 1-septate, moderately thick-walled, wall externally smooth, roughened on the inner surface, oval to ovoid, widest in the center, apex obtuse, base truncate or rounded.

Material examined: RUSSIA, Rostov region, Oktyabrsky District, near natural sanctuary «Persianovskaya steppe», Khoruli hollow, ravine grove (47.5006484° E, 40.1385927° N), on *Rhamnus cathartica* (*Rhamnaceae*), 26 April 2014, T.S. Bulgakov (MFLU 15–3541, **holotype**); ex-type culture, MFLUCC 14–0902.

Notes: The genus *Dothiorella* was established by Saccardo (1880) to accommodate *D. pyrenophora* (Berk.) ex Sacc., and is characterized by branched, septate conidiophores, holoblastic conidiogenesis, and smooth to finely verruculose but not striate, brown, 1-euseptate conidia (Crous and Palm 1999). Phillips et al. (2005) re-introduced *Dothiorella* as a distinct *Botryosphaeriaceae* asexual morph with brownish conidia, which become septate while still attached to the conidiogenous cells. *Dothiorella rhamni* also has sepia to dark brown, 1-septate conidia, similar to other members in *Dothiorella*. Phylogenetically *D. rhamni* clustered in a sister group with *D. sarmentorum* (CBS 115038 and IMI 63581b) and *Diplodia acerina* (CBS 910.73), but *D. rhamni* separates from them with good statistical support.

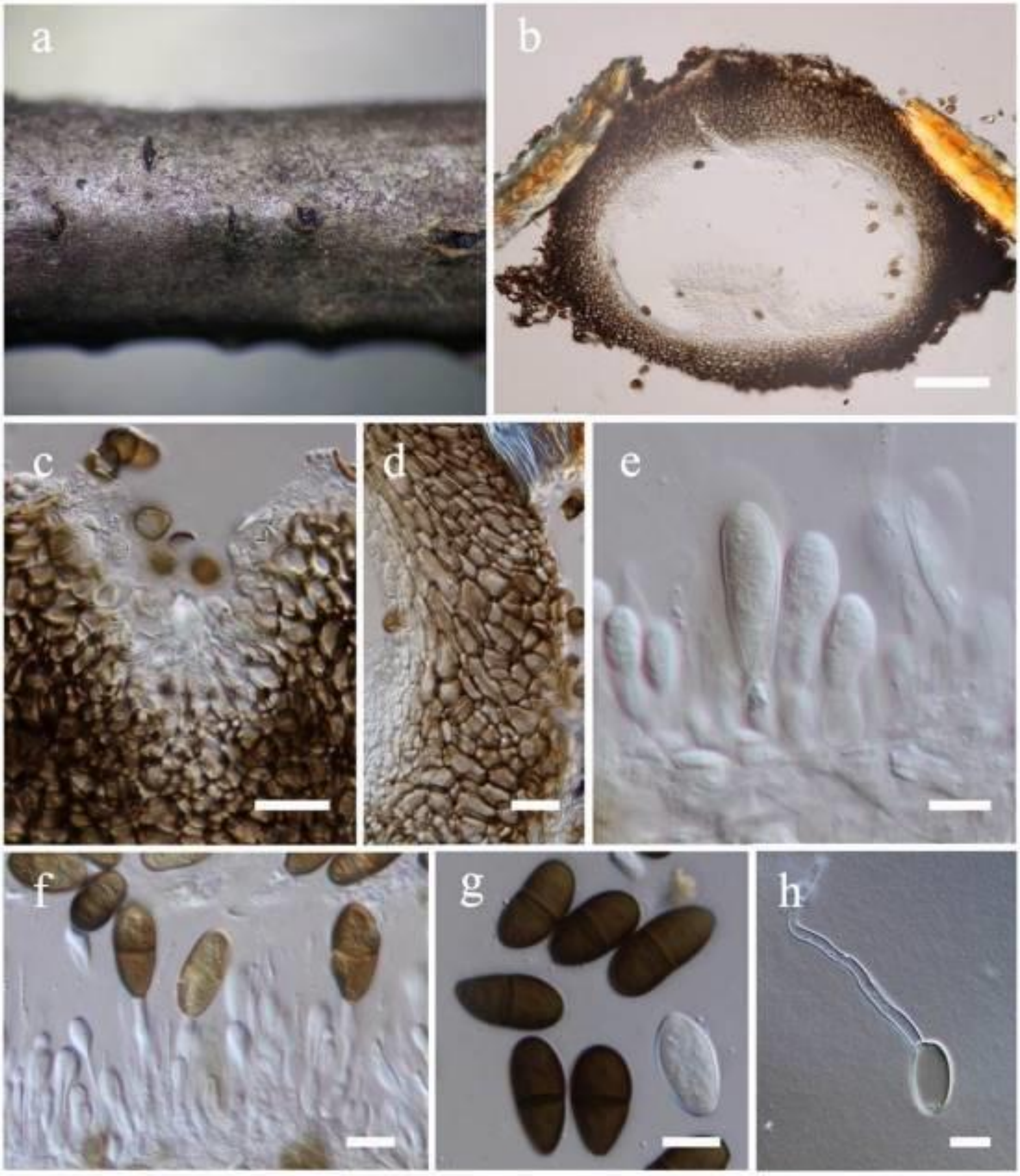


Fig. **3** ***Dothiorella rhamni*** (**holotype**) **a** Appearance of conidiomata on host substrate **b** Vertical section through a conidioma **c** Close up of ostiole **d** Peridium of conidioma **e, f** Mature and immature conidia attached to conidiogenous cells **g** Mature and immature conidia **h** Germinated conidium. Scale bars: b = 100 *µm*, c, d = 20 *µm*, e–h = 10 *µm*.

254. ***Dothiorella vidmadera*** Pitt et al., Fungal Diversity 61: 216, 2013

Facesoffungi number: FoF 01326, Fig. 4

Saprobic on dead branch of *Fraxinus ornus* L. **Sexual morph** *Ascostromata* 320–410 *µm* diam., dark brown to black, globose, submerged in the substrate, partially erumpent at maturity, ostiolate. *Ostiole* circular, central, papillate. Peridium 50–80 *µm* thick, composed of dark brown thick-walled cells of *textura angularis*, becoming thin-walled and hyaline towards the inner region. *Pseudoparaphyses* 3–5 *µm* wide, thin-walled, hyaline. *Asci* 150–220 × 12–22 *µm*, 8-spored, bitunicate, cylindric-clavate, endotunica thick-walled, with a well-developed ocular chamber. *Ascospores* 17–26 × 8–10 *µm* ($\bar{x}$ = 22 × 9 *µm*, n = 20), obliquely uniseriate or irregularly biseriate, initially hyaline and becoming dark brown, oblong to ovate, widest in center, straight, 1-septate, constricted at the septum, moderately thick-walled, surface smooth. **Asexual morph** *Conidiomata* 380 *µm* wide, globose, pycnidial, stromatic, solitary, composed of dark brown, thick-walled cells of *textura angularis*. *Conidiogenous cells* 8–14 × 3–6 *µm*, lining the pycnidial cavity, holoblastic, hyaline, subcylindrical. *Conidia* 17–22 × 9–10 *µm* ($\bar{x}$ = 21 × 10 *µm*, n = 20) initially hyaline and aseptate, becoming pigmented brown and 1-septate while attached to conidiogenous cell, slightly constricted at the septum, ovoid with a broadly rounded apex and truncate base.

Culture characteristics: Colonies on PDA, covering 20 mm diam. in Petri-dishes after 30 days in the dark at 25°C; circular, initially white, after 1 week becoming greyish brown to black; reverse grey to dark greyish green; flattened, fluffy, fairly dense, aerial, surface smooth with crenate edge, filamentous and conidia produced on pine needles after 3 weeks at 18°C.

Material examined: ITALY, Province of Forlì-Cesena [FC], Corniolo - Santa Sofia, on dead branch of *Fraxinus ornus* (*Oleaceae*), 6 December 2013, Erio Camporesi IT 1562 (MFLU 15–3483, **reference specimen designated here**), ex-type living cultures MFLUCC 15–0759, KUMCC 15–0129, GZCC 15–0007.

Notes: The sexual morph of *Dothiorella vidmadera* is morphologically similar to *D. sarmentorum* and *D. iberica* in having globose ascostromata with a central ostiole, lined with hyaline cells, a wide peridium, bitunicate asci with a thickened endotunica, and dull brown or dark reddish brown, septate, ellipsoid-obovoid, ascospores, constricted at the septum. It however differs in spore dimensions and molecular phylogeny. The asexual morph of *Dothiorella vidmadera* was observed in culture and is similar to that described by Pitt et al. (2013b) and differs from the other asexual morphs of *Dothiorella* species (Phillips et al. 2013; Abdollahzadeh et al. 2014; Crous et al. 2015a). Our strains of *D. vidmadera* (MFLUCC 15–0759) clustered in the *Dothiorella* clade with 94% bootstrap support (Fig. 1) and this is the first report of the sexual morph for *Dothiorella* other than *D. sarmentorum* and *D. iberica*.

Fig. 4 ***Dothiorella vidmadera*** (MFLU 15–3483, **reference specimen**) **a** Appearance of ascostromata on host substrate **b** Cross section of ascoma **c** Peridium **d–f** Immature asci **g–i** Mature asci **j** Mature brown ascospore **k, l** Culture on PDA **m** Immature and mature conidia attached to conidiogenous cells **n** Immature hyaline conidia **o** Mature conidia. Scale bars: b, c = 100 *µm*, d–g = 30 *µm*, h–j = 20 *µm*, k, l = 1 cm, m–o = 20 *µm*.

Eutiarosporella Crous

This genus was introduced by Crous et al. (2015b) named because of its similarity to the genus *Tiarosporella*, and is distinguished from *Tiarosporella* by having conidiomata with long necks, and holoblastic conidiogenesis. *Tiarosporella* was introduced by Höhnel (1919), and is considered as an asexual genus in

Botryosphaeriaceae (Jami et al. 2012; Phillips et al. 2013; Slippers et al. 2013) and mainly occurs on grasses, conifers and members of *Asteraceae* and *Zygophyllaceae* (Karadžić 2003; Jami et al. 2012). Thambugala et al. (2014a) introduced the sexual morph of *Tiarosporella*, *T. dactylidis* and detailed descriptions and illustrations were provided. The sexual morph of *T. dactylidis* which is illustrated here, is morphologically similar to *Botryosphaeria* in having globose ascomata, with a central ostiole, a two layered peridium, hyphae-like pseudoparaphyses and hyaline, aseptate, fusoid to ovoid ascospores, with a mucilaginous sheath (Thambugala et al. 2014a). Crous et al. (2015b) described *Eutiarosporella tritici* (B. Sutton & Marasas) as the type species of the genus. Species of *Eutiarosporella* have been reported from *Celtis Africana* N.L. Burm (*Rosales*), *Triticum aestivum* L. (*Poales*), *Acacia karroo* Hayne (*Fabales*) and *Dactylis glomerata* L. (*Poales*) (Thambugala et al. 2014a; Crous et al. 2015b). Here we report the sexual morph of *Eutiarosporella* for the first time from *Avenella flexuosa* L. (*Poales*).

255. *Eutiarosporella dactylidis* (K.M. Thambugala, E. Camporesi & K.D. Hyde) Dissanayake, Camporesi & K.D. Hyde, ***comb. nov.***

Basionym: *Tiarosporella dactylidis* Thambugala, E. Camporesi & K.D. Hyde, Cryptog. Mycol.35: 359–367 (2014).

Index Fungorum number: IF 551751, *Facesoffungi number*: FoF 01650, Fig. 5

Saprobic on stem of grasses (*Avenella* sp.). **Sexual morph** *Ascostromata* 150–195 *µm* high × 175–240 *µm* diam., visible as black spots on host tissue, uniloculate, scattered or gregarious, globose to subglobose, ostiolate. *Ostiole* circular, central, papillate. *Peridium* up to 25–45 *µm* wide, comprising 2 layers: outer layer of thin, small, brown to dark brown cells of *textura angularis*, inner layer of thick, large, hyaline to lightly pigmented, cells of *textura angularis*. *Hamathecium* comprising 2–3 *µm* wide, hyphae-like, hyaline, sparse pseudoparaphyses. *Asci* 120–180 × 15–23 *µm* ($\bar{x}$ = 145 × 19 *µm*, n = 30), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, pedicellate, apically rounded, with an ocular chamber. *Ascospores* 22–28 × 7–8.5 *µm* ($\bar{x}$ = 25 × 8 *µm*, n = 30), uni to bi-seriate in the upper half, uniseriate at the base, hyaline, becoming olivaceous-brown at maturity, aseptate, ellipsoidal to fusiform, usually wider in the center, thick-walled, smooth-walled, surrounded by a mucilaginous sheath. **Asexual morph** see asexual morph description in Thambugala et al. (2014a).

Material examined: ITALY, Province of Forlì-Cesena [FC], Montebello - Modigliana, on dead stem of *Avenella flexuosa* L. (*Poaceae*), 24 November 2014, Erio Camporesi IT 2251 (MFLU 15–3502), living cultures MFLUCC 15–0915.

Notes: The genus *Tiarosporella* was introduced by Höhnel (1919) and is considered as an asexual genus in the family *Botryosphaeriaceae*. Thambugala et al. (2014a) introduced a sexual morph for the genus *Tiarosporella*; *T. dactylidis* Thambugala et al., based on the multi-gene phylogeny. Since the type species of *Tiarosporella*; *T. paludosa* (Sacc. & Fiori ex P. Syd.) Höhn clusters in a distinct clade in *Botryosphaeriaceae* apart from the species accommodated in *Tiarosporella*; Crous et al. (2015b) introduced a new genus *Eutiarosporella* to accommodate tiarosporella-like taxa, based on *E. tritici* (B. Sutton &Marasas) on *Triticum aestivum* L. from South Africa. The genus comprises three species, *Eutiarosporella africana* Jami et al., *E. tricti* and *E. urbis-rosarum* Jami et al. Based on the multigene phylogenetic analysis (Fig. 1), the ex-type strain of *Tiarosporella dactylidis* (MFLUCC 13–0276) clusters with other species in *Eutiarosporella*. With the species combined in *Eutiarosporella* here, the number of species in this genus increases to four.

Fig. 5 ***Eutiarosporella dactylidis*** sexual morph (MFLU 15–3502) **a** Appearance of ascostromata on host surface **b** Section through ascostroma **c, d** Immature asci **e-g** Mature bitunicate asci **h, i** Ascospores with inconspicuous mucilaginous sheath. Scale bars: b = 100 *µm*, c, d = 50 *µm*, e, f = 40 *µm*, g–i = 20 *µm*.

Mucoharknessia Crous, R.M. Sánchez & Bianchin.

The genus *Mucoharknessia* was introduced by Crous et al. (2015b) for a genus resembling *Harknessiaceae*, in *Diaporthales*. *Mucoharknessia* can be distinguished from *Harknessiaceae* in having pycnidia that lack furfuraceous tissue surrounding its ostiole, and conidia that have a mucoid apical appendage. The type species is *Mucoharknessia cortaderiae* (Crous et al. 2015b).

256. ***Mucoharknessia anthoxanthi*** Dissanayake, Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551752, *Facesoffungi number*: FoF 01651, Fig. 6

Etymology: Referring to the host *Anthoxanthum odoratum* L.

Holotype: MFLU 15–3477

Saprobic on dead stems of *Anthoxanthum odoratum*. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 240–320 *µm* high × 215–280 *µm* diam., globose, immersed to erumpent, brown, wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–14 × 4–5 *µm* lining the inner cavity, hyaline, smooth, ampulliform to subcylindrical, proliferating percurrently at the apex. *Paraphyses* 25–45 × 3–4 *µm* intermingled among conidiogenous cells, hyaline to pale brown, smooth to verruculose, subcylindrical with obtuse ends. *Conidia* 18–30 × 8–10 *µm* ($\bar{x}$ = 24 × 9 *µm*, n = 30), solitary, hyaline, smooth-walled, guttulate, fusoid-ellipsoid to subcylindrical, straight to curved, apex apiculate, tapering at base, apex with flared mucoid appendage, up to 20 *µm* long, 15 *µm* diam.

Material examined ITALY. Province of Forlì-Cesena [FC], Passo delle Forche - Galeata, on dead stem of *Anthoxanthum odoratum* (*Poaceae*), 24 November 2012, Erio Camporesi IT 981 (MFLU 15–3477), ex-type living cultures MFLUCC 15–0904, CGMCC.

Notes: The genus *Mucoharknessia* was introduced in *Botryosphaeriaceae* by Crous et al. (2015b) based on *Cortaderia selloana* L. from Argentina. Based on multi-gene phylogenetic analyses (Fig. 1), our isolate clustered close to *M. cortaderiae*. In this paper we introduce a new species, *Mucoharknessia anthoxanthi* based on its distinct morphological characters.

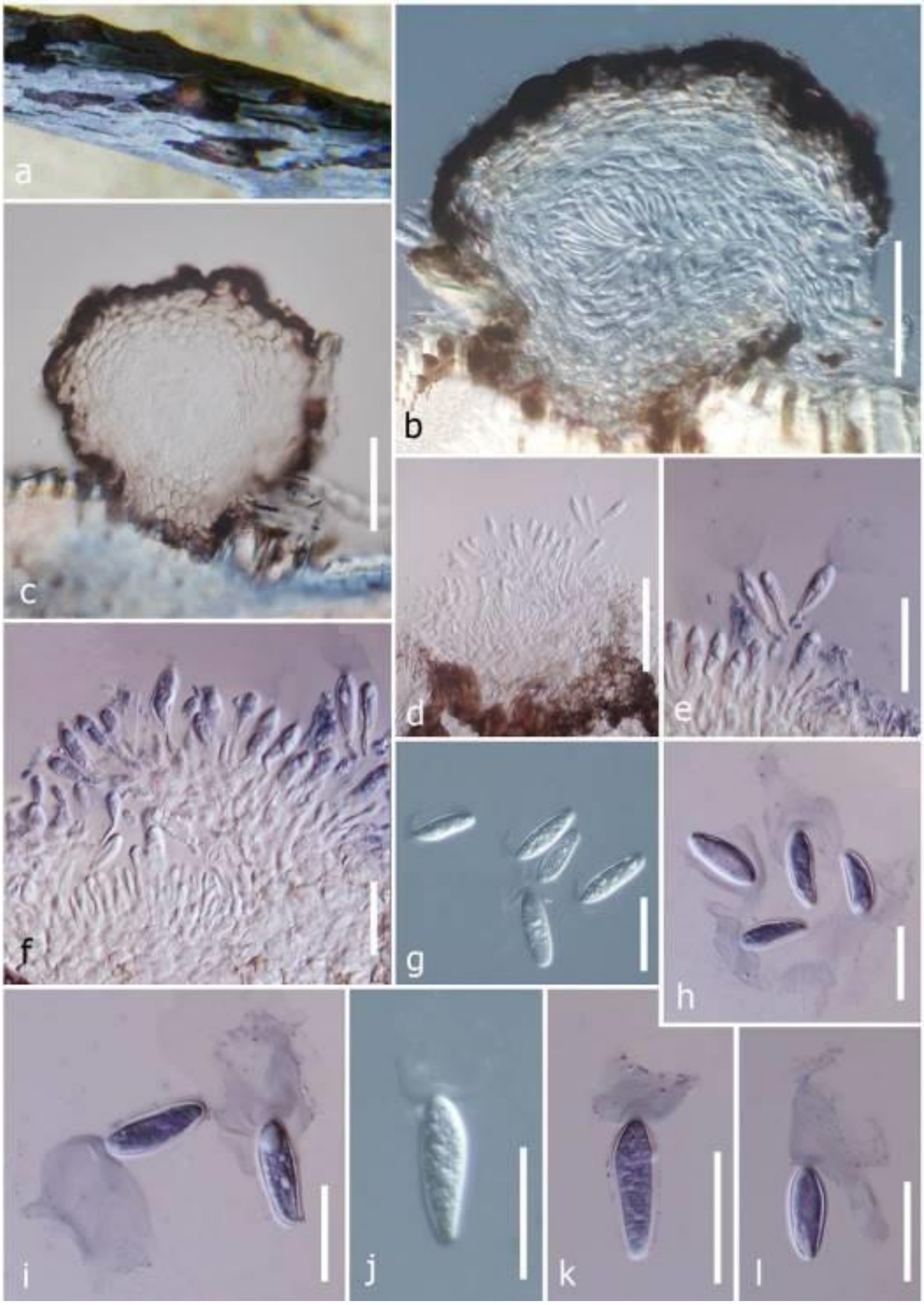


Fig. 6 ***Mucoharknessia anthoxanthi*** (**holotype**) **a** Appearance of conidiomata on host surface **b, c** Sections through conidiomata **d–f** Immature conidia attached to conidiogenous cells **g** Conidia with mucoid appendage **h–l** Conidia with mucoid appendage stained in Indian ink. Scale bars: b, c = 100 *µm*, d = 50 *µm*, e–l = 25 *µm*.

Dothideales

The order *Dothideales* was introduced by Lindau (1897) to accommodate a single family *Dothideaceae* Chevall. Subsequently, Theissen and Sydow (1917) introduced *Dothioraceae* Theiss. & Syd. in *Dothideales*. *Dothideales* however, has a rather varied past as various authors treated this order with a number of different families (Thambugala et al. 2014b). However, recently Thambugala et al. (2014b) revised the order *Dothideales* and synonymized *Dothioraceae* under *Dothideaceae*, and accepting only two families: *Dothideaceae* and *Aureobasidiaceae* K.M. Thambugala & K.D. Hyde. Thambugala et al. (2014b) introduced *Aureobasidiaceae* to accommodate *Aureobasidium* Viala & G. Boyer, *Saccothecium* and five other genera, but this family is a homonym of *Aureobasidiaceae* Cif., which had been previously introduced (Ciferri 1958). Later *Saccotheciaceae* Bonord. was proposed (instead of *Aureobasidiaceae)* as *Saccotheciaceae* is the oldest available name for the family that contains *Aureobasidium* and *Saccothecium* (Liu et al. 2015). The phylogenetic tree for *Dothideales* is presented in Fig. 7.

Dothideaceae

The family *Dothideaceae* was introduced by Chevallier (1826) as 'Dothideae', and later Fuckel (1870) established this family with *Dothidea* as the type genus and *D. gibberulosa* (Fr.) Fr. as the type species. *Dothideaceae* is characterized by 'immersed to erumpent or superficial, uni or multi-loculate ascostromata, 8- or polyspored, bitunicate asci and hyaline or brown, transversely septate, sometimes muriform ascospores' (Thambugala et al. 2014). Thambugala et al. (2014) revised the family and included ten sexual genera (*Phaeocryptopus*, *Sydowia*, *Pringsheimia*, *Delphinella*, *Plowrightia*, *Stylodothis*, *Dictyodothis*, *Dothidea*, *Endodothiora* and *Dothiora*) and five asexual genera (*Endoconidioma*, *Cylindroseptoria*, *Neocylindroseptoria*, *Kabatina* and *Coleophoma*).

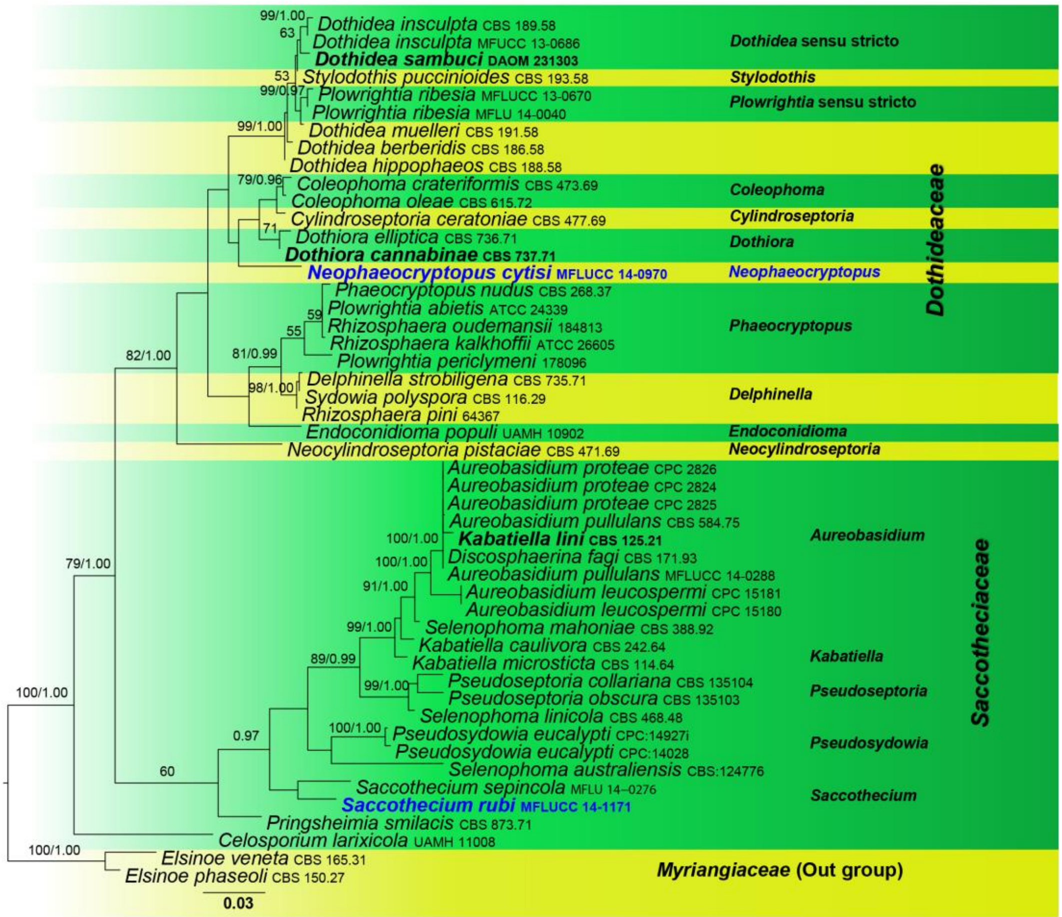


Fig. 7 Phylogram generated from maximum likelihood analysis based on analysis of combined LSU, SSU and ITS sequence data of species of *Dothideales*. Maximum likelihood bootstrap support values greater than 50 % and Bayesian posterior probabilities greater than 0.90 are near the nodes. The ex-type strains are in bold and the new isolates are in blue. The scale bar indicates 0.03 changes. The tree is rooted with *Elsinoe veneta* and *Elsinoe phaseoli*.

257. ***Neophaeocryptopus*** Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 551785, *Facesoffungi number*: FoF 01669

Etymology: Named after its morphological similarity to the genus *Phaeocryptopus*.

Type species: *Neophaeocryptopus cytisi* Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde

Saprobic on stems and twigs of herbaceous and woody plants in terrestrial habitats. **Sexual morph** *Ascostromata* superficial, semi-immersed to erumpent, solitary, scattered, broadly oblong, dark brown to black, coriaceous, uniloculate. *Peridium* comprising 5–8 layers, outer part comprising heavily pigmented, thick-walled, angular cells. *Hamathecium* lacking pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, clavate to broadly-clavate, short pedicellate, thickened and rounded at apex, with an ocular chamber. *Ascospores* overlapping 1–2-seriate, hyaline, broadly fusiform, rounded at both ends, 1-septate, with a median septum, constricted at the septum, smooth-walled, lacking a mucilaginous sheath. **Asexual morph** *Conidiomata* stromatic, immersed in agar to superficial, uni- to multi-loculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Conidiomata walls* composed of several layers of hyaline to dark brown, pseudoparenchymatous cells, organized in a *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata, mostly reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, phialidic, discrete, ampulliform to cylindric-clavate, hyaline, aseptate, smooth-walled. *Conidia* solitary, one-celled, fusiform to falcate, with narrowed ends, initially hyaline, becoming pale brown at maturity, aseptate, smooth and thin-walled, guttulate, contents granular.

Notes: Phylogenetic analyses of LSU, SSU and ITS sequence data indicate that *Neophaeocryptopus* is a distinct genus in *Dothideaceae*, which forms a clade sister to the *Coleophoma*, *Cylindroseptoria* and *Dothiora* clades. *Neophaeocryptopus*, however differs from these genera, having uni-loculate ascostromata, while *Coleophoma*, *Cylindroseptoria* and *Dothiora* having multi-loculate ascostromata. *Neophaeocryptopus* is morphologically most closely related to *Phaeocryptopus* which has uniloculate ascostromata, cylindrical, clavate asci and partially overlapping, hyaline, 1-septate ascospores, with rounded ends (Thambugala et al. 2014b). However, this is not supported by sequence data, as *Neophaeocryptopus* forms a remote clade from *Phaeocryptopus* (Fig. 7). Nevertheless, we could not include the type species *Phaeocryptopus abietis* Naumov sequences in the phylogenetic analysis, since they are not available. The type of *Phaeocryptopus* needs to be recollected and sequenced in order to resolve the conformity of *Neophaeocryptopus* with *Phaeocryptopus* in *Dothideaceae*.

258. *Neophaeocryptopus cytisi* Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551786, *Facesoffungi number*: FoF 01670, Fig. 8

Etymology: Named after the host genus on which it occurs, *Cytisus*.

Holotype: MFLU 15–3542

Saprobic on dead and hanging branches of *Cytisus* sp. **Sexual morph** *Ascostromata* 180–250 ×170–210 *µm* ($\bar{x}$ = 212.8 × 187.1 *µm*, n = 10), superficial, semi-immersed to erumpent, solitary, scattered, broadly oblong, dark brown to black, coriaceous, uniloculate. *Peridium* 35–45 *µm* wide at the base, 30–40 *µm* wide at the sides, comprising 5–8 layers, outer part heavily pigmented, thick-walled, comprising a blackish to dark brown, amorphous layer, inner part composed of dark brown, thick-walled, angular cells, becoming flattened and hyaline inwardly. *Hamathecium* lacking pseudoparaphyses. *Asci* 70–90 × 20–30 *µm* ($\bar{x}$ = 81.9 × 25.3 *µm*, n = 40), 8-spored, bitunicate, fissitunicate, clavate to broadly-clavate, short pedicellate, thickened and rounded at apex, with an ocular chamber. *Ascospores* 25–35 × 7–10 *µm* ($\bar{x}$ = 29.1 × 9.2 *µm*, n = 50), overlapping 1–2-seriate, hyaline, broadly fusiform, rounded at both ends, 1-septate, with a median septum, constricted at the septum, smooth-walled, lacking a mucilaginous sheath. **Asexual morph** *Conidiomata* stromatic, immersed in agar to superficial, uni- to multi-loculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Conidiomata walls* composed of several layers of hyaline to dark brown, pseudoparenchymatous cells, organized in a *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata, mostly reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, phialidic, discrete, ampulliform to cylindric-clavate, hyaline, aseptate, smooth-walled. *Conidia* 25–35 × 6–9 *µm* ($\bar{x}$ = 28.3 × 7.3 *µm*, n = 50), solitary, 1-celled, fusiform to falcate, with narrowed ends, initially hyaline, becoming pale brown at maturity, aseptate, smooth and thin-walled, guttulate, contents granular.

Material examined: ITALY, Arezzo Province: Croce di Pratomagno, dead and hanging branches of *Cytisus scoparius* (L.) Link (*Fabaceae*), 30 June 2014, E. Camporesi (MFLU 15–3542, **holotype**); ex-type culture, MFLUCC 14–0970, MUCL.

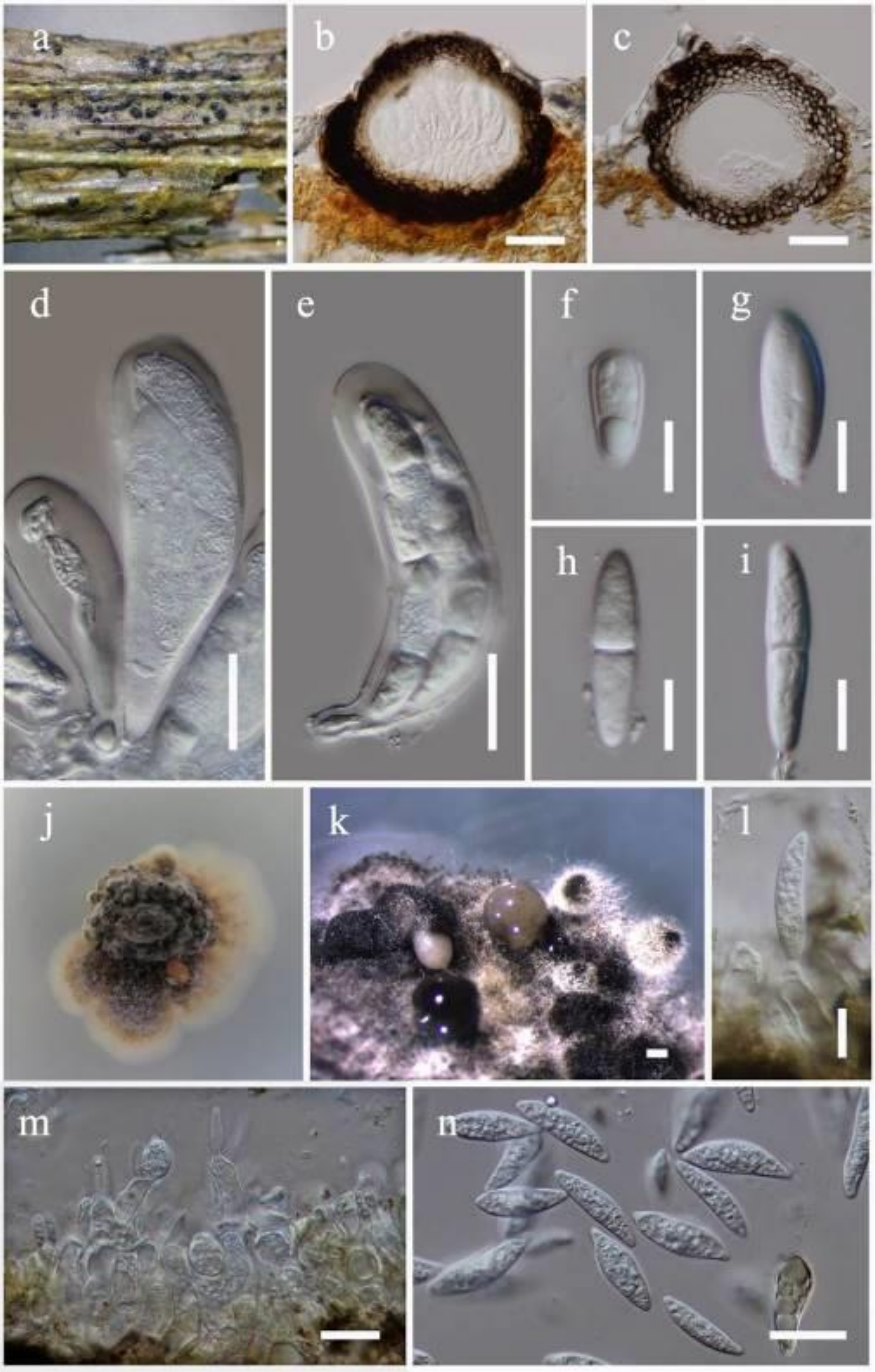


Fig. 8 ***Neophaeocryptopus cytisi*** (**holotype**) **a** Appearance of ascostromata on host substrate **b, c** Sections of the ascostromata **d**, **e** Asci **f**–**i** Ascospores **j, k** Conidiomata produced on PDA **l, m, n** Mature and immature conidia attached to conidiogenous cells **g** Mature and immature conidia. Scale bars: b, c = 50 μm, d, e = 20 μm, f–i, l = 10 μm, k = 500 μm, m, n = 20 μm.

Saccotheciaceae Bonord. [as 'Saccotheciei'], Abh. naturforsch. Ges. Halle 8: 82 (1864)

= *Aureobasidiaceae* Cif., Man. Mic. Med., Edn 2 (Pavia) 1: 178 (1958)

= *Aureobasidiaceae* Thambugala & K.D. Hyde in Hyde et al., Fungal Diversity 68 (1): 133 (2014), isonym.

Type: *Saccothecium* Fr., Fl. Scan.: 349 (1836)

Notes: *Saccotheciaceae* was introduced by Bonorden (1864) in order to accommodate *Saccothecium* Fr., while Theissen and Sydow (1917) introduced *Dothioraceae* Theiss. & Syd. in *Dothideales* which was typified by *Dothiora* Fr. Doweld (2012) suggested to conserve *Dothioraceae* against the older *Saccotheciaceae*. However, Thambugala et al. (2014b) based on morphology and molecular phylogeny introduced *Aureobasidiaceae* K.M. Thambugala & K.D. Hyde to accommodate *Aureobasidium* Viala & G. Boyer, *Saccothecium* and five other genera. The family *Aureobasidiaceae* had in fact already been introduced by Ciferri (1958). However, *Aureobasidiaceae* should be synonymized under *Saccotheciaceae* because the latter is the oldest available name for the family that contains *Aureobasidium* and *Saccothecium*. The phylogenetic tree is presented in Fig. 7.

Saccothecium Fr.

Thambugala et al. (2014b) have discussed this genus with the new placement in the order *Dothideales*. They have collected *S. sepincola* from Italy and directly isolated DNA from the ascostromata. This collection of *S. sepincola* from Italy clustered in *Saccotheciaceae* in the phylogenetic analysis. Therefore, they assigned *Saccothecium* in family *Saccotheciaceae*.

259. *Saccothecium rubi* Jayasiri, Wanasinghe, Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum Number: IF 551769, *Facesoffungi number*: FoF 01663, Figs 9, 10

Etymology: In reference to host genus.

Holotype: MFLU 15–3400

Saprobic on dead spines of *Rubus ulmifolius* Schott. **Sexual morph** *Ascostromata* 94–110 *µm* high, 110–120 *µm* diam. ($\bar{x}$ = 98 × 115 *µm*, n = 10), black, immersed to erumpent, solitary or scattered, globose to subglobose, usually uniloculate, rarely biloculate without a distinct ostiole. *Peridium* 20–30 *µm* ($\bar{x}$ = 23 *µm*, n = 15) wide, a single layer, composed of brown to inner hyaline cells of *textura angularis*, near the base connected to the host tissue. *Hamathecium* lacking pseudoparaphyses. *Asci* 47–62 × 12–16 *µm* ($\bar{x}$ = 50 × 15 *µm*, n = 20), 8-spored, bitunicate, saccate to broadly clavate or cylindric-, with a short bifurcate pedicel and a distinct ocular chamber. *Ascospores* 14–18 × 4–5 *µm* ($\bar{x}$ = 16 × 4.5 *µm*, n = 25), overlapping biseriate, hyaline, 3-septate, lacking vertical septate, asymmetric, obovoid, fusiform to clavate, with broadly to narrowly rounded ends, with broad upper cells, smooth-walled. **Asexual morph** *Conidiomata* acervular to sporodochial, amphigenous, substomatal, subepidermal, pulvinate, dry or crystaline in appearance, dark brown to black, discrete. *Conidiogenous cells* on hyaline hyphae, lateral, terminal or intercalary, cylindrical, clavate or globose, integrated, terminal, with holoblastic, polyblastic conidiogenesis, with numerous synchronously produced conidia. *Conidia* blastic, hyaline, smooth-walled, aseptate, straight, ellipsoidal to sphaerical, reniform to sickle-shaped, sometimes cylindrical with obtuse ends and occasionally with a slightly truncate base, rather variable in shape and size.

Material examined: ITALY, Province of Forlì-Cesena [FC], near Poderone – Corniolo - Santa Sofia, on dead spines of *Rubus ulmifolius* (*Rosaceae*), 3 October 2014, Erio Camporesi IT 2136 (MFLU 15–3400, **holotype)**, *Ibid*., (**isotype** in KUN); ex-type living culture (MFLUCC 14–1171, KUNCC).

Culture characteristics: Colonies on MEA at 18 ºC attaining about 70–80 mm diam. after 14 days, appearing smooth and slimy due to abundant sporulation, pinkish white. Within first 6 weeks' colonies filamentous and thereafter develop white, setae-like mycelia, then turning to brown and then black at the irregular margin.

Notes: In this study we have collected a new species of this genus from Italy, with different ascospore and ascus morphology, which also separates in the phylogenetic tree. Wehmeyer (1957) and Holm (1957) proposed to lectotypify the genus with *Saccothecium sepincola*. *Saccothecium* has been assigned to *Dothideaceae*, *Dothideales* (Barr 1972, 1987 and 2001; Kirk et al. 2008; Lumbsch and Huhndorf 2010; Thambugala et al. 2014b). In this study, we could obtain the asexual morph of this species, which is similar to *Aureobasidium pullulans* (de Bary) G. Arnaud var. (type species of genus *Aureobasidium*). Hence we can confirm placement of *Saccothecium* with in family *Saccotheciaceae*. This is the first record of species from host *Rubus ulmifolius* in the family *Saccotheciaceae*.

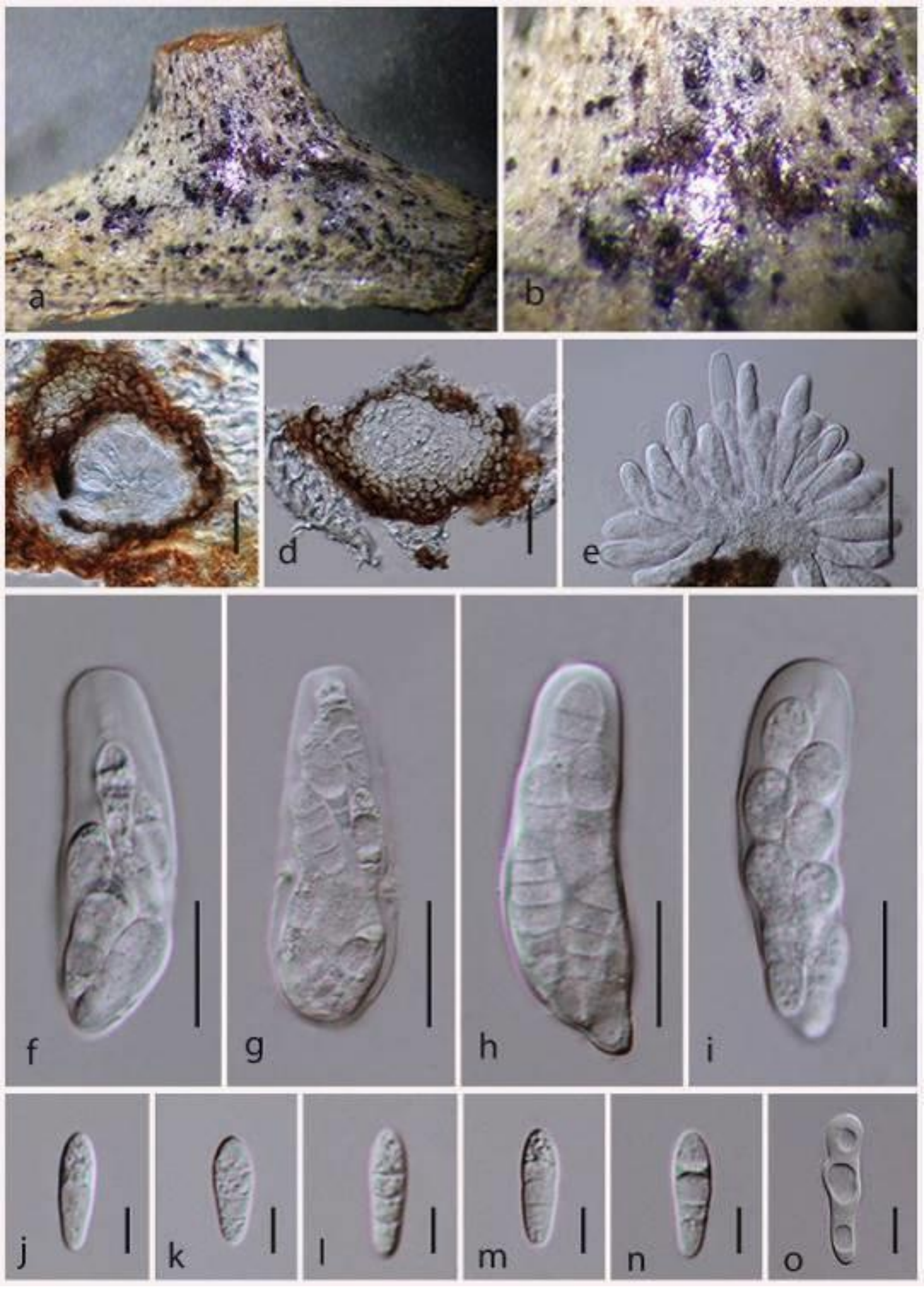


Fig. 9 ***Saccothecium rubi*** (**holotype**) **a, b** Appearance of immersed ascostromata on the host surface **c, d** Section through ascostromata **e** Arrangement of asci in ascostromata **f**–**h** Asci **j**–**n** Spores **o** Germinating ascospore. Scale bar: c, d = 30 *µm*, e = 50 *µm*, f–i = 20 *µm*, j–o = 5 *µm*.

Fig. 10 ***Saccothecium rubi*** asexual morph from the culture (**ex-type**) **a, b** Culture on MEA incubated for 2 weeks, a from above, b from below **c** Asexual structures in the MEA **d**–**g** Conidiophores and conidiogenesis **h, i** Conidia. Scale bars: a, b = 3 cm, c = 200 *µm*, d–i = 10 *µm*.

Subclass Pleosporomycetidae

Hysteriales

Hysteriaceae

The family *Hysteriaceae* was introduced by Chevallier (1826) and is characterized by carbonaceous, immersed to erumpent to entirely superficial hysterothecia, distinctly navicular in outline, bearing a pronounced longitudinal slit running the length of the long axis and hyaline to pigmented, 1-multi-septate or muriform ascospores (Boehm *et al*., 2009 a, b; Hyde *et al*., 2013; de Almeida *et al*., 2014; Thambugala et al. 2016). Hyde *et al*. (2013) and Wijayawardene *et al*. (2014b) accepted 13 genera including *Actidiographium*, *Coniosporium*, *Gloniella*, *Gloniopsis*, *Hysterium*, *Hysterobrevium*, *Hysterocarina*, *Hysteropycnis*, *Oedohysterium*, *Ostreichnion*, *Psiloglonium*, *Rhytidhysteron* and *Sphaeronaema* in the family, while de Almeida *et al*., (2014) introduced a new genus *Hysterodifractum*. The phylogenetic tree is presented in Fig. 11.

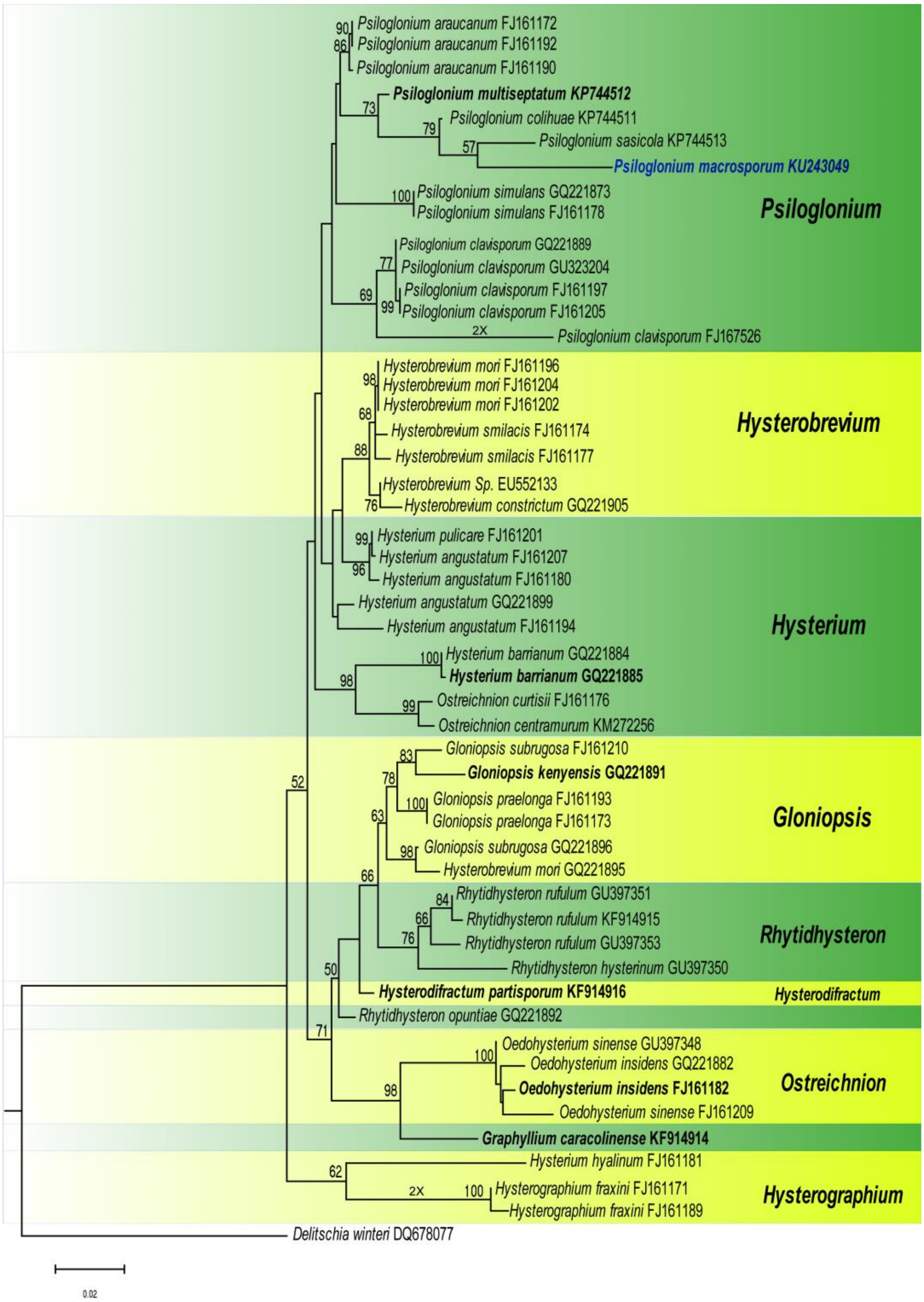


Fig. 11 Phylogram generated from Maximum Likelihood (RAxML) analysis based on LSU sequence data of *Hysteriaceae*. Maximum likelihood bootstrap support values equal or greater than 50 % are indicated above and below the nodes. New taxa are in blue and sequences based on type material have names in bold. The tree is rooted with *Delitschia winteri*.

Psiloglonium Höhn.

Psiloglonium was introduced by von Höhnel (1918) and Petrak (1923a) designated *P. lineare* (Fr.) Petr as the type species. Zogg (1962) synonymised *Psiloglonium* species which were introduced by von Höhnel (1918) and Petrak (1923 a, b) under the genus *Glonium*. von Arx & Müller (1975) reduced the genus *Psiloglonium* to a synonym of *Glonium*. However, Boehm et al. (2009a) re-established *Psiloglonium* within the *Hysteriaceae*, to accommodate non-subiculate species with apically obtuse didymospores. Boehm et al. (2009b) introduced eight new combinations for the genus *Psiloglonium*, to accommodate species previously classified under the genus *Glonium* in *Gloniaceae*. Liu et al. (2015) introduced a new *Psiloglonium* species, *P. multi-septatum* Phookamsak & K.D. Hyde, based on morphological traits and phylogenetic placement and currently there are 19 epithets listed in Index Fungorum (2016).

260. *Psiloglonium macrosporum* Thambugala, Senan. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551806, *Facesoffungi number*: *FoF* 01774, Fig. 12

Etymology: Referring to its relatively large ascospores

Holotype: MFLU 14–0610

Saprobic on decaying wood. **Sexual morph** *Ascomata* 600–1400 *µm* long × 275–475 *µm* wide × 270–415 *µm* high ($\bar{x}$ = 921 × 348 × 327 *µm*, n = 6), hysterothecial, scattered, superficial, base immersed in the substrate, elongate and depressed conchate, globose, surface black, shiny, longitudinally striate, apex compressed, opening by a longitudinal slit. *Peridium* 30–60 *µm* ($\bar{x}$ = 42, n = 15) wide, carbonaceous, brittle, comprising heavily pigmented, small, prosenchymatous cells. *Hamathecium* comprising 0.5–1 *µm* wide, hyaline, aseptate, branched, trabeculate pseudoparaphyses, in a gelatinous matrix. *Asci* 168–215 × 50–60 *µm* ($\bar{x}$ = 187 × 55 *µm*, n = 15), bitunicate, 8-spored, oblong to clavate, with a very short pedicel or apedicellate, apically thickened, with a distinct ocular chamber. *Ascospores* 80–115 × 25–31 *µm* ($\bar{x}$ = 98 × 28.4 *µm*, n = 25), crowded to biseriate, fusiform when young, oblong at maturity 80–113 × 25–31 *µm* ($\bar{x}$ = 98 × 28.35 *µm*, n = 20), hyaline when young and becoming brown at maturity, smooth-walled, ornamented, surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: THAILAND, Chiang Mai Province, Chom Thong District, Doi Inthanon National Park, on dead twig, 2 November 2012, I.C. Senanayake TL026 (MFLU 14–0610, **holotype**); *ibid* (PDD, **isotype**), ex-type living culture (MFLUCC 13–0448, ICMP 20755).

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies growing on PDA 2 cm diam. after 21 days at 25 °C, slow growing, circular, effuse, dense, gray, smooth surface with entire to slightly undulate edge.

Notes: *Psiloglonium macrosporum* is introduced here as a new species based on morphological traits and phylogeny. In the present phylogenetic analysis *P. macrosporum* grouped with other *Psiloglonium* species (Fig. 11) and is closely related to *P. sasicola* (N. Amano) E. Boehm & C. L. Schoch. *Psiloglonium macrosporum* differs from other *Psiloglonium* species in having 4-spored asci and relatively large, brown ascospores with ornamentation

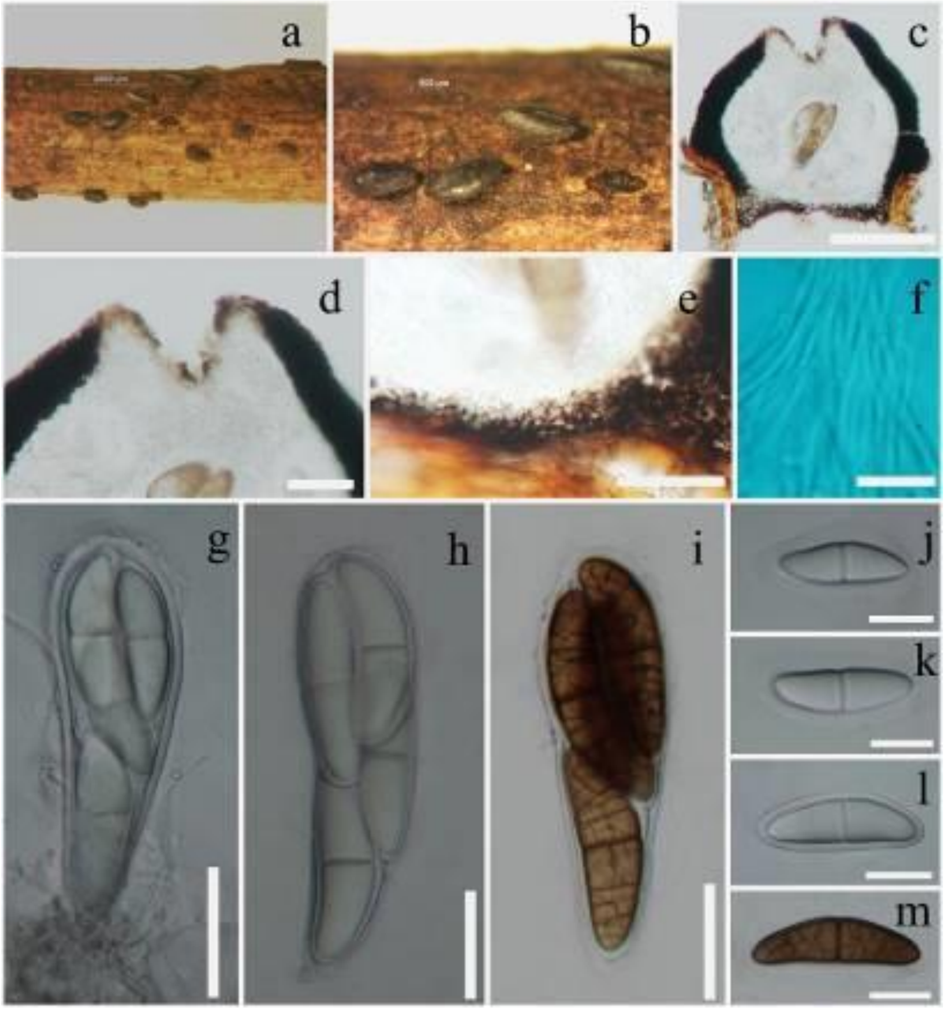
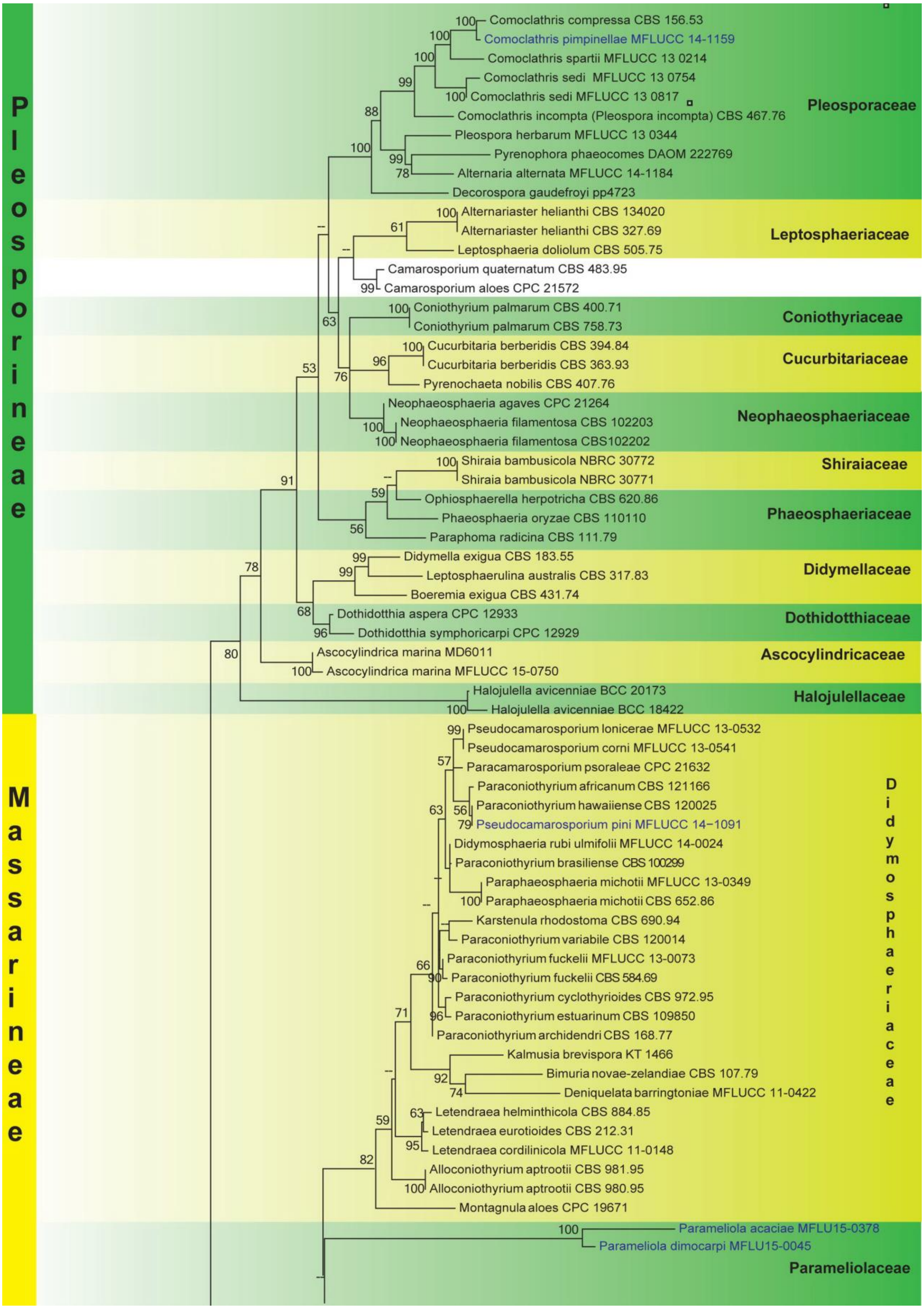


Fig. 12 ***Psiloglonium macrosporum*** **(holotype) a, b** Hysterothecia on host **c** Vertical section of hysterothecium **d** Apex of the hysterothecia **e** Peridium **f** Pseudoparaphyses **g–i** Asci **j–m** Ascospores. Scale bars: c = 150 *µm*, d, e, g–i = 50 *µm*, f = 10 *µm*, j–m = 40 *µm*.

Pleosporales

For an account of *Pleosporales* see Hyde et al. (2013).


Pleosporineae
Comoclathris compressa CBS 156.53
Comoclathris pimpinellae MFLUCC 14-1159
Comoclathris spartii MFLUCC 13 0214
Comoclathris sedi MFLUCC 13 0754
Comoclathris sedi MFLUCC 13 0817
Comoclathris incompta (Pleospora incompta) CBS 467.76
Pleospora herbarum MFLUCC 13 0344
Pyrenophora phaeocomes DAOM 222769
Alternaria alternata MFLUCC 14-1184
Decorospora gaudefroyi pp4723
Pleosporaceae
Alternariaster helianthi CBS 134020
Alternariaster helianthi CBS 327.69
Leptosphaeria doliolum CBS 505.75
Leptosphaeriaceae
Camarosporium quaternatum CBS 483.95
Camarosporium aloes CPC 21572
Coniothyrium palmarum CBS 400.71
Coniothyrium palmarum CBS 758.73
Coniothyriaceae
Cucurbitaria berberidis CBS 394.84
Cucurbitaria berberidis CBS 363.93
Pyrenochaeta nobilis CBS 407.76
Cucurbitariaceae
Neophaeosphaeria agaves CPC 21264
Neophaeosphaeria filamentosa CBS 102203
Neophaeosphaeria filamentosa CBS102202
Neophaeosphaeriaceae
Shiraia bambusicola NBRC 30772
Shiraia bambusicola NBRC 30771
Shiraiaceae
Ophiosphaerella herpotricha CBS 620.86
Phaeosphaeria oryzae CBS 110110
Paraphoma radicina CBS 111.79
Phaeosphaeriaceae
Didymella exigua CBS 183.55
Leptosphaerulina australis CBS 317.83
Boeremia exigua CBS 431.74
Didymellaceae
Dothidotthia aspera CPC 12933
Dothidotthia symphoricarpi CPC 12929
Dothidotthiaceae
Ascocylindrica marina MD6011
Ascocylindrica marina MFLUCC 15-0750
Ascocylindricaceae
Halojulella avicenniae BCC 20173
Halojulella avicenniae BCC 18422
Halojulellaceae
Massarineae
Pseudocamarosporium lonicerae MFLUCC 13-0532
Pseudocamarosporium corni MFLUCC 13-0541
Paracamarosporium psoraleae CPC 21632
Paraconiothyrium africanum CBS 121166
Paraconiothyrium hawaiiense CBS 120025
Pseudocamarosporium pini MFLUCC 14-1091
Didymosphaeria rubi ulmifolii MFLUCC 14-0024
Paraconiothyrium brasiliense CBS 100299
Paraphaeosphaeria michotii MFLUCC 13-0349
Paraphaeosphaeria michotii CBS 652.86
Karstenula rhodostoma CBS 690.94
Paraconiothyrium variabile CBS 120014
Paraconiothyrium fuckelii MFLUCC 13-0073
Paraconiothyrium fuckelii CBS 584.69
Paraconiothyrium cyclothyrioides CBS 972.95
Paraconiothyrium estuarinum CBS 109850
Paraconiothyrium archidendri CBS 168.77
Kalmusia brevispora KT 1466
Bimuria novae-zelandiae CBS 107.79
Deniquelata barringtoniae MFLUCC 11-0422
Letendraea helminthicola CBS 884.85
Letendraea eurotioides CBS 212.31
Letendraea cordilinicola MFLUCC 11-0148
Alloconiothyrium aptrootii CBS 981.95
Alloconiothyrium aptrootii CBS 980.95
Montagnula aloes CPC 19671
Didymosphaeriaceae
Parameliola acaciae MFLU15-0378
Parameliola dimocarpi MFLU15-0045
Parameliolaceae

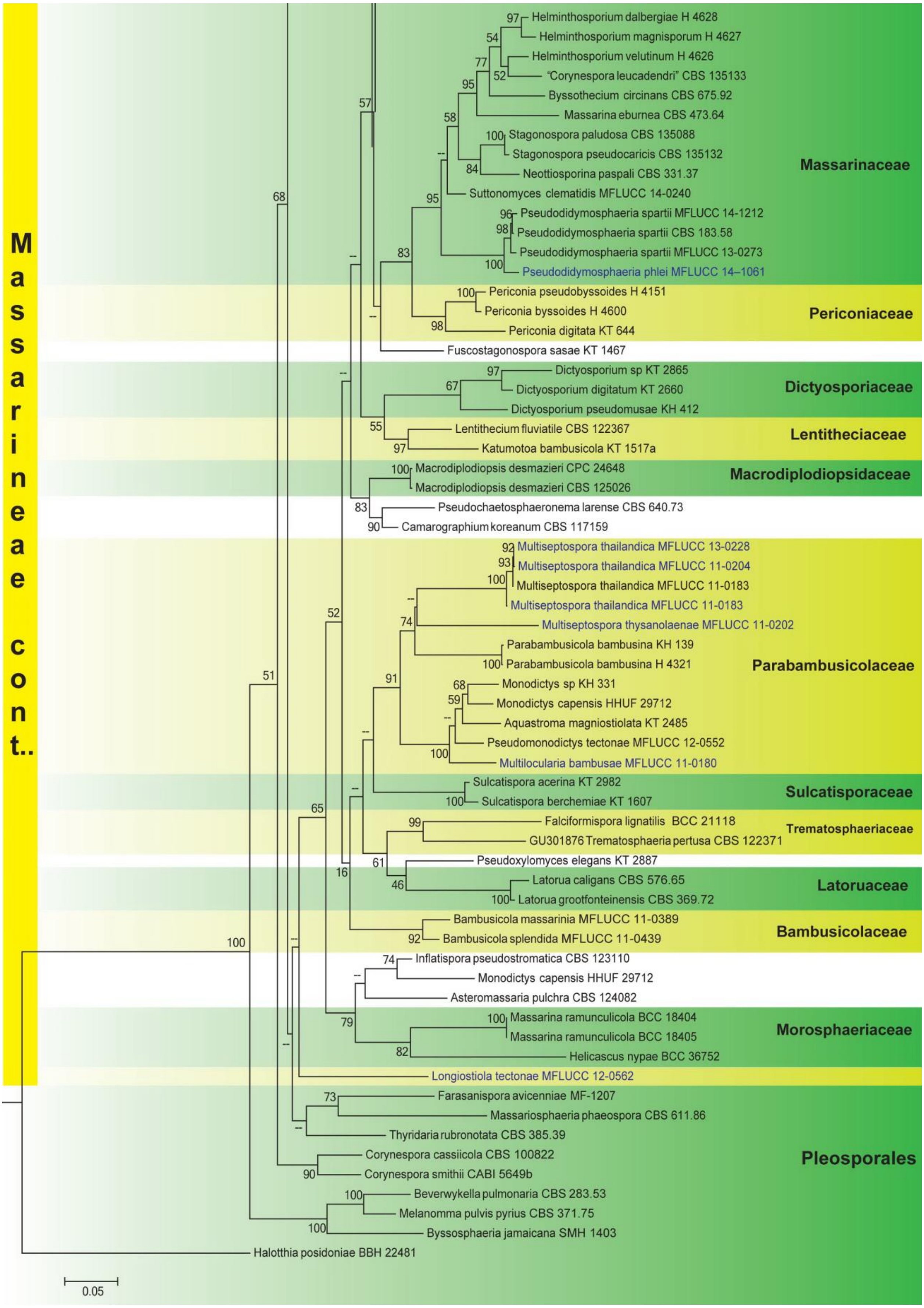

Massarineae cont..
97 Helminthosporium dalbergiae H 4628
54 Helminthosporium magnisporum H 4627
Helminthosporium velutinum H 4626
77
52 "Corynespora leucadendri" CBS 135133
95 Byssothecium circinans CBS 675.92
57
Massarina eburnea CBS 473.64
58
100 Stagonospora paludosa CBS 135088
--
Stagonospora pseudocaricis CBS 135132
84 Neottiosporina paspali CBS 331.37
Massarinaceae
68
Suttonomyces clematidis MFLUCC 14-0240
95
96 Pseudodidymosphaeria spartii MFLUCC 14-1212
98 Pseudodidymosphaeria spartii CBS 183.58
--
83
Pseudodidymosphaeria spartii MFLUCC 13-0273
100 Pseudodidymosphaeria phlei MFLUCC 14–1061
100 Periconia pseudobyssoides H 4151
Periconia byssoides H 4600
--
Periconiaceae
98 Periconia digitata KT 644
Fuscostagonospora sasae KT 1467
97 Dictyosporium sp KT 2865
--
67 Dictyosporium digitatum KT 2660
Dictyosporiaceae
Dictyosporium pseudomusae KH 412
55 Lentithecium fluviatile CBS 122367
Lentitheciaceae
97 Katumotoa bambusicola KT 1517a
100 Macrodiplodiopsis desmazieri CPC 24648
Macrodiplodiopsidaceae
Macrodiplodiopsis desmazieri CBS 125026
83 Pseudochaetosphaeronema larense CBS 640.73
90 Camarographium koreanum CBS 117159
92 Multiseptospora thailandica MFLUCC 13-0228
93 Multiseptospora thailandica MFLUCC 11-0204
100 Multiseptospora thailandica MFLUCC 11-0183
--
Multiseptospora thailandica MFLUCC 11-0183
52
74 Multiseptospora thysanolaenae MFLUCC 11-0202
Parabambusicola bambusina KH 139
100 Parabambusicola bambusina H 4321
Parabambusicolaceae
51
91
68 Monodictys sp KH 331
59 Monodictys capensis HHUF 29712
--
Aquastroma magniostiolata KT 2485
--
Pseudomonodictys tectonae MFLUCC 12-0552
100 Multilocularia bambusae MFLUCC 11-0180
Sulcatispora acerina KT 2982
--
100 Sulcatispora berchemiae KT 1607
Sulcatisporaceae
65
99 Falciformispora lignatilis BCC 21118
Trematosphaeriaceae
GU301876 Trematosphaeria pertusa CBS 122371
61 Pseudoxylomyces elegans KT 2887
16
46 Latorua caligans CBS 576.65
Latoruaceae
100 Latorua grootfonteinensis CBS 369.72
Bambusicola massarinia MFLUCC 11-0389
Bambusicolaceae
100
--
92 Bambusicola splendida MFLUCC 11-0439
74 Inflatispora pseudostromatica CBS 123110
--
Monodictys capensis HHUF 29712
Asteromassaria pulchra CBS 124082
100 Massarina ramunculicola BCC 18404
79
Massarina ramunculicola BCC 18405
Morosphaeriaceae
--
82 Helicascus nypae BCC 36752
Longiostiola tectonae MFLUCC 12-0562
73 Farasanispora avicenniae MF-1207
Massariosphaeria phaeospora CBS 611.86
--
Thyridaria rubronotata CBS 385.39
Corynespora cassiicola CBS 100822
Pleosporales
90 Corynespora smithii CABI 5649b
100 Beverwykella pulmonaria CBS 283.53
Melanomma pulvis pyrius CBS 371.75
100 Byssosphaeria jamaicana SMH 1403
Halotthia posidoniae BBH 22481
0.05

Fig. 13 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, RPB2 and TEF sequence data of *Pleosporineae* and *Massarineae*, *Pleosporales*, *Dothideomycetes*. Maximum likelihood bootstrap support values greater than 50% are near the nodes. The ex-type strains are in bold and the new isolates are in blue. The tree is rooted with *Halotthia posidoniae* BBH 22481.

Didymosphaeriaceae

The family *Didymosphaeriaceae* was introduced by Munk (1953) and is typified by *Didymosphaeria* with *D. epidermidis* (Fr.) Fuckel as the type species. Ariyawansa *et al*. (2014a) synonymized *Montagnulaceae* under *Didymosphaeriaceae* based on priority of the oldest name. Ariyawansa *et al*. (2014a) detailed the family and accepted 16 genera. *Austropleospora*, *Cucubidothis*, *Munkovalsaria*, *Spegazzinia*, *Sporidesmiella*, *Paracamarosporium*, *Pseudocamarosporium*, *Pseudopithomycetes*, *Pseudotrichia*, *Verrucoconiothyrium*, and *Xenocamarosporium* were later introduced to the family based on morphology and phylogenetic analysis (Thambugala *et al*. 2014c, Wijayawardene *et al*. 2014a, Ariyawansa *et al*. 2015a, Crous *et al*. 2015a, Tanaka *et al*. 2015). However, the strains of *Munkovalsaria appendiculata* Aptroot that cluster with *Montagnula* species and *Sporidesmiella fusiformis* W.P. Wu were not ex-type species. Therefore, Wanasinghe et al. (2016) synonymized *Munkovalsaria* under *Montagnula*, when introducing a new genus, *Laburnicola* in *Didymosphaeriaceae*. The family now contains 28 genera. A phylogenetic tree for the family is presented in Wanasinghe et al. (2016) and in this paper we used the genera closest to *Pseudocamarosporium* (Fig. 14).

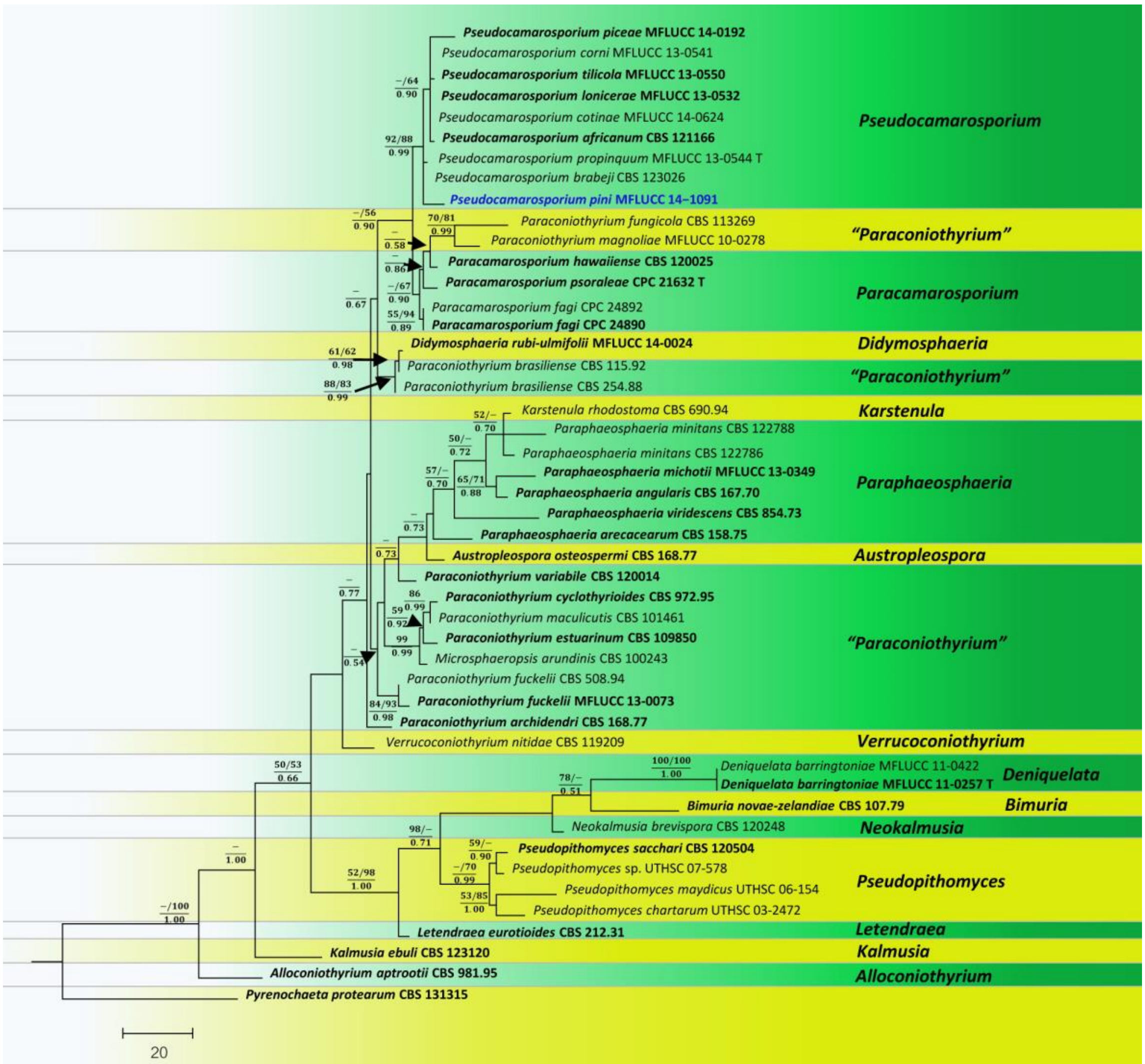


Fig. 14 Phylogram generated from maximum parsimony analysis based on combined LSU, ITS and SSU sequenced data from species of *Didymosphaeriaceae*. Maximum parsimony/likelihood bootstrap support values greater than 50 % and Bayesian posterior probabilities greater than 0.50 are shown in above and below. The ex-type strains are in bold and the new isolates is in blue. The tree is rooted with *Pyrenochaeta protearum*.

Pseudocamarosporium Wijayaw. & K.D. Hyde

The genus *Pseudocamarosporium* is typified by *P. propinquum* and *Paracamarosporium* is typified by *P. psoraleae* and were introduced to accommodate camarosporium-like species that cluster in *Didymosphaeriaceae* (Wijayawardene *et al*., 2014a). Based on morphology both genera are similar, but *Paracamarosporium* has paraphyses and microconidia which are lacking in *Pseudocamarosporium*.

261. *Pseudocamarosporium pini* (Westend.) Phukhamsakda, Camporesi & K.D. Hyde, ***comb. nov.***

Index Fungorum number: IF 551896; *Facesoffungi number*: FoF 01817, Fig. 15

Basionym: *Hendersonia pini* Westend., Bull. Acad. R. Sci. Belg., Cl. Sci.: tab. 9, no. 7 (1857)

≡ *Camarosporium pini* (Westend.) Sacc., Syll. fung. (Abellini) 3: 465 (1884)

Saprobic on dead cone of *Pinus nigra* J.F. Arnold. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 105–174 *µm* high × 188–244 wide *µm* ($\bar{x}$ = 145 × 210 *µm*, n = 5) diam., pycnidial, solitary, uniloculate, scattered, immersed to erumpent, subglobose, but sometimes irregular, brown to dark brown, ostiole central. *Pycnidial wall* 14–28 *µm* (–40 *µm* at apex), composed of 5 layers of brown-walled cells of *textura angularis*, hyaline inner layer lining bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–6 × 3–5 *µm* ($\bar{x}$ = 4 × 4 *µm*, n = 20) diam., enteroblastic, phialidic, determinate, smooth-walled, hyaline. *Conidia* 7–18 × 4–8 *µm* ($\bar{x}$ = 14 × 6 *µm*, n = 50), oval to oblong, curved at the apex, with 1–3 transverse septa, and 1–2 longitudinal septa at the second and third cells, initially hyaline, brown to dark brown at maturity, narrowly rounded at both ends, smooth-walled.

Culture characteristics: Colonies on PDA 60 mm diam. after 4 weeks at 16°C, cream to white at the margins, pale-brown to yellowish at the center; reverse yellowish to cream and orangish-white at the center, medium dense, circular, umbonate, fairly fluffy, without diffusible pigments.

Material examination: ITALY, Forlì-Cesena Province, Monte Mirabello - Predappio, on dead and terrestrial cone of *Pinus nigra* (*Pinaceae*), 13 Octorber 2014, E. Camporesi (MFLU 15–3290, HKAS 91937, **reference specimen designed here**), ex-type living culture, MFLUCC 14–1091, KUMCC 15–0550.

Note: Several *Camarosporium* species has been reported from *Pinus* spp., such as *C. propinquum* (Sacc.) Sacc., *C. brabeji* Marincowitz *et al*., and *C. pini* (Westend.) Sacc. (Grove 1937, Botella *et al*. 2010, Botella and Diez 2011). Wijayawardene *et al*. (2014a) treated *C. propinquum* under *Pseudocamarosporium* typified by *P. propinquum*. The strain clustered in *Didymosphaeriaceae*, separate from the type of *Camarosporium*, *C. quaternatum*, which clustered in *Pleosporinae*. Crous *et al*. (2015a) synonymized *Camarosporium brabeji* Marincowitz *et al*. under *Pseudocamarosporium brabeji* as the molecular data placed them in *Didymosphaeriaceae*. *Camarosporium pini* was originally described by Westendorp (1857) as *Hendersonia pini*, and the species is recorded from *Pinus silvestris* (Grove 1937). When comparing the morphology of our species with *C. pini*, they are similar in the host and morphology. The conidiomata are similar in size, with thick walls up to 40 *µm* wide. The dimension of conidia overlap and are oblong, rounded at both ends, with one or two longitudinal septa in the middle cells. Based on phylogenetic analysis (Fig. 14) our strain clusters within *Pseudocamarosporium* in *Didymosphaeriaceae* with relative high support (92% MP /88 % ML /0.99 PP). We therefore synonymize *Camarosporium pini* under *Pseudocamarosporium pini* based on morphology and phylogeny, and designate our collection as a reference specimen (*sensu* Ariyawansa *et al*. 2014c), which we illustrate here.

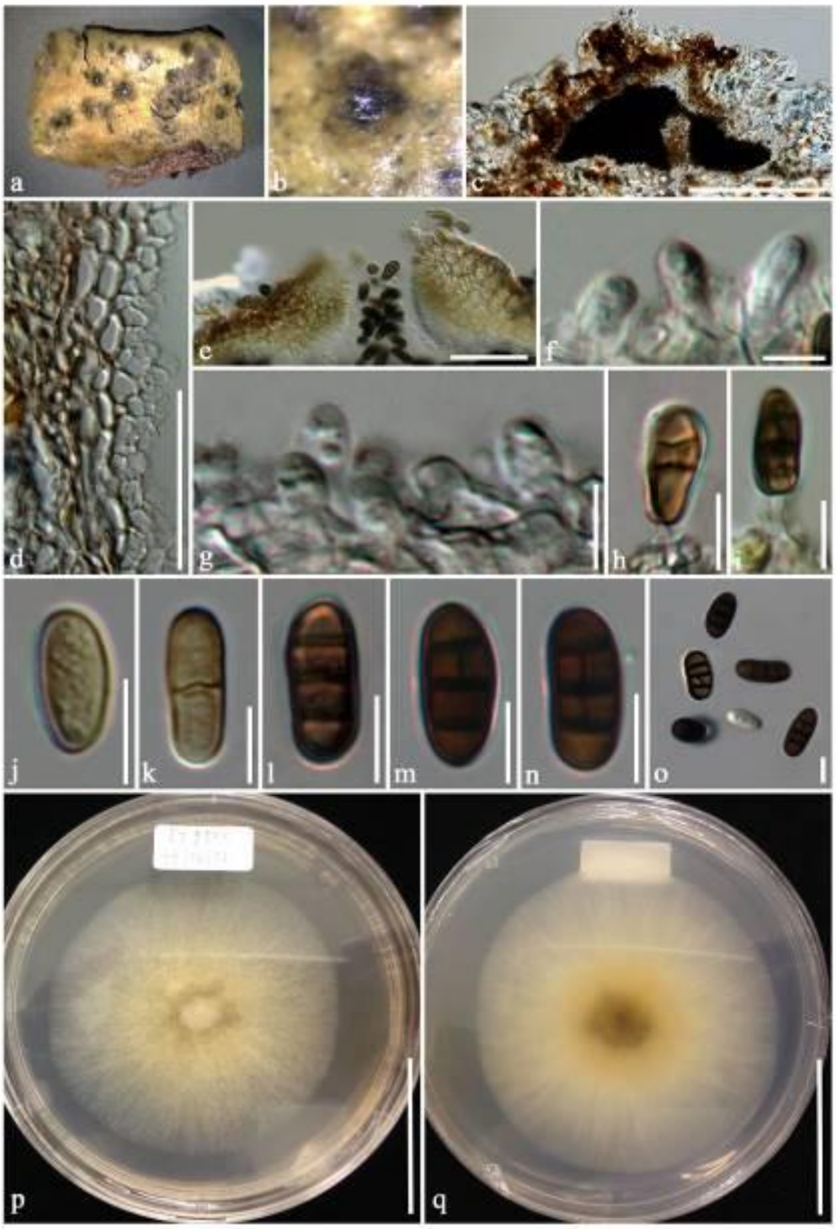


Fig. 15 ***Pseudocamarosporium pini*** (MFLU 15–3290, **reference specimen**) **a, b** Appearance of conidiomata on *Pinus nigra* cone **c** Vertical section of conidioma **d** Peridium **e** Ostiole **f–i** Developing stages of conidia **j–o** Conidia **p–q** Culture characters on PDA. Scale bars: c = 100 *µm,* d–e = 20 *µm,* f–o = 5 *µm*, p–q = 30 mm.

Lentitheciaceae

The family *Lentitheciaceae* was introduced to accommodate *Lentithecium* and some other related taxa (Zhang et al. 2009a) with species occurring on herbaceous plants and on submerged wood in freshwater environments (Zhang et al. 2012). There have been several studies on *Lentitheciaceae* (Hirayama et al. 2010, Quaedvlieg et al. 2013, Wanasinghe et al. 2014, Ariyawansa et al. 2015b, Knapp et al. 2015, Liu et al. 2015, Phookamsak et al. 2015, Singtripopa et al. 2015, Tanaka et al. 2015, Wijayawardane et al. 2015). Currently there are eleven accepted genera included including the new genus introduced in this study (*Darksidea*, *Katumotoa*, *Keissleriella*, *Lentithecium*, *Murilentithecium*, *Neoophiosphaerella*, *Phragmocamarosporium*, *Poaceascoma*, *Setoseptoria*, *Tingoldiago* and *Towyspora*). The phylogenetic tree is presented in Fig. 16.

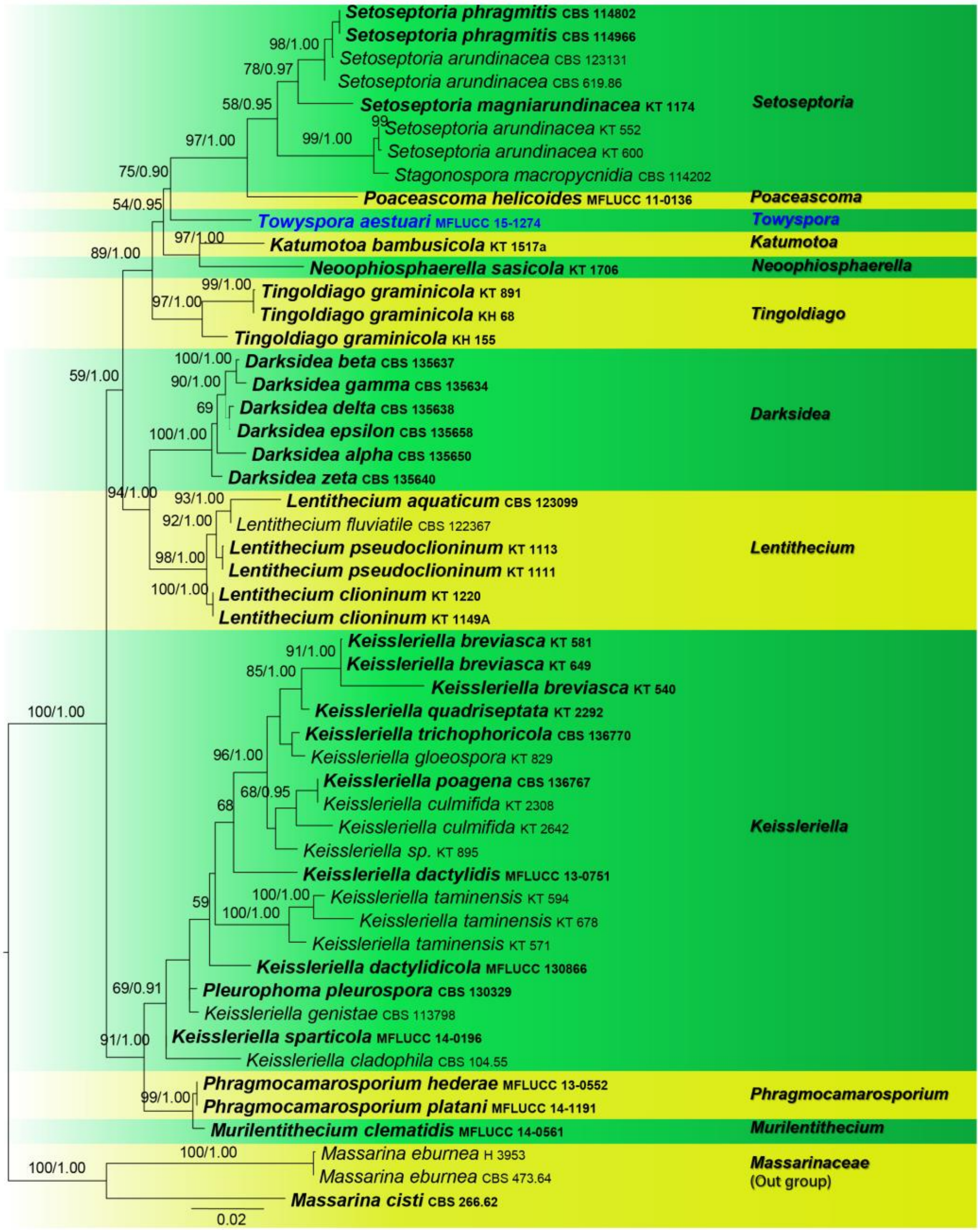


Fig. 16 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF and ITS sequence data for species of *Lentitheciaceae*. Maximum likelihood bootstrap support values greater than 50 % and Bayesian posterior probabilities greater than 0.90 are near the nodes. The ex-type strains are in bold and the new isolates are in blue. The scale bar indicates 0.02 changes. The tree is rooted with *Massarina eburnea* and *M. cisti*.

262. *Towyspora* Wanasinghe, E.B.G. Jones & K.D. Hyde, *gen. nov.*

Index Fungorum number: IF 551787, *Facesoffungi number*: FoF 01671

Etymology: Named after the River Towy where this species was collected and from the Latin, *spora* meaning spore.

Saprobic on dead shrubs in aquatic habitats. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, stromatic, mostly solitary, semi-immersed to immersed in the host, uni- to multi-loculate, globose to subglobose, dark brown to black, ostiolate, apapillate. *Peridium* comprising 2–3 layers, pigmented, thin-walled, comprise blackish to dark brown, angular cells. *Conidiogenous cells* phialidic, discrete, ampulliform to cylindric-clavate, hyaline, aseptate, smooth. *Conidia* hyaline, 1-celled, oblong to cylindrical, with rounded or obtuse ends, aseptate, smooth-walled, thin-walled, guttulate.

Type species: ***Towyspora aestuari*** Wanasinghe, E.B.G. Jones & K.D. Hyde

Notes: *Towyspora* gen. et sp. nov. is introduced in the family *Lentitheciaceae* to accommodate, *T. aestuari* based on both morphology and phylogeny. *Towyspora* shares most similarities with *Setoseptoria* in having hyaline, subcylindrical conidiogenous cells and transversely euseptate, hyaline, smooth-walled, subcylindrical conidia, with one large central guttule per cell. *Towyspora* however, differs from *Setoseptoria* in having comparatively smaller conidia. This is also supported phylogenetically as *Towyspora aestuari* forms a remote clade from *Setoseptoria* with high bootstrap support (Fig. 16).

263. *Towyspora aestuari* Wanasinghe, E.B.G. Jones & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF 551788, *Facesoffungi number*: FoF 01672, Fig. 17

Etymology: aestuari from estuary, the habit of the species

Holotype: MFLU 15–3543

Saprobic on *Phragmites communis* (Cav.) Trin. ex Steud. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 300–400 *µm* high × 200–250 *µm* diam. ($\bar{x}$ = 347.9 × 223.2 *µm*, n = 10), pycnidial, stromatic, mostly solitary, semi-immersed to immersed in the host, uni- to multi-loculate, globose to subglobose, dark brown to black, ostiolate, apapillate. *Peridium* 5–10 *µm* wide at the base, 7–12 *µm* wide in sides, comprising 2–3 layers, pigmented, thin-walled, comprising blackish to dark brown, angular cells. *Conidiogenous cells* 5–8 *µm* high × 2–4 *µm* wide, phialidic, discrete, ampulliform to cylindric-clavate, hyaline, aseptate, smooth. *Conidia* 7–12 × 2.5–3.5 *µm* ($\bar{x}$ = 9.6 × 2.8 *µm*, n = 50), hyaline, 1-celled, oblong to cylindrical, with rounded or obtuse ends, transversely euseptate, smooth and thin-walled, guttulate.

Material examined: UK, Lanstephan, 8 July 2015, on *Phragmites communis* (*Poacaeae*), E.B.G. Jones (MFLU 15–3543, **holotype**); ex-type culture, MFLUCC 15–1274, MUCL.

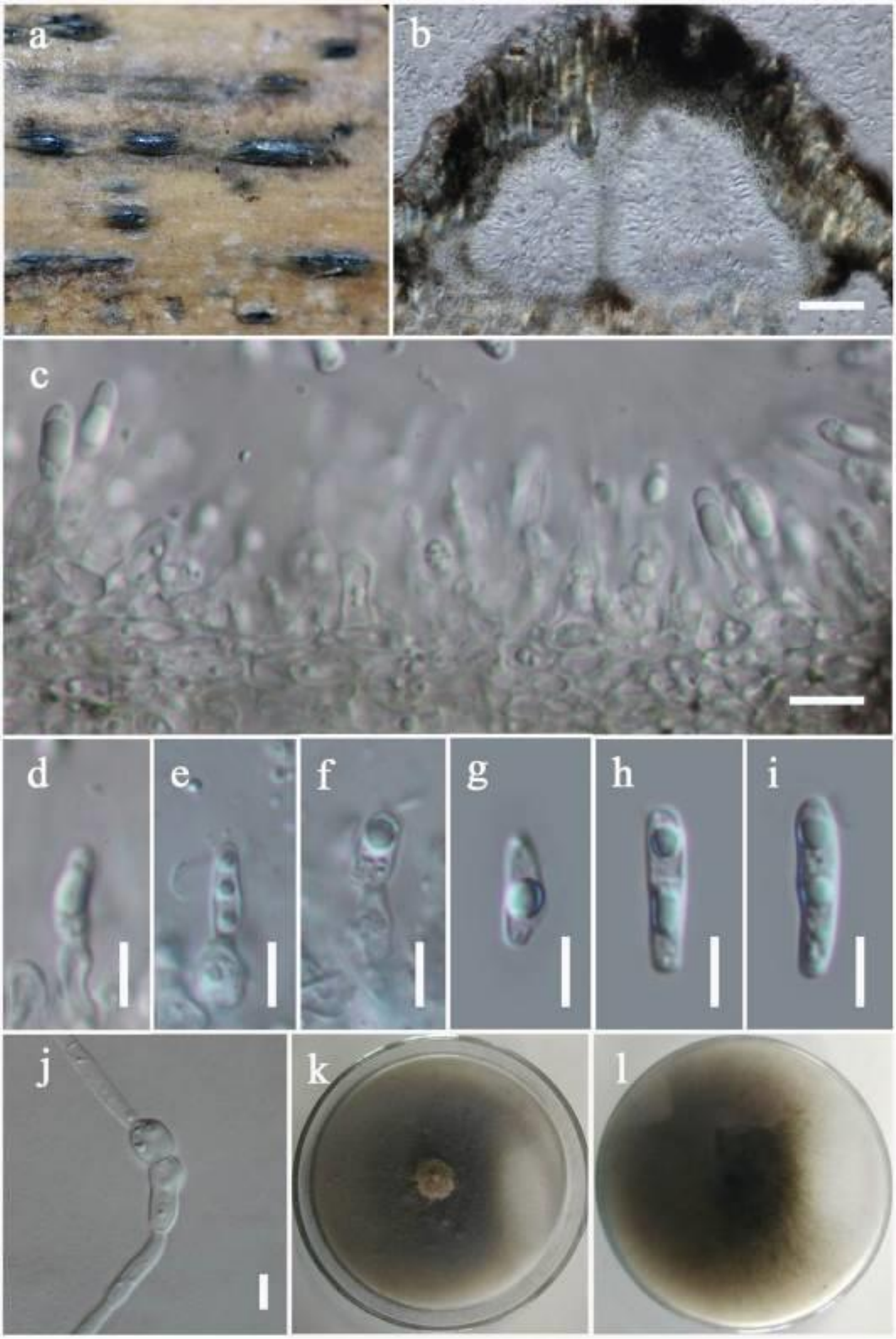


Fig. **17** ***Towyspora aestuari*** **(holotype)** **a** Appearance of conidiomata on host substrate **b** Vertical section through conidioma **c**–**f** Mature and immature conidia attached to conidiogenous cells **g–i** Mature and immature conidia **j** Germinated conidium **k, l** Culture on PDA (note l reverse). Scale bars b = 50 *µm*, c = 20 *µm*, d–j = 5 *µm*.

Lindgomycetaceae

Lindgomyces K. Hiray. et al.

Lindgomyces K. Hiray. et al. (*Lindgomycetaceae*, *Pleosporales*, *Dothideomycetes*) is a recently established ascomycetous genus from submerged wood in freshwater habits (Hirayama et al. 2010). *Lindgomyces* is characterized by globose to subglobose ascomata, fissitunicate, clavate to cylindrical asci, and clavate to cylindrical, hyaline ascospores with a gelatinous sheath (Hirayama et al. 2010). *Lindgomyces* currently includes eight species, viz. *L. ingoldianus* (Shearer & K.D. Hyde) K. Hiray. et al. (type species), *L. apiculatus* K. Hiray. & Kaz. Tanaka, *L. breviappendiculatus* (Kaz. Tanaka et al.) K. Hiray. & Kaz. Tanaka, *L. cinctosporus* Raja et al., *L. lemonweirensis* Raja et al., *L. rotundatus* K. Hiray. & Kaz. Tanaka, *L. angustiascus* Raja et al. and *L. griseosporus* Ying Zhang et al. (Hirayama et al. 2010; Raja et al. 2011, 2013; Zhang et al. 2014). The phylogenetic tree is presented in Fig. 18.

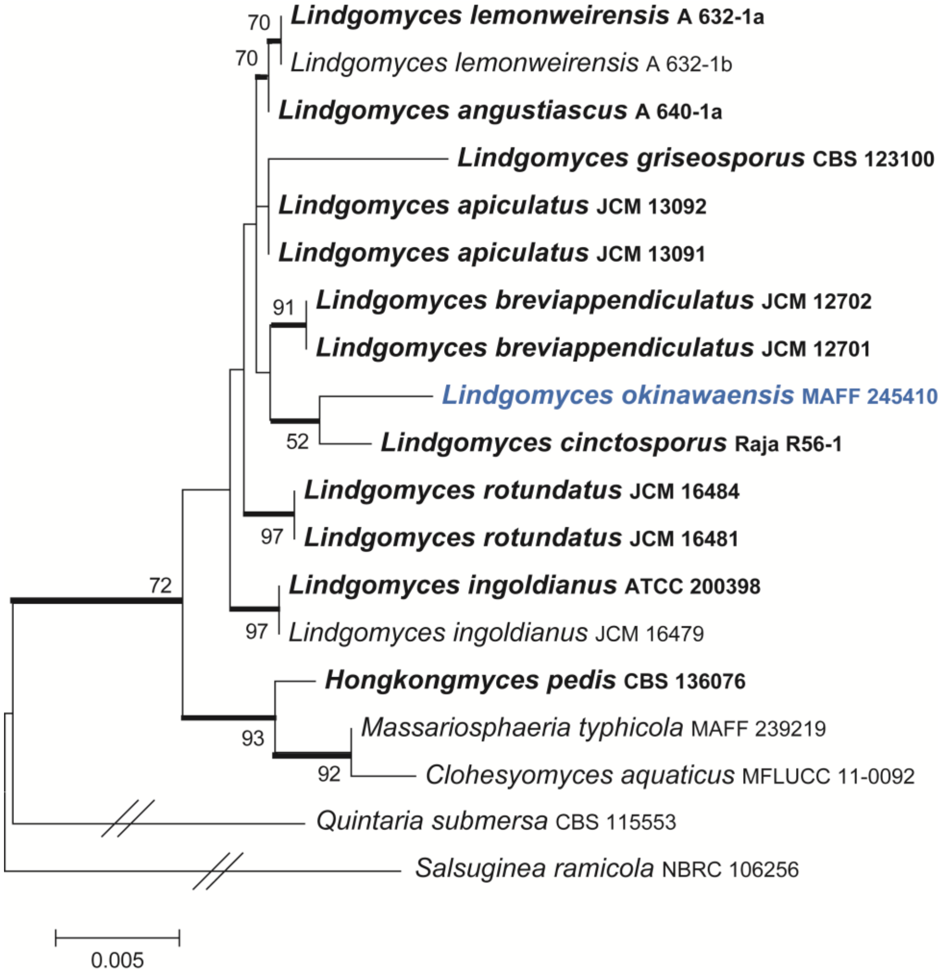


Fig. 18 Maximum-likehood tree of *Lindgomyces okinawaensis* based on SSU and LSU sequence data. Bootstrap values greater than 50 % are presented at the nodes. New taxa are in blue and ex-types in bold.

264. *Lindgomyces okinawaensis* Tak. Takah. & Kaz. Tanaka, *sp. nov.*

MycoBank number: MB 815296; *Facesoffungi number*: FoF 02022, Fig. 19

Etymology: In reference to the locality, Okinawa where the new species was collected.

Holotype: HHUF 30498

Saprobic on submerged dead wood. **Sexual morph** *Ascomata* 260–290 *µm* high, 310–340 *µm* diam., globose to subglobose, black, scattered to grouped, immersed to erumpent. *Neck* 50–60 *µm* long, 50–75 *µm* wide, short papillate, central. *Peridium* 35–41 *µm* thick, composed of an inner layer of polygonal to subglobose, hyaline to pale brown, thin-walled, 8–12 × 6–7.5 *µm* cells, and an outer layer of brown-walled cells. *Hamathecium* comprising numerous, 1.5–3 *µm* wide, anastomosed, branched, cellular pseudoparaphyses. *Asci* 134.5–183(–208) × (18.5–)23–31(–40.5) *µm* ($\bar{x}$ = 160.9 × 26.5 *µm*, n = 12), 8-spored, fissitunicate, clavate, rounded at the apex, with an apical chamber. *Ascospores* (38–)40–48(–51) × (10–)12–19 *µm* ($\bar{x}$ = 44.9 × 14.9 *µm*, n = 50), L/W 2.2–4.3 ($\bar{x}$ = 3.1, n = 50), overlapping biseriate to triseriate, hyaline, pale brown with age, clavate with acute ends, straight or slightly curved, with the primary septum almost submedian 0.46–0.58 ($\bar{x}$ = 0.52, n = 50), filled with small lipid droplets, slightly constricted at the primary septum, with a broad upper cell, smooth-walled, becoming 3-septate with age. **Asexual morph** Undetermined.

Material examined: JAPAN, Okinawa, Kunigami, Aha, Tanagakumui, small river, on submerged dead twigs of woody plant, 19 May 2015, collector K. Tanaka et al., KT 3531 (HHUF 30498, **holotype**); ex-type living culture, MAFF 245410.

Notes: *Lindgomyces okinawaensis* has relatively wide ascospores. The morphological features of ascospores are similar to those of *L. cinctosporus* (Hirayama et al. 2010). However, the ascospores of *L. okinawaensis* do not have an entire gelatinous sheath. The identities of ribosomal ITS sequences between *L. okinawaensis* and *L. cinctosporus* were low [GenBank JF419905; Identities = 408/432 (94.4%), Gaps = 2/432 (0.5%)].

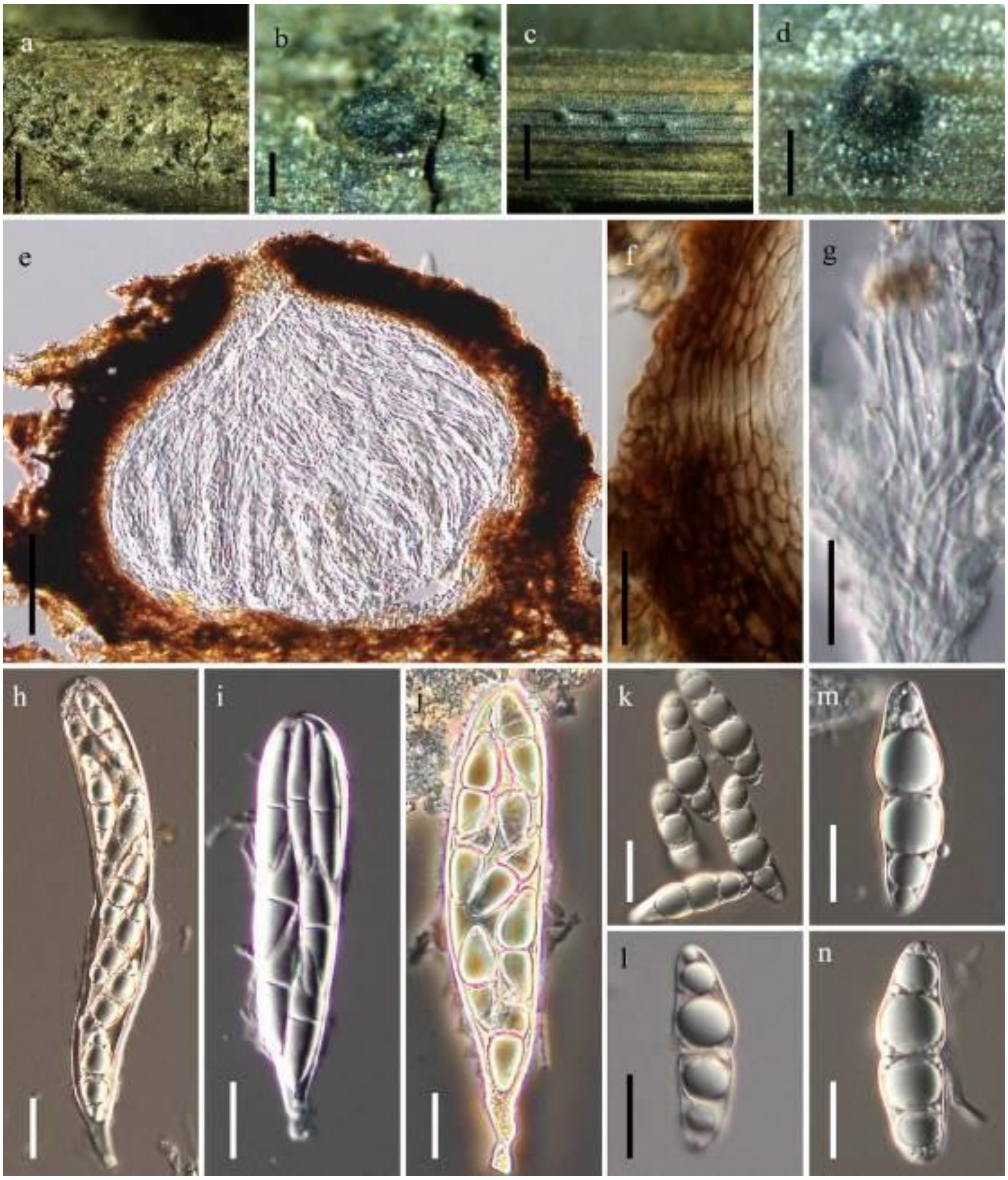


Fig. 19 ***Lindgomyces okinawaensis*** **a**, **b** Appearance of ascomata on host surface **c, d** Ascomata formed in culture **e** Ascoma in longitudinal section **f** Peridium in longitudinal section **g** Pseudoparaphyses **h**–**j** Asci **k**–**n** Ascospores **a**, **b**, **e**, **g**, **i** from HHUF 30498 **(holotype)**; **c**, **d**, **f**, **h**, **j**–**n** from MAFF 245410 **(ex-holotype)**. Scale bars: a, c = 1 mm, b, d = 200 *µm*, e = 50 *µm*, f–n = 20 *µm*.

Lophiostomataceae

The family *Lophiostomataceae* was revisited by Thambugala et al. (2015a). Based on morphology and phylogenetic analyses of the lophiostomataceous genera, *Lophiostomataceae* is presently a large family comprising 16 genera. One new species is each introduced in the genera *Lophiostoma* and *Sigarispora* in this study; the phylogenetic trees for *Lophiostomataceae* are presented in Figs 20 and 21.

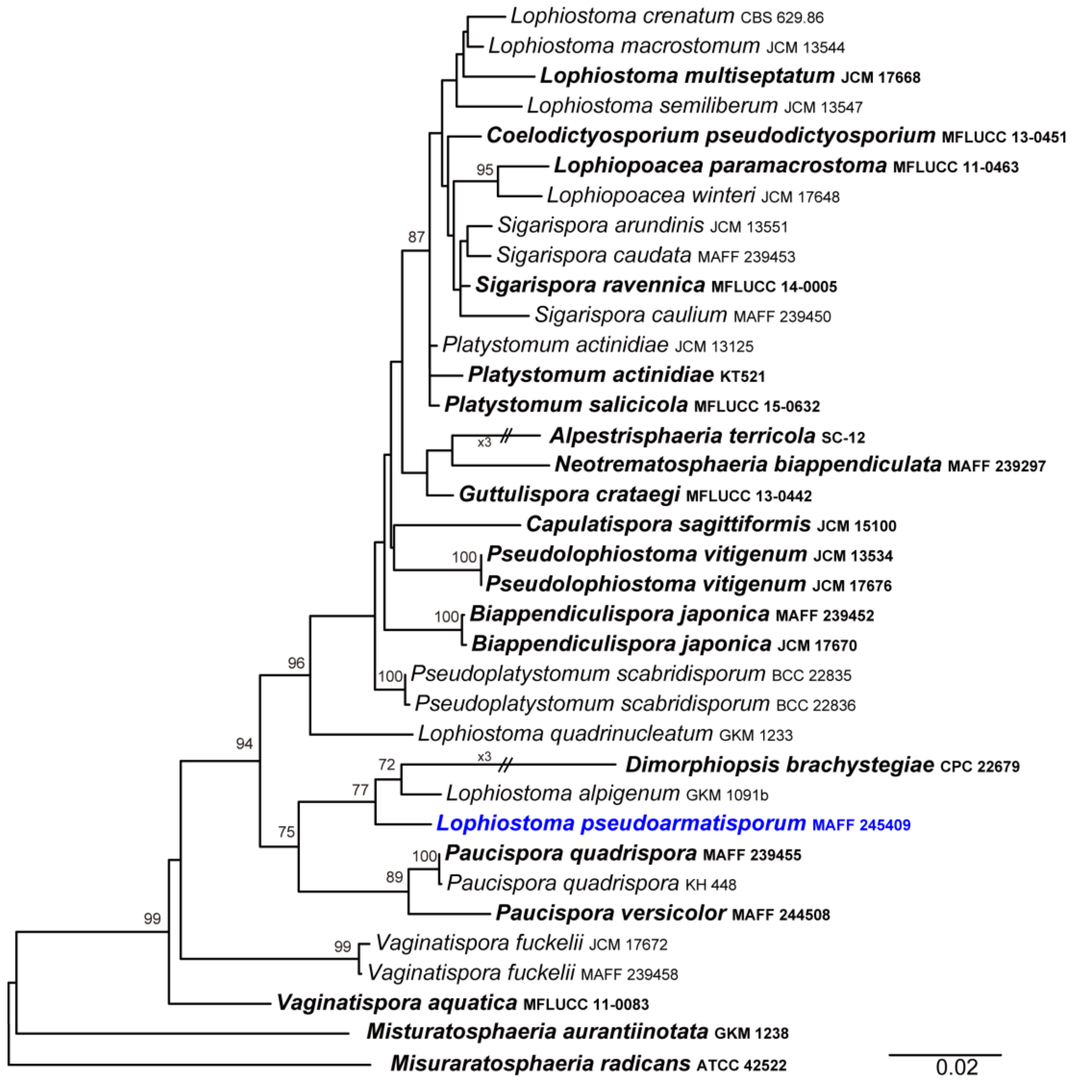


Fig. 20 ML tree based on an analysis of combined LSU, SSU and TEF sequence data. Bootstrap values greater than 70% are indicated at the nodes. New taxa are in blue and ex-type strains are in bold.

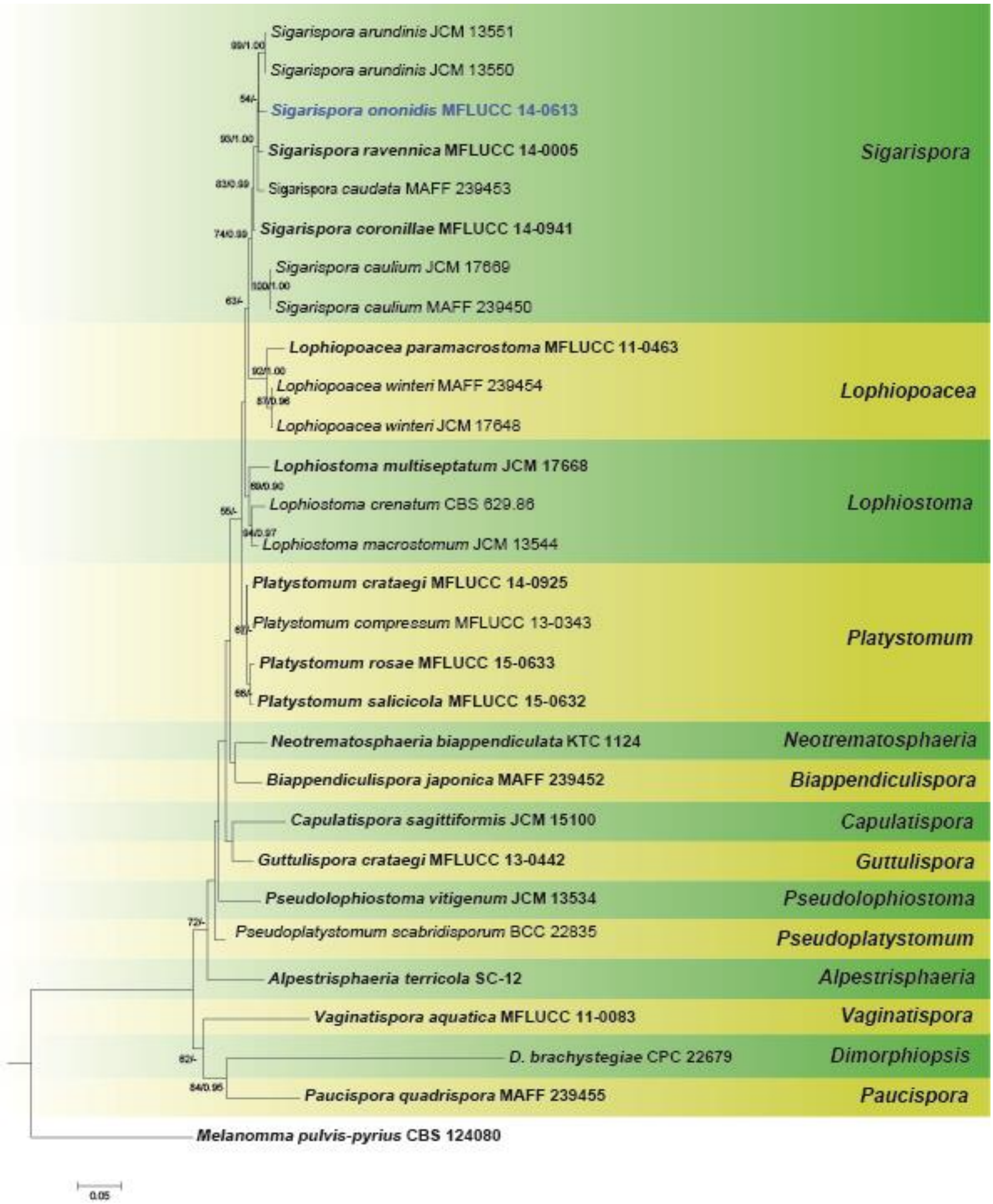


Fig. 21 Phylogram generated from Maximum likelihood (RAxML) analysis based on combined LSU, SSU, ITS and TEF1 sequence data of species of *Lophiostomataceae*. Maximum likelihood bootstrap support values greater than 50 % are indicated above or below the nodes, and branches with Bayesian posterior probabilities greater than 0.90 are given. New taxa are in blue and ex-type strains are in bold. The tree is rooted with *Melanomma pulvis-pyrius*.

265. *Lophiostoma pseudoarmatisporum* Hay. Takah., K. Hiray. & Kaz. Tanaka, ***sp. nov.***

MycoBank number: MB 815298, *Facesoffungi number*: FoF 02023, Fig. 22

Etymology: In reference to the similarity of the ascospore with that of *Lophiostoma armatisporum*.

Holotype: HHUF 30497

Saprobic on dead wood. **Sexual morph** *Ascomata* 390–515 *µm* high, 555–645 *µm* diam., immersed, subglobose to ellipsoidal, black, with a slit-like ostiole. *Peridium* in longitudinal section, 25–38 *µm* thick at sides, composed of 3–5 layers of angular, hyaline to brown, 10–15 × 2.5–5 *µm* cells. *Hamathecium* comprising 1.5–2 *µm* wide pseudoparaphyses. *Asci* 105–152 × 15.5–25 *µm* ($\bar{x}$ = 131.3 × 19.7 *µm*, n = 50), 8-spored, clavate, fissitunicate, pedicellate, with an ocular chamber. *Ascospores* 29–40 × 9.5–13 *µm* ($\bar{x}$ = 34.4 × 11.3 *µm*, n = 100), 1–2-seriate, fusiform, hyaline, with the primary septum mostly submedian (0.48–0.56; $\bar{x}$ = 0.52, n = 100), the cell above the septum usually broader than the lower one, smooth-walled, with thin mucilaginous appendages, 6–10 *µm* long. **Asexual morph** Undetermined.

Material examined: JAPAN, Kagoshima, Yakushima Island, Yakusugi land, on dead twigs of unknown woody plant, 15 March 2007, collector K. Tanaka and H. Yonezawa, KT 2237 (HHUF 30497, **holotype**); ex-type living culture, MAFF 245409.

Notes: Morphologically, this taxon has ascospores which are similar to *Lophiostoma armatisporum* (Hyde et al. 1992). However, *L. pseudoarmatisporum* has wider ascospores than those of *L. armatisporum* (vs. 28–39 × 7–9.8 *µm*; Hyde et al. 1992), and the ITS sequence similarity between these two taxa is rather low (405/544 = 74.4 %, with gaps 32/544 = 5.9 %; Liew et al. 2002). Multi-gene phylogenetic analysis (Fig. 20) indicated that *L. pseudoarmatisporum* has a close relationship with *Lophiostoma alpigenum*, but the latter has longer and slender ascospores (40–45 × 10 *µm*) with 9–11-septa (Holm and Holm 1988) than those of *L. pseudoarmatisporum*.

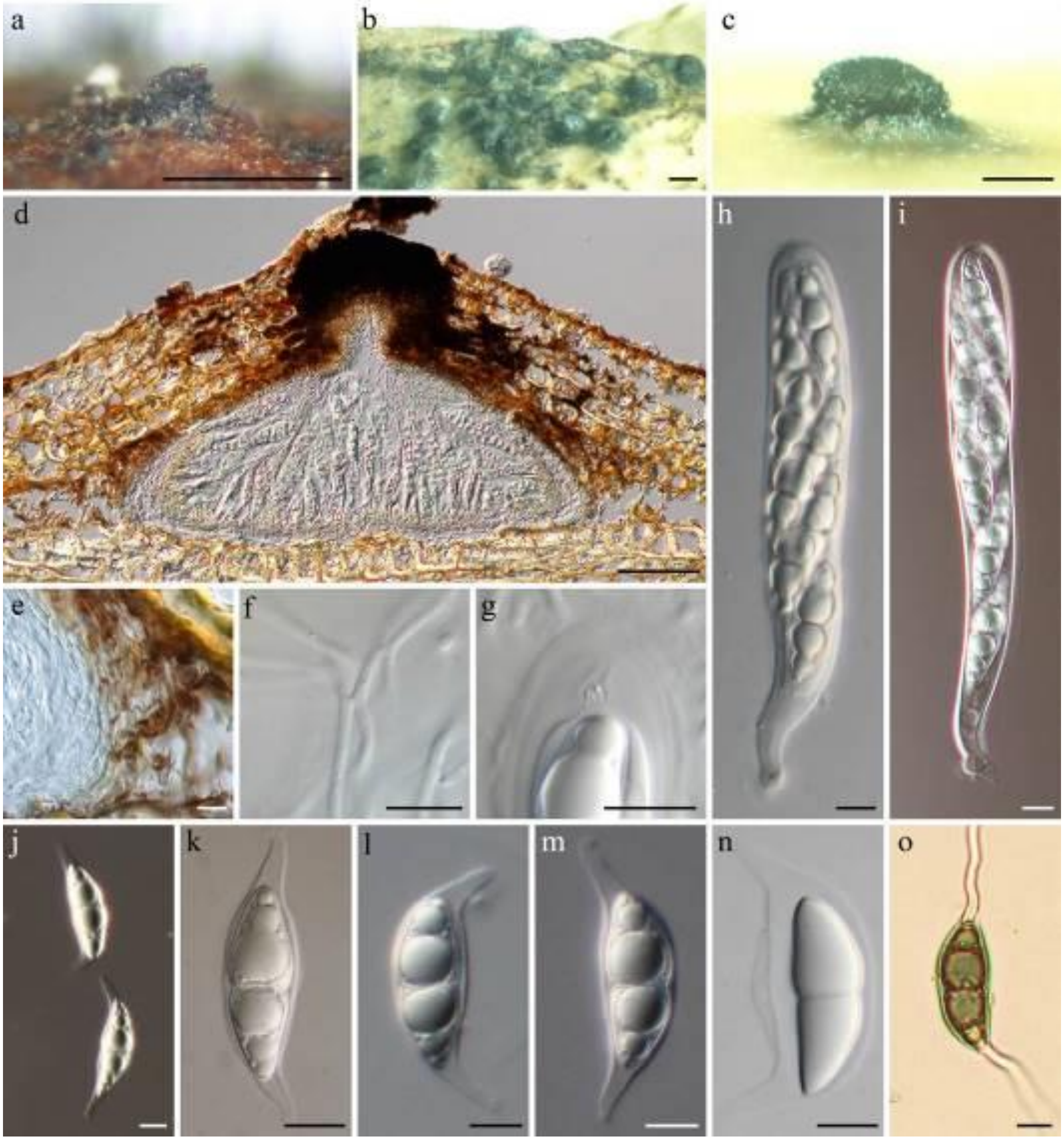


Fig. 22 ***Lophiostoma pseudoarmatisporum*** **a** Ascoma on host surface **b, c** Ascoma formed in culture **d** Ascoma in longitudinal section **e** Peridium **f** Pseudoparaphyses **g** Ascus apex **h, i** Asci with 8 ascospores **j–n** Ascospores **o** Germinating ascospore **a, d–h, n, o** from HHUF 30497 **(holotype)**; **b, c, i–m** from culture MAFF 245409 **(ex-holotype)**. Scale bars: a–c = 500 *µm*, d = 100 *µm*, e–o = 10 *µm*.

266. ***Sigarispora*** Thambug. & K.D. Hyde, in Thambugala et al., Fungal Diversity: 199–266, [40] (2015)

Index Fungorum number: IF 551255, *Facesoffungi number*: FoF 00823

Notes: *Sigarispora* was introduced by Thambugala et al. (2015a) based on morphological characters and phylogenetic analyses and is typified by *S. ravennica* (Tibpromma et al.) Thambugala & K.D. Hyde. It is characterized by immersed to semi-immersed ascomata, a small crest-like ostiole, and brown, cigar-shaped, multi-septate ascospores. In this study, the new species clustered together with *S. arundinis* (Pers.) Thambug. et al., *S. ravennica* (Tibpromma et al.) Thambugala & K.D. Hyde, *S. caudata* (Fabre) Thambug. et al., *S. coronillae* Wanas. et al. and *S.*

caulium (Fr.) Thambug. et al. and formed a distinct clade in *Lophistomataceae* (Fig. 21).

266. *Sigarispora ononidis* Qing Tian, Thambug., Camporesi & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF 551729, *Facesoffungi number*: FoF 01639, Fig. 23

Etymology: In reference to its occurrence on *Ononis* sp., ononidis meaning "of *Ononis*".

Holotype: MFLU 15–2667

Saprobic on the dead stem of *Ononis spinosa* L. in terrestrial habtats. **Sexual morph** *Ascomata* 240–311.5 *µm* diam. ($\bar{x}$ = 287.2 *µm*, n = 10), perithecial, solitary, scattered to gregarious, immersed or semi-immersed to erumpent, gregarious, circular, globose or subglobose, coriaceous, black, ostiolate, smooth-walled. *Ostiole* central, rounded, with a pore-like opening. *Peridium* 250–320 *µm* wide × 196–250 *µm* high ($\bar{x}$ = 279 × 220.5 *µm*, n = 10), two-layered, outer layer composed of irregular, thick-walled, brown to dark brown cells of *textura angularis* and inner layer with slightly, smaller cells of *textura angularis*. *Hamathecium* comprising 1–3 *µm* wide, branched or simple, septate, cellular, pseudoparaphyses, embedded in agelatinous matrix, between and above the asci. *Asci* 96–169 × 17–19 *µm* ($\bar{x}$ = 120.6 ×18 *µm*, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical to clavate or broader-clavate, long pedicellate, apically rounded, with an ocular chamber. *Ascospores* 27–34 × 11–12 *µm* ($\bar{x}$ = 29 × 11.7 *µm*, n = 10), overlapping uni-seriate or bi-seriate, yellowish brown to dark brown, ellipsoid to fusiform or cigar-shaped, 3–5-septate or rarely muriform with one vertical septa, slightly curved, constricted at the central septum, darkened, with rounded ends, smooth-walled, without a sheath. **Asexual morph** Undetermined.

Material examined: ITALY, Province of Forlì-Cesena, Valbura-Premilcuore, on dead stem of *Ononis spinosa* (*Fabaceae*), 18 June 2014, Erio Camporesi, IT1941 (MFLU 15–2667, **holotype**); *ibid*., (HKAS 92413, **isotype**); ex-type living cultures, MFLUCC 14–0613, KUMCC 15–0524.

Notes: *Sigarispora ononidis* is introduced here as a new species which is morphologically similar with species in *Sigarispora*, a genus established by Thambugala et al. (2015a). *Sigarispora ononidis* differs from other species of *Sigarispora* in having 3–5-septate or rarely muriform ascospores, without a mucilaginous sheath (Fig. 23). Phylogenetic analyses of combined genes indicated that the ex-type strain of *S. ononidis* clustered within the clade of *Sigarispora* (Fig. 21).

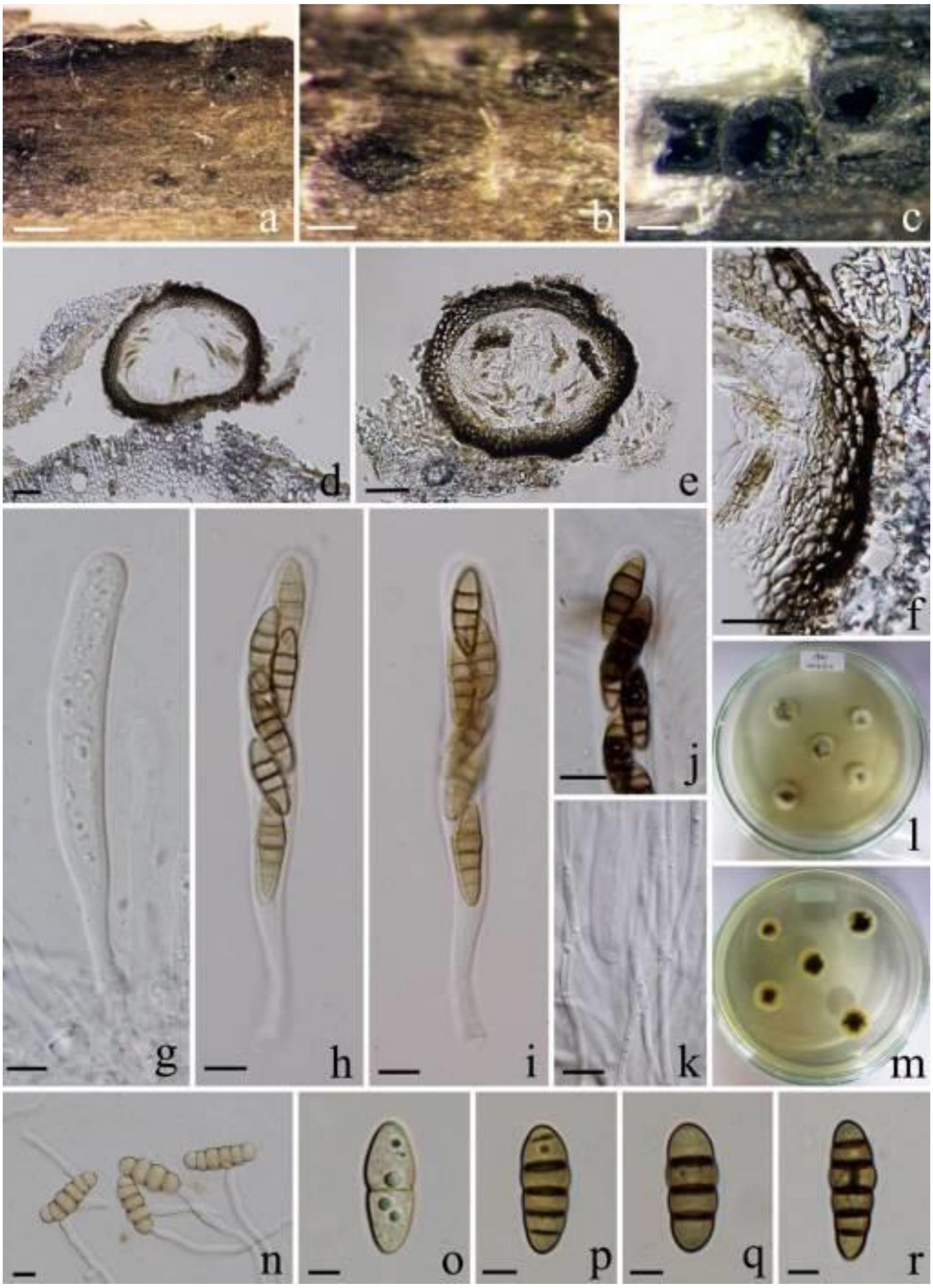


Fig. 23 ***Sigarispora ononidis*** **(holotype)** **a–c** Appearance of ascomata semi-immersed in the host **d, e** Vertical section of ascoma **f** Vertical section of peridium **g** Immature ascus **h–j** Mature asci with ascospores **k** Hamathecium **n** Germinated ascospore **o–r** Ascospores **l** Colony on MEA from above **m** Colony on MEA from below. Scale bars: a = 500 *µm*, b, c = 200 *µm*, d, e = 50 *µm*, f = 20 *µm*, g–k, n = 10 *µm*, o–r = 5 *µm*.

Melanommataceae

The family *Melanommataceae* was introduced by Winter (1885) and is characterized by globose or depressed perithecial ascomata, bitunicate and fissitunicate asci, hyaline or brown and 1 to multi-septate ascospores (Zhang et al.

2012; Hyde et al. 2013; Tian et al. 2015). Barr (1990) reviewed the family and included *Ostropella*, *Keissleriella*, *Strickeria*, *Byssosphaeria* and *Melanomma*. Subsequently various authors had included and excluded different species in *Melanommataceae* at various times. Tian et al. (2015) revised the family and accepted 20 genera, including seven asexual morphs. The phylogenetic tree is presented in Fig. 24.

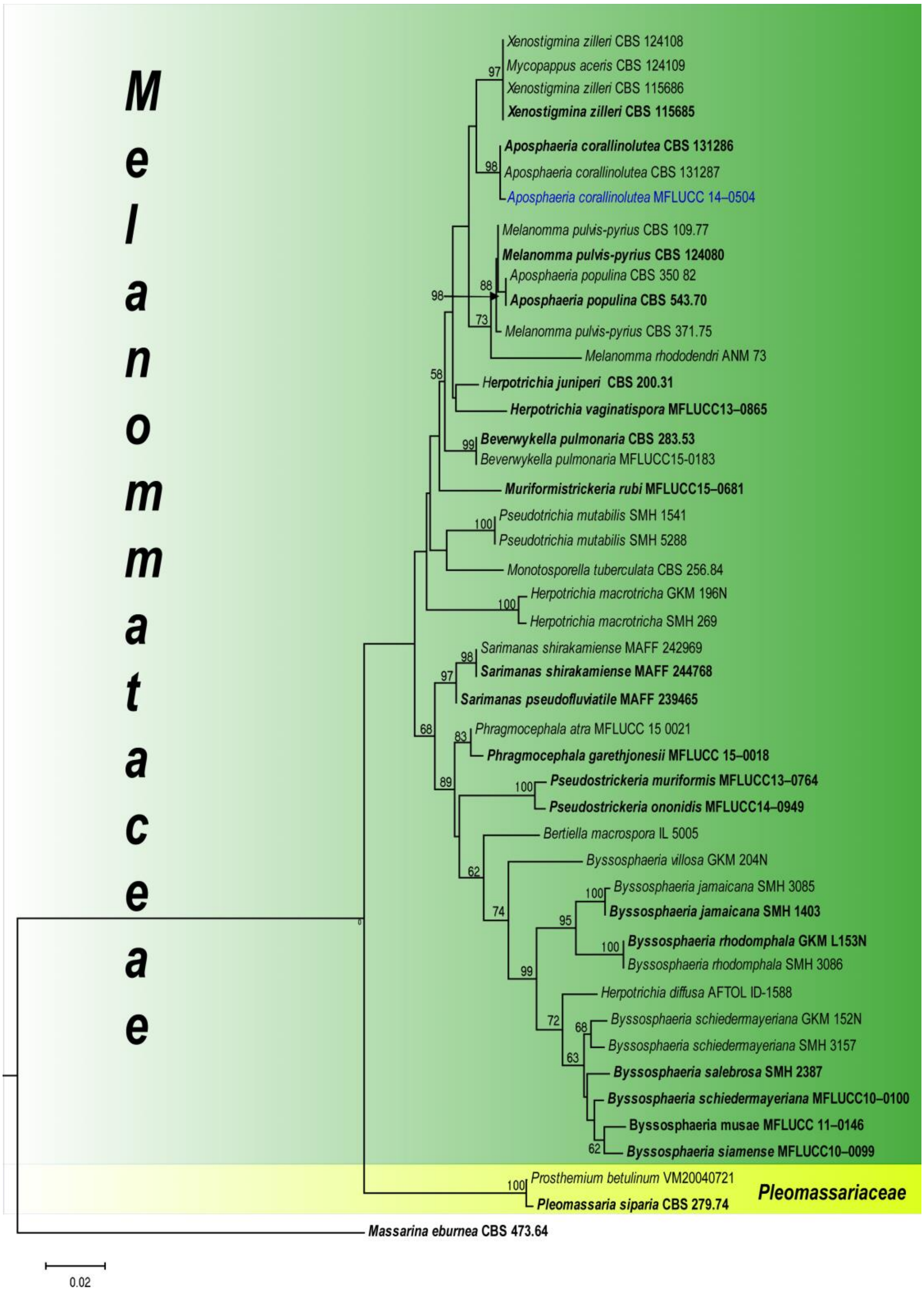


Fig. 24 Phylogram generated from Maximum Likelihood (RAxML) analysis based on combined LSU and EF sequence data of taxa from *Melanommataceae* and *Pleomassariaceae*. Maximum likelihood bootstrap support values greater than 50 % are indicated above and below the nodes. New taxa are in blue and ex-type strains are in bold. The tree is rooted with *Massarina eburnea*.

Aposphaeria Berk.

Aposphaeria is a poorly known genus and recent studies have been classified this genus in *Melanommataceae* based on sequence data (De Gruyter et al. 2012; Tian et al. 2015). *Aposphaeria* or aposphaeria"- like species have been reported for different genera such as *Chaetomastia*, *Massariosphaeria*, *Melanomma*, *Mytilinidion* and *Rhytidhysteron* (Sivanesan 1984; Barr 1989; Zhang et al. 2012; Hyde et al. 2013; Tian et al. 2015). However, sequence data of the type species, *A. pulviscula* (Sacc.) Sacc., are essential to confirm the phylogeny of *Aposphaeria* in *Melanommataceae*. This genus is characterized by pycnidial, unilocular conidiomata, short, cylindrical, branched conidiophores and hyaline, aseptate, cylindrical or ellipsoidal conidia (Tian et al. 2015).

267. *Aposphaeria corallinolutea* Gruyter et al., in Gruyter et al., Stud. Mycol. 75: 28 (2012)

Facesoffungi number: FoF 01647, Fig. 25

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Pycnidia* 200–320 *µm* diam., superficial, globose to subglobose, black, shiny, aggregated or solitary, with or without a distinct ostiole. *Pycnidial wall* comprising several lightly pigmented to dark brown cells of *textura angularis*. *Conidiophores* 6–26 × 1–2 *µm* ($\bar{x}$ = 14.4 × 1.5 *µm*, n = 25), branched, cylindrical, septate, hyaline and formed from the inner wall cells of the pycnidial wall. *Conidiogenous cells* enteroblastic, phialidic, determinate, ampulliform to filiform, hyaline, smooth. *Conidia* 2.6–4.2 × 1–1.5 *µm* ($\bar{x}$ = 3.8 × 1.2, n = 50), ellipsoidal, hyaline, aseptate, eguttulate or with some small, polar guttules, smooth-walled.

Culture characteristics: Colonies on PDA 14–16 mm diam. after 9 d, margin entire to somewhat lobate; colony white to pale white with white, felty aerial mycelium; reverse brown to greenish olivaceous, greenish grey at centre, white near margin.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University Garden, 1 December 2014, Kasun M. Thambugala, TL 987 (MFLU 15–3203), living culture MFLUCC 14–0504.

Notes: *Aposphaeria* was introduced by Saccardo (1880) and currently there are 207 epithets listed in this genus (Index Fungorum 2016), but sequence data is available for only a few species. *Aposphaeria corallinolutea* was introduced by de Gruyter et al. (2012) and our strain clustered with the ex-type strain (CBS 131287) of *A. corallinolutea* (Fig. 24). *Aposphaeria corallinolutea* has been reported on *Kerria japonica* (*Rosaceae*) and *Fraxinus excelsior* (*Oleaceae*) in Netherlands (Gruyter et al. 2012). This is the first report of A. corallinolutea in Thailand.

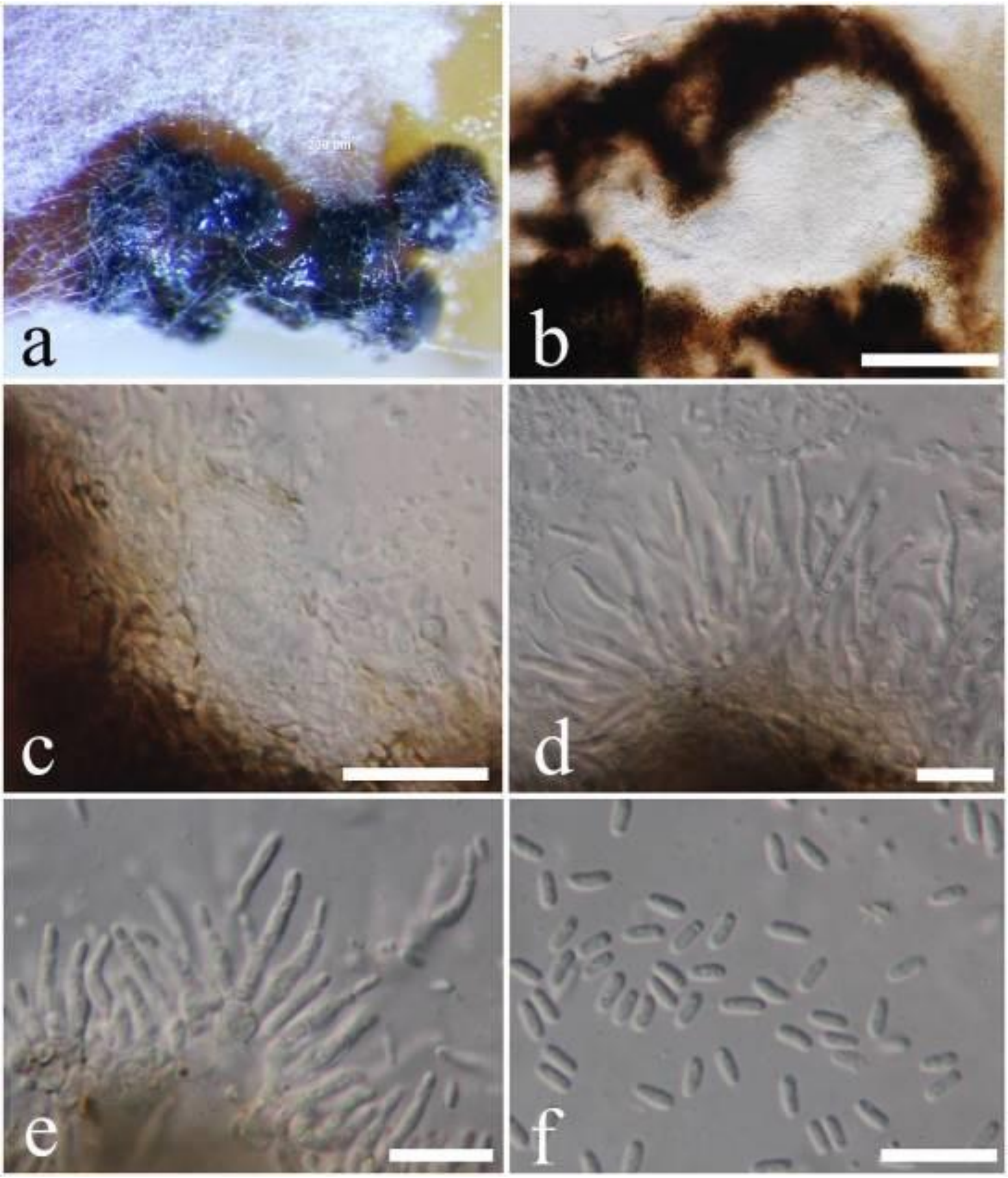


Fig. 25 ***Aposphaeria corallinolutea*** (MFLUCC 14–0504) **a** Pycnidia on PDA **b** Section through stromatic pycnidia **c** Pycnidial wall **d**–**e** Conidiophores and conidiogenous cells **f** Conidia. Scale bars: b = 100 μm, c = 20 μm, d–f = 10 μm.

Parabambusicolaceae

Parabambusicolaceae was introduced by Tanaka et al. (2015) and is typified by *Parabambusicola* Kaz. Tanaka & K. Hiray. The family was introduced to accommodate *Massarina*-like species from bamboo and grasses, and initially included the sexual genera *Aquastroma*, *Multiseptospora* and *Parabambusicola* (Tanaka et al. 2015). Two unnamed *Monodictys* species also clustered in this family, but *Monodictys* is obviously heterogenous (Tanaka et al. 2015). In this paper, we introduce a new genus, *Multilocularia* to accommodate a single Dothideomycetes species, which was collected from bamboo in Thailand. Additionally, a new species of *Multiseptospora*, *M. thysanolaenae* is introduced.

268. ***Multilocularia*** Phookamsak, Ariyawansa & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 551946, *Facesoffungi number*: FoF 01658

Etymology: The generic epithet "*Multilocularia*" refers to the multi-loculate ascostroma

Saprobic on bamboo. **Sexual morph** *Ascostromata* gregarious, clustered, immersed, visible as raised, black rows, on host surface, multi-loculate, elongate, glabrous, ostiolate. *Locules* clustered, immersed in ascostromata, globose to subglobose, or elongate hemisphaerical, ostiole individually central. *Peridium* thin- to thick-walled, slightly thick at the rim, composed of several layers of dark brown to black, pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* composed of dense, broad cellular pseudoparaphyses, filamentous, distinctly septate, anastomosing among the asci, embedded in a hyaline, gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, clavate, long pedicellate, apically rounded, with well-developed ocular chamber. *Ascospores* overlapping 1–2-seriate, hyaline, ellipsoidal, with rounded ends, slighty curved, septate, slightly constricted at the central septum, smooth-walled, with small guttules. **Asexual morph** Undetermined.

Type species: ***Multilocularia bambusae*** Phookamsak, Ariyawansa & K.D. Hyde

Notes: *Multilocularia* is introduced as a monotypic genus to accommodate the Dothideomycetes species, forming elongate ascostromata with multi-loculate and phragmosporous, hyaline, ellipsoidal ascospores. The genus is commonly found on bamboo as saprobes, similar to the genus *Munkovalsaria* Aptroot in forming ascostromata on the host, with asci have long pedicellate and ellipsoidal ascospores. However, *Multilocularia* differs from *Munkovalsaria* in having a greater number of locules than *Munkovalsaria* and ascospores are hyaline, while in *Munkovalsaria* ascospores are brown. *Multilocularia* clusters with *Aquastroma magniostiolata*, *Pseudomonodictys tectonae* and *Monodictys* species in *Parabambusicolaceae* in the phylogenetic tree (Fig. 13), whereas, *Munkovalsaria* belongs in *Didymosphaeriaceae* (Ertz et al. 2015) which is synonymized under *Montagnula* by Wanasinghe et al. (2016). *Multilocularia* differs from *Pseudomonodictys tectonae* and *Monodictys* species based on its phylogenetic distinctiveness. *Pseudomonodictys* and *Monodictys* species are presently only know as asexual morphs, while *Multilocularia* is known in its sexual morph. *Aquastroma* differs from *Multilocularia* in having globose ascostromata, short pedicellate asci, clavate to fusiform, multi-septate ascospores and an aquatic habitat.

269. ***Multilocularia bambusae*** Phookamsak, Ariyawansa & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551947, *Facesoffungi number*: FoF 01659, Fig. 26

Etymology: The specific epithet "*bambusae*" refers to the host

Holotype: MFLU11–0216

Saprobic on bamboo. **Sexual morph** *Ascostromata* 200–240 *µm* high, 1100–1900 *µm* long, gregarious, clustered, immersed, raised, in black rows on host surface, multi-loculate, elongate, glabrous, ostiolate. *Locules* 130–240 *µm* high, 200–700 *µm* diam., clustered, immersed in ascostromata, globose to subglobose, or elongate hemisphaerical, ostiole individually central. *Peridium* 10–40 *µm* wide, thin- to thick-walled, slightly thick at the rim, composed of several layers of small, brown to dark brown pseudoparenchymatous cells, arranged in a *textura prismatica* to *textura angularis*, and arranged in *textura porrecta* at the sides among the locules. *Hamathecium* composed of dense, 1.2–2 *µm* wide, cellular pseudoparaphyses, distinctly septate, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* (64–)70–90(–94) × (10–)11–14(–17) *µm* ($\bar{x}$ = 82.5 × 14.2 *µm*, n = 30), 8-spored, bitunicate, fissitunicate, clavate, long pedicellate (30–50 × 3–5 *µm*), apically rounded, with well-developed ocular chamber. *Ascospores* (11–)12–15(–16) × (3–)4–5 (–7) *µm* ($\bar{x}$ = 14.2 × 4.7 *µm*, n = 30), overlapping 1–2-seriate, hyaline, ellipsoidal, with rounded ends, slighty curved, 3-septate, rarely 1- to 4-septate, slightly constricted at the central septum, smooth-walled, with small guttules. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 30–40 mm diam. after 4 weeks at 25–30°C, colony from above, dark greenish to black at the margin, white to orange in the middle, white at the centre; from below, dark greenish to black; medium dense, irregular, slightly raised to umbonate, surface slightly rough, dull with umbonate edge, concave at the centre, fluffy to floccose, with white tufts at the centre; producing brown pigmentation in agar.

Material examined: THAILAND: Chiang Rai Province, Mae Jun District, Huai kang Pla Waterfall, on dead stem of bamboo (*Poaceae*), 25 October 2010, R. Phookamsak, RP0096 (MFLU 11–0216, **holotype**), ex-type living culture, MFLUCC 11-0180, BCC.

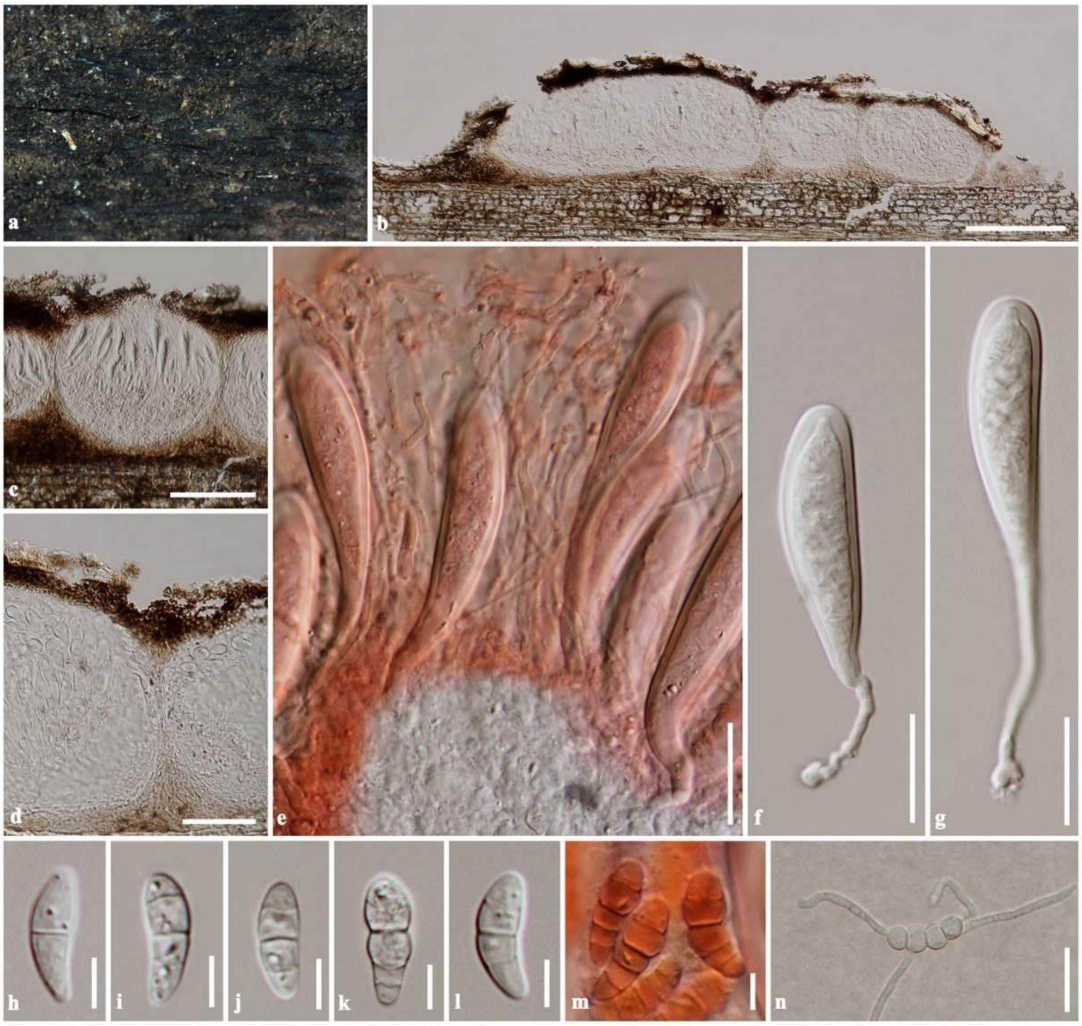


Fig. 26 ***Multilocularia bambusae*** (**holotype**) **a** Appearance of ascostromata on host surface **b** Section through an ascostroma **c** Appearance of locules **d** Section through peridium **e** Asci with pseudoparaphyses, stained in congo red **f, g** Asci **h–l** Ascospores **m** Ascospore stained congo red **n** Spore germination on WA after 8 hours. Scale bars: b = 200 *µm*, c = 100 *µm*, d = 50 *µm*, e–g = 20 *µm*, n = 10 *µm*, h–m = 5 *µm*.

Multiseptospora Phookamsak & K.D. Hyde

The genus *Multiseptospora* Phookamsak & K.D. Hyde was introduced in Liu et al. (2015) to accommodate a single species *M*. *thailandica* Phookamsak & K.D. Hyde, which was collected on *Thysanolaena maxima* Kuntze. The genus was introduced in the *Pleosporales* genera *incertae sedis* (Liu et al. 2015). However, Tanaka et al. (2015) added the genus to *Parabambusicolaceae* when they introduced this family based on their phylogenetic relationships. In this study, a new species, *M*. *thysanolaenae* is introduced. The new species was also collected on *Thysanolaena maxima* in Thailand.

270. ***Multiseptospora thysanolaenae*** Phookamsak, Ariyawansa & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551948, *Facesoffungi number*: FoF 01660, Fig. 27

Etymology: The specific epithet "*thysanolaenae*" refers to the host.

Holotypus: MFLU 11–0238

Saprobic on *Thysanolaena maxima* Kuntze. **Sexual morph** *Ascostromata* 190–270 *µm* high, 300–350 *µm* diam., gregarious, scaterred, immersed, visible as raised, black dots on host surface, uni-loculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Peridium* 12–40 *µm* wide, thin- to thick-walled, slightly thick at the sides towards apex, composed of several layers of flattened, pseudoparenchymatous cells, inner layers comprising flattened, hyaline cells, arranged in a *textura prismatica*, outer layers comprising brown to dark brown cells, arranged in a *textura angularis*. *Hamathecium* composed of dense, 1.8–4 *µm* wide, cellular pseudoparaphyses, slightly constricted at the septum, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* (93–)100–120(–143) × (26–)28–32(–35) *µm* ($\bar{x}$ = 114.3 × 30.4 *µm*, n = 30), 8-spored, bitunicate, fissitunicate, broadly cylindric-clavate to clavate, subsessile to short pedicellate, apically rounded, with an indistinct ocular chamber. *Ascospores* (55–)60–65(–73) × (8–)9–11(–13) *µm* ($\bar{x}$ = 64.6 × 10.5 *µm*, n = 30), overlapping 3–4-seriate, initially hyaline, becoming brown to dark brown at maturity, fusiform, with slightly rounded ends, slighty curved, (6–)7-septate, not constricted at the septa, smooth-walled, surrounded by thin, mucilaginous sheath, with small appendages at both ends. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA fast growing, reaching 70–80 mm diam. after 4 weeks at 25–30°C, colony from above, light brown to dark brown; from below: black; dense, circular, slightly raised to umbonate, surface smooth, dull with entire edge, concave at the centre, fluffy to floccose, producing brown pigmentation in agar.

Material examined: THAILAND, Chiang Mai, Doi Suthep-Pui, on dead leaf sheath of *Thysanolaena maxima* (*Poaceae*), 5 June 2011, R. Phookamsak, RP0118 (MFLU 11–0238, **holotype**), ex-type living culture, MFLUCC 11–0202, BCC.

Notes: *Multiseptospora thysanolaenae* is similar to the type species, *M. thalandica* in having multi-septate ascospores and is associated with *Thysanolaena maxima* Kuntze. However, *M. thysanolaenae* differs from *M. thailandica* due to its glabrous ascostromata, with brown ascospores. *Multiseptospora thysanolaenae* has larger ascomata, asci and ascospores than *M. thailandica*, but has less ascospore septation (ascospores septation: 10–11-septate in *M. thailandica* versus 6–7-septate in *M. thysanolaenae*. Based on phylogenetic analysis, *M. thysanolaenae* clusters with *M. thailandica* (Fig. 13).

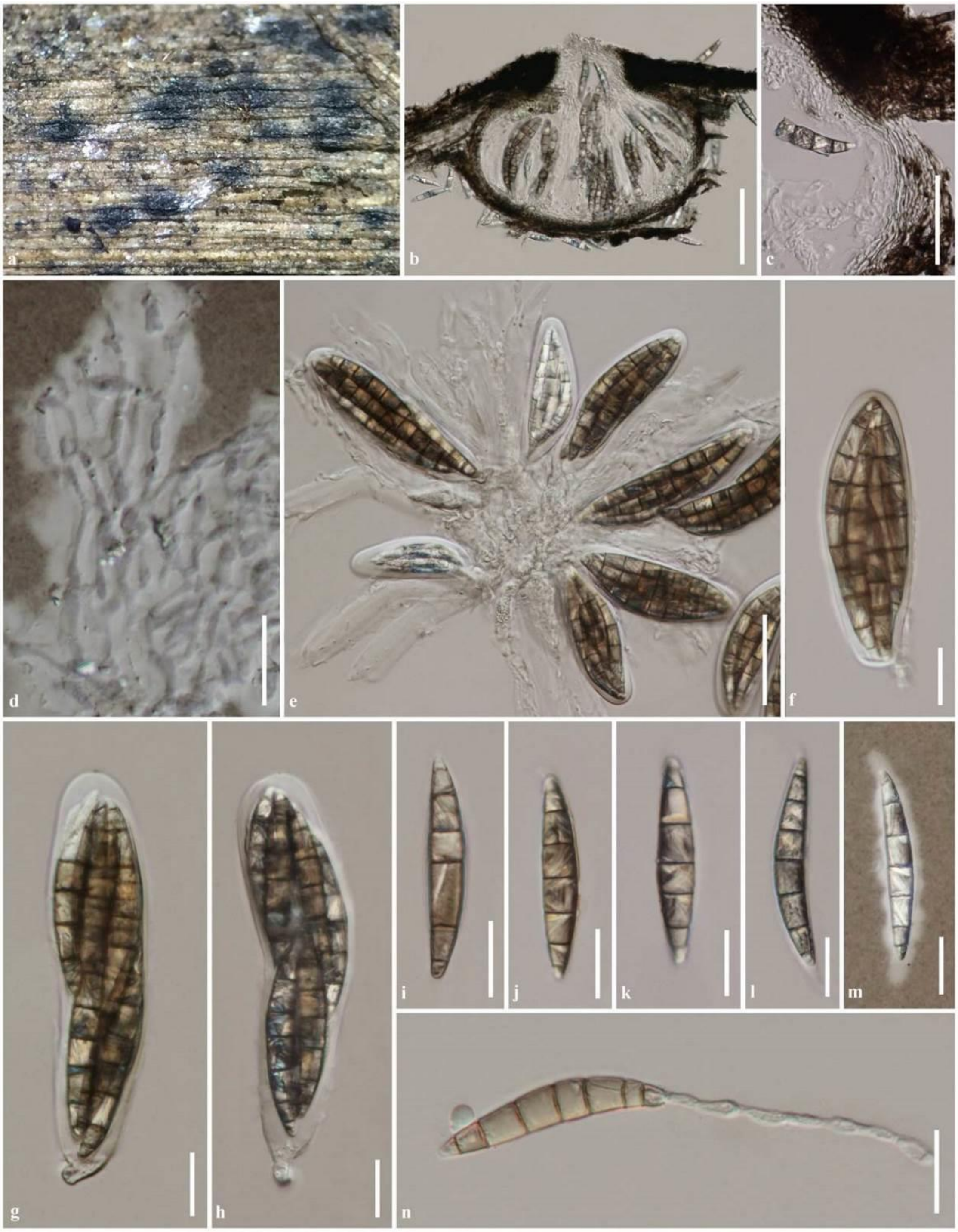


Fig. 27 ***Multiseptospora thysanolaenae*** (**holotype**) **a** Appearance of ascostromata on host surface **b** Section through an ascostroma **c** Section through peridium **d** Pseudoparaphyses stained in Indian ink **e** Asci with pseudoparaphyses **f**–**h** Asci **i**–**l** Ascospores **m** Ascospore stained in Indian ink **n** Spore germination on WA after 8 hours. Scale bars: b = 100 *µm*, c, e = 50 *µm*, d, f–n = 20 *µm*.

Phaeosphaeriaceae

The family *Phaeosphaeriaceae* (*Pleosporales*) was introduced by Barr (1979a) and is a heterogeneous group of taxa comprising plant pathogens, saprobes and endophytes, associated with a wide variety of plant hosts (Zhang et al. 2012; Hyde et al. 2013; Phookamsak et al. 2014). The family is typified by *Phaeosphaeria* with *P. oryzae* as the type species. Initially the family comprised 15 genera (Barr 1979a), and now comprises more than 35 sexual and asexual genera (Hyde et al. 2013; Phookamsak et al. 2014). Various phylogenetic studies have been carried out on *Phaeosphaeriaceae* and several new genera has been introduced, while some has been transferred to other families (Zhang et al. 2012; Hyde et al. 2013; Phookamsak et al. 2014; Trakunyingcharoen et al. 2014; Crous et al. 2015c, d; Ertz et al. 2015; Li et al. 2015c). In the present study, a backbone tree for the family is presented (Fig. 28) with the genera *Allophaeosphaeria*, *Ampelomyces*, *Chaetosphaeronema*, *Coniothyrium*, *Dematiopleospora*, *Didymocyrtis*, *Edenia*, *Entodesmium*, *Galliicola*, *Leptospora*, *Loratospora*, *Muriophaeosphaeria*, *Neosetophoma*, *Neostagonospora*, *Neosphaerellopsis*, *Nodulosphaeria*, *Ophiobolus*, *Ophiosphaerella*, *Paraphoma*, *Parastagonospora*, *Phaeosphaeria*, *Phaeosphaeriopsis*, *Poaceicola*, *Populocrescentia*, *Sclerostagonospora*, *Scolicosporium*, *Septoriella*, *Setomelanomma*, *Setophoma*, *Sulcispora*, *Stagonospora*, *Vagicola*, *Vrystaatia*, *Wojnowicia*, *Wojnowiciella*, *Xenophoma*, and *Xenoseptoria*. The phylogenetic tree is presented in Fig. 28.

Notes: Our phylogenetic analyses of taxa of *Phaeosphaeriaceae*, uses combined LSU and ITS sequence data, and comprises 106 strains, representing 37 genera, with *Didymella exigua* (CBS 183.55) as the outgroup taxon. The phylogenetic analyses provides good evidence for one new species, *Parastagonospora cumpignensis* (strain MFLUCC 13–0573), which clusters with their respective genus with strong support. *Parastagonospora cumpignensis* forms a distinct clade with *P. dactylidis* (strain MFLUCC 13–0375), with a relatively high 100% MP and 96% ML bootstrap support, and a high Bayesian posterior probability (1.0 PP).

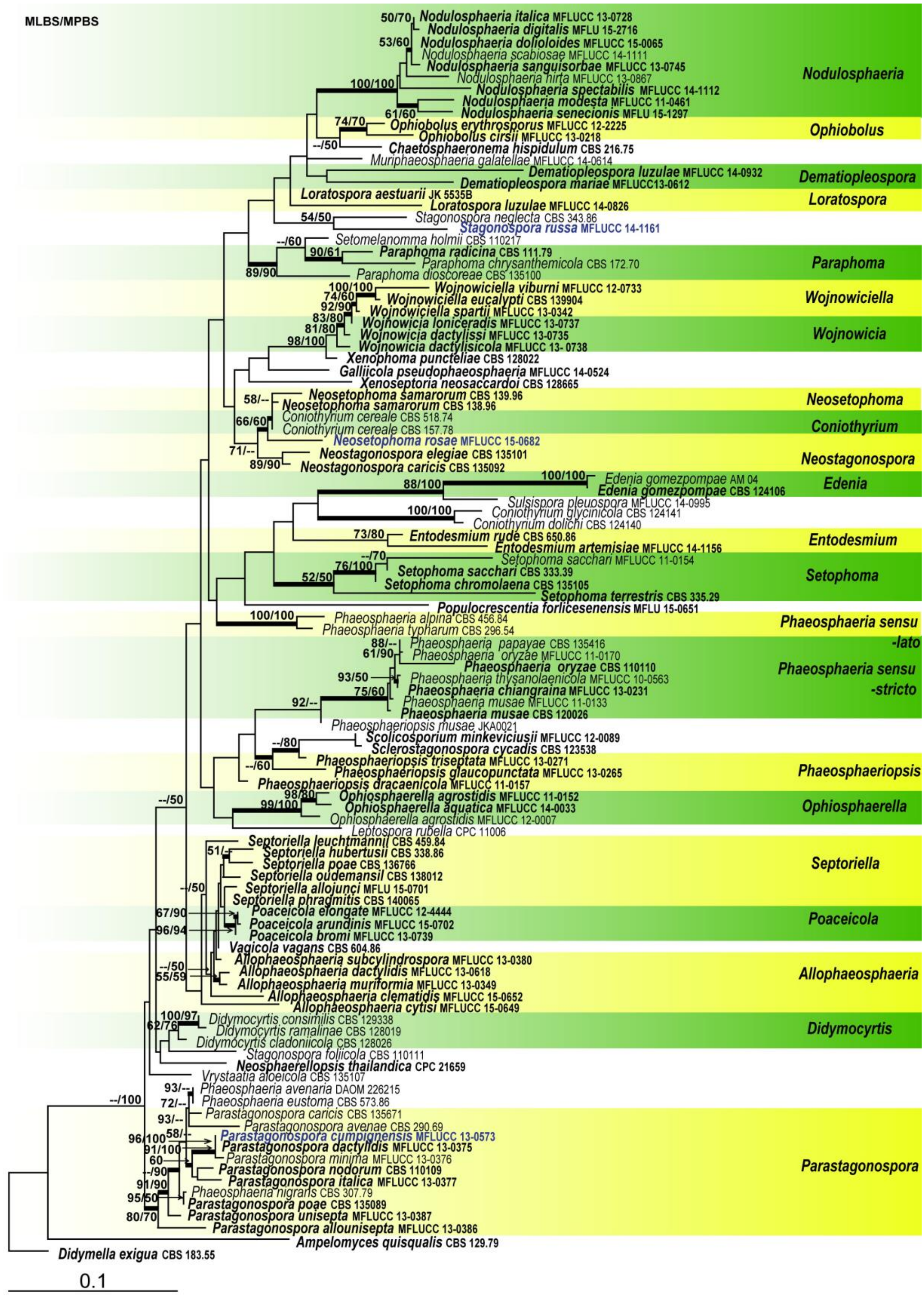


Fig. 28 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequenced data of species of *Phaeosphaeriaceae*. Branches of maximum parsimony and maximum likelihood bootstrap support values greater than 50% and Bayesian posterior

probabilities greater than 0.90 are indicated in bold. New taxa are in blue and ex-type strains are in bold. The scale bar indicates 0.1 changes. The tree is rooted with *Didymella exigua* CBS 183.55.

Parastagonospora Quaedvl. et al.

Parastagonospora was introduced by Quaedvlieg et al. (2013) with *P. nodorum* (Berk.) Quaedvl. et al. as the type species. *Parastagonospora* is a plant pathogenic genus accommodating taxa that were formerly placed in either *Septoria*/*Stagonospora*, or *Leptosphaeria*/*Phaeosphaeria* (Quaedvlieg et al., 2011, 2013; de Gruyter et al. 2013; Ariyawansa et al. 2015c). The sexual and asexual characters of this genus were described in Quaedvlieg et al. (2013).

271. *Parastagonospora cumpignensis* Tibpromma, Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551804, *Facesoffungi number*: FoF 01767, Fig. 29

Etymology: Name reflects the locality, Campigna, where this species was collected.

Holotype: MFLU 15–1480

Saprobic on *Dactylis glomerata* L. in terrestrial habitats. **Sexual morph** *Ascomata* 205–310 *µm* high × 197–217 *µm* diam. ($\bar{x}$ = 245 × 207 *µm*, n = 5), scattered, immersed in host tissue, globose to subglobose, thin-walled, solitary, with short neck, dark brown to black. *Peridium* 14–19 *µm*, thin-walled, comprising 2 layers of hyaline to brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1.5–3 *µm* wide, septate, branched, pseudoparaphyses. *Asci* 62–92 × 9–12 *µm* ($\bar{x}$ = 78 × 10 *µm*, n = 10), 8-spored, bitunicate, cylindrical to narrowly fusoid, short pedicellate, with a relatively a small ocular chamber. *Ascospores* 26–31 × 6–7 *µm* ($\bar{x}$= 28 × 7 *µm*, n = 15), obliquely uniseriate, ellipsoid to narrowly obovoid, hyaline, becoming 3-septate with age, constricted at each septum, cells above central septum often broader than the lower ones, with acute rounded ends, constricted at the septa, with 1–2 distinct oil droplets in each cell, smooth-walled, without a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: on MEA reaching 4 *cm* diam. after 2 weeks at 16°C, later with dense mycelium, with entire edge, flat, smooth with raised elevation, white-grey; hyphae septate branched, grey, thin-walled.

Material examined: ITALY, Campigna, Santa Sofia, Forlì-Cesena Province, on dead stem of *Dactylis glomerata* (*Poaceae*), 23 June 2012, Erio Camporesi, IT458 (MFLU 15–1480, **holotype**)**;** ex-type living culture, MFLUCC 13–0573, MUCL; *Ibid*. (MFLU 16-0065bis, HKAS 92500tris, **paratypes**).

Notes: The phylogeny of the family *Phaeosphaeriaceae* is reconstructed based on analysis combined LSU and ITS sequence data (Fig. 28). *Parastagonospora cumpignensis* clusters with *P. dactylidis* W.J. Li et al. and *P. minima* W.J. Li et al. with high support. *Parastagonospora dactylidis* and *P. minima* are asexual morphs with 3-septate, hyaline conidia, while *P. cumpignensis* is a sexual morph which shares 3-septate, hyaline ascospores with *P. dactylidis* and *P. minima* (Li et al. 2015c). *Parastagonospora cumpignensis* is introduced as new species with an illustrated account and the phylogenetic trees of combined LSU and ITS sequence data confirm its placement in *Parastagonospora*.

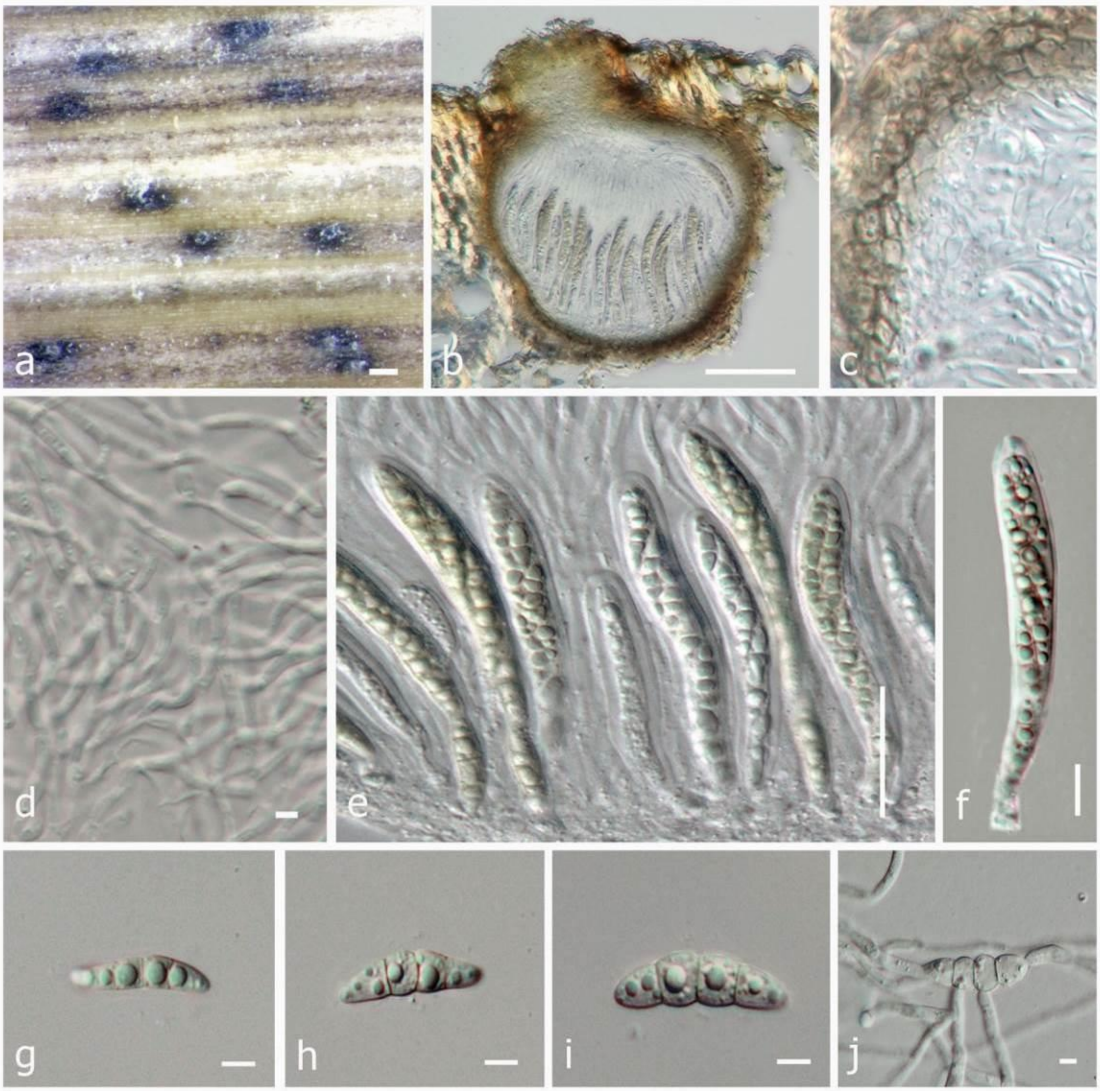


Fig. 29 ***Parastagonospora cumpignensis*** (**holotype**) **a** Appearance of ascomata on host substrate **b** Section of ascoma **c** Section of peridium **d** Paraphyses **e**, **f** Asci **g–i** Ascospores **j** Germinated ascospore. Scale bars: a = 200 *µm*, b = 50 *µm*, c = 20 *µm*, d = 5 *µm*, e, f = 20 *µm*, g–j = 10 *µm*.

Pleosporaceae

The family was recently detailed by Ariyawansa et al. (2015a) and this is followed here.

Comoclathris Clem.

Comoclathris was introducing by Clements (1909) and is typified by *Comoclathris lanata* Clem. *Comoclathris* is characterized by ascomata with circular lid-like openings and applanate, reddish brown to dark reddish brown, muriform ascospores, with single longitudinal septa (Zhang et al. 2012; Ariyawansa et al. 2014b; Crous et al. 2014a).

272. ***Comoclathris pimpinellae*** Konta, Bulgakov & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551949, *Facesoffungi number*: FoF 01769, Fig. 30

Etymology: The specific epithet refers to the host genus *Pimpinella*.

Holotypus: MFLU 15–0010

Saprobic on dead stems of *Pimpinella tragium* Vill. subsp. *titanophila* (Woronow) Tutin (syn. *Pimpinella titanophila* Woronow) appearing as black spots on host surface, or small black lines arising from cracks in the epidermal cells. **Sexual morph** *Ascomata* 155–135 wide × 88–95 *μm* high ($\bar{x}$ = 149 × 95 *μm*, n = 10), solitary or aggregated, semi-immersed or rarely somewhat superficial, globose to subglobose, dark brown to black. *Peridium* 10–19 *μm* wide, comprising an outer layer of dark brown cells of *textura angularis* and inner layer of mostly hyaline to pale brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1.3–2.1 *μm* wide, septate, pseudoparaphyses. *Asci* 58–75 × 14–16 *μm*, ($\bar{x}$ = 62 × 16 *μm*, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, rounded at the apex, with indistinct, shallow, ocular chamber. *Ascospores* 14–16 × 5–8 *μm* ($\bar{x}$ = 15 × 7 *μm*, n = 10), overlapping biseriate, yellow to light brown, transversely septate or muriform, with 3 transverse septa, central segments with 2 longitudinal septa, end segments with 2 angular septa, surrounded by a thick, hyaline, a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on MEA, reaching 5–6.5 cm diam. after 2 weeks at 16°C, smoky-grey to dark green, margins smooth, medium dense, with fairly fluffy surface.

Material examined: RUSSIA, Rostov region, Shakhty City, near Grushevsky Pond, stony steppe, dead stems of *Pimpinella tragium* Vill. subsp. *titanophila* (Woronow) Tutin (syn. *Pimpinella titanophila* Woronow), 18 May 2014, T.S. Bulgakov (MFLU 15–0010, **holotype**, HKAS, **isotype**); ex-type living culture, MFLUCC 14–1159.

Notes: *Comoclathris* is characterised by ascomata with circular lid-like openings and applanate, reddish brown to dark reddish brown, muriform ascospores, with single longitudinal septa (Zhang et al. 2012). This genus includes 36 species names in Index Fungorum (2016) and the type species is *C. lanata* Clem. In this paper we introduce *C. pimpinellae* based on morphology and phylogeny. Maximum Likelihood analysis of combined LSU, SSU, RPB2 and TEF sequence data (Fig. 13) indicates that *C. pimpinellae* is closest to *C. compressa* with high bootstrap support (100% ML) and groups in the *Comoclathris* clade, but is distinct with other species in this genus. The sexual morph of *C. pimpinellae* differs from *C. compressa*, *C. lanata* (type) and *C. sedi* in having ascomata not surrounded by radiating brown hypha (Fig. 30 a–c viz Fig. 8 a and Fig. 9 a, d in Ariyawansa et al. 2015b), and yellow to light brown ascospores with 3 transverse septa, with central segments with 2 longitudinal septa and end segments with 2 angular septa (Fig. 30 j–m viz Fig. 8 g–i and Fig. 9 i in Ariyawansa et al. 2015). No *Comoclathris* species have been described from

Pimpinella. Therefore, we introduce *C. pimpinellae* as a new species based on morphology, phylogeny and host association.

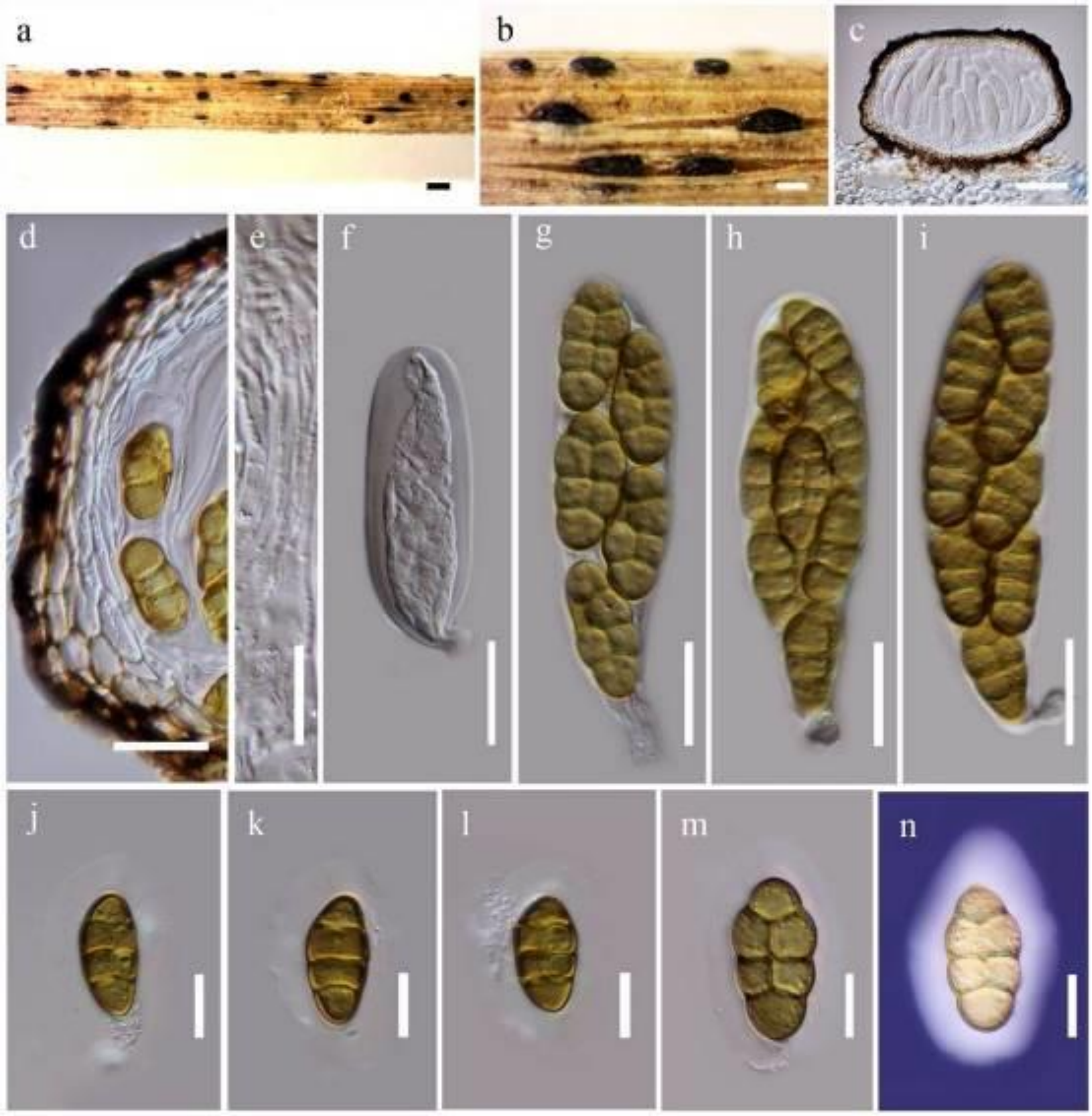
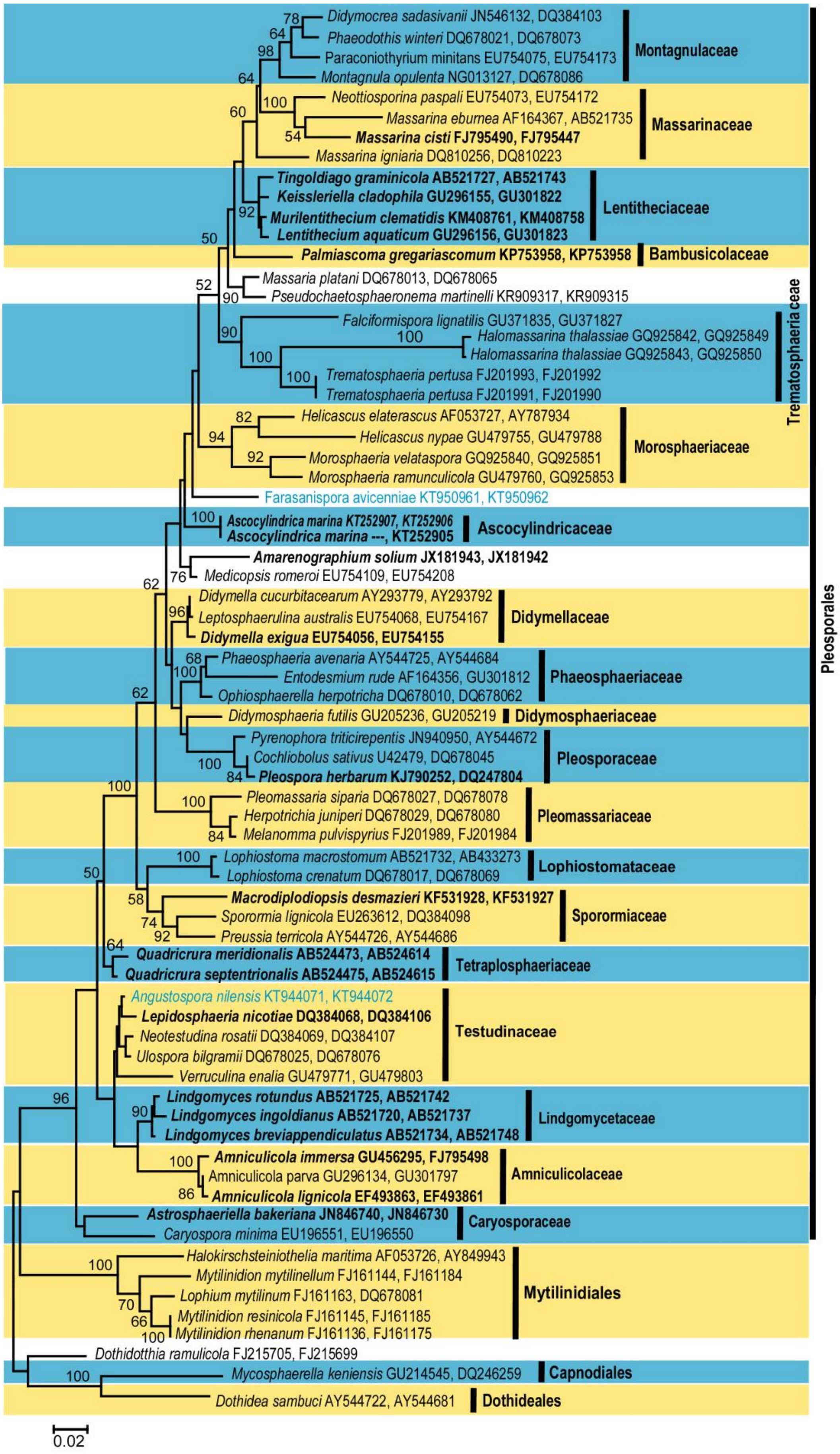


Fig. 30 ***Comoclathris pimpinellae*** (**holotype**) **a** Appearance of ascomata on host substrate **b** Close up of ascomata **c** Section of ascoma **d** Peridium **e** Pseudoparaphyses **f–i** Asci **j–n** Ascospores. Scale bars: a = 500 *µm*, b = 200 *µm*, c = 50 *µm*, d–i = 20 *µm*, j–n = 10 *µm*.

Testudinaceae

A family of *Pleosporales* that was introduced by von Arx (1971) to accommodate“astomatous ascomata with a dark peridium, which is often made up of plates, with bitunicate asci, and dark 2-celled ascospores, about 10 *µm* long”. The family contains five genera namely: *Lepidosphaeria*, *Neotestudina*, *Testudina* (type genus), *Ulospora* and *Verruculina*. Species belonging to the family are either saprobic in the terrestrial habitats (*Lepidosphaeria*, *Testudina* and *Ulospora*), dermatophytes (*Neotestudina*) or marine fungi (*Verruculina*). Further information about the family is available in Hyde et al. (2013).


78 Didymocrea sadasivanii JN546132, DQ384103
64 Phaeodothis winteri DQ678021, DQ678073
98 Paraconiothyrium minitans EU754075, EU754173
64 Montagnula opulenta NG013127, DQ678086
Montagnulaceae
100 Neottiosporina paspali EU754073, EU754172
60 Massarina eburnea AF164367, AB521735
54 Massarina cisti FJ795490, FJ795447
Massarina igniaria DQ810256, DQ810223
Massarinaceae
Tingoldiago graminicola AB521727, AB521743
Keissleriella cladophila GU296155, GU301822
92 Murilentithecium clematidis KM408761, KM408758
Lentithecium aquaticum GU296156, GU301823
Lentitheciaceae
50 Palmiascoma gregariascomum KP753958, KP753958
Bambusicolaceae
52 Massaria platani DQ678013, DQ678065
90 Pseudochaetosphaeronema martinelli KR909317, KR909315
90 Falciformispora lignatilis GU371835, GU371827
100 Halomassarina thalassiae GQ925842, GQ925849
Halomassarina thalassiae GQ925843, GQ925850
100 Trematosphaeria pertusa FJ201993, FJ201992
100 Trematosphaeria pertusa FJ201991, FJ201990
Trematosphaeriaceae
82 Helicascus elaterascus AF053727, AY787934
94 Helicascus nypae GU479755, GU479788
92 Morosphaeria velataspora GQ925840, GQ925851
Morosphaeria ramunculicola GU479760, GQ925853
Morosphaeriaceae
Farasanispora avicenniae KT950961, KT950962
100 Ascocylindrica marina KT252907, KT252906
Ascocylindrica marina ---, KT252905
Ascocylindricaceae
Amarenographium solium JX181943, JX181942
76 Medicopsis romeroi EU754109, EU754208
62 Didymella cucurbitacearum AY293779, AY293792
96 Leptosphaerulina australis EU754068, EU754167
Didymella exigua EU754056, EU754155
Didymellaceae
68 Phaeosphaeria avenaria AY544725, AY544684
100 Entodesmium rude AF164356, GU301812
Ophiosphaerella herpotricha DQ678010, DQ678062
Phaeosphaeriaceae
62 Didymosphaeria futilis GU205236, GU205219
Didymosphaeriaceae
Pyrenophora triticirepentis JN940950, AY544672
100 Cochliobolus sativus U42479, DQ678045
84 Pleospora herbarum KJ790252, DQ247804
Pleosporaceae
100 Pleomassaria siparia DQ678027, DQ678078
100 Herpotrichia juniperi DQ678029, DQ678080
84 Melanomma pulvispyrius FJ201989, FJ201984
Pleomassariaceae
100 Lophiostoma macrostomum AB521732, AB433273
50 Lophiostoma crenatum DQ678017, DQ678069
Lophiostomataceae
58 Macrodiplodiopsis desmazieri KF531928, KF531927
74 Sporormia lignicola EU263612, DQ384098
92 Preussia terricola AY544726, AY544686
Sporormiaceae
64 Quadricrura meridionalis AB524473, AB524614
Quadricrura septentrionalis AB524475, AB524615
Tetraplosphaeriaceae
Angustospora nilensis KT944071, KT944072
Lepidosphaeria nicotiae DQ384068, DQ384106
Neotestudina rosatii DQ384069, DQ384107
Ulospora bilgramii DQ678025, DQ678076
Verruculina enalia GU479771, GU479803
Testudinaceae
96 Lindgomyces rotundus AB521725, AB521742
90 Lindgomyces ingoldianus AB521720, AB521737
Lindgomyces breviappendiculatus AB521734, AB521748
Lindgomycetaceae
100 Amniculicola immersa GU456295, FJ795498
Amniculicola parva GU296134, GU301797
86 Amniculicola lignicola EF493863, EF493861
Amniculicolaceae
Astrosphaeriella bakeriana JN846740, JN846730
Caryospora minima EU196551, EU196550
Caryosporaceae
Pleosporales
100 Halokirschsteiniothelia maritima AF053726, AY849943
Mytilinidion mytilinellum FJ161144, FJ161184
70 Lophium mytilinum FJ161163, DQ678081
66 Mytilinidion resinicola FJ161145, FJ161185
100 Mytilinidion rhenanum FJ161136, FJ161175
Mytilinidiales
Dothidotthia ramulicola FJ215705, FJ215699
100 Mycosphaerella keniensis GU214545, DQ246259
Capnodiales
Dothidea sambuci AY544722, AY544681
Dothideales
0.02

2016

Fig. 31 Phylogram generated from maximum likelihood analysis (MEGA6) based on combined dataset of SSU and LSU sequence data of the two new genera and related taxa in *Pleosporales*. Representatives of the orders *Mytilinidiales*, *Capnodiales* and *Dothideales* are used as outgroup taxa. Maximum Likelihood bootstrap values greater than 50 % are indicated at the nodes. The new genera are in blue. Ex-type strains are in bold.

273. ***Angustospora*** Abdel-Aziz, ***gen. nov.***

Index Fungorum number: IF 551714, *Facesoffungi number*: FoF 01632

Etymology: In reference to the striate ascospores.

Type species: *Angustospora nilensis* Abdel-Aziz

Saprobic on decayed wood in freshwater habitats. **Sexual morph** *Ascomata* globose to subglobose, immersed to erumpent, solitary, ostiolate, papillate, periphysate, coriaceous to sub-carbonaceous, dark-brown to black. *Peridium* comprising two strata, outer stratum dark-brown to black, forming a *textura angularis*, inner stratum comprising hyaline, thick-walled, flattened cells arranged in a *textura angularis*. *Hamathecium* comprising numerous, 1–2.5 *µm* wide, distantly septate, branched, trabeculate pseudoparaphyses, within a gelatinous matrix, anastmosing above asci. *Asci* 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded, with a wide, shallow ocular chamber and faint ring. *Ascospores* overlapping biseriate, dark-brown to black, (3)–5–(7) septate, polar cells lighter when young and apical cells with two-walls, surrounded by thin, gelatinous, striate layer. **Asexual morph** Undetermined.

Notes: The phylogenetic analyses of both SSU and LSU sequence data place the genus *Angustospora* within the family *Testudinaceae* (Fig. 31). This phylogenetic placement was consistent with various degrees of bootstrap support in all the phylogenetic analyses performed (data not shown). Arx (1971) established the family *Testudinaceae* to accommodate four genera namely: *Lepidosphaeria*, *Neotestudina*, *Pseudophaeotrichum* and *Testudina* (type genus). Suetrong et al. (2009) assigned the monotypic marine genus *Verruculina* to the family *Testudinaceae*, based on multi-gene analyses. *Verruculina enalia* (Kohlm.) Kohlm. & Volkm.-Kohlm. is characterized by small ascomata (less than 500 *µm* in diam.), that are subglobose, ampulliform or depressed ellipsoidal, immersed to erumpent, ostiolate, papillate, clypeate, carbonaceous, black and solitary. Asci are 8-spored, cylindrical, pedicellate, bitunicate, thick-walled, physoclastic, without apical apparatuses. Ascospores are obliquely uniseriate, ellipsoidal, 1-septate, constricted at the septum, dark brown, verrucose, with a hyaline tubercle at each apex which is probably a germ pore (Kohlmeyer and Kohlmeyer 1979). *Angustospora* is not congeneric with *Verruculina* as their morphology is quite different and they are phylogenetically distant (Fig. 31). The genus *Angustospora* is reminiscent of *Caryospora* in having large ascospores with a median septum and additional septa near poles of the ascospores. However, *Angustospora* is different from species of *Caryospora* in having small ascomata and 8-spored, clavate asci (Barr 1979b, 1990; Hawksworth 1982; Abdel-Wahab and Jones 2000; Raja and Shearer 2008; Zhao and Zhao 2012; Ariyawansa et al. 2015b). Ten species currently are recognized in the genus *Caryospora*, of which five were recorded from aquatic habitats (Abdel-Wahab and Jones 2000; Raja and Shearer 2008; Jones et al. 2015; Ariyawansa et al. 2015b). Ariyawansa et al. (2015) established the new family *Caryosporaceae* for two species of *Caryospora* and the marine genus *Acrocordiopsis* Borse & K.D. Hyde. The family *Caryosporaceae* formed a basal clade to *Testudinaceae* (Ariyawansa et al. 2015b, Fig. 30). *Angustospora nilensis* has smaller ascomata than most of the described *Caryospora* species and different dimensions of asci and ascospores. Raja and Shearer (2008) described *C. obclavata* Raja & Shearer from decayed wood in freshwater habitats, with small ascomata, however, *A. nilensis* has larger asci and ascospores.

274. *Angustospora nilensis* Abdel-Aziz, ***sp. nov.***

Index Fungorum number: IF 551715, *Facesoffungi number*: FoF 01633, Fig. 32

Etymology: In reference to the habitat where the fungus was first collected.

Holotype: CBS

Saprobic on decayed submerged wood in freshwater habitats. **Sexual morph** *Ascomata* 225–420 *µm* high, 325–390 *µm* diam., globose to subglobose, immersed to erumpent, solitary, ostiolate, papillate, periphysate, coriaceous to sub-carbonaceous, dark-brown to black. *Papilla* 100–180 *µm* long, 110–160 *µm* wide, protruding above the wood surface. Ostiolar canal 150–300 *µm* long, 80–160 *µm* wide, cylindrical to triangular, filled with periphyses that are 30 to 50 *µm* long and 2–3 *µm* wide. Peridium 57–85 *µm* thick, comprising two strata; outer stratum 39–54 *µm* thick, dark-brown to black, forming a *textura angularis*; inner stratum 18–31 *µm* thick comprising hyaline, thick-walled, flattened cells, arranged in a *textura angularis*. *Hamathecium* comprising numerous, 1–2.5 *µm* wide, distantly septate, branched, trabeculate pseudoparaphyses, embedded in a gelatinous matrix, anastmosing above the asci. *Asci* 150–240 × 48–83 *µm* ($\bar{x}$ = 193.9 × 59.9 *µm*, n = 10), 8-spored, bitunicate, fissitunicate, clavate, semi-persistent, short pedicellate, apically rounded, with a wide, shallow ocular chamber and faint ring. *Ascospores* 45–68 × 26–35 *µm* ($\bar{x}$ = 58.6 × 30 *µm*, n = 50), overlapping biseriate, dark-brown to black, (3)–5–(7)-septate, polar cells are lighter when young and apical cells with two-walls, surrounded by thin gelatinous, striate layer. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching a 20–30 mm diam. after 15 days at 25 °C, with gray to dark-brown aerial and immersed mycelium, dark-brown to black in reverse, producing fertile ascomata after 40 to 60 days of incubation, ascomata, asci and ascospores produced in culture with dimensions similar to those recorded on natural wood.

Material examined: EGYPT, Sohag City, on decayed wood submerged in the River Nile, 8 March 2005, F.A. Abdel-Aziz (CBS, **holotype**); ex-type living culture in CBS.

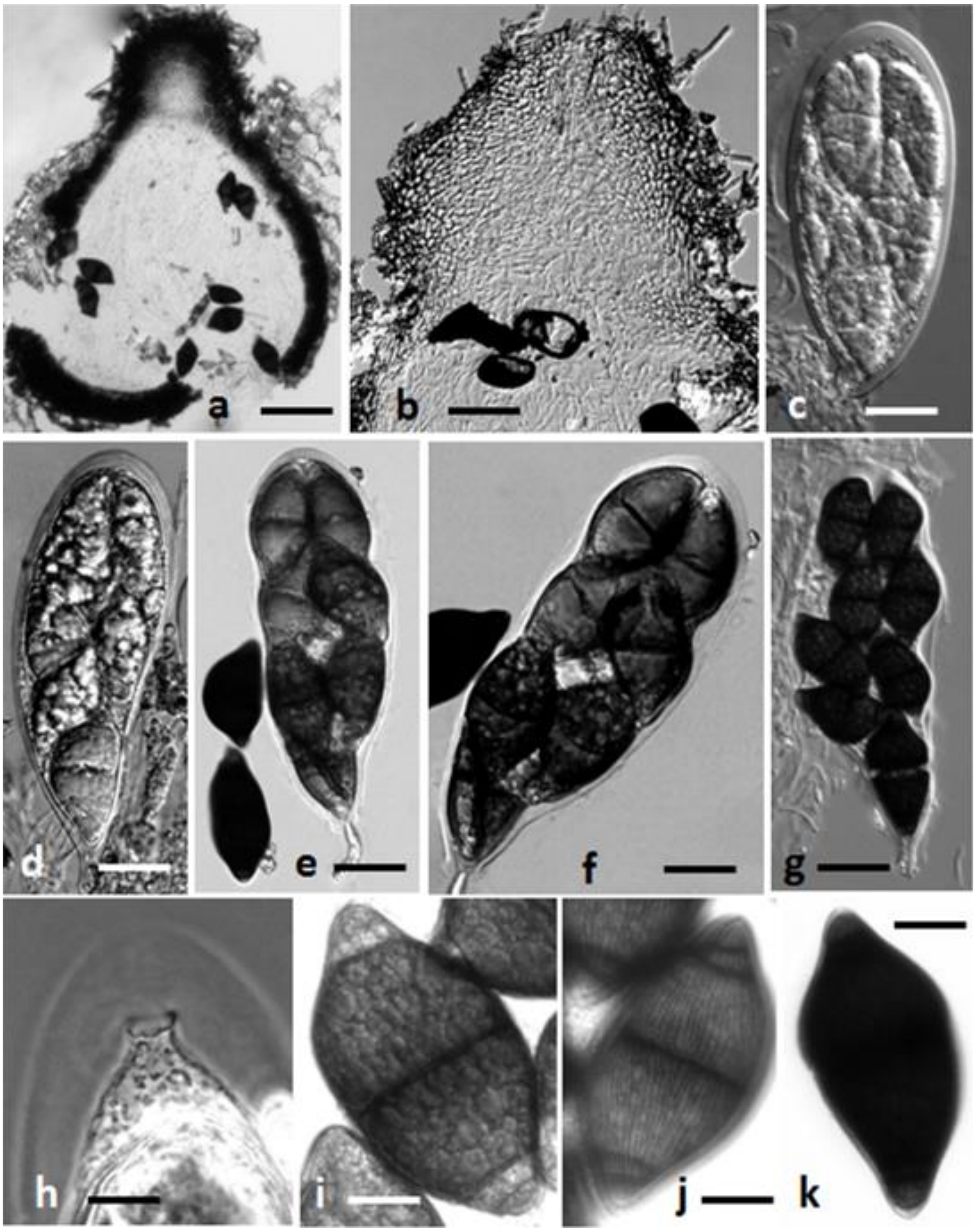


Fig. 32 ***Angustospora nilensis*** **(holotype) a** Vertical section of ascoma **b** Magnified part of the vertical section of the ascoma showing the papilla and ostiolar canal **c, d** Immature asci **e, g** Mature asci **h** Ocular chamber in ascus and faint ring **i, k** Variously shaped ascospores at different stages of maturity with striate gel coating (evident in j). Scale bars: a = 100 *µm*, b = 50 *µm*, c = 40 *µm*, d–g = 30 *µm*, h–k = 12 *µm*.

Tetraplosphaeriaceae

The family *Tetraplosphaeriaceae* accommodates *Tetraploa*, *Triplosphaeria*, *Polyplosphaeria*, *Pseudotetraploa*, and *Quadricrura* (Tanaka et al. 2009; Hyde et al. 2013). Of these, the genera *Tetraploa*, *Polyplosphaeria* and *Triplosphaeria* have

Massarina-like sexual morphs with almost hyaline 1(–3)-septate ascospores and *Tetraploa*-like asexual morphs with several setose appendages (Tanaka et al. 2009; Hyde et al. 2013;). The sexual morph of the genera *Pseudotetraploa* and *Quadricrura* are undetermined. The phylogenetic tree is presented in Fig. 33.

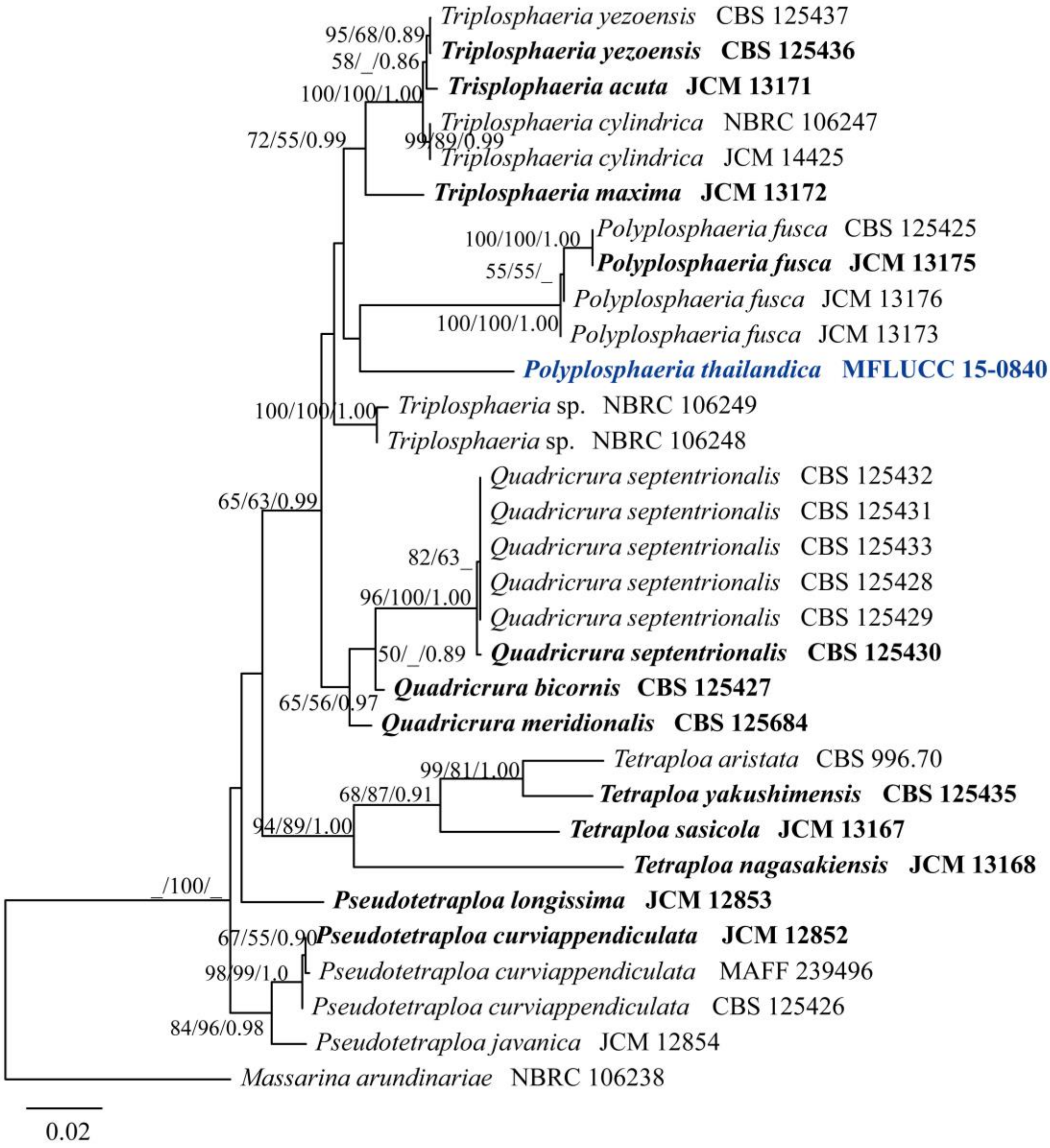


Fig. 33 Phylogenetic tree generated from Maximum Likelihood (ML) analysis based on combined ITS and LSU sequence data of family *Tetraplosphaeriaceae*. Bootstrap support values for maximum likelihood (ML) and maximum parsimony (MP) greater than 50 % and Bayesian posterior probabilities greater than 0.75 are indicated above or below the nodes as MLBS/MPBS/PP. The ex-type strains are in bold; the new isolates are in blue. The tree is rooted with *Massarina arundinariae*.

Polyplosphaeria Kaz. Tanaka & K. Hiray.

The genus was introduced by Tanaka et al. (2009) to accommodate *Polyplosphaeria fusca* Kaz. Tanaka & K. Hiray. The asexual morph of

Polyplosphaeria produces globose to subglobose conidia with several setose appendages (Tanaka et al. 2009). Only one species was accepted in this genus, *viz*. *P. fusca* Kaz. Tanaka & K. Hiray.

275. *Polyplosphaeria thailandica* C.G. Lin, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551791, *Facesoffungi number*: FoF 01676, Fig. 34

Etymology: Referring to the country where the fungus was first collected.

Holotype: MFLU 15–3273

Saprobic on bamboo culms. *Mycelium* superficial. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* absent. *Conidiogenous cells* monoblastic. *Conidia* solitary, dry, acrogenous, muriform, globose, obovoid, pyriform, ellipsoidal, occasionally two conidia associated together at the basal cell, brown, 20.5–43 *µm* long excluding the appendages, 17.5–54 *µm* wide at the broadest part, verrucose; with 2–5 appendages, grey to brown, straight, septate, 23–117 *µm* long, 2–4.5 *µm* thick, rounded at the apex; basal cell usually cylindrical, obconical, dark brown, smooth-walled.

Culture characteristics: Colonies on PDA slow growing, attaining a diam. of 0.5–0.8 cm at room temperature (25°C) in 7 days, effuse, hairy, olive green to gray on above, green to gray yellow from below.

Material examined: THAILAND, Phetchaburi, Cha-am District, Kao Yai, Khao Nang Panthurat Forest Park, 12°49'48.5"N 99°57'05.5"E, on decaying bamboo, 28 July 2015, Chuan-Gen Lin, KNP 8-2 (MFLU 15-3273, **holotype**; GZAAS 16-0001, **isotype**); ex-type living culture, MFLUCC 15-0840, GZCC 16-0001.

Notes: This species belongs to family *Tetraplosphaeriaceae*, and its placement is supported by morphological and phylogenetic analysis. Phylogenetic analysis of ITS and LSU sequence data indicates that our new species belongs in the genus *Polyplosphaeria* (Fig. 33). It differs from *P. fusca* Kaz. Tanaka & K. Hiray which has globose to subglobose, 43–100(–125) *µm* diam. conidia (Tanaka et al. 2009; Hyde et al. 2013).

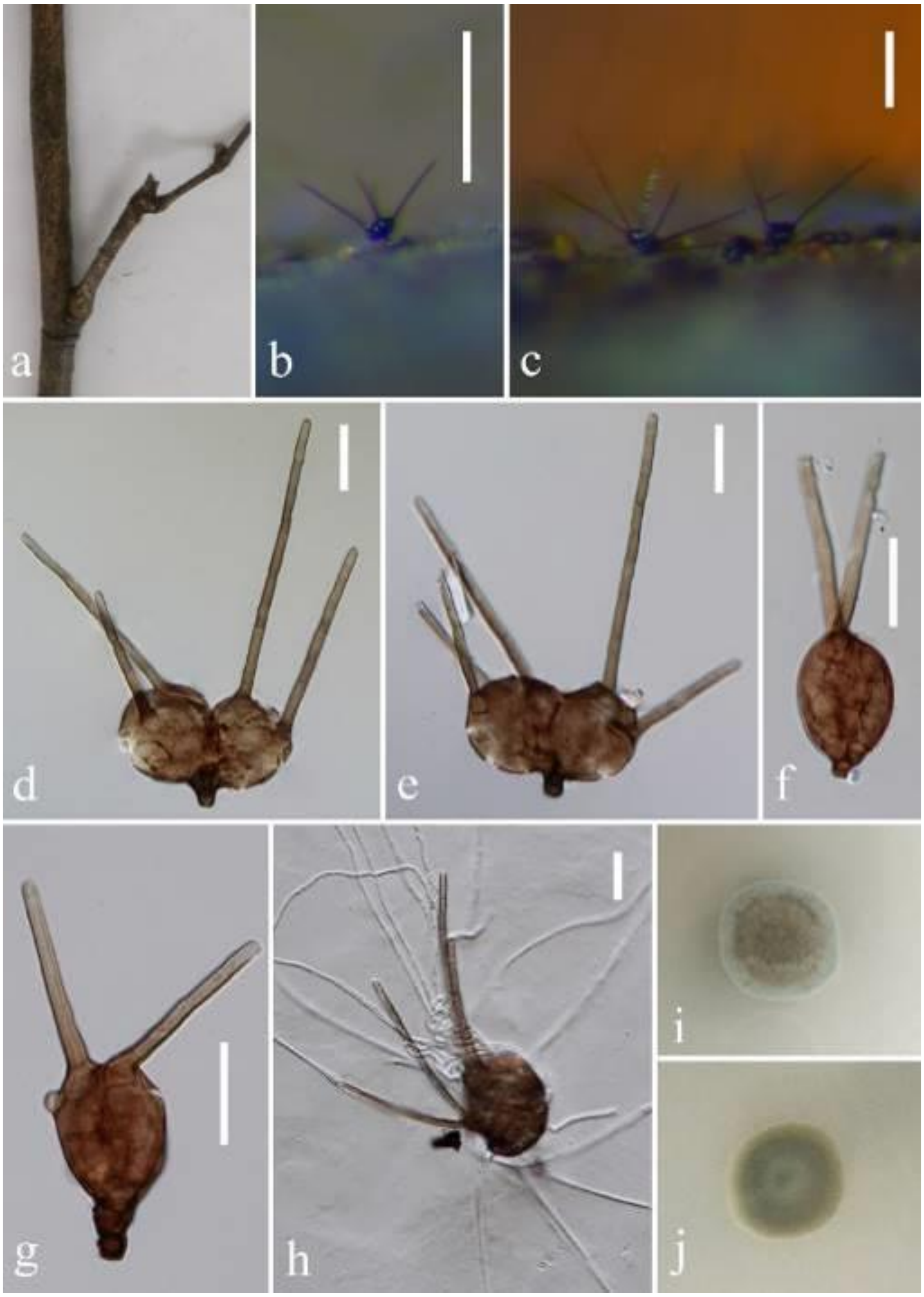


Fig. 34 ***Polyplosphaeria thailandica*** (**holotype**) **a** Host (decaying bamboo) **b, c** Conidiophores on the host surface **d–g** Conidiophores, conidiogenous cell and conidia **h** Germinating conidium **i, j** Colonies on PDA culture. Scale bars: b = 200 *µm*, c = 100 *µm*, d–h = 20 *µm*.

Pleosporales suborder *Massarineae, incertae sedis*

Massarinaceae

The suborder was treated by Tanaka et al. (2015*) and this is followed here.

276. *Longiostiolum* Doilom, Ariyawansa & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 551899, *Facesoffungi number*: FoF 01881

Etymology: Name refers to the long ostiole.

Saprobic on dead bark of *Tectona*. **Sexual morph** *Ascostromata* black, solitary to gregarious, scattered, immersed to semi-immersed, locules visible as white contents, uniloculate, globose to subglobose, with a central ostiole. *Ostiole* long, circular, central, periphysate. *Peridium* comprising two types of cell layers, outer layer black to brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline and thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, hypha-like, filiform, septate, branched, cellular, pseudoparaphyses. *Asci* 8–spored, bitunicate, clavate, apically rounded with ocular chamber. *Ascospores* mostly overlapping biseriate to 3-seriate, hyaline when young later pale brown, fusoid to narrowly fusoid, with narrowly rounded ends, constricted at the center septa, with 7–10 transverse septa, smooth-walled. **Asexual morph** Undetermined.

Type species: ***Longiostiolum tectonae*** Doilom, Ariyawansa & K.D. Hyde

277. *Longiostiolum tectonae* Doilom, D.J. Bhat & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551900, *Facesoffungi number*: FoF 01882, Figs 35, 36

Etymology: Name refers to the host genus *Tectona*.

Holotype: MFLU 15–3532

Saprobic on dead bark of *Tectona grandis* L.f. **Sexual morph** *Ascostromata* (255–) 295–375 (–500) *µm* high × (230–) 275–335 (–385) *µm* diam. ($\bar{x}$ = 340 × 300 *µm*, n = 10), black, solitary to gregarious, scattered, immersed to semi-immersed, when cut horizontally, locules visible as white contents, uniloculate, globose to subglobose, with a central ostiole. *Ostiole* 110–220 *µm* high, 100–170 *µm* diam., circular, long, central, periphysate. *Peridium* 58–85 *µm* thick, comprising two types of cell layers, outer layer black to brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline and thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 1.8–2.9 *µm* wide, hypha-like, filiform, septate, branched, cellular, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* (105–) 135–150 (–195) × 22–33 *µm* ($\bar{x}$ = 140 × 27 *µm*, n = 15), 8-spored, bitunicate, clavate, with a short pedicel, apically rounded, with an ocular chamber. *Ascospores* (52–) 57–59 (–63) × 8–12 *µm* ($\bar{x}$ = 57× 10 *µm*, n = 20), mostly overlapping biseriate to tri-seriate, hyaline when young later pale brown, fusoid to narrowly fusoid, with narrowly rounded ends, constricted at the central septum, slightly constricted at other septa, with 7–10 transverse septa, smooth-walled. **Asexual morph** (see culture characteristics).

Culture characteristics: Ascospores germinating on PDA within 24 h. Colonies on MEA reaching 12–17 mm diam. after 7 days in the dark at 25 °C ($\bar{x}$ = 14.1 mm, n = 5), undulate, fluffy in the center of old mycelium plug, aerial, medium spare, flat or effuse, initially white, becoming brown, grey (7D1) in the center and white (7A1) at the edge from above, light brown (7D6–7D7) from below. Colonies producing yellow to brown pigments on MEA and PDA. *Mycelium* 1–4.5 *µm* wide, white to pale brown, branched, septate. *Conidia*–like structures (3–) 6–8 (–11) × (4–) 6–7 (–9) *µm* ($\bar{x}$ = 7 × 6 *µm*, n = 30), produced on aerial mycelium, subglobose to ellipsoidal, aseptate, initially hyaline, becoming olivacious brown and finally black, terminal and lateral, thick-walled.

Material examined: THAILAND, Chiang Mai Province, Mae Tang District, on dead bark of *T. grandis* (*Lamiaceae*), 22 May 2012, M. Doilom, (MFLU 15–3532, **holotype**), ex-type living culture MFLUCC 12–0562, MKT 078, ICMP.

Notes: *Longiostiolum* is introduced as a monotypic genus in the suborder *Massarineae* with *L. tectonae* as the type species. The genus has black, immersed to semi-immersed, uniloculate, globose to subglobose ascostromata, with white contents, with a long central ostiole and phragmosporous ascospores. *Longiostiolum* clearly differs from other genera in suborder *Massarineae* based on phylogenetic analysis and morphology. Although, in this study, the combined phylogeny of LSU, SSU, TEF1α and RPB2 sequence data shows weak support, *L. tectonae* (isolate MFLUCC 12–0562) however, grouped in a distinct lineage within the suborder *Massarineae* (Fig. 13). Therefore, we introduce a new monotypic genus to accommodate the taxon.

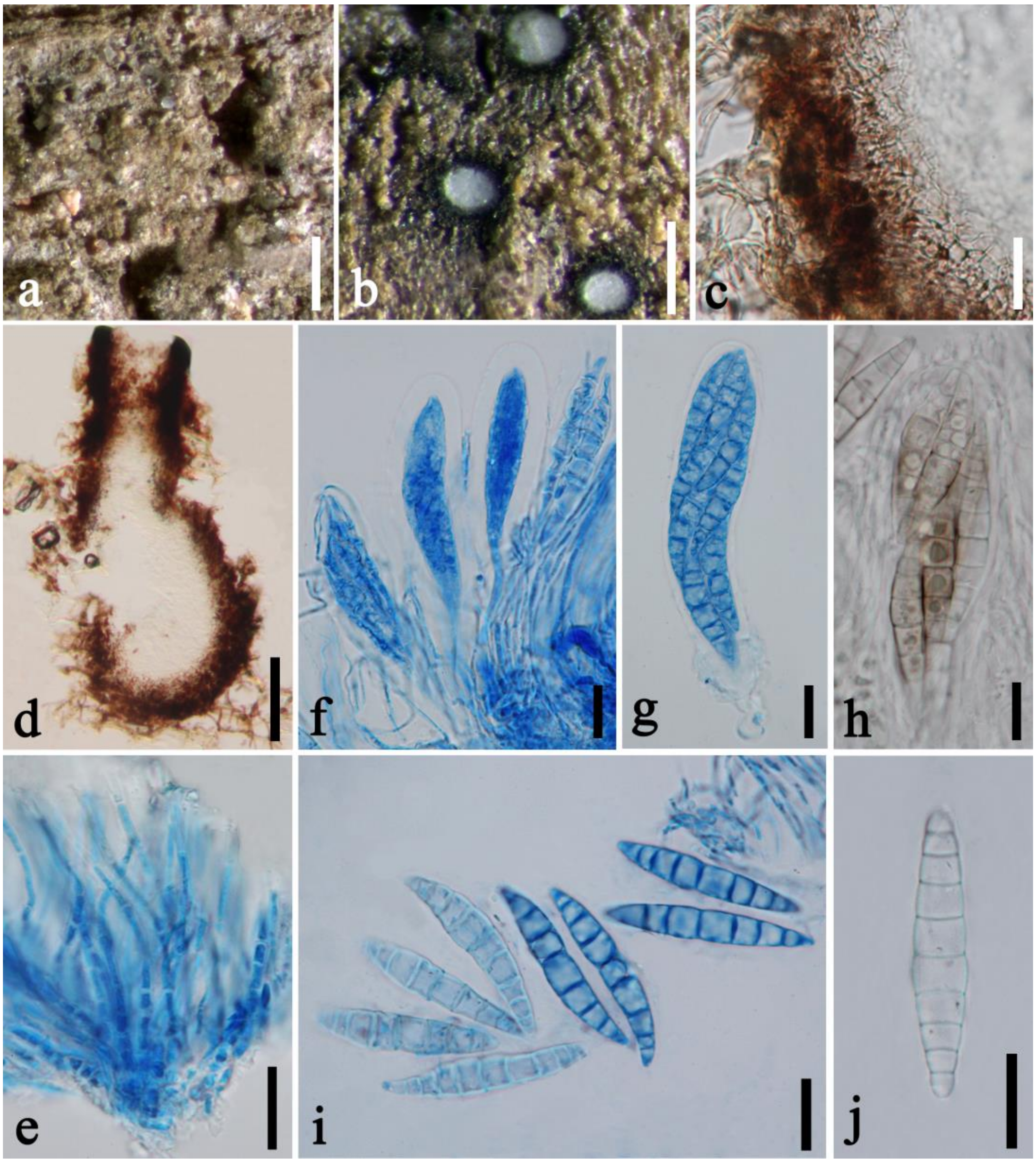


Fig. 35 ***Longiostiolum tectonae*** (**holotype**) **a** Ascostromata immersed in dead bark of *Tectona grandis* **b** Ascostroma cut horizontally showing the white contents **c** Peridium **d** Ascostroma in section **e** Pseudoparaphyses **f, g** Immature asci with ascospores **h** Mature ascus **i, j** Ascospores. Notes: **e**–**g, i** stained with lactophenol cotton blue. Scale bars: a = 500 *µm*, b = 200 *µm*, c, d = 100 *µm*, e = 10 *µm*, f–j = 20 *µm*.

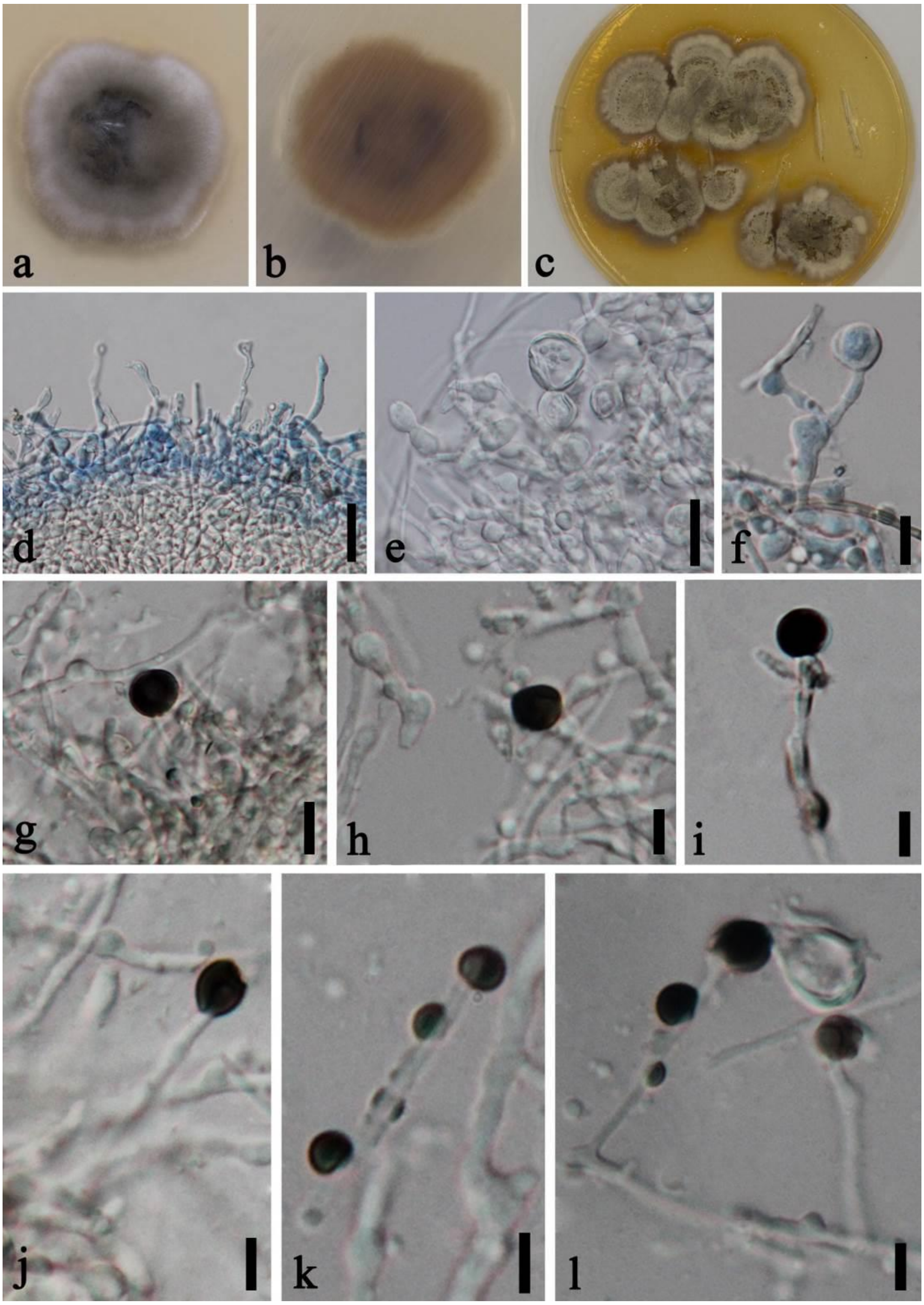


Fig. 36 ***Longiostiolum tectonae*** (**holotype**) on MEA **a, b** Colony on MEA after 7 days (a = above view, b = below view) **c** Colony producing yellow pigment on MEA after 2 months **d** Mycelia **e–l** Conidia–like structures. Notes: d, f stained with lactophenol cotton blue. Scale bars: d, e, i = 20 *µm*, f, g = 10 *µm*, h, j–l = 5 *µm*.

Pseudodidymosphaeria Thambugala & K.D. Hyde

Thambugala et al. (2015b) introduced *Pseudodidymosphaeria*, typified by *P. spartii* (Fabre) Thambugala et al., and accommodated it in the family *Massarinaceae*. In this paper a second species is introduced. The phylogenetic tree is presented in Fig. 13.

278. *Pseudodidymosphaeria phlei* Phukhamsakda, Camporesi, & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF 551895, *Facesoffungi number*: FoF 01816, Fig. 37

Etymology: Names base on the host.

Saprobic on dead stem of *Phleum pretense* L. **Sexual morph** *Ascomata* 200–368 *µm* diam. ($\bar{x}$ = 290.7 *µm*, n = 15), solitary, scattered or gregarious on host, semi-immersed to superficial, globose to subglobose, base flattened, slightly tapering to apex, lacking ostioles. *Peridium* 9–24 *µm* wide, composed of 2–3 wall layers, outer layer of light brown to dark brown cells of *textura prismatica*, inner layer, 1–2 thin gelatinous layers. *Hamathecium* comprising numerous, long, 2–5 *µm* wide ($\bar{x}$ = 2.5 *µm*, n = 50), transversely septate, branched, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 60–100 × 10–20 *µm* ($\bar{x}$ = 73.49 × 13.86 *µm*, n = 20), 8-spored, bitunicate, fissitunicate, clavate to sub-cylindrical, short pedicellate, ocular chamber clearly visible when immature. *Ascospores* 15–21 × 6–10 *µm* ($\bar{x}$ = 16.8 × 7.5 *µm*, n = 50) bi-seriate or overlapping, ovoid to sub-oval, slightly narrow at the apex, 1-transversely septate, slightly constricted at the septa, mucilaginous sheath clearly visible, immature spores hyaline, light brown to brown when mature, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospore geminating on PDA within 48 hours, germ tubes developed from both ends of the ascospores. Colonies on PDA reaching 30 mm diam. after 4 weeks. Culture incubated at 16℃, at first white, after 2 weeks pale green from center and bottom of colonies. After four weeks olive-green. Colonies morphology, umbonate, with dense mycelium, slightly papillate on the surface, circular, with dentate margin.

Material examined: ITALY, Forlì-Cesena Province, Monte Fumaiolo – Verghereto, on a dead stem of *Phleum pretense* (*Poaceae*), 31 July 2014, E. Camporesi (MFLU 15–3281, **holotype**; **isotype** HKAS 91937), ex-type living culture, MFLUCC 14–1061, KUMCC 15–0551.

Notes: *Pseudodidymosphaeria phlei* is introduced from vertical dead stems of *Phleum pretense* L. (*Poaceae*). *Pseudodidymosphaeria phlei* is closely related to the type species, *P. spartii* (Fabre) Thambugala et al., as in phylogenetic analysis they form sister clades with high support values (100 % ML). *Pseudodidymosphaeria phlei* nevertheless is distinct in having semi-immersed to superficial ascomata, larger peridium cell walls, with 2–3 wall layers, and ascospores with less distinctly rounded ends. Therefore, we introduce *Pseudodidymosphaeria phlei* as a new species.

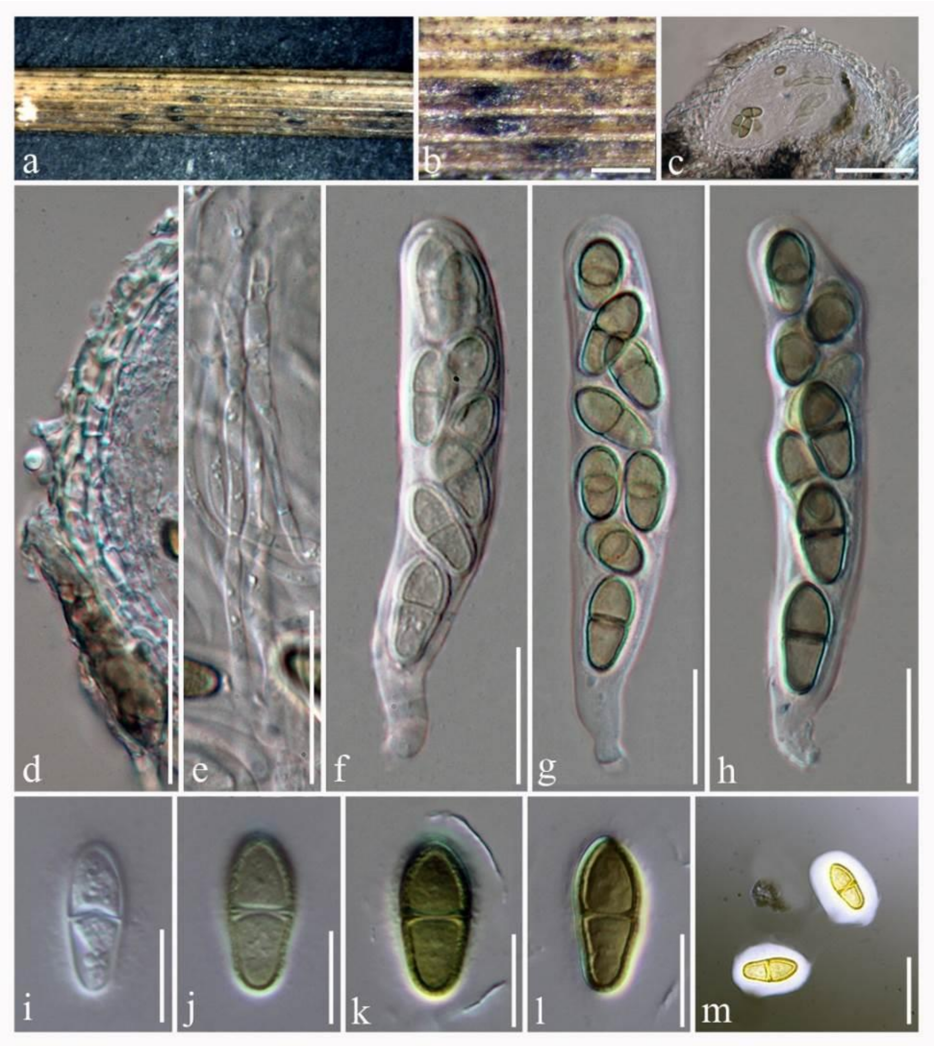


Fig. 37 ***Pseudodidymosphaeria phlei*** (**holotype**) **a, b** Appearance of ascomata on host surface **c** Section throught ascoma on host **d** Section of peridum **e** Hyaline cellular pseudoparaphyses **f** Immature asci **g**–**h** Mature asci **i**–**l** Ascospores **m** Ascospores stained in Indian ink to show sheath. Scale bar: b = 200 *µm*, c = 100 *µm*, d = 50 *µm*, e–h, m = 20 *µm*, i–l = 10 *µm*.

Pleosporales* genera, *incertae sedis

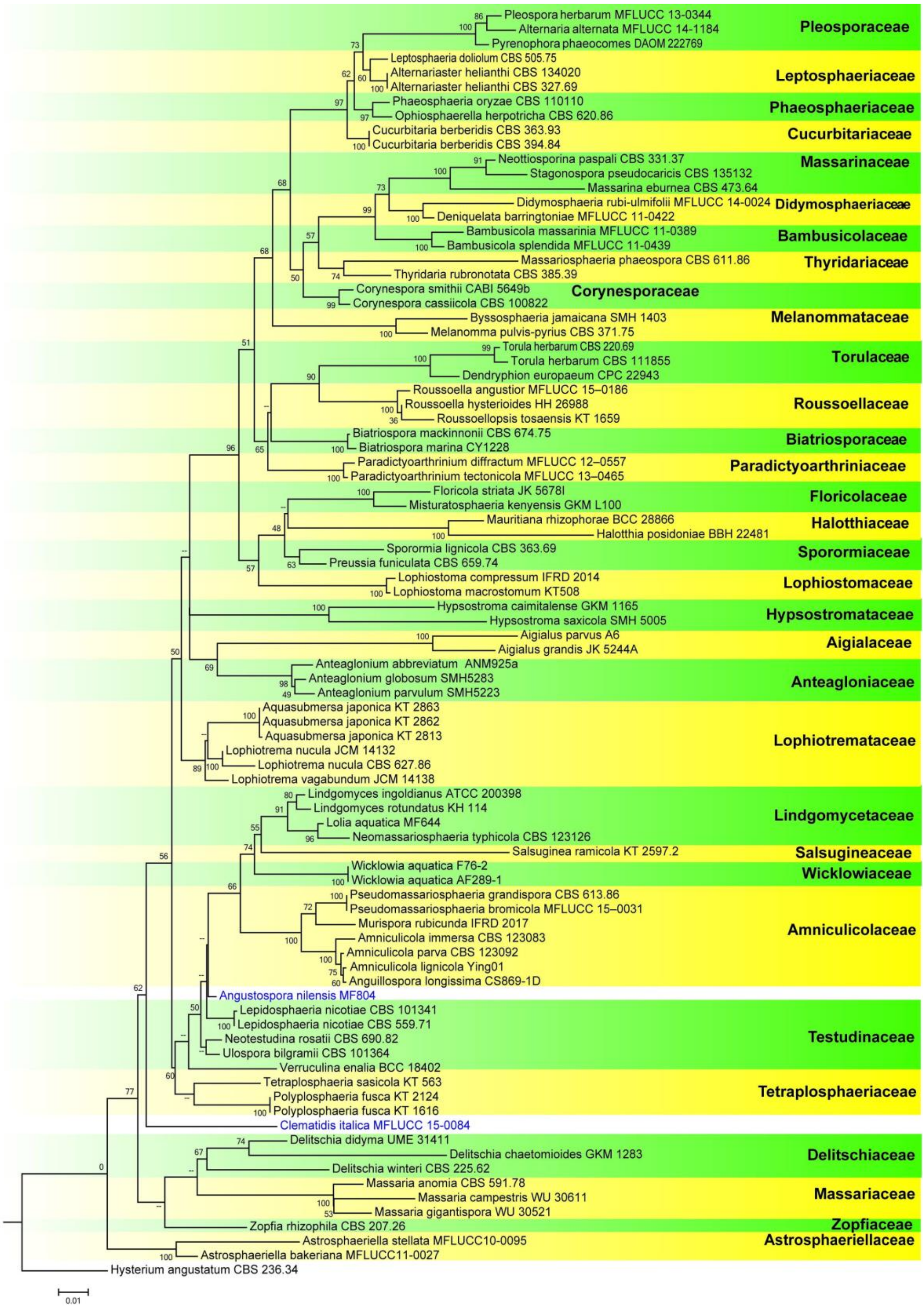


Fig. 38 Phylogram generated from maximum likelihood analysis based on combined LSU and SSU sequence data of *Pleosporales*. Maximum likelihood bootstrap support values greater than 50% are near the nodes. New isolates are in blue. The tree is rooted with *Hysterium angustatum* CBS 236.34

279. *Clematidis* Tibpromma, Camporesi & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 551867, *Facesoffungi number*: FoF 01813

Etymology: named for its occurrence on the host plant genus (*Clematis*)

Saprobic on *Clematis vitalba* L. in terrestrial habitats. **Sexual morph** *Ascomata* solitary or scattered on the host surface, superficial, globose to subglobose, with flattened base, ostiole in the center, black. *Peridium* composing several layers of brown to dark brown, flattened pseudoparenchymatous cells arranged in a *textura angularis*. *Hamathecium* of 1.3–1.7 *µm* wide, long, cylindrical, cellular, anastomosed, guttulate, septate, pseudoparaphyses. *Asci* 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate or sessile. *Ascospores* overlapping 2–3-seriate, hyaline, fusiform, 1-septate in center, swollen with large guttules in each cell, lacking a mucilaginous sheath.

Type species: ***Clematidis italica*** Tibpromma, Camporesi & K.D. Hyde

Notes: *Clematidis italica* is morphologically similar to *Lophiotrema* (*Lophiotrema nucula*). *Clematidis* can be distinguished morphologically from *Lophiotrema nucula* (Fr.) Sacc. 1878 by having fusiform, 1-septate, straight or slightly curved and hyaline ascospores, but *L. nucula* has elliptic-fusiform brown ascospores with 3-septa (Tanaka and Harada 2003). *Clematidis italica* is introduced as new genus based on morphology and combined LSU and SSU sequence phylogenetic support (Fig. 38).

280. *Clematidis italica* Tibpromma, Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551868, *Facesoffungi number*: FoF 01814, Fig. 39

Etymology: Name reflects the country, where this species was collected

Holotype: MFLU 14–0669

Saprobic on *Clematis vitalba* L. in terrestrial habitats. **Sexual morph** *Ascomata* 170–182 *µm* high × 137–168 *µm* diam. ($\bar{x}$ = 174 × 149 *µm*, n = 5), superficial, solitary or scattered on the host surface, globose to subglobose, with flattened base, ostiole in the center, not easy to removed, black, without papilla. *Peridium* 14–20 *µm* wide, composed of several layers of brown to dark brown, flattened pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* of 1.3–1.7 *µm* wide, long cylindrical, cellular, anastomosed, septate, pseudoparaphyses. *Asci* 79–114 × 13–18 *µm* ($\bar{x}$ = 93 × 15 *µm*, n = 15), 8-spored, bitunicate, cylindrical to cylindric-clavate, rounded at the apex, short pedicellate or sessile. *Ascospores* 21–30 × 5–8 *µm* ($\bar{x}$ = 26 × 6 *µm*, n = 20), overlapping 2–3-seriate, hyaline, fusiform, straight or slightly curved, 1-septate in center, slightly constricted at the median septa, swollen with large guttules in each cell, lacking a mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: on MEA reaching 2 cm diam. after 2 weeks at 16°C, later with dense mycelium, with irregular colony, edge undulate, surface smooth with raised elevation, white-gray; hyphae septate branched, grey, thin-walled.

Material examined: ITALY, Corniolino, Santa Sofia, Forlì-Cesena Province, on dead stem of *Clematis vitalba* (*Ranunculaceae*), 2 March 2013, Erio Camporesi, IT1086 (MFLU 14–0669, **holotype**); ex-type living culture, MFLUCC 15–0084); *Ibid*. (HKAS92499 bis, **paratypes**).

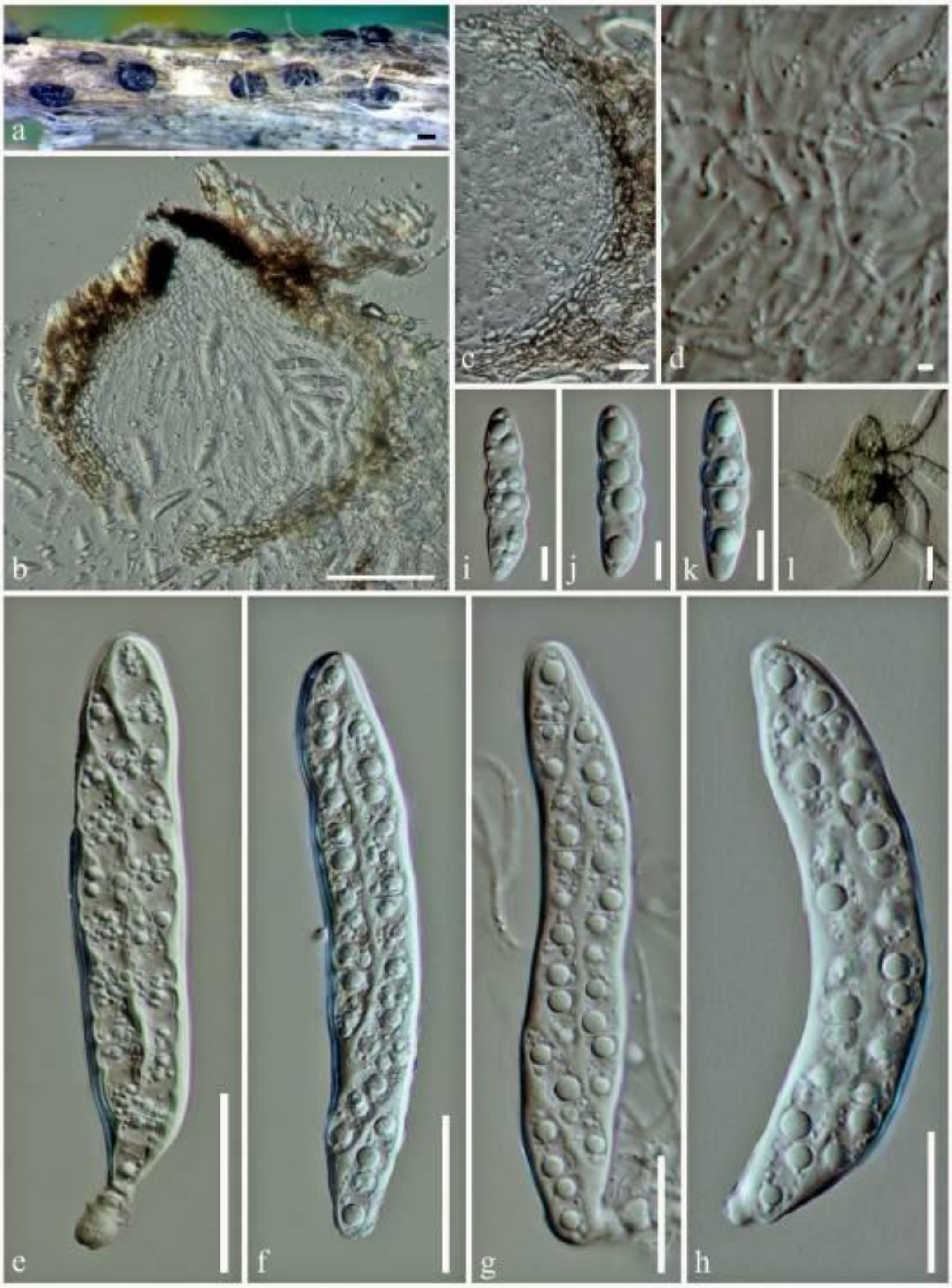


Fig. 39 ***Clematidis italica*** (**holotype**) **a** Appearance of ascomata on host substrate. **b** Section of ascoma **c** Section of peridium **d** Pseudoparaphyses **e**–**h** Ascus with minute pedicel **i**–**k** Ascospores **l** Germinated spore. Scale bars: a = 200 *µm*, b = 50 *µm*, c = 10 *µm*, d = 2 *µm*, e–h = 20 *µm*, i–l = 5 *µm*

281. ***Crassiparies*** Matsumura, K. Hiray & Kaz. Tanaka, ***gen. nov.***

MycoBank number: MB 815294, *Facesoffungi number*: FoF 02024

Etymology: From the Latin *crassi*-, meaning thick, and *paries*, meaning wall, in reference to the thick ascomatal wall.

Saprobic on dead twigs of *Acer* sp. **Sexual morph** *Ascomata* scattered, sometimes in groups of 2–3, immersed to superficial, hemisphaerical, ostiolate. *Peridium* composed of 2 strata; outer stratum composed of brown, angular cells; inner stratum composed of hyaline, prismatic cells. *Hamathecium* comprising numerous, cellular, septate pseudoparaphyses. *Asci* 4-spored, fissitunicate, cylindrical to clavate, pedicellate. *Ascospores* 1–2-seriate, hyaline, broadly fusiform, straight, thick-walled, with a submedian septum, 1-septate, smooth-walled. *Spermatia* subglobose to elliptic, hyaline, smooth-walled. **Asexual morph** Undetermined.

Notes: *Crassiparies* is similar to *Massarina* typified by *M. eburnea* (Tul. & C. Tul.) Sacc. in that both have cylindrical, bitunicate asci and broadly fusiform, 1-septate, hyaline ascospores (Bose 1961; Aptroot 1998). *Crassiparies*, however, differs from *Massarina* in having thick ascomatal walls, ascomatal necks without clypei, and 4-spored asci. *Massarina* belongs to *Massarinaceae*, *Massarineae* (Hyde et al. 2013), but *Crassiparies* nests between *Massarineae* and *Pleosporineae* (Fig. 40).

In phylogenetic analysis based on a combined dataset of SSU and LSU sequence data, this genus formed a sister clade to *Medicopsis* (Fig. 40). However, sequence similarity of ITS region between *Crassiparies* and *Medicopsis romeroi* (Borelli) Gruyter et al., the type species of *Medicopsis* (CBS 252.60) was rather low (426/480 = 88.8 %), with 1.7 % gaps (8/480). *Crassiparies* occurs on woody plants (*Acer*), while *Medicopsis* is known as a human pathogen (Borelli 1959; Ahmed et al. 2014). Therefore, *Crassiparies* is introduced as a new genus.

Type species: ***Crassiparies quadrisporus*** Matsumura, K. Hiray. & Kaz. Tanaka

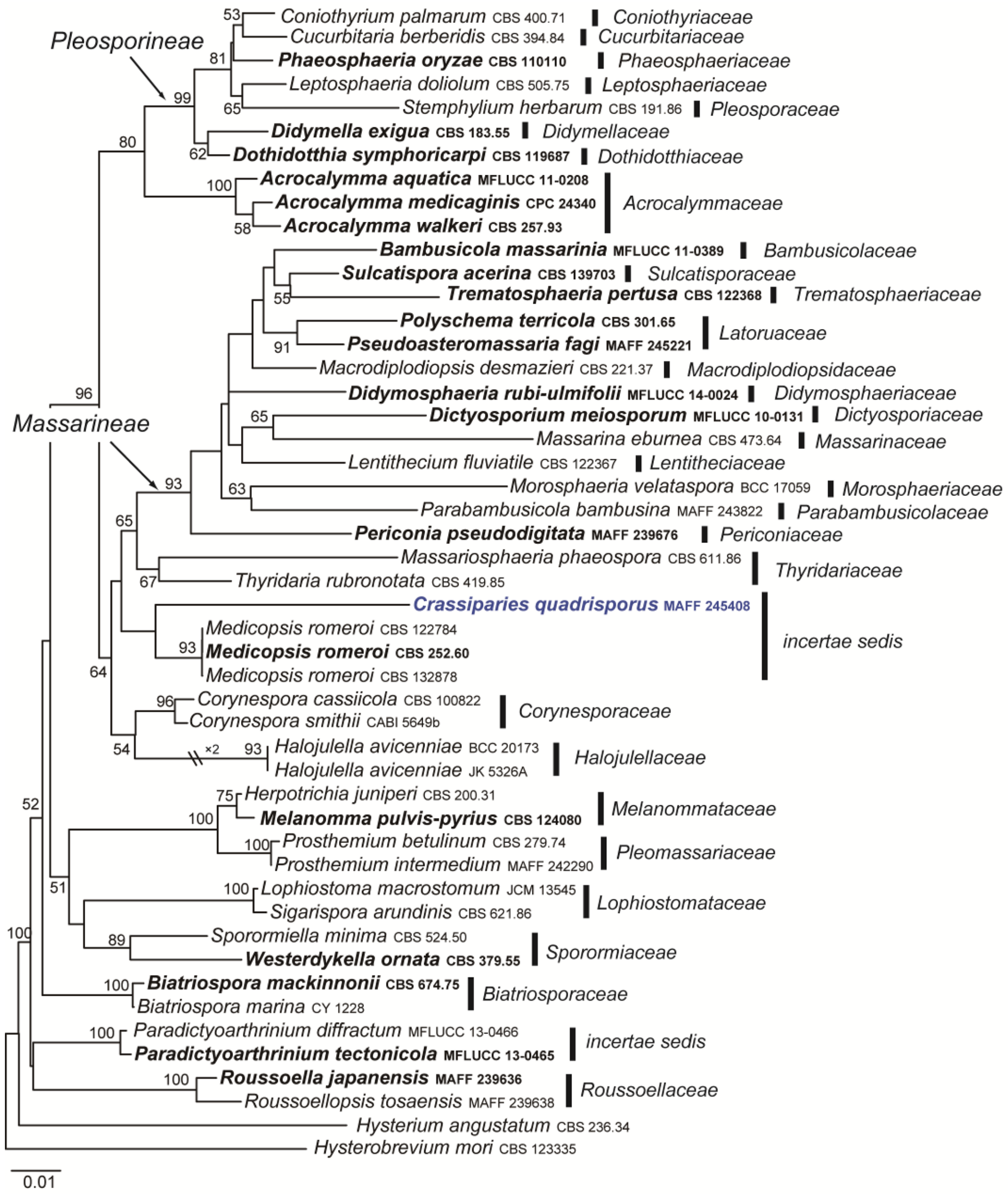


Fig. 40 Maximum-likelihood tree of *Crassiparies* based on analysis of combined SSU and LSU sequence data of *Pleosporales*. Bootstrap values greater than 50 % are presented at the nodes. The ex-types are in bold. New species is annotated in blue.

282. *Crassiparies quadrisporus* Matsumura, K. Hiray. & Kaz. Tanaka, ***sp. nov.***

MycoBank number: MB 815295, *Facesoffungi number*: FoF 02025, Fig. 41

Etymology: In reference to the 4-spored asci.

Holotype: HHUF 30409

Saprobic on dead twigs of *Acer* sp. **Sexual morph** *Ascomata* 300–590 *µm* high, 400–820 *µm* diam., scattered, sometimes in groups of 2–3, immersed to superficial, hemisphaerical in section, with a central ostiole. *Peridium* 63–125 *µm* thick at the base, 75–150 *µm* thick at sides, composed of 2 strata; outer stratum composed of brown, angular cells (7.5–11 × 5–10 *µm*); inner stratum composed of hyaline, prismatic cells. *Hamathecium* comprising numerous, 2–3 *µm* wide, septate, branched, cellular pseudoparaphyses. *Asci* 87–110(–124.5) × 17.5–22.5 *µm* ($\bar{x}$ = 101.3 × 20.3 *µm*, n = 20), 4-spored, fissitunicate, cylindrical to clavate, pedicellate [(17–)22.5–37.5 *µm* long]. *Ascospores* 27–37 × 9–15 *µm* ($\bar{x}$ = 31.4 × 12 *µm*, n = 30), L/W (2–)2.4–3 ($\bar{x}$ = 2.6, n = 30), 1–2-seriate, hyaline, broadly fusiform, straight, thick-walled, with a septum mostly submedian (0.48–0.56; $\bar{x}$ = 0.52, n = 30), 1-septate, smooth-walled. *Spermatia* 3–5.5 × 2–2.5 *µm*, subglobose to elliptic, hyaline, smooth-walled. **Asexual morph** Undetermined.

Material examined: JAPAN, Mie, Tsu, Mie University, on dead twigs of *Acer* sp., 30 May 2008, collector K. Tanaka, KH 111 (HHUF 30409, **holotype)**; ex-type living culture, MAFF 245408.

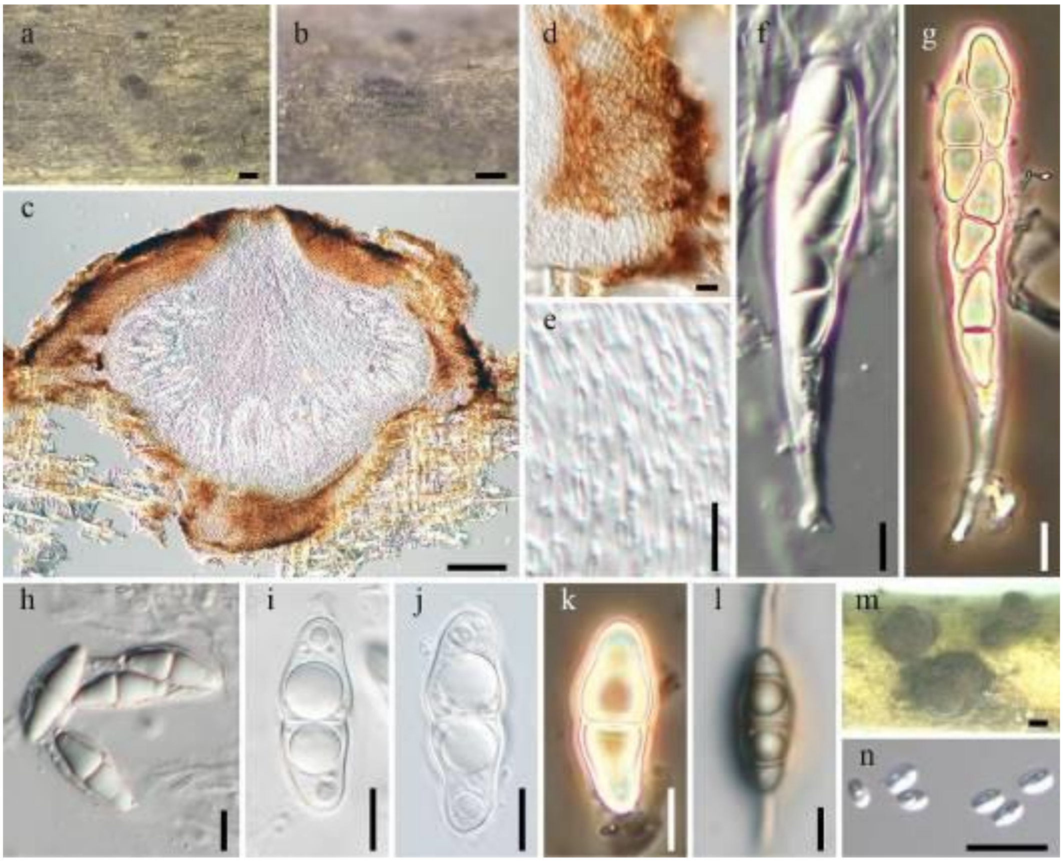


Fig. 41 ***Crassiparies quadrisporus*** **a, b** Appearance of ascomata on host surface **c** Ascoma in longitudinal section **d** Peridium **e** Pseudoparaphyses **f, g** Asci **h**–**k** Ascospores **l** Germinating ascospore **m** Spermogonia formed in culture **n** Spermatia **a–l** from HHUF 30409 (**holotype**); **m, n** from culture MAFF 245408 (**ex-holotype**). Scale bars: a, b, m = 500 *µm*, c = 100 *µm*, d–l, n = 10 *µm*.

283. ***Farasanispora*** Abdel-Wahab, Bahkali & E.B.G. Jones, ***gen. nov.***

Index Fungorum number: IF 551712, *Facesoffungi number*: FoF 01634

Etymology: In reference to the Farasan Island where it was recorded.

Saprobic on submerged mangrove wood. **Sexual morph** *Ascomata* globose to subglobose, immersed to erumpent, solitary, ostiolate, papillate, coriaceous, dark-brown to black. *Peridium* thick at the upper part, two-layered; outer layer comprising polygonal, brown to dark-brown, thick-walled cells; inner layer 12–15 µm wide, comprising hyaline, thin-walled, flattened cells, hard to distinguish from the host cells. *Hamathecium* comprising numerous, 1.5–3 *µm* wide, septate, branched, trabeculate pseudoparaphyses, within a gelatinous matrix, anastomosing above asci and emerging through the ostiolar canal. *Asci* 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* overlapping biseriate, hyaline, 1-septate, senescent ascospores light brown, flattened, striate, rough, 2–3-septate. **Asexual morph** Undetermined.

Notes: During an ongoing study of marine fungi from Saudi Arabia (Hodhod et al. 2012; Abdel-Wahab et al. 2014) an undescribed *Massarina*-like fungus was recorded on decaying intertidal wood of *Avicennia marina* from Farsan Island mangroves. Phylogenetic analyses of SSU and LSU sequence data placed the new taxon in the order *Pleosporales* with affinities to the marine families: *Trematosphaeriaceae*, *Ascocylindricaceae* and *Morosphaeriaceae* however, it did not group with any known family and form a distant clade and it is described in here as a new genus and species (Fig. 31). The genus *Farasanispora* closely resembles species of *Massarina* in having hyaline, 1-septate ascospores, that become light brown and rough-walled when senescent (Aptroot 1998). The genus *Massarina* is polyphyletic and several new genera have been named to accommodate *Massarina* species, e.g., *Halomassarina* to accommodate *M. thalassiae* Kohlm. & Volkm.-Kohlm. (Suetrong et al. 2009); *Lindgomyces* to accommodate *M. ingoldiana* Shearer & K.D. Hyde (Hirayama et al. 2010); *Morosphaeria* to accommodate *M. ramunculicola* K.D. Hyde and *M. velatispora* K.D. Hyde & Borse (Suetrong et al. 2009).

Type species: ***Farasanispora avicenniae*** Abdel-Wahab, Bahkali & E.B.G. Jones

284. *Farasanispora avicenniae* Abdel-Wahab, Bahkali & E.B.G. Jones, ***sp. nov.***

Index Fungorum number: IF 551713, *Facesoffungi number*: FoF 01635, Fig. 42

Etymology: In reference to the host, *Avicennia marina*.

Holotype: CBS

Saprobic on submerged intertidal mangrove wood. **Sexual morph** *Ascomata* 180–270 *µm* in diam., globose to subglobose, immersed to erumpent, ostiolate, solitary, coriaceous, dark-brown to black. *Peridium* 25–35 *µm* thick at the upper part, two-layered, forming *textura angularis*; outer layer 10–15 *µm* comprising polygonal, brown to dark-brown thick-walled cells; inner layer 12–15 *µm* wide, comprising hyaline thin-walled flattened cells; peridium at the lower part of the ascomata is one-layered, hyaline to light brown comprising of 10–15 *µm* diam. polygonal flattened cells. *Hamathecium* comprising numerous, 1.5–3 *µm* wide, septate, trabeculate pseudoparaphses, branched, within a gelatinous matrix, anastomosing above the asci and emerging through the ostiolar canal. *Asci* 115–162 × 23–34 *µm* ($\bar{x}$ = 37.2 × 29.3 *µm*, n = 25), 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 30–39 × 9–13 *µm* ($\bar{x}$ = 34.9 × 11.4 *µm*, n = 60), overlapping biseriate, hyaline, 1–septate, the septum is sub-median, upper cell longer and wider, slightly curved, guttulate; senescent ascospores are larger 38–43 × 11–14 *µm* ($\bar{x}$ = 40.5 × 12.5 *µm*, n = 15), light brown, flattened, striate, verrculose, 2–3-septate. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching a 25–30 mm radius after 22 days at 25°C, with white to gray aerial and immersed mycelium, from below brown.

Material examined: SAUDI ARABIA, Jizan City, Farasan Island, 16° 44′ 22″ N 42° 4′ 41″ E, on decayed wood of *Avicennia marina* at a mangrove stand, 8 March 2012, M.A. Abdel-Wahab (CBS, **holotype**); ex-type living culture, MF 1207.

Notes: *Farasanispora avicenniae* has ascospore dimensions that overlap with *Halomassarina thalassiae* (Kohlm. & Volkm.-Kohlm.) Suetrong et al., however, *Farasanispora avicenniae* have smaller ascomata without a clypeus or papillae and the ostiolar canal is not periphysate. Ascospores in *Halomassarina thalassiae* has a prominent and larger gelatinous sheath (Kohlmeyer and Volkmann-Kohlmeyer 1987). Phylogenetically *H. thalassiae* and *Farasanispora avicenniae* are distantly related, where the latter formed a basal clade to the families *Morosphaeriaceae* and *Trematosphaeriaceae* and its phylogenetic placement is not well-resolved (Fig. 31).

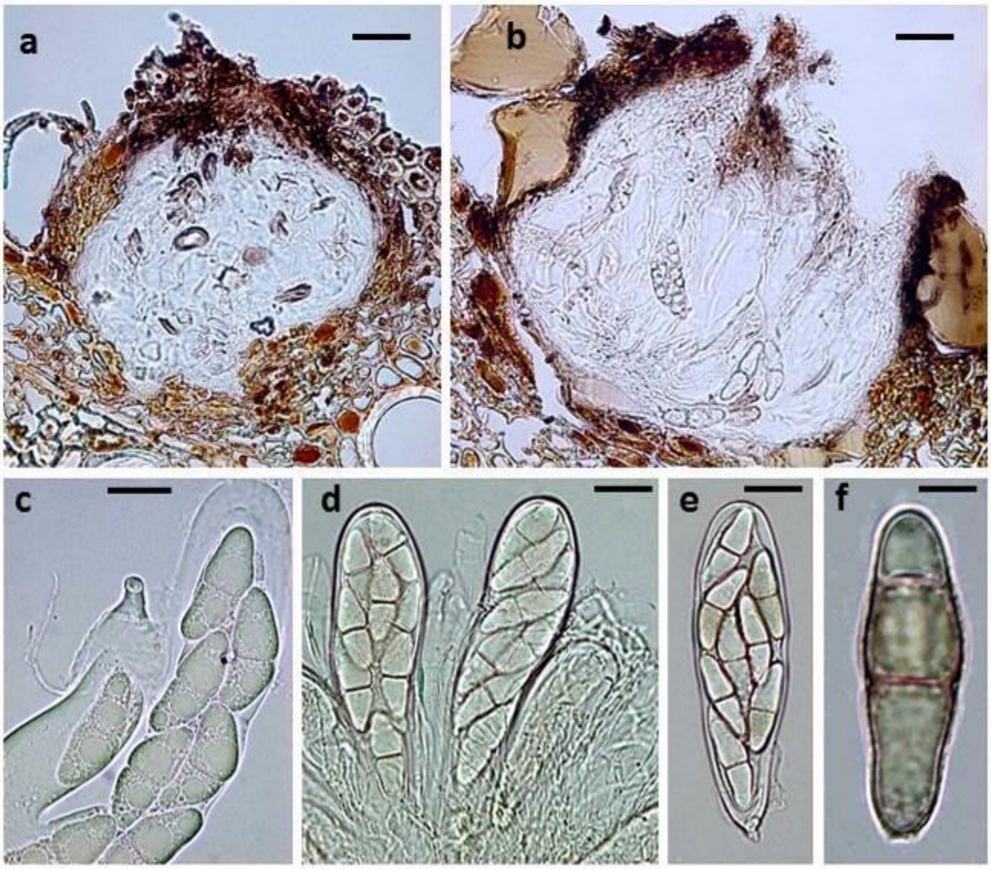


Fig. 42 ***Farasanispora avicenniae*** (**holotype**) **a, b** Vertical section of ascomata **c** Ascus dehiscence **d–e** Mature asci **f** Senescent ascospore. Scale bars: a–b = 40 *µm*, c = 15 *µm*, d–e = 20 *µm*, f = 5 *µm*.

285. ***Parameliola*** Hongsanan, Peršoh & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 551765, *Facesoffungi number*: FoF 01664

Etymology: From Greek *Para* meaning near or beside, *meliola* is from the genus name, in reference to the occurrence on *Meliolaceae*.

Hyperparasite on the surface of hyphae of *Meliola thailandicum* Hongsanan & K.D. Hyde. On superficial hyphae of *M. thailandicum*, growing on the lower surface of living leaves, branched, septate, darker at the septum, brown to dark brown, with hyphopodia, later forming outwardly radiating black colonies with capitate hyphopodia, mostly alternate or sometimes opposite on hyphae, near to hyphal septum, 2-celled, brown and hyphal setae 5 *μm* diam., aseptate, brown to reddish brown, pale brown to hyaline at the apex. *Conidiomata* of *Parameliola* superficial, solitary, globose to subglobose, attached to the superficial hyphae of *Meliola thailandicum*, ostiole absent, thin-walled, brown to dark brown. *Peridium* comprising 2 layers of *textura angularis*, inner layer very thin and hyaline, outer layer dark brown. *Hamathecium* lacking pseudoparaphyses. *Conidiophores* not observed. *Conidiogenous* cells holoblastic in cavity of conidiomata, cylindrical, hyaline, smooth-walled. *Conidia* borne singly at the apex of the conidiophore, ellipsoid to cylindrical, both ends broadly rounded, aseptate, hyaline, smooth-walled.

Notes: *Parameliola* was found on the surface of leaves based of a black sooty mould collected in northern Thailand. The species develops among the setae and on the hyphae of *Meliola thailandicum* Hongsanan & K.D. Hyde, as a hyperparasite. The morphology of *Parameliola* is typical of *Coniothyrium* in having globose, black conidiomata and unicellular hyaline conidia. It is distinct from *Coniothyrium* and other genera in *Pleosporales* in being hyperparasitic on the thallus or hyphae of *Meliola* species. DNA extraction of *Parameliola dimocarpi* and *P. acaciae* were made directly from dry fruiting bodies which contained many conidia to obtain sequence data. Molecular analyses of LSU and SSU sequence data indicate that these two species are separated from other known genera in *Pleosporales*. Therefore, *Parameliola* should be a new genus in *Pleosporales*, typified by *P. dimocarpi*. Furthermore, *Parameliola* species do not clusterd in any family of *Pleosporales* in phylogenetic tree. More collections are needed to confirm their placement which is possibly a new family in *Pleosporales*.

Type species: ***Parameliola dimocarpi*** Hongsanan & K.D. Hyde

286. *Parameliola dimocarpi* Hongsanan & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551927, *Facesoffungi number*: FoF 01962, Fig. 43

Etymology: *dimocarpi* referring to the host.

Holotypus: MFLU15–0045

Hyperparasite on the surface of hyphae of *Meliola thailandicum*. *Conidiomata* 90–98 *μm* diam. ($\bar{x}$ = 96 *μm*, n = 10), superficial, solitary, globose to subglobose, attached to the superficial hyphae of *M. thailandicum*, ostiole absent, thin-walled, brown to dark brown. *Peridium* 7–10 *μm* ($\bar{x}$ = 8 *μm*, n = 10), comprising cell layers of *textura angularis*, inner layer hyaline, outer layer dark brown. *Hamathecium* lacking pseudoparaphyses. *Conidiophores* reduesed to conidiogenous cells. *Conidiogenous cells* 5–4 × 2–3 *μm* ($\bar{x}$ = 4.5 × 3 *μm*, n = 5), holoblastic in cavity of conidiomata, cylindrical, hyaline, smooth-walled. *Conidia* 6–9 × 2–3 *µm* ($\bar{x}$ = 7 × 2.5 *µm*, n = 10), borne singly at the apex of the conidiophore, ellipsoid to cylindrical, both ends broadly rounded, aseptate, hyaline, smooth-walled.

Material examined: THAILAND, Chiang Rai, Amphoe Thoeng, on the living leaves of *Dimocarpus longan* Lour. (*Sapindaceae*), 18 January 2015, S. Hongsanan (MFLU15–0045 **holotype**; KIB, **isotype**).

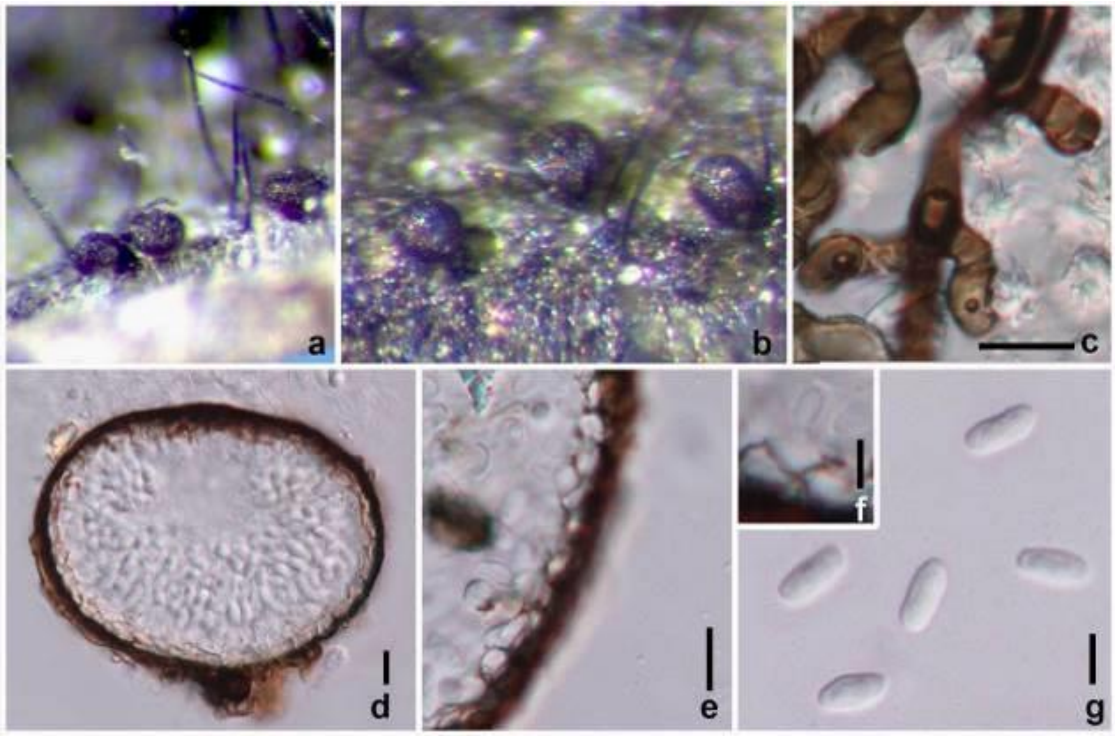


Fig. 43 ***Parameliola dimocarpi*** (**holotype**) **a, b** Conidiomata developing as hyperparasites on the thallus or hyphae of *Meliola thailandicum* **c** Hyphae of *M. thailandicum* with hyphopodia **d** Section through conidioma in 10% lactic acid **e** Peridium of conidiomata **f** Conidiogenous cell **g** Conidia in 10% lactic acid Scale bars: c–e = 10 *µm*, f, g = 5 *µm*

287. ***Parameliola acaciae*** Hongsanan & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551928, *Facesoffungi number*: FoF 01963, Fig. 44

Etymology: *acaciae* referring to the host.

Holotypus: MFLU15–0378

Hyperparasite on the surface of hyphae of *Meliola thailandicum*. *Conidiomata* 84–88 *µm* diam. ($\bar{x}$ = 85 *µm*, n = 10), superficial, solitary or gregarious, globose to subglobose, attached to the superficial hyphae of *Meliola thailandicum*, ostiole absent, thin-walled, brown to dark brown. *Setae* 5 *µm* diam., aseptate, brown to reddish brown, pale brown to hyaline at the apex. *Peridium* 10 *µm* ($\bar{x}$ = 8 *µm*, n = 10), comprising 2 layers of *textura angularis*, inner layer hyaline, outer layer dark brown. *Hamathecium* lacking pseudoparaphyses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 × 1–2 *µm* ($\bar{x}$ = 4.5 × 1.5 *µm*, n = 5) wide, holoblastic in cavity of conidiomata, cylindrical, hyaline, smooth-walled. *Conidia* 7–10 × 3–4 *µm*

($\bar{x}$ = 9 × 3.5 μm, n = 10), borne singly at the apex of the conidiophore, cylindrical to oblong, both ends broadly rounded, aseptate, hyaline, smooth-walled.

Material examined: THAILAND, Chiang Rai, Mueang, Agricultural Research Center, on living leaves of *Acacia auriculiformis* A. Cunn. ex Benth. (*Fabaceae*), 23 January 2015, S. Hongsanan (MFLU 15–0378; KIB, **isotype**).

Notes: *Parameliola acaciae* is similar to *P*. *dimocarpi*, however, it differs in having cylindrical to oblong ascospores, which are slightly larger than those of *P*. *dimocarpi*. *Parameliola acaciae* was found among the colonies of *Meliola thailandicum* growing on dead leves of *Acacia auriculiformis*, while *Parameliola dimocapi* was found among the colonies of *Meliola thailandicum* growing on leaving leaves of *Dimocarpus longan* (Hongsanan et al. 2015). Phylogenetic analyses indicate that *Parameliola*. *acaciae* is closely related to the type species of *Parameliola*, but is a distinct species, therefore the placement of *Parameliola* in *Pleosporales* is supported.

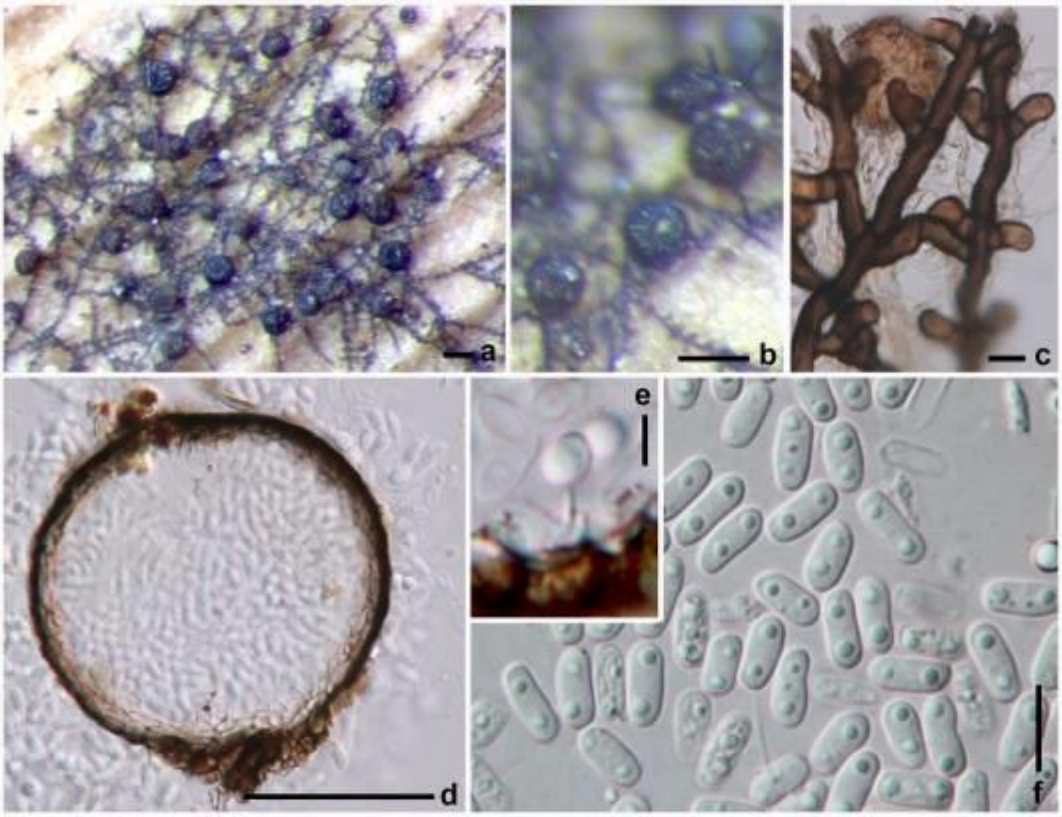


Fig. 44 ***Parameliola acaciae*** (**holotype**) **a, b** Conidiomata developing as hyperparasites on the thallus or hyphae of *Meliola thailandicum* **c** Hyphae of *M*. *thailandicum* with hyphopodia **d** Section through conidiomata in 10% lactic acid **e** Conidiogenous cell **f** Conidia. Scale bars: a, b = 100 μm, c = 10 μm, d = 50 μm, e, f = 5 μm.

Dothideomycetes* family, *incertae sedis

Kirschsteiniotheliaceae

Boonmee et al. (2012) established the new family *Kirschsteiniotheliaceae* based on morphological features and phylogenetic analysis. The family is typified by

Kirschsteiniothelia aethiops (Berk. & M.A. Curtis) D. Hawksw. and its asexual morph is *Dendryphiopsis atra* (Corda) S. Hughes (Kirk et al. 2008; Su et al. 2016), and Wijayawardene et al. (2014b) proposed the correct name for the type species as *Kirschsteiniothelia atra* (Corda) D. Hawksw. Two species of *Kirschsteiniothelia*, *K. elaterascus* Shearer and *K. maritima* (Linder) D. Hawksw. have been transferred to *Morosphaeria* (*Morosphaeriaceae*) and a new genus *Halokirschteiniothelia* (*Mytilinidiaceae*) by Boonmee et al. (2012) respectively. *Kirschsteiniothelia* comprises 19 species according to Index Fungorum (2016). *Kirschsteiniothelia tectonae* is introduced as a new species in *Kirschsteiniotheliaceae*. The phylogenetic tree is presented in Fig. 45.

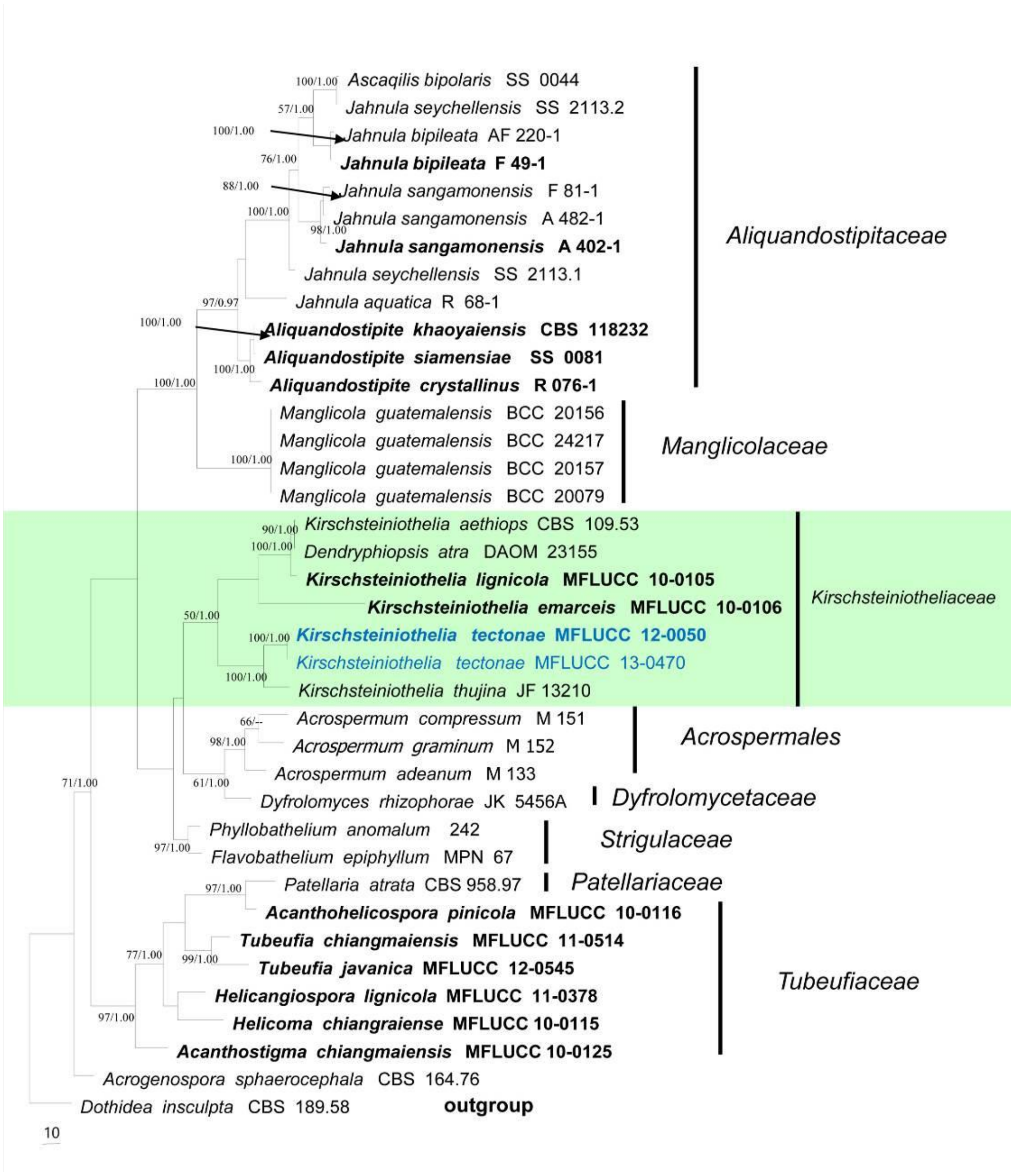


Fig. 45 Phylogram generated from combined LSU, SSU and ITS sequence data. The tree is rooted to *Dothidea insculpa* CBS 189.58. Maximum parsimony bootstrap values ≥50%,

Bayesian posterior probabilities ≥ 0.95, (MPBS/PP) are given at the nodes. The ex-type strains are in bold and the new isolates are in blue.

288. ***Kirschsteiniothelia tectonae*** Doilom, D.J. Bhat & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551992, *Facesoffungi number*: FoF 01883, Fig. 46

Etymology: Name refers to the host genus *Tectona* on which the fungus was collected.

Holotype: MFLU 15–1883.

Saprobic on dead branches and twigs of *Tectona grandis* (L. f.). **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate, superficial, hairy, dark brown, scattered, single or in groups. *Conidiophores* up to 200 *µm* long, 4–8 *µm* wide at the swollen base, superficial on host surface, macronematous, mononematous, simple, erect to slightly curved, unbranched or branched, septate, slightly constricted at septa, pale brown to dark brown, cylindrical. *Conidiogenous cells* 7.5–9.5 × 3.5–5 *µm*, monoblastic, integrated, terminal, cylindrical, determinate. *Conidia* (85–)135–150(–212) × (15–)16–17(–19) *µm* ($\bar{X}$ = 137 × 16 *µm*, n = 30), 9–25 or more transverse septa, cylindric-obclavate, elongate, straight or slightly curved, rounded at the apex and slightly paler, with sheath at apex, obconically truncate at the base, dark reddish brown, thick–walled, smooth; secession schizolytic.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on MEA reaching 14–16 *mm* diam. after 7 days in the dark at 25 °C ($\bar{X}$ = 14.9 *mm*, n = 5), entire edge, circular, flat or effuse, raised at the edge, superficial at the center, dense, fluffy, grey (5E1) from above, brownish (5F2) from below. *Mycelium* 1.5–4.7 *µm* wide, aerial, reddish brown to dark brown, septate, branched hyphae, slightly constricted at septa. *Conidiophore*s up to 45 *µm* long, 3.5–8 *µm* wide, semi-macronematous, mononematous, erect to slightly curved, indeterminate, branched, reddish brown to dark brown. *Conidiogenous cells* holoblastic, doliiform, integrated, terminal. *Conidia* (33–) 70–110 (–200) *µm* long × (7–) 11–13 (–18) *µm* thick at the broadest part ($\bar{X}$ = 83 × 12 *µm*, n = 30), produced on aerial mycelium, initially subglobose and acellular, becoming cylindric-obclavate, 1–29 or more transverse septa, flexuous, slightly curved, rounded at the apex and slightly paler, obconically truncate at the base, dark reddish brown, thick-walled.

Material examined: THAILAND, Phrae Province, Denchai District, Ban Maejour Subdistrict, on dead branches of *Tectona grandis* (*Lamiaceae*), 29 October 2011, M. Doilom (MFLU 15–1883, **holotype**), ex-type living culture MFLUCC 12–0050, MKT 016, MUCL55897; Chiang Rai Province, Mae Chan District, on dead twigs of *T. grandis*, 3 March 2013, M. Doilom, MFLU 15–1884, living culture MFLUCC 13–0470, MKT 111.

Notes: *Kirschsteiniothelia tectonae* was found only in its asexual morph, while *K. thujina* is known only as the sexual morph. Thus, a morphological comparison could not be made, and *K. tectonae* is only compared to *K. atra*, *K. emarceis* and *K. lignicola*. These three species have been reported with asexual morphs both on natural substrates and cultures. It differs from these species in size and shape of conidiophores and conidia both on natural substrates and cultures. The conidia of *K. tectonae* are longer than those of the other three species (Table. 2). Based on its morphology (Fig. 46) and the fact it is phylogenetically separate from other species in *Kirschsteiniothelia* (Fig. 45), we introduce it a new species. The combined LSU, SSU and ITS sequence analysis shows that *K. tectonae* isolate MFLUCC 12–0050 and MFLUCC 13–0470 grouped close to, but is distinguishable from *K. thujina* with strong bootstrap support 100% MPBS and 1.00 PP (Fig. 45).

Table. 2 Comparison of morphological characters of asexual morph of *Kirschsteiniothelia*

Species	**Morphology on natural substrate**		**Morphology on MEA culture**		**Reference**
	Conidiophores (*µm*)	**Conidia (*µm*)**	**Conidiophores (*µm*)**	**Conidia (*µm*)**	
K. tectonae	Up to 200, 4–8 wide at the swollen base	(85–) 135–150 (–212) long × (15–) 16–17 (–19) thick in broadest part, 9–25 or more transverse septa, cylindric–obclavate, elongate	up to 45, 3.5–8 wide	(33–) 70–110 (–200) long × (7–) 11–13 (–18) thick in broadest part, 1–29 or more transverse septa, cylindric–obclavate	This study
K. aethiops	Up to 500 long, 8–11 thick.	40–80 × 12–25	Not reported	Not reported	Ellis 1971
K. emarceis	162–271 × 7–14	(40–)45– 56(–67) × (10–)14–15(–17), 3–4(–5) septate, oblong to obclavate	32–92 long, 5–7 thick, branched at apex	(21–)27–28(–36) × 9– 13(–15), 1–2(–3) transverse septate, fusiform to obclavate	Boonmee et al. 2012
K. lignicola	287–406 × 11–13	39–48(–52) × 21–25(–28), 1–2 transverse septa, obovoid to broadly	39–148 long, 4–7 thick	24.5–35(–41) × 14–16(–19), 1–2 transverse septa, broadly obovoid	Boonmee et al. 2012

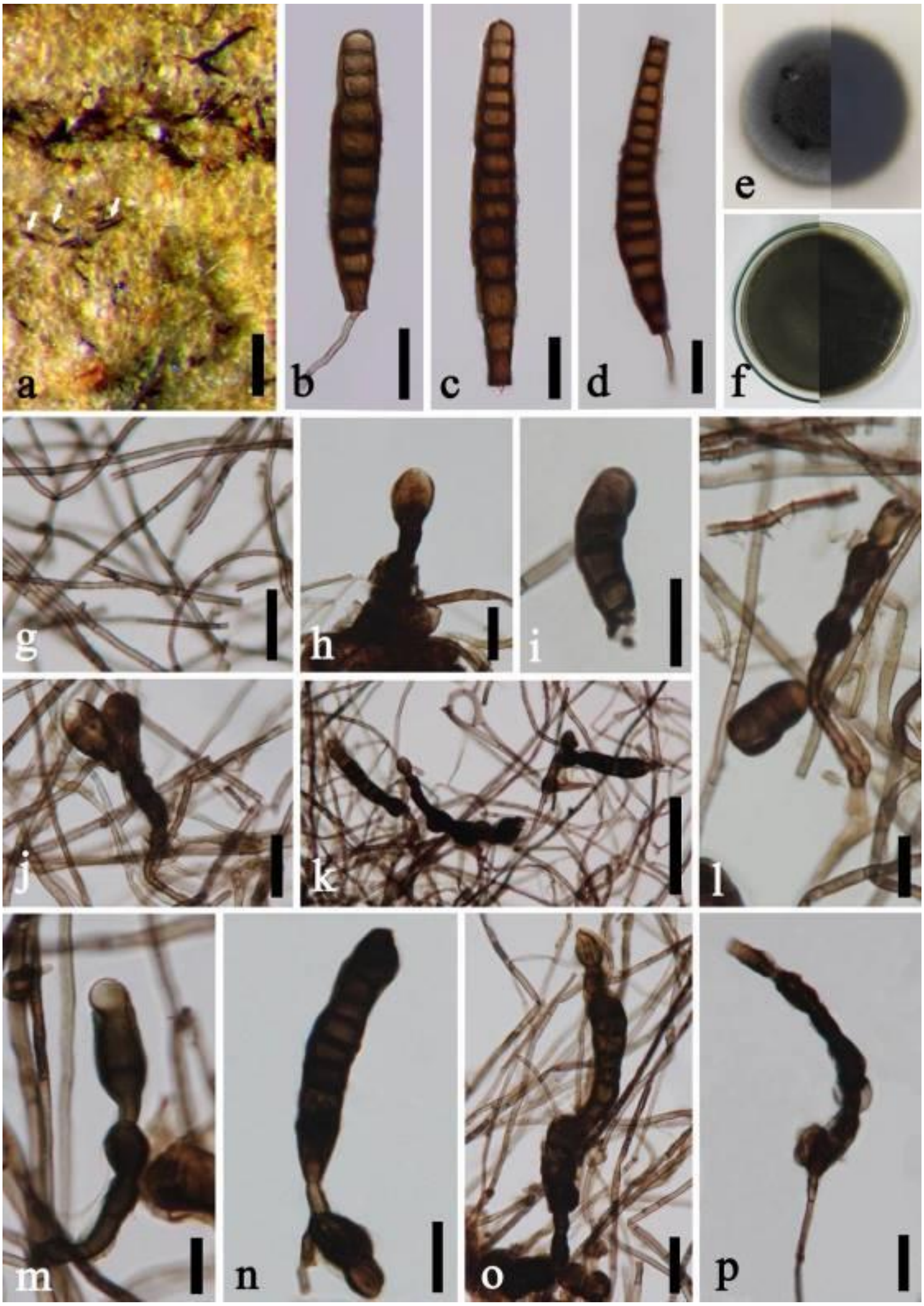


Fig. 46 ***Kirschsteiniothelia tectonae*** **(holotype)** **a** Conidia host surface (arrows) **b–d** Conidia **e** Colony on MEA for 7 days (above and below views) **f** Colony on PDA for 2 months (above and below views) **g** Mycelia **h** Immature conidia attached to conidiophore **i** Conidia **j–m**, **o** Conidia attached to conidiophores with mycelia **n**, **p** Conidia attached to conidiophores **a–d** Morphology on host **g–p** Morphology on MEA culture. Scale bars: a = 200 *µm*, b–d, g, j, n–p = 20 *µm*, h, i, l, m = 10 *µm*, k = 50 *µm*.

Lecanoromycetes

Ostropales

Graphidaceae

Graphidaceae is the second largest family of lichenized fungi, with approximately 2,100 species in nearly 80 genera and an additional 1,800 species predicted (Rivas Plata et al. 2012a; Lücking et al. 2014; Jaklitsch et al. 2016). Here we described three new species of *Graphidaceae* discovered in the course of collaborative inventory work in Sri Lanka and adjacent areas (Weerakoon 2015; Weerakoon et al. 2012a, b, c, 2014, 2015; Weerakoon & Aptroot 2013, 2014). All belong to the *Ocellularia* clade, a clade that has been recognized as hyper diverse in recent molecular and revisionary studies (Rivas Plata et al. 2012b; Cáceres et al. 2014; Lücking 2014, 2015; Kraichak et al. 2015), surpassing the genus *Graphis* and relatives in species richness. Since *Ocellularia* and relatives are mostly found in well-preserved tropical forests (Rivas Plata et al. 2008), it is predicted that the remaining forest ecosystems still yield a high number of undiscovered species (Lücking et al. 2014). This is also true for Sri Lanka, which has only begun to be studied systematically with regard to its lichen biota (Weerakoon & Aptroot 2014; Weerakoon 2015), but where tropical forest has largely been degraded, leaving a few pristine, highly diverse areas. Although we were unable to generate molecular data for the newly described species, our broad molecular framework of the family (Rivas Plata et al. 2012b, 2013) has helped us to establish a much refined species concept in the *Ocellularia* clade, leading to numerous recent discoveries (Lücking 2014, 2015; Lücking & Pérez-Ortega 2015), including the three species described here.

Ocellularia

289. *Ocellularia arachchigei* Weerakoon, Lücking & Lumbsch, ***sp. nov.***

MycoBank number: MB 815548, *Facesoffungi number*: FoF 02026, Fig. 47a

Etymology: In honor of the collector of the type specimen, Mr. Omal Selika Arachchige.

Holotype: O. S. Arachchige 107A (F).

Diagnosis: Differing from *Ocellularia papillata* and *O. rongklaensis* in the grey thallus with large internal clusters of calcium oxalate crystals and the whitish cover of the columella.

Thallus corticolous, epiperidermal, up to 5 cm diam., continuous; surface smooth to uneven, light grey; prothallus absent. Thallus in section 70–100 *µm* thick, with prosoplectenchymatous cortex, 15–20 *µm* thick, photobiont layer 30–50 *µm* thick, and medulla 30–50 *µm* thick, strongly encrusted with numerous clusters of calcium oxalate crystals, thicker near apothecial margin (up to 100 *µm*). *Photobiont Trentepohlia*; cells rounded to irregular in outline, in irregular groups, yellowish green, 8–10 × 5–7 *µm*. *Ascomata* immersed-erumpent, with complete thalline margin, 0.8–1.2 mm diam.; disc covered by 0.2–0.5 mm wide pore; proper margin distinct, entire, visible as thin, white rim around the pore; thalline margin entire, smooth, white. *Excipulum* entire, yellowish to orange-brown (difficult to separate from modified periderm), together with periderm 50–100 *µm* wide, fused with thalline margin; laterally covered by algiferous, corticate thallus containing periderm and large crystals of calcium oxalate crystal layers up to 100–150 *µm*. *Columella* present, finger-like to barrel-shaped, becoming irregular, 150–200 *µm* broad, yellowish brown with whitish cover. *Hypothecium* prosoplectenchymatous, 10–15 *µm* high, colourless. *Hymenium* 150 µm high, colourless, clear. *Epithecium* indistinct, 10–15 *µm* high, colourless. *Paraphyses* unbranched, apically smooth; periphysoids absent. *Asci* cylindrical, 120–140 × 20–25 *µm*. *Ascospores* 8 per ascus, ellipsoid, 7–9-septate, 30–35 × 9–10 *µm*, 3–4 times as long as wide, hyaline, distoseptate with lens-shaped lumina, I+ violet-blue. *Secondary chemistry*: No substances detected by TLC.

Material examined: SRI LANKA, Central Province, Matale District, Gammaduwa; 7° 31' N, 80° 40' E, 360 m; low altitude, on tree bark of home garden; January 2015, O. S. Arachchige 107A (PDA **holotype** and F **Isotype**).

Distribution and ecology: The new species was collected from a home garden in the central region of Sri Lanka. It is thus far only known from the type locality.

Notes: This new species keys out close to *Ocellularia papillata* (Leight.) Zahlbr. and *O. rongklaensis* (Homchant. & Coppins) Lücking. All three agree in lacking secondary metabolites, having a non-carbonized excipulum, a smooth to uneven thallus, immersed to erumpent ascomata, and ascospores over 20 *µm* long. However, *O. papillata* differs in the pale olive thallus lacking large clusters of calcium oxalate crystals, the completely immersed apothecia, and the distinctly brown apothecial rim and columella, with the columella becoming more distinctly irregular. In contrast, *O. ronklaensis* has a pale olive, indistinctly verrucose thallus, due to clustered distribution of calcium oxalate crystals, more erumpent apothecia, and the columella appears dark with only a thin whitish pruina. Other similar species are *O. laeviusculoides* Sipman & Lücking, differing chiefly in its carbonized columella, and *O. bonplandii* (Fée) Müll. Arg. and *O. auberianoides* (Nyl.) Müll. Arg., which both produce protocetraric acid and the columella becomes distinctly irregular in the latter.

290. *Ocellularia ratnapurensis* Weerakoon, Lücking & Lumbsch, ***sp. nov.***

MycoBank number: MB 815549, *Facesoffungi number*: FoF 02027, Fig. 47b

Etymology: Referring to the type locality.

Holotype: G. Weerakoon 1005 (F).

Diagnosis: Differing from *Ocellularia guptei* in the larger ascospores and the only partially (upper half) carbonized columella.

Thallus corticolous, epiperidermal, up to 5 cm diam., continuous; surface uneven to verrucose, brownish yellow; prothallus absent. Thallus in section 50–80 *µm* thick, with paraplectenchymatous cortex, 5–10 *µm* thick, photobiont layer 30–60 *µm* thick, and medulla 30–50 *µm* thick, strongly encrusted with clusters of calcium oxalate crystals, near apothecial margins much thicker, up to 150 *µm*; in addition with numerous small, grey granules. *Photobiont Trentepohlia*; cells rounded to irregular in outline, in irregular groups, yellowish green, 8–11 × 5–8 *µm*. *Ascomata* rounded, erumpent to prominent, with complete thalline margin, 0.7–1.2 mm diam., 0.2–0.3 mm high; disc covered by 0.15–0.25 mm wide pore; proper margin distinct, entire, visible as brownish rim around the pore; thalline margin entire, smooth, light yellowish. *Excipulum* entire, yellowish to orange-brown, upper half carbonized, 50–70 *µm* thick, covered by periderm layer, 70–100 *µm* thick, orange, fused with thalline margin. *Columella* present, finger-like to barrel-shaped, 100 *µm* broad, upper half carbonized; hypothecium prosoplectenchymatous, 10–15 *µm* high, colourless. *Hymenium* 300 *µm* high, colourless, clear; epithecium indistinct, 10–15 *µm* high, colourless. *Paraphyses* unbranched, apically smooth; periphysoids absent. *Asci* cylindrical, 200–250 × 50–70 *µm*. *Ascospores* 1–2 per ascus, muriform, 200–250 × 40–50 *µm*, about 5 times as long as wide, hyaline, distoseptate with lens-shaped lumina, I+ violet-blue. *Secondary chemistry*: No substances detected by TLC.

Material examined: SRI LANKA. Sabaragamuwa Province: Ratnapura District, Coolbone Tea Estate, on tree bark, 7° 02' N, 80° 23' E, 1288 (PDA **holotype** and F **Isotype**).

Distribution and ecology: The new species was collected from montane forest patches in a Tea estate in the Sabaragamuwa region of Sri Lanka. It is thus far only known from the type locality.

Notes: *Ocellularia ratnapurensis* belongs in a small group of species with carbonized excipulum and columella, large, muriform ascospores, and absence of secondary substances. Among these, the neotropical *O. sanfordiana* Zahlbr. differs by the carbonization of the excipulum and columella reaching down to the base, the larger apothecia, and the smaller ascospores (130–170 × 25–35 *µm*). The paleotropical *Ocellularia kalbii* Mangold also differs in the basal carbonization of excipulum and columella and in addition has less erumpent apothecia with gently sloping sides and much longer ascospores (300–600 × 25–50 *µm*). *Ocellularia guptei* (Nagarkar, Sethy & Patw.) D. D. Awasthi, from India, apart from a fully carbonized columella, differs in its smaller ascospores (100–180 × 15–30 *µm*). All other similar species differ in their chemical components, mostly producing hypoprotocetraric or isonotatic and norisonotatic acid.

Rhabdodiscus

291. *Rhabdodiscus albodenticulatus* Weerakoon, Lücking & Lumbsch *sp. nov.*

MycoBank number: MB 815550, *Facesoffungi number*: FoF 02028, Fig. 47c, d

Etymology: Referring to the white teeth-like apothecial columella.

Holotype: G. Weerakoon 880 (F).

Diagnosis: Differing from *Rhabdodiscus integer* by the thicker, verrucose thallus and the smaller, more immersed apothecia.

Thallus corticolous, up to 5 cm diam., continuous, olive-grey to olive- green, uneven-verrucose; prothallus not observed. Thallus in section 200–300 *µm* thick, with prosoplectenchymatous cortex 10–20 *µm* thick, photobiont layer 50–70 *µm* thick, and medulla 150–200 *µm* thick, strongly encrusted with numerous large crystals of calcium oxalate, forming clusters that cause the verrucae. *Photobiont Trentepohlia*; cells rounded to irregular in outline, in irregular groups, pale green, 7–11 × 4–6 *µm*. *Apothecia* erumpent, 0.8–1.2 mm diam.; disc partially covered by 0.2–0.4 mm wide pore, rim around the pore whitish to pale yellowish, pore mostly filled by columella. *Columella* present, broad-stump-shaped but becoming ruptured in to 3–6 irregular teeth, 100–200 *µm* broad, carbonized but with whitish top. *Excipulum* 30–50 *µm* broad, carbonized; periphysoids absent. *Hymenium* 120 *µm* high, clear. *Paraphyses* unbranched. *Asci* 100 × 20 *µm*, fusiform. *Ascospores* 8 per ascus, submurifom, 3 transverse septa and 0–1 longitudinal septa, 15–18 × 7–8 *µm*, ellipsoid, with thick septa and lens-shaped lumina, brown, I+ violet-blue (amyloid). *Secondary chemistry*: Psoromic, subpsoromic and 2'-*O*-demethylpsoromic acids.

Material examined: SRI LANKA, Central Province, Matale district, Siyabalabokka-Rattota, 7° 31' N, 80° 40' E, 360 m, low altitude, on tree bark of home garden; January 2015, G. Weerakoon 880 (PDA **holotype** and F **Isotype**); Along Karagastanna road, 7° 34' N, 80° 42' E, 990 m, mid elevation, January 2015, G. Weerakoon *205*, *237* (F); *Meepiliyamana* -Nuwaraeliya, 6° 56' N, 80° 47' E, 1350 m, high elevation, January 2015, Weerakoon 732 (F).

Distribution and ecology: The new species was collected in high elevation disturbed montane forest patches.

Notes: This new species is most similar to *Rhabdodiscus integer* (Müll. Arg.) Rivas Plata & Lumbsch, which which it shares the submuriform, brown ascospores, the columella rupturing into teeth, and the psoromic acid chemistry. However, *R. integer* has a thinner, smooth to uneven thallus and much larger, strongly prominent apothecia. *Rhabdodiscus marivelensis* (Vain.) Rivas Plata & Lumbsch differs in the minutely grainy thallus caused by columnar clusters of calcium oxalate crystals, the thicker apothecial margin, and the larger ascospores (20–30 × 8–18 *µm*).

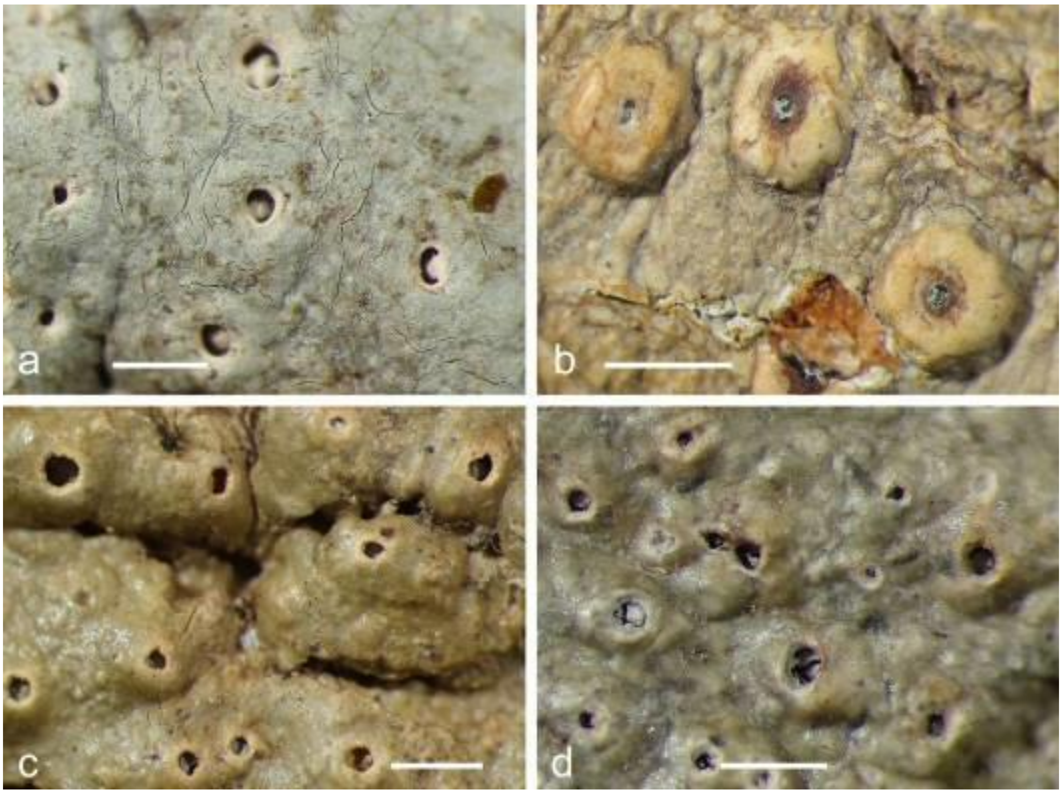


Fig. 47 ***Ocellularia arachchigei*** (**holotype**) **a** Thallus with ascomata. ***Ocellularia ratnapurensis*** (**holotype**) **b** Thallus with ascomata. ***Rhabdodiscus albodenticulatus*** (**c holotype**, **d paratype**) **c**, **d** Thallus with ascomata. Scale bars: a–d = 1 mm.

Sordariomycetes

Chaetosphaeriales

Chaetosphaeriales was established as distinct order in the Class *Sordariomycetes* based on phylogenetic analysis of LSU sequence data (Huhndorf et al. 2004). At present, two families, *Chaetosphaeriaceae* (Réblová et al. 1999) and *Helminthosphaeriaceae* (Samuels et al. 1997) are recognized as members of this order (Maharachchikumbura et al. 2015).

Chaetosphaeriaceae

Species of *Chaetosphaeriaceae* are widely distributed and are saprobic on various plants (Fernández and Hundorf 2005). The representative genus *Chaetosphaeria* is characterized by non-stromatic perithecia, cylindrical asci, and transversely septate ascospore in its sexual morph, but the genus has been reported to have morphologically diverse asexual morphs (Réblová and Winka 2000). Phylogenetic studies also suggest that the genus is polyphyletic (Fernández et al. 2006; Jeewon et al. 2009). To date, 32 asexual hyphomycetous genera have been reported in this family (Wijayawardene et al. 2012). Additionally, eight coelomycetous genera, *Brunneodinemasporium*, *Dendrophoma*, *Dinemasporium*, *Infundibulomyces*, *Neopseudolachnella*, *Pseudodinemasporium*, *Pseudolachnea* and *Pseudolachnella* are known as members of *Chaetosphaeriaceae* (Somrithipol et al. 2008; Crous et al. 2012; Wijayawardene et al. 2012; Hashimoto et al. 2015a, b; Liu et al. 2015).

Pseudolachnella

The genus *Pseudolachnella* was established by Teng (1936) to segregate species with multi-septate conidia from *Pseudolachnea*. The generic concept has been recently revised based on detailed morphological observations and molecular analysis (Hashimoto et al. 2015b). It is characterized by setose condiomata with thin basal stroma and less-developed excipulum, and condia bearing appendages. Sixteen species of *Pseudoalchnella* have been described from bamboo (Nag Raj 1993; Zhao et al. 2004; Sato et al. 2008; Hashimoto et al. 2015b), but *P. guaviyunis* occurred on *Myrcianthes pungens* (*Myrtaceae*) (Crous et al. 2014b). The phylogenetic tree for *Pseudolachnella* is presented in Fig. 48.

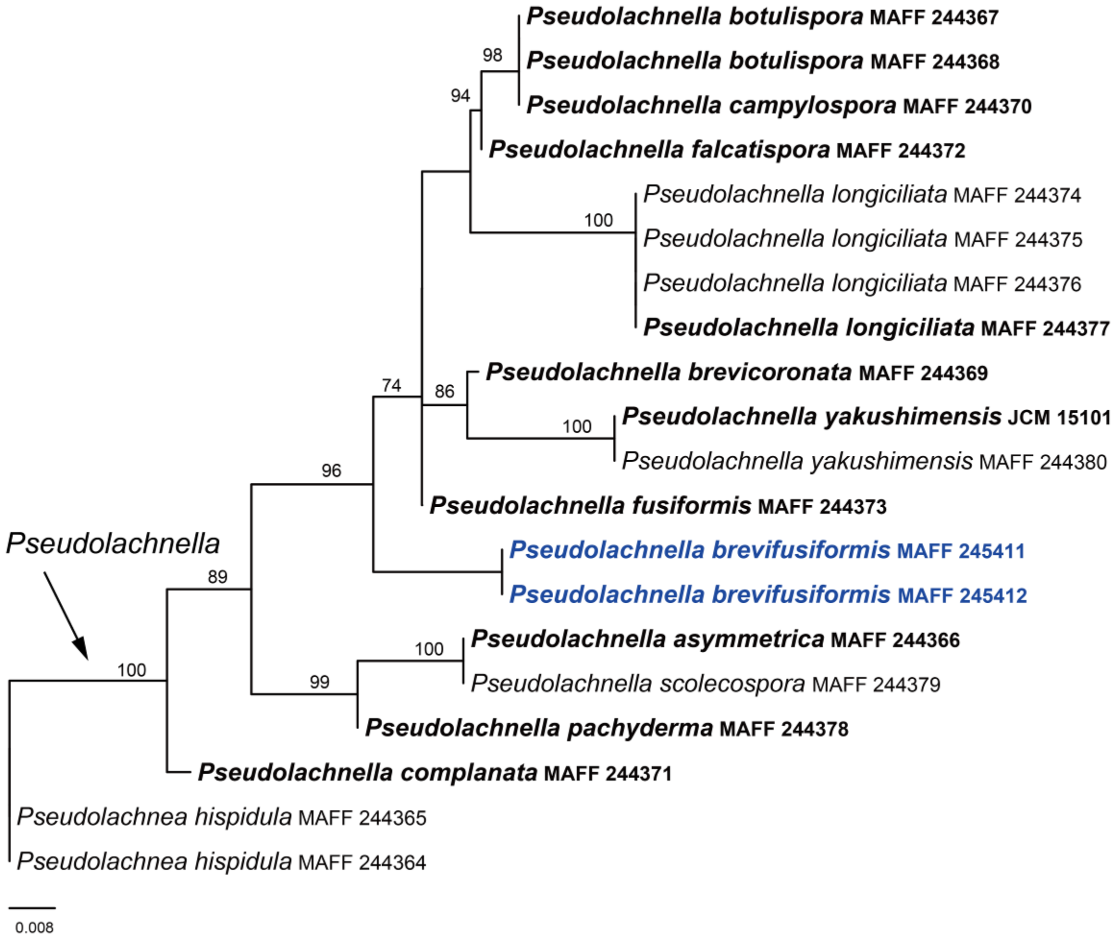


Fig. 48 Maximum-likehood tree of *Pseudolachnella* spp. based on analysis of ITS sequence data. Bootstrap values greater than 50 % are presented at the nodes. New taxa are in blue extypes in bold.

292. *Pseudolachnella brevifusiformis* A. Hashim. & Kaz. Tanaka, ***sp. nov.***

MycoBank number: MB 815299, *Facesoffungi number*: FoF 02029, Fig. 49

Etymology: named after its resemblance to *Pseudolachnella fusiformis*, but with smaller conidia.

Holotype: HHUF 30495

Saprobic on dead sheath of bamboo. **Sexual morph:** Undetermined. **Asexual morph**: *Conidiomata* stromatic, acervular, setose, shallow-cupulate, superficial, globose to oval, up to 295 *µm* high, (325–)450–700(–895) *µm* diam., scattered to occasionally 2–5 grouped, conical in sectional view; basal stroma 6.5–15 *µm* thick, composed of brown, globose, thick-walled, 2–2.5 *µm* diam. cells; excipulum 30–44.5(–50) *µm* thick, poorly developed, composed of globose, pale brown cells. *Setae* marginal, cylindrical, straight to slightly curved, aseptate, brown to dark brown, thick-walled, (315–)380–520 *µm* long, acute and 2–3.5 *µm* wide at the apex, 3–4 *µm* wide at the base. *Conidiophores* absent. *Conidiogenous cells* phialidic, cylindrical to lageniform, hyaline, smooth, 6.5–14 × 1.5–2.5 *µm*. *Conidia* (9.5–)10.5–18(–19) × 2–3.5 *µm* ($\bar{x}$ = 14 × 2.9 *µm*, n = 78), L/W 3.4–7.6(–8.7) ($\bar{x}$ = 5, n = 78), (1–)3-septate, clavate to cylindrical, obtuse at the apex, truncate at the base, hyaline, smooth, bearing (2–)3–6 unbranched appendages at each end; apical appendage (2.5–)3–6 *µm* long ($\bar{x}$ = 4.3 *µm*, n = 61), central; basal appendage (2.5–)3–5.5(–6.5) *µm* long ($\bar{x}$ = 4 *µm*, n = 61), eccentric.

Material examined: JAPAN, Okinawa, Kunigami, Yona, Mt. Fuenchiji, on dead sheath of *Pleioblastus linearis*, 19 May 2015, collector K. Tanaka et al., KT 3536 (HHUF 30495, **holotype**); ex-type living culture, MAFF 245411; *ibid*., KT 3537 (HHUF 30496, **paratype)**; ex-paratype living culture, MAFF 245412.

Notes: In terms of the similar conidial size and multiple conidial appendages, *Pseudolachnella brevifusiformis* resembles *P. fusiformis*, but can be distinguished from the latter by its smaller conidia (vs. 15–20 × 4–6.5 *µm*; Hashimoto et al. 2015b) in addition, there were 25 base differences with 12 gaps in their ITS sequence data.

Pseudolachnella brevifusiformis was collected from *Pleioblastus linearis*. *Pseudolachnella ryukyuensis* was also recorded from same host plant (Hino and Katumoto 1958; Nag Raj 1993). Morphologically, *P. brevifusiformis* has smaller conidia, as compared with those of the latter (vs. 30–40 × 2.5–3 *µm*; Nag Raj 1993).

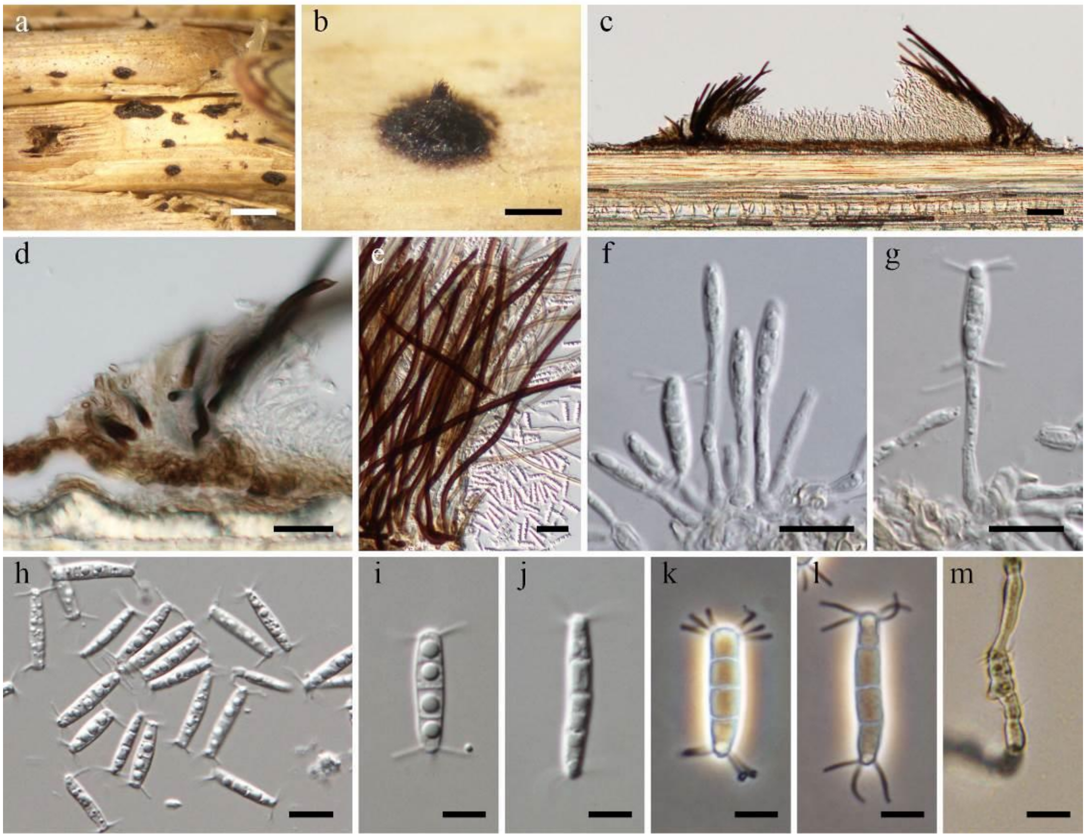


Fig. 49 ***Pseudolachnella brevifusiformis*** **a, b** Appearance of conidiomata on substrate **c** Conidioma in longitudinal section **d** Excipulum of conidioma **e** Conidiomatal setae **f, g** Conidiogenous cells and immature conidia **h–l** Conidia **m** Germinating conidium **a–d**, **i**, **k**, **m** from HHUF 30495 **(holotype)**; **e–h**, **j**, **l** from HHUF 30496 **(paratype)**. Scale bars: a = 1 mm, b = 250 *µm*, c = 50 *µm*, d, e = 20 *µm*, f–h, m = 10 *µm*, i–l = 5 *µm*.

Diaporthales

Gnomoniaceae

The family *Gnomoniaceae* was established by Winter (1886) based on the genus *Gnomonia*. *Gnomoniaceae* is simialr with *Obryzaceae*, which is considered to be a lichenicolous family, while *Gnomoniaceae* is a well-known plant pathogenic family (McNeill et al. 2006). Hawksworth and Eriksson (1988) proposed that the name *Obryzaceae* should be rejected to conserve *Gnomoniaceae* and the proposal was accepted (McNeill et al. 2006). *Gnomoniaceae* is characterised by immersed, rarely erumpent or superficial astromatic ascomata, arranged solitary, or aggregated with a rudimentary stroma, dark brown to black, and generally soft-textured, and pseudoparenchymatous and thin-walled, with necks. Generally the asci have a distinct apical ring (Sogonov et al. 2008). Species of this family are found in herbaceous plant material, especially in leaves, twigs or stems, rarely in bark or wood (Sogonov et al. 2008).

Phragmoporthe Petr.

The genus *Phragmoporthe* was introduced based on *P. ploettneriana* (Henn.) Petr. as the type species (Petrak 1934). *Phragmoporthe* is characterised by multi-septate ascospores and 8-spored asci (Sogonov et al. 2008). The closest genus to *Phragmoporthe* is *Ditopella*, which differs from *Phragmoporthe* in having 1-septate, rarely aseptate ascospores and polysporous asci (Sogonov et al. 2008). The phylogenetic tree is presented in Fig. 50.

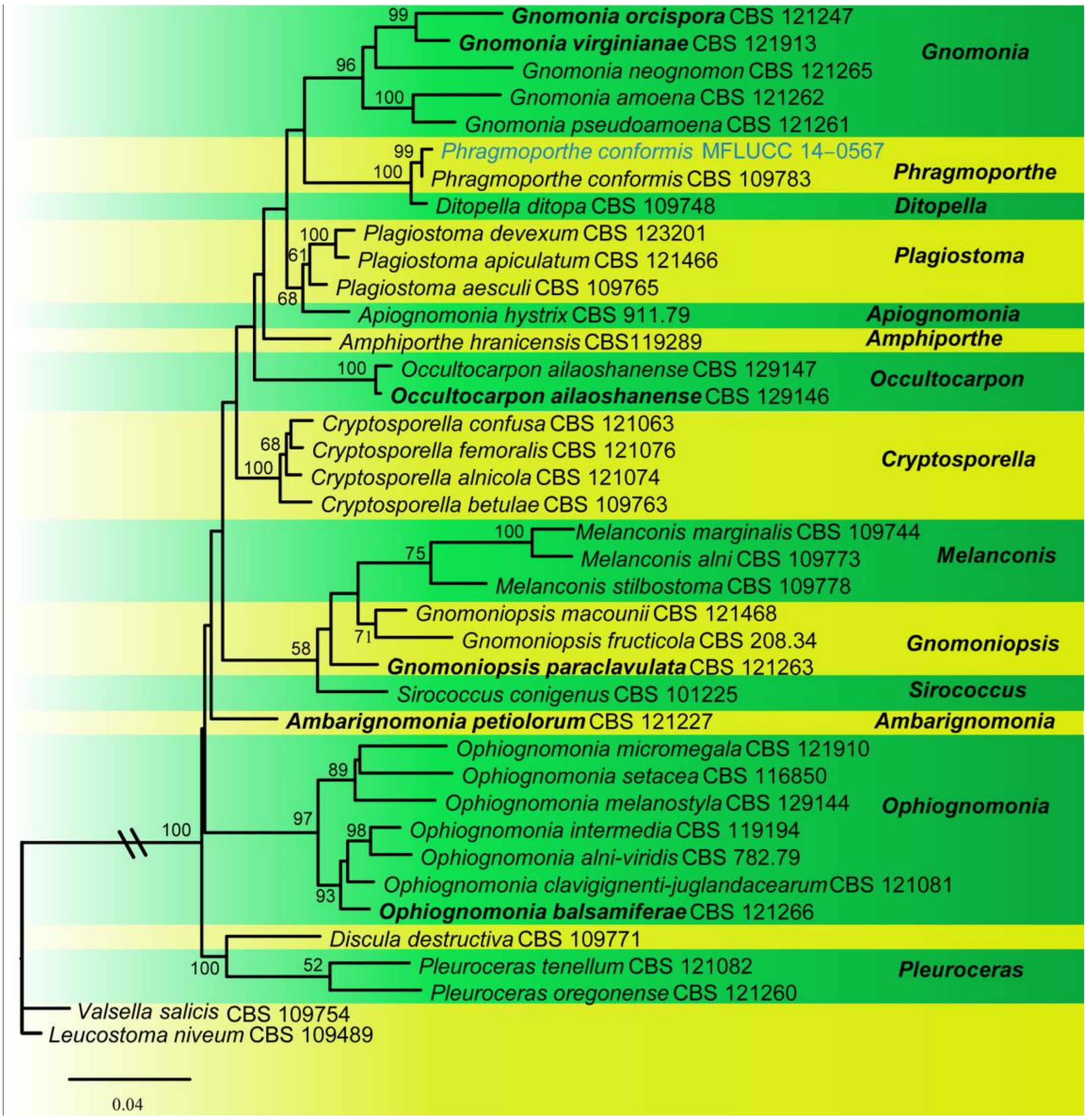


Fig. 50 Maximum Likelihood tree resulting from analysis of combined LSU, ITS and TEF-1α sequence data for taxa of the family *Gnomoniaceae*. Maximum likelihood bootstrap support values greater than 50% are shown near the nodes. New taxa are in blue and ex-type strains in bold. The tree is rooted with *Valsella salicis* and *Leucostoma niveum*.

293. *Phragmoporthe conformis* (Berk. & Broome) Petr., Annls mycol. 39(4/6): 285 (1941)

Facesoffungi number: FoF 01794, Fig. 51

Basionym

Sphaeria conformis Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 9: 325 (1852)

Synonym

= *Gnomonia conformis* (Berk. & Broome) Ferd. & Winge

= *Metasphaeria conformis* (Berk. & Broome) Sacc., Miscell. mycol. 1: 6 (1884)

= *Calospora conformis* (Berk. & Broome) Starbäck, Bih. K. svenska VetenskAkad. Handl., Afd. 3 15(no. 2): 16 (1889)

= *Sphaeria ditopa* f. octospora Cooke

= *Valsa alnicola* Cooke & Massee, Grevillea 16(no. 78): 47 (1887)

= *Calospora alnicola* (Cooke & Massee) Sacc., Syll. fung. (Abellini) 9: 872 (1891)

= *Phragmoporthe alnicola* (Cooke & Massee) Petr., Annls mycol. 38(2/4): 209 (1940)

= *Sphaerulina* alni A.L. Sm., Trans. Br. mycol. Soc. 6(2): 151 (1918)

Saprobic on *Alnus glutinosa* L. **Sexual morph** Appearing as conical, pustules on the host surface. *Ascomata* perithecial, minutely stromatic, immersed, erumpent. *Perithecia* 700–770 *µm* diam. (n = 20), solitary, immersed in or directly below the host epidermis, globose, membranous, dark brown to black, with a periphysate ostiole. *Peridium* 14–38 *µm* ($\bar{x}$ = 22 *µm*, n = 10) wide, comprising 7–15 cell layers, outer layers heavily pigmented, thin-walled, comprising dark brown cells of *textura angularis*, inner layers composed of hyaline to brown, thin-walled, flat cells of *textura angularis*. *Hamathecium* lacking paraphyses. *Asci* 60–80 × 17–24 *µm* ($\bar{x}$ = 72 × 19.5 *µm*, n = 30), 8-spored, unitunicate, clavate, straight, short pedicellate, apically rounded or truncate, with a refractive, J- apical ring. *Ascospores* 19–24 × 6.5–8 *µm* ($\bar{x}$ = 22 × 7 *µm*, n = 50), multi-seriate, fusiform, mainly with 3 transverse septa, occasionally constricted at septum, hyaline, smooth and thick-walled, without a mucilaginous sheath or appendages. **Asexual morph** Undetermined

Culture characteristics: Colonies growing on MEA, slow growing, reaching 4 cm diam. in 21d at 16 °C on MEA, white, dense, moderate aerial mycelium on the surface, underneath similar in colour, margins even.

Material examined: ITALY, Forlì-Cesena Province, Lago Pontini-Bagno di Romagna, dead branches of *Alnus glutinosa* (L.) Gaertn. (*Betulaceae*), 26 May 2014, Erio Camporesi, IT 1892 (MFLU 15–2662 **reference specimen designated here**), also in HKAS 92498, living culture, MFLUCC 14–0567.

Notes: The putatively named strain of *Phragmoporthe conformis* (CBS 109793) clustered with our newly collected strain (MFLU 14–0567), collected from Italy, on a dead a stem of *Alnus glutinosa*. Berkeley and Broome (1852) originally described *Phragmoporthe conformis* as *Sphaeria conformis* on *Alnus* spp. from the UK. Later Petrak (1941) synonymized *Sphaeria conformis* under *Phragmoporthe conformis*. The ascomata, size of asci and ascospores of our strain are typical of *P. conformis* (Petrak 1941) and the molecular data is identical to CBS 109793. We therefore designate our collection as a reference specimen of *P. conformis* to stabilize the taxonomy of the genus.

Fig. 51 ***Phragmoporthe conformis*** (MFLU 15–2662, **reference specimen**) **a, b** Appearance of ascomata on host substrate **c** Section of ascoma **d** Transverse section through ostiole **e, f** Periphyses **g** Close up of peridium **h–j** Asci **k** Close up of apical ascus strained in Melzer's reagent **l–n** Ascospores **o** Germinating spore **p, q** Colonies growing on MEA. Scale bars: c = 500 *µm*, d, e = 100 *µm*, f–j = 50 *µm*, k = 20 *µm*, l–o = 10 *µm*.

Valsaceae

The family *Valsaceae* was introduced by Tulasne and Tulasne (1861) and placed in *Diaporthales* by Barr (1978). Most of *Valsaceae* species are plant pathogens causing canker and dieback disease, with damage to several economic crops worldwide (Adams et al. 2005; Fan et al. 2014a, b, 2015a, b; Ariyawansa et al. 2015b). *Valsaceae* was restricted to *Cytospora* (asexual morph), *Valsa*, *Leucostoma*, *Valsella*, and *Valseutypella*; sexual morph for the last four genera (Fries 1823; Saccardo 1884; Gvritishvili 1982; Spielman 1985; Adams et al. 2002, 2005; Castlebury et al. 2002; Bulgakov 2010; Yang et al. 2015). However, all sexual genera were synonymized under *Valsa* as a subgenus or species without additional infrageneric rank (Adams et al. 2005). According to the International Code of Nomenclature for Algae, Fungi, and Plants (ICN) in 2011, a single name is needed for a biological species and for genera, the older and more commonly encountered genus *Cytospora* (1818) was chosen over that of its sexual morph, *Valsa* (1849), for placement on the list of protected fungi (Adams et al. 2005; Fotouhifar et al. 2010, Fan et al. 2015a; Wingfield et al. 2012; Crous et al. 2015e; McNeill et al. 2012; Rossman et al. 2015). *Cytospora* is characterized by single or labyrinthine locules, filamentous conidiophores (or clavate to elongate obovoid asci), and allantoid, hyaline conidia (Spielman 1983, 1985; Adams et al. 2005). In moist conditions, conidia emerge from the fruiting bodies as yellow masses, and become orange to red gelatinous tendrils later (Adams et al. 2005, 2006). The genus *Cytospora* comprised 110 species (Kirk et al. 2008), however, 572 epithets are recorded in Index Fungorum (2015). Ex-type sequence data, is however, available for a few species. Thus it is difficult to identify species (Liu et al. 2015; Ariyawansa et al. 2015b). A systematic account of the genus *Cytospora* is needed to clarify cryptic species in *Cytospora* (Adams et al. 2002; Fotouhifar et al. 2010; Hyde et al. 2010, 2014; Fan et al. 2015a, b; Liu et al. 2015; Ariyawansa et al. 2015b, Yang et al. 2015). The phylogenetic trees for *Cytospora* are presented in Figs 52 and 53.

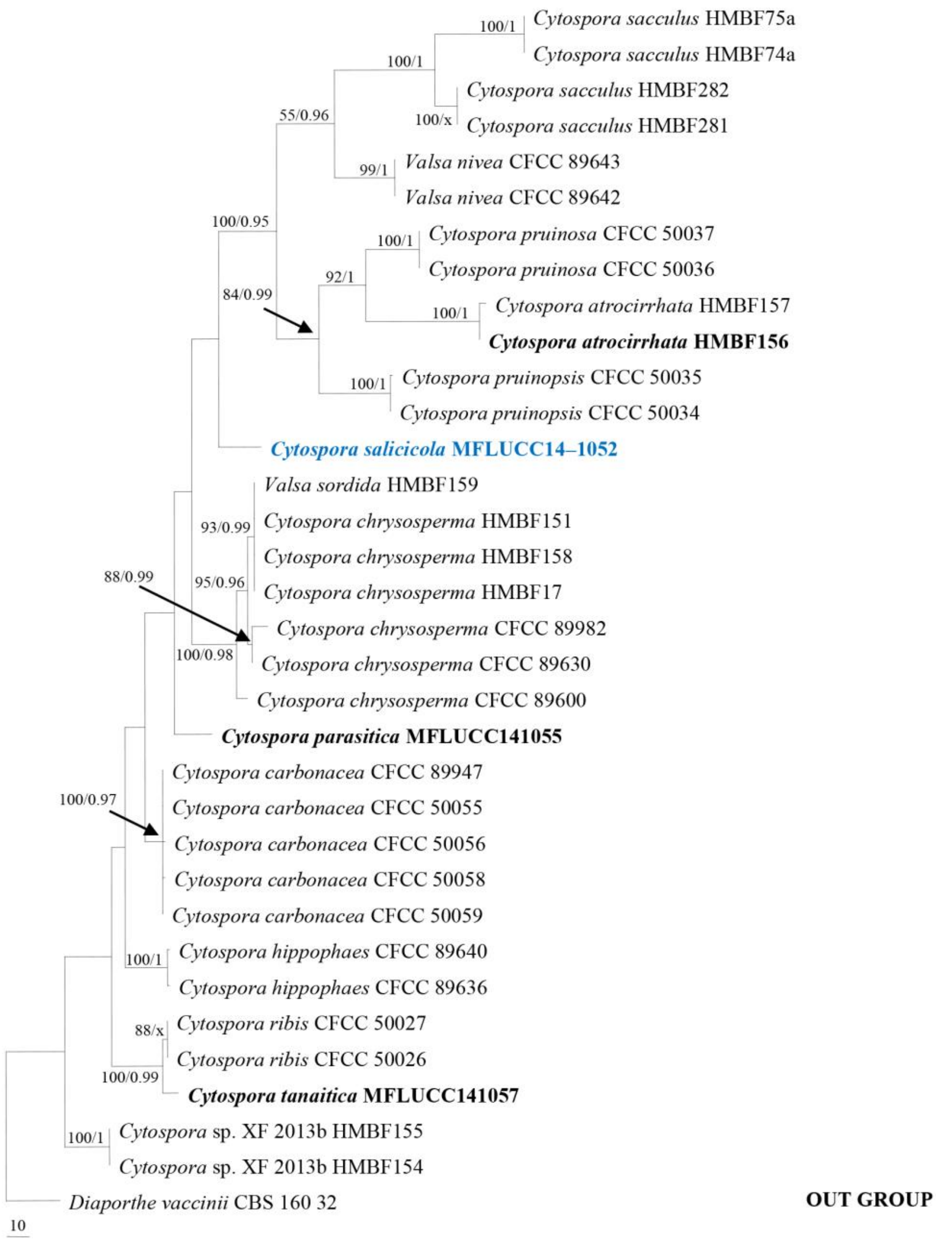


Fig. 52 Maximum Parsimony (MP) majority rule consensus tree for the analyzed *Cytospora* isolates based on a combined dataset of ACT, ITS and LSU sequence data. MP bootstrap support values higher than 50% and Bayesian posterior probabilities (PP) above 95% (MP/PP). The tree is rooted with *Diaporthe vaccinii* (CBS 160.32). The strain numbers are mentioned after the species names. The species obtained in this study is in blue bold and ex-type strains in black bold.

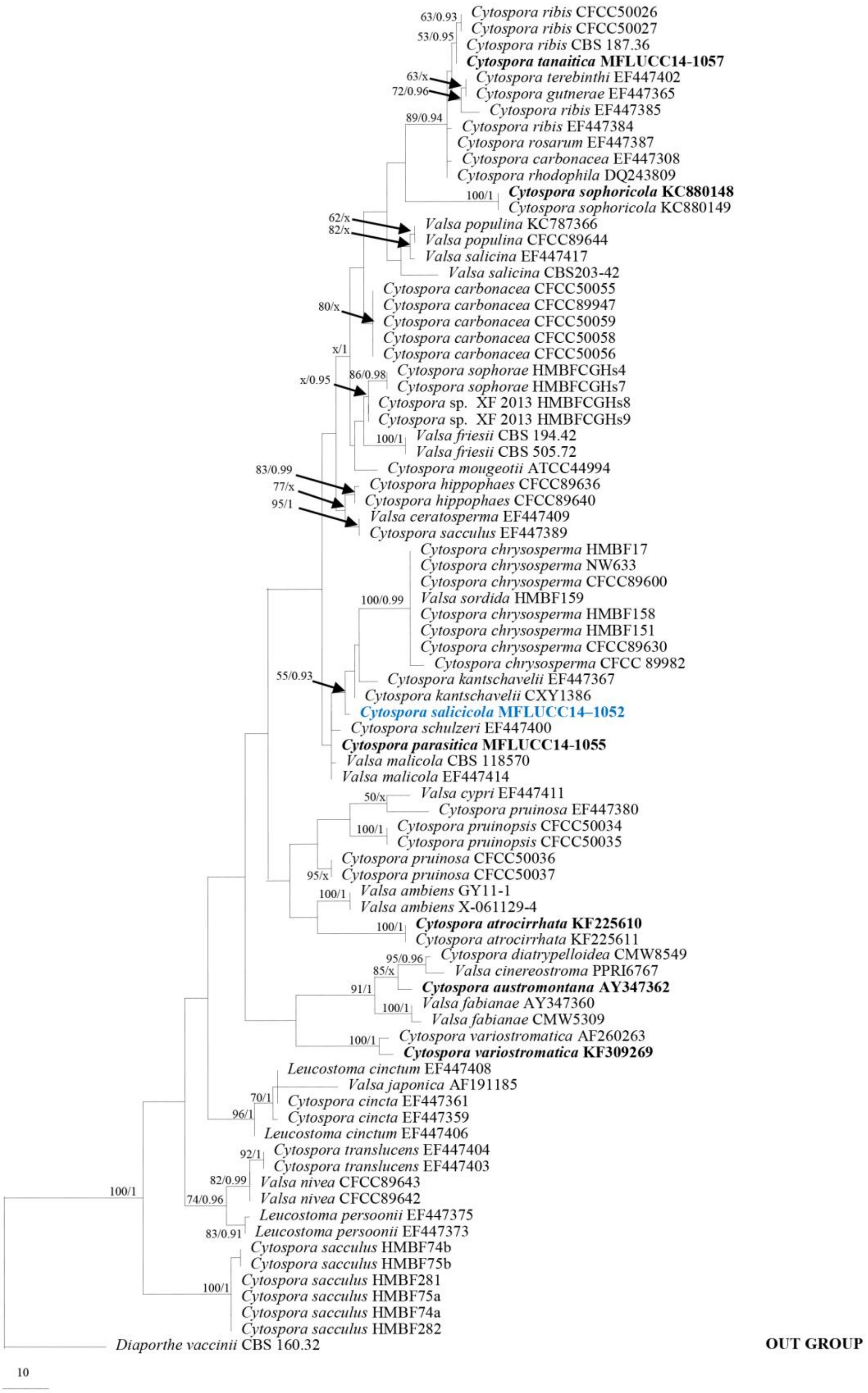


Fig. 53 Phylogenetic tree based on an alignment of the sequences of the ITS sequence data for *Cytospora*, *Leucostoma*, and *Valsa* species, which was generated using the MP and Bayesian posterior probabilities (PP) in PAUP. Numbers separated by a slash represent MP bootstrap values >50% and Bayesian posterior probabilities (PP) above 95% are given at the nodes

(MP/PP). The tree is rooted in outgroup taxon *Diaporthe vaccinii* (CBS 160.32). New strains are in blue bold and ex-type strains are in black bold.

294. *Cytospora salicicola* C. Norphanphoun, Bulgakov & K.D. Hyde, ***sp. nov***

Index Fungorum number: IF 551803, *Facesoffungi number*: FoF 01768, Fig. 54

Etymology: Named after the host genus on which the fungus occurs.

Holotype: MFLU 14–0785

Pathogen causing dieback of twigs and branches of *Salix alba* L. *Conidiomata* 500–300 *µm* diam. ($\bar{x}$ = 400 × 350 *µm*, n = 10), pycnidial, solitary, immersed in host tissue, unilocular, dark brown, ostiolate. *Ostiole* 150–40 *µm* diam. ($\bar{x}$ = 145 × 40 *µm*, n = 10), at the same level as the disc surface. *Peridium* comprising a few to several layers of cell of *textura angularis*, with inner most layer thin, hyaline, outer layer brown to dark brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* blastic, enteroblastic phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth. *Conidia* (3.4–) 4.3–5.3 × 0.7–0.8 (–1) *µm* ($\bar{x}$ = 4.3 × 0.8 *µm*, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled. **Sexual morph** Undetermined.

Culture characteristics: Colonies on PDA, reaching 3.5 cm diam. after 10 days at 25 °C, producing dense mycelium, circular, rough margin white, after 5 days, flat or effuse on the surface, without aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, riparian forest, on dead twigs and branches of *Salix alba* L. (*Salicaceae*), 21 May 2014, T.S. Bulgakov (MFLU 14–0785, **holotype**; PDD, **isotype**); ex-type-living cultures, MFLUCC 14–1052, ICMP.

Notes: *Cytospora salicicola* belongs in *Valsaceae* based on morphology and phylogeny. The new species has immersed, uniloculate conidiomata, with a single ostiole and shares common walls with the host tissue. *Cytospora salicicola* is most similar to *C. schulzeri* Sacc. & P. Syd. in conidia size [4.5–8(6.3) × 0.9–1.3(1.1) *µm*]. It however, differs in having a single locule, while *C. schulzeri* has multiple locules with 2-11 ostioles per disc (Mehrabi et al. 2011). Phylogenetic analyses, using ITS sequence data (Fig. 53) indicate that *C. salicicola* can be distinguished from other species within the genus *Cytospora*. The tree using ACT, ITS and LSU sequence data (Fig. 52) demonstrate that *C. salicicola* separates from other sequenced species in *Cytospora*, and should be introduced as a new species.

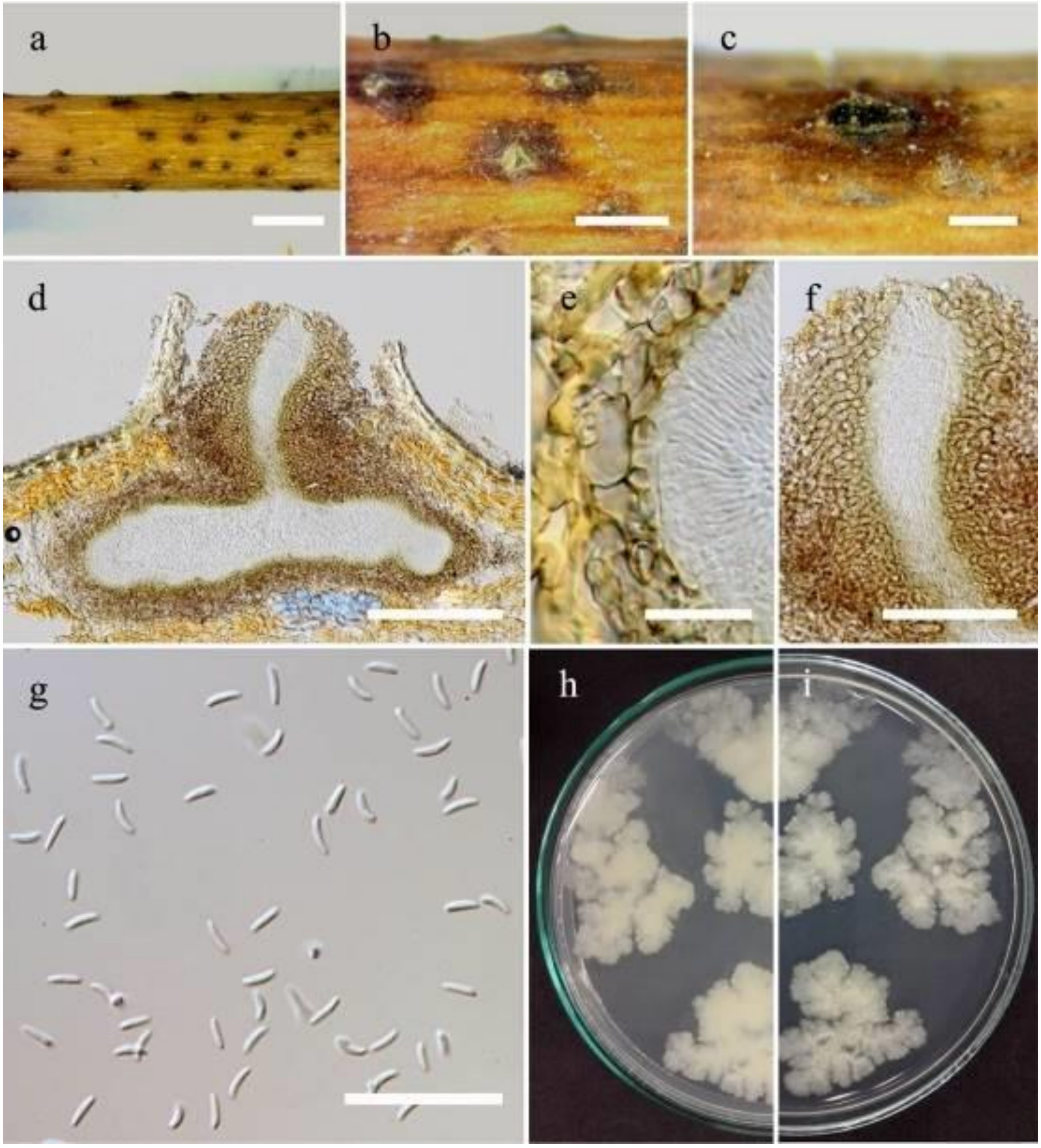


Fig. 54 ***Cytospora salicicola*** (**holotype**) **a** Appearance of fruiting bodies in wood **b** Fruiting bodies on substrate **c** Surface of fruiting bodies **d** Cross section of the conidioma **e** Peridium **f** Ostiole of conidioma **g** Conidia **h–g** Colonies on PDA (P from below). Scale bars: a = 2 mm, b–c = 1 mm, d = 100 *µm*, e = 10 *µm*, f = 50 *µm*, and g = 20 *µm*.

Glomerellales

Chadefaud (1960) proposed the order "*Glomerellales*" to accommodate a group of endophytic and pathogenic fungi with ascomata varying from endostromatal to apostromatal and ascospores that are often unicellular and hyaline. Réblová et al. (2011) validated this order and accepted three families namely *Australiascaceae*, *Glomerellaceae* and *Reticulasceae* in the class *Sodariomycetes*. This introduction was based on analysis of ITS, LSU, and SSU datasets, and a combined data set of LSU SSU and RPB2. Maharachchikumbura et al. (2015) included *Plectosphaerellaceae* in to this order based on a combined data set of LSU SSU TEF and RPB2. The phylogenetic tree for *Colletotrichum* is presented in Fig. 55.

Glomerellaceae

The family *Glomerellaceae* was invalidly published by Locquin (1984), validated in Zhang et al. (2006), and it was accepted as one of the three families of *Glomerellales* in Réblová et al. (2011). *Glomerellaceae* is a monotypic family characterized by the *Glomerella* sexual morph and the *Colletotrichum* asexual morph (Maharachchikumbura et al. 2015).

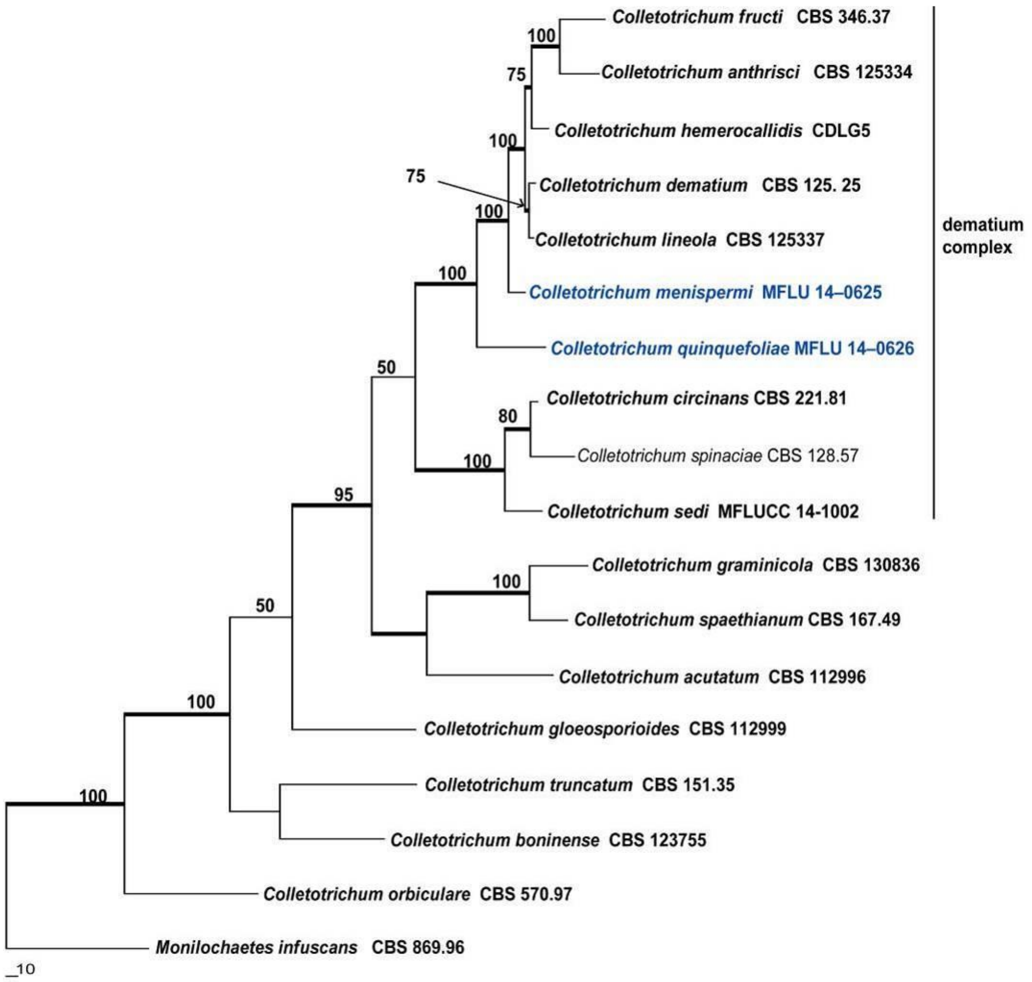


Fig. 55 Phylogram generated from parsimony analysis based on combined ITS, GADPH, CHS, ACT and β-tubulin sequence data of *Colletotrichum*. Parsimony bootstrap support values greater than 50 % are indicated above or below the nodes, and branches with Bayesian posterior probabilities greater than 0.95 are given in bold. The ex-type strains are in bold; the new isolates are in blue. The tree is rooted with *Monilochaetes infuscans* CBS 869.96.

Colletotrichum Corda

Réblová et al. (2011) placed *Colletotrichum* in *Glomerellaceae*, and its placement has been further confirmed by the study of Maharachchikumbura et al. (2015). In the latter study the use of the name *Colletotrichum* over its sexual name

Glomerella was suggested. Hyde et al. (2009), Cai et al. (2009) and Cannon et al. (2012) have treated this genus subsequently, and the most recent treatment is of Hyde et al. (2014). This genus comprises plant pathogens, endophytes and saprobes (Cannon et al. 2012).

295. *Colletotrichum menispermi* Chethana, Jayawardena, Bulgakov & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551744, *Facesoffungi number*: FoF 01648, Fig. 56

Etymology: The specific epithet *menispermi* is named after the host genus *Menispermum* from which the taxon was collected.

Holotype: MFLU 14–0625

Saprobic on dead twigs of *Menispermum dauricum* DC. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 180–265 *µm* ($\bar{x}$ = 229 *µm*, n = 10) diam., solitary, acervulus, black, oval. *Setae* 59–109 *µm* long, pale to dark brown, smooth-walled, straight, 2–3-septate, base cylindrical, 4–9 *µm* diam. and rounded apex. *Conidiophores* simple, to 33 *µm* long, hyaline to pale brown, smooth-walled. *Conidiogenous cells* reduced. *Conidia* 6–18 × 2–5 *µm* ($\bar{x}$ = 12 × 4 *µm*, n = 20), L/W ratio 3.0, hyaline, aseptate, smooth-walled, both sides gradually tapering towards the round to slightly acute apex, truncate base and guttulate. *Appresoria* not observed.

Material examined: RUSSIA, Rostov region, Rostov-on-Don city, Botanical Garden of Southern Federal University, introductional nursery, on dead twigs of *Menispermum dauricum* (*Menispermaceae*), 5 March 2014, T.S. Bulgakov, (MFLU 14–0625, **holotype**), **(isotype** in GZAAS, under the code of GZAAS 15–0102).

Note: Based on phylogenetic analyses and morphological comparison *Colletotrichum menispermi* clusters in the *Colletotrichum dematium* species complex, forming a separate branch with 100 % bootstrap support and 1.00 Bayesian posterior probabilities. *Colletotrichum menispermi* separates from *C. quinquefoliae* with 100 % bootstrap support and 1.00 Bayesian posterior probabilities. Morphologically it differs from *C. quinquefoliae* in having larger conidiomata with minute 2–3-septate setae which cannot be observed by unaided eye.

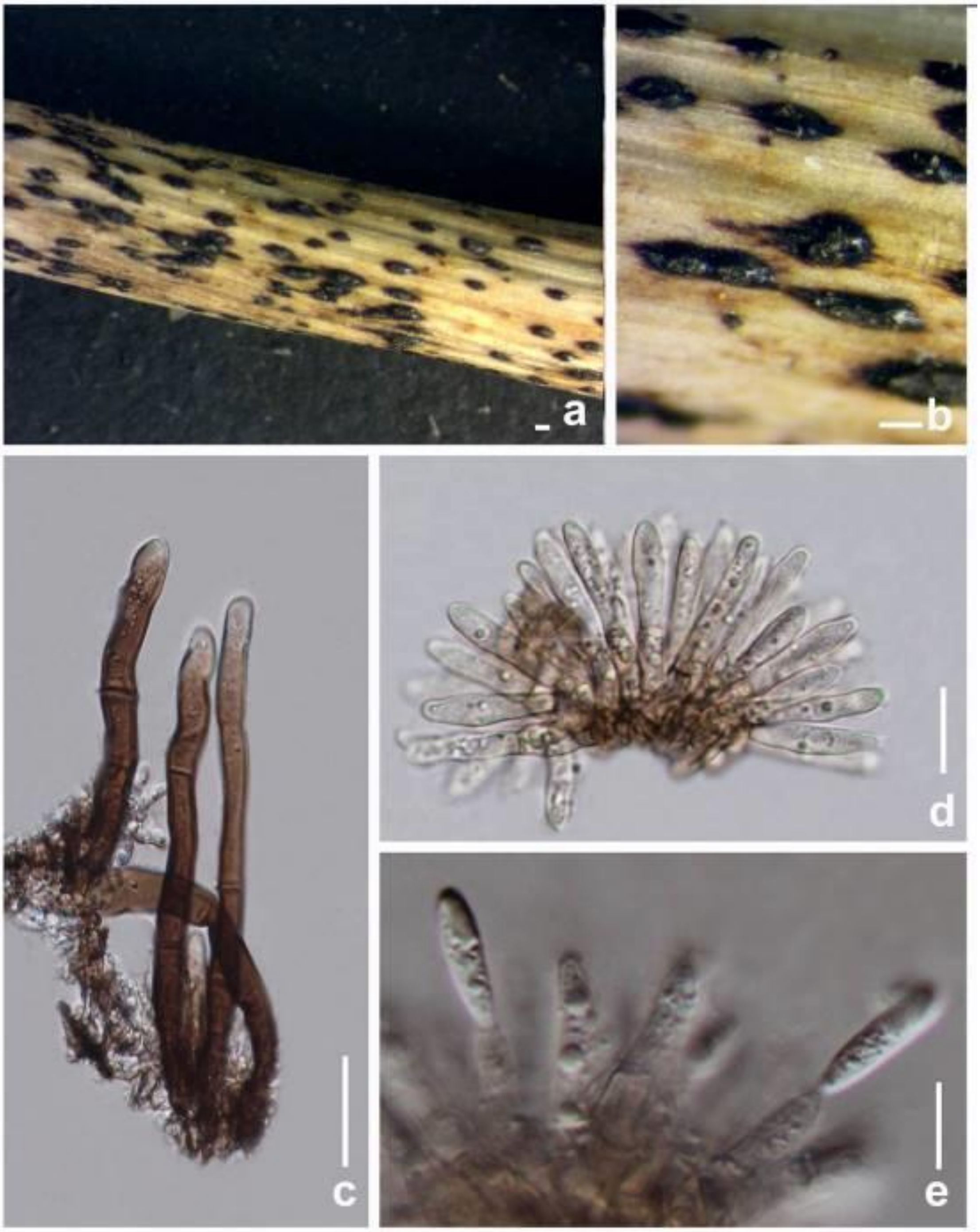


Fig. 56 ***Colletotrichum menispermi*** **(holotype)** **a** Appearance of the conidiomata on the host substrate **b** Close up of black conidioma **c** Brown 4-septate setae **d** Hyaline conidiogenous cells **e** Hyaline conidia. Scale bars: a, b = 100 *µm*, c–e = 10 *µm*.

296. ***Colletotrichum quinquefoliae*** Jayawardena, Bulgakov & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551745, *Facesoffungi number*: FoF 01649, Fig. 57

Etymology: The specific epithet *quinquefoliae* is named after the host *Parthenocissus quinquefolia* (L.) Planch. from which the taxon was collected.

Holotype: MFLU 14–0626

Saprobic and weak pathogen on dying and dead leafstalks, twigs and tendrils of *Parthenocissus quinquefolia*. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 267–517 *µm* ($\bar{x}$ = 410 *µm*, *n* = 10) diam., black, acervulus, oval, solitory, gregarious. *Setae* straight or ± bent, abundant, dark brown, becoming paler towards the apex, opaque, smooth-walled, septa difficult to distinguish, 1–5-septate, 58–258 *µm* long, base cylindrical, 6.8–10.5 *µm* diam., tip somewhat acute. *Conidiophores* medium brown, smooth–walled, simple, to 35 *µm* long. *Conidiogenous cells* 7.3–12.8 × 1.4–3.3 *µm* ($\bar{x}$ = 8.5 × 2.5 *µm*, *n* = 20), hyaline to pale brown, smooth–walled, cyllindrical to slighty inflated, opening 0.5–1 *µm* diam., collarette or periclinal thickening not observed. *Conidia* 5.9–15.8 × 2.2–5.2 *µm* ($\bar{x}$ = 9.9 × 3.3 *µm*, *n* = 40), L/W ratio 3.0, hyaline, smooth or verruculose, aseptate, curved, both sides gradually tapering towards the round to slightly acute apex and base, guttulate.

Material examined: RUSSIA, Rostov region, Rostov-on-Don city, Botanical Garden of Southern Federal University, Higher Park, underwood, on *Parthenocissus quinquefolia* (*Vitaceae*), 5 March 2014, T.S. Bulgakov (MFLU 14–0626, **holotype**), **(isotype** in GZAAS, under the code of GZAAS 15–0101).

Notes: *Colletotrichum dematium* species complex is mainly characterized by having curved conidia (Damm et al. 2009). *Colletotrichum quinquefoliae* falls within the *Colletotrichum dematium* species complex and forms a separate clade which is supported by 100% bootstrap value and 1.00 Bayesian posterior probability (Fig. 55). This species differ from *C. menispermi* in having larger conidiomata, 1–5-septate, long setae, with a larger base and conidia with an acute base. This species differs from *C. circinans* and *C. spinaceae* in having longer setae with 1–5 septa and simple conidiophores.

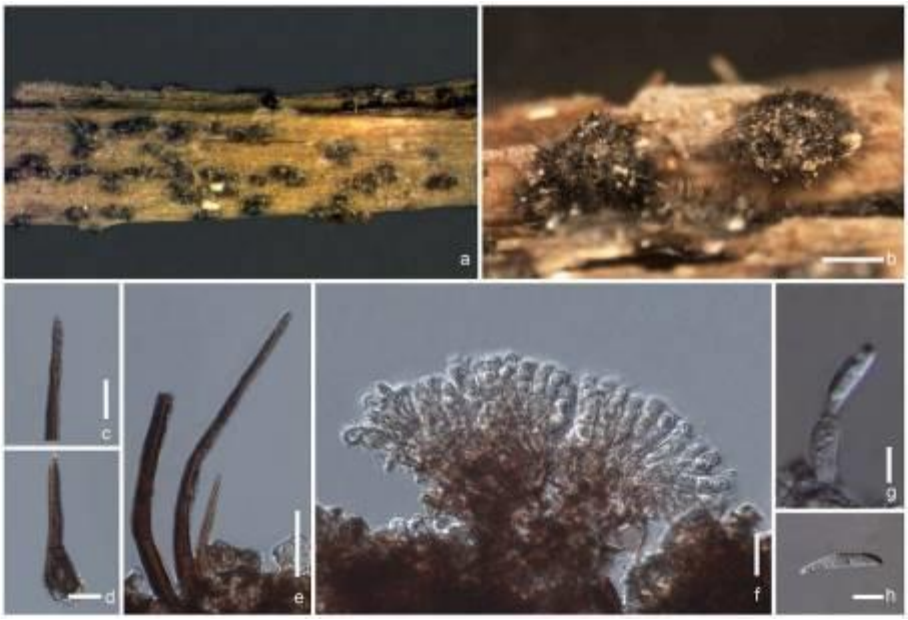


Fig. 57 ***Colletotrichum quinquefoliae*** (**holotype**) **a** Conidiomata on host **b** Black acervuli with setae **c** Acute tip of the setae **d** Base of the setae **e** Seta **f** Conidiophores **g** Conidiogenous cell **h** Conidium Scale bars: b = 200 *µm*, c = 50 *µm*, d = 5 *µm*, e = 150 *µm*, f = 20 *µm*, g–i = 5 *µm*.

Hypocreales

Bionectriaceae

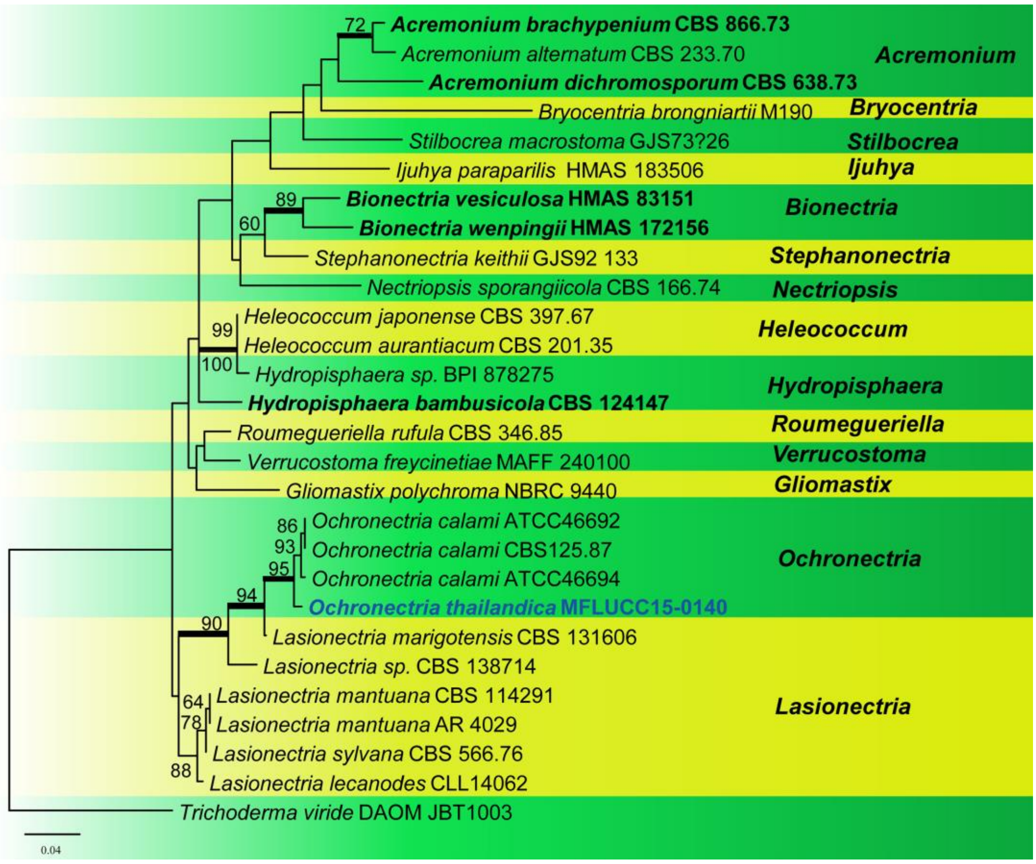


Fig. 58 Phylogram generated from maximum likelihood analysis based on LSU sequence data of the family *Bionectriaceae*. New taxa are in blue ex-type strains are in bold. The tree is rooted with *Trichoderma viride*.

Ochronectria

Ochronectria was established by Rossman and Samuels (1999) and is typified by *Ochronectria calami* (Henn. & E. Nyman) Rossman & Samuels. The genus has subglobose to globose ascomata, that are cupulate when dry, a three layered peridium, clavate asci and fusiform ascospores with guttules (Rossman et al. 1999; Lechat 2010). Ochronectria includes two species epithets (Index Fungorum 2016).

297. *Ochronectria thailandica* Q.J. Shang, D.Q. Dai & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551918, *Facesoffungi number*: FoF 01815, Fig. 59

Etymology: The specific epithet "*thailandica*" refers to the country where the fungus was first collected.

Holotype: MFLU 16–0030

Saprobic on bark. **Sexual morph** *Ascomata* 71–189 *µm* high, 78–223 diam., solitary to gregarious, superficial, black, globose, cup-like, or collapsing laterally when dry. *Ostioles* brown to dark brown, 28–32 *µm* diam., with paraphyses. *Peridium* 31–52 *µm* wide, composed of three layers, inner 1–3 layers, comprising of hyaline, thin-walled, elongated cells, central 3–4 layers of yellow to brown cells arranged in a *textura angularis*, outer 5–6 layers, comprising dark brown to black, thick-walled cells of *textura angularis* to *globosa*, having yellow oily droplets between the cells. *Hamathecium* comprising 1.2–3 *µm* wide, hyaline, aseptate paraphyses. *Asci* 34–56 × 6–9 *µm* ($\bar{x}$ = 45 × 7 *µm*, n = 30), 8-spored, unitunicate, clavate, with short pedicel, slightly rounded to truncate at the apex. *Ascospores* 12–17 × 3–4 *µm* ($\bar{x}$ = 14 × 3 *µm*, n = 50), overlapping 2-seriate, fusiform, hyaline, 2-celled, straight to curved, smooth-walled, with small guttules. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h. Germ tubes produced from any cell. Colonies on MEA reaching 1.5–2 mm diam. after 7 d in the dark at 25 °C, edge entire, flat or effuse or umbonate, sparse, forming ascomata on MEA in the centre. After 7 d colonies white (n) above, from below reddish yellow (o).

Material examined: THAILAND, Chiang Rai, Mae Sai, Pong Ngam Village, Tham Pla Cave, on unidentificated wood in the water, 25 November 2014, Qiu Ju Shang, SHTM02–4 (MFLU 16–0030, **holotype)**, ex-type living culture, MFLUCC 15–0140, (**isotype** in KUN-HKAS, under the code of KUN-HKAS 93730), ex-living culture KUMCC 16-0001).

Notes: Based on phylogenetic analyses and morphological comparison, our isolate belongs to the genus *Ochronectria* in the family *Bionectriaceae*. The morphology of *Ochronectria thailandica* fits well with the description provided by Rossman and Samuels (1999). It differs from the type, *O. calami* (Henn. & E. Nyman) Rossman & Samuels and *O. courtecuissei* Lechat based on the size and colour of ascomata, peridium colour and number of septa and dimensions of the ascospores. *Ochronectria thailandica* has black ascomata, a peridium composed of black brown outer layers and yellow middle layers, while, *O. calami* has white or yellow to orange ascomata, a peridium composed of hyaline middle and outer layers, and *O. courtecuissei* has yellow to brown ascomata and a peridium composed of yellow to orange outer layers and hyaline middle layers (Rossman et al. 1999; Rossman et al. 2001; Lechat 2010). Furthermore, *O. thailandica*, which has 1-septate ascospores can be distinguished from *O. calami* which forms multi-septate ascospores. Phylogenetic analysis based on LSU sequence data of the family *Bionectriaceae* showed that *O. thailandica* is closely related to *Ochronectria calami*, forming a distinct lineage within the sclade (Fig. 58).

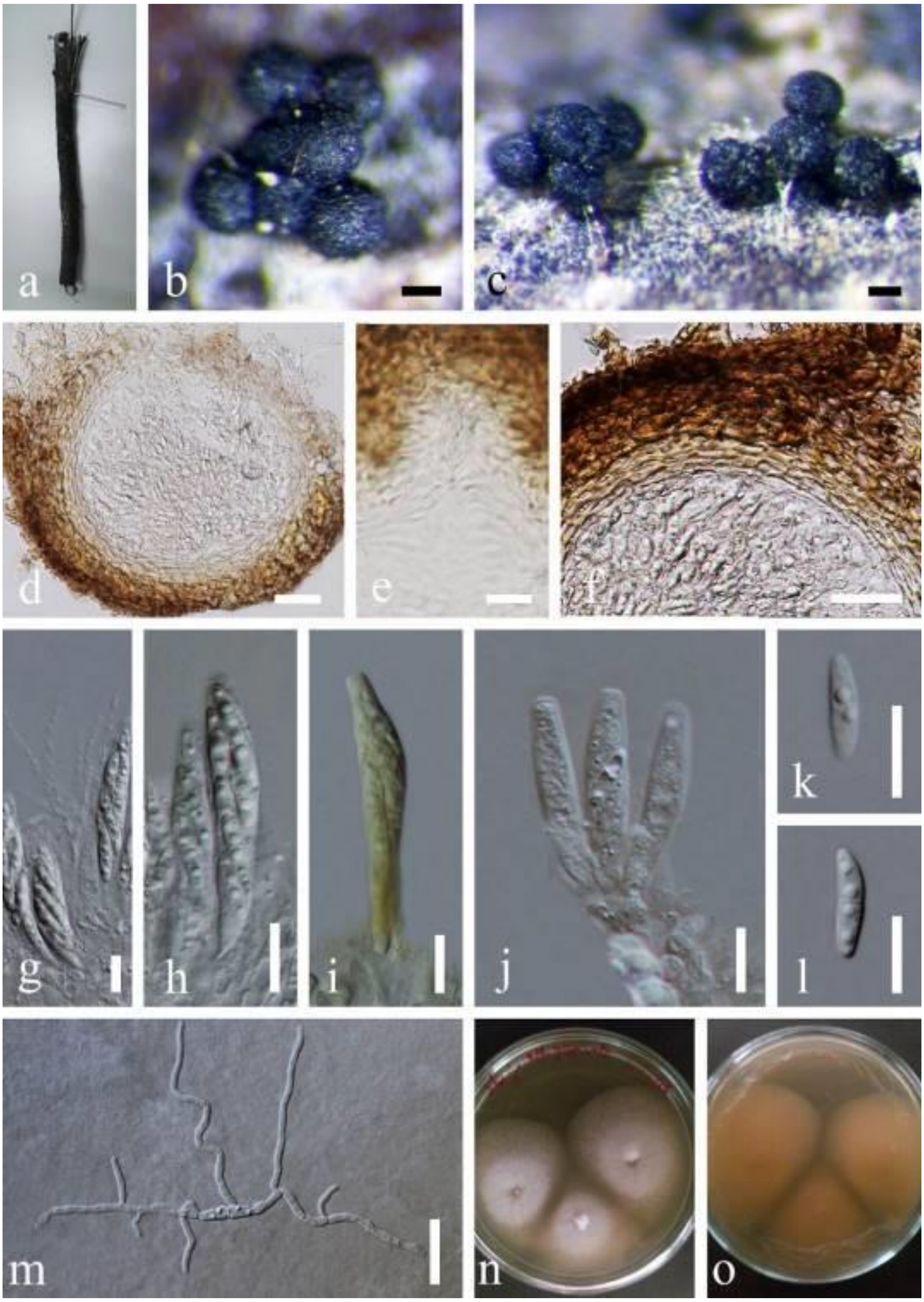


Fig. 59 ***Ochronectria thailandica*** (**holotype**) **a** Host **b**, **c** Ascomata on host **d** Vertical section of ascoma **e** Periphysate ostiole **f** Section of peridium **g** Paraphyses and asci **h**–**j** Asci; note **i** stained in Melzer's reagent **k, l** Ascospores **m** Germinating ascospore **n, o** Culture on MEA. Scale bars: b, c = 100 μm, d = 25 μm, e, g–l = 10 μm, f, m= 20 μm.

Clavicipitaceae

The family *Clavicipitaceae* (*Hypocreales*) is a very heterogeneous group of fungi that are associated with a broad range of invertebrate animals, plants and occasionally with other fungi (Sung et al. 2007, Schardl et al. 2014, Kepler et al. 2012). The plant-associated *Clavicipitaceae* includes mutualistic symbionts, such as the grass endophytes *Epichloë* and *Balansia*, as well as plant pathogens, many of which produce alkaloids (*e.g*. *Claviceps purpurea*) with diverse neurotropic effects on vertebrate and invertebrate animals, with important implications for human health, agriculture and food security (Spatafora et al. 2007). The invertebrate-associated *Clavicipitaceae* comprises many pathogens of scale insects and whiteflies, such as *Conoideocrella*, *Hypocrella*, *Moelleriella*, *Orbiocrella*, *Regiocrella*, and *Samuelsia* (Chaverri et al. 2008). *Paecilomyces*, *Pochonia* and *Metarhizium* are also other invertebrate-pathogens that infect a wide range of insect hosts (Kepler et al. 2014). The sexual morphs in this family produce various types of stromata and colors, but all produce filiform asci with ascospores that may or may not disarticulate into part-spores.

Moelleriella infects scale insects and white flies and was recently separated from the genus *Hypocrella* together with *Samuelsia* (Chaverri et al. 2008). The delimitation and separation of *Moelleriella* was based on molecular data and morphology: its ascospores disarticulate inside the ascus. The asexual morph of *Moelleriella* is *aschersonia*-like, i.e., it is similar to *Aschersonia sensu stricto* (sexual morph *Hypocrella sensu lato*; Chaverri et al. 2008). Species in *Aschersonia sensu lato* are characterized mostly by the shape and colour of the stromata that cover the hosts, pycnidium-like conidiomata, phialides, and presence or absence of paraphyses. These characters have been useful in distinguishing between subgenera of *Aschersonia* (Petch 1921; Mains 1959a, b; Chaverri et al. 2008). The combined analysis of LSU and RPB1 in comparison with related species, support *M. phukhiaoensis* and *M. pongdueatensis* as new species from Thailand. The phylogenetic tree is presented in Fig. 60.

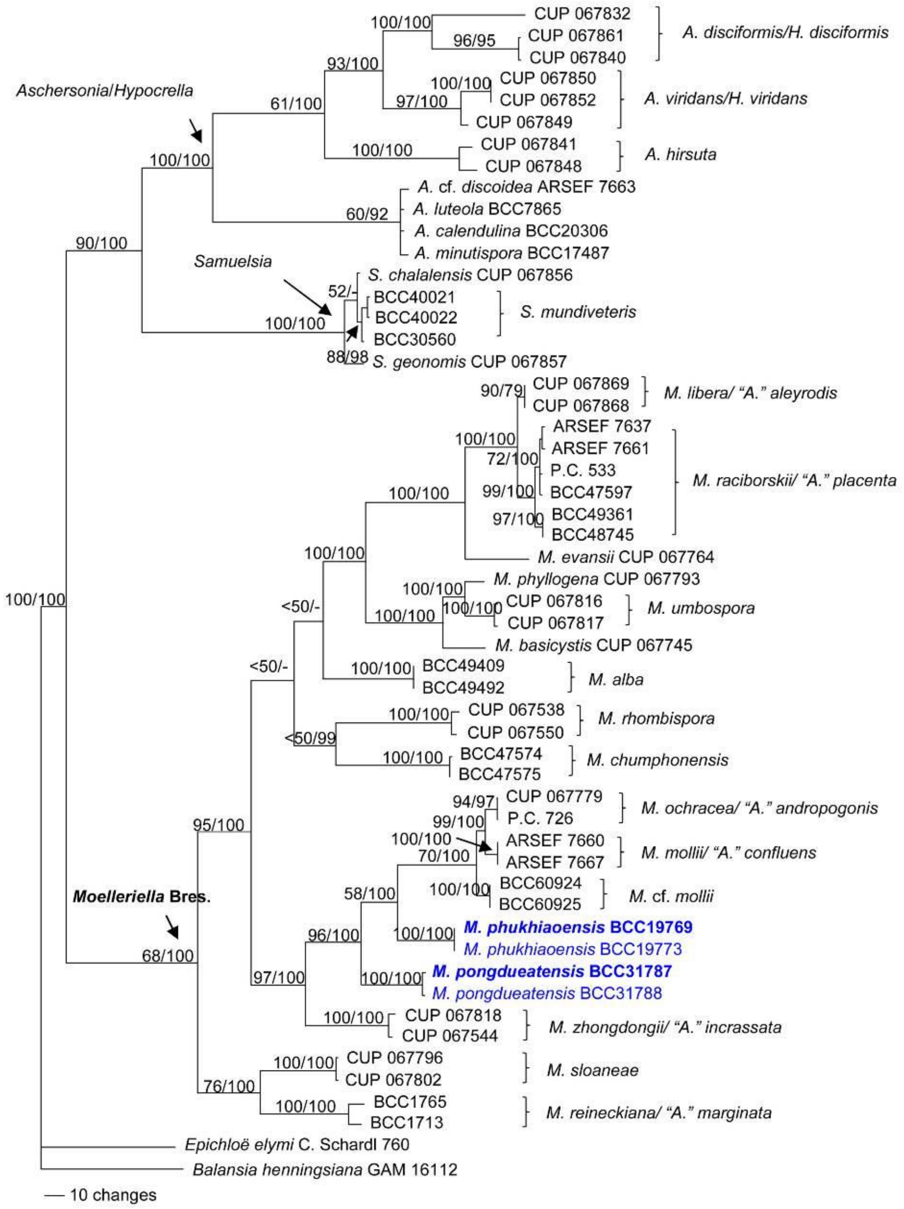


Fig. 60 Phylogenetic relationships between *Moelleriella phukhiaoensis*, *M. pongdueatensis* and related species generated from a combined LSU and RPB1 gene dataset using maximum parsimony and Bayesian analysis. The numbers on each branch represent the bootstrap values/Bayesian PP. New taxa are in blue and species for ex-type strains in bold.

298. ***Moelleriella phukhiaoensis*** Mongkol., Thanakitp. & Luangsa-ard, ***sp. nov.***

Index Fungorum number: IF 551609, *Facesoffungi number*: FoF 02030, Fig. 61

Etymology: The specific epithet refers to Phu Khiao Wildlife Sanctuary, the collection location

Holotype: BBH 17305

Specimens were found on the underside of dicotyledonous leaves. Hosts are scale insect nymphs (*Hemiptera*). *Stromata* flattened pulvinate, sometimes surrounded by a membranous hypothallus; up to 5 mm diam. and 2 mm high, dark orange to golden yellow. **Sexual morph** *Perithecia* 400–520 × 150–200 *µm*, crowded, immersed, elongate flask-shaped, ostioles slightly projecting, translucent. *Asci* 195–220 × 8–12 *µm*, cylindrical, with cap approx. 4–6 thick. *Ascospores* disarticulating into 12.5–17.5 × 2–3 µm part-spores inside the ascus, cylindrical with somewhat rounded ends. **Asexual morph** *Conidiomata* orifice scattered or circularly arranged, ultimately hidden by the orange-yellow mass or extruded conidia, oval or elongate flask shaped, up to 430 *µm* deep, up to 100 diam. *Conidiogenous cells* cylindrical, up to 25 *µm* long, 1–2 *µm* wide. *Conidia* 16–17 *µm* × 2.5–3.5 *µm*, cylindrical narrow, tapering slightly towards the ends. *Paraphyses* present, linear, filiform, up to 90 *µm* long; 1–2 *µm* wide.

Culture characteristics: Cultures were obtained from germinating ascospores and conidia. The ascospores and conidia germinated within 48 h on PDA. The colonies on PDA grew slowly, to approx. 5 mm diam. after 4 wk at 20°C. The stromatic colonies derived from germinating ascospores or conidia formed a compact mycelium. The conidial mass yellow to orange yellow appearing as abundant slimy masses scattered over the surface of stromatic colonies.

Material examined: THAILAND, Chaiyaphum Province, Bueng Pan Protect Forest Unit, Phu Khiao Wildlife Sanctuary, 15 October 2005, S. Mongkolsamrit, R. Ridkaew, B. Thongnuch, K. Tasanathai (BBH 17305, **holotype**); ex-type living culture, BCC19769.

Notes: The sexual morph of *M. phukhiaoensis* is rarely found when compared with the asexual morph. The asexual morph of *M. phukhiaoensis* was compared with the Thai material of *Aschersonia placenta* (sexual morph *M. raciborskii*) based on the pale yellow to light orange stromata. Although the asexual morph of *M. phukhiaoensis* morphologically resembles *A. placenta*, it differs significantly from the latter in having longer conidia (12–14 × 2–2.5 *µm*) as reported for *A. placenta* by Luangsa-ard et al. (2007). *Moelleriella phukhiaoensis* has only been collected in the Phukhiao Phu Khiao Wildlife Sanctuary.

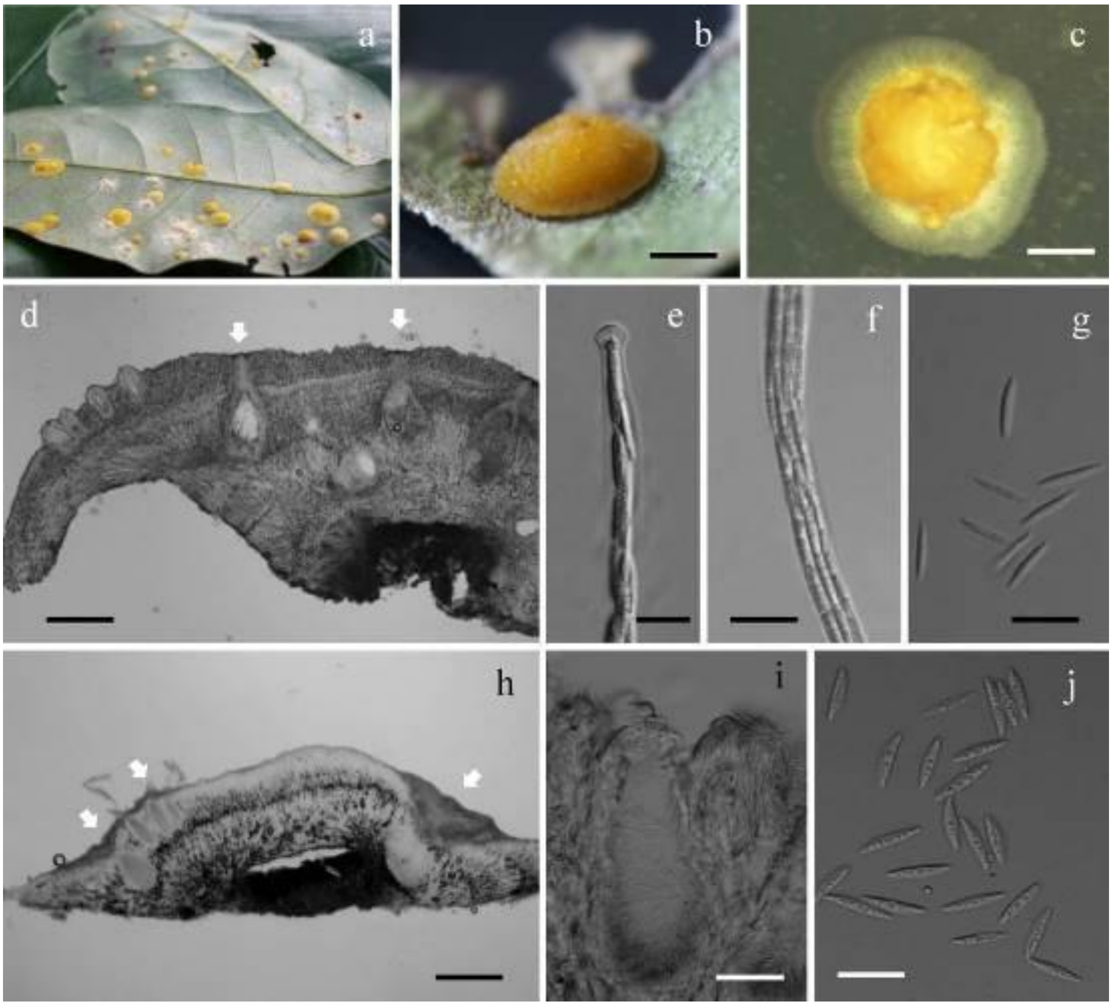


Fig. 61 ***Moelleriella phukhiaoensis*** **(holotype) a**, **b** Fungi on hosts **c** Culture derived from ascospores on PDA (sporulation present) **d** Side view of ascostroma showing flask-shaped perithecia (arrows) **e** Ascus showing a thickened cap **f** Part of ascus showing ascospores **g** Ascospores **h** Longitudinal section through the stroma showing conidiomata with conidia (arrows) **i** Conidiogenous cells and paraphysis **j** Conidia. Scale bars: b, c = 1 mm; d = 500 *µm*; e, f = 10 *µm*, g, j =20 *µm*, h, i = 100 *µm*.

299. ***Moelleriella pongdueatensis*** Mongkol., Thanakitp. & Luangsa-ard, ***sp. nov.***

Index Fungorum number: IF 551610; *Facesoffungi number*: FoF 02031, Fig. 62

Etymology: The specific epithet refers to Pong Dueat Pa Pae Geyser, the collection location

Holotype: BBH 24730

Specimens were found on the underside of bamboo leaves. Hosts are scale insect nymphs (*Hemiptera*). *Stromata* usually discoid, distinctly stud-shaped, up to 4 mm diam. and 2 mm high, pale yellow, base surrounded by a membranous hypothallus. **Sexual morph** No stromata observed. **Asexual morph** *Conidiomata* scattered around a narrow neck, extruding an orange yellow mass of conidia. *Conidiogenous cells* cylindrical, up to 23 *µm* long, 1–2 *µm* wide. *Conidia* fusoid, 9–12.5 *µm* × 1.5–2.5 *µm*. Paraphyses present, linear, filiform, up to 110 *µm* long; 1–2 *µm* wide. The *hirsutella*-like synanamorph is scattered on the upper surface of the stroma, phialides with a long thin neck, up to 20 *µm*, 1–2 *µm* wide, conidia citriform, 2–3 × 1–2.5 *µm*.

Culture characteristics: Cultures were obtained from germinating conidia. The conidia germinated within 24 h on PDA. The colonies on PDA grew slowly, to approx. 5 mm diam. after 2 wk at 20°C. The stromatic colonies formed a compact mycelium. The cream to pale yellow conidial mass covers the stromatic colonies.

Material examined: THAILAND, Chiang Mai Province, Pong Dueat Pa Pae Geyser, 5 July 2008, S. Mongkolsamrit, B. Thongnuch, K. Tasanathai, P. Srikitikulchai, A. Khonsanit (BBH 24730, **holotype**); ex-type living culture, BCC31787

Notes: The sexual morph of this species was not found in the field although several attempts to find it were made throughout the year. The asexual state of *Moelleriella pongdueatensis* is similar to *Aschersonia basicystis* Berk. & M.A. Curtis (sexual morph *Moelleriella basicystis* P. Chaverri & K.T. Hodge) reported from Costa Rica, Cuba and Panama by Chaverri et al. (2008) based on stud-shaped and pale yellow stroma, and yellow mass of extruded conidia, around a narrow neck. The conidia of *M. pongdueatensis*, however, are somewhat smaller; the conidia are fusoid, 9–12.5 × 1.5–2.5 *µm*, with paraphyses up to 110 *µm* long. In contrast, *Aschersonia basicystis* conidia are ventricose, (11–)13–13.5 (–15.5) × (3–)4–4.2(–5) *µm*, with acute ends, paraphyses are absent. Based on our study, *Moelleriella pongdueatensis* is the second species that show the presence of *hirsutella*-like synanamorphs simultaneously occurring on stromata in nature. Tadych et al. (2009) first reported *M. zhongdongii* having both *Aschersonia* and *hirsutella*-like synanamorphs on stromata in nature along with the *Moelleriella* sexual morph.

Phylogenetic analysis

Independent maximum parsimony analyses were done for each gene. Comparisons of the bootstrap supports for the nuclear large subunit rRNA gene (LSU) and RNA polymerase II subunit one (RPB1) gene datasets showed no significant contradictory nodes, and where the bootstrap supports were ≥70% the strains were prepared to make a combined data set for both LSU and the RPB1 for analysis. The combined dataset for the LSU and RPB1 sequence data consisted of 1447 characters, 986 of which are constant, 50 are variable and parsimony-uninformative, while 411 are parsimony-informative. Maximum parsimony analysis of the combined dataset of LSU and RPB1 resulted in 12 most parsimonious trees. Maximum parsimony analyses of this data set yielded one parsimonious tree (tree length 1540; CI = 0.455, RI = 0.802, RC = 0.365, HI = 0.545) as shown in Fig. 60.

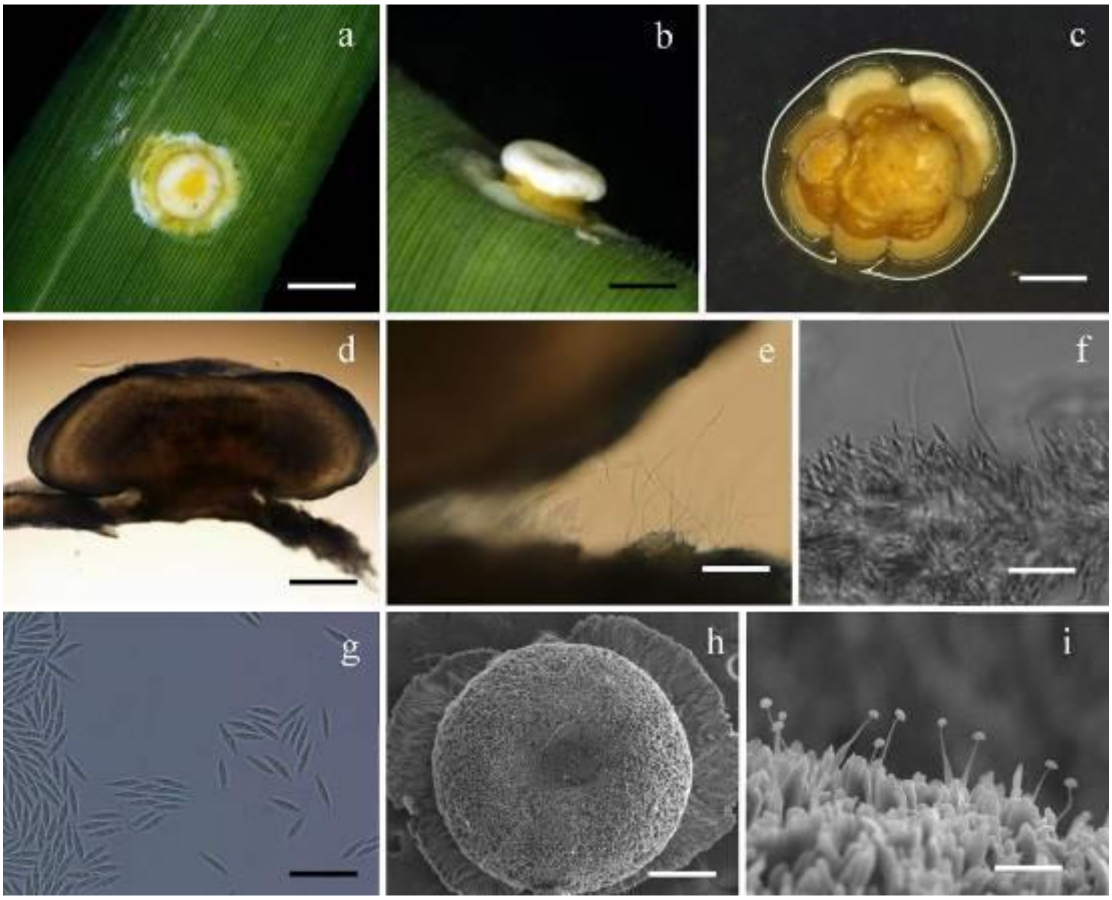


Fig. 62 ***Moelleriella pongdueatensis*** **(holotype) a**, **b** Fungi on hosts **c** Culture derived from conidia on PDA (sporulation present) **d** Side view of stroma showing stud-shaped **e** Paraphyses **f** Conidiogenous cells and paraphysis **g** Conidia **h** SEM derived from stroma **i** SEM of *hirsutella*-like on stroma. Scale bars: a–d, h = 1 mm, e = 50 *µm*, f, g, i = 20 *µm*.

Ophiocordycipitaceae

The family *Ophiocordycipitaceae* (order) was introduced by Sung et al. (2007) based on phylogenetic analyses and later emended by Kirk et al. (2013) and Quandt et al. (2014). Kirk et al. (2013) listed eleven genera under this family, while Quandt et al. (2014) refined it and proposed six genera, including *Drechmeria*, *Harposporium*, *Ophiocordyceps*, *Polycephalomyces*, *Purpureocillium* and *Tolypocladium*. Maharachchikumbura et al. (2015) confirmed this system and Spatafora et al. (2015) introduced some necessary species combinations based on this classification. Most species of *Ophiocordycipitaceae* are known to produce dark 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). The phylogenetic tree is presented in Fig. 63.

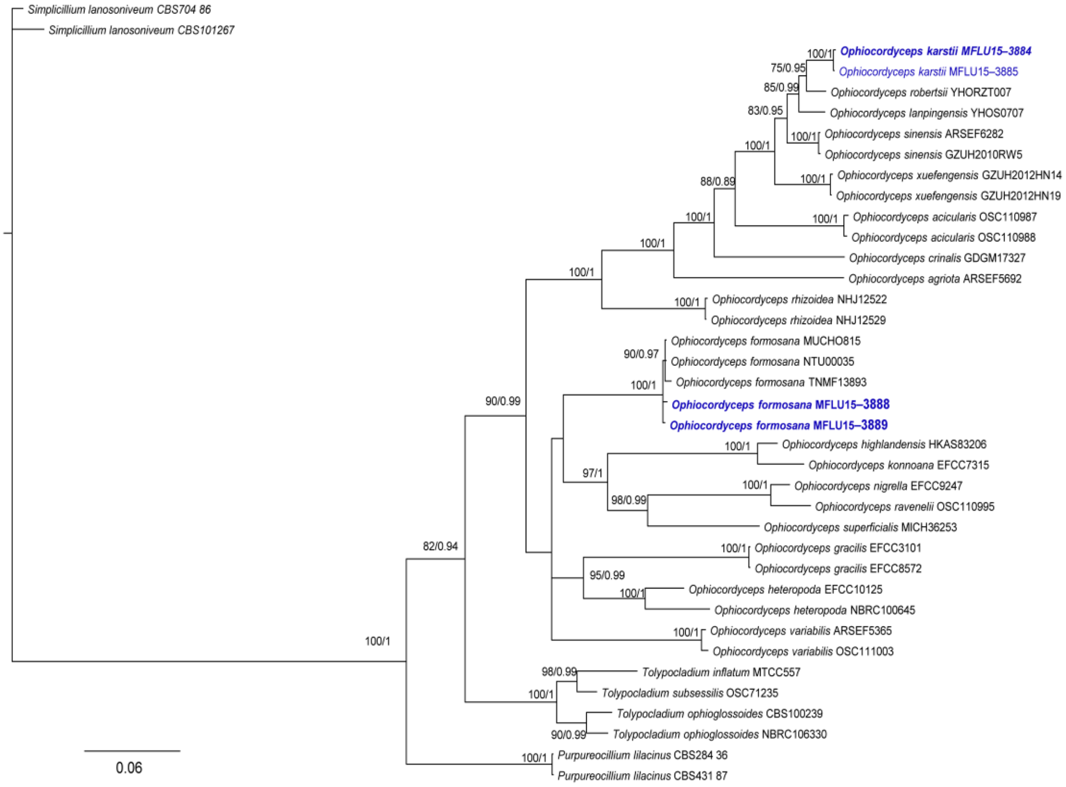


Fig. 63 Phylogram of *Ophiocordyceps* generated from Maximum likelihood analysis of SSU, rpb1 and tef1-α sequence data. *Simplicillium lanosoniveum* (J.F.H. Beyma) Zare & W. Gams is used as outgroup taxon. Maximum likelihood bootstrap values greater than 50 % and Bayesian posterior probabilities over 0.90 are indicated above or below the nodes. The new species are indicated in blue.

300. *Ophiocordyceps formosana* Y.W. Wang et al. in Wang et al., Evidence-Based Complementary and Alternative Medicine (no. 189891): 4 (2015)

Facesoffungi number: FoF 01796, Fig. 64

Parasitic in larva of *Coleoptera* (Superfamily Tenebrionoidea), forming yellow to orange ascostromata. **Sexual morph** Ascomycetous. *Stromata* 14 mm long, 2-5 mm wide, growing from the head and the tail of *Coleoptera* larva, simple or branched, yellow to orange, stipitate. *Stipe* 1.9–3.7 cm long, 2–4 cm wide, yellow, cylindrical, surface rough. *Fertile head* 30 mm long, 2–2.5 mm wide, orange, mostly elliptic barely branched, head-like, with orange, pseudoparenchymatous, epidermal tissues, surface mastoid, differentiated from stipe. *Ascomata* 453–546 × 265–298 *µm* ($\bar{x}$ = 479 × 270, n = 30), completely immersed, orange, flask-shaped to oval, with the ostioles opening on the surface of the head. *Peridium* 26–38 *µm* wide ($\bar{x}$ = 30, n = 60), comprising three layers. *Asci* 366–498× 8–11 *µm* ($\bar{x}$ = 437 × 10, n = 60), 8-spored, hyaline, cylindrical, with apical cap, breaking into secondly ascospores. *Secondary ascospores* 2–6 × 1–3 *µm* ($\bar{x}$ = 4 × 2, n = 60), hyaline, cylindrical. **Asexual morph** Undetermined.

Material examined: CHINA. Province of Hunan, on dead larva of Tenebrionoidea, 23 October 2014, Ping Zhang, ZP8282 (MFLU 15–3888); ZP828i (MFLU 15–3889, MFLU 15–3890, MFLU 15–3891).

Notes: *Ophiocordyceps formosana* was introduced by Kobayashi (1979) as *Cordyceps formosana* Kobayasi & Shimizu. Wang et al. (2015a) revised it as *Ophiocordyceps formosana*. This species is frequently used in Traditional Chinese Medicine and has a long history of use as tonics and folk medicines that can be used as anticancer and diabetes treatments and contains antioxidants (Wang et al. 2015a). This species was previously known from Fujian and Taiwan (Wang et al. 2015a). We collected this species in Hunan Province, China, which is a new record for the province. We also provide a colour figure for this species which includes asci and cap and entire ascospores, which are illustrated for the first time.

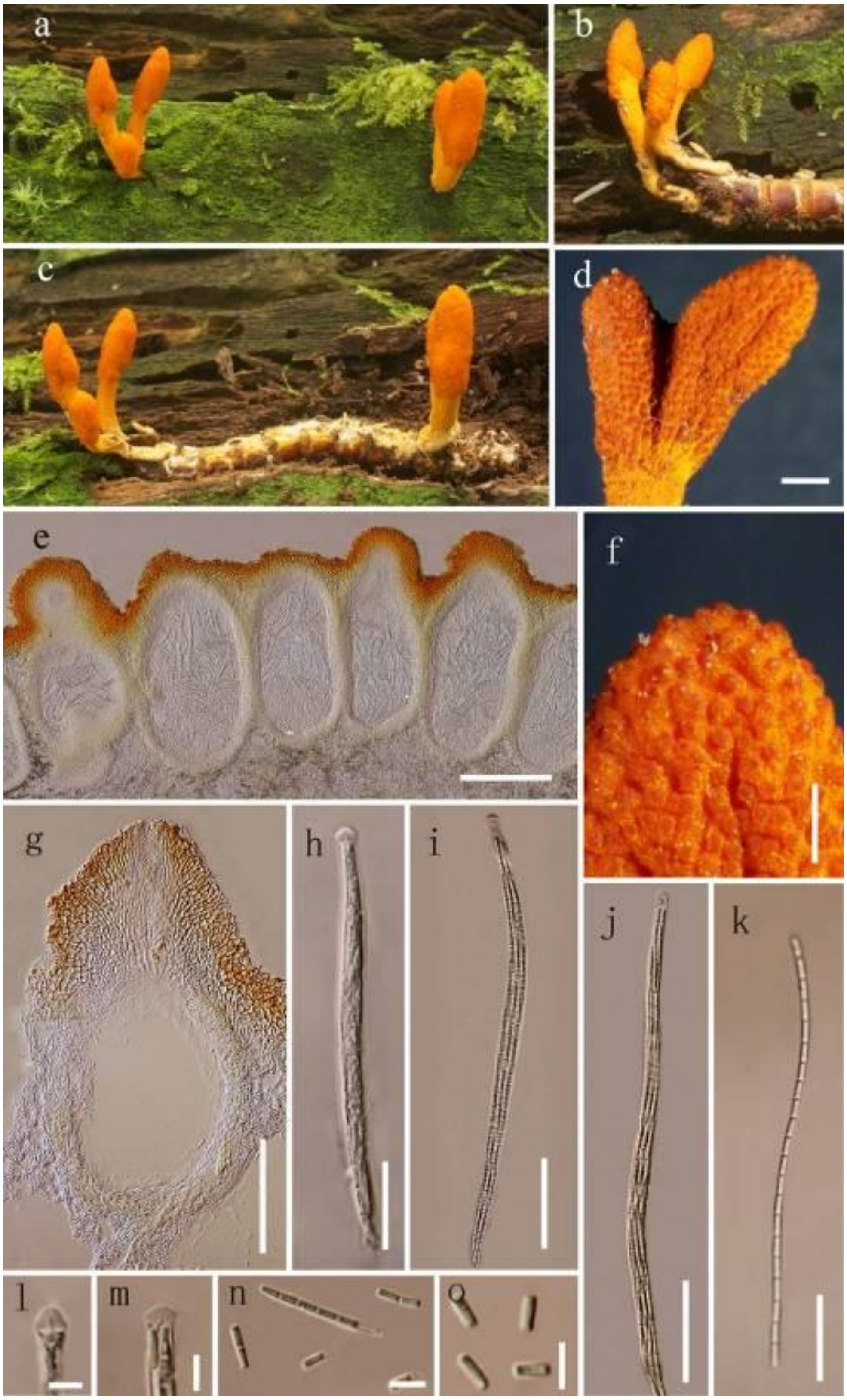


Fig. 64 ***Ophiocordyceps formosana*** (MFLU 15–3888) **a** Stromata appearing from the tree **b** Yellow, superficial stroma appearing from host head **c** Overview of the stromata and the host **d**, **f** Apical part of the stroma **e** Vertical section of stroma **g** Cross section showing the complete perithecia **h**–**j** Asci at immature and mature stages **k** Entire ascospore **l**, **m** Asci with

apical cap **n**, **o** Secondly ascospores. Scale bars: d = 1000 *µm*, e, f = 200 *µm*, g = 100 *µm*, h, k = 20 *µm*, i, j = 50 *µm*, l–o =5 *µm*.

301. *Ophiocordyceps karstii* T.C. Wen, Y.P. Xiao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551814, *Facesoffungi number*: FoF 01795, Fig. 65

Etymology: Name referring to the location which the specimen was collected.

Holotype: MFLU 15–3884

Parasitic in larva of *Hepialus jianchuanensis*, brown to dark brown, forming yellow to brownish stromata. **Sexual morph** *Thallus* within host white, composed of intercalary hyphal bodies. *Stromata* mostly single, 140–145 × 2–4 mm, stipitate arising from head of the host. *Stipe* 12 cm long, 2 mm wide, clavate, with a fertile apex, becoming golden yellow to brownish yellow when mature. *Fertile head* 20–25 mm long, 2–4 mm diam., clavate, light yellow to yellow-brown, upper surface roughened, covered with white non compact mycelium. *Ascomata* 600–765 × 247–323 *µm* ($\bar{x}$ = 683 × 285 *µm*, n = 30), superficial, yellow to brown, flask-shaped, thick-walled, ostiole on the top. *Peridium* 63–42 mm ($\bar{x}$ = 52 *µm*, n = 60) wide, three layers. *Asci* 186–228 × 8–12 *µm* ($\bar{x}$ = 207 × 10 *µm*, n = 60), 8-spored, hyaline, narrow cylindrical, with a thickened apex. *Apical cap* 5–7 *µm* ($\bar{x}$ = 6 *µm*, n = 60) diam. *Ascospores* 173–202 × 3–5 *µm* ($\bar{x}$ = 188 × 4 *µm*, n = 60) fasciculate, fusiform, smooth, as long as asci, hyaline, 10–18 septate, not breaking into secondly spores. **Asexual morph** Undetermined.

Material examined: CHINA. Guizhou Province, Chishui, on dead larva of *Hepialus jianchuanensis*, 23 October 2014, TingChi Wen CS2014102301 (MFLU 15–3884, **holotype**); CS2014102304 (MFLU 15–3885, MFLU 15–3886, MFLU 15–3887, **paratype**).

Notes: *Ophiocordyceps* was introduced by Petch (1931) with *Ophiocordyceps blattae* (Petch) Petch as the type species and used by Sung et al. (2007) as the type genus of *Ophiocordycipitaceae*. According to morphological and phylogenetic analysis, *Ophiocordyceps karstii* closedly matches *O. lanpingensis* Hong Yu bis & Z.H. Chen bis and *O. robertsii* (Hook.) G.H. Sung et al. This species is characterized by fusiform ascospores (173–202 × 3–5 *µm*, $\bar{x}$ = 188 × 4 *µm*, n = 60), which do not break into secondly ascospores and superficial ascomata. Phylogenetic analysis of th of combined TEF1, RPB1 and SSU sequence data (Fig. 63) confirms that *Ophiocordyceps karstii* clusters with *O. robertsii* in *Ophiocordyceps* with high bootstrap support. Therefore, we proposed *O. karstii* as a new species.

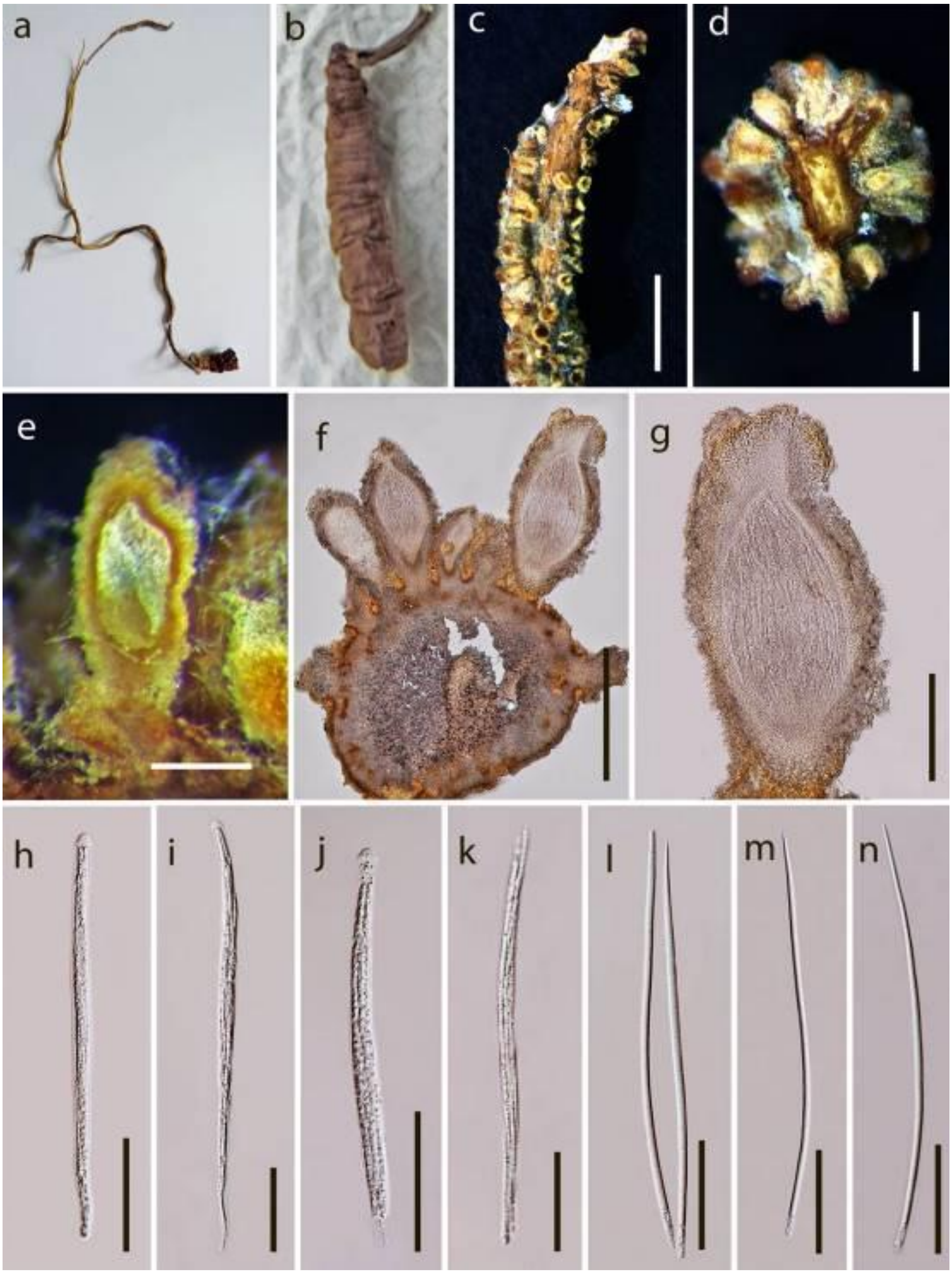


Fig. 65 ***Ophiocordyceps karstii*** (**holotype**) **a** Overview of the host and stromata **b** Host: *Hepialus jianchuanensis* **c** Stroma **d** Vertical section of stroma **e** Vertical section showing the superficial perithecia **f**, **g** Perithecia **h**–**k** Asci at immature to mature stages **l**–**n** Ascospores. Scale bars: c = 2 mm, d, f = 500 μm, e–g = 200 μm, h–n = 50 μm.

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

Species	Stromata (mm)	Ascomata (μm)	Asci (μm)	Ascospores (μm)	Secondly spores	Reference

					(μm)	
O. karstii	140–150 × 2–4	600–765 × 247–323	186–228 × 8–12	173–202 × 3–5	Not breaking	This study
O. lanpingensis	50–160 × 0.2–1.3	310–370 × 200–240	240–300 × 5.1–6.5	240–300 × 1.4	Not breaking	Chen et al. 2013
O. robertsii	100–380 × 3–4	600–880 × 300–400	280–400 × 9–10	280 × 3	5–6 × 3	Cunningham 1921
O. sinensis	40–110	380–550 × 140–240	240–485 × 12–16	160–470 × 5–6	Not breaking	Liang et al. 2007
O. xuefengensis	140–460 × 2–7	416–625 × 161–318	191–392 × 4.5–8.9	130–380 × 1.4–5.2	Not breaking	Wen et al. 2013

Microascales

Halosphaeriaceae

The family *Halosphaeriaceae* was introduced by Müller and von Arx (1962) with *Halosphaeria* as the type genus (Barghoorn and Linder 1944). Morphological characters include the perithecioid ascomata, presence of catenophyses that generally deliquesce, clavate to fusiform, unitunicate thin-walled asci; hyaline, septate ascospores sometimes with polar appendages (Jones 1995, Sakayaroj et al. 2011, Jones et al. 2015). Members of *Halosphaeriaceae* constitute the largest group of marine Ascomycota mainly found in marine habitats, with few transitional species found in freshwater and brackish water (Jones 1995; Pang et al. 2003; Jones et al. 2009, Sakayaroj et al. 2011). The phylogenetic tree is presented in Fig. 66.

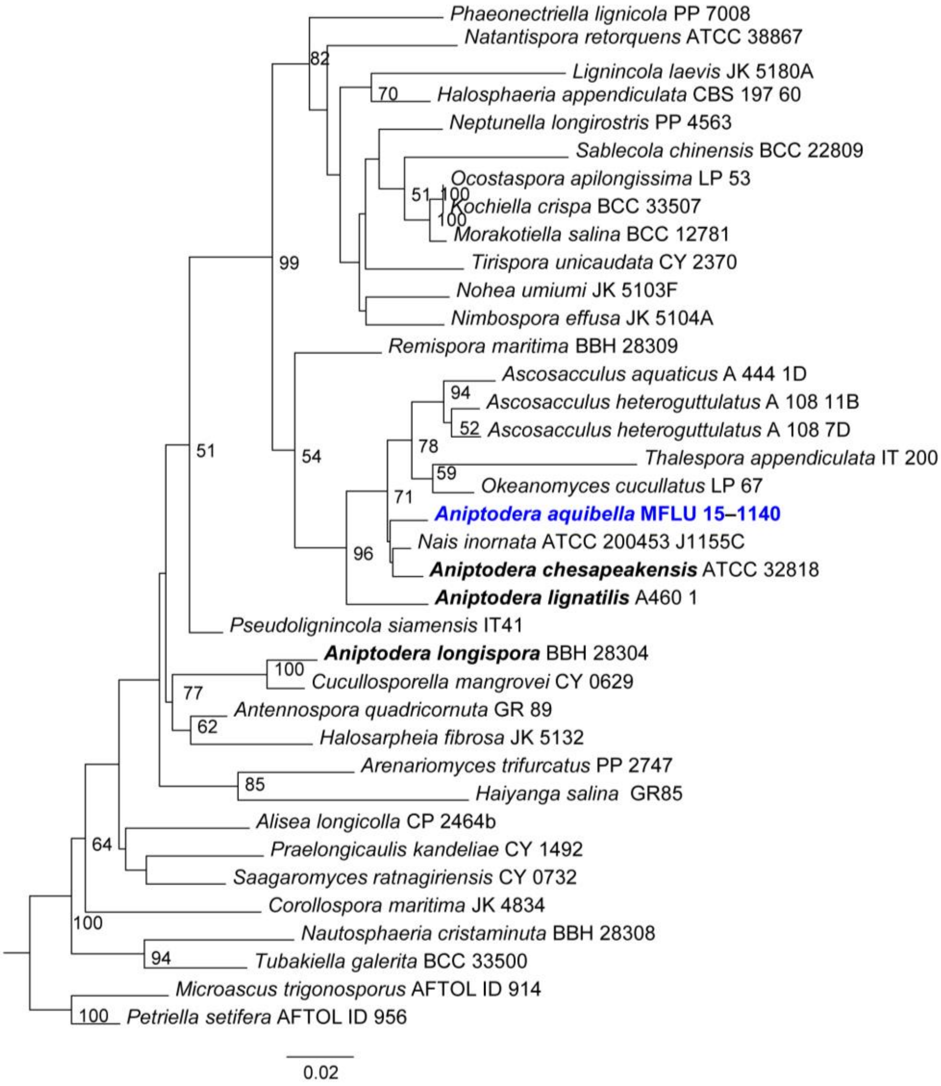


Fig. 66 Maximum likelihood (ML) majority rule consensus tree for the analyzed *Halosphaeriaceae* isolates based on a dataset of combined LSU and SSU sequence data. RAxML bootstrap support values (ML) are given at the nodes (ML). The scale bar represents the expected number of changes per site. The tree is rooted with *Microascus trigonosporus* and *Petriella setifera*. The original isolate numbers are noted after the species names. The new strain is in blue bold and other strains in *Aniptodera* are in black bold.

302. *Aniptodera aquibella* J. Yang & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF 551897, *Facesoffungi number*: FoF 01818, Fig. 67

Etymology: from the Latin aqua = water, bellus = lovely, referring to the freshwater habitat.

Holotype: MFLU 15–1140

Saprobic on decaying, submerged twigs in freshwater habitats, shining on the host surface. **Sexual morph** *Ascomata* 130–160 × 150–200 *µm*, superficial or immersed, globose or subglobose, scattered, hyaline or greyish, membranous. *Neck*

80–110 × 40–60 *µm*, cylindrical to conical, hyaline, with periphyses. *Peridium* 7–15 *µm* thick, composing several layers of hyaline-walled cells of *textura globosa*. *Catenophyses* sparse, hyaline, septate, consisting of elongated cells, slightly constricted at the septa. *Asci* 60–110 × 25–45 *µm* (x = 90 × 30, n = 20), 8-spored, thin-walled, clavate, becoming balloon-shaped or swollen, flattened at apex, tapering to a pointed pedicel, unitunicate, wall thickened at the apex, subapical cytoplasm retracted, mostly persistent, with a J-, apical thickening, which has an apical pore. *Ascospores* 25–30 × 7–10 *µm* (x = 28 × 8, n = 50), 1-euseptate, slightly constricted at the septa, thin-walled, hyaline, smooth-walled, ellipsoidal, 2–3-seriate, guttulate, sometimes with indistinct appendages at both ends. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes produced from the poles of both cells. Colony on MEA slow-growing, reaching 5–10 mm diam. at 14 days, dark brown in the middle, conspicuous paler and sparser at edge, with dense white mycelium on surface in the middle of colony; in reverse with a dark brown middle and olive-green smooth margin. Mycelium immersed and superficial in the media, composed of branched, septate, smooth-walled, hyaline aerial hyphae and dark brown hyphae near or within the media.

Habitat and distribution: On submerged wood in freshwater, Thailand.

Material examined: THAILAND, Prachuap Khiri Khan Province, Hua Hin, Kaeng Krachan, near Pala-U Waterfall, stream outside national park, on submerged wood, 25 December 2014, Jaap van strien (MFLU 15–1140, **holotype**), ex-type living culture, MFLUCC 15–0605, GZCC 15–0055.

Notes: The genus *Aniptodera* was established by Shearer and Miller (1977) with *A. chesapeakensis* Shearer & M.A. Mill. as the type species. The genus was described as having hyaline or light colored ascomata, catenophyses, apically thickened persistent asci with a distinct pore and subapical retraction of cytoplasm, and hyaline, thick-walled, 1-septate ascospores with or without appendages (Shearer and Miller 1977; Raja and Shearer 2008). *Aniptodera aquibella* fits well within *Aniptodera*. It is most similar to *A. chesapeakensis*, except that the ascospores are smaller and the ascospore walls are thinner than those of *A. chesapeakensis* (Shearer and Miller 1977). *Aniptodera aquibella* differs from other species in the genus by conspicuous differences in the size and shape of asci and ascospores. *Aniptodera intermedia* K.D. Hyde & Alias has the shortest asci (46–62 × 16–19 *µm*) and smallest ascospores (10.5–13 × 7–8 *µm*), while *A. longispora* K.D. Hyde has the longest asci (145–201 × 24–31 *µm*) and larger ascospores (39–51 × 9–13.5 *µm*) in the genus (Hyde 1990, 1999). *Aniptodera megaloascocarpa* Raja & Shearer differs distinctly from *A. aquibella* because it has the largest ascomata (1060–1360 × 430–530 mm) of all the species in *Aniptodera* (Raja and Shearer 2008). *Aniptodera margarition* Shearer and *A. mangrovei* K.D. Hyde lack any apical thickening and the subapical retraction of cytoplasm and the former also lacks a distinguishable apical pore characteristic of all *Aniptodera* species (Shearer 1989). *Aniptodera triseptata* K.D. Hyde is the only species with 3-septate ascospores in the genus (Hyde 2002).

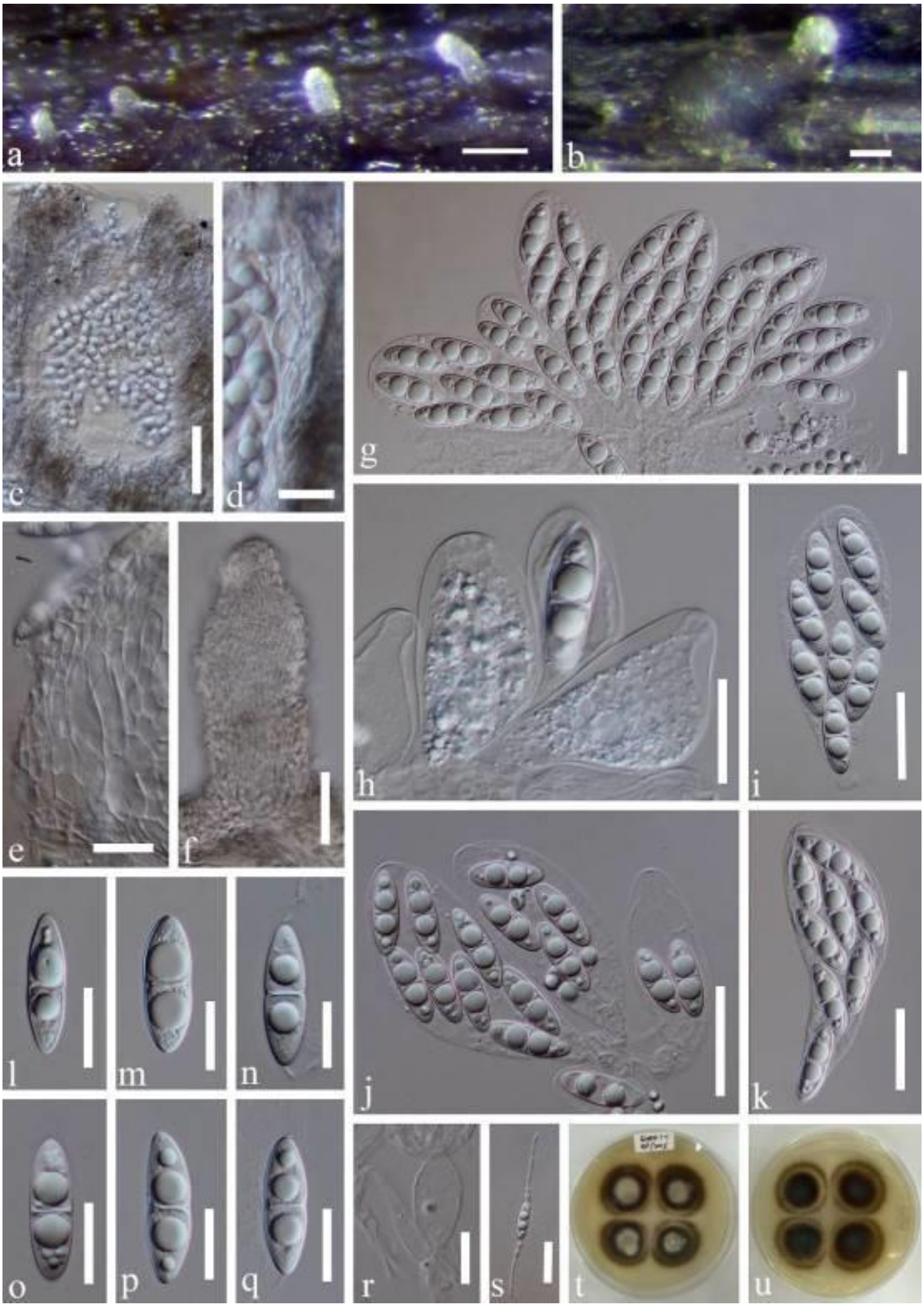


Fig. 67 ***Aniptodera aquibella*** **(holotype)** **a, b** Appaerance of ascomata on submerged wood **c** Section of an ascoma **d** Section through peridium **e** Peridium in surface view **f** Surface of periphysate neck **g**–**k** Asci **l**–**q** Ascospores **r** Catenophyses **s** Germinated spore **t**–**u** Culture on MEA **t** from above. Scale bars: a = 100 *µm*, b–c = 50 *µm*, d–e, h = 20 *µm*, f–g, i–k, s = 30 *µm*, l–q = 15 *µm*, r = 10 *µm*.

Sordariales

The order Sordariales was detailed by Maharachchikumbura et al. (2015) and this is followed here.

Chaetomiaceae

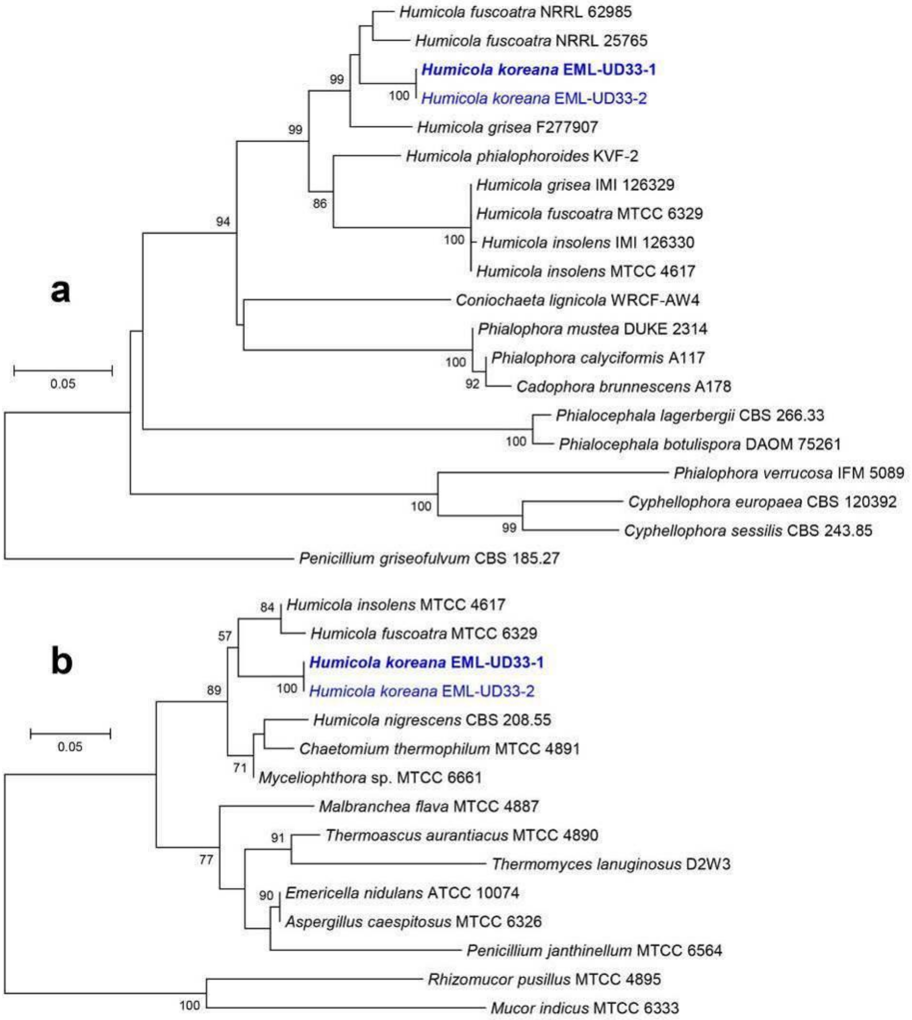


Fig. 68 Phylogenetic tree for *Humicola koreana* EML-UD33-1 and EML-UD33-2 and related species based on Maximum likelihood analysis of **a** ITS, **b** LSU sequence data. Sequences of *Penicillium griseofulvum*, *Mucor indicus* and *Rhizomucor pusillus* were used as outgroups. Numbers at the nodes indicate the bootstrap values (>50%) from 1000 replications. The *bar* indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold.

Humicola Traaen

The genus *Humicola* was established by Traaen (1914) for two species, *H. fuscoatra* Traaen and *H. grisea* Traaen which were isolated from Norwegian soil. Species belonging to this genus are slow growing and form solitary, dark, globose to elongate, single-celled conidia (Omvik 1955; De Bertoldi et al. 1972). However, until now, the taxonomy of the genus have not yet been studied in detail. About six species including some varieties are recognized in this genus (Ko et al. 2011). The genus is likely to be polyphyletic with some species being the asexual morphs of *Chaetomium*.

Several species of the genus, *Humicola* are rich in organic matter and are able to produce strong cellulolytic enzymes and may have important economical application (White and Downing 1953; Sharma et al. 2008; Du et al. 2013). Species may also reduce disease caused by *Aspergillus flavus*, *Phytophthora capsici* and *Alternaria brassicicola* (Wicklow et al. 1998; Ko et al. 2011). Thus, the purpose of this study was to investigate the morphological charateristics of a *Humicola* species isolated from soil and to conduct molecular phylogenetic analyses to establish their placement in Ascomycota.

During a study on the *Sordariales* from a soil sample of Ulleung-do island which is about 161 km far from the mainland of Korea, a *Humicola* species that differs morphologically and phylogenetically from the other species of the genus was isolated and is described as new to science.

303. ***Humicola koreana*** Hyang B. Lee & T.T.T. Nguyen, ***sp. nov.***

MycoBank number: MB 814402, *Facesoffungi number*: FoF 02068, Fig. 69

Etymology: koreana. Referring to the country which from the species was first isolated (Korea)

Holotype: EML-UD33-1

Colonies of strain grow slowly on PDA, initially nearly buff and then changing to luteus, reaching 59–61 mm in diam. at 25°C after 7 days of incubation. The reverse of colonies is yellow in the center with a lighter margin and irregular zonation. *Conidia* are formed laterally, the shapes are commonly round, ovovoid to some ellipsoid, and measure 8–10.7 *µm* in diam. The conidia have outwardly melanized thick wall layers. At maturity, conidia are detached from the conidiophores having scars.

Notes: *Humicola koreana* is morphologically similar to *H. fuscoatra* and *H. grisea*, but differs from the related species in having smaller spores and producing yellow pigment when cultivated on PDA.

Material examined: REPUBLIC OF KOREA, from a soil sample from Ulleung-do island; EML-UD33-1 (EML-UD33-1, **holotype** a dried culture, stored at Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Korea) ex-type living culture at the Culture Collection of National Institute of Biological Resources (NIBR), Incheon, preserved as glycerol stock at -80°C in the CNUFC and deposited at Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012183).

The isolate was observed to grow over a wide range of temperatures with varying growth rates on PDA, MEA (malt extract agar), and CDA (czapek dox agar). The average growth rates of EML-UD33-1 on PDA, MEA, and CDA were 7 mm, 6 mm, and 7.5 mm per 24 hours, respectively. Optimal growth was observed around 25–27°C, slow growth was observed at below 20°C, and no growth at 37°C.

Humicola koreana appears to be phylogenetically related to *H. fuscoatra*, the type of the genus *Humicola* (Fig. 68).

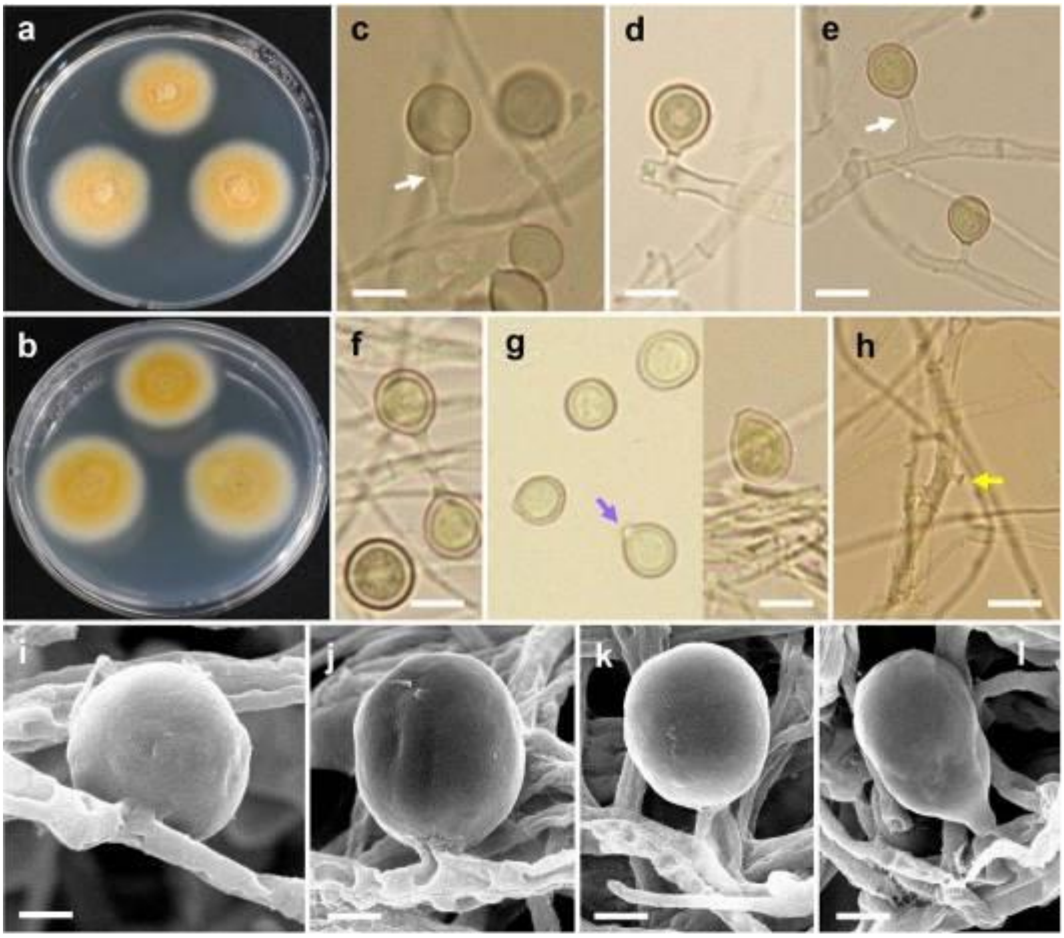


Fig. 69 ***Humicola koreana*** (**holotype**) **a**, **b** Yellow colonies in potato dextrose agar (PDA) (**a** from above, **b** from below) **c**–**f**, **i**–**l** Two different types of conidiophores (white arrows) and aleuriconidia, vase-shaped conidiophore **c** Column-shaped conidiophore **e** Ground to obovoid conidia with scar (purple arrow) and thick wall layer **h** Scar on the conidiophore after detachment (yellow arrow). Scale bars: c–h = 20 *µm*, i, k = 10 *µm*, j, l = 15 *µm*.

Amphisphaeriales

Amphisphaeriaceae

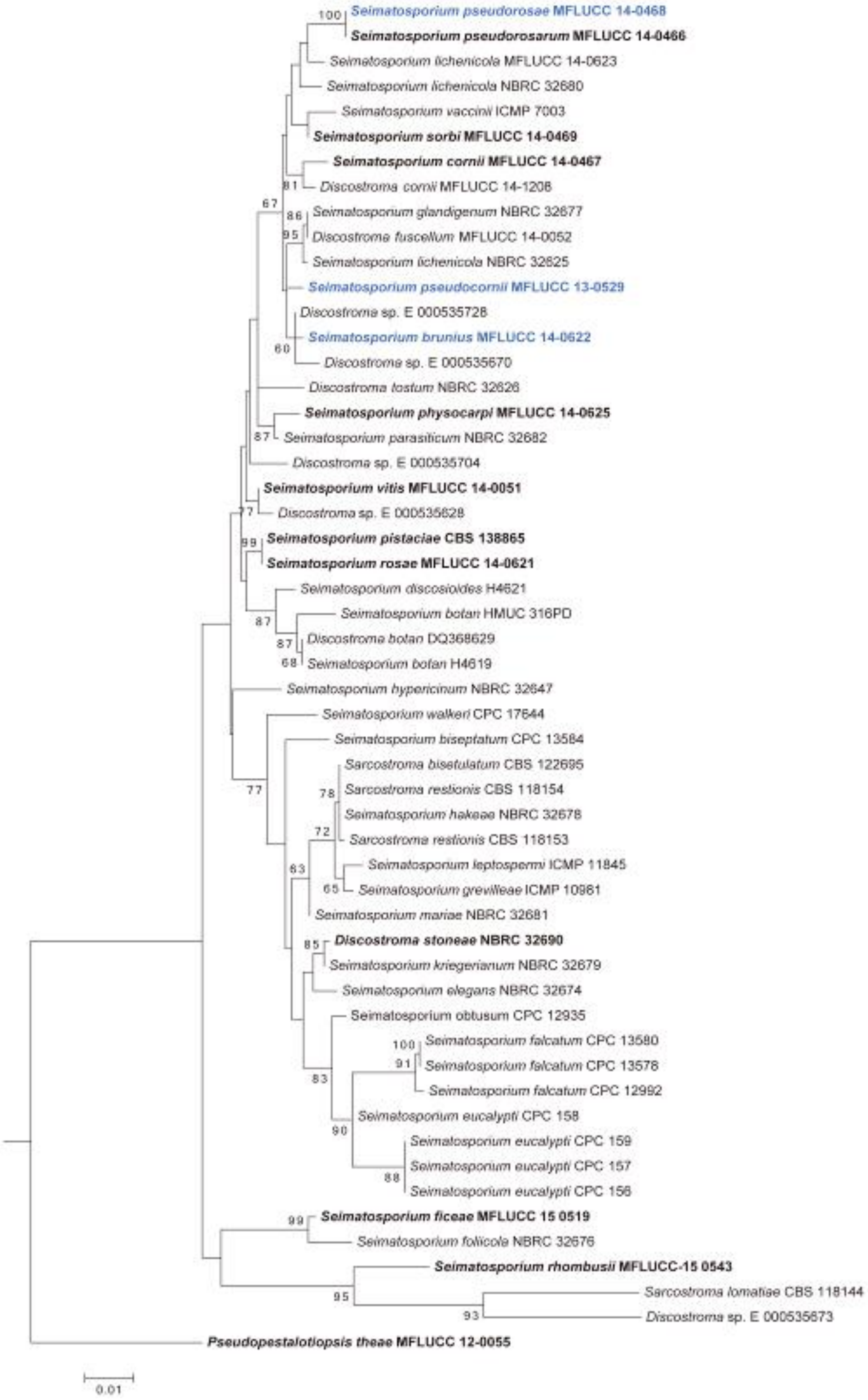


Fig. 70 Phylogram generated from maximum likelihood analysis (ML) based on combined LSU and ITS sequence data of *Seimatosporium*. Maximum likelihood bootstrap support values greater than 50% are near the nodes. New taxa are in blue and ex-type strains are in bold. The tree was rooted to *Pseudopestalotiopsis theae* (MFLUCC 12–0055).

Seimatosporium

The genus *Seimatosporium* was introduced by Corda (1833) with *S. rosae* as the type species, and Shoemaker (1964), Shoemaker and Muller (1964), Sutton (1980) and Nag Raj (1993) revisited the genus. Barber et al. (2011), Tanaka et al. (2011), Norphanphoun et al. (2015) and Senanayake et al. (2015) re-visited the genus and discussed the taxonomic placement based on sequence analyses.

Nag Raj (1993) and Okane et al. (1996) stated *Discostroma* was the sexual morph of *Seimatosporium*. Recent publications also showed that both *Seimatosporium* and *Discostroma* grouped in a monotypic clade (Barber et al. 2011; Tanaka et al. 2011; Norphanphoun et al. 2015; Senanayake et al. 2015). Norphanphoun et al. (2015) designated the epitype for *Seimatosporium rosae*, the type species of *Seimatosporium*.

304. *Seimatosporium pseudocornii* Wijayaw., Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551754, *Facesoffungi number*: FoF 01653, Fig. 71

Etymology: Named as its morphological similarity to *Seimatosporium rosae*

Holotype: MFLU 15–3558

Saprobic on dead branches and stems of *Cornus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 320–350 *µm* diam., 50–120 *µm* high, acervular, unilocular, subglobose, superficial to subepidermal, solitary to gregarious, dark brown to black, non papillate ostiole. *Conidiomata wall* multi-layered, outer wall thick, composed of brown cells of *textura angularis*, inner wall thin, hyaline. *Conidiophores* 5–30 × 2–4 *µm*, long, cylindrical, branched, hyaline, smooth-walled. *Conidiogenous cells* holoblastic, annellidic, simple, integrated, determinate, hyaline. *Conidia* 31–42 × 5–7 *µm* ($\bar{x}$ = 38.1 × 6.1 *µm*, n = 20), obovoid to fusiform, occasionally truncate base, obtuse apex, straight to slightly curved, 3-transverse septate, brown to dark brown septa, constricted at the septa, often guttulate at immaturity, medium brown, hyaline to sub-hyaline basal cell, smooth-walled, appendage absent.

Culture characteristics: On PDA slow growing, attaining a diam. of 2 cm in 7 days at 18 ºC, white to pale brown from top, greyish white from below, with sparse mycelium, flat, uneven margin.

Material examined: ITALY, Forlì-Cesena [FC] Province, near Monte Riccio - Bagno di Romagna, on dead branch of *Cornus* sp. (*Cornaceae*), 5 January 2013, Erio Camporesi, IT 1000 (MFLU 15–3558, **holotype**); (HKAS **isotype**), ex-type living cultures MFLUCC 13–0529, GUCC IT 1000, KIB.

Notes: Farr and Rossman (2015) reported *Seimatosporium lichenicola* (Corda) Shoemaker & E. Müll. (conidial dimensions 13–15 × 5.5–6.5 *µm fide* Sutton 1980) and *S. salicinum* (Corda) Nag Raj (11–17 × 4–6 *µm fide* Nag Raj 1993) from *Cornus* spp. Senanayake et al. (2015) reported *Seimatosporium corni* Wijayawardene et al. (conidial dimensions 21–29 × 9–11 *µm*). In morphology our new collection is distinct from these species, thus we introduce a new species based on morphology, host association and phylogenetic analyses.

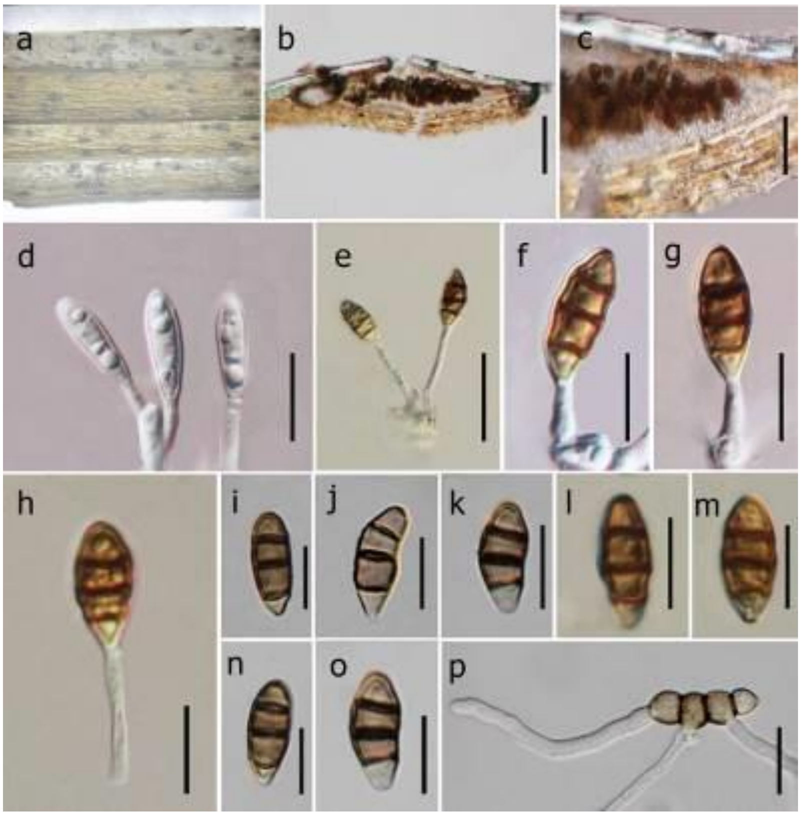


Fig. 71 ***Seimatosporium pseudocornii*** (**holotype**) **a** Appearance of conidiomata on dead branch of *Cornus* sp. **b, c** Cross sections of conidiomata **d**–**h** Different stages of conidiogenesis **i**–**o** Conidia **p** Germinating conidium. Scale bars: b = 50 *µm*, c–o = 25 *µm*, p = 30 *µm*.

305. *Seimatosporium pseudorosae* Wijayaw., Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551753, *Facesoffungi number*: FoF 01652, Fig. 72

Etymology: Named as its morphological similarity to *Seimatosporium rosae*

Holotype: MFLU 15–3559

Saprobic or *endophytic* on living branches and stems of *Rosa villosa* (*Rosaceae*). **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 175–250 *µm* diam., 200–250 *µm* high, acervular, unilocular, subglobose, superficial to subepidermal, solitary, dark brown to black, with apapillate ostiole. *Conidiomata wall* multi-layered, with thick outer wall, composed of brown walled-cells of *textura angularis*, with thin, hyaline, inner wall. *Conidiophores* 10–60 × 2–4 *µm*, long, cylindrical, branched, hyaline, smooth-walled. *Conidiogenous cells* holoblastic, annellidic, simple, integrated, determinate, hyaline. *Conidia* 12–17.5 × 3–6 *µm* ($\bar{x}$ = 13.54 × 4.79 *µm*, n = 20), obovoid to fusiform, truncate at base, obtuse at apex, straight, with 3-transverse septa, brown to dark brown at septa, constricted at the septa, eguttulate, medium brown, hyaline to sub-hyaline at basal and apical cell, smooth-walled, with or without tubular basal and apical appendages; basal appendage when present 6–15 *µm*, unbranched; apical appendage when present unbranched, 8–25 *µm*.

Culture characteristics: On PDA slow growing, attaining a diam. of 1.5 cm in 7 days at 18 ºC, white to light brown from above, pale brown from below, with sparse mycelium, flat, uneven margin.

Material examined: ITALY, Province of Trento [TN], Marilleva 900 - Val di Sole, on dead branch of *Rosa villosa* L. (*Rosaceae*), 29 July 2013, Erio Camporesi, IT 1392 (MFLU 15–3559, **holotype**); (HKAS **isotype**), ex-type living cultures MFLUCC 14–0468, GUCC IT1392

Notes: Farr and Rossman (2015) list several *Seimatosporium* species which were recorded from *Rosa* spp. Among these, only *Seimatosporium rosae* shows both apical and basal appendages (Sutton 1980; Nag Raj 1993). Crous et al. (2014a) introduced *S. pistaciae* Crous & Mirab which also has apical and basal appendages. Our collection is morphologically distinct from both these species and the key is provided below to distinguish the three species.

Molecular analysis shows our collection groups with *S. pseudorosarum* (MFLUCC 14–0466), but the latter species lacks apical appendages. Norphanphoun et al. (2015) introduced *Seimatosporium physocarpi* C. Norphanphoun et al. from *Physocarpi* sp. (15–16 × 3.5–4.8 *µm*) which has both apical and basal appendages and has conidial dimensions similar with our collection. However, our collection has longer conidiophores (10–60 *µm*), while in *S. physocarpi* conidiophores are only up to 20 *µm*. The new taxon is phylogenetically distinct from *Seimatosporium physocarpi* (Fig. 70) and it is thus introduced as a new species.

Key to distinguish *Seimatosporium* spp. with apical and basal appendages

1. Conidia longer than 17 *µm*...***S. pistaciae***
1. Conidia shorter than 15 *µm*.. 2
2. Conidia12–17.5 × 3–6 *µm* 3
2. Conidia 10–15 × 3–4 *µm* ....***S. rosae***
3. Conidiophores up-to 20 *µm* ....***S. physocarpi***
3. Conidiophores 10–60 *µm*...***S. pseudorosae***

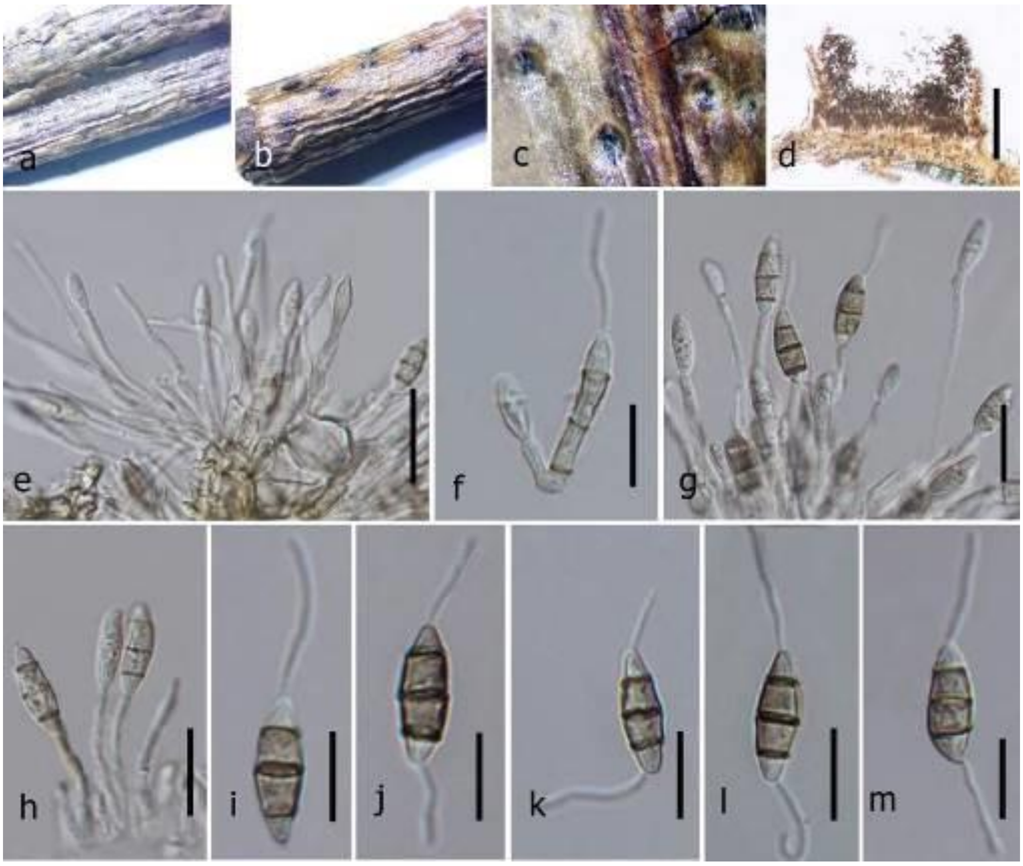


Fig. 72 ***Seimatosporium pseudorosae*** (**holotype**) **a**–**c** Appearrance of conidiomata on dead branches of *Rosa villosa* **d** Cross section of conidiomata **e** Conidia baring conidiophore and paraphyses **f**–**h** Different stages of conidiogenesis **i**–**m** Conidia. Scale bars: d = 200 *µm*, e–h = 20 *µm*, i–m = 10 *µm*.

Xylariales

Diatrypaceae

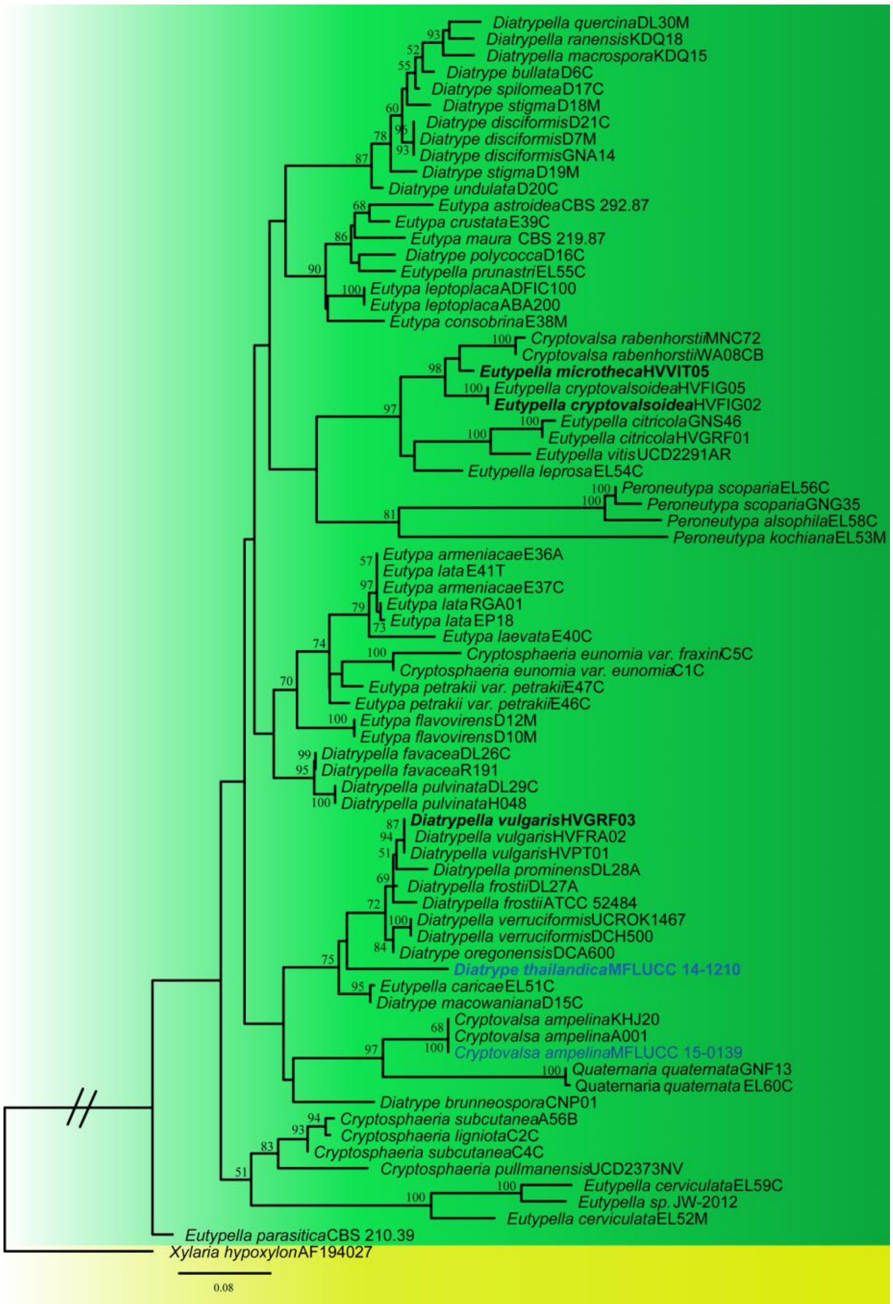


Fig. 73 Phylogram generated from maximum likelihood analysis based on ITS sequence data of the family *Diatrypaceae*. The new isolates are in red and ex-type strains are in bold. The tree is rooted with *Xylaria hypoxylon*.

Cryptovalsa Ces. & De Not. ex Fuckel

Cryptovalsa is a common diatrypaceous genus known to occur on grapevines in the family *Diatrypaceae* which was typified by *C. protracta* (Pers.) De Not. (Mostert et al. 2004; Mehrabi et al. 2015). The genus was characterized by eutypoid ascostromata, polysporous asci and allantoid ascospores (Spooner 1981; Vasilyeva and Stephenson 2005; Trouillas et al. 2011). Currently, there are 58 epithets in Index Fungorum (2016), while four species have been transferred to other genera in *Diatrypaceae*, *Massariaceae* and *Xylariaceae* (Index Fungorum 2016). Molecular data are only available for *C. ampelina* (Nitschke) Fuckel and *C. rabenhorstii* (Nitschke) Sacc. (Trouillas et al. 2011; Mehrabi et al. 2015; EBI 2016; NCBI 2016). *Cryptovalsa ampelina* is the most studied species in *Cryptovalsa* (Nitschke 1867; Mostert et al. 2004; Vasilyeva and Stephenson 2005; Luque et al. 2006; Martín et al. 2009; Trouillas et al. 2010; Trouillas et al. 2011; Mehrabi et al. 2015).

306. *Cryptovalsa ampelina* (Nitschke) Fuckel, Jb. nassau. Ver. Naturk. 23-24: 212 (1870) [1869-70]

Basionym: *Valsa ampelina* Nitschke, Pyrenomycetes Germa-nici 1, p. 156, 1867.

Index Fungorum number: IF 241474, *Facesoffungi number*: FoF 01800, Fig. 74

Saprobic on bark. **Sexual morph** *Stromata* poorly developed, immersed in bark, with occasionally protruding perithecial necks, single or in groups, irregularly scattered. *Ascomata* 510–580 *µm* high, 340–440 *µm* diam. ($\bar{x}$ = 530 × 391 *µm*, n = 8), solitary to gregarious, immersed, dark brown to black, arranged in a single layer, singly arising, in rows globose to subglobose, often compressed, ostiolate, with cylindrical necks, raising above the epidermis and forming black, blister-like areas, periphysate. *Peridium* 35–45 *µm* wide, composed of two layers; outwardly comprising several layers of thick-walled, dark brown to black cells of *textura angularis*, inwardly comprising 3–5 layers of thin-walled, hyaline cells of *textura angularis* to *textura prismatica*. *Hamathecium* comprising dense, 2–4 *µm* wide, hyaline, aseptate, anastomosing paraphyses. *Asci* (98–)118–133(–146) × (7–)7–11(–14) *µm* ($\bar{x}$ = 119 × 9 *µm*, n = 30), polysporous, unitunicate, cylindric-clavate, long pedicellate, apically rounded to truncate with indistinct, amyloid apical annulus. *Ascospores* (7–)7.5–9(–10) × (1–)2–2.5(–3) *µm*, ($\bar{x}$ = 8.3 × 2.4 *µm* n = 60), crowded, pale yellowish to pale brown at maturity, allantoid–reniform, 1-celled, smooth-walled, with small guttules. **Asexual morph** Coelomycetous, forming on MEA. *Conidiomata* 150–260 mm diam., pycnidial, superficial, solitary or aggregated, dark brown to black, globose to subglobose, covering by yellow to light brown interwoven, thick-walled, hyphae. *Conidiophores* 10–22 × 1.5–2 µm ($\bar{x}$ = 18 × 2 µm, n = 10), septate, bicellately to verticillately branched, arranged in dense palisades, cylindrical, hyaline, smooth, arising from the base. *Conidiogenous cells* 8–14 × 1–2 µm ($\bar{x}$ = 11 × 1.5 µm, n = 20), holoblastic, sympodial to synchronous, straight or curved, subcylindrical, hyaline, apically distorted on conidial secession. *Conidia* 16.5–20 × 1–1.5 *µm* ($\bar{x}$ = 18.6 × 1.3 *µm*, n = 55), hyaline, cylindrical to filiform, unicellular, slightly curved, apically rounded, with truncate base.

Culture characteristics: Ascospores germinating on MEA within 24 hours, germ tubes produced at both ends cell, colonies on MEA reaching 4 mm diam. after 7 days in darkness condition at 25 °C, medium dense, raised, circular with fimbriate edge, fluffy to fairy fluffy, white from above, light yellowish from below, forming asexual morph, with black, stromatic after 15 days.

Material examined: ITALY, Fiumana di Predappio, Province of Forlì-Cesena [FC], on dead branch of *Vitis vinifera* L. (*Vitaceae*), 5 January 2015, E. Camporesi, (MFLU 16–0007, KUN-HKAS 93731, **reference specimen designate here**), living culture, MFLUCC15–0139, KUMCC 16-0003).

Notes: *Cryptovalsa ampelina* is a pathogen of grapevines (*Vitis vinifera* L.) and is abundant on pruned canes and necrotic wood of living plants (Mostert et al. 2004; Luque et al. 2006; Trouillas et al. 2010; Pitt et al. 2013a). The species was reported as a pathogen from South Africa, Australia, North East of Spain, California and Eastern United States (Mostert et al. 2004; Vasilyeva and Stephenson 2005; Luque et al. 2006; Trouillas et al. 2010; Pitt et al. 2013a). *Cryptovalsa ampelina* causes internal wood discoloration, similar to that caused by *Eutypa lata* (Pers.) Tul. & C. Tul (Ferreira 1987; Mostert et al. 2004). However, the species can be distinguished from *E. lata* in having polysporous asci and pigmented allantoid ascospores (Luque et al. 2006).

The asexual morph of *Cryptovalsa ampelina* has been reported in the coelomycetous genus *Libertella*, which is characterized by sporodochium-like conidiomata, hyaline, branched conidiophores, with hyaline, subcylindrical, conidiogenous cells which proliferate sympodially and hyaline, filiform, slightly curved to hamate, unicellular conidia, with a truncate, flattened base (Mostert et al. 2004; Luque et al. 2006). In this study, the asexual morph formed in culture on MEA after 20 days. The characters of our taxon are similar to previous studies, although our taxon differs due to its slightly smaller conidia.

Based on phylogenetic analysis of ITS gene dataset (Fig. 73), *Cryptovalsa ampelina* clearly separates from *Eutypa lata* and clusters with *Quaternaria quaternata* (GNF13, EL60C). However, *C. ampelina* can be distinguished from *Q. quaternata* by its polysporous asci. Our strain (MFLU 15-0139) forms a well-supported clade (100% ML) with other strains of *C. ampelina* (KHJ 20 and A 001) in the family *Diatrypaceae* (Fig. 73). Our isolate is similar to the protolgue described by Nitschke (1867) as well as Trouillas et al. (2010). Nevertheless, it differs from the type protoloque in having larger asci (from Saccardo (1882), 75–90 × 8–9 versus (98–)118–133(–146) × (7–)7–11(–14), this study) and slightly smaller ascospores (from Saccardo (1882), 9–10 × 2.5 versus, (7–)7.5–9(–10) × (1–)2–2.5(–3), this study). Therefore, we propose our new collection as a reference specimen.

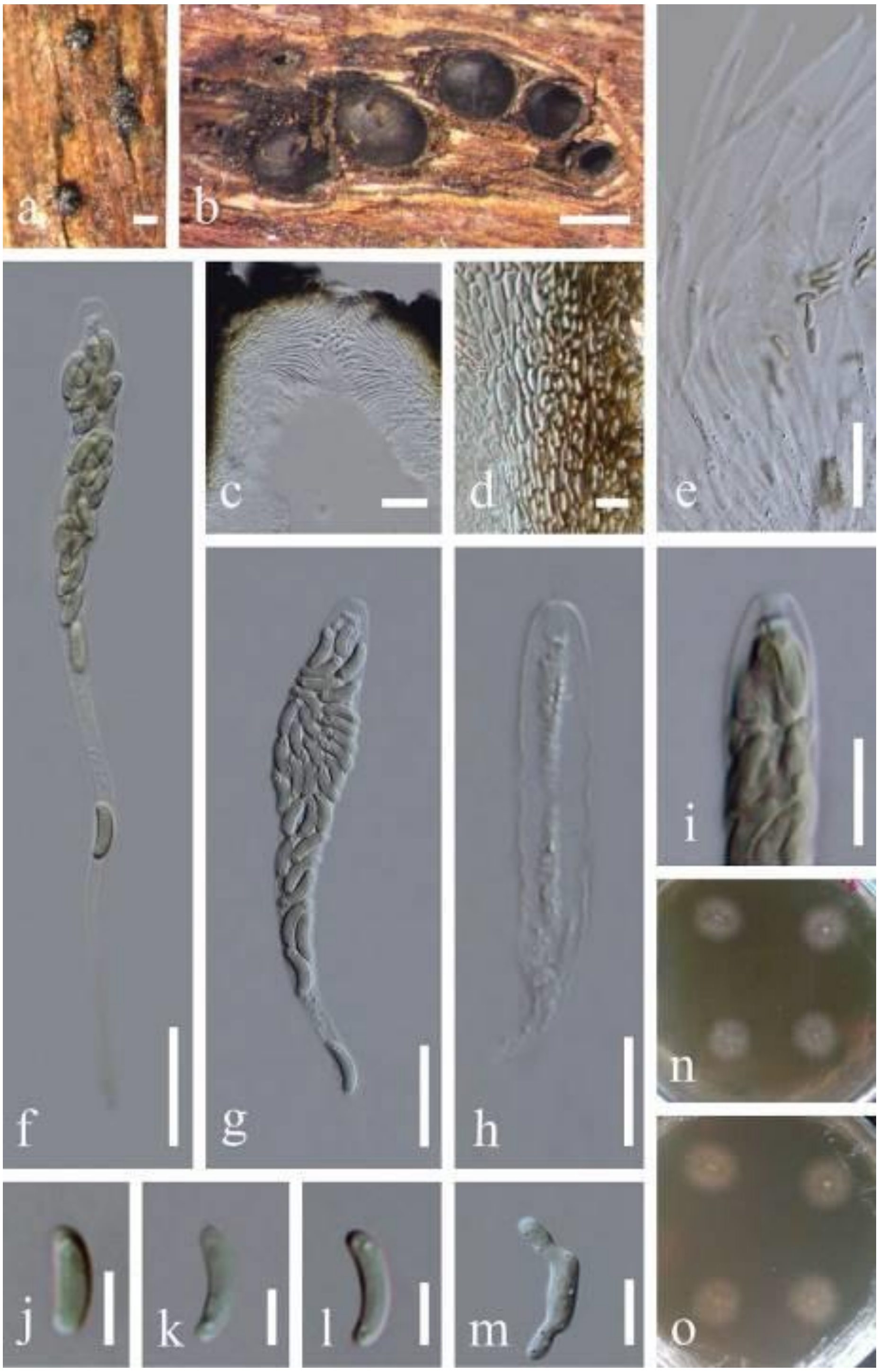


Fig. 74 ***Cryptovalsa ampelina*** (MFLU 16–0007, **reference specimen**) **a** Appearance of stromata on host surface **b** Longitudinal section through stromata showing globose ascomata embedded in stromatal tissues **c** Ostiole with periphysate ostiolar neck **d** Peridium **e** Paraphyses **f, g** Asci **h** Immature ascus **i** Ascus with apical apparatus inconspicuously bluing in Melzer's reagent **j–l** Ascospores **m** Germinating ascospore **n, o** Culture in MEA, note n is from above and o is from below. Scale bars: a = 200 μm, b = 500 μm, c = 30 μm, d = 50 μm, e–g = 20 μm, h, i, m= 10 μm, j–l = 5 μm.

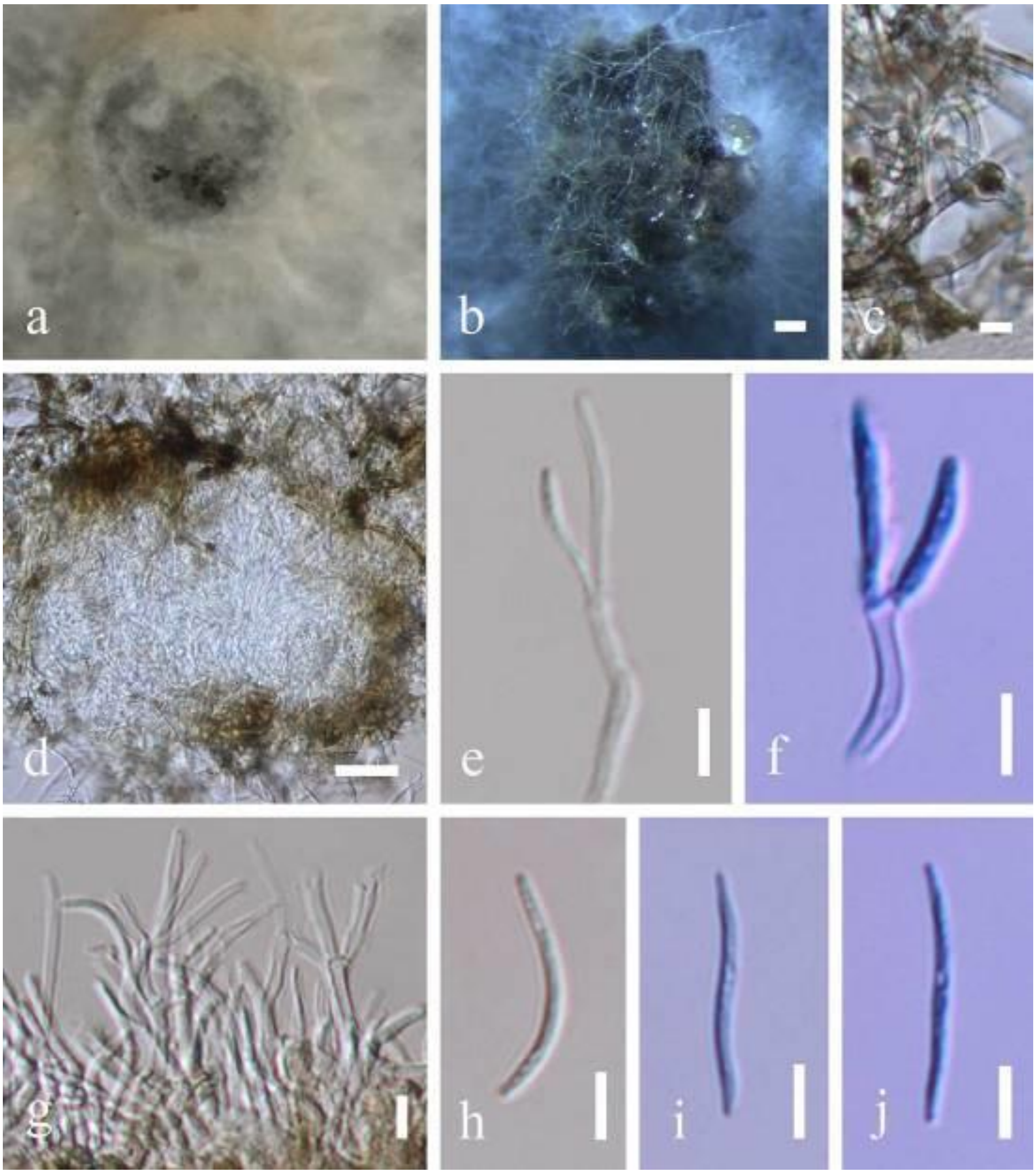


Fig. 75 Culture of ***Cryptovalsa ampelina*** in PDA (MFLU 15–0139) **a, b** Conidiomata on the culture **c** Hyphae on conidiomatal surface **d** Section of conidiomata **e** Conidiophore with young conidia **f** Conidiogenous cells with conidia **g** Conidiophores **h–j** Conidia. (Note: f, i, j with cotton blue) Scale bars: b = 200 *µm*, d= 20 *µm*, c, e–j = 5 *µm*.

307. *Diatrype thailandica* R.H. Perera, J.K. Liu & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 552008, *Facesoffungi number*: FoF 01797, Figs 76, 77

Etymology: The specific epithet *thailandica* refer to the country in which the fungus was first collected.

Holotype: MFLU 15–3662

Saprobic on wood. **Sexual morph** *Stromata* 1–1.2 mm wide, scattered on host, erumpent, arising through the cracks in bark epidermis, with 4 ascomata immersed in a single stromata, comprising an outer, dark brown to black, small, tightly packed, thin parenchymatous cell layer, inner layer yellowish, loosely packed, with parenchymatous cells, with ostioles opening to outer surface, appearing as black spots. *Ascomata* 226–336 *µm* high, 177–235 *µm* diam., ($\bar{x}$ = 282 × 209 *µm*, n = 20), perithecial, immersed in stromatic tissues, aggregated, globose to subglobose, narrowing towards the apex, pale brown, ostiolate. *Ostiolar necks* emerging separately, short, immersed in only dark outer layer of stromata, conical, periphysate. *Peridium* 6.5–15 *µm* wide ($\bar{x}$ = 11 *µm*, n = 20), comprising strata of 4–8 layers of cells of hyaline to dark brown cells of *textura angularis*. *Hamathecium* comprising 2.2–4.5 *µm* wide ($\bar{x}$ = 3 *µm*, n = 20), aseptate, paraphyses, longer than the asci, wider at the apex. *Asci* 55–80 × 5–7 *µm* ($\bar{x}$ = 67 × 6 *µm*, n = 25), 8-spored, unitunicate, with narrow, long, thin-walled pedicel, with cylindrical, thick-walled, swollen upper portion, apex flat, with J-, conspicuous apical apparatus. *Ascospores* 3.8–6.9 × 1–1.4 *µm* ($\bar{x}$ = 5.4 × 1.2 *µm*, n = 20), multi-seriate to overlapping pale brown, allantoid to cylindrical, unicellular, with small, fat globules at the ends, smooth-walled**. Asexual morph** Coelomycetous, libertella-like, *Mycelial clumps* white. *Conidiomata* pycnidial, 0.4–1 mm diam., brownish yellow, becoming dark brown when mature, watery, bubble-like, rounded, conidial masses forming from mycelial clumps. *Pycnidia* superficial, solitary or aggregated, subconical, globose to subglobose, shiny, with smooth surface, yellow, dark brown, comprising brown, thick-walled cells of *textura angularis*. *Conidiophores* 12–16 *µm* high, 1.8–2.3 *µm* wide ($\bar{x}$ =14 × 2.1 *µm*, n = 20) branched, arising from pseudoparenchymatous cells or interwoven hyphae. *Conidiogenous* cells 5.9–10 *µm* high, 1.1–1.8 *µm* wide ($\bar{x}$ = 8.4 × 1.6 *µm*, n = 20), cylindrical, in dense palisades, straight or curved, apically distorted or bearing annellations. *Conidia* 14.2–18 × 0.7–1 *µm* ($\bar{x}$ = 16.7 × 0.9 *µm*, n = 20), filiform, curved or rarely straight, with flattened base and blunt apex, hyaline.

Culture characteristics: Fast growing, reaching 6.7 cm within 14 days on PDA, at 25 °C, circular, flat, with diffuse margin, white, and becoming yellowish-white, dull yellow to brownish with age.

Material examined: THAILAND, Doi Mae Salong, on stems of unidentified plant, 12 March 2015, R.H. Perera, RHP 27 (MFLU 15–3662, **holotype);** *ibid.*, HKAS 92497, isotype), ex-type living culture, MFLUCC 14–1210, CUMCC 15-0019.

Notes: Based on the phylogenetic analysis of ITS sequence data, *Diatrype thailandica* form a separate branch as a sister group with *Diatrypella* and *Diatrype* species. Previous studies by Trouillas et al. (2011) and Acero et al. (2004) suggested that both *Diatrypella* and *Diatrype* are polyphyletic within the family. However *Diatrype thailandica* is morphologically similar to the members of the genus *Diatrype* in both sexual and asexual morph characteristics. In the phylogenetic analysis it has a close relationship with *D. macowaniana* which was isolated from dead branches of *Cassina capensis* in South Africa. *Diatrype thailandica* is different from *D. macowaniana* in having yellow inner cells in the stromata, with smaller, pale brown, mostly allantoid ascospores, and longer asci, while *D. macowaniana* is characterized by stromata with white inner cells, larger, cylindrical ascospores and smaller asci. *Diatrypaceae* is a taxonomically confused family and it is presently difficult to segregate genera (Trouillas et al. 2011; Vasilyeva et al. 2006; Liu et al. 2015).

Therefore, the placement of this isolate into the genus *Diatrype* may require reconsideration in the future together with a revision for the entire family.

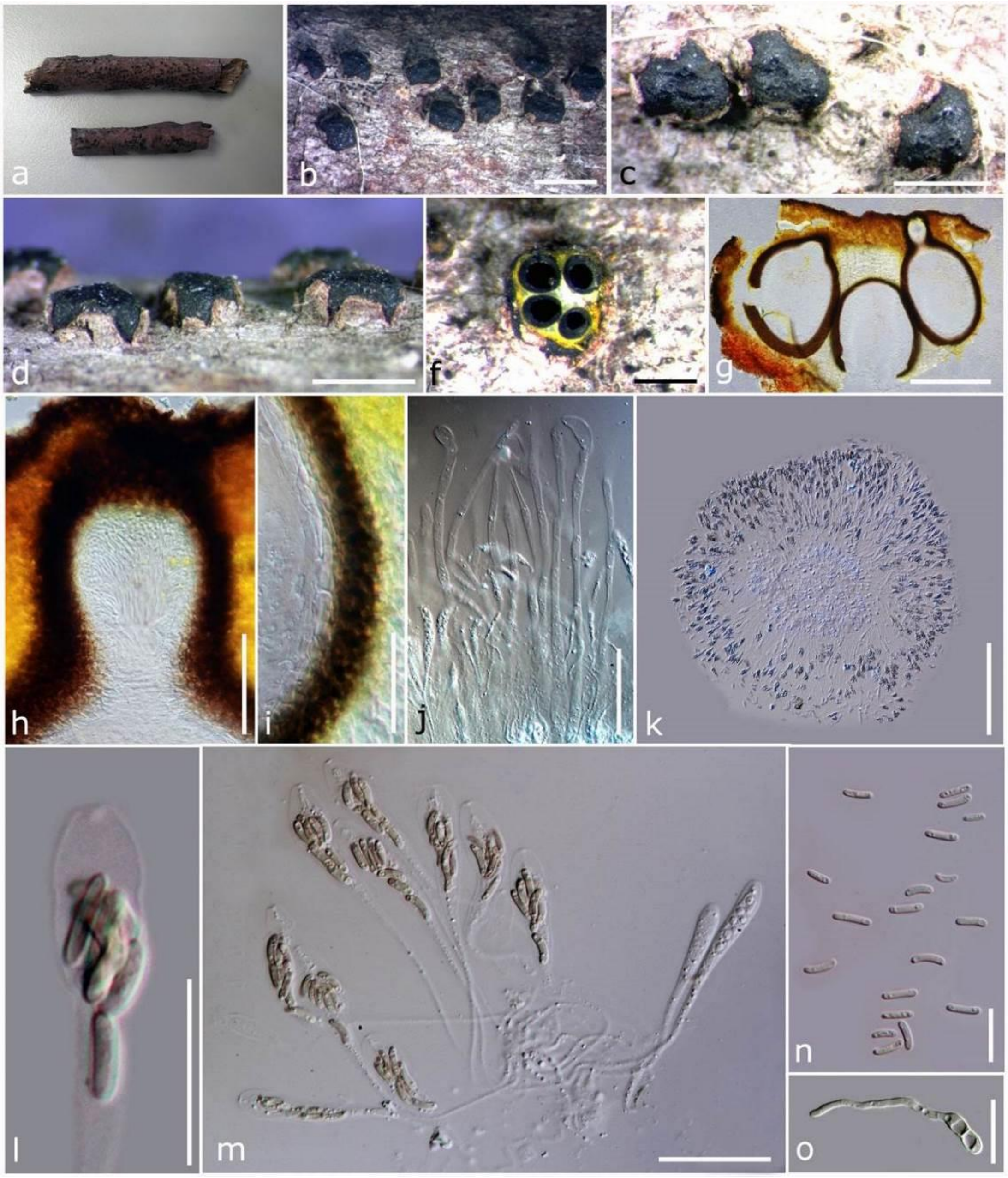


Fig. 76 ***Diatrype thailandica*** (**holotype**) **a** Herbarium material **b–d** Appearance of stromata on host substrate. **e** Longitudinal section through stroma **f** Vertical section through stroma showing ascomata **g** Close up of the ostiole **h** Close up of the peridium **i** Paraphyses **j** Arrangement of asci **k** Ascus in Melzer's reagent **l** Immature and mature asci **m** Ascospores **n** Germinating ascospore. Scale bars: b = 2 mm, c–e = 500 *µm*, f = 50 *µm*, g–j = 20 *µm*, k = 100 *µm*, l = 10 *µm*, m = 20 *µm*, n, o = 10 *µm*.

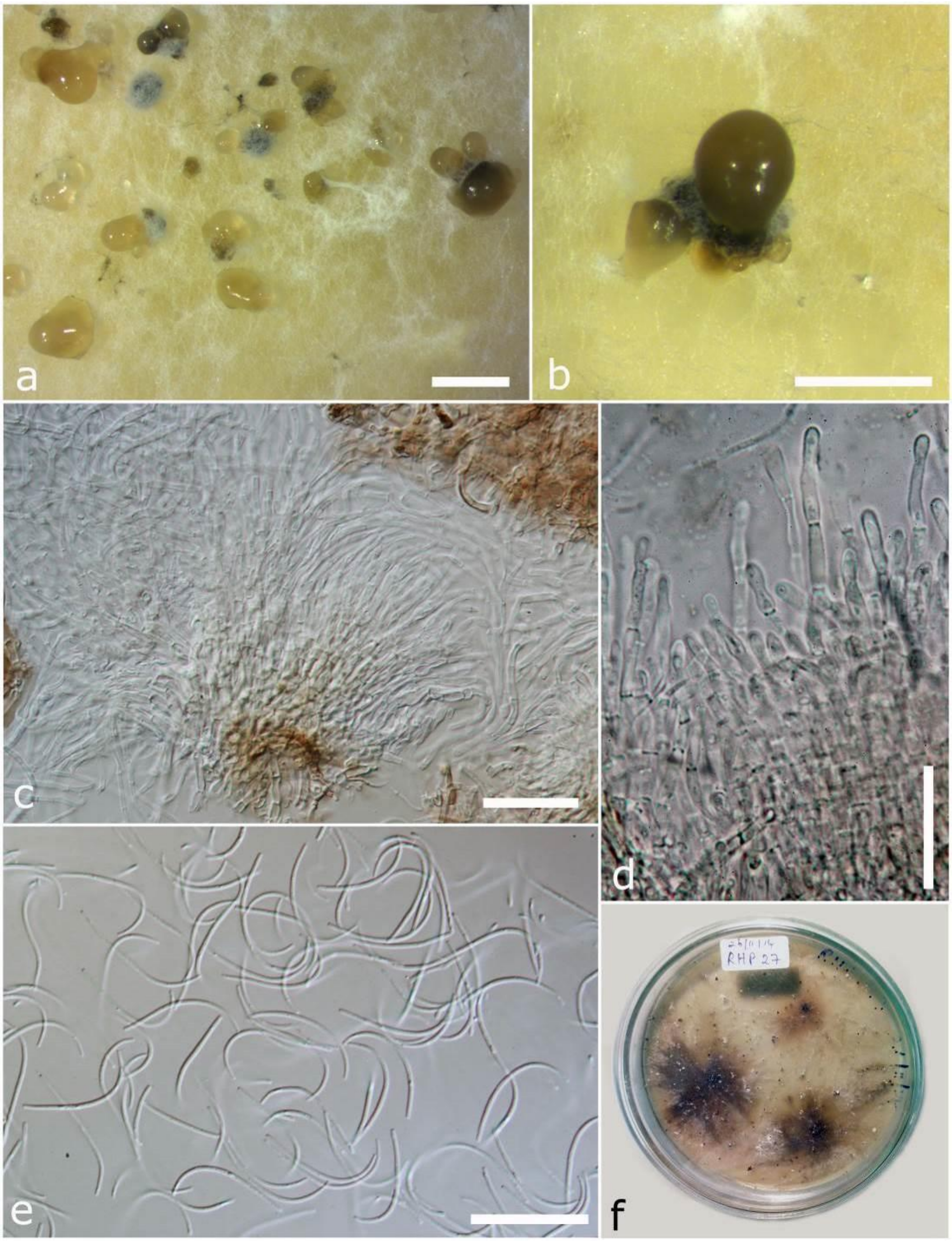


Fig. 77 ***Diatrype thailandica*** (**holotype**) **a, b** Conidiomata on PDA **c** Cross section of conidioma **d** Conidia attached to conidiophores **e** Conidia **f** Sporulation on one month old culture on PDA, 25 °C. Scale bars: a, b = 1 mm, c–e = 20 *µm*.

Xylariaceae

The family *Xylariaceae* is defined as one of the largest families of pyrenomycetous fungi with unitunicate asci and pigmented ascospores. This family comprises about 85 genera (Maharachchikumbura et al. 2015, 2016) with more than 1300 accepted species (Stadler et al. 2013). The majority of *Xylariaceae* are saprotrophs on decaying wood, animal dung, fruits and seeds, leaves and herbaceous stems, while some are endophytes of vascular plants and some are even associated with termite nests (Rogers 2000; Stadler 2011). Morphological characteristics of the sexual morph, such as the stromata, perithecia, asci, ascospore, apical apparatus and germ slit, or of the asexual morph, such as nodulisporium-like and geniculosporium-like are used to delineate species. Phylogenetic analysis of multi-gene sequence data (ITS, LSU, RPB2 and β-tubulin) has shown that *Xylariaceae* comprising two major groups representing the subfamilies *Xylarioideae* and *Hypoxyloideae*. The *Xylarioideae* comprises the genus *Xylaria*, and the asexual morph is known to be geniculosporium-like. The Hypoxyloideae comprises four subclades with the major subclade containing the genera *Hypoxylon* and *Annulohypoxylon* and the second subclade consists of *Daldinia*, *Entonaema* and *Ruwenzoria* and two small subclades of *Rhopalostroma* and *Phylacia* clustering separately in the poorly supported tree. The asexual morphs are either nodulisporium-like or virgariella-like (Stadler et al. 2013). The phylogenetic tree is presented in Fig. 78.

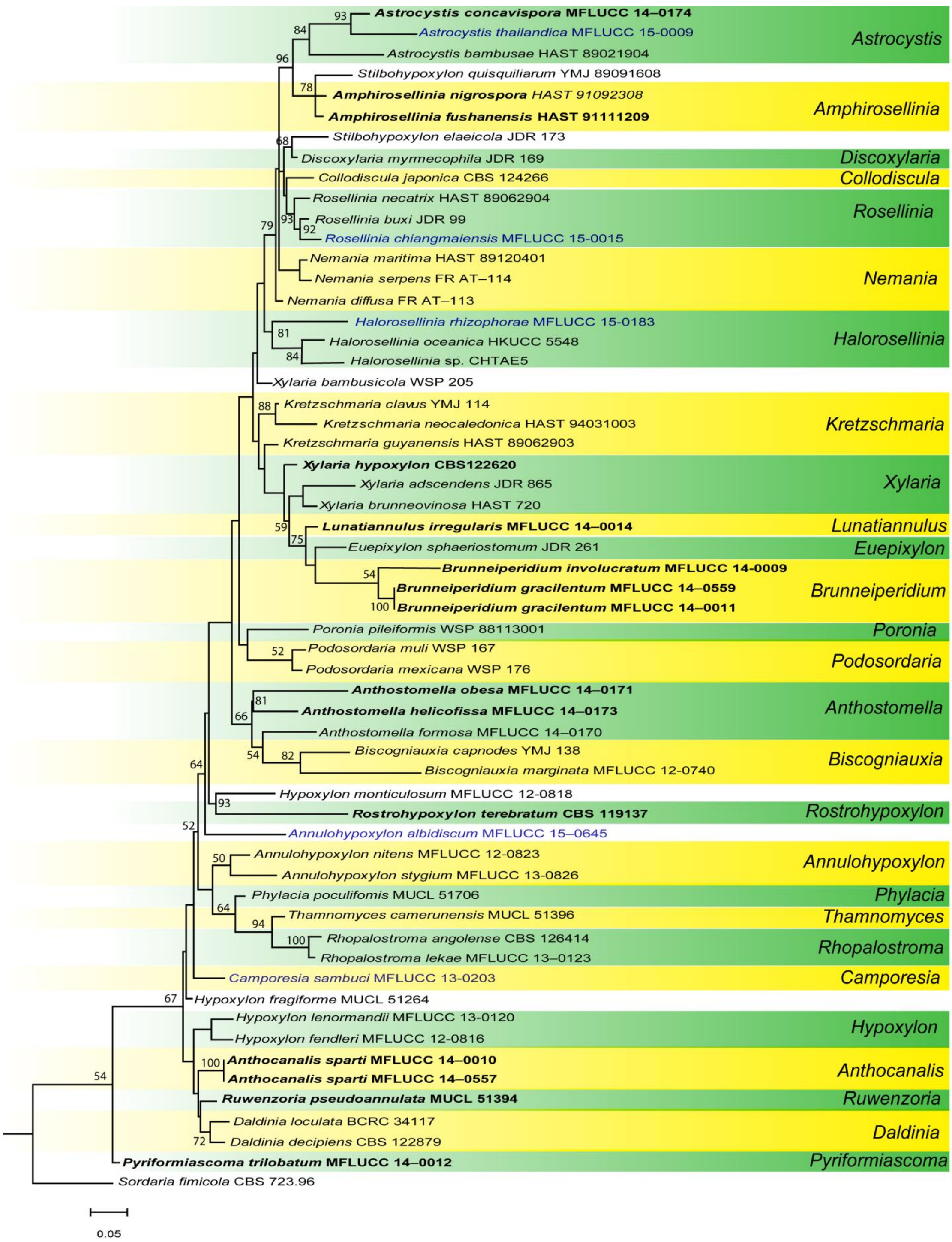


Fig. 78 Phylogram generated from RAxML analysis based on combined ITS, LSU, RPB2 and β-tubulin sequenced data of species of *Xylariaceae*. Maximum Likelihood values equal or greater than 50 are indicated above or below the nodes and branches. The tree is rooted to *Sordaria fimicola*. New taxa are in blue and ex-type strains in bold.

Annulohypoxylon Y.M. Ju, J.D. Rogers & H.M. Hsieh

The genus *Annulohypoxylon* was introduced by Hsieh *et al*. (2005) with the type species *Annulohypoxylon truncatum* (Schwein.) Y.M. Ju, J.D. Rogers & H.M. Hsieh and 53 species are listed to date (Index Fungorum 2016). *Annulohypoxylon* is characterized by effused-pulvinate or pulvinate, glomerate stromata, sphaerical or obovoid perithecia with a carbonaceous stromata layer, with KOH-extractable pigments in most cases, cylindrical, stipitate asci with an apical apparatus and light- to dark-coloured, ellipsoid or short fusoid, nearly equilateral ascospores, with narrowly of broadly rounded ends and a germ slit, and perispore dehiscence or indehiscence in KOH 10% (Hsieh *et al*. 2005). Molecular analysis showed this genus is closely related with *Hypoxylon* with strong support. However, it differs from the *Hypoxylon* in having a carbonaceous stromata layer, discretely enclosing each perithecium, and the ostioles are always higher than the surrounding stromatal surface, usually encircled with a distinct annulate disk (Hsieh *et al*. 2005). The phylogenetic tree for *Annulohypoxylon* is presented in Fig. 79.

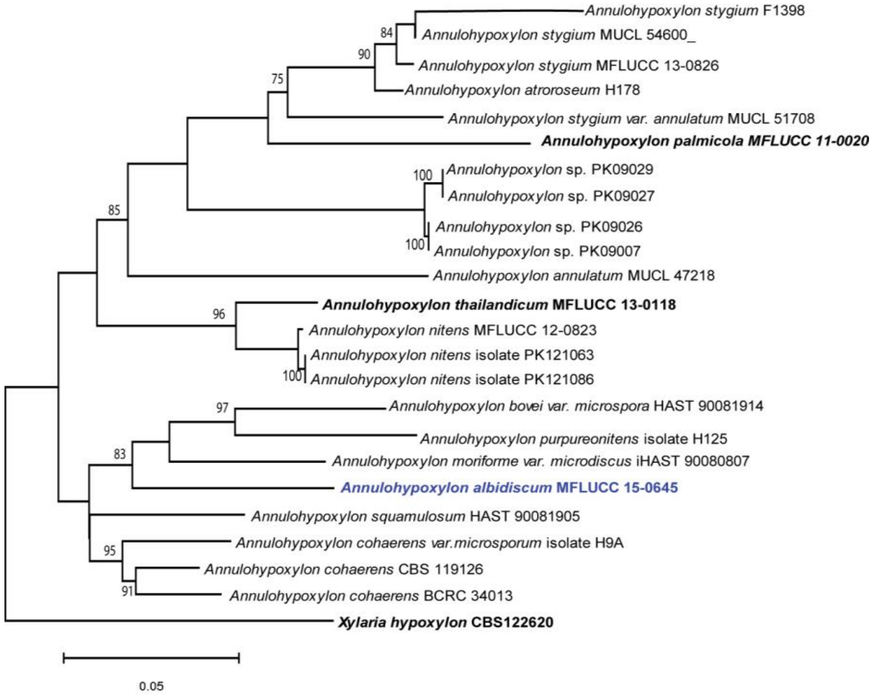


Fig. 79 Phylogram generated from RAxML analysis based on ITS sequence data of species of *Annulohypoxylon*. Maximum Likelihood values equal or greater than 50 are indicated above or below the nodes and branches. The tree is rooted to *Xylaria hypoxylon*. Newly introduced taxa in this study are highlighted in blue and ex-types are in bold.

308. *Annulohypoxylon albidiscum* J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, ***sp. nov.***

Indexfungorum number: IF 551809, *Facesoffungi number*: FoF 01812, Fig. 80

Holotype: MFLU 15–3883

Etymology: From the Latin *albus* referring to white, and *discus* meaning disc, in reference to the morphology of stromata, which have a white, flattened truncatum-type disc, encircling the ostioles.

Saprobic on decorticated wood. **Sexual morph** *Stromata* 1.5–7.5 × 1–4.5 × 0.2–0.5 cm, ($\bar{x}$ = 5.2 × 2.8 × 0.35 cm), glomerate, pulvinate to effused-pulvinate, with conspicuous perithecial mounds, surface shiny black, sphaerical to hemisphaerical, carbonaceous, blackish granules immediately beneath surface and between perithecia, with KOH-extractable pigments greenish-olivaceous (90). *Ostioles* conical, papillate, encircled with a white, flattened *truncatum*-type disc. *Perithecia* 0.4–0.8 mm diam., sphaerical. *Peridium* laterally 43–51 *µm* thick, composed of carbonaceous, thick-walled, dark brown to black cells of *texura angularis*. *Hamathecium* comprising long, septate paraphyses, 4.5–5.3 *µm* wide at the base, 1.5–2.5 *µm* wide at the apex, with hyaline, guttulate cells. *Asci* (61–)77–87(–97) × 3.5–5 *µm* ($\bar{x}$ = 83.5 × 4.3 *µm*, *n* = 20), 8-spored, unitunicate, cylindrical, long pedicellate, with a wedge-shaped, J+, subapical apparatus, 0.7 × 1.6 *µm*. *Ascospores* 7.1–7.9(–8.4) × (3.4–)3.6–4.2(–4.8) *µm* ($\bar{x}$ = 7.7 × 3.8 *µm*, *n* = 30), uniseriate, 1-celled, inequilaterally ellipsoidal, with narrowly rounded ends, light brown to brown, with or without guttules when young, germ slit straight, running along the entire spore-length on flattened side **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on WA within 12 h and germ tubes produced from ends. Colonies growing fast on PDA, reaching 7 cm in 7 days at 25–28 °C, whitish colonies, azonate with diffuse margins, reverse at first whitish and turning light brown after 5 days.

Material examined: THAILAND, Chiang Rai, Muang District, Mae Chang Hot Spring, on limestone outcrops, on decorticated wood of unidentified host, 25 November 2014, JinFeng Zhang, ZJF–16 (MFLU 15–3883, **holotype**), ex-type living culture, MFLUCC 15–0645.

Notes: This is a typical *Annulohypoxylon* species with pulvinate to effused-pulvinate stromata, long cylindrical asci and pale brown, inequilaterally ellipsoidal ascospores. As well it is reminiscent to *A. stygium* (Lév.) Y.M. Ju et al. and *A. nitens* (Ces.) Y.M. Ju et al., regarding the stromatal characters. However, *A. albidiscum* differs from *A. stygium* in having larger perithecia (0.4–0.8 mm vs. 0.2–0.3 mm), a wider ascal apical apparatus (1.6 *µm* vs. 0.7 *µm*) and having white, flattened *truncatum*-type disc encircling the ostioles. In addition, the KOH-extractable pigments of this specimen is greenish-olivaceous (90), whereas, the latter is greenish olivaceous (90) or dull green (70) (Ju and Rogers 1996). *Annulohypoxylon albidiscum* is distinct from *A. nitens* (Ces.) because the latter has a vinaceous reddish tone in the younger stages (Ju and Rogers 1996), as well as the asci of *A. albidiscum* are significantly shorter than the latter (77–87 *µm* long vs. 110–140 *µm* long). The phylogenetic analysis showed that the *A. albidiscum* clustered with other *Annulohypoxylon* species and is phylogenetically closely related to *A. bovei* var. *microspora* (J.H. Mill.) Y.M. Ju et al., *A. moriforme* var. *microdiscus* (Y.M. Ju & J.D. Rogers) Y.M. Ju et al. and *A. purpureonitens* (Y.M. Ju & J.D. Rogers) Y.M. Ju et al., but they have different morphological characters.

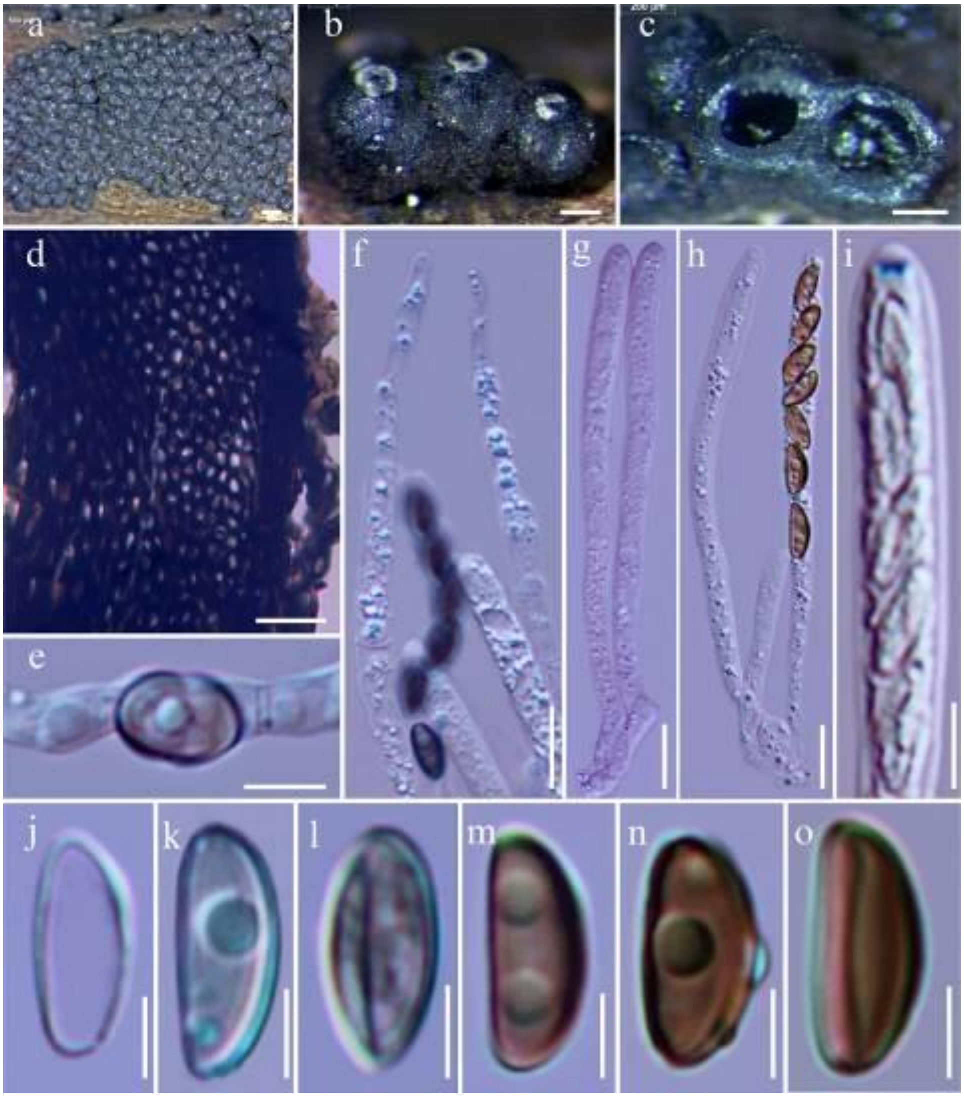


Fig. 80 ***Annulohypoxylon albidiscum*** (**holotype**) **a** Stromata habit on wood **b** Stromata in side view **c** Cross section of the stromata showing perithecia **d** Section of peridium **e** Germinating ascospore **f** Long, hyaline paraphyses **g–h** Asci with ascospores in water **i** Ascus in Melzer's reagent, showing the J+, subapical ring **j–o** Ascospores. Scale bars: a = 500 *µm*, b, c = 200 *µm*, d, f–i = 10 *µm*, j–o = 3 *µm*.

Astrocystis Berk. & Broome

Astrocystis was introduced based on *A. mirabilis* Berk. & Broome, a bamboo-inhabiting xylariaceous taxon. The stellate or coronate appearance of the stromata is characteristic feature of the *Astrocystis* species (Læssøe and Spooner 1994). The genus is mostly confined to monocotyledons such as bamboo and has superficial, uniperitheciate stromata, which may develop beneath the host cuticle. The asci are relatively short-stipitate, with a relatively small, amyloid and stopper-shaped ascal apparatus (Smith et al. 2001). Index Fungorum (2015) listed 24 *Astrocystis* species epithets.

309. ***Astrocystis thailandica*** Daranagama & K. D. Hyde, ***sp. nov.***

Indexfungorum Number: IF 551727, *Facesoffungi number*: FoF 01637, Fig. 81b

Etymology: Referring to the country, Thailand where the species was collected.

Holotype: MFLU 15–3525

Saprobic on bamboo clumps. **Sexual morph** *Stromata* superficial, gregarious, black, shiny, smooth, carbonaceous, multi-peritheciate, with 2–3 perithecia, 650–1075 × 250–375 *µm* ($\bar{x}$ = 720 × 310 *µm*, n = 10), globose to hemisphaerical, carbonaceous, with black, stellate area of mixed host and stromatic material encircling the base of stromata. *Ostioles* papillate, black. *Peridium* >50 *µm* wide, comprising several thick layers of compressed cells, black. *Hamathecium* comprising numerous, 2 *µm* wide, filamentous, septate, paraphyses, embedded in a gelatinous matrix. *Asci* 88–125 × 8.2–12.2 *µm* (x = 93.5 × 10.5 *µm*, n = 25), 8–spored, unitunicate, cylindrical–clavate, short pedicellate, apically rounded, with a J+, wedge-shaped apical apparatus, 4.5–5 × 2.5–3 *µm*. *Ascospores* 17–24 × 6.2–7.5 *µm* (x = 20 × 6.8 *µm*, n = 25), overlapping uniseriate, dark brown, equilaterally ellipsoidal, unicellular, germ slit full-length or ¾ of the length, with a conspicuous mucilaginous sheath, forming slimy caps at both ends. **Asexual morph** Undetermined.

Culture characteristics: Colonies on Difco OA plates at 25–28 °C reaching 5 cm edge Petri-dish in 2 weeks, at first whitish, felty, azonate, with diffuse margins, after 3 weeks become citrine; reverse turning light brown.

Material examined: THAILAND, Chaing Mai Province, road to Wat Pa Dang, on clumps of fallen bamboo clumps, 14 August 2014, Anupama Daranagama AXL 323 (MFLU 15–3525, **holotype,** HKAS 92485, **isotype**), living culture, MFLUCC 15–0009, KIBCC.

Notes: *Astrocystis thailandica* displayed a close relationship with *A. eleiodoxae* A. Pinnoi et al., which was also encountered in Thailand on submerged petioles of *Eleiodoxa conferta* (Pinnoi et al. 2010). However *A. thailandica* differs from *A. eleiodoxae* because of its unique characters such as, superficial stromata with black, stellate stromatic material encircling the base, shorter and wider asci and ascospores with a thick, conspicuous mucilaginous sheath forming slimy caps at both ends. According to the phylogenetic analysis the species clustered with other *Astrocystis* species with 93 bootstrap support forming a monophyletic clade. As well as the phylogenetic analysis of the genus (Fig. 81a) confirmed the placement of *Astrocystis thailandica* with a high bootstrap support, as a distinct species from other *Astrocystis* species.

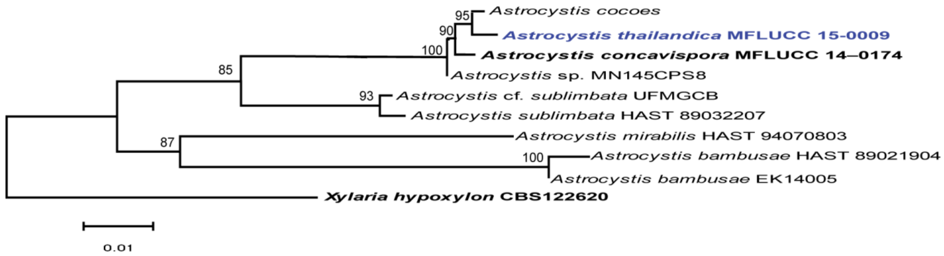


Fig. 81a Phylogram generated from RAxML analysis based on ITS sequenced data of *Astrocystis*. Maximum Likelihood values equal or greater than 50 are indicated above

or below the nodes and branches. The tree is rooted to *Xylaria hypoxylon*. Newly introduced taxa in this study are highlighted in blue.

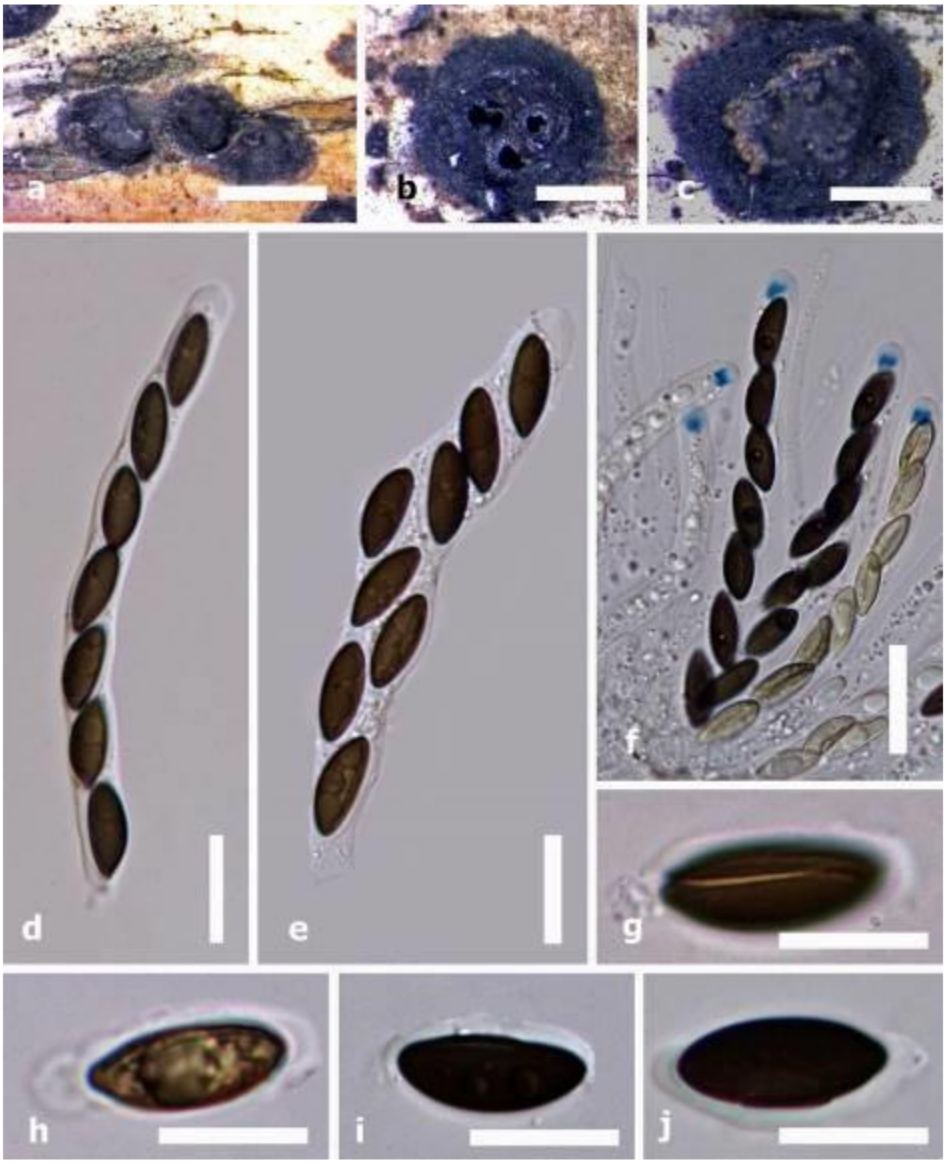


Fig. 81b ***Astrocystis thailandica*** (**holotype**) **a** Stromata on host surface **b** Multi-peritheciate ascomata **c** Papillate ostiole **d, e** Mature asci **f** Apical apparatus bluing in Melzer's reagent **g** Ascospore with straight germ slit **h, i** Developmental stages of ascospores with sheath. Scale bars. a = 2000 *µm*, b, c = 500 *µm*, d–j = 10 *µm*.

310. ***Camporesia*** W.J. Li & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF 552005; *Facesoffungi number*: FoF 01822

Etymology: Named after the collector Erio Camporesi

Type species: *Camporesia sambuci* W.J. Li & K.D. Hyde

Saprobic on dead stems of plant host. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* pycnidial, globose, superficial to subepidermal, separate, unilocular, thick-walled, ostiolate. *Peridium* composed of cells of *texura angularis*, with inner layers hyaline gradually merging with the outer dark brown layers. *Conidiophores* short, unbranched, hyaline, formed from the innermost layer of wall cells. *Conidiogenous cells* hyaline, phialidic, ampuliform, smooth-walled, with a periclinal wall thickening at the tip. *Conidia* pale brown, fusiform, rounded at both ends, 2–3-septate, smooth-walled.

Notes: The asexual morph of *Xylariaceae* has mainly been linked to hyphomycetous (i.e. genicolosporium-like and nodulisporium-like) (Ju and Rogers 1996). Subsequently, the asexual structures were extended to libertella-like coelomycetous genera (Ju et al. 1993, Stadler et al. 2013, Senanayake et al. 2015). *Camporesia sambuci* was collected form *Sambucus ebulus* L. and is characterized by globose pycnidia and pale brown, fusiform conidia with 2–3-septa. *Camporesia sambuci* is morphologically distinct from libertella-like species, which have hyaline, long slender falcate conidia. The phylogeny of the family *Xylariaceae* is reconstructed based on combined gene (LSU, ITS, RPB2 and β-tubulin) analysis, showing that *Camporesia sambuci* clusters away from any other genera in *Xylariaceae* (Fig. 78). Thus *Camporesia* is introduced as a novel genus in this study.

311. ***Camporesia sambuci*** W.J. Li & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 552006 *Facesoffungi number*: FoF 01823, Fig. 82

Etymology: Named after the host genus *Sambucus*

Saprobic on dead stems of *Sambucus ebulus*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 100–150 *µm* high, 200–250 *µm* diam., pycnidial, globose, superficial to subperidermal, separate, unilocular, thick-walled, ostiolate. *Peridium* 30–50 *µm* wide, composed of 6-8 layers, with outer 4–5 layers of dark brown and inner 2-3 layers of pale brown to hyaline cells *texura angularis*. *Conidiophores* short, unbranched, hyaline, formed from the innermost layer of wall cells. *Conidiogenous cells* 10–15 × 2–4 *µm*, phialidic, ampuliform, hyaline, smooth, with a periclinal wall thickening at the tip. *Conidia* 8–15 × 4–5 *µm* ($\bar{x}$ = 10 × 4.5 *µm*; n = 20), pale brown, fusiform, rounded at both ends, 2–3-septate, smooth.

Culture characteristics: *Colonies* fast growing on PDA, reaching 20 mm diam. after one week at 20–25 °C, with circular margin, whitened, flattened, felt-like, with filamentous, dense, aerial mycelium on the surface, reverse similar in colour.

Material examined: ITALY, Province of Arezzo [AR], near Passo della Consuma, on dead stem of *Sambucus ebulus* (*Adoxaceae*), 19 June 2012, Erio Camporesi, IT–450 (MFLU 15–3905, **holotype**); ex-type living culture, MFLUCC 13–0203, ICMP 20775.

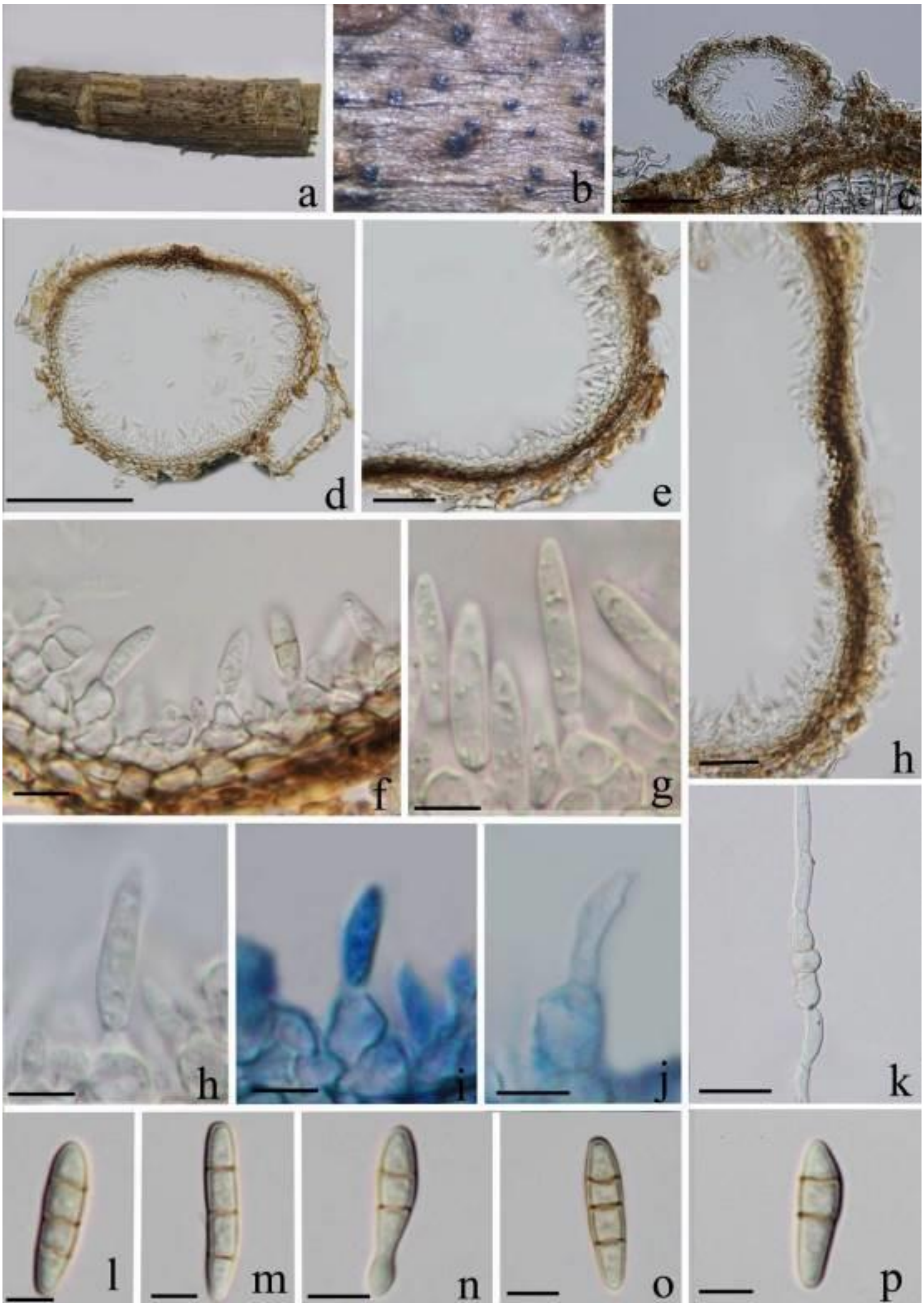


Fig. 82 ***Camporesia sambuci*** (**holotype**). **a** Herbarium specimen **b** Appearance of black coniodiomata on the host **c**, **d** Vertical sections of conidiomata **h** Section of peridium **f**–**j** Conidiophores, conidiogenous cells and developing conidia **k** Germinated spore **l**–**p** Conidia. Scale bars c–d = 100 *µm*, e = 20 *µm*, f–j = 5 *µm*, k = 10 *µm*, 1–p = 5 *µm*.

Durotheca Læssøe et al.

The genus *Durotheca* was introduced by Læssøe et al. (2013) with *D. depressa* Læssøe & Srikitik. as type species and *D comedens* (Ces.) Læssøe & Srikitik. and *D. rogersii* (Y.M. Ju & H.M. Hsieh) Læssøe & Srikitik. transferred from *Theissenia* based on morphology and molecular phylogeny. *Durotheca* is characterized by stromata which are erumpent through bark or wood, initially covered in white pruina, highly carbonaceous tissue, globose to cylindrical perithecia, with or without columella, and filiform and distantly septate paraphyses. Mature asci deliquescent early and young asci are clavate, without an apical apparatus. Ascospores are moderate to very thick-walled, pale to medium brown, ellipsoid–oblong to allantoid, and with or without a germ slit. The phylogenetic tree is presented in Fig. 83.

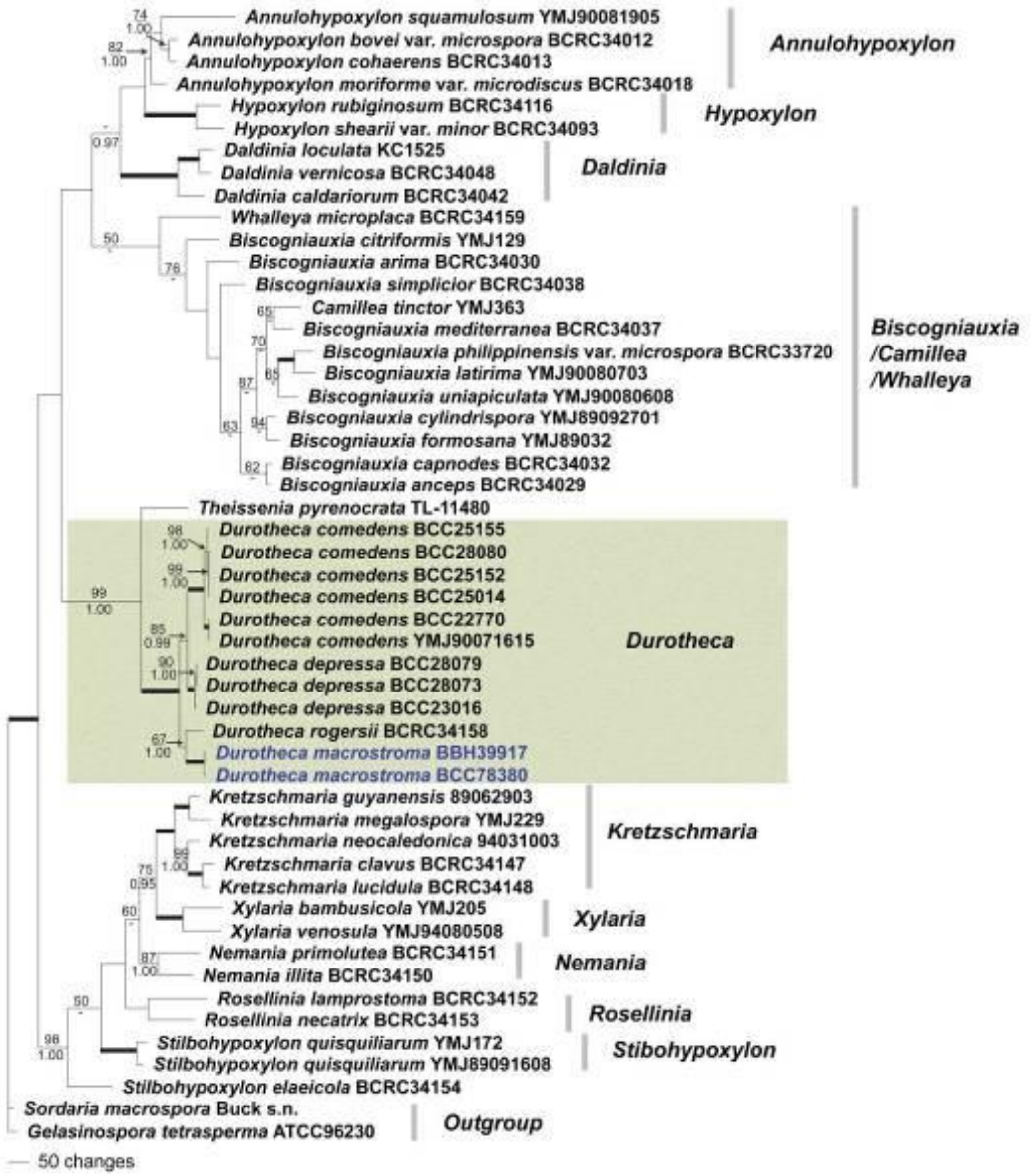


Fig. 83 One of four MPTS inferred from combined β-tubulin and α-actin gene dataset generated with maximum parsimony and Bayesian analysis. Maximum parsimony bootstrap value greater than 50% and Bayesian posterior probabilities greater than 0.95 are given above and below each clade, respectively. The internodes that are highly supported by bootstrap

(100%) and posterior probabilities (1.00) are shown as a thicker line. New taxa are in blue and ex-type strains in bold.

312. *Durotheca macrostroma* Srikitik., Wongkanoun & Luangsa-ard, ***sp. nov.***

Index Fungorum number: IF 551628, *Facesoffungi number*: FoF 02033, Fig. 84

Etymology: based on the large stroma when compare with other *Durotheca* species.

Holotype: BBH39917

Saprobic on bark of dead *Castanopsis acuminatissima* (Blume) A.DC. **Sexual morph** *Stromata* superficial, solitary, subglobose 1 cm thick × 2.3–2.4 cm diam., stromata surface smooth, chalky white, creamy, owing to the presence of a thin pruina, when mature surface greyish green (28C3), crust and tissue highly carbonaceous, with beveled margin. *Perithecia* completely immersed, usually monostichous, globose-ovoid, 1.8–2 mm high × 0.8–1 mm diam. *Ostioles* umbilicate/lower than stromatal surface. Paraphyses not observed. *Asci* 8-spored, deliquescing, mature asci not observed, young asci 77–93.5 × 11–13 *µm*, cylindrical, and long stalked, apical apparatus lacking, and no reaction with Melzer's reagent. *Ascospores* light brown, unicellular, oblong to allantoid in side view, smooth-walled, (13–) 14–16 (–17.5) × (5–) 6–7 (–8) *µm* ($\bar{x}$ = 15.03 × 6.67 *µm*, n = 54), germ slit lacking; perispore non-dehiscent in 10% KOH. **Asexual morph** Undetermined.

Culture characteristics: Colony on PDA reaching 49–51 mm diam. in 10 days, the culture produced botryose structures from the type and paratypes after 4 weeks. Mycelia initially white and fluffy, turning to yellow brown after 2 weeks.

Material examined: THAILAND, Chaiyaphum, Phu Khiao Wildlife Sanctuary, 12 August 2015, on *Castanopsis acuminatissima* wood (*Fagaceae*), P. Srikitikulchai & S. Wongkanoun (BBH39917, **holotype**); ex-type living culture, BCC78380.

Distribution: Only known from a single site in Phu Khiao Wildlife Sanctuary in northeastern Thailand.

Notes: Molecular phylogenetic analyses of combined β-tubulin and α-actin gene datasets based on maximum parsimony and Bayesian analysis has placed *D. macrostroma* in *Durotheca*. *Durotheca macrostroma* differs from other *Durotheca* species in having a large stroma; the shape of *D. macrostroma* is subglobose, 10 mm thick, while other species are widely effused-pulvinate and are not over than 2.5 mm thick. The ascospores of *D. macrostroma* are smaller than other *Durotheca* species. In addition, the phylogenetic tree supported the position of *D. macrostroma* as closely related to *D. rogersii* with 100% bootstrap support. They differ in the shape of stromata and ascospore shape and size. *Durotheca rogersii* has a widely effused-pulvinate 2.5 mm thick stroma (Ju et al. 2007), while that of *D. macrostroma* is very thick (10 mm) and subglobose. Ascospores of *D. rogersii* have very thick walls (3–4.5 *µm*) and are larger (25–36 × 19–24 *µm*) than *D. macrostroma*, but all lack a germ slit.

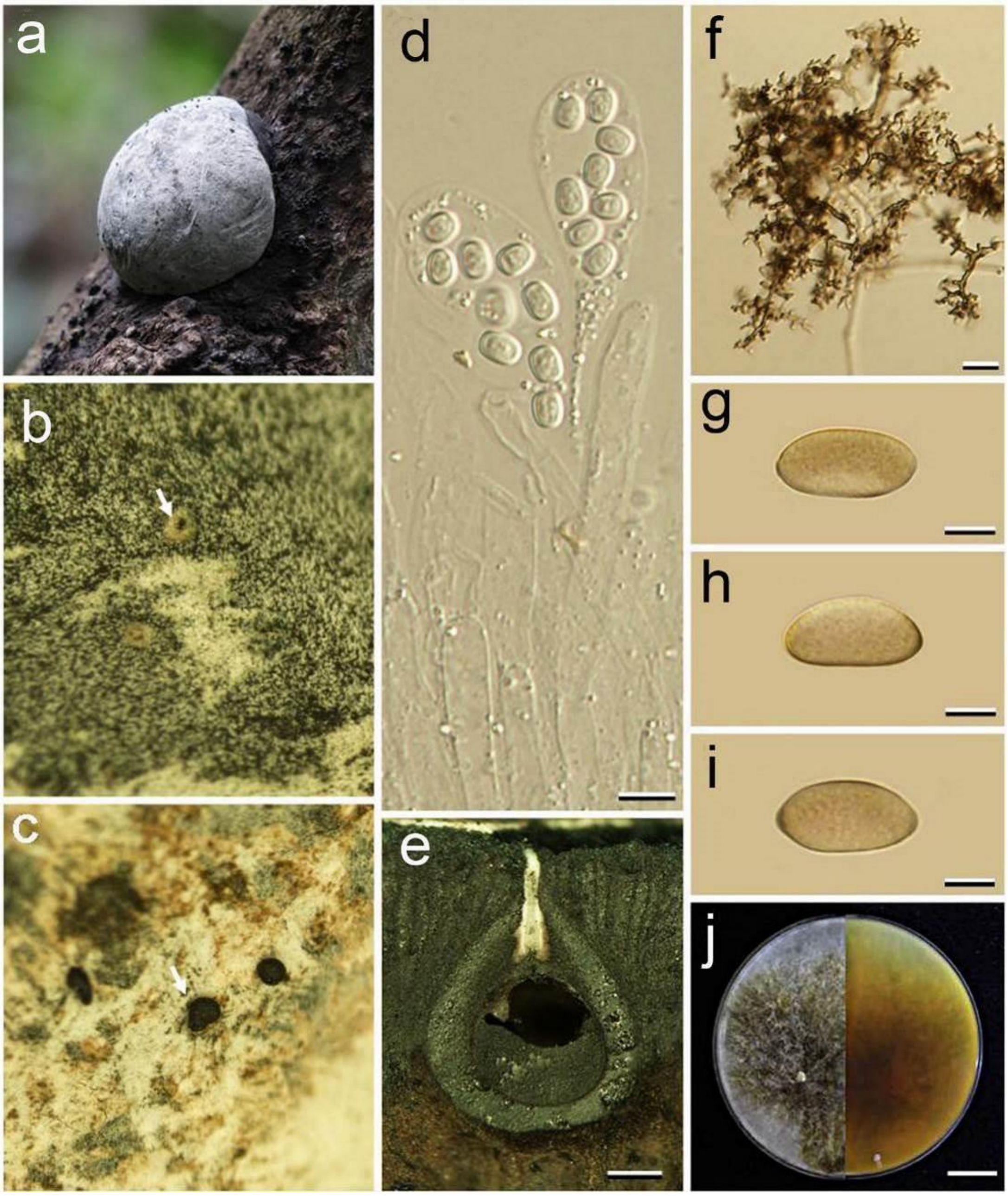


Fig. 84 ***Durotheca macrostroma*** **(holotype)** **a** Stroma on bark **b** Stroma surface and ostiole, arrow: ostioles **C** Ascospore release on apex of ostioles, arrow: black spore mass **d** Young asci **e** Perithecium **f** Botryose structures produced in culture **g–i** Ascospores **j** Colony on PDA plate after 2 weeks. Scale bars: d = 5 *µm*, e = 0.25 mm, g–i = 5 *µm*, f = 10 *µm*, j = 1 cm.

Halorosellinia Whalley et al.

Halorosellinia is a monophyletic genus with a single species *Hypoxylon oceanicum* S. Schatz which is characterized by uniperitheciate ascomata which are immersed in a pseudostroma (Whalley et al. 1999).

313. ***Halorosellinia rhizophorae*** Dayarathne, Jones E.B.G. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551858, *Facesoffungi number*: FoF 01811, Fig. 85

Etymology: Name referring to the host genus *Rhizophora*.

Holotype: MFLU 15–0183

Saprobic on dead root of *Rhizophora* sp. submerged in marine habitats. **Sexual morph** *Pseudostromata* 1.5–2.5 × 0.9–1 *mm* ($\bar{x}$ = 2 × 0.8 *mm*; n = 10), semi-immersed, pulvinate to hemisphaerical, in clusters of up to 20 uni peritheciate pseudostromata, surface black, carbonaceous, lacking ascomatal projections. In section pseudostromata comprises host cells, filled with amorphous black fungal material. *Ascomata* 350–380 × 96–114 *µm* ($\bar{x}$ = 365 × 105 *µm*; n = 10), immersed in pseudostroma, subglobose to hemisphaerical, black, ostioles papillate. *Peridium* 25–38 *µm* wide, two-layered, outer layer of cells of *textura angularis*, black, fusing at the outside with the pseudostromata, inner layer of elongate cells, dark brown to black. *Paraphyses* 1–3 *µm* wide, hyaline, abundant, persistent, aseptate. *Asci* 165–270 × 12–18 *µm* ($\bar{x}$ = 217.5 × 15 *µm*; n = 20), overlapping, 6–8-spored, cylindrical, long pedicellate, unitunicate, with J^+, rectangular apical ring. *Ascospores* 24–36 × 10–15 *µm* ($\bar{x}$ = 30 × 12.5 *µm*; n = 20) overlapping uniseriate, light brown when immature, dark to opaque brown when mature, more or less equilaterally ellipsoid, ventral side varying in degree of convex curvature, upper end broadly rounded, lower end slightly pointed, 1-celled, 1–2-guttulate, without appendages, germ slit on the ventral side, straight, ¾ total length of spore. **Asexual morph** Undetermined.

Culture characteristics: *Colonies* on PDA at 25–28 °C reaching 5 cm in 7 days, whitish, zonate with diffuse margins, reverse at first whitish and turning light brown after 3–4 days.

Material examined: THAILAND, Krabi Province, Krabi, 8°25'52" N, 98°31'42" E, 0 m asl., on submerged root of *Rhizophora* sp., 7 December 2014, Monika Dayarathne, KRB018 (MFLU 15–0183, **holotype**, HKAS 92496 **isotype**); ex-type living culture, MFLUCC 15–1281, KUMCC 16-0004.

Notes: Distinctive features of *Halorosellinia* include a poorly developed pseudostromata which lack extractable pigments in KOH, asci with a relatively large apical apparatus, that become dark blue in Melzer's reagent and ascospores with a prominent, straight germ slit on the ventral side (Whalley et al. 1999). The new species, *Halorosellinia rhizophorae* is clearly different from the type, *Halorosellinia oceanica* (S. Schatz) Whalley et al. in lacking ascomatal projections (Table 4). They are approximately similar in ascospore morphology being 1-celled, light brown to opaque brown, more or less equilaterally ellipsoid, with the ventral side varying in the degree of convex curvature, the upper end broadly rounded, lower end slightly pointed, and with 1–2 guttules. A *Geniculosporium*-like asexual morph was reported from the ex-type culture of *H. oceanica* (Whalley et al. 1999). However, an asexual morph was not found associated with *H. rhizophorae* on host substrate or in culture media. *Halorosellinia rhizophorae* also has morphological affinities to *Nemania maritima* having more or less inequilaterally ellipsoid ascospores with germ slits. However, ascospores of *H. rhizophorae* are larger than that of *N. maritima* [9–12 × 5–6(–6.5) *µm*]. When considering the differences between these taxa, in *H. rhizophorae* the ascomata are immersed in a pseudostroma, asci have a long stipe with a well-developed apical ring. In *N. maritima* ascomata are aggregated and submerged in the carbonaceous stroma and asci are short-stalked. Maximum likelihood analysis of combined ITS and LSU sequence data confirmed the placement of *H. rhizophorae* within the family *Xylariaceae*, where it forms a sister clade to the type, *H. oceanica* with 81% bootstarp support (Fig. 78). However, *H. rhizophorae* is distantly placed from *Nemania* spp. in the phylogenetic analyses.

Table 4 Comparison of the measurments of *Halorosellinia oceanica* and *H. rhizophorae*.

Characters	***H. oceanica***	***H. rhizophorae***
Pseudostromata	0 ± 4–0 ± 8 mm in diam.	1.5–2.5 × 0.9–1 mm ($\bar{x}$ = 2 × 0.8 mm; n = 10)
Peridium	25–35 *µm*	25–38 *µm*
Asci	177–219 *µm*	165–270 *µm*
Ascospores	(17 ± 9–)18 ± 7–26(–28)¬7 ± 5–13(–13 ± 5) *µm*	24–36 × 10–15 *µm* ($\bar{x}$ = 30 × 12.5 *µm*; n = 20)
Paraphyses	2–2 ± 5 *µm* wide	1–3 *µm* wide

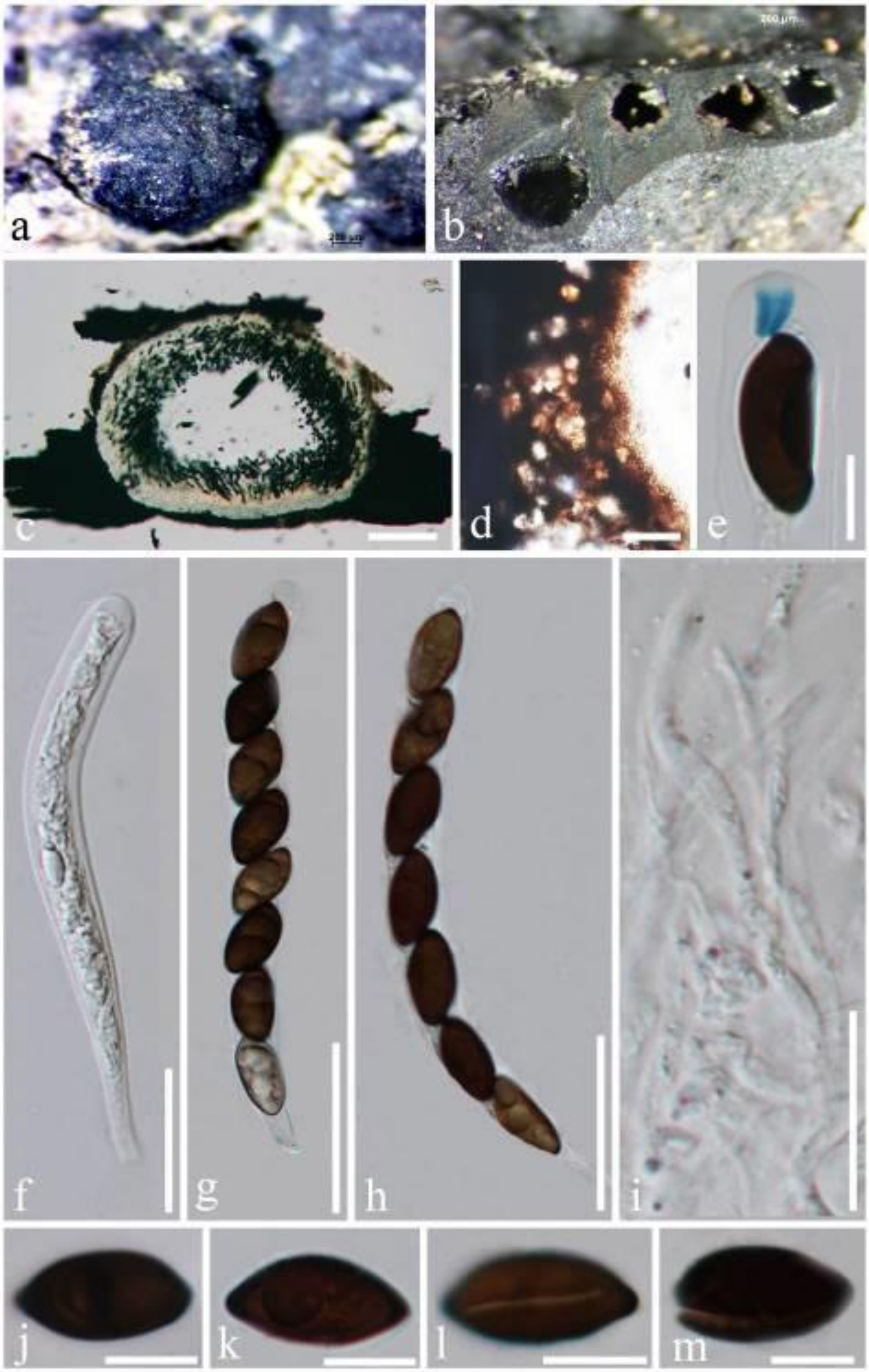


Fig. 85 ***Halorosellinia rhizophorae*** (**holotype**) **a, b** Appearance of pseudostromata on host **b** Horizontal section through pseudostroma **c** Section through pseudostromata **d** Peridium **e** Apical apparatus stained blue in Melzer's reagent **f**–**h** Asci **i** Paraphyses **j**–**m** Ascospores. Scale bars: b = 200 *µm*, c = 100 *µm*, d, e = 20 *µm*, f–i = 50 *µm*, j–m = 20 *µm*.

Hypoxylon Bull.

The genus *Hypoxylon* is one of the largest genera within the family *Xylariaceae* with currently 159 accepted taxa. Its species are distributed world-wide with the highest diversity in the tropics. Their sexual morph is usually associated with dead hardwood and can often be found along with the respective asexual morph. The generic concept is mainly based on the monograph by Ju & Rogers (1996), which was later improved by Hsieh et al. (2005). In most cases the stromata contain large quantities of secondary metabolites, which show characteristic colour reactions in potassium hydroxide solutions, a feature that is used to discriminate between species. Moreover, Stadler and coworkers employed analytical chromatographic methods (HPLC) to identify the stromatal compounds and to generate respective secondary metabolite profiles (Kuhnert et al. 2014). These chemical profiles are often species specific and help to validate the erection of new species. The phylogenetic tree is presented in Fig. 86.

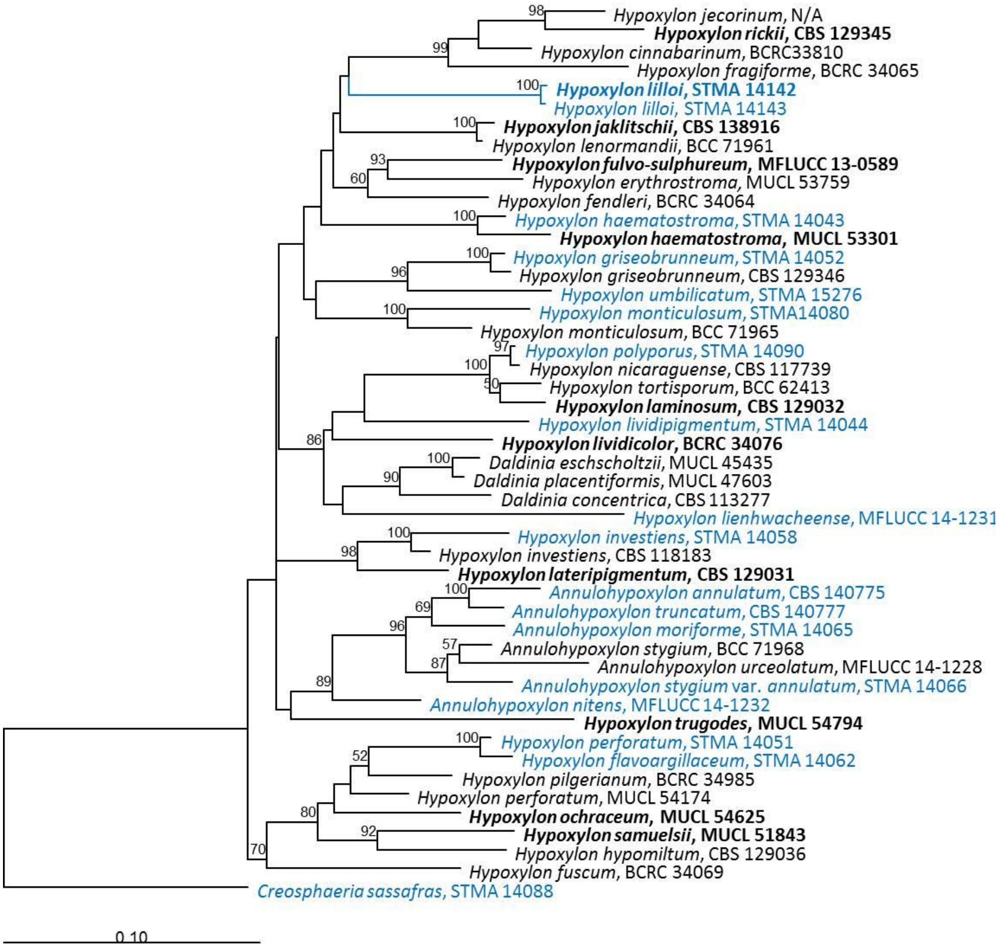


Fig. 86 Phylogenetic relationships among *Hypoxylon lilloi* and related *Xylariaceae* as inferred from β-tubulin gene sequences. Likelihood (ML) bootstrap support values above 50%, from 1000 RAxML replicates are assigned to the tree topology of the most likely tree found by RAxML. The tree is rooted to *Creosphaeria sassafras*. Species names are followed by strain numbers. Ex-type strains are highlighted in bold and new isolates are in blue.

314. ***Hypoxylon lilloi*** Sir, Lambert & Kuhnert, ***sp. nov.***

Mycobank number: MB 814982, *Facesoffungi number*: FoF 02034, Figs 87–89

Etymology: In honor of Dr. Miguel Lillo, a pioneer biologist in Tucuman province (Argentina).

Holotype: ARGENTINA, Salta, Depto. Anta, Parque Nacional El Rey, 30 April 2014, Sir & Hladki 739 (LIL, ex-type culture STMA 14142)

Differs from Hypoxylon vogesiacum by livid purple stromatal pigments in 10% KOH, as well as in having an amyloid apical apparatus and smaller ascospores.

Sexual morph *Stromata* effused-pulvinate, 14–30 mm long × 5–26 mm broad × 1 mm thick; plane or with inconspicuous perithecial mounds; surface Purplish Gray (128) or Vinaceous Grey (116); pruinose; brown to dark red granules immediately beneath surface and between perithecia; with KOH-extractable pigments Livid Purple (81), the tissue below the perithecial layer inconspicuous, black, 0.2–0.5 mm thick. *Perithecia* obovoid to lanceolate-tubular 0.5–0.8 mm high × 0.2–0.3 mm diam; ostiolar openings lower than the stromatal surface, umbilicate with white area surrounding ostioles. *Paraphyses* 2–4 *μm* wide at base, tapering above asci. *Asci* 8-spored, cylindrical, 92–134.5 *μm* total length, the spore-bearing parts 56–46 *μm* long × 5–6.5 *μm* broad, the stipes 40–82.5 *μm* long; with amyloid, discoid apical apparatus 0.7–0.9 *μm* high × 1.9–2.3 *μm* broad. *Ascospores* brown to dark brown, unicellular, ellipsoid-inequilateral, with narrowly rounded ends, slightly curved, 7.4–8.9 (9.7) × 3.2–4.2 *μm* (n = 60, Me = 8.3 × 3.8 *μm*); with straight germ slit spore-length on convex side; perispore dehiscent in KOH; with inconspicuous coil-like ornamentation by light microscopy, revealing reticulate ornamentation by SEM (5000×); epispore smooth. **Asexual morph** In culture, *Conidiophores* with virgariella-like branching pattern, usually borne on aerial hyphae, hyaline, smooth. *Conidiogenous cell*s hyaline, smooth, 10–27 × 1–2.5 *μm*. *Conidia* 4–5 × 1.5–2.5 *μm*, ellipsoid, hyaline, smooth-walled.

Culture: Colonies on OA covering Petri dish in 2 week, at first whitish, becoming Olivaceous Grey (121) to Dull Green (70), felty, zonate, with entire margin; reverse Apricot (42), later turning Dark Green (21) in places. Sporulating regions scattered over entire surface of colony.

Secondary metabolites: Stromata of this species contain two unknown major metabolites in its stromatal extracts (Fig. 89) in addition to some other yet unknown minor metabolites, besides binaphthalene tetrol (BNT).

Additional material examined: ARGENTINA, Jujuy Province, Depto. Santa Bárbara, Reserva provincial Las Lancitas, 13 May 2012, Sir & Hladki 278 (LIL); Salta, Depto. Anta, Parque Nacional El Rey, 30 April 2014, Sir & Hladki 744 (LIL, culture STMA 14143).

Notes: *Hypoxylon lilloi*, which was found in the course of a study on Xylariaceae of the Argentine cloud forest "Las Yungas" (Sir et al. 2016) might be confused with *H. vogesiacum* (Pers. ex Curr.) Sacc. due to their similar purplish gray or vinaceous grey stromatal surfaces. However, *H. lilloi* differs in having livid purple KOH-extractable pigments, smaller ascospores and in lacking a dotted band in the centre of the ascospores. This new taxon resembles the group of species with purplish KOH-extractable pigments, such as *H. lienhwacheense* Y.M. Ju & J.D. Rogers, *H.*

lividicolor Y.M. Ju & J.D. Rogers, *H. lividipigmentum* F. San Martín et al. and *H. texcalense* F. San Martín et al. Those can be easily differentiated from *H. lilloi* by the colour of the stromatal surface and granules. In addition *H. lienhwacheense* has smaller ascospores (6–7.5 × 3–3.5 *µm* vs. 7.4–9.7 × 3.6–4.6 *µm*) and a smooth perispore. *Hypoxylon lividicolour* differs in having longer perithecia (0.5–1.3 × 0.2–0.4 mm vs. 0.5–0.8 × 0.2–0.3 mm), larger ascospores (11–12.5 × 4.5–5 *µm* vs. 7.4–9.7 × 3.6–4.6 *µm*) and sporothrix-like conidiogenous structures and *H. lividipigmentum* can be differentiated by its larger ascospores (10–15 × 4.5–6 *µm* vs. 8.5–10 × 4–4.5 *µm*) and nodulisporium-like conidiogenous structures. In comparison with *H. texcalense*, the latter has also much larger ascospores (17–24 × 6.5–9.5 *µm* vs. 7.4–9.7 × 3.6–4.6 *µm*), and lack ascal apical rings and nodulisporium-like conidiogenous structures.

The type of secondary metabolites produced in the stromata seems to be a unique feature of the species, because they were not detected in more than 1000 studied specimens. Only BNT could be identified, which is common in hypoxyloid genera of the *Xylariaceae*.

In the phylogenetic reconstruction based on β-tubulin gene sequences (Fig. 86), *H. lilloi* forms a separated clade. The latter is located between the *H. fragiforme* clade and *H. lenormandii* clade. Besides huge morphological differences of those species compared to *H. lilloi*, they can be easily distinguished by their orange KOH-extractable pigments due to the production of azaphilones such as the mitorubrins (*H. cinnabarinum* Henn.) Y.M. Ju & J.D. Rogers, *H. fragiforme* (Pers.) J. Kickx f., *H. jecorinum* Berk. & Ravenel, *H. rickii* Y.M. Ju & J.D. Rogers) and the lenormandins (*H. lenormandii* Berk. & M.A. Curtis; cf. Kuhnert et al. 2016).

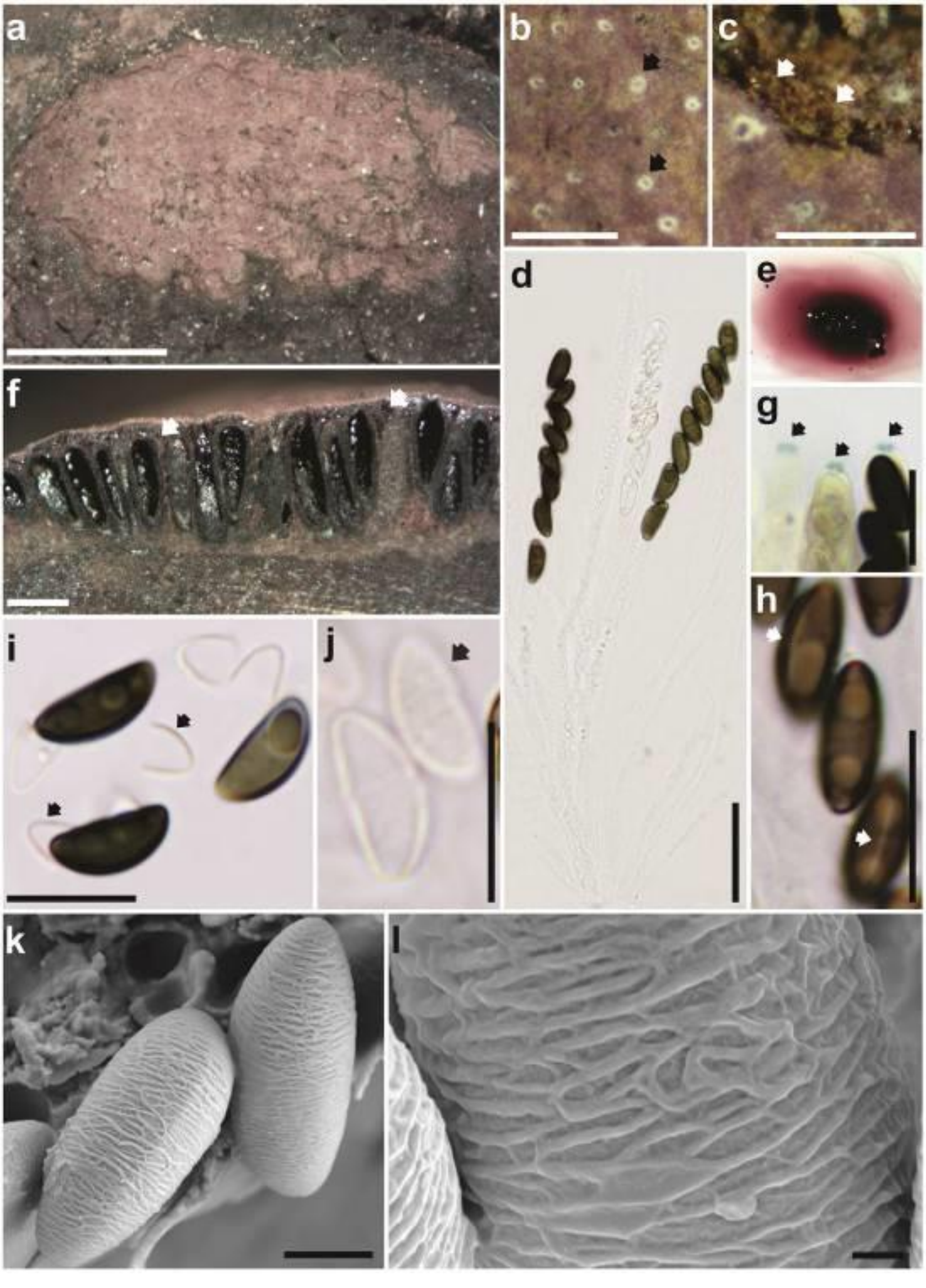


Fig. 87 ***Hypoxylon lilloi*** **(holotype)** **a** Stromatal habit **b** Close-up view of stromatal surface with white area surrounding umbilicate ostioles (black arrow) **c** Bown granules beneath surface and between perithecia (white arrow) **d** Asci **e** extractable pigments in 10% KOH **f** Section through stroma showing perithecia and dark red granules (white arrow) **g** Apical ring bluing in melzer´s iodine reagent (black arrow) **h** Ascospores showing germ slit (white arrow) **i** Ascospores showing perispore dehiscent in KOH (black arrow) **j** Perispore showing inconspicuous ornamentation **k, l** Ascospores showing reticulate ornamentation on perispore

under SEM. Scale bars: a = 5 mm, b, c and f = 0.5 mm, d = 20 *µm*, g, h, i and j = 10 *µm*, k = 2 *µm*, l = 200 nm.

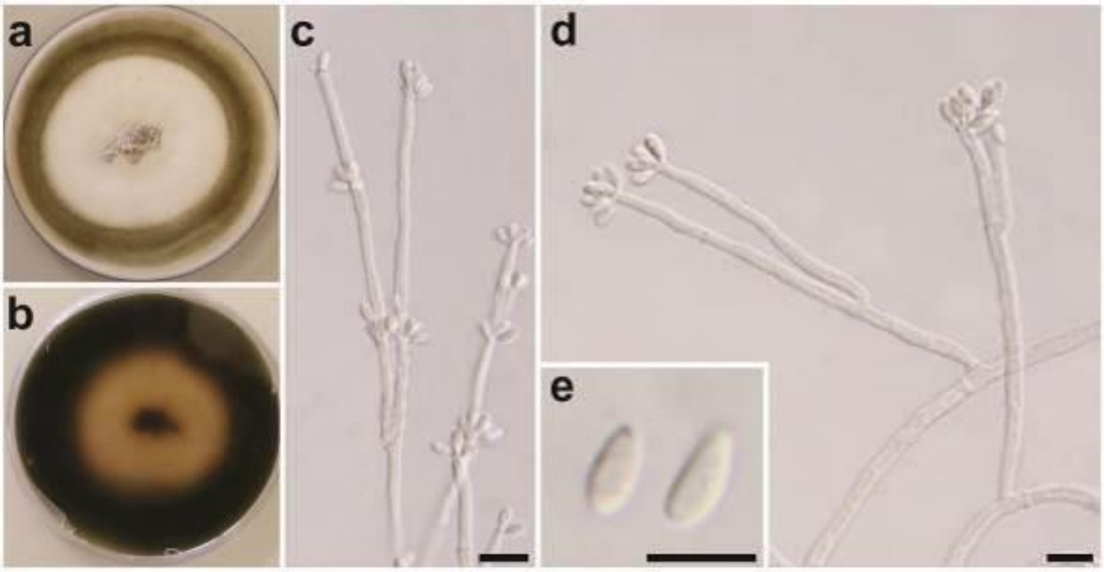


Fig. 88 ***Hypoxylon lilloi*** (**ex-type**) Culture of on OA after 3 weeks **a** top view **b** reverse **c**, **d** Conidiophores with virgariella-like branching patterns **e** Conidia. Scale bars: c–e = 5 *µm*).

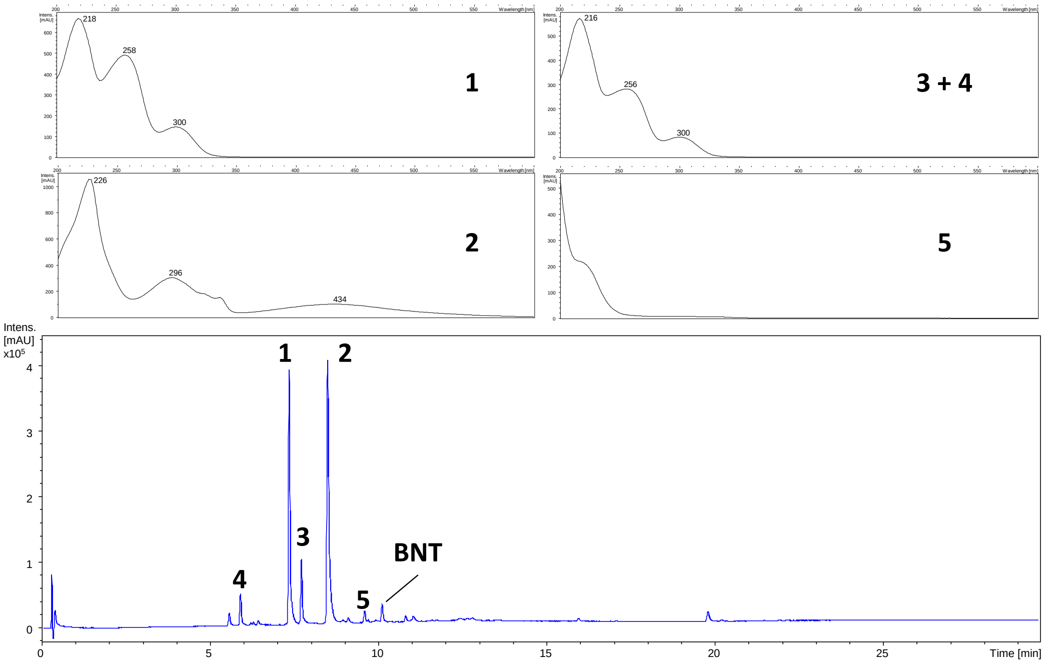


Fig. 89 Stromatal HPLC-UV profiles of *H. lilloi* derived from EBS278 and corresponding DAD spectra of the unknown main metabolites.

Rosellinia De Not.

The genus is typified by *Rosellinia aquila* (Fr.) Ces. & De Not. and was introduced to accommodate species with uniperitheciate, superficial, ostiolate stromata seated on a subiculum with cylindrical, stipitate asci usually with an amyloid apical apparatus and produce dark brown ascospores (Petrini 1992). *Rosellinia* is a relatively large genus in *Xylariaceae*. Index Fungorum (2016) includes 496 records under the name However according to the world monograph by Petrini (2013) only 142 species are accepted, of which 37 species are described as new species.

315. *Rosellinia chiangmaiensis* Daranagama & K. D. Hyde, ***sp. nov.***

Index Fungorum Number: IF 551728, *Facesoffungi number*: FoF 01638, Fig. 90b

Etymology: Referring to the province Chiang Mai, where the species was encountered.

Holotype: MFLU 15–3524

Saprobic on dead dicotyledonous wood. **Sexual morph** *Stromata* globose, with a pointed top, 1220–1400 × 800–1080 *µm* ($\bar{x}$ = 72.5 × 4.8 *µm*, n = 20), chestnut brown, shiny, smooth, solitary, in small groups, uniperitheciate, surrounded by woolly to felty, pale yellow subiculum, confined to the stroma base, black entostroma, reduced at the base. *Ostioles* black, distinctively papillate, pointed. *Ascomata* globose, 400–500 × 500–600 *µm* ($\bar{x}$ = 467 × 560 *µm*, n = 20). Peridium thick-walled, > 70 *µm*, carbonaceous. *Hamathecium* comprising long, dehiscent, filamentous, few paraphyses, 2*µm* wide, longer than asci. *Asci* 150–200 × 4.5–6.4 *µm* ($\bar{x}$ = 172 × 5.2 *µm*, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, apical narrowly rounded, with a J+, inverted hat-shaped, apical apparatus, upper width 4–6 *µm*, lower width 2–3 *µm*, with rounded bulge at upper rim. *Ascospores* 70–90 × 7–10 *µm* ($\bar{x}$ = 84 × 9 *µm*, n = 20), overlapping uniseriate, dark brown, elongate fusiform, with acute ends, with thin mucilaginous sheath, germ slit and appendages absent.

Culture characteristics: Colonies on Difco OA plates at 25–28°C reaching 5 cm edge of Petri-dish in 2–3weeks, at first citrine, felty, azonate, with diffuse margins, reverse turning yellow.

Material examined: THAILAND, Chiang Mai Province, garden of Mushroom Research Center, on decorticated bark of a fallen log, 17 August 2014, Anupama Daranagama, AXL 342 (MFLU 15–3524, **holotype**, HKAS 92486, **isotype**), ex-type living culture, MFLUCC 15–0015, KIBCC.

Notes: *Rosellinia chiangmaiensis* is reminiscent to *R. macrosperma* Speg. and *R. procera* Syd. & P. Syd. because its large length: width ascospore ratio, lacking germ slits and generally large stromata more than 1 mm high (Petrini 2013). However the new species possess longer ascospores with thin mucilaginous sheath with acute ends and a white to pale yellow subiculum restricted to the stromatal base. These characters make this species unique from other known, morphologically similar species. According to the description by Petrini (2013) this new species belongs to the *R. emergens* group, which is a phylogenetically heterogeneous group. The reconstructed phylogenetic trees for the family *Xylariaceae* (Fig. 83) and the genus *Rosellinia* (Fig. 90a) confirmed the placement of *Rosellinia chiangmaiensis* with high bootstrap support.

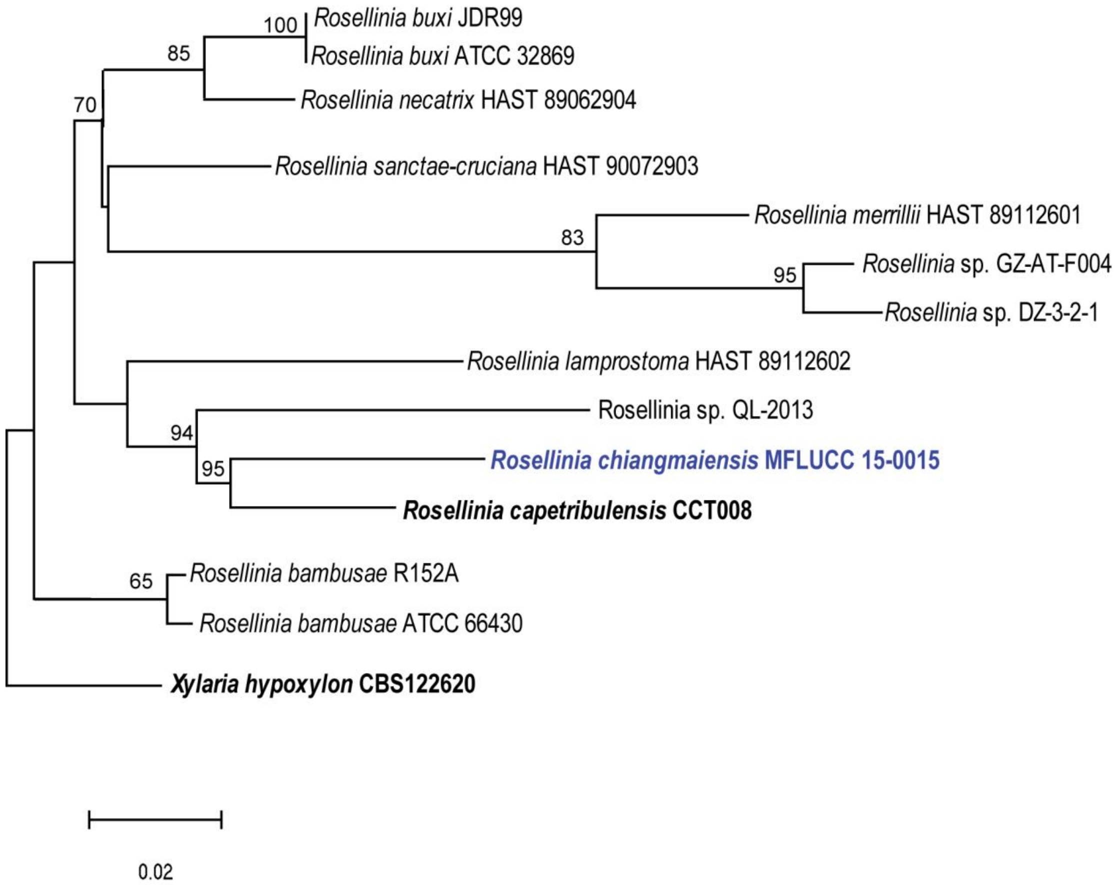


Fig. 90a Phylogram generated from RAxML analysis based on ITS sequenced data of *Rosellinia*. Maximum Likelihood values equal or greater than 50 are indicated above or below the nodes and branches. The tree is rooted with *Xylaria hypoxylon*. Newly introduced taxa in this study are highlighted in blue and ex-type strains are in bold.

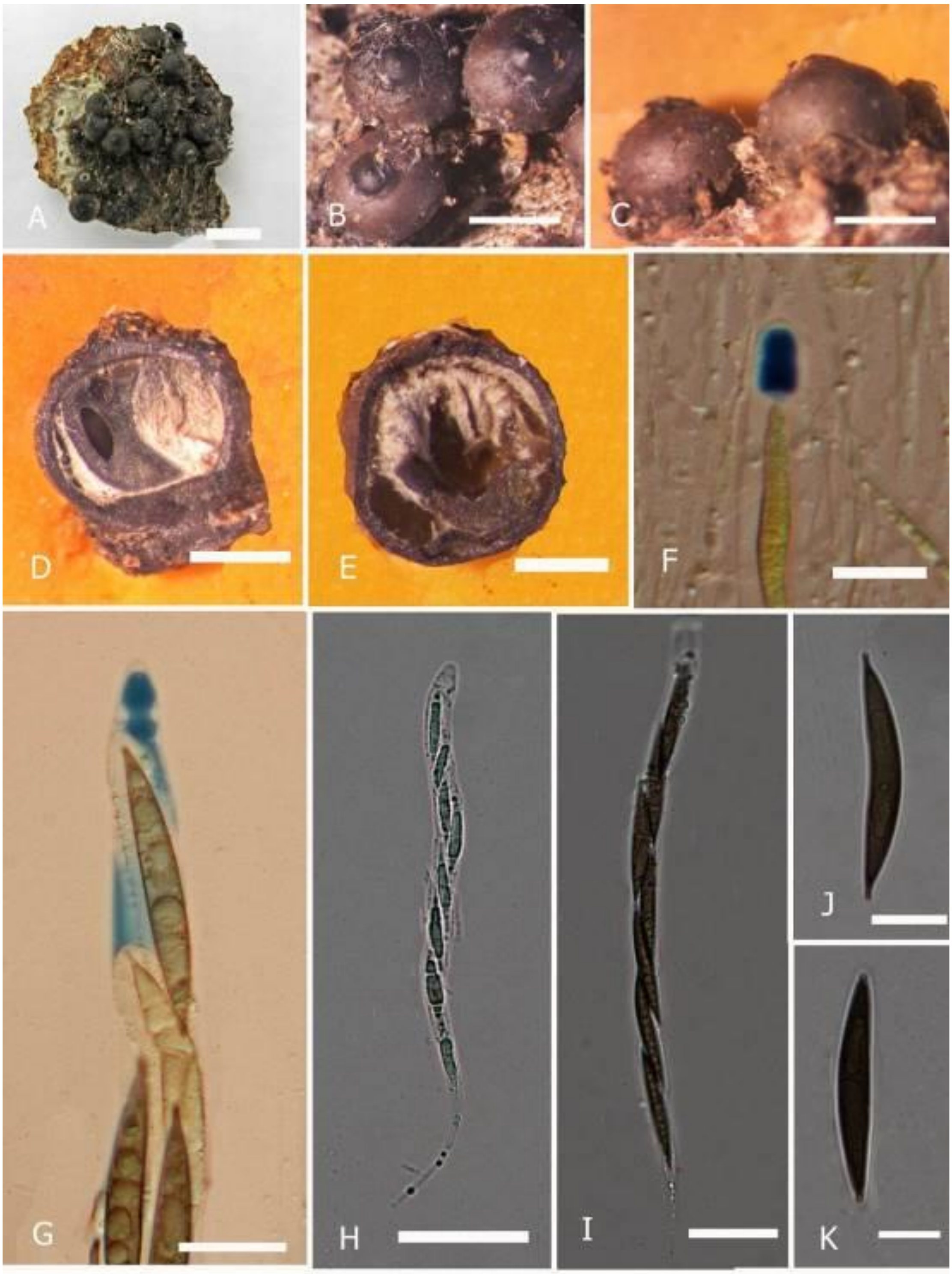


Fig. 90b ***Rosellinia chiangmaiensis*** **(holotype) a** Ascomata in host surface **b** Papillate ostioles **c** Side view of ascomata **d** Cross section through stroma **e** Vertical section of stroma **f, g** Asci with J+, apical apparatus in Melzer's reagent **h, i** Asci in water **j, k** Ascospores in water. Scale bars: a = 500 *μm*, b, c = 1000 *μm*, d, e = 200 *μm*, f, g = 10 *μm*, h, i = 50 *μm*, j, k = 30 *μm*.

Ascomycota, genera *incertae sedis*

Petrakia Syd. & P. Syd.

Petrakia is typified by *Petrakia echinata* and characterized by having dark brown, rounded to oval, muriform conidia bearing cellular, long, hyaline appendages. Butin et al. (2013) described sexual morph of *P. echinata* based on field collections, culture studies and ITS sequence data and assigned it to the genus *Mycodidymella*. Following the rulings of the current ICN, we propose to use the oldest name, *Petrakia* over *Mycodidymella*. The phylogenetic tree is presented in Fig. 91 which shows that *Petrakia* probably belong in *Dothideomycetes* genera, *incertae sedis*.

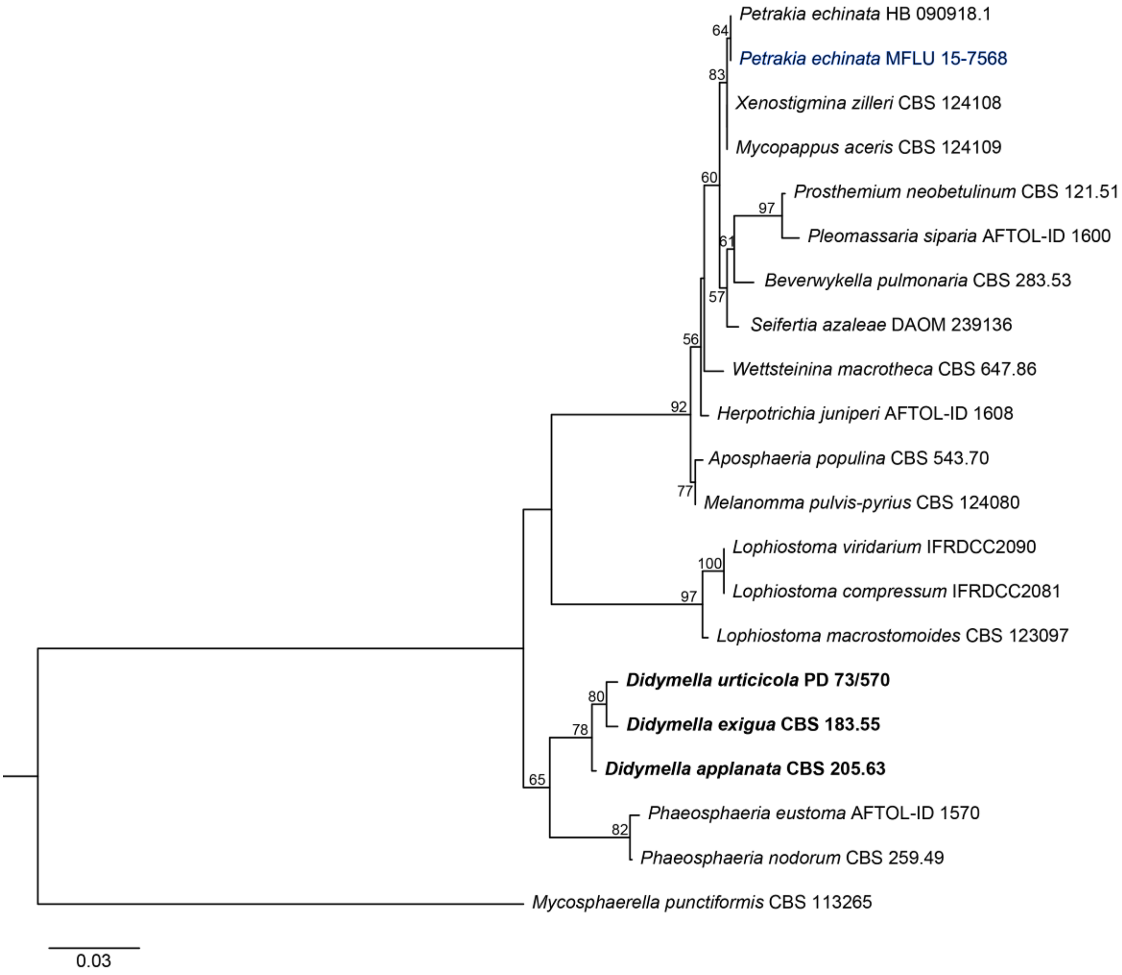


Fig. 91 Best scoring RAxML tree of *Petrakia echinata* and related species obtained from analysis of LSU sequence data. RAxML bootstrap support values (equal to or greater than 50% based on 1.000 replicates) are shown at the nodes. The tree is rooted to *Mycosphaerella punctiformis* CBS 113265. New taxa are in blue and species for which obtained sequences are based on type material have names in bold.

316. *Petrakia echinata* (Peglion) Syd. & P. Syd., Annls mycol. 11(5): 406 (1913)

Index Fungorum number: IF 192652, *Facesoffungi number*: FoF 01821

≡ *Epicoccum echinatum* Peglion, Malpighia 8: 459 (1895)

Parasitic on living leaves of *Acer pseudoplatanus* L., forming numerous, conspicuous rounded, black, sporodochia. **Sexual morph** *Mycodidymella* (Butin et al. 2013).

Asexual morph *Sporodochia* 90–110 *µm* high, 100–150 *µm* diam., dark brown to black, solitary, scattered to gregarious, occasionally confluent, superficial, erumpent, elliptical or irregular in outline, with a basal stroma variably developed, 20–30 *µm* thick, composed of cells of *textura angularis* to *textura globulosa*. *Conidiophores* reduced to conidiogenous cell arising from the uppermost cells of the basal stroma. *Conidiogenous cells* 12–35 × 3–10 *µm*, hyaline to pale yellow, integrated, annellidic, with 2–3 annellations, cylindrical, thick-walled, smooth. *Conidia* 22–45 × 12–32 *µm* ($\bar{x}$ = 32 × 25 *µm*, n = 30), rounded to oval or broadly ellipsoidal, muriform, with multi-transverse and longitudinal septa or oblique septa in the central zone, constricted at septa, thick-walled, smooth, at first hyaline, later becoming brown or dark brown, bearing 8–33 × 3–9 *µm*, cellular, long appendages; appendages, arising as a tubular extension of the body of the conidium, unbranched, narrow and attenuated, subhyaline, cylindrical, smooth-walled.

Culture characteristics: *Colonies* on PDA slow growing, reaching 15 mm diam. after one week, circular, white to pale grey, velvety, felty, sparse, aerial, surface smooth with crenate edge, filamentous; reverse black at the central zone, white at the margin.

Material examined: ITALY, Province of Forlì-Cesena [FC], Camposonaldo, Santa Sofia, on living leaves of *Acer pseudoplatanus* L. (*Sapindaceae*), 20 February 2013, Erio Camporesi IT-1570 (MFLU 15–7568, **reference specimen designated here**), living culture MFLUCC 15–0582.

Notes: In the phylogenetic analysis, strain MFLUCC 15–0582 is closely related to *Petrakia echinata* (Fig. 92). The comparisons of ITS sequence data from both strains show 100% similarity. Morphologically, strain MFLUCC 15–0582 has similar sporodochia and conidia characteristics to those of *P. echinata*, and the only distinguishing character is the dimension of the conidia. Strain MFLUCC 15–0582 has slightly larger conidia (22–45 × 12–32 µm, versus 16–28 × 18–22 *µm*) than *P. echinata*. However, the differences noted here similarly reflect reasonable intraspecific variation. *Petrakia echinata* has been reported as an pathogen in Austria, Caucasus, Germany Switzerland and the Czech Republic (Kirisits 2007, Butin et al. 2013), and this is first record of the species in Italy. Details of the conidiogenous cells are also provided.

Fig. 92 ***Petrakia echinata*** (MFLU 15–7568, **reference specimen**) **a** Herbarium specimen **b, c** Appearance of black sporodochia on the host **d** Vertical section of sporodochia **e**–**h** Conidiogenous cells and developing conidia **i** Germinating conidium **j**–**m** Conidia **n**, **o** Culture on PDA note o reverse. Scale bars: b = 200 *µm*, c = 100 *µm*, d = 50 *µm*, e, f = 5 *µm*, g, h, m = 10 *µm*, i–l = 20 *µm*, n, o = 10 mm.

Contributions to *Basidiomycota*

Agaricomycetes

Agaricales

Agaricaceae

Agaricaceae is the type family of the order *Agaricales*, which is distributed widely around the world. This family contains 1340 species in 85 genera (Kirk et al. 2008). Species in this family mostly have a fleshy basidiome, with pileus and stipe, some of them also have an annulus, such as the genera *Agaricus* and *Micropsalliota*. Besides the agaricoid, secotioid and gasteroid taxa are also included in this family. The phylogenetic tree for *Agaricaceae* is presented in Fig. 96.

Agaricus L.

The genus *Agaricus* (*Agaricaceae*) is a well known group with many cultivable species. Its systematics has been well-studied in recent years (Parra 2008, 2013; Zhao et al. 2011; Chen et al. 2012, 2015a; Wang et al. 2015b; Zhao et al. 2016). There are some sections of this genus, such as sections *Sanguinolenti* and *Sppisicaules*, that have been revealed to be polyphyletic (Zhao et al. 2011; 2016). However, section *Minores* has been stable since it was introduced by Fries (1874), based on its morphology and molecular phylogeny (Zhao et al. 2011; Parra 2013; Lebel 2013). Section *Minores* is characterized by relatively small-sized basidiomes, a simple annulus, the surfaces of the pileus and stipe often discolouring yellow on scratching, a context yellow discolouring on exposure, and a pleasant odour (Heinemann 1978; Parra 2013). Historically the species of section *Minores* have been limited in number. Recent research has revealed a high biodiversity of species in Europe (Parra 2013), Thailand (Liu et al. 2015), Australia (Lebel 2013) and China (He et al. 2015). Herein we add two more new species of this section from China. The phylogenetic tree for *Agaricus* is presented in Fig. 93.

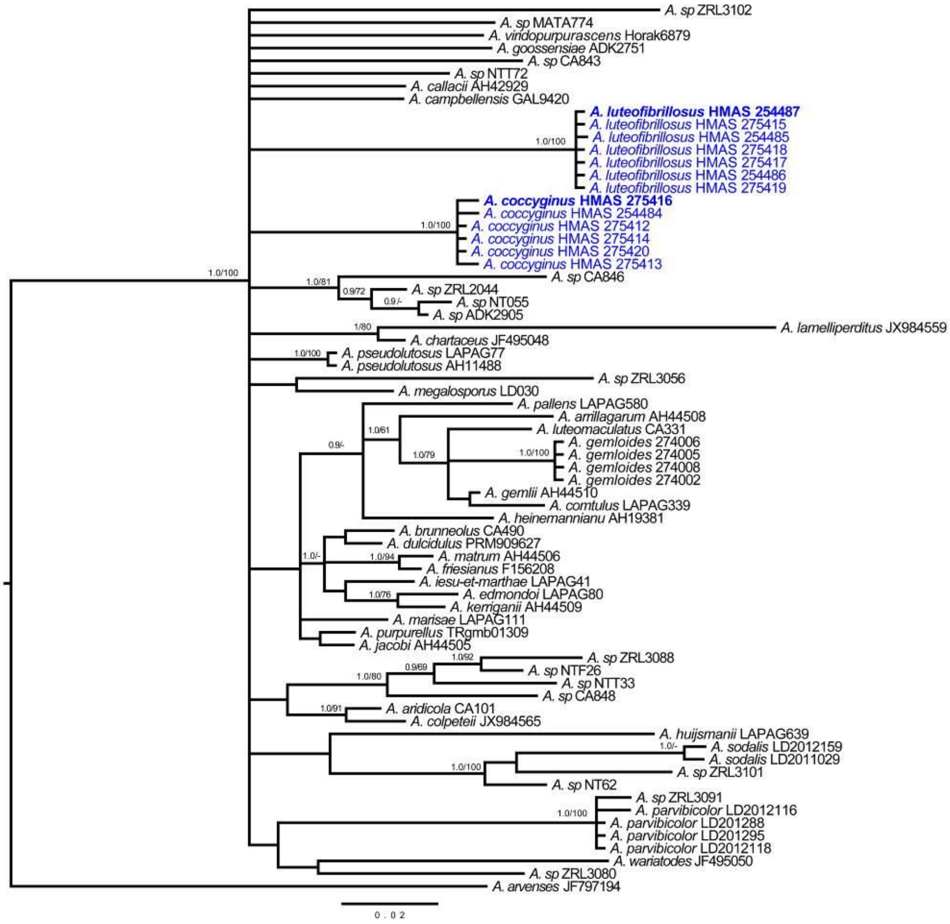


Fig. 93 Phylogeny of species of *Agaricus* section *Minores* generated from Bayesian analysis of ITS sequence data rooted with *Agaricus arvensis*. Bayesian posterior probability (PP) values above 90% and parsimony bootstrap support (BS) above 50% are given at the internodes (PP/BS). New taxa are in blue ex-types in bold.

317. ***Agaricus coccyginus*** M.Q. He & R.L. Zhao, ***sp. nov.***

Fungal Names number: FN 570238, *Facesoffungi number*: FoF 02035, Fig. 94

Etymotogy: the epithet "*coccyginus"* refers to the purple red squamules on the cap of this species.

Holotype: HMAS 275416

Macroscopical characters: *Pileus* 35–110 mm in diam., umbonate at disc, parabolic when young, then convex, finally plane with age; margin straight, decurved, sometimes little exceeding; surface dry, covered by tiny fibrils on the whole cap, appressed, denser on the disc and broken into radially triangular squamules toward margin, purple red, brown, or reddish brown on the lighter background. *lamellae* free, crowded, 3–8 mm broad, white or pink at first, then grayish brown, brown finally. *Context* white, fresh, 2–6 mm thick at disc, white, turns yellow on cutting first, then reddish brown after several minutes. *Annulus* membranous or cortinate-membranous, simple, pendant, white, 4–10 mm in diam., smooth on both sides of surface. *Stipe* 64–160 × 4–9 (base 9–21) mm, cylindrical or slightly clavate, hollow, white, smooth or fine fibrils below the annulus, always with rhizomorphs. Basidiome surface strongly discolouring yellow when touching or bruising, then reddish brown after several minutes. Odour of strong almond.

Macrochemical reaction: KOH reaction strongly yellow; Schäffer's reaction orange.

Microscopical characters: *Basidiospores* 5.5–6.5 (– 6.8) × 4.3–4.5 *µm*, [x = 6 ± 0.3 × 3.8 ± 0.2, Q = 1.4–1.8, Q_m = 1.6 ± 0.1, n = 20], ellipsoid to elongate, smooth, thick-walled, brown, no germ pore. *Basidia* 14.1–19 × 5.6–7.8 *µm*, clavate, hyaline, 4-spored, smooth. *Cheilocystidia* 16–60 × 9.2–22 *µm*, mostly pyriform and clavate, sometimes oblong, pheropedunculate, rarely septa at base, smooth, hyaline, with yellow pigment inside. *Pleurocystidia* absent. *Pileipellis* a cutis composed of 5.9–14.5 *µm* in diam. hyphae, smooth, cylindrical, brown, constricted at septa.

Habitat: Solitary on the soil of forest.

Material examined: CHINA, Tibet, Bomi, Baga Village, 26 July 2012, Su-ShengYu, *ZRL2012485* (HMAS 275416, **holotype**); Tibet, Milin County, Nanyigou, Li Guang-Ping *ZRL2012597* (HMAS275413,); Yunnan Province, Weixi County, 4 August 2014, He Mao-Qiang, Dai Rong-Chun, Su Sheng-Yu, *ZRL2014354* (HMAS 275412,), *ZRL2014364* (HMAS275414), *ZRL2014415* (HMAS275420), *ZRL2014430* (HMAS 254484).

Notes: see under *Agaricus luteofibrillosus*.

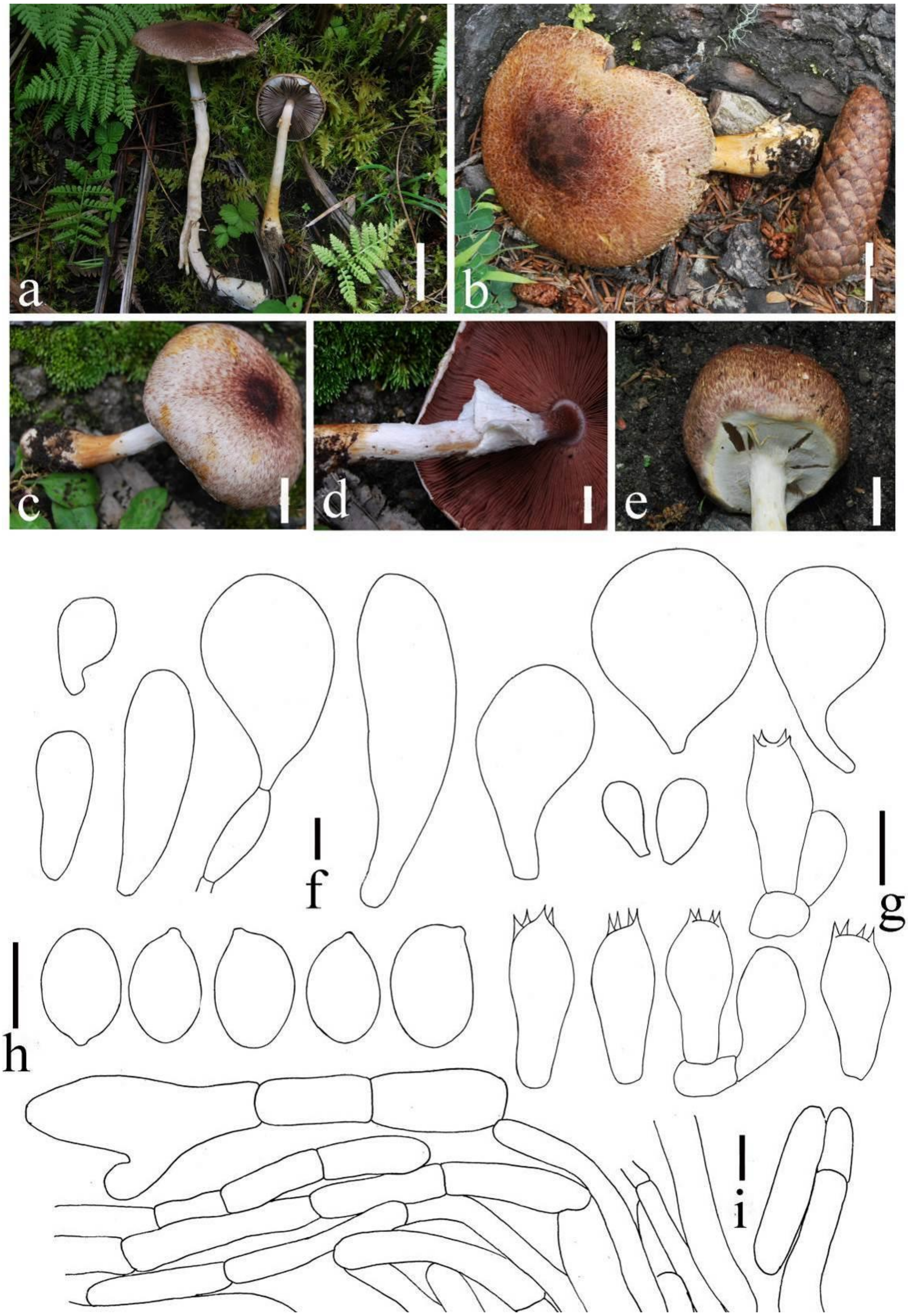


Fig. 94 ***Agaricus coccyginus*** **a, b** Basidiome **c, e** Annulus **d** Discoloration on stipe **f** Cheilocystidia **g** Basidia **h** Basidiospores **i** Hyphae of Pileipellis Scale bars: a from **holotype** ZRL2012485, b, d from ZRL2012597, c from ZRL2014415, e from ZRL2012576. Scale bars: a = 3 cm, b–d = 2 cm, e = 1 cm, f, g, i = 10 µm, h = 5 µm.

318. ***Agaricus luteofibrillosus*** M.Q. He, L.J. Chen & R.L. Zhao, ***sp. nov.***

Fungal Names number: FN 570234, *Facesoffungi number*: FoF 02036, Fig. 95

Etymotogy: the epithet "luteo" refer to the yellow colour; and "fibrillosus" refers to the fibrils on the pileus and stipe.

Holotype: HMAS 254487

Marcoscopical characters: *Pileus* 35–94 mm in diam., parabolic at first, then convex, finally plane, sometimes with slightly subumbonate disc with age; margin slightly decurved when young, then straight; surface dry, fibrillose, yellowish brown against white to light brown background, appressed, denser at disc, then broken into triangular fibrillose squamules towards the margin. *Context* 3–8 mm thick at disc, fresh, white, and yellow discolouring on exposure. *Lamellae* 4–8 mm broad, free, crowded, pink when young, then brown when mature. *Annulus* simple, membranous, pendant, white, lower surface floccose with light brown tiny squamose. *Stipe* 60–141 × 5–14 (base 8–25) mm, white, cylindrical, base clavate or subbulbose, surface smooth and white above the annulus, fibrillose squamose or floccose and light brown below the annulus, hollow. Basidiome surface yellow discolouring on touching or bruising. Odour of almond.

Macrochemical reaction: KOH reaction strongly yellow; Schäffer's reaction orange.

Microscopical characters: *Basidiospores* 5–6.5 (–7.2) × 3–4.2 *µm* [x = 5.8 ± 0.4 × 3.4 ± 0.2, Q = 1.5–2, Q_m = 1.7 ± 0.1, n = 20], ellipsoid to cylindric, smooth, thick-walled, brown, no germ pore. *Basidia* 14–18 × 5.6–7.3 *µm*, clavate, hyaline, 4-spored, smooth. *Cheilocystidia* 9.4–28 × 6.4–17 *µm*, mostly globose and clavate, sometimes pyriform and pheropedunculate, septa at base sometimes, smooth, hyaline, some with yellow pigment inside. *Pleurocystidia* absent. *Pileipellis* a cutis composed of hyphae of 3.2–13.2 *µm* in diam., smooth, cylindrical, light brown, constricted at septa. *Annulus* composed of hyphae with 3–9.5 *µm* in diam., hyaline, cylindrical, not constricted at septa.

Habitat: Solitary on soil of forest.

Material examined: CHINA, Yunnan Province, Baoshan, Gaoligong Mountain, Wanzi Village, He Mao-Qiang *ZRL 2013484* (HMAS 254487, **holotype**); Yunnan Province, Yongde County, Pingtian Village, Li Guang-Ping *ZRL 2012359* (HMAS 275419); Yunnan Province, Cangyuan County, Nanban Village, Zhao Rui-lin *ZRL 2012121* (HMAS 254486), ZRL 2012200 (HMAS 275415).

Notes: In the phylogenetic tree (Fig.3), the proposed new species *A. coccyginus* and *A. luteofibrillosus* are represented by two clades respectively with strong PP and BS support. Their phylogenetic positions are also clearly distinguished from other known species in section *Minores*. In morphology, they both have related larger basidiomes which the cap reaching 110 mm in diam. There are only two species with such large-sized basidiomes in section *Minores*, one is *A. brunneolus* (J.E. Lange) Pilát and the other is *A. megalosporus* J. Chen et al. *Agaricus brnneolus* is the most similar species to *A. coccyginus*. They both have the same shape of cap, stipe and same colour of fibrils on the basidiome. Also, under the microscope they have the similar cheilocystidia. There are some distinguishable autapomorphies between these two species. *Agaricus coccyginus* has the longer basidiospores than those of *A. brunneolus* (length 4.5–6.2 *µm*). The yellow pigment of cheilocystidia in *A. coccyginus* is also another difference from *A. brunneolus*. *Agaricus megalosporus* is the most similar species to *A. luteofibrillosus*, because both species have similar basidiomes, they both have coloured fibrils on the cap, annulus and stipe. Both have the same size of basidospores, but *Agaricus luteofibrillosus* has a yellowish brown cap, while in *A. megalosporus* it is purplish brown. Under the microscope they have different cheilocystidia: in *A. megalosporus* they are broadly clavate to pyriform, and white, while in *A. luteofibrillosus* they are pheropedunculate, septa at base and contain yellow pigment.

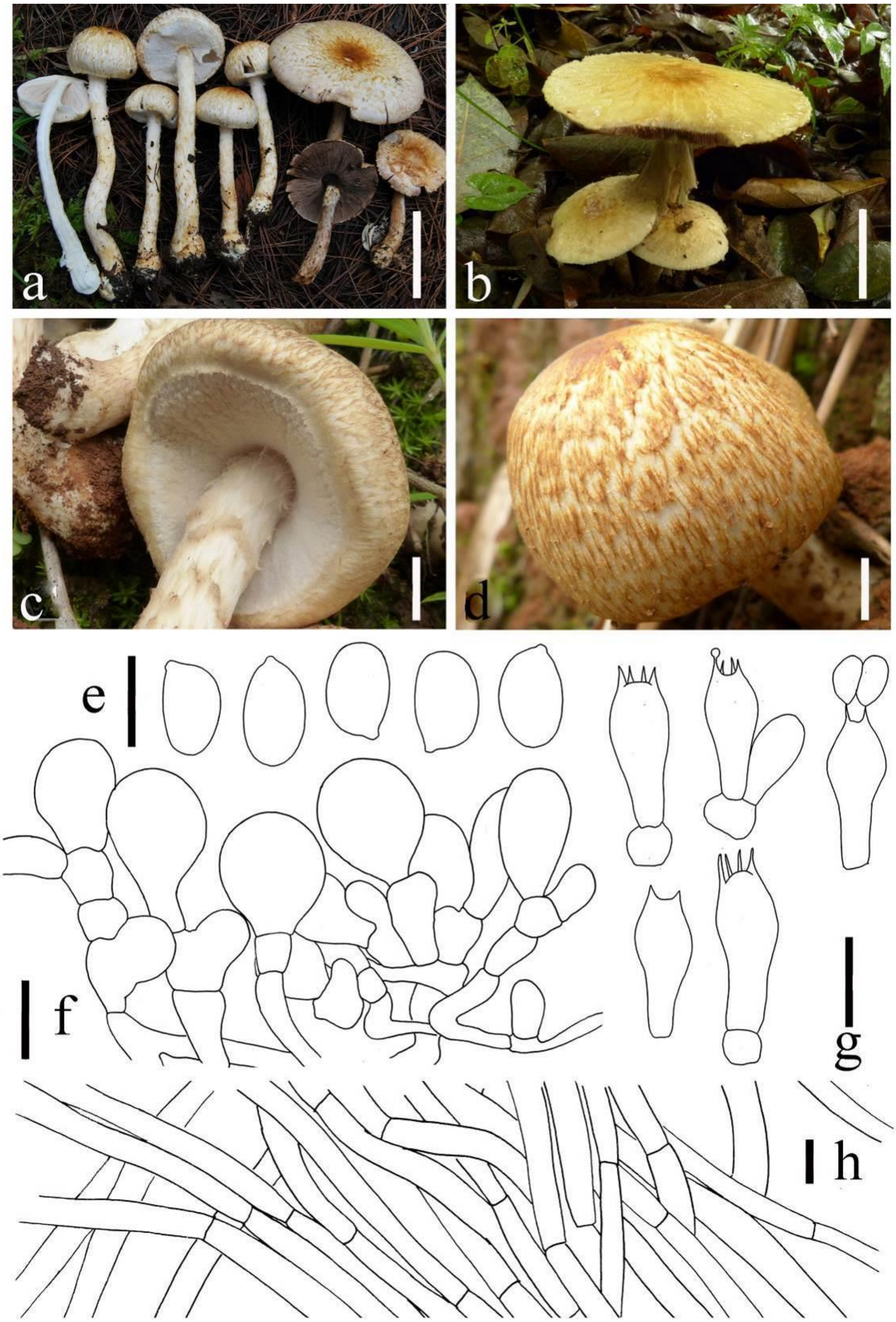


Fig. 95 ***Agaricus luteofibrillosus*** **a, b** Basidiome **c** Annulus **d** Fibrils on cap **e** Basidiospores **f** Cheilocystidia **g** Basidia **h** Hyphae of pileipellis. Scale bars: a from **holotype** ZRL2013484, b from ZRL2012359, c, d from ZRL2012121. Scale bars: a = 5 cm, b = 3 cm, c, d = 1 cm, e = 5µm, f–h = 10 µm.

Clarkeinda Kuntze

The genus *Clarkeinda* belongs to the family *Agaricaceae*, and was circumscribed by Kuntze (1891). According to the Dictionary of the Fungi the widespread genus contains five species and Index Fungorum lists 14 records (Kirk et al. 2008; Clements 1909; Index Fungorum 2016). Species in this genus, especially *Clarkeinda trachodes*, are only distributed in south and southeast Asia (Yang 1991; Kuntze 1891; Hosen and Ge 2011).

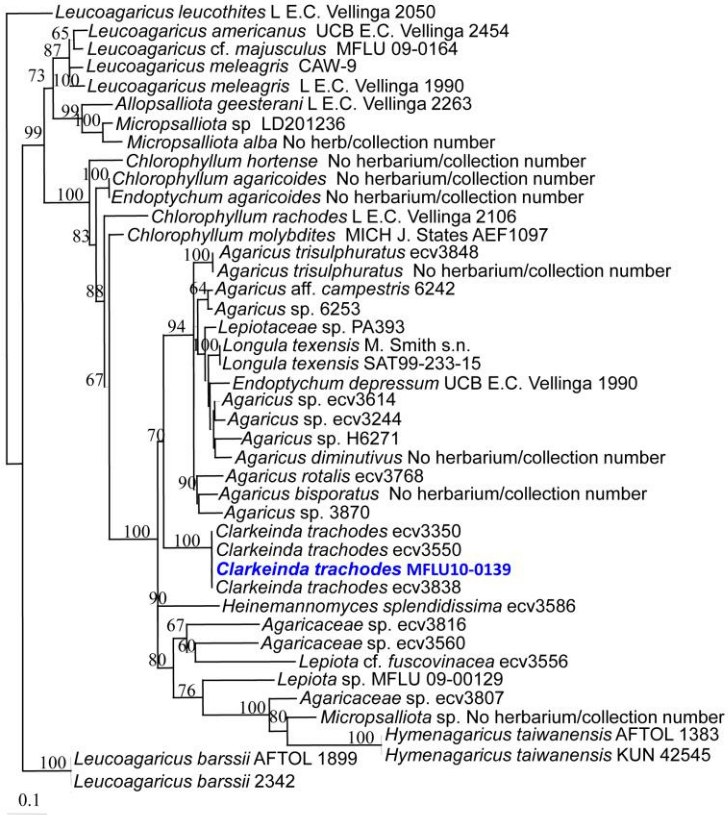


Fig. 96 Phylogeny of *Clarkeinda trachodes* and satellite genera in the *Agaricaceae* based on analysis of ITS sequence data, inferred by maximum likelihood (ML) analysis. Numbers at internodes refer to confidence estimates based on 100 rapid ML bootstraps (only those >50 are indicated). *Clarkeinda trachodes* from Sri Lanka is highlighted. *Leucoagaricus barssii* and *Leucoagaricus leucothites* are outgroup taxa. New sequences are in blue and ex-type and reference specimens are in bold.

319. *Clarkeinda trachodes* (Berk.) Singer, Lilloa 22: 413, 1951.

Facesoffungi number: FoF 01844, Figs 97, 98

Description: Basidiomes medium to large, fleshy. Pileus 120 mm in diam., hemisphaerical when young, and becoming convex to applanate at maturity; pellicle on the cap brown to coffee or chocolate brown, thin when young and thick when mature, and brown to grayish brown at maturity; the whole surface except the pellicle area covered with grayish brown to vinaceous brown squamules, with numerous, small, loosely floccose, brown squamules; context up to 8–9 mm thick in the center of the pileus, white, instantly turning reddish with exposure. Lamellae free and distant from the stipe, white to dirty white when young, turning to olive brown when mature, becoming reddish brown after bruised, crowded with lamellulae, entire margin, concolorous. Stipe 140 × 45 mm, central, subcylindrical, fistulose in mature specimens; surface dirty white to white at the apex, light brown to brown towards the base, glabrous above the annulus, lower half densely covered with minute, brown, furfuraceous squamules. Annulus present on the upper part of the stipe but not the top, up to 20 mm, thick, membranous and remaining up to maturity, adaxial part glabrous with fine longitudinal striate but abaxial part rough with squamules. Volva presents, grayish, dirty white to white, membranous, usually closely appressed to stipe and eventually inconspicuous. Basidiospore deposit not obtained. Basidia 17–28 × 5.5–9 *μm*, mostly clavate to subclavate, thin-walled, tetrasporic, but seldom 1-, 2- or 3-spored, bearing four short sterigmata, hyaline, smooth, lacking incrustations, clamp connections absent. Basidioles narrowly clavate to clavate. Hymenophoral trama interwoven, hyphae cylindrical to slightly inflated, up to 14 *μm* wide, thin-walled, hyaline, and without clamp connections. Basidiospores (Fig. 98b) (5–)5.5–6 (–7) × (3.5–)3.9–4(–4.5) *μm*, mean Q = 1.4–1.5, ovoid, occasionally broadly ellipsoid to ellipsoid, glabrous, thick-walled, apiculus eccentric, apex or germinating pore prominent and truncate with slightly depressed, olive brown to dark, umber brown in deposit, dextrinoid in Melzer's solution, not metachromatic in Cresyl blue. Cheilocystidia 25–33 × 10.5–15.5 *μm*, abundant, scattered to more or less crowded, narrowly clavate, clavate to broadly clavate, obpyriform, hyaline, thin-walled, smooth, lacking incrustations, sometimes with long pedicel and narrow. Pleurocystidia absent. Pileipellis consisting of short branching chains of 4–7 cells, slightly interwoven, terminal cells 12–23 × 8–14.5 *μm*, dull brown vacuolar pigment inside the cells in glycerin, water and 5% KOH solutions, thin-walled, clavate, cylindrical, obpyriform to fusiform or spindle-shaped in rare cases, occasionally branching with lateral cells that are mostly clavate, basal cells nearly subglobose to clavate or cylindrical.

Habit, *habitat*, *distribution*: The basidiomes of *C*. *trachodes* normally fruit as isolated individuals or in groups of two in disturbed habitats and at forest edges. Our collection was collected on grassland in Royal Botanic Gardens, Peradeniya, Sri Lanka. It is also known from China, India, Indonesia, Bangladesh and Malaysia.

Material examined: Sri Lanka. Central Province: Peradeniya, Royal Botanic Gardens, 7°15'35.03"N 80°36'4.07"E, elev. 590 m, 15 July 2009, Samantha C. Karunarathna (MFLU 10–0139, **reference specimen designated here**)

Notes: *Clarkeinda trachodes* is distinguished by its large basidiome size, prominent chocolate or coffee brown to dark brown pellicle on the pileus disc surface, presence of an annulus, olive brown to umber brown spore deposit, slightly thick-walled basidiospores with a truncate apex, and a context that changes from white to reddish brown when exposed. Since Berkeley (1847) first described the species from Sri Lanka, it has been reported from south and Southeast Asia by Petch and Bisby (1950, as *Chitoniella*), Leelavathy et al. (1981), and Pegler (1985, 1986). Yang (1991) has also reported it from the tropical region of Yunnan, China. This is the first report with the molecular phylogenetic confirmation after Berkeley (1847) first described this from Sri Lanka. We therefore designate it as a reference specimen.

Fig. 97 ***Clarkeinda trachodes*** (MFLU 10–0139, **reference specimen**) **a** Basidiomes in the field **b** Pellicle on the cap **c** Longitudinal section of the basidiome **d** Veil. Scale bars: a–d = 10 cm.

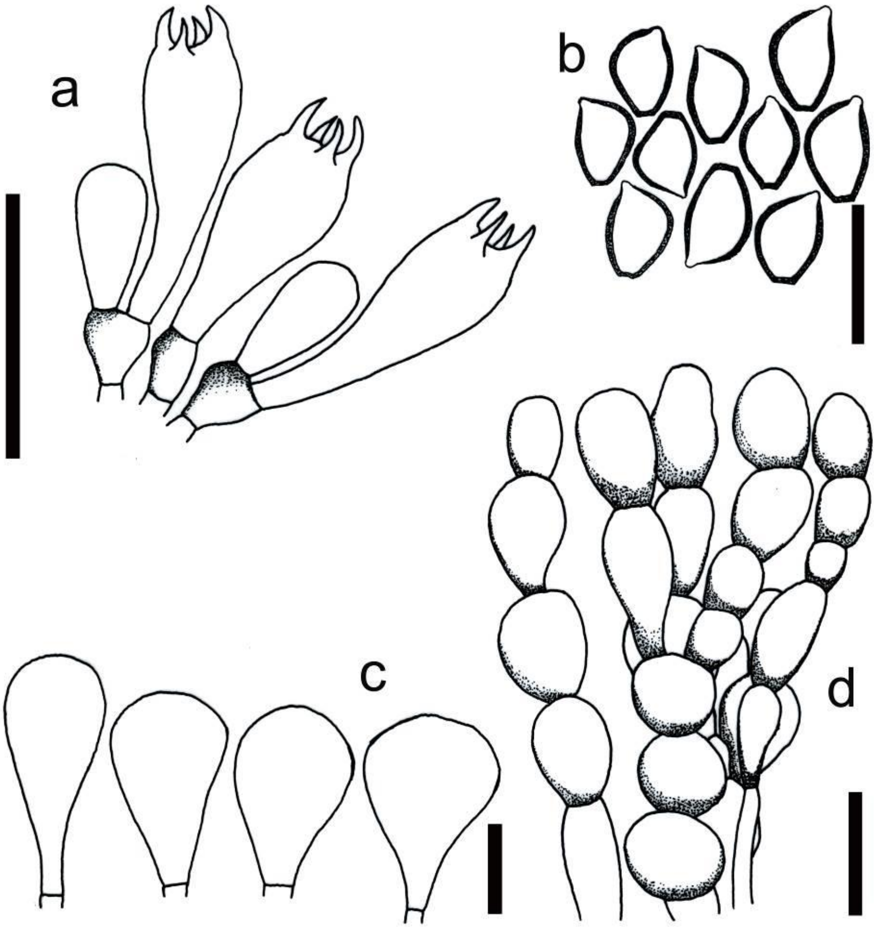


Fig. 98 ***Clarkeinda trachodes*** (MFLU 10–0139, **reference specimen**) **a** Basidia with basidioles **b** Basidiospores **c** Cheilocystidia **d** Pileipellis. Scale bars: a = 30 μm, b = 10 μm, c = 15 μm, d = 20 μm.

Amanitaceae

Amanita Pers.

Amanita Pers. is a widespread basidiomycete genus, with about 700 described species (Tulloss and Yang 2016, http://www.amanitaceae.org). It is divided into two subgenera, *Amanita* and *Lepidella* (E.-J. Gilbert) Veselý. The subgenus *Amanita* includes sections *Amanita*, *Caesareae* Singer, and *Vaginatae* (Fr.) Quél., while the subgenus *Lepidella* includes sections *Amidella* (E.-J. Gilbert) Konrad & Maubl., *Lepidella*, *Phalloideae* (Fr.) Quél., and *Validae* (Fr.) Quél. (Yang 1997; Yang et al. 2004). Most *Amanita* species are known to form ectomycorrhizal (ECM) associations with trees. The phylogenetic tree of *Amanita* is presented in Figs 99 and 100.

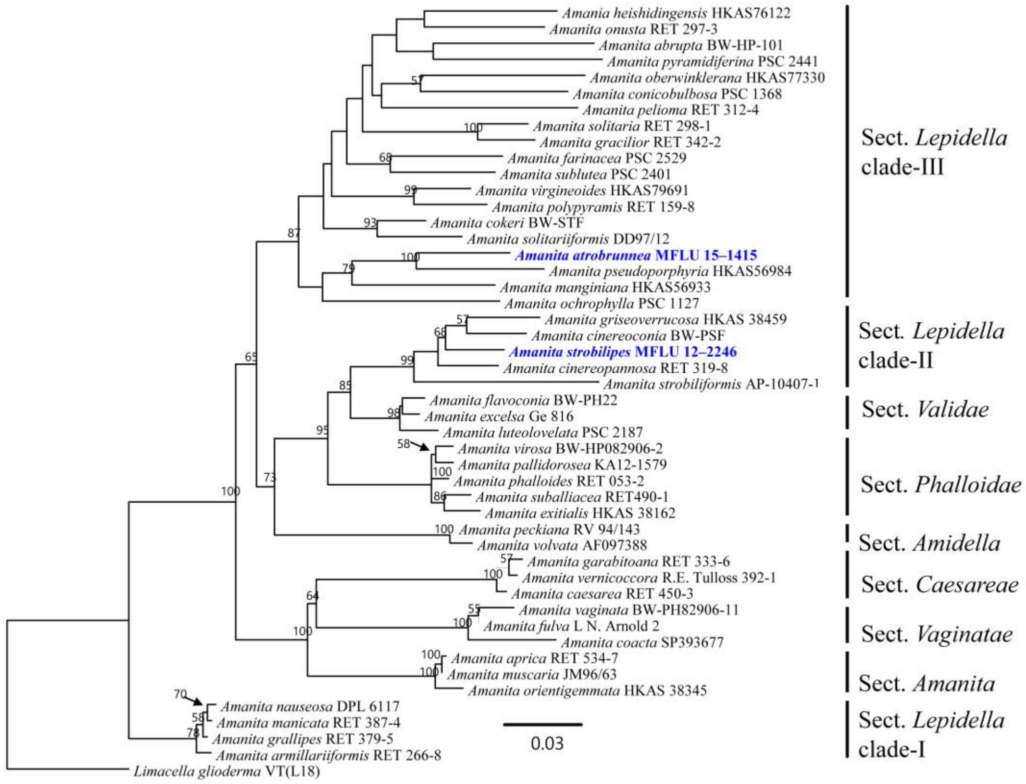


Fig. 99 Phylogram inferred by Maximum Likelihood analysis of LSU sequences. Bootstrap support values greater than 50% are indicated above the nodes. New taxa are in blue and species for which obtained sequences are based on type material have names in bold. The tree is rooted with *Limacella glioderma*.

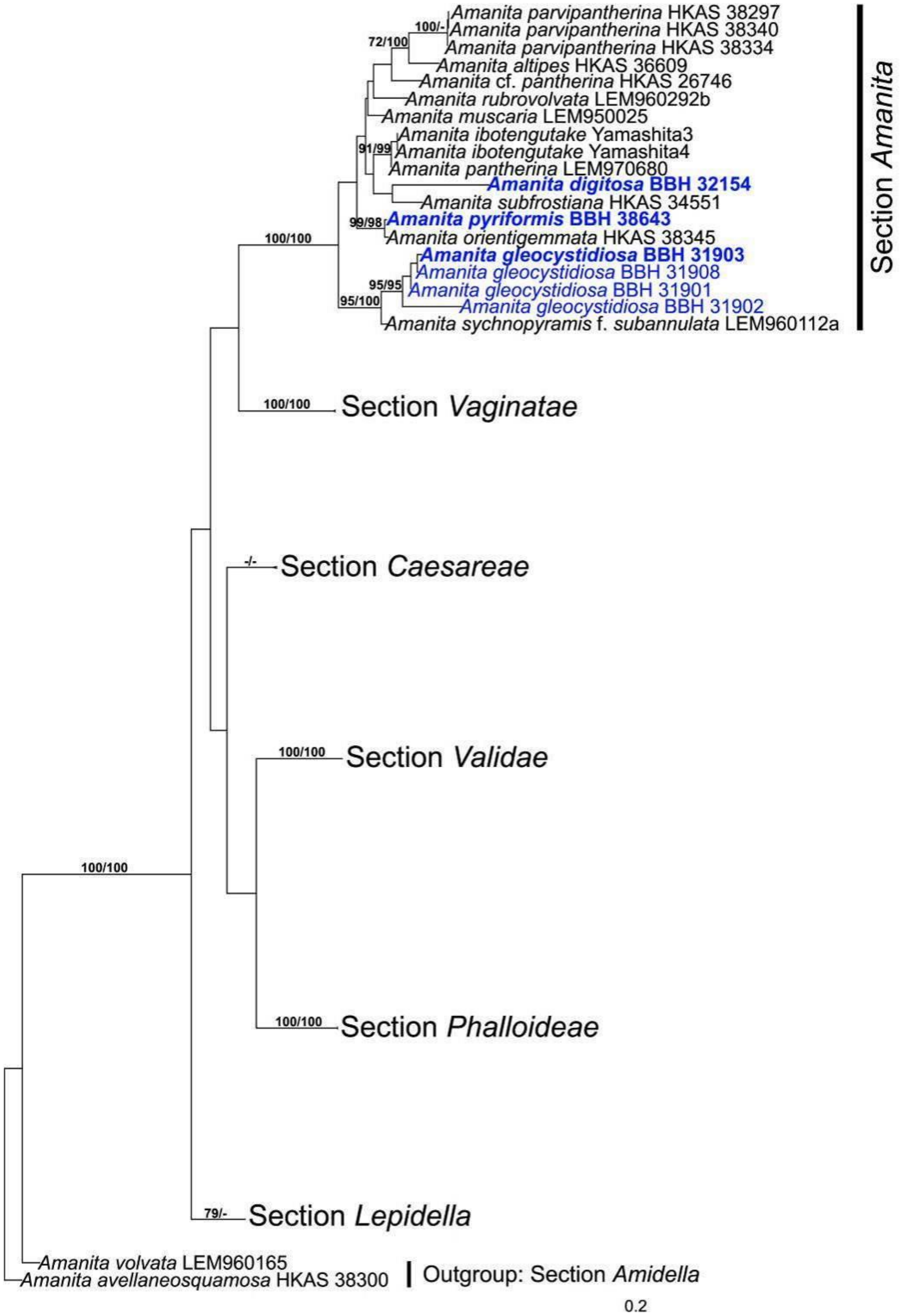


Fig. 100 Maximum likelihood tree depicting infrageneric relationships of *Amanita* based on nuclear ITS dataset. ML and MP bootstrap values ≥ 70% are shown above branches. Sequences derived from three new toxic species are in bold.

320. ***Amanita atrobrunnea*** Thongbai, Raspé & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551652, *Facesoffungi number*: FoF 02070, Fig. 101

Etymology: the epithet refers to the dark brown colour of the pileus

Holotype: MFLU 15–1415

Pileus 120 mm in diam., conic to paraboloid when young, then plano-convex, becoming convex and broadly umbonate when mature, dark brown to chestnut brown (6F7, 6F8), darker in the center, paler and becoming teak brown to leather brown (6F5) towards the margin, minutely rimose, sub-viscid when wet; margin lacking striations, slightly appendiculate, sometimes with scattered annulus remnants; context 1 mm thick at mid-radius, white. *Lamellae* free, white, crowded, up to 8 mm high; lamellulae attenuate, with two to three series. *Stipe* 170 × 15 mm, slender, slightly tapering upwards, white to pale yellowish, finely fibrillo-squamulose; context white, solid, unchanging when bruised. *Bulb* 15–25 mm wide, inconspicuous, subfusiform, white (1A1). *Volva* limbate, slightly firm, up to 20 mm high, white (1A1). *Annulus* membranous, easily broken, white. Odour absent.

Lamellar trama bilateral; mediostratum 30–35 *µm* wide, composed of ellipsoid to fusiform, 35–45 × 10–18 *µm* cells, mixed with abundant, filamentous 3–6 µm wide, branching hyphae. *Subhymenium* 20–35 *µm* thick, with two to three layers of subglobose to irregularly-shaped cells, 12–25 × 10–15 *µm*. *Basidia* 36–41 × 9–12 *µm*, 4-spored, clavate, thin-walled; sterigmata 4–6 *µm* long. *Basidiospores* 7.3–*8.3*–9.5 × 5.4–*6.6*–7.8 *µm*, *Q* = 1.15–*1.26*–1.46 (*N* = 40), broadly ellipsoid to ellipsoid, thin-walled, colourless, amyloid, smooth, with small apiculus. *Lamellar edge* composed of numerous, subglobose, (15–25 × 8–18 *µm*) cells, and rare filamentous, thin-walled, hyaline, 3–9 *µm* wide hyphae. *Pileipellis* 90–100 *µm* thick, composed of two distinct layers, the upper layer gelatinized, made up of radially arranged, thin-walled, filamentous, 3–8 *µm* wide, colourless hyphae, with inflated, sometimes cylindrical, rarely subglobose to elliptical terminal cells; the lower layer mostly non-gelatinized, composed of filamentous, sometimes branching, 4–10 *µm* wide hyphae with pale brown pigment, mixed with abundant inflated cells. *Velar remnants* from stipe base composed of thin-walled to slightly thick-walled, filamentous, 3–8 *µm* wide hyphae, mixed with abundant inflated cells, with yellowish to pale brown intracellular pigments. *Annulus* composed of thin to slightly thick-walled, filamentous, 3–8 µm wide, branching hyphae, mixed with ellipsoid to subglobose, hyaline, inflated, thin-walled cells. No clamps observed in any tissue.

Habitat: Terrestrial in forest dominated by *Fagaceae* species.

Material examined: THAILAND, Chiang Mai Province, Doi Saket District, Sub-District Tepsadet, N18° 57’ 1.0016” E99° 20’ 1.0452”, 30 June 2014, collector B. Chuankid, BZ–2014–09 (MFLU 15–1415, **holotype**)

Notes: *Amanita atrobrunnea* is a member of *Amanita* subgenus *Lepidella* (J.-E. Gilbert) Veselý, section *Lepidella* (Bas 1969). Remarkable features of *A. atrobrunnea* are the dark brown pileus, the broad umbo at the disc, the slender basidiocarp, the absence of membranous velar remnants on the pileus, even when young, the abundant inflated cells in the pileal surface and the broadly elipsoid to ellipsoid basidiospores. The most morphologically similar species are *A. manginiana sensu* W.F. Chiu and *A. pseudoporphyria* Hongo, which share several characters with *A. atrobrunnea*, such as an inconspicuous bulb, dark pileus, and velar remnants on the pileus consisting of inflated cells (Zhang et al. 2010). However, *A. atrobrunnea* can easily be distinguished from *A. manginiana* and *A. pseudoporphyria* by its distinctive umbonate pileus at maturity. In addition, the inflated cells of the pileipellis, a key character of *A. atrobrunnea*, are not present in the other species. Like *A. atrobrunnea*, *A. pallidorosea* P. Zhang & Zhu L. Yang possesses a conspicuous umbo, but the pallid rose colour of latter is very different. *Amanita manginiana* and *A. pseudoporphyria* were initially placed in section *Phalloideae* (Hongo 1982, Yang 1997, Zhang et al. 2004, Zhang et al. 2010). However, recent phylogenetic analyses clearly showed that both species belong to section *Lepidella* (Cai et al. 2014). Our molecular phylogenetic analysis indicates that *A. atrobrunnea* is a sister species to *A. manginiana* and *A. pseudoporphyria*.

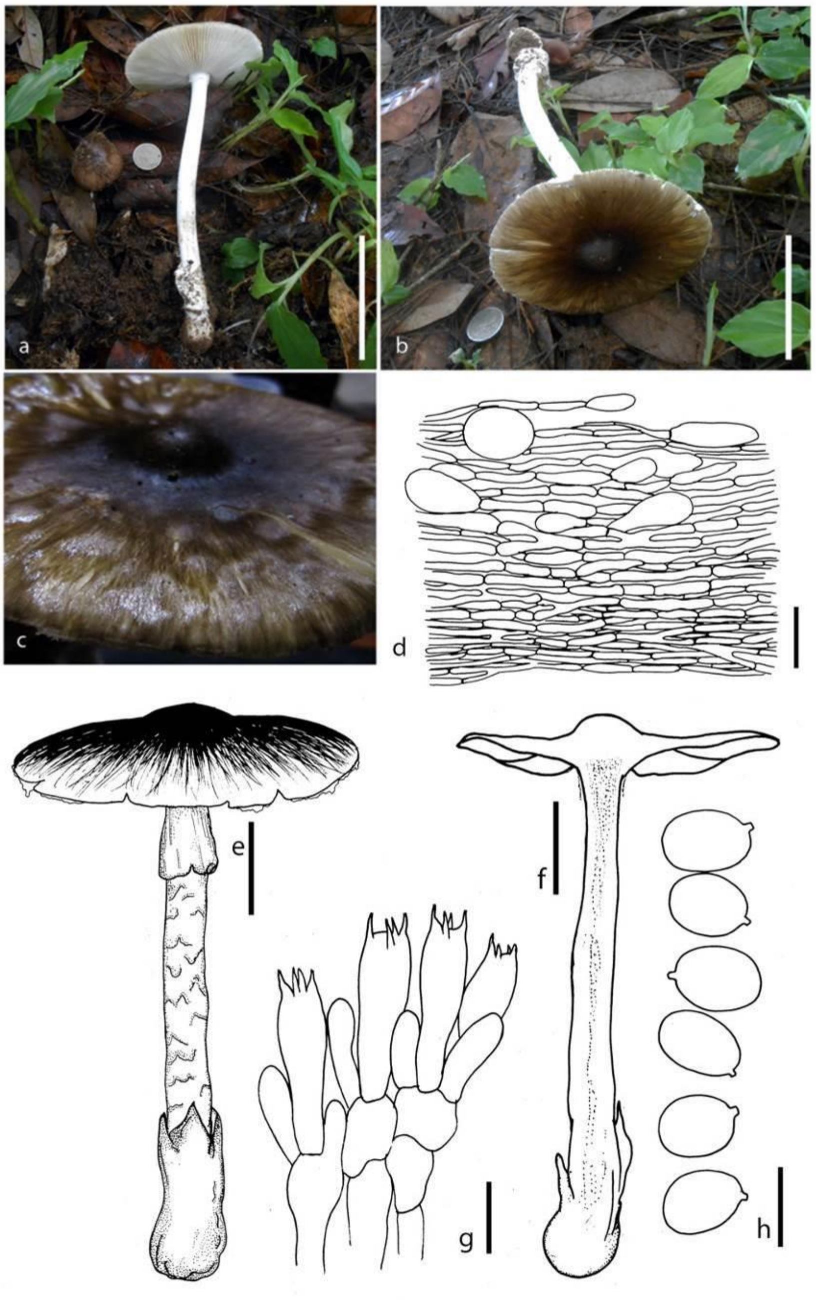


Fig. 101 ***Amanita atrobrunnea*** (**holotype**) **a**–**c** Basidiome **d** Radial section of pileipellis **e, f** Basidiome **g** Basidia and subhymenium **h** Basidiospores. Scale bars: a, b = 8 cm, d = 20 *µm*, e, f = 30 mm, g = 20 *µm*, h = 10 *µm*

321. ***Amanita digitosa*** Boonprat. & Parnmen, ***sp. nov.***

Index Fungorum number: IF 551619, *Faceoffungi number*: FoF 02069, Fig. 102

Etymology: The specific epithet refers to *Amanita* with abundant digitate cell types among other elements of the volva.

Holotype: BBH 32154

Pileus 13.5–29 mm, paraboloid when young, convex to applanate with age, smooth, yellowish brown 5(D–E) 8 at disc, towards half of pileus and pale yellow 3(A)4 in the middle of the pileus to margin, or the whole pileus yellowish brown 3(A)4, smooth from disc towards the half of pileus and striate from the middle of pileus towards the margin, with dry and even margin. *Pileus context* off white, soft. *Lamellae* free, unequal, subsistent, broad, fimbriate, lamella edge and face pale yellow 3(A)4. *Stipe* 4.5–6 × 21–53 mm, central, cylindrical to tapering from base to apex, yellowish white 1(A)2, soft, context reaction yellow with 3%KOH, base bulbous: width 12–16 mm. Annulus not observed. Volva white membranous saccate.

Basidiospores 8–10 × 7–9 [x = 8 ± 0.65 × 9 ± 0.65 *µm*, Q = 1.13 ± 0.01, n = 25 spores, 1 collection] subglobose, smooth, hyaline, inamyloid, thin-walled, sometimes with wart-like to network-like interior ornamentation. *Basidia* 30–37.5 × 10.5–12.5 *µm*, clavate with 2 and 4-spores, clamp connection absent, smooth, hyaline, inamyloid, thin-walled. *Basidioles* 16–28 × 4.7–9.5 *µm*, clavate, smooth, hyaline, inamyloid, thin-walled. *Pleurocystidia* 31–34 × 5.5–9.4 *µm*, clavate, smooth, hyaline, inamyloid, thin-walled. *Cheilocystidia* absent. *Lamellae trama* divergent, composed of broadly clavate to broadly ellipsoid cells, smooth, hyaline, dextrinoid, thin-walled, base of hymenial layer directly arising from a few layers of cellular cells connected to trama element. *Pileipellis* composed with cutis of repent hyphae, cylindrical, smooth, hyaline, inamyloid, thin-walled. *Stipilipellis* composed with cutis of repent hyphae, 3–5 *µm* diam., smooth, hyaline, inamyloid, thin-walled. *Stipe trama* composed of two types of element: repent hyphae and broadly clavate to broadly ellipsoid hyphae, smooth, hyaline, inamyloid, thin-walled. *Volva* composed of three types of elements: apex 19–21 × base 6 *µm* of digitate cells, 16–68 × 2.5–8.9 *µm* of clavate cells and 21–32 × 10.5–23 *µm* of broadly clavate to broadly ellipsoid cells, smooth, hyaline, inamyloid, thin-walled. *Clamp* absent in all parts of basidiomata.

Notes: *Amanita digitosa* differs from *A. subfrostiana* Zhu L. Yang (Yang 1997) in having brown and smaller basidiomata, while in *A. subfrostiana* they are red over the disc to orange at the margin. Micro-characters include pleurocystidia, while these are absent in the protologue of *A. subfrostiana*.

Habitat: Terrestrial in mixed forest.

Material examined: THAILAND, Si Sa Ket Province, Phu Sing District, Khok Tan Tambon, 3 September 2012, collector SRRT Team, Bureau of Epidemiology, Department of Disease Control Ministry of Public Health (BBH 32154, **holotype**).

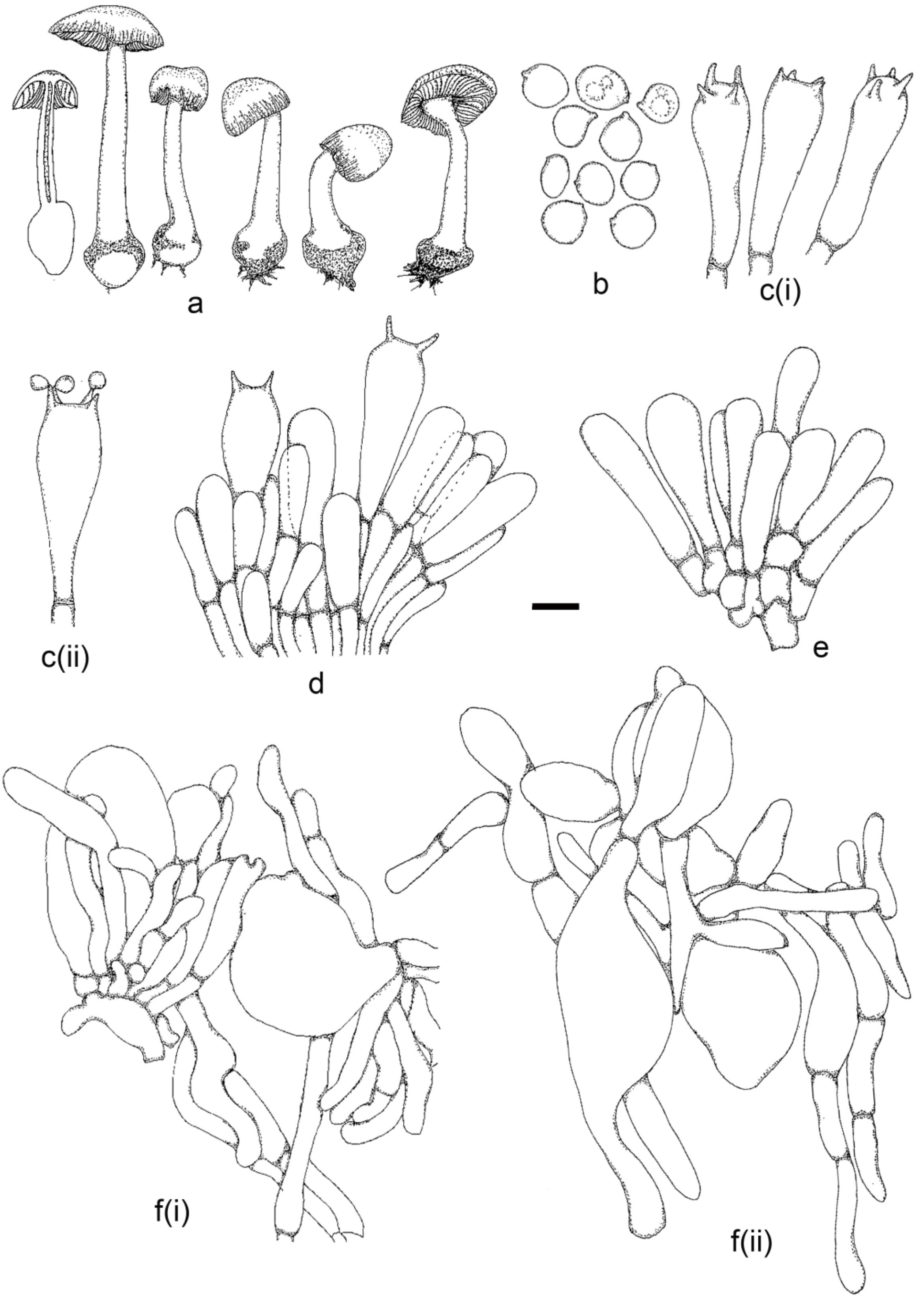


Fig. 102 ***Amanita digitosa*** (**holotype**) **a** Basidiomata **b** Basidiospores **c(i-ii)** Basidia **d** Basidia with basidioles **e** Pleurocystidia **f(i-ii)** Veil trama. Scale bars: a = 10 mm, b-f = 10 *μm*.

322. ***Amanita gleocystidiosa*** Boonprat. & Parnmen, ***sp. nov.***

Index Fungorum number: IF 551614, *Faceoffungi number*: FoF 02071, Fig. 103

Etymology: The specific epithet refers to *Amanita* with abundant of yellow gleocystidium, *'gleocystidium' (n, neuter = versiform cystidia which have granular content) + '-osus' (adjA suffix = abundant)*

Holotype: BBH31903

Pileus 22–45 mm diam. at first, first convex to parabolic when young, expanding to applanate with age, sometimes depressed, sulcate, sticky, moist, colour ranges from dark brown 8(F)5–8 at disc to grayish yellow 1(A)3–5 at margin when young; olive yellow 2–3(C–E)6–8 at disc to yellowish white 2–3(A)2 at margin with age, sometimes dark brown 8(F)5–8 at disc to grayish yellow 1(A)3–5 at margin with age, with striate and even margin. *Pileus context* off white, 2–3 mm thick, soft and moist. *Lamellae* free, broad, average, 3 series, sub-distant, yellowish white 2–3(A)2. *Stipe* 75–100 × 6–9 mm, central, tapered from base to apex, clavate-bulbous base, fistulose, longtitudinal striate, pale orange to orange white 5(A)2–3 with grayish orange striate 5(B)3–6 after bruising. *Annulus* with single layer, pale yellow to brown, apical and partial veil still intact when young, many of disappearing with age but few present at a center of stipe. *Volva* constricted, adherent with flaring margin, white.

Basidiospores 7–10 (–11) × 7–10 *µm* [x = 8.76 ± 0.91 × 8.12 ± 0.13 *µm*, Q = 1.07 ± 0.10, n = 25 spores per collection, 2 collections], globose subglobose, smooth, hyaline, inamyloid, thin-walled. *Basidia* 27–41 × 9.5–12.5 *µm*, clavate 2-spored, clamp connection absent, smooth, hyaline, inamyloid, thin-walled. *Basidioles* 18–21 × 6.5–7.5 *µm*, clavate, smooth, hyaline, inamyloid, thin-walled. *Pleurocystidia* with two types of clavate and lanciolate, smooth, hyaline, inamyloid, thin-walled, clavate pleurocystidia 30–35 × 7.5–12.5 *µm*, lanciolate pleurocystidia 35–50 × 8.5–12.5 *µm*. *Cheilocystidia* apex 12–13 *µm* × middle 5–7 × base 3–4 *µm*, broadly clavate to pyriform, smooth, hyaline, inamyloid, thin-walled. *Gleocystidia* abundant among basidioles, pleurocystidia and cheilocystidia, shape and size dependent on the position of appearance, contains yellow granules, smooth, hyaline, inamyloid, thin-walled. *Lamellae trama* divergent, broadly clavate to broadly ellipsoid, smooth, hyaline, dextrinoid, thin-walled, base of hymenial layer directly arising from a few layers of cellular cells, which connects to the trama element. *Pileipellis* composed of cutis of repent hyphae, smooth, hyaline, inamyloid, thin-walled. *Stipilipellis* composed with cutis of repent hyphae, 2.5–5 *µm* diam., smooth, hyaline, inamyloid, thin-walled. *Stipe trama* composed of two types of element: repent hyphae and broadly clavate to broadly ellipsoid hyphae 73–105 × 31–34 *µm*, smooth, hyaline, inamyloid, thin-walled. *Volva* composed of two types of elements: 22–31 × 3.5–7 *µm* of clavate cells and 14–28 × 6.3–11.5 *µm* of broadly clavate to broadly ellipsoid cells, smooth, hyaline, inamyloid, thin-walled. *Clamp* absent in all parts of basidiomata.

Habitat: Terrestrial in mixed forest.

Material examined: THAILAND, Phetchabun Province, Lom Kao District, Na Sang Tambon, 28 May 2012, collector SRRT Team, Bureau of Epidemiology, Department of Disease Control Ministry of Public Health (BBH31903, **holotype**); *Ibid*., BBH31901, BBH31902 and BBH31908, paratypes, all collections were from Phetchabun Province, Lom Kao District, Na Sang Tambon, collector SRRT Team, Bureau of Epidemiology, Department of Disease Control Ministry of Public Health, 28 May 2012, specimen scattered around temple.

Notes: *Amanita gleocystidiosa* is similar to *A*. *sychnopyramis* f. *subannulata* Hongo (Yang et al. 2001) in having a similar macroscopic morphology and basidiospore shape and size, but *A*. *gleocystidiosa* differs from *A*. *sychnopyramis* f. *subannulata* in having pleurocystidia and cheilocystidia, while those two types of cystidia were absent in *A*. *sychnopyramis* f. *subannulata*. The most important feature in *A*. *gleocystidiosa* are gleocystidia containing yellow granular cells, abundantly dispersed among cells in the hymenial layer.

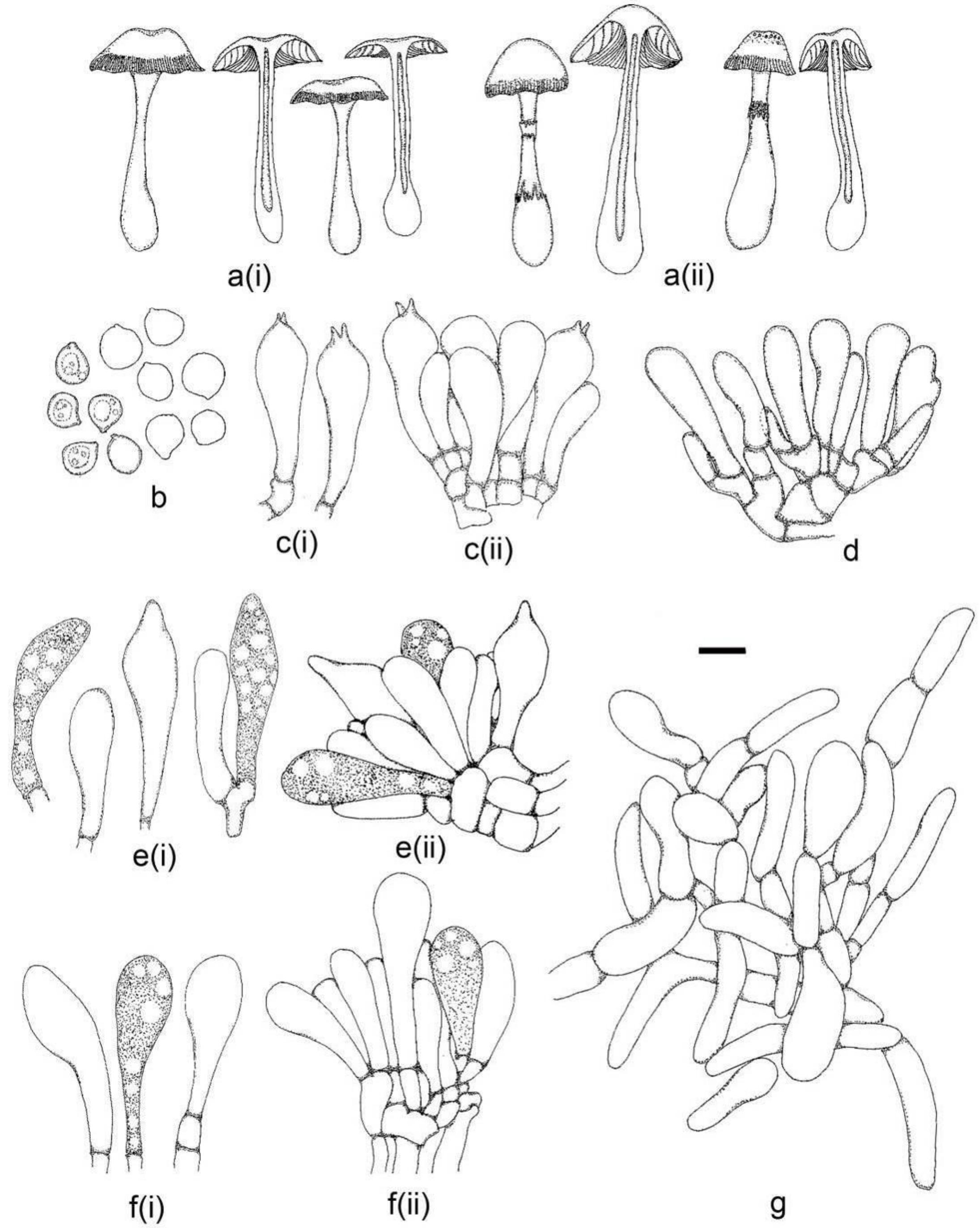


Fig. 103 ***Amanita gleocystidiosa*** **(holotype) a (i–ii)** Basidiomata **b** Basidiospores **c(i)** Basidia **c(ii)** Basidia with basidioles **d** Basidioles **e(i)** Pleurocystidia **e(ii)** Pleurocystidia and basidioles mixed with gleocystidia in the different shapes **f(i)** Cheilocystidia **f(ii)** Cheilocystidia with basidioles **g** Veil trama. Scale bars: a = 10 mm, b–g = 10 *μm*.

323. ***Amanita pyriformis*** Boonprat. & Parnmen, ***sp. nov.***

Index Fungorum number: IF 551620, *Faceoffungi number*: FoF 02072, Fig. 104

Etymology: The specific epithet refers to a type of pleurocystidia *'pyriformis'* = pear-shaped, narrowly obovoid with a tapering base.

Holotype: BBH 38643.

Pileus 33–55 mm, convex when young, plane with age, rugulose, umbonate, the whole pileus grayish yellow 1(B)3–7 and yellowish orange 4(A–B)7–8 at margin, dry, striate 1/8 from margin toward to disc, margin even. *Pileus context* off white, soft. *Lamellae* free, unequal, subdistant, broad, eroded, grayish yellow 1(B)3–7. *Stipe* 79–112 × 3–7.5 mm, central, cylindrical, enlarged base, grayish yellow 1(B)3–7 with yellowish orange 4(A–B)7–8 at stipe base near volva, soft. *Annulus* cream, hanging about 1/3 of pileus from stipe apex, single, sheathing, smooth, white, thin, apical attachment 19–27 mm from base toward the apex. *Volva* constricted, adherent with flaring margin, white.

Basidiospores (7–) 8–10 × (6–) 7–9 *μm* [x = 9.12 ± 0.97 × 7.76 ± 0.83 *μm*, Q = 1.18 ± 0.14, n = 25 spores, 1 collection] broadly ellipsoid, smooth, hyaline, inamyloid, thin walled. *Basidia* 29.5 × 11.5 *μm*, clavate with 4-spores, clamp connection absent, smooth, hyaline, inamyloid, thin-walled. *Basidioles* 16–26 × 6.5–11 *μm*, clavate to broadly clavate, sometimes pyriform, smooth, hyaline, inamyloid, thin-walled. *Pleurocystidia* 28–30 × 7–8 *μm*, clavate to pyriform, smooth, hyaline, inamyloid, thin-walled. *Cheilocystidia* absent. *Lamellae trama* divergent, composed with broadly clavate to broadly ellipsoid cells, smooth, hyaline, dextrinoid, thin-walled, base of hymenial layers directly arising from a few layer of cellular cells which connects to trama element. *Pileipellis* composed with cutis of repent hyphae, cylindrical, smooth, hyaline, inamyloid, thin-walled. *Stipilipellis* composed with cutis of 3.5–7.5 *μm* diam. of repent hyphae, sometime obclavate cells, found among simple cylindrical cells, smooth, hyaline, inamyloid, thin-walled. *Stipe trama* composed of two types of element: repent hyphae and broadly clavate to broadly ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Volva* composed of three types of element: 2–6.8 *μm* diam. of repent hyphae, broadly clavate to broadly ellipsoid cells 32–52 × 11.5–26 *μm* and branching of repent hyphae, smooth, hyaline, inamyloid, thin-walled. *Clamp* absent in all parts of basidiomata.

Habitat: Terrestrial in mixed forest.

Material examined: THAILAND, Chiang Mai Province, Omkoi District, Mae Tun Tumbon, 27 June, 2014, collector SRRT Team, Bureau of Epidemiology, Department of Disease Control Ministry of Public Health (BBH38643, **holotype**)

Notes: *Amanita pyriformis* is similar to *A. orientigemmata* Zhu L. Yang & Yoshim. Doi (Yang and Doi 1999) in having broadly ellipsoid basidiospores, but differs from *A. orientigemmata* in having smaller, umbonate, pale yellow basidiomata and presence of pleurocystidia, while *A. orientigemmata* has larger basidiomes, up to 100 mm wide, floccose patches on the pileus and the absence of pleurocystidia.

ITS sequence data belonging to core taxa of different sections of *Amanita* were selected based on current classification and phylogeny of the genus *Amanita* (Zhang *et al*. 2004). A matrix of 1,005 unambiguously aligned nucleotide characters was constructed and 276 characters were constant. The topology of the trees from the maximum likelihood (ML) and maximum parsimony (MP) analyses did not show any conflict and hence, only the ML tree is shown here (Fig. 100). The boundary of each section is supported as monophyletic. In this study, we focused on the toxic mushroom samples from the outbreaks of mushroom poisoning cases in 2012 and 2014. These samples clustered in section *Amanita*. In our phylogenetic analysis based on ITS sequence data, *Amanita gleocystidiosa*, *A. digitosa* and *A. pyriformis* were placed near *A. sychnopyramis* f. *subannulata* (Yang *et al*. 2001), *A. subfrostiana* (Yang 1997) and *A. orientigemmata* (Yang and Doi 1999), respectively. Only *Amanita gleocystidiosa* contains a high quality of toxic amanitin.

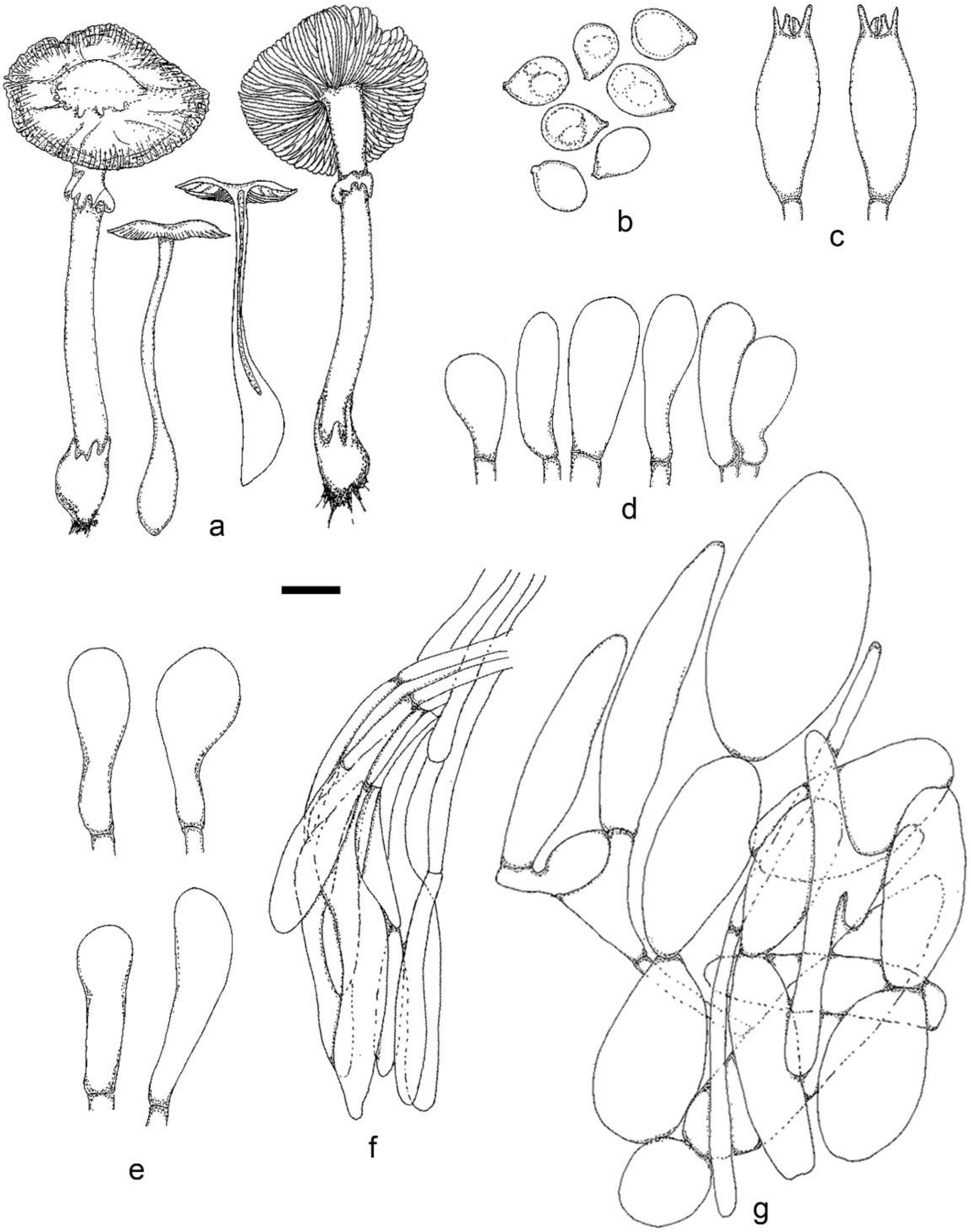


Fig. 104 ***Amanita pyriformis*** (**holotype**) **a** Basidiomata **b** Basidiospores **c** Basidia **d** Basidioles **e** Pleurocystidia **f** Stipilipellis **g** Veil trama. Scale bars: a = 10 mm, b–f = 10 *µm*.

324. ***Amanita strobilipes*** Thongbai, Raspé & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551651, *Facesoffungi number*: FoF 02073, Fig. 105

Etymology: Refers to base of stipe like a pine cone.

Holotype: MFLU 12–2246

Pileus 105 mm in diam., slightly convex then plane, pale gray or grayish white (1A2, 1C1) with dark gray (1E1, 1F1) conical or pyramidal warts over the center, progressively becoming brownish gray (5D2, 5D3) squamules towards the margin, slightly pulverulent-flocculose, margin paler, lacking striations, slightly appendiculate, edge fibrillose, dry; context 1.5 mm thick at mid-radius, white. *Lamellae* sub-free to free, crowded; lamellulae attenuate, with more than 4 series, white to very pale ochraceous (1A1, 1A2). *Stipe* 120 × 20 mm, subcylindrical, bulbous, inflated near the pileus, surface mostly white to smoke gray, pale grayish below, covered with cottony-fibrillose pulverulence all over, which is easily lost when touched; context white, solid, unchanging when bruised. *Bulb* maximum 30 mm wide, spindle-shaped, covered with white to slightly ochraceous (1A1, 1A2) curved scales. *Annulus* membranous, fibrillose, fragile, white. Odour absent.

Lamellar trama bilateral; mediostratum 25–40 *µm* wide, mainly consisting of filamentous, 2–5 *µm* wide, branching hyphae; lateral stratum made up of intercalary inflated, 25–45 × 5–20 *µm*, connected with subhymenium. *Subhymenium* 20–30 *µm* thick, with three to four layers of subglobose to broadly ellipsoid cells. *Basidia* 30–55 × 9–11 *µm*, 4-spored, clavate, thin to slightly thick-walled, sterigmata 4–6 *µm* long, clamps absent at base. *Basidiospores* (6.8) 7–*8.2*–9.8 (10.1) × (4.4) 5.2–*5.6*–6 (8.5) *µm*, *Q* = 1.04–*1.46*–1.87, (*N* = 40), ellipsoid to elongate, colourless, amyloid, smooth, thin-walled, with apiculus. *Lamellar edge* sterile, mainly consisting of subglobose to clavate, 12–20 × 4–8 *µm*, thin-walled cells, mixed with filamentous, 2–3 celled, brownish hyphae. *Pileipellis* 250–300 *µm* thick, composed of filamentous, subcylindric, occasionally branching, 3–8 *µm* wide, slightly gelatinized to gelatinized, hyphae, with pale yellow vacuolar pigments. *Velar remnants* from pileus consisting of abundant globose to ellipsoid, 30–60 × 25–65 *µm* cells, sometimes mixed with cylindrical, branching, thin-walled, filamentous 1.5–7 µm wide, hyaline or with brownish to yellowish pigments hyphae with terminal inflated cells. *Annulus* composed of clavate, 42–71 × 16–32 *µm* to cylindrical, 36–50 × 9–15 µm cells, with brownish to yellowish pigments. No clamps observed in any tissue.

Habitat: Terrestrial in forest with *Fagaceae* species.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, N19° 07.20’ E98°44.04’, 25 June 2012, collector B. Thongbai, BZ–2012–22 (MFLU 12–2246, **holotype**)

Notes: *Amanita strobilipes* is a member of *Amanita* subgenus *Lepidella* (J.-E. Gilbert) Veselý emend section *Lepidella* (Bas 1969) subsection *Solitariae*. The pale gray or grayish white pileus with brownish gray squamules on the surface, pyramidal dark gray warts over the center, whitish stipe covered with white gray to grayish cottony-fibrillose pulverulence, white to slightly ochraceous, recurved scales on the spindle-shaped bulb, and amyloid, ellipsoid to elongate basidiospores characterize this species. Within the subsection *Solitariae*, the morphologically most similar species is *Amanita griseoverrucosa* Zhu L. Yang, originally described from China. Both species share some similarities, namely the pale gray or grayish white pileus. However, *A. griseoverrucosa* produces larger basidiomes, wider basidiospores and the pileus of *A. strobilipes* is more distinctively covered with dark gray pyramidal warts to brownish gray squamules. *Amanita strobilipes* also can easily be differentiated from *A. griseoverrucosa* by its distinctively spindle-shaped bulb, covered with white to slightly ochraceous, curved scales, whereas *A. griseoverrucosa* has a rather ventricose to subglobose, subradicate bulb, with the upper part covered with grey to greyish warts or irregularly formed velar remnants. *Amanita cinereopannosa* Bas, originally described from the USA, resembles *A. strobilipes* in the ellipsoid to elongate basidiospores, a subcylindric stipe and grayish white pileus. However, in *A. cinereopannosa* the pileus is covered with rather abundant, soft, pulverulent-subfelty, low irregular warts, to flat or more angular patches. Additionally, the upper part of bulb of *A. cinereopannosa* is usually covered with a few transverse bands or concentric rows of greyish flocculose-pulverulent patches. Another species that shares some similarities is *A. heishidingensis* Fang Li & Qing Cai, originally described from China, which also shows dark gray pyramidal warts on the pileus, a whitish stipe covered with white-gray to grayish cottony-fibrillose pulverulence, but its pileus is rather dirty white to whitish and viscid, the bulb is larger and napiform, subclavate to ventricose. Moreover, *A. heishidingensis* appears not to be very closely phylogenetically related to *A. strobilipes*.

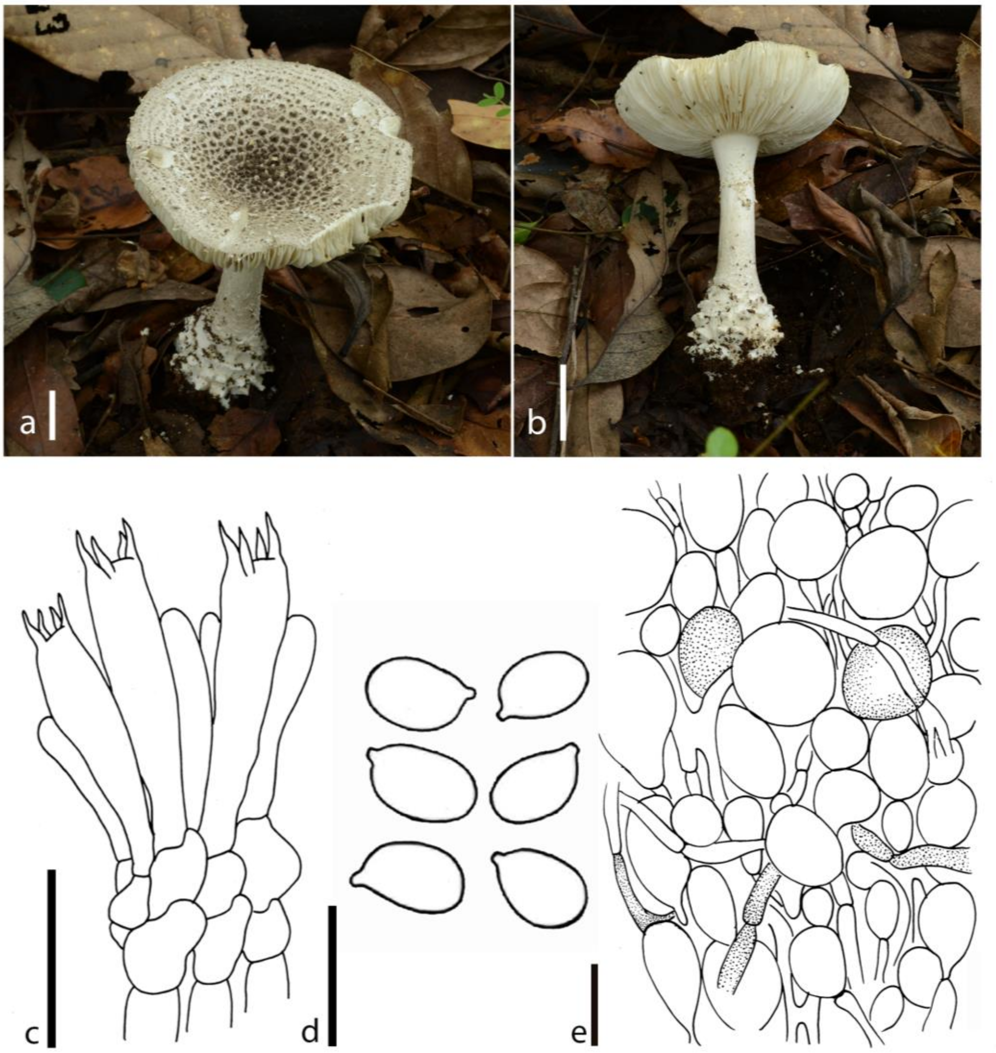


Fig. 105 ***Amanita strobilipes*** (**holotype**) **a, b** Basidiome **c** Basidia and subhymenium **d** Basidiospores **e** Longitudinal section of velar remnants from pileus. Scale bars: a, b = 20 mm, c = 20 *µm*, d = 10 *µm*.

Cortinariaceae

The limits of the family *Cortinariaceae* remain unclear at this time. The majority of the species are in the genus *Cortinarius*. Many genera formerly placed in the *Cortinariaceae*, e.g., *Phaeocollybia*, *Hebeloma*, *Galerina*, and some others have been moved to other families in *Agaricales*. On the other hand, the sequestrate genera, *Thaxterogaster*, *Quadrispora*, *Protoglossum* and *Hymenogaster p.p.*, as well as *Cuphocybe*, *Rapacea* and species of *Rozites*, once thought to be genera within the *Cortinariaceae*, are currently included in the genus *Cortinarius* (Peintner et al. 2001, 2002). The basidiocarps range from agaricoid to sequestrate, and many have poorly to well-developed veils. The basidiospores are typically ornamented and cinnamon brown in deposit.

Cortinarius (Pers.) Gray

Cortinarius is the largest genus of *Agaricales* with a cosmopolitan distribution and over 2000 described species. The species are important ectomycorrhizal fungi and are associated with different trees and shrubs, belonging to the families *Fagaceae*, *Salicaceae, Caesalpiniaceae, Cistaceae*, *Dipterocarpaceae*, *Myrtaceae*, *Rhamnaceae*, *Rosaceae* and *Pinaceae*, as well as some herbaceous plants in the *Cyperaceae* and *Polygonaceae*. Some species form arbutoid mycorrhizae with *Arbutus*, *Arctostaphylos*, and *Comarostaphylis*. Revealing the true diversity of species using only morphological and ecological characteristics has proven to be a difficult if not an impossible task. The use of sequence data has made it possible to elucidate phylogenetic relationships within the genus, to show patterns of speciation, and to help define new, convergent and cryptic species.

In recent years several workers have investigated *Cortinarius* species associated with oak and mixed oak-conifer forests and woodlands along the Pacific coast from California north to Victoria, British Columbia (Bojantchev & Davis 2011, Bojantchev 2013, Bojantchev 2015, Ceska 2013, Garnica et al. 2011, Harrower et al. 2011, Liimatainen 2015). In most instances, the studies show that the species in these habitats are new to science and often represent unique and/or significant additions to our understanding of the phylogenetic relationships in *Cortinarius*.

Below we introduce nine new species of *Cortinarius*, subgenus *Telamonia* that represent a number of evolutionary lineages. The majority of the specimens were collected in *Quercus garryana* Dougl. dominated woodlands of southwestern Klickitat County, Washington. All collecting was carried out in a 44 km long region, immediately north of the Columbia River. Elevations ranged from 30 meters to 427 meters. Average annual rainfall is 790 mm/year at the west end and 365 mm/year at the east end of the oak study area. Further west, oak forests are replaced by Douglas fir (*Pseudotsuga menziesii* (Mirb.) Franco) dominated forests, with oaks only found on the very steep, warmer and dryer south-facing slopes. Mushrooms were rarely seen on these steep, dry slopes. Further east, the oaks are mainly found in the colder and wetter north facing slopes where fewer of these mushrooms were found. Nor were *Cortinarius* species found under higher elevation oaks where nighttime temperatures were much colder. In some portions of the oak woodlands, the oaks may be mixed with Grand fir (*Abies grandis* (Douglas ex D. Don) Lindley) and Ponderosa pine (*Pinus ponderosa* Douglas ex C.Lawson). Specimens collected on British Columbia, Canada are from Vancouver Island and Salt Spring Island. The average total annual precipitation is about 880 mm near Victoria. *Quercus garryana* reaches its global distribution limit south of the 50° parallel on Vancouver Island near Courtenay and on Savory Island, northwest of Powell River. Its distribution on Vancouver Island and adjacent Gulf Islands is determined by the rain shadow of the Olympic and Vancouver Island Mountains. On the other hand, *Arbutus menziesii* Pursh that is missing in Klickitat Co. is a common associate of *Quercus garryana* in British Columbia. It is an important co-dominant of *Quercus garryana* stands on shallow soil and a constant species at the *Quercus garryana/Pseudotsuga menziesii* ecotone. The phylogenetic tree for *Cortinarius* is presented in Fig. 106.

Several factors appear to explain why such high portions of the *Cortinarius* species in these oak woodlands are new to science. In past decades few *Cortinarius* collectors visited these relatively dry habitats. Poison oak (*Toxicodendron diversilobum* (Torr. & A. Gray) Greene) may have prevented some people from entering these woodlands. The fall fruiting often occurs after leaves have fallen from the trees, thickly covering the ground. The fungi themselves tend to fruit from deep in the soil and often only just barely stick up above the soil. These two factors make the mushrooms hard to find. The fruiting window can be very narrow and occurs after mushrooms have largely ceased fruiting in other near-by areas. The mushrooms often fruit in small hot spots, often with five to ten species appearing within 30 meters of each other and no *Cortinarius* species elsewhere in the oak grove. In some years fruiting is poor or completely absent in these rather dry habitats.

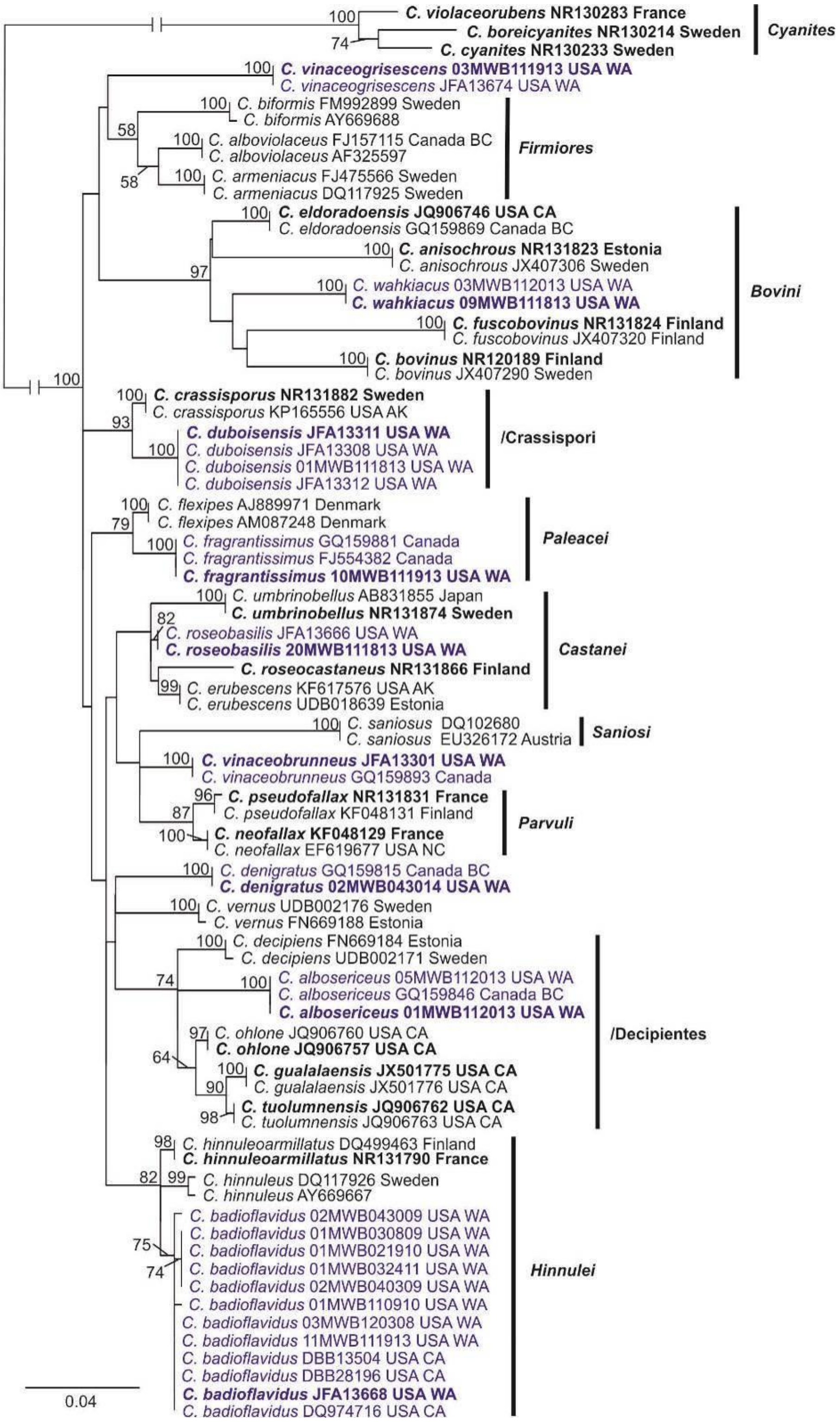


Fig. 106 Phylogram resulting from the RaXML (Stamatakis 2014) analysis of ITS regions. Bootstrap values greater than 50% are indicated above branches. The names in blue represent the new species of *Cortinarius* and the specimens in boldface the type specimens of the species. The tree is rooted with section *Cyanites*.

325. ***Cortinarius albosericeus*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, ***sp. nov.***

Index Fungorum number: IF 551701, *Facesoffungi number*: FoF 02037, Fig. 107

Etymology: Name based on white thinly sheathing veil of stipe and pileus.

Holotype: Michael Beug 01MWB112013 (WTU)

Pileus 30–40 mm diam., convex to broadly umbonate, silky dry, Mahogany Red to chestnut brown becoming Amber Brown then Tilleul Buff, margin white, hygrophanous. *Lamellae* adnate, subdistant, light pinkish cinnamon to cinnamon or cinnamon brown when mature, edge pale. *Stipe* 55–80 mm long, 5–7 mm thick, ± equal, slightly rooting, dry, apex sometimes with bluish tints, light vinaceous cinnamon to whitish buff. *Universal veil* white fibrillose, thinly sheathing the surface of the stipe with indistinct belts. *Basal mycelium* white. *Context* pale brown. *Odour* fungoid or slightly of radish. *Taste* slight fungoid to mild. *Macrochemical reaction (40 % KOH)*: pileus context and surface clove brown, raw umber, bronze, stipe apex pinkish cinnamon to light ochraceous buff, stipe base warm buff to fuscous black. *Exsiccatae*: pileus margin light brown, disc darker brown, lamellae rust brown from spores, stipe pallid to light brown, white basal mycelium, context pallid to light brownish. *Basidia* 4-spored, 7–8.1 × 28–31 *µm*, clavate, hyaline or slightly brownish. *Basidiospores* (7) 7.4–8.5 × 4.6–5.5 *µm* (20 spores, holotype specimens), ellipsoid, broadly ellipsoid, or some amygdaloid, slightly to somewhat curved apiculus, moderately to coarsely verrucose, slightly to moderately or strongly dextrinoid. *Lamella trama hyphae* hyaline to yellowish brown or brownish, walls yellow refractive, encrusted in KOH. *Pileipellis in KOH*: Surface layer thin, hyphae cylindrical, 4–6 *µm* wide, hyaline or rarely yellowish. Subtending layer of ± enlarged hyphae 8–30 *µm* wide, hyaline, walls yellow refractive, hyaline to somewhat yellowish. Beneath a light yellow brown to light brown pigmented layer of cylindrical to enlarged hyphae, mostly 4–20 *µm* wide that gradually grade into trama hyphae. *ITS sequence* distinct from the other known members of the *Decipientes*, and differs from them in the ITS region by more than 15 substitutions and indel positions.

Ecology and distribution: In mixed forests of *Quercus garryana* and *Pinus ponderosa* or *Quercus garryana*, *Pseudotsuga* and *Arbutus menziesii*. Producing basidiomata in late autumn. Known from British Columbia, Canada and Washington USA, Western North America.

Material examined: CANADA, British Columbia, Observatory Hill, Saanich, behind smaller dome, 48.52° N, 123.416° W, margin of mixed forest (*Quercus garryana*., *Pseudotsuga menziesii*, *Arbutus menziesii*) and open mossy rock outcrops on SW slope, 26 Nov 2005, *leg*. Oluna Ceska OC188, F17260 (UBC). USA, Washington. Klickitat County, Land Trust property, N45°44'20.65" W121°13'11.9", *Quercus garryana*, 20 Nov 2013, *leg*. Michael Beug 01MWB112013 (**holotype**, WTU), (**isotype**, K(M):200657). Klickitat County, Wahkiacus, N45°49'20.6" W121°05'38.5", *Quercus garryana* and *Pinus ponderosa*, 20 Nov 2013, *leg*. Michael Beug 05MWB112013 (WTU, K).

Notes: Based on the phylogenetic analysis *C. albosericeus* belongs to clade Decipientes (Fig. 106). The species in this clade are small and have chestnut brown to blackish brown pileus, white universal veil, and often some kind of smell in lamellae (cedar wood-like, spicy, or raphanoid). The stipe apex in almost all species sometimes has bluish tints. *Cortinarius albosericeus* is most similar to *C. ohlone* Bojantchev, but *C. ohlone* has cedar wood-like smell, nondextrinoid spores and occurs with coast live oak (*Quercus agrifolia*) and interior live oak (*Q. wislizenii*) in California.

Fig. 107 ***Cortinarius albosericeus*** (05MWB112013, reference specimen) **a** Basidiomata **b** Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 μm.

326. ***Cortinarius badioflavidus*** Ammirati, Beug, Niskanen, Liimat. & Bojantchev, ***sp. nov.***

Index Fungorum number: IF 551702, *Facesoffungi number*: FoF 02038, Fig. 108

Etymology: Name based on coloration of pileus and stipe.

Holotype: Joseph Ammirati JFA13668 (WTU)

Pileus 20–60 mm diam., rounded conic, convex to plano–convex, umbonate or broadly umbonate or uplifted, margin incurved to decurved then plane, non-striate to striate, expanded, finely pale yellowish to white silky, silky fibrillose or fibrillose scaly, more or less glabrescent, colour some shade of red brown (brown Russet, Xanthine Orange, Dresden Brown, Mars Brown, Prout's Brown, Cinnamon Brown, Vinaceous Cinnamon), faded more medium brown, edge pale (faded) in older pilei, disc paler brown at times, hygrophanous. *Lamellae* distinctly adnexed, subdistant to distant, sometimes intervenose, moderately broad, moderately thick then thicker in age, light medium brown, becoming rich brown (brownish Chamois, Cinnamon, Buckthorn Brown, Tawny Olive, Sudan Brown, Brussels Brown, Amber Brown, Argus Brown, Carob Brown), edges even to uneven in age, remaining pale for some time, then concolor. *Stipe* 43–88 mm long, apex 5.5–15 mm thick, equal or strongly tapered to base, tough, rigid, yellowish Cream Colour, Light Ochraceous Buff, Light Buff, Colonial Buff to Chamois, buff and yellow becoming mixed with brown, lower stipe developing watery red brown areas, often dull watery red brown to watery dull yellow brown., stipe surface longitudinally fibrillose, fibrils white to faintly yellowish or orange buff. *Universal veil* white, forming a ring and incomplete girdles or almost a sock-like sheath on the stipe. *Basal mycelium* white. *Context* rather thin in pileus, watery concolour with surface, above stipe apex yellowish white or sometimes pinkish cinnamon, in stipe central area stuffed whitish to yellowish white, cortex watery yellow brown to brown or dark brown or red brown (Sudan Brown, Brussels

Brown, Argus Brown, Antique Brown) in base the cortex somewhat darker brown. *Odour* sharply fragrant to that of green corn. *Taste* slightly unpleasant or astringent. *Macrochemical reaction (40 % KOH)*: pileus cuticle Xanthine Orange, context pale yellow orange, stipe apex Xanthine Orange, stipe base Seal Brown. *Exsiccatae*: pileus light brown to dark brown or somewhat blackish, lamellae rich medium brown, stipe pallid to brownish or somewhat yellowish, with some blackish area, context dull whitish to pallid or slightly brownish. *Basidia* 4-spored, 8.7–9.2 × 29–31 *µm*, clavate, hyaline or commonly rich orange brown to yellow brown. *Basidiospores* 8.1–10.5 × 5.8–6.5 *µm* (20 spores, holotype specimens), broadly ellipsoid to broadly amygdaloid, very coarsely verrucose, moderately to strongly dextrinoid. *Lamella trama hyphae* heavily pigmented, red brown, orange brown, yellow brown, strongly encrusted in KOH. *Pileipellis in KOH*: Surface hyphae ± cylindrical to broadly cylindrical, 6–11 *µm* wide, hyaline or yellowish; subtending layer of ± enlarged hyphae 7–24 *µm* wide, hyaline to yellowish brown; beneath a yellow brown to orange brown pigmented layer of cylindrical to enlarged hyphae, 6–25 *µm* wide adjacent to trama hyphae. *ITS sequence* distinct from the other known members of the section *Hinnulei*, and differs from them in the ITS region by more than 6 substitutions and indel positions.

Ecology and distribution: Collections have been made in mixed forests of *Quercus garryana*, *Q. douglasii*, *Pseudotsuga menziesii*, *Abies grandis*, and *Pinus ponderosa*, *Salix scouleriana* has also been present in some areas. Producing basidiomata in late autumn-winter and spring. Known from Western North America, from California to Washington.

Material examined: USA, California, Contra Costa County, Tilden Park, N37°54'14.5" W122°15'32.1", *Quercus agrifolia* and *Pseudotsuga menziesii*, 23 Nov 2009, *leg*. Dimitar Bojantchev DBB28196. Marin County, Marin Watershed, N37°56'44.1", W122°35'32.6", *Quercus agrifolia* and *Pseudotsuga menziesii*, 09 Jan 2009, *leg*. Dimitar Bojantchev DBB13504. Yuba County, Southern Sierra Research Station src94, *Quercus douglasii* woodland, 14 Feb 2001 *leg*. Matthew Smith (UCB), Washington, Klickitat County, 45°48’36.71“N, 121°30”55.72 “W, *Quercus garryana*, 19 Feb 2010, *leg*. Michael Beug 01MWB021910 (WTU, K). Beug Farm, near air field, *Quercus garryana*, *Pseudotsuga menziesii*, *Salix* sp., 20 Nov 2010, *leg*. Joseph Ammirati JFA13668 (**holotype**, WTU) (**isotype**, K(M): 200672), JFA13669. Beug Property, 45° 48.607 N, 121° 30.986 W, *Quercus garryana*, 3 April 2009 *leg*. Michael Beug 02MWB040309 (WTU, K). Oak grove (*Quercus garryana*, *Pseudotsuga menziesii* and *Abies grandis*) behind Beug house, 45° 48.606 N, 121° 30.973 W, 8 March 2009, *leg*. Michael Beug 01MWB030809 (WTU, K). Behind house, 194 Spring Creek, Husum, 24 March 2011, *Quercus garryana*, *leg*. Michael Beug 01MWB032411 (WTU, K). One thousand feet west of Beug property, 45°48.430 N, 121°31.135 W, *Quercus garryana*, 3 Dec 2008, *leg*. Michael Beug 03MWB120308 (WTU, K). Lindserth Old Road, 45° 48.419 N, 121°31.122 W, *Quercus garryana*, *Pseudotsuga menziesii* and *Abies grandis*, 9 Nov 2010, *leg*. Michael Beug 01MWB110910 (WTU, K). 45° 48.611 N, 121° 30.936W, *Quercus garryana*, *Pseudotsuga menziesii* and *Abies grandis*, 30 Apr 2009 *leg*. Michael Beug 02MWB043009 (WTU, K). SDS west of Beug Farm, N45°48’24”, W121°31’06”, *Quercus garryana*, *Pseudotsuga menziesii*, 19 Nov 2013, *leg*. Michael Beug 11MWB111913, (WTU, K).

Notes: *Cortinarius badioflavidus* looks like a typical member of section *Hinnulei* (Fig. 106). The overall coloration of the basidiocarp is red brown to brown, the stipe is equal or tapered, lamellae are distant and the smell of lamellae is green corn-like. The broadly ellipsoid to broadly amygdaloid spores differentiate it from *C. hinnuleus* collections which have subglobose to obovoid-subglobose spores. European *Cortinarius hinnuleoarmillatus* is otherwise very similar to *C. badioflavus*, but it has orange red universal veil.

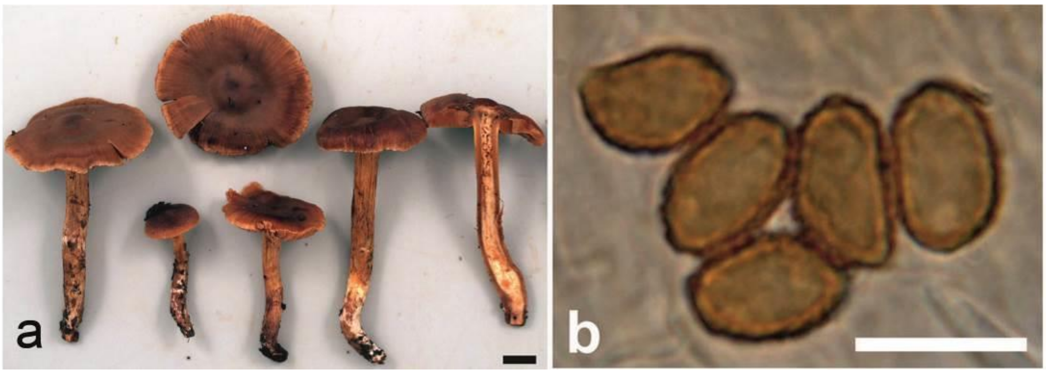


Fig. 108 ***Cortinarius badioflavidus*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photographs Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *μm*.

327. ***Cortinarius denigratus*** Ammirati, Beug, Niskanen, Liimat. & O. Ceska, ***sp. nov.***

Index Fungorum number: IF 551703, *Facesoffungi number*: FoF 02039, Fig. 109

Etymology: Name based on blackening of the basidiocarps on drying.

Holotype: Michael Beug 02MWB043014 (WTU)

Pileus 10–20 mm diam., papillate umbo, dry, Dresden Brown to Mars Yellow, edge blackens dried (in sun), minutely fibrillose, hygrophanous. *Lamellae* adnexed, ± distant, tan rusty. *Stipe* 30–40 mm long, 2–4 mm thick, ± equal, minutely fibrillose, buckthorn brown. *Universal veil* not recorded. *Basal mycelium* white. *Context* in stipe context ochraceous buff to yellowish tan. *Odour* indistinct. *Macrochemical reaction (40 % KOH)*: all parts instantly black. *Exsiccatae*: pileus brown to blackish, lamellae dark dull brown to blackish, stipe brown to blackish, some white mycelium at base, context brown. *Basidia* 4-spored, 9–10 × 27–37 *μm*, clavate, hyaline, light brown or dark brown in KOH. *Basidiospores* 9–11.2 × 4.8–6 *μm* (20 spores, holotype specimens), narrowly to broadly amygdaloid, distinct apiculus, moderately to very coarsely verrucose, apex ± extended and less ornamented, slightly to somewhat moderately dextrinoid. *Lamella trama hyphae* hyaline, light brown or very dark brown, walls yellow refractive, heavily brown encrusted and with brown interhyphal plaques in KOH. *Pileipellis in KOH*: Surface layer thin, somewhat compressed, hyphae ± cylindrical, 4–12 *μm* wide, hyaline or yellowish, some encrusted. Subtending layer of cylindrical to enlarged hyphae 7–25 *μm* wide, yellow brown to orange brown, walls yellow refractive, some heavily encrusted with brown pigment. Beneath a darker brown pigmented layer of encrusted hyphae with interhyphal brown plaques, cylindrical to enlarged, mostly 7–22 *µm* wide, that gradually grade into trama hyphae. *ITS sequence* distinct from other species of *Cortinarius* subgenus *Telamonia*.

Ecology and distribution: Found from forests of *Quercus garryana* and *Pinus ponderosa*, and *Pseudotsuga menziesii* and *Arbutus menziesii*. Producing basidiomata in spring in April. Known from British Columbia, Canada and Washington USA, Western North America.

Material examined: CANADA, British Columbia, Salt Spring Island, Mt. Tuam, 48.72° N 123.485° W, along the trail through mixed forest (*Pseudotsuga*, *Arbutus*), 19 April 2007, *leg*. Oluna Ceska OC155, F17227 (UBC). USA, Washington, Klickitat County, Beug Farm, N45°48'36.6" W121°30'59.04", *Quercus garryana* and *Pinus ponderosa*, 30 April 2014, *leg*. Michael Beug 02MWB043014 (**holotype**, WTU), (**isotype**, K(M): 200659).

Notes: *Cortinarius denigratus* is easily recognized since it produces fruitbodies in the spring when not that many other *Cortinarius* species are fruiting. Characteristic for the species are small, brown basidiomata, highly brown pigmented lamella trama hyphae, and amygdaloid, rather large spores with ± extended apex. *Cortinarius denigratus* is not very closely related to any of the known *Telamonia* species, but groups together with other small *Telamonias* in our phylogenetic analysis (Fig. 106).

Fig. 109 ***Cortinarius denigratus*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

328. ***Cortinarius duboisensis*** Ammirati, Beug, Niskanen & Liimat, ***sp. nov.***

Index Fungorum number: IF 551704, *Facesoffungi number*: FoF 02040, Fig. 110

Etymology: Named for DuBois Lake, the original name of Roland Lake in Washington, USA

Holotype: Joseph Ammirati JFA13311(WTU)

Pileus 50–135 mm diam., broadly obtuse-umbonate to plano-umbonate then ± plane to uplifted, margin decurved at first, mature becoming irregular and lacerated, easily broken, surface moist to dry, not striate, center often with whitish bloom, margin in places silky or with thin coating of whitish fibrils, colour variable, when moist watery dark brown to watery grey brown, faded areas ochraceous tawny, light brown, brownish buff or light buff, center sometimes very pale, margin frequently finely rivulose-variegated or streaked with brown colors, sometimes with darker areas or blotches, hygrophanous. *Lamellae* adnexed, close to subdistant, very broad, moderately thick to thick, somewhat easily broken, pale brown at first or in non-spore covered areas, rich deep brown when mature, edges irregular. *Stipe* 45–135 mm long, 10–32 mm thick above, base 23–35 mm thick, varies from narrow clavate to bulbous, upper surface shiny, sometimes twisted striate, whitish to pallid-white, with some thin darker watery buff brown streaks, without veil remains above. *Universal veil* white. *Basal mycelium* white and extends up onto base of the stipe. *Context* whitish to pallid or brownish white, darkening with age and with exposure, watery brown streaked in stipe, cortex rather tough, lower stipe flesh soon grayish then much darker brown, especially in stipe base. *Odour* strong fungoid to mildy woodsy. *Taste* mild, fungoid. *Macrochemical reaction (40 % KOH)*: on pileus surface raw umber, pileus context bronze, stipe apex, pinkish buff exterior, interior of stipe including stipe base, fuscous black. *Exsiccatae*: pileus grey brown to rather dark grey brown, lamellae dark brown, stipe whitish to pallid or greyish with a few blackish areas, context similar to stipe surface, basal mycelium white. *Basidia* 4-spored, 8.5–9 × 29–48 *µm*, clavate, hyaline or pale brownish in KOH. *Basidiospores* 8.9–10.2 × 5–6.2 *µm* (20 spores, holotype specimens), ellipsoid, broadly ellipsoid or somewhat amygdaloid, moderately verrucose, somewhat to strongly dextrinoid. *Lamella trama hyphae* smooth, not encrusted in KOH. *Pileipellis in KOH*: Surface hyphae ± cylindrical, 4–14 *µm* wide, hyaline or brownish, some encrusted. Subtending layer of cylindrical to enlarged hyphae 4–20 *µm* wide, hyaline, not encrusted. Beneath a brown pigmented layer of cylindrical to enlarged hyphae 8–22 *µm* wide, grading into trama hyphae. *ITS sequence* distinct from the other known members of the subgenus *Telamonia*, and differs from them in the ITS region by more than 15 substitutions and indel positions.

Ecology and distribution: Collections have been made under *Quercus garryana*, *Pinus ponderosa* or a mixture of *Quercus garryana*, *Pinus ponderosa* and *Abies grandis*. Producing basidiomata in late autumn. Known from Washington, Western North America.

Material examined: USA, Washington, Klickitat County, Roland Lake, 47.36N 122.73W, ecology, *Quercus garryana* and *Pinus ponderosa*, 28 Nov 2008, *leg*. Joseph F. Ammirati JFA13308 (WTU, K), JFA13311 (**holotype**, WTU), (**isotype**, K), JFA13312 (WTU). Klickitat County, Lower Staats Road, N45°50’38.5”, W121°24’ 44.1”, *Quercus garryana*, *Pinus ponderosa* and *Abies grandis*, 18 Nov 2013, *leg*. Michael Beug 01MWB111813 (WTU, K).

Notes: *Cortinarius duboisensis* is a rather large species with dark brown to watery grey brown pileus with a whitish bloom in the center and clavate to bulbous stipe. Typical are also exsiccatae with grey brown to rather dark grey brown pileus and whitish to greyish stipe. *Cortinarius duboisensis* is related to *C. crassisporus* Kytöv., Niskanen & Liimat. which also has basidiomata with bulbous stipe and brown pileus (Fig. 106). *Cortinarius crassisporus*, however, has larger spores (10.7–13.6 x 7.5–9.1 *µm*) and occurs in hemiboreal–boreal and mountain coniferous forests on calcareous soil. The species are morphologically most reminiscent to those of section *Bovini*, but do not seem to belong to that section based on our phylogenetic analysis.

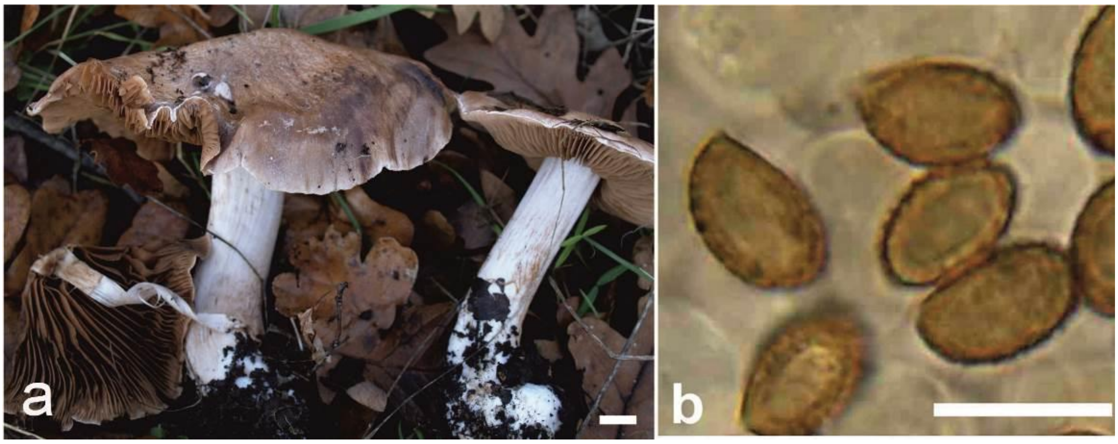


Fig. 110 ***Cortinarius duboisensis*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photographs Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

329. *Cortinarius fragrantissimus* Ammirati, Beug, Liimat., Niskanen & O. Ceska, ***sp. nov.***

Index Fungorum number: IF 551705, *Facesoffungi number*: FoF 02041, Fig. 111

Etymology: Name based on fragrant Odour.

Holotype: Michael Beug 10MWB111913 (WTU)

Pileus 15–30 mm, rounded-umbonate to obtuse umbonate to plano-umbonate, umbo ± acute, surface silky, dry, fuscous to pale ochraceous salmon, hygrophanous. *Lamellae* adnexed, subdistant, dark vinaceous purple when young, buffy brown when mature. *Stipe* 55–70 mm long, 3–5 mm thick above, ±equal, dry, pale pinkish buff, hollow. *Universal veil* white. *Basal mycelium* white. *Odour* slightly fragrant sweet. *Taste* mild. *Macrochemical reaction (40 % KOH)*: pileus cuticle raw umber, stipe apex bronze, base fuscous black. *Exsiccatae*: pileus pallid to brown, greyish brown and some blackish areas, lamellae brown, stipe pale shiny at apex, below pallid to light brownish or blackish with whitish areas from universal veil, basal mycelium white. *Basidia* 4-spored, 8.7–9.2 × 29–31 *µm*, clavate, hyaline or commonly brown in KOH. *Basidiospores* (7.4) 7.8–9 (9.3) × 4.8–6 *µm* (20 spores, holotype specimens), ellipsoid to broadly ellipsoid, coarsely verrucose, apiculus ±curved, slightly to somewhat dextrinoid. *Lamella trama hyphae* hyaline or more commonly brown pigmented, commonly brown encrusted, many brown plaques in KOH. *Pileipellis in KOH*: Surface hyphae ± cylindrical, 4–11 *µm* wide, hyaline, walls refractive. Subtending distinct layer of ± enlarged hyphae 7–26 *µm* wide, hyaline to yellowish brown, walls refractive. Beneath a brown to yellow brown pigmented layer of cylindrical to enlarged hyphae, 7.5–22 *µm* wide, encrusted and with pigment plaques, grading into trama hyphae. *ITS sequence* distinct from the other known members of the section *Paleacei*, and differs from them in the ITS region by more than 8 substitutions and indel positions.

Ecology and distribution: Collections have been made from mixed forests of *Quercus garryana* and *Abies grandis*, and *Pseudotsuga menziesii* and *Arbutus* *menziesii*. Producing basidiomata in late autumn. Known from British Columbia, Canada and Washington USA, Western North America.

Material examined: CANADA, British Columbia, Cobble Hill, off Thain Rd., 48.686° N, 123.6° W, mixed forest (*Pseudotsuga menziesii*, *Arbutus menziesii*), 25 Nov 2000, *leg*. Oluna Ceska OC66, F17138 (UBC). Skulow Lake, forest soil from the long-term soil productivity (LTSP) site, Aug 2007, environmental sample. USA, Washington. Klickitat County, SDS west of Beug Farm, N45°48'24", W121°31'06.5", *Quercus garryana* and *Pseudotsuga menziesii*, 19 Nov 2013, leg. Michael Beug 10MWB111913 (**holotype**, WTU), (**isotype**, K(M): 200664).

Notes: *Cortinarius fragrantissimus* belongs to section *Paleacei* (Fig. 106). Typical for the species of the section is the fragrant smell in lamellae, often reminiscent of that of *Pelargonium*, as well as small basidiomata and white universal veil. Several species also have purplish tints in lamellae and/or stipe apex. *Cortinarius fragrantissimus* can be separated from the other species of the section by the combination of smooth cap with more or less acute umbo and ellipsoid 8–9 ×5–6 *µm*, coarsely verrucose spores.

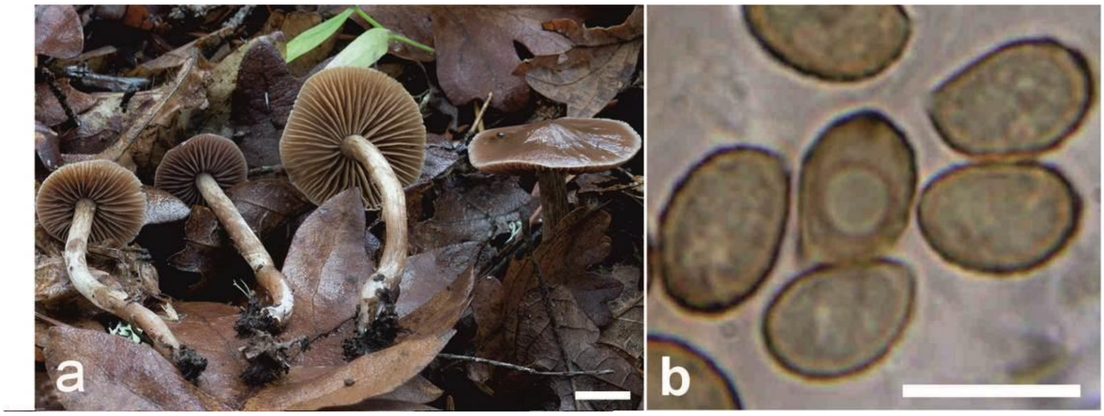


Fig. 111 ***Cortinarius fragrantissimus*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

330. ***Cortinarius roseobasilis*** Ammirati, Beug, Niskanen & Liimat., ***sp. nov***.

Index Fungorum number: IF 1551706, *Facesoffungi number*: FoF 02042, Fig. 112

Etymology: Name based on reddish stipe base.

Holotype: Michael Beug 20MWB111813 (WTU)

Pileus 42–75 mm diam., obtuse-umbonate to plano-umbonate then uplifted-irregular umbonate, margin decurved to straight, becoming lacerate-split in age, non–striate or only short striate at edge in a few places, very little veil materials on edge, silky dry, colour Blackish Brown (1) to Dusky Brown or Dresden Brown streaked with light ochraceous buff where faded, edge grayish to greyish brown, hygrophanous. *Lamellae* adnexed with a decurrent line, distant, thick, becoming irregular, deep brown with Vinaceous Drab mixed in, becoming Dresden Brown. *Stipe* up to 80 mm (often 70–80 mm) long, above up to 8 (or sometimes to 20) mm thick, equal above, strongly tapered to base, with some dull whitish fibrillose areas, otherwise buffy brown to lighter brown then watery brown to watery vinaceous brown. *Universal veil* white, sparse. *Basal mycelium* white. *Context* of pileus thin, watery and concolor, faded whitish, in stipe drab with pale drab gray streaks, hollow. *Odour* not distinctive. *Taste* mild or not distinctive. *Macrochemical reaction (40 % KOH)*: pileus cuticle fuscous, pileus context buffy brown, stalk apex pale ochraceous salmon, stipe base fuscous black. *Exsiccatae*: pileus dark brown to blackish, lamellae brown to dark brown, stipe pallid, brownish or blackish, lower stipe whitish in one, context pallid to darkened in lower stipe. *Basidia* 4-spored, 6.5–8 × 28–31 *µm*, clavate, hyaline or slightly brownish. *Basidiospores* 6.7–8.9 × 4.5–4.8 (5.5) *µm* (20 spores, holotype specimens), ellipsoid, broadly ellipsoid, rarely subglobose, slightly curved apiculus, coarsely verrucose, moderately to very strongly dextrinoid. *Lamella trama hyphae* hyaline to yellowish brown or brownish, somewhat encrusted in KOH. *Pileipellis in KOH*: Surface layer thin, hyphae cylindrical, 5.2–9 *µm* wide, hyaline or yellowish, some slightly encrusted. Subtending layer of ± enlarged hyphae 8.9–26 *µm* wide, hyaline, walls refractive, somewhat yellowish beneath a light yellow brown to light brown pigmented layer of cylindrical to enlarged hyphae, 4.5–25 *µm* wide adjacent to trama hyphae. *ITS sequence* distinct from the other known members of the /Castanei, and differs from them in the ITS region by more than 7 substitutions and indel positions.

Ecology and distribution: Gregarious under *Quercus garryana* or in mixed forests of *Q. garryana*, *Crataegus*, and *Populus tremuloides*. Producing basidiomata in late autumn. Known from Washington USA, Western North America.

Material examined: USA, Washington. Klickitat County, Balch Farm, 45°42.896N, 121°18.939W, *Quercus garryana* with *Populus* and *Crataegus*, 20 Nov 2010, *leg*. Joseph F. Ammirati JFA13666 (WTU, K). Klickitat County Lower Staats Road, N45°50’39”W121°24’50”, *Quercus garryana*, 18 Nov 2013, *leg*. Michael Beug 20MWB111813 (**holotype**, WTU), (**isotype**, K).

Notes: In our phylogenetic analysis *C. roseobasilis* is placed in *Castanei* although the group is not well-supported (Fig. 106). However, the species in the group are morphologically similar. They have dark brown to blackish brown pileus; reddening, but first white, universal veil and/or stipe base; and indistinctive smell in lamellae. *Cortinarius rosebasilis* is most reminiscent of European *C. erubescens* M.M. Moser, but the spores of *C. erubescens* are narrowly ellipsoid and almost smooth.

Fig. 112 ***Cortinarius roseobasilis*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

331. ***Cortinarius vinaceobrunneus*** Ammirati, Beug, Liimat., Niskanen & O. Ceska, ***sp. nov.***

Index Fungorum number: IF 551707, *Facesoffungi number*: FoF 02043, Fig. 113

Etymology: Named for the colour of the pileus and stipe.

Holotype: Joseph Ammirati JFA13301 (WTU)

Pileus 47–60 mm diam., obtusely rounded to obtuse-uplifted, with slight umbo at times, margin incurved to straight but often folded and irregular, opaque, edge whitish fibrillose from veil, colour evenly deep vinaceous brown with a pale sheen from thin layer of silky fibrils, hygrophanous. *Lamellae* deeply adnexed, intervenose, close to subdistant, thick, deep rich brown with paler brown edges, light medium brown viewed from edges, edges uneven. *Stipe* 82–100 mm long, apex 10–14 mm thick, tapered below, deeply inserted in soil, shiny, silky streaky, dull watery light vinaceous brown ground color. *Universal veil* white, sparse, forming a few surface fibrils on stipe, no zones. *Basal mycelium* white, sparse. *Context* watery brown in cortex (rather thick and tough), interior of stipe pale brownish white, dark watery brown in pileus cuticle, flesh thin, brownish white above stipe apex. *Odour* pleasant, like parsley. *Taste* mild. *Macrochemical reaction (40 % KOH)*: not recorded. *Exsiccatae*: pileus blackish with slight purplish cast, lamellae rich brown or a few blackish, stipe blackish or with some pallid greyish or brownish areas, context is a light bright cinnamon brown. *Basidia* 4-spored, 8.1–8.5× 28–35 *µm*, clavate, hyaline to light brown in KOH. *Basidiospores* 8.1–9.6 × 4.8–5.9 *µm* (20 spores, holotype specimens), ellipsoid to broadly ellipsoid or somewhat amygdaloid, distinct, ± curved apiculus, moderately to coarsely verrucose, slightly to moderately (a few darker) dextrinoid. *Lamella trama hyphae* hyaline to brown, walls yellow refractive, some encrusted (not heavily so) in KOH. *Pileipellis in KOH*: Surface layer of ± cylindrical hyphae, 3–11 *µm* wide, hyaline or yellowish, wall refractive, some encrusted; subtending layer of ± cylindrical to enlarged hyphae 7–26 *µm* wide, colourless to yellowish or slightly brownish, walls yellow refractive, some encrusted. Beneath a somewhat darker brown layer of cylindrical to enlarged hyphae, mostly 8–22 *µm* wide, hyaline or with brown pigments, grading into trama hyphae; hyaline to dark brown lactiferous hyphae scattered throughout trama. *ITS sequence* distinct from other species of *Cortinarius* subgenus *Telamonia* and deviating from them by more than 15 substitutions and indel positions in the ITS region.

Ecology and distribution: With *Quercus garryana*. Producing basidiomata in late autumn. Known from British Columbia, Canada and Washington USA, Western North America.

Material examined: CANADA, British Columbia, Elkington property Reserve, Duncan, 48.805° N, 123.622° W, *Quercus garryana* stand, 25 Nov 2001, *leg*. Oluna Ceska OC78, F17150 (UBC). USA, Washington, Klickitat County, Balch Farm, 45°42.896N,121°18.939W, *Quercus garryana*, 2 Nov 2008, *leg*. Joseph Ammirati JFA13301 (**holotype**, WTU), (**isotype**, K(M): 200667).

Notes: *Cortinarius vinaceobrunneus* is a small to medium-sized species of subgenus *Telamonia*. From many other similar looking species it can be distinguished by the combination of vinaceous brown pileus, silky white rooting stipe almost without veil remnants, and the parsley-like smell in lamellae. The exact phylogenetic position of the species is not known, but in our analysis it is grouped in the same large clade with section *Hinnulei* and many small *Telamonias* (Fig. 106).

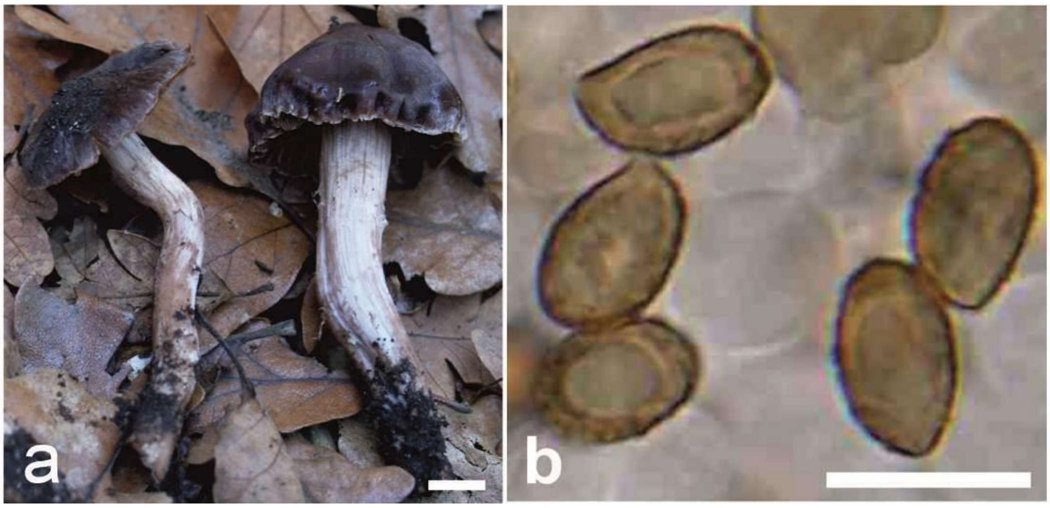


Fig. 113 ***Cortinarius vinaceobrunneus*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photographs Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

332. *Cortinarius vinaceogrisescens* Ammirati, Beug, Liimat. & Niskanen, ***sp. nov.***

Index Fungorum number: IF 551708, *Facesoffungi number*: FoF 02044, Fig. 114

Etymology: Name based on coloration of the stipe.

Holotype: Michael Beug 03MWB111913 (WTU)

Pileus 30–65 mm diam., convex, at times subumbonate, becoming uplifted silky, red brown to Light Pinkish Cinnamon, hygrophanous. *Lamellae* adnexed, subdistant, reddish brown to dark brown (Natal Brown) when mature. *Stipe* 60–100 mm long, 5–10 mm thick, equal, dry, at first white, later pale greyish vinaceous brown (Tilleul Buff) at apex, lower down grey vinaceous brown (Wood Brown). *Universal veil* white. *Basal mycelium* white. *Odour* very slightly fragrant, pleasant. *Taste* mild. *Macrochemical reaction (40 % KOH)*: pileus cuticle and stipe base Chaetura Black, context and stipe apex Chamois. *Exsiccatae*: pileus light brown to brown with blackish areas, lamellae brown, stipe brownish to blackish with whitish veil covering above base, basal mycelium white, context pallid to brownish. *Basidia* 4-spored, 8.5–9 × 35–42 *µm*, clavate, hyaline or brownish. *Basidiospores* 8.5–10 × 5.4–6.4 *µm* (20 spores, holotype specimens), broadly ellipsoid, moderately to coarsely verrucose, somewhat to moderately dextrinoid. *Lamella trama hyphae* hyaline to brown, some encrusted. *Pileipellis in KOH*: surface hyphae cylindrical, 5–9.5 *µm* wide, hyaline or yellowish to brownish, some encrusted; subtending layer of cylindrical to enlarged hyphae 5–18 *µm* wide, hyaline, walls refractive, interhyphal and encrusted pigment common, grading into trama hyphae. ITS sequence distinct from other species of *Cortinarius* subgenus *Telamonia*. With an isolated position and deviating from the other members of the subgenus in the ITS region by more than 20 substitutions and indel positions.

Ecology and distribution: Collections have been made in mixed forests of *Quercus garryana* and *Pseudotsuga menziesii*. Producing basidiomata in late autumn. Known from Washington and Oregon, Western North America. The Oregon record is based on a sequence (GenBank no. JQ393038) from a mycorrhizal root tip of *Arbutus menziesii* (*Ericaceae*). It differs by some bases from the type material but the differences might be artificial.

Material examined: USA, Washington, Klickitat County, Beug Farm, N 45 48.624, W 121 30.969, mixed forest of *Quercus garryana* and *Pseudotsuga menziesii*, 20 Nov 2010, *leg*. Joseph F. Ammirati JFA13674 (WTU, K). Klickitat County, SDS west of Beug Farm, N45°48’24”, W121°31’06”, mixed forest of *Quercus garryana* and *Pseudotsuga menziesii*, 19 Nov 2013, *leg*. Michael Beug 03MWB111913 (**holotype**, WTU), (**isotype**, K(M): 200668).

Notes: *Cortinarius vinaceogriseus* can be recognized by a combination of brown pileus, first white, later vinaceous brown stipe, rather large, broadly ellipsoid spores and rather dark exsiccatae. It is not very closely related to any previously known species/sections of *Telamonia* (Fig. 106).

Fig. 114 ***Cortinarius vinaceogrisescens*** (**holotype**) a Basidiomata and b Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

333. ***Cortinarius wahkiacus*** Ammirati, Beug, Liimat. & Niskanen, ***sp. nov.***

Index Fungorum number: IF 551709, *Facesoffungi number*: FoF 02045, Fig. 114

Etymology: Named for Wahkiacus Washington, USA

Holotype: Michael Beug 09MWB111813 (WTU).

Pileus 45–60 mm diam., convex to ± plane, silky dry, streaked with yellow brown (Raw Umber) and cinnamon buff or umber brown on light vinaceous cinnamon. *Lamellae* adnexed, distant to subdistant, cinnamon or light brown to yellowish brown (Buckthorn Brown) when mature. *Stipe* 70–80 mm long, 8–12 mm thick above, ± equal down to an ± enlarged base inserted in soil, surface dry, honey yellow to cinnamon buff or light vinaceous cinnamon. *Universal veil* white, sheathing lower stipe, forming inferior ring. *Basal mycelium* white, with white rhizomorphs. *Taste* mild. *Odour* slightly musty to fishy. *Macrochemical reaction (40 % KOH)*: on pileus surface fuscous to olivaceous black, stipe apex olive to fuscous, interior citrine drab to olive, stipe base fuscous black to dark olive, rhizomorphs white. *Exsiccatae*: Pileus dark brown to dark reddish brown, one with large, central white veil patch. Lamellae dark brown. Stipe surface light brown to pale in some places above but often blackish. Basal mycelium, sheathing veil above base and rhizomorphs white. Context pale to brownish discolored blackish. *Basidia* 4-spored, 8–10 × 31–38 *µm*, clavate, hyaline or brownish in KOH. *Basidiospores* 10–11.6 × 5.4–6.6 *µm* (20 spores, holotype specimens), amygdaloid to ± ellipsoid, moderately to coarsely verrucose, apiculus somewhat curved, somewhat to strongly dextrinoid. *Lamella trama hyphae* smooth, not encrusted in KOH. *Pileipellis in KOH*: Surface hyphae cylindrical to broadly cylindrical, 8–10 *µm* wide, hyaline or brownish, some encrusted. Subtending layer, hyphae 8–21 *µm* wide, hyaline, walls refractive, some encrusted, gradually grading into trama hyphae. *ITS sequence* distinct from the other known members of the section *Bovini*, and differs from them in the ITS region by more than 20 substitutions and indel positions.

Ecology and distribution: Found from forests of *Quercus garryana* or *Q. garryana* and *Pinus ponderosa*. Producing basidiomata in late autumn. Known from Washington, Western North America.

Material examined: USA, Washington, Klickitat County, Lower Staats Road, N 45°50’36.4”, W121°24’ 33.7”, under *Quercus garryana*, 18 Nov 2013, *leg*. Michael Beug 09MWB111813 (**holotype**, WTU), (**isotype**, K(M): 200670). Klickitat County, Wahkiacus, under *Quercus garryana and Pinus ponderosa*, N 45°49’20.6”, W121°05’ 38.9”, 20 Nov 2013, *leg*. Michael Beug 03MWB112013 (WTU, K).

Notes: *Cortinarius wahkiacus* is a medium-sized, brown species with a white, sheath-like universal veil covering the lower part of the stipe, and with rather large, amygdaloid, moderately to coarsely verrucose, dextrinoid spores. It belongs to section *Bovini* (Fig. 106) and as other members of the group has exsiccatae with dark brown to blackish brown pileus. *Cortinarius eldoradoensis* Bojantchev is another species of section *Bovini* encountered in Western North America, but it fruits in the spring and has somewhat shorter spores, 8.5–10.5 × 5–6 *µm*.

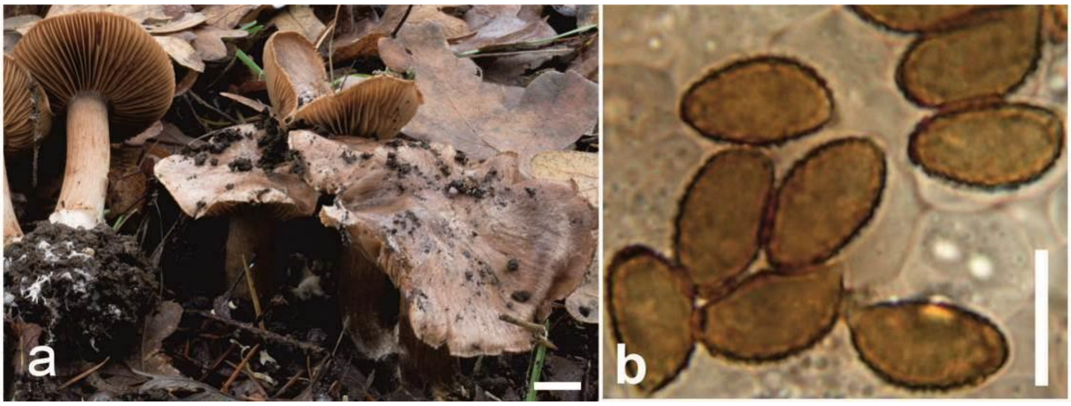


Fig. 115 ***Cortinarius wahkiacus*** (**holotype**) **a** Basidiomata **b** Basidiospores. Photograph a Michael Beug, b Joseph Ammirati. Scale bars: a = 10 mm, b = 10 *µm*.

Tricholomataceae R. Heim ex Pouzar

The family *Tricholomataceae*, as traditionally circumscribed (Singer 1986), includes 98 genera with a pale spore print (white, cream, light pink, pale violet, light green, or pale greyish), lamellae variously attached to the stipe (rarely free, adnate, sinuate, or decurrent); hymenophoral trama regular to subregular, irregular, interwoven, bilateral; spores amyloid or inamyloid; clamp-connections present or absent; mainly saprotrophic or symbiotic. The family was demonstrated to be polyphyletic in several molecular analyses (Hofstetter et al. 2002; Moncalvo et al. 2000, 2002; Matheny et al. 2006; Garnica et al. 2007). Some taxa previously included in *Tricholomataceae* have been placed in other families such as *Lyophyllaceae* Jülich (Hofstetter et al. 2002), "*Marasmiaceae*" (Wilson and Desjardin 2005), *Mycenaceae* Overeem (Moncalvo et al. 2002), *Omphalotaceae* Bresinsky (Moncalvo et al. 2002), "*Physalacriaceae*" (Binder et al. 2006), and *Hygrophoraceae* Lotsy (Lodge et al. 2014).

Based on a multi-gene analysis, Sánchez-García et al. (2014) recognized a *Tricholomataceae sensu stricto* which encompasses only seven genera, *Albomagister* Sánchez-García, Birkebak & Matheny, *Corneriella* Sánchez-García, *Dennisiomyces* Singer, *Leucopaxillus* Boursier, *Porpoloma* Singers.str., *Pseudotricholoma* (Singer) Sánchez-García & Matheny, *Tricholoma* (Fr.) Staude. Vizzini et al. (2016) added to the family the genus *Pseudoporpoloma* Vizzini & Consiglio.

***Pseudoclitocybe-Musumecia* clade**

Binder et al. (2010) and Vizzini et al. (2011) showed a well-supported phylogenetic relationship between *Infundibulicybe* Harmaja and *Pseudoclitocybe* (Singer) Singer at the base of the Tricholomatoid clade. Vizzini et al. (2011) and Sánchez-García et al. (2014) found also a significant relationship between *Musumecia*, *Pseudoclitocybe*, and the genus *Pogonoloma* (Singer) Sánchez-García (= *Porpoloma* subgen. *Pogonoloma* Singer), while *Aspropaxillus* Kühner & Maire and *Notholepista* Vizzini & Contu were found also to represent basal lineages to the Tricholomatoid group. This clade is characterized by the absence or scarce number of cystidia and clamp connections in most species, as well as the cutis-like pileipellis, elongated basidia and acyanophilous spores. The phylogenetic tree for *Pseudoclitocybe-Musumecia* clade is presented in Figs 116 and 117.

Musumecia Vizzini & Contu

The genus *Musumecia* is a small genus in the so called Tricholomatoid clade (Matheny et al. 2006, Sánchez-García et al. 2014). Its name was originally proposed by Vizzini et al. (2011) to honor the Swiss mycologist Enzo Musumeci, who was the first to collect this genus from Alsace (France). Molecular data revealed that this genus is closely related to *Pseudoclitocybe*. The genus *Musumecia* was established to encompass clitocyboid fungi phylogenetically close to *Pseudoclitocybe* with a hygrophoroid habit (non-depressed convex pileus and distant thick lamellae), a cutis-like pileipellis, regular hymenophoral trama, elongated basidia, smooth acyanophilous and inamyloid spores, absence of hymenial cystidia and clamp-connections (Vizzini et al. 2011). The type species, *M*. *bettlachensis* Vizzini & Contu (Vizzini et al. 2011), is whitish and grows caespitose in *Abies alba*, *Fraxinus* sp., and *Fagus* sp. forests, while the only other known taxon, *M*. *vermicularis* Musumeci (Musumeci 2014), has a zonate brownish dark pileus, is gregarious but not caespitose, grows under *Carpinus betulus*, and produces rhizomorphs. Although the genus *Musumecia* was originally described with inamyloid spores (Vizzini et al. 2011), the spores of *M*. *bettlachensis* (holotypus TO HG2284) examined under a standardized procedure by some of the authors turned out to be weakly amyloid in grey colour. Moreover, the spores of *M*. *sardoa* are clearly amyloid. Thus, the amyloidity feature should not be used to qualitatively discriminate spores of *Musumecia* and *Pseudoclitocybe*, and so, the generic diagnosis has to be amended accordingly.

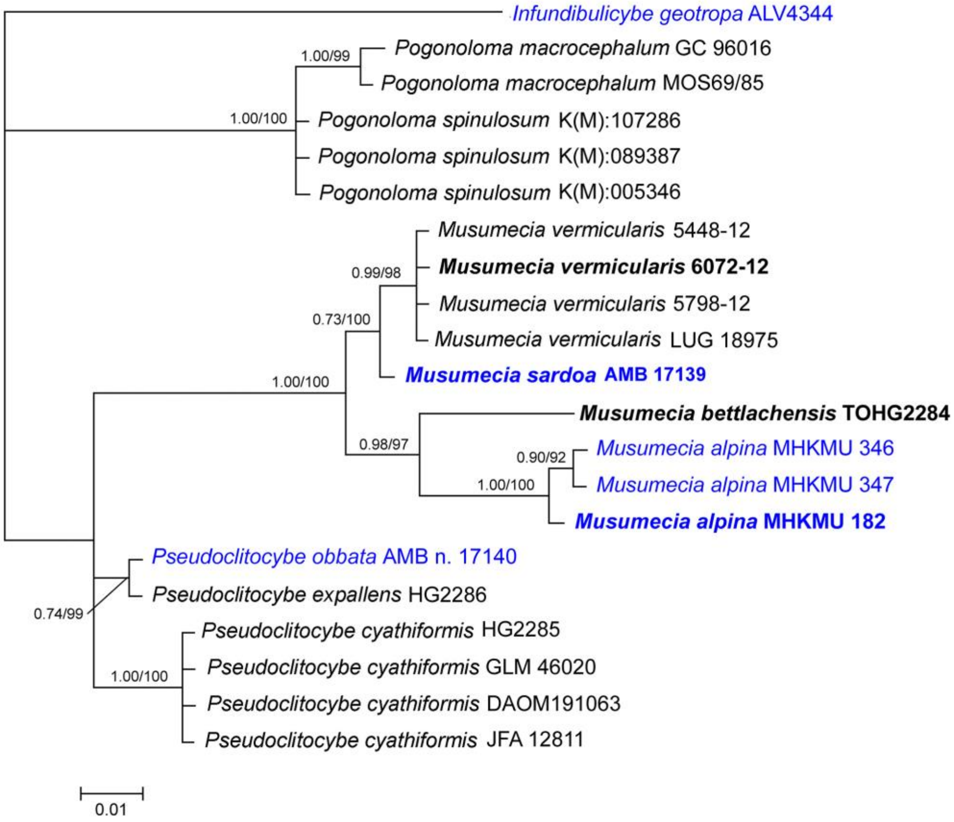


Fig. 116 Phylogenetic relationships of *Musumecia* based on LSU sequences. Bayesian posterior probabilities (PP ≥ 0.90) and RAxML bootstrap values (BP ≥ 70%) are shown above or below the branches. New taxa are in blue ex-type specimens in bold.

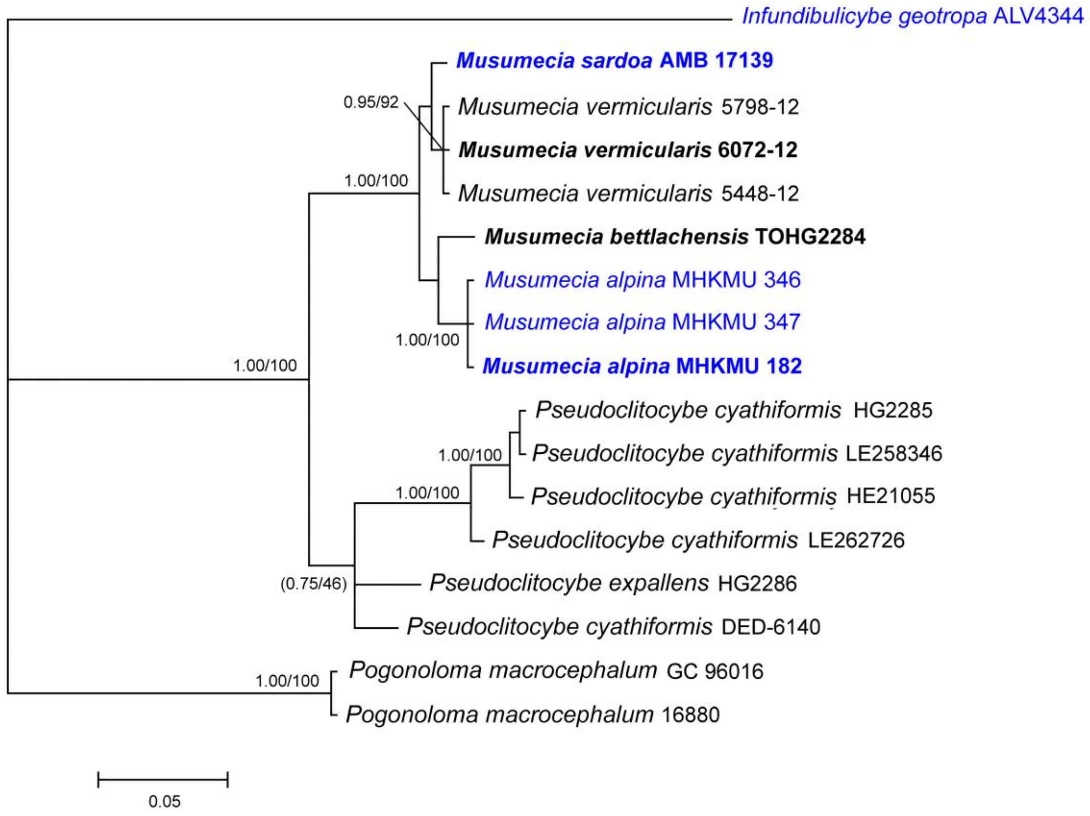


Fig. 117 Phylogenetic relationships of *Musumecia* based on ITS sequences data. Bayesian posterior probabilities (PP ≥ 0.90) and RAxML bootstrap values (BP ≥ 70%) are shown above or below the branches. New taxa are in blue and ex-type specimens in bold.

Key to the known species of *Musumecia*

1. Pileus ivory-white to cream-white………………………………*M. bettlachensis*
1. Pileus dark coloured…………………………………………………………2
2. Spores minutely ornamented, presence of hymenial cystidia and clamp-connections abundant in all tissues………………………………………………*M. alpina*
2. Spores smooth, absence of hymenial cystidia and clamp-connections rare and scattered……………………………………………………………………..3
3. With abundant white rhizomorphs at the stipe base; pileipellis with cystidioid terminal elements………………………………………………*M. vermicularis*
3. Without rhizomorphs; pileipellis without cystidioid elements …………*M. sardoa*

334. ***Musumecia alpina*** L.P. Tang, J. Zhao & S.D. Yang, ***sp. nov.***

MycoBank number: *MB* 812873, *Facesoffungi number*: FoF 02046, Figs 118–120

Etymology: Derived from latin alpinus, relative to the Alps, in reference to their preference for mountain habitats.

Holotype: MHKMU 182

Colour codes follow Kornerup and Wanscher (1981).

Habit mycenoid. *Pileus* 3–4 cm in diam., applante or slightly depressed around umbo, dark grey (1E1-2, 4E1) to grey-black (4E2, 7E2, 8E2) over centre, paler towards the margin, greyish-black (1D3, 2D1–2) to greyish-white (2C2, 3C2), with a vague to evident, greyish to pale grey zone at margin; surface covered with dense tomentum or pubescence; margin slightly inflexed or involute, greyish-white (2B1, 3B1–2, 4B1); pileus context colour not changing when injured. *Lamellae* 0.4–0.6 cm in width, adnate, crowded to subdistant, sinuous, grey (3C1–2) to greyish white (1B1), interspersed with lamellulae. *Stipe* 5–7.5 × 0.5–0.6 cm, single, central attached to subcentral, subcylindrical to cylindrical, slightly narrowing upwards, greyish (3B1) to white (3A1); surface slightly smooth; base slightly enlarged, with whitish (2A1, 3A1) to white (1A1) mycelium or rhizomorphs; solid to loose when young, then fistulose; stipe context fibrous, consistent when handled, greyish-white (2B13, B1–2) to cream-white or white (3A1, 2A1). Smell and taste faint, not distinct. *Spores* [80/4/3] (6.5–) 7.5–9 (–10) × (3.5–) 4–5 (–5.5) *µm*, Q= (1.35–) 1.58–2.16 (–2.49), Qm= 1.89 ± 0.22, ellipsoid to oval, with a small apiculus, inamyloid, thin-walled, hyaline, colourless in KOH, densely covered with irregular rugulose ornaments (ornaments not clearly in KOH, but clearly observed in Cotton Blue and under SEM). *Basidia* 35–38 × 4–5 *µm*, clavate, hyaline, colourless in KOH, thin-walled, 2–4 spored, predominantly 2-spored, sterigmata 6–8 *µm* in length. *Cheilocystidia* and *pleurocystidia* clustered or scattered, quite similar in shape and size, 24–30 × 3–5 *µm*, clavate, thin-walled, hyaline, clamped. *Hymenophoral trama* composed of subparallel filamentous hyphae, 3–7 *µm* wide, thin-walled, hyaline, colourless in KOH. *Pileipellis* made up of subparallel filamentous hyphae, 6–8 *µm* wide, thin-walled, hyaline, clamped. *Stipitipellis* composed of subparallel filamentous hyphae, 5–7 *µm* in diametre, slightly thick-walled (up to 1 *µm*), hyaline. *Clamp-connections* abundant in every part of basidioma.

Habitat and known distribution: Alpine mountain in southwestern China.

Material examined: CHINA, Yunnan Province, Eryuan County, Ma'an mountain, N 26°15′21.74", E100°06′04.02", alt. 3500m asl, in broad leaved forest with *Ericaceae* (*Rhododendron anthosphaerum, R. fictolacteum,* and *R. irrotatum* subsp. *irrotatum*) and *Fagaceae* (*Quercus monimotricha*), 22 August 2014, L.P. Tang 1778 (MHKMU 182, **holotype**). Yunnan Province, Eryuan County, Ma'an mountain, N 26°15′21.74", E 100°06′04.02", alt. 3560m, in broad leaved forest with *Ericaceae* (*Rhododendron anthosphaerum, R. fictolacteum,* and *R. irrotatum* subsp. *irrotatum*) and *Fagaceae* (*Quercus monimotricha*), 22 August 2014, S.D. Yang 89 (MHKMU 346). Ibid. S.D. Yang 90 (MHKMU 347).

Notes: see under *M. sardoa*.

Fig. 118 ***Musumecia alpina*** **a, b** Basidiomes from L.P. Tang 1778 **(holotype)** **a** Mature basidiomes with a tomentose-fibrillose to pubscent pileus **b** Clustered basidiomes with base enlarged stipe and white rhizomorphs at the base of stipes **c, d** Basidiomes from S.D. Yang 90 (MHKMU 347) **c** Single basidiome **d** Basidiomes with grey-whitish, curving lamellae and hollow stipe. Scale bars = 1 cm.

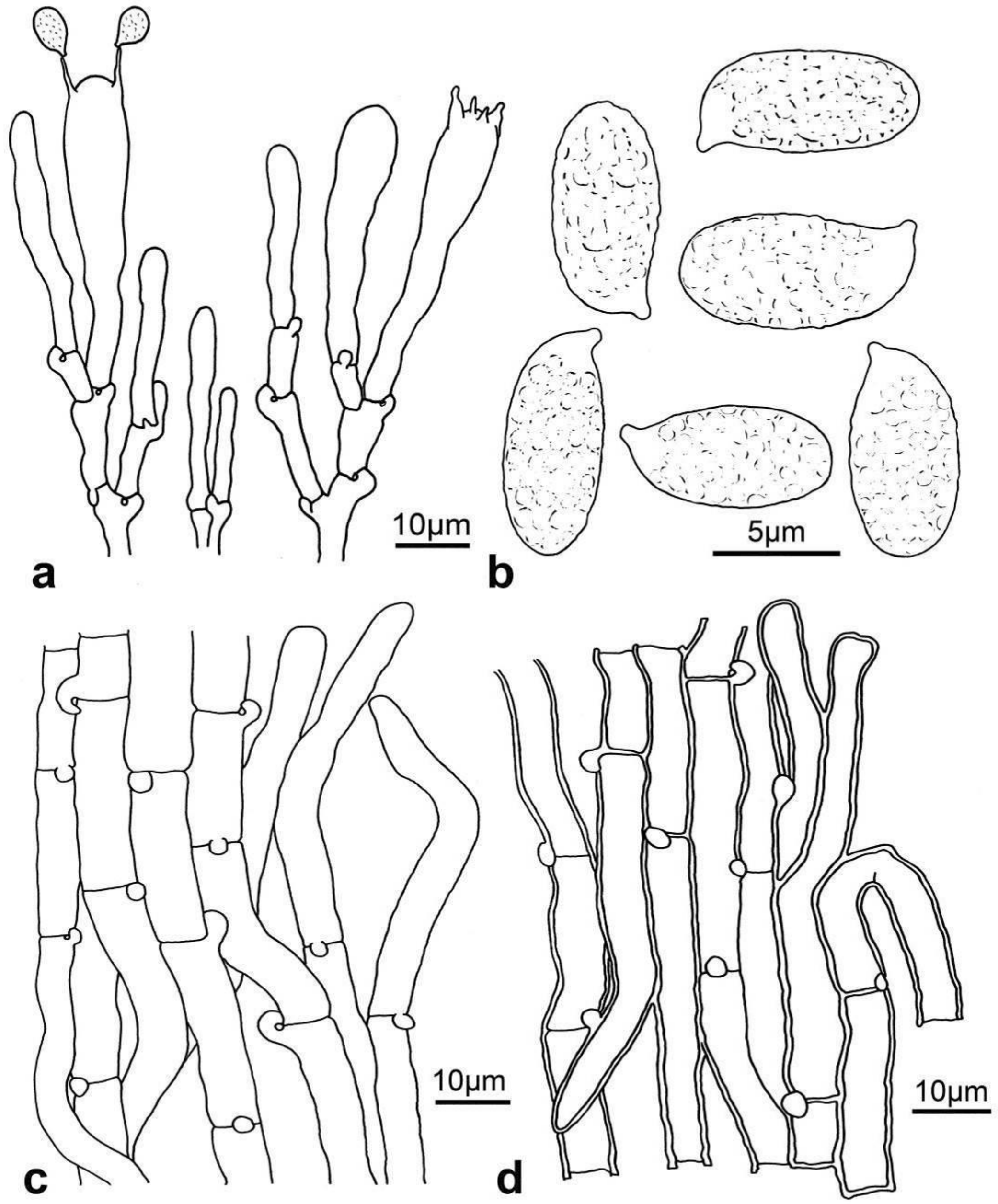


Fig. 119 ***Musumecia alpina*** (**holotype**) **a** Basidia, cheilocystidia, and pleurocystidia **b** Spores **c** Pileipellis **d** Stipitipellis.

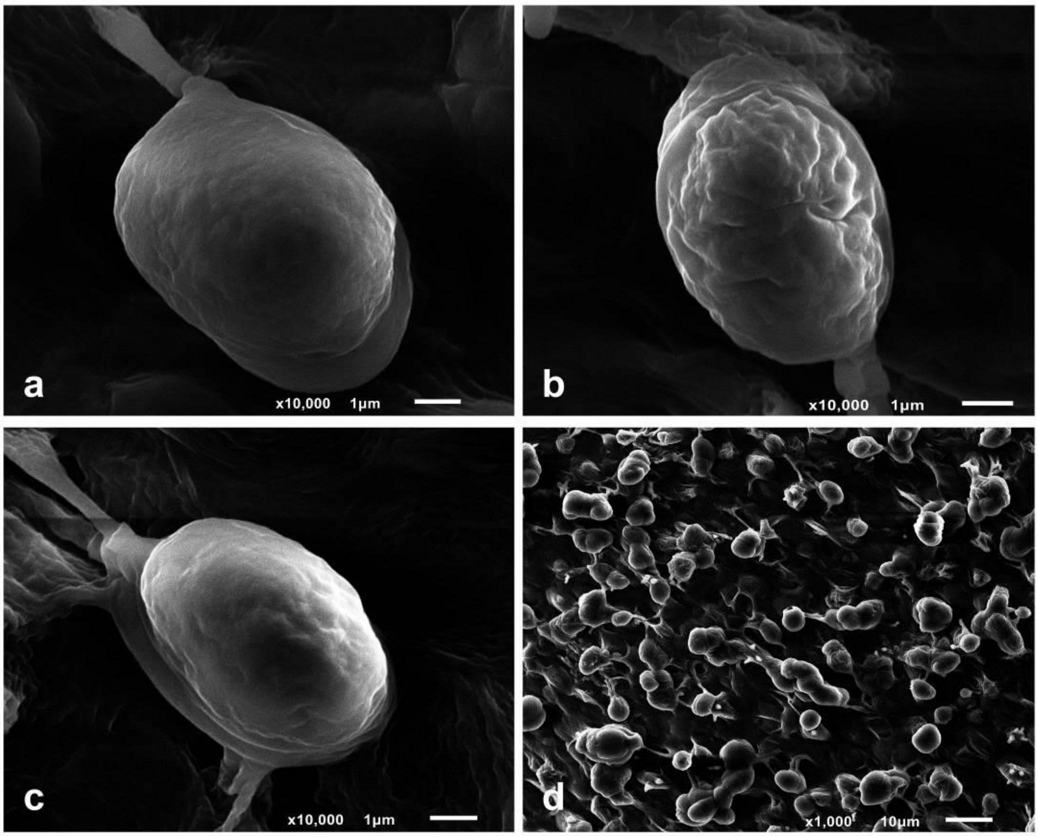


Fig. 120 Spores under SEM of ***Musumecia alpina*** (**holotype** MHKMU 182) **a–d** Basidiospores under SEM.

335. ***Musumecia sardoa*** G. Consiglio, A. Vizzini & L. Setti, ***sp. nov.***

MycoBank number: MB 812779, *Facesoffungi number*: FoF 02047, Fig. 121

Etymology: Derived from latin *sardous*, relative to the Sardinia, the region where it was first found.

Holotype: AMB n. 17139

Colour codes follow Kornerup and Wanscher (1981).

Habit mycenoid. *Pileus* 2–4 cm in diam., funnel shaped or infundibuliform, dark reddish brown (9E3, 10E3); surface pubescent; margin strongly involute; colour not changing when injured. *Lamellae* interspersed with lamellulae, decurrent, about 0.4–0.6 cm in width, rather broad, rather crowded, whitish cream. *Stipe* 3–5 × 0.8–1.5 cm, single, centrally attached to subcentral, subcylindrical to obclavate, slightly widening upwards, whitish cream to slightly brownish (5A2, 5C6); surface smooth; solid when young, becoming hollow or fistulose when mature; flesh fibrous, whitish cream (3A1, 2A1) or slightly brownish (5B3, 6B3). Odour faintly herbaceous. *Spores* [60/1/1] (5.8–) 5.9–8.5 (–9.5) × (3.5–) 3.8–4.2 (–4.9) *µm*, *Q*= (1.43–) 1.53–2.00 (–2.17), Q_{m}= 1.76 ± 0.18, long ellipsoid to cylindrical, sometimes dacryoid, with an apiculus up to 1 *µm*, thin-walled, hyaline; containing small refractive droplets greenish in 5% ammonia, cyanophilous in Cotton Blue; smooth; amyloid, in Melzer's reagent the spore contour stains blackish blue, including the apiculus which stains more intensely. The basidiospores show a tendency to form tetrads. *Basidia* 25–32 ×

6–8 μm, subcylindrical to subclavate, hyaline, containing small droplets greenish in 5% ammonia, thin-walled, 4-spored, sterigmata up to 5 μm long; basidioles more or less cylindrical, rare septa with clamps at the base of basidia and basidioles. *Hymenial cystidia* absent. *Hymenophoral trama* subregular to irregular, composed by cylindrical hyphae, 3.5–10 μm wide, hyaline, septate, sometimes the septa slightly contracted, some hyphae with plates of encrusting parietal pigment. *Subhymenium* composed by short elements, 3–6 μm wide. *Pileipellis* made up of a thin layer of periclinal cylindrical hyphae, 4–10 μm wide, slightly entangled, with rare septa, with an evenly grey cytoplasmic content and covered with plates of ochraceous parietal encrusting pigment. Scattered superficial hyphae forming small erect tufts and small more or less hemisphaerical warts. *Stipitipellis* composed by cylindrical, more or less parallel, septate hyphae with a pale ochraceous citoplasmatic pigment and small plates, 4.5–10 μm wide, of parietal encrusting pigment. At the stipe apex short tufts of hyaline smooth septate hyphae, with a rounded and reclined apex. Thromboplerous hyphae present in pileipellis and stipitipellis, 3–7 μm wide, with an evenly greenish yellow content. *Context* dextrinoid (more or less deep orange). *Clamp-connections* rare and scattered, present in subpellis and in pileitrama.

Habitat and known distribution: Only known from Sardinia (Italy).

Material examined: ITALY, Sardinia, Desulo (NU), in a *Pinus halepensis* forest, 2 November 2004, leg. *G. Consiglio, F. Franceschetti, A. Garbellotto & C. Orlandini* (Holotype Herbarium AMB n. 17139, **holotype**).

Notes: Species in the genus *Musumecia* are characterized by their clitocyboid basidiomata, stipe more or less enlarged at the base, and more or less amyloid basidiospores. However, *M. alpina* has a dark grey, zonate, and fibrous-tomentose or pubescent pileus with the disc subumbonate in age, slightly larger basidiospores with granular decorations on the surface, often 2-spored basidia, and this species has cheilocystidia, pleurocystidia, and abundant clamps. Three European species have slightly larger basidiomata, shallowly depressed or infundibuliform or pileus in age, commonly 4-spored, smooth basidiospores without any decorations on the surface, absence of cheilocystidia and pleurocystidia. Additionally, there are no or rare clamp-connections in their basidiome. *Musumecia bettlachensis* has an ivory-white or cream-white glabrous pileus sometimes with a small umbo when young, somewhat smaller basidiospores (5.5–8.5 × 3.5–5 μm), and lacks rhizomorphs (Vizzini et al. 2011). *Musumecia sardoa* has an infundibuliform, dark reddish brown, pubescent pileus, and amyloid spores. *Musumecia vermicularis* has an infundibuliform minutely tomentose pileus lacking umbo, and smaller basidiospores (6.5–7.5 × 3.5–5 μm) (Musumeci 2014). The discovery of *M. alpina* in southwestern China suggests that *Musumecia* has a much wider geographical distribution ranging from East Asia to Europe. *Musumecia alpina* is here reported from an alpine region of southwestern China, growing in very different climate conditions.

Musumecia alpina and *M. sardoa* introduce some aberrant features for the genus: the first displays minutely ornamented spores, abundant clamp-connections, and hymenial cystidia; the second is characterized by its amyloid spores. As a matter of fact, the genus *Musumecia* shows a marked macro- and micromorphological heterogeneity while evident shared morphological features are currently unknown. In contrast, its molecular homogeneity is very high and all *Musumecia* species so far known appear as a well supported monophyletic clade. Future work will be necessary to assess the presence of yet undescribed unifying morphological and/or physiological characters. To date, four taxa were reported in this genus. A key to the known species in *Musumecia* is provided above.

Yunnan region is one of the major biodiversity hotspots in the world. Over 4000 species of fungi from different groups have been identified in this area during the last decades (Zhang et al. 2005; Li et al. 2009, 2011b, 2014; Yang et al. 2012, 2013, 2015; Zeng et al. 2013, 2014; Hao et al. 2014; Song et al. 2014; Tang et al. 2014; Zhao et al. 2014). Research is needed to confirm if this is a truly disjoint distribution or else there exist specimens of *M. alpina* or other related taxa in the intermediate regions of Central Asia.

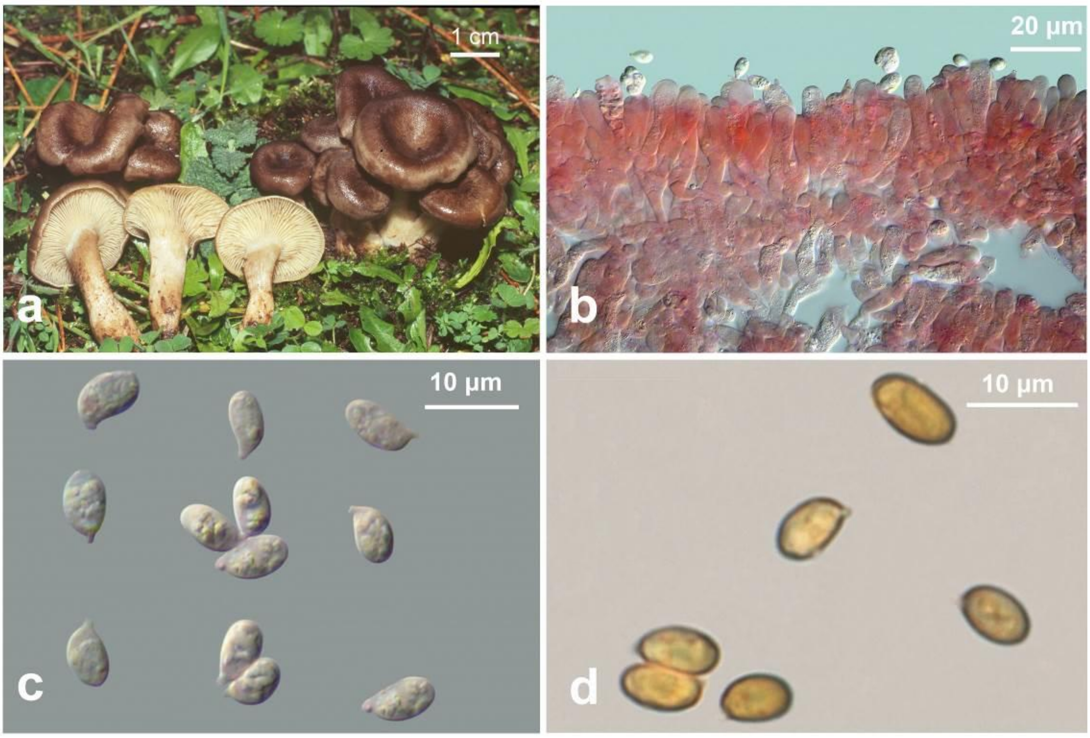


Fig. 121 ***Musumecia sardoa*** (**holotype**) **a** Basidiomes **b** Lamella edge (interferential contrast) **c** Basidiospores (interferential contrast) **d** Basidiospores in Melzer's (light fase).

Boletales

Boletaceae

The mushroom family *Boletaceae* is composed of >1000 species in ~70 genera. They are distributed worldwide primarily as obligate ectomycorrhizal mutualists with vascular plants. Species in this family are characterised by producing soft, fleshy stipitate-pileate basidiomata with a tubulose or sometimes lamellate to loculate fertile layer (hymenophore), gasteroid basidiomata (truffles), and few secotioid basidiomata.

Cyanoboletus Gelardi, Vizzini & Simonini

The genus *Cyanoboletus* was erected in 2014 to accommodate three existing species that were phylogenetically shown as a clade distinct from *Boletus* (Wu et al. 2014, Vizzini 2014). It is typified by the European *Cyanoboletus pulverulentus* (Opat.) Gelardi, Vizzini & Simonini. All three species exhibit an intense bluing colour reaction in the flesh when exposed to air, which, although not unique to the group, is a distinctive field character uniting them. They associate with both coniferous and broadleaf trees worldwide. According to Species Fungorum (www. speciesfungorum. org) and this report, five species are currently accepted for the genus. The phylogenetic tree for *Cyanoboletu* is presented in Fig. 122.

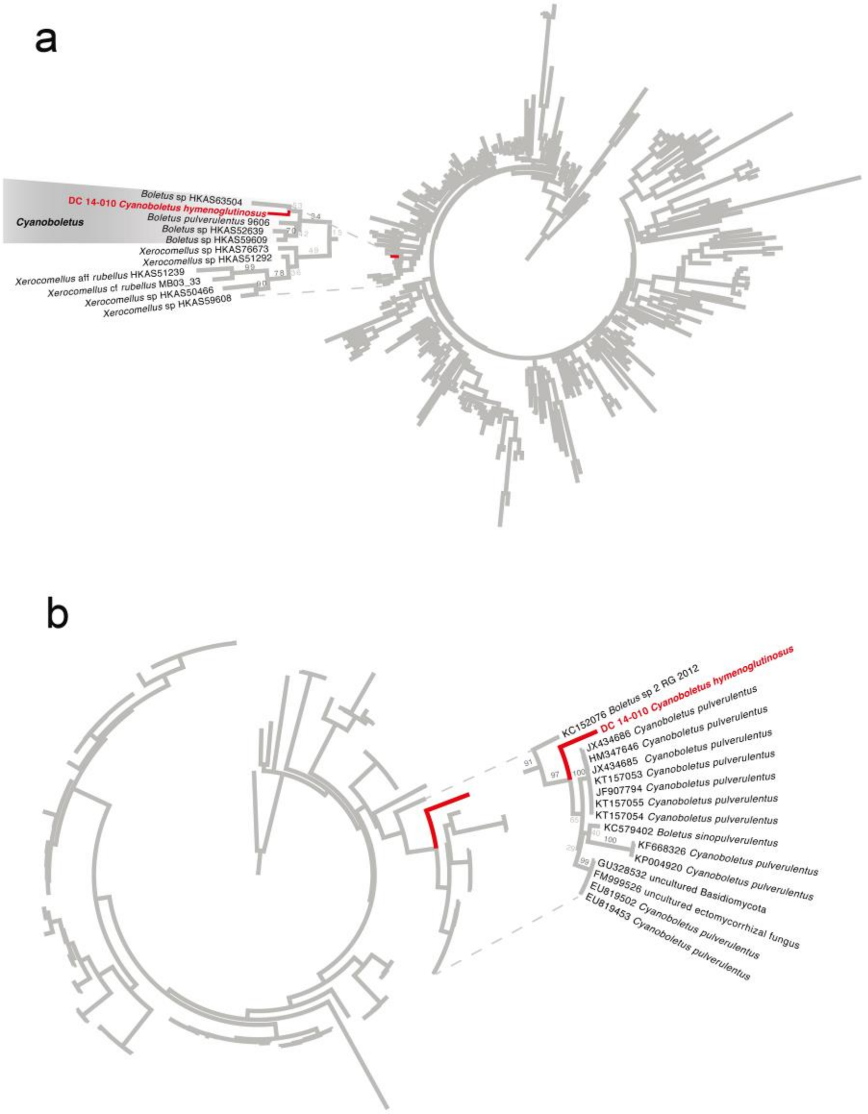


Fig. 122 Phylogenetic placement of the new species *Cyanoboletus hymenoglutinosus*. a Best maximum likelihood circle phylogram recovered using RAxML of an LSU dataset including the new species *Cyanoboletus hymenoglutinosys* (DC14-010) and the alignment of Wu et al. (2014). Tree is rooted with *Suillus* spp. (HKAS57622 and HKAS57748), following the topology of Wu et al. (2014). The clade containing *C. hymenoglutinosus* is magnified to the left. Numbers on branches are percent nonparametric bootstraps. b Best maximum likelihood circle phylogram recovered using RAxML of an ITS dataset including the new species *Cyanoboletus hymenoglutinosys* (DC14-010) and the 100 best hits on GenBank identified

using blastn. Tree is arbitrarily rooted using *Xerocomus badius*. The *Cyanoboletus* clade containing *C. hymenoglutinosus* is magnified at right. Numbers on branches are percent nonparametric bootstraps.

336. *Cyanoboletus hymenoglutinosus* D. Chakr., K. Das, A. Baghela, S.K. Singh & Dentinger, ***sp. nov.***

Index Fungorum number: IF 551541, *Facesoffungi number*: FoF 02048, Figs 123, 124

Etymology: Named after characteristic highly glutinous hymenium layer

Holotypus: D. Chakraborty & K. Das DC 15-010 (H).

Diagnosis: Distinguished from American species: *Cyanoboletus pulverulentus* by its highly glutinous hymenium layer, pileipellis and differently coloured (yellowish orange to brownish orange) pore surface.

Pileus 16–25 mm. diam.; hemisphaerical when young, becoming convex with maturity; surface rough, highly glutinous, brown (6E5–6) or brownish orange (6C6–7), mostly darker after maturity; margin entire with narrow sterile flap of tissue. *Pore surface* narrowly depressed near stipe, yellowish orange, orange to greyish orange or brownish orange (5B5–6, 6C5) instantly becoming bluish black (20F4–5) on bruising; pore 2–3/mm, simple, rounded, mostly stuffed. *Tube* 3–5 mm long, narrowly adnate-sinuate, pale yellow to pastel yellow (1A3–4), becoming bluish black (20F4–5) after bruising. *Stipe* 50–65 ×5–8 mm, central, cylindrical, with slightly bulbous base, yellow at apex (near pileus juncture), greyish red (7–8B5) or darker up to black on bruising, surface scaly-pruinose with longitudinal striations on the upper half, highly glutinous. *Context* solid (in pileus and stipe); context in pileus pale yellow to pastel yellow (1A3–4), immediately becoming blue on exposure, reddish yellow to melon yellow (4A7–5A6) with $FeSO_4$, but, unchanging colour change with guiacol and KOH. *Spore print* not found.

Basidiospores 11.6–**12.8**–14.8 × 4.8–**5.2**–5.8 *µm* (n = 20, Q = 2.31–2.71–2.79), inequilateral, smooth under light microscope and SEM. *Basidia* 34–49 × 6–8 *µm*, 2–4 spored, clavate to subclavate, covered by very thick gluten. *Hymenial cystidia* 34–50 × 5–8 *µm,* emergent 15–20 *µm,* cylindrical to subfusiform or fusiform, content mostly hyaline, some brown pigmented, mostly associated or partly to completely submerged in gluten. *Hymenophoral* trama divergent. *Pileipellis* 65– 100 *µm* thick, ixotrichoderm, composed of erect elements, terminal cell 17–36 × 6–7 *µm*, mostly with oval to subfusoid apices, brown pigmented, heavily encrusted, wall up to 0.7 *µm*. *Stipitipellis* 320–340 *µm,* somewhat ixocutis, composed of subrepent to loosely interwoven hyphae submerged under moderately thick gluten, fertile, with caulobasidia and caulocystidia in groups. *Caulocystidia* 19–48 × 8–10 *µm*, encrusted, gelatinous.

Habitat and distribution: Under *Castanopsis* sp. in upper Phadamchen area, humid temperate mixed (broadleaf and coniferous) forests dominated by species of *Cryptomeria*, *Pinus*, *Castanopsis* and bamboos. Producing basidiomata in the rainy season. Uncommon, found in East district of Sikkim (India).

Material examined: INDIA, Sikkim, East district, Upper Phadamchen, 29 July 2014, D. Chakraborty & K. Das, DC 14-010 (**holotype**, CAL; isotype, AMH).

Notes: LSU sequence data from the holotype (DC 14-010) was added to a dataset consisting of all LSU used in Wu et al. (2014). Multiple sequence alignment was achieved using the Practical Alignment using Sate and TrAnsitivity (PASTA) algorithm (Mirarab et al. 2014). The resulting alignment was used for maximum likelihood analysis implemented in RAxML v8.1.17 (Stamatakis 2006, 2014; Ott et al. 2007) using a GTRGAMMA model and branch support assessed using rapid bootstrapping set to terminate automatically based on the MRE criterion. The LSU sequence of DC 14-010 was strongly supported (94% bootstrap) in a clade with *Cyanoboletus pulverulentus* and three unidentified taxa (Fig. 122a). The ITS sequence of DC 14-010 was queried against GenBank (Benson et al. 2013) using blastn (Altschul et al. 1990). The top 100 best hits in GenBank were downloaded and combined with the newly generated sequence. Multiple sequence alignment and phylogenetic analysis were carried out as above. Similar to the LSU dataset, DC 14-010 was strongly supported (97% bootstrap) in a clade composed of multiple sequences from *Cyanoboletus pulverulentus*, *C. sinopulverulentus*, and two environmental sequences (Fig. 122b). Taken together, independent phylogenetic analyses of LSU and ITS sequences unequivocally place DC 14-010 with close affinity to *Cyanoboletus* spp.

Cyanoboletus hymenoglutinosus is characterized by highly glutinous basidiomata (always associated with mud particles on gluten), yellow- to brown-orange pore surface with stuffed pores, instantaneously changing (to blue-black) pore surface and context, typically highly glutinous hymenial layer, basidia distinctly covered by thick gluten and the apparent association with *Castanopsis*. Morphologically, *Cyanoboletus pulverulentus* (Opat.) Gelardi, Vizzini & Simonini (Europe, North America), *C. sinopulverulentus* (Gelardi & Vizzini) Gelardi, Vizzini & Simonini (similar distribution: China, adjacent to Sikkim, India) and *C. rainisii* (Bessette & O.K. Mill.) Gelardi, Vizzini & Simonini (North America) look very similar to the present species. But, both *C. pulverulentus* and *C. rainisii* lack the typical glutinous pileipellis (cutis in *C. pulverulentus* and trichoderm in *C. rainisii*). All three earlier species never shows entirely glutinous hymenial layer and gluten-covered basidia, which is the striking feature of the present species i.e. *C. hymenoglutinosus* (Smith and Thiers 1971, Bessette et al. 2010, Gelardi et al. 2013, Vizzini 2014). Moreover, *C. pulverlentus* is separated by differently coloured pore surface (“yellow when young, darkening to golden yellow to brownish yellow when mature” as in Bessette et al. 2010). Similarly, *C. sinopulverulentus* has deep yellow pore surface (never with orange pore surface like *C. hymenoglutinosus*) and unstuffed pores (Gelardi et al. 2013) whereas, in *C. rainisii* the pore surface becomes dark green (not blue-blak) when bruised and the spores are much larger (10–17 × 4.2–7 *µm* as mentioned in Bessette et al. 2010).

Fig. 123 ***Cyanoboletus hymenoglutinosus*** (**holotype**) **a**, **c** Fresh basidiomata **b** Pore surface before and after bruising **d** Longitudinal section through plugged tubes **e** Hymenial layer submerged in gluten **f**, **g** Basidia covered by thick gluten **h** Tube edge **i** Transverse section through pileipellis **j** Transverse section through stipitipellis **k** Caulocystidia **l**, **m** Basidiospores. Scale bars: a, b = 1cm, d = 100 μm, e–m = 10 μm.

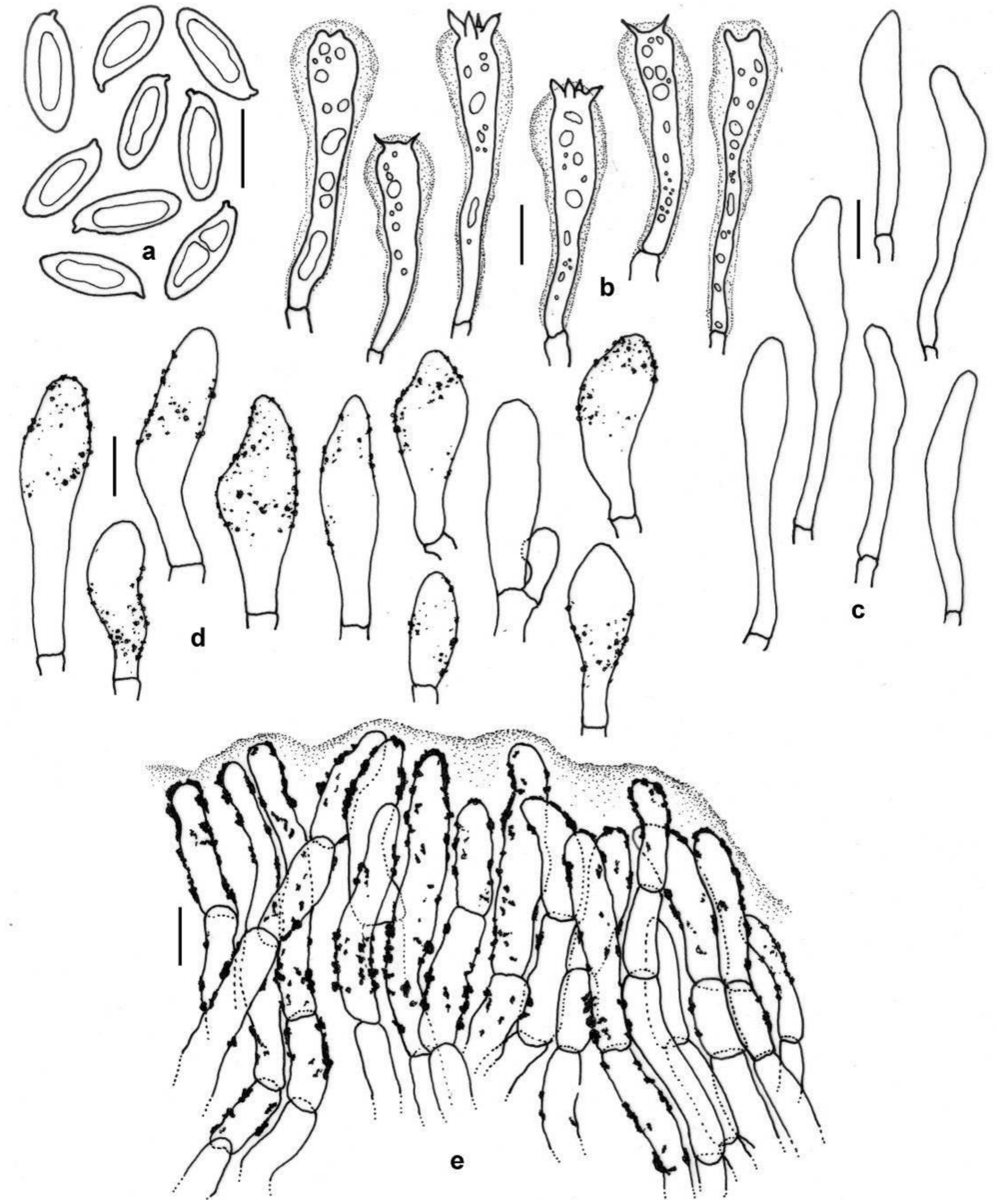


Fig. 124 ***Cyanoboletus hymenoglutinosus*** (**holotype**) **a** Basidiospores **b** Basidia **c** Hymenial cystidia **d** Caulocystidia **e** Transverse section through pileipellis. Scale bars: a–e = 10 *µm*.

Leccinellum Bresinsky & Manfr. Binder

In the family *Boletaceae* (Basidiomycota, *Agaricomycetes*, *Boletales*), leccinoid members (boletes with scabrous stipe surfaces) are some of the dominant ectomycorrhizal fungi that associate with coniferous and broadleaf trees in the Himalayas. *Leccinellum* was segregated from *Leccinum* to accommodate taxa with a pileipellis composed of a palisade of swollen hyphal tips and a yellow hymenophore, but not including three taxa with similar features, now belonging to *Hemileccinum* Šutara (Šutara 2008), based on phylogenetic evidence (Bresinsky and Besl 2003). Together, these two new genera represent *Leccinum* sect. *Luteoscabra* Singer, who separated these boletes with scabrous stipe surfaces but yellow hymenophores from the remainder of *Leccinum* (Singer 1947). According to Species Fungorum (www.speciesfungorum.org) and this report, 9 species are currently accepted for the genus. The phylogenetic tree for *Leccinellum* is presented in Fig. 125.

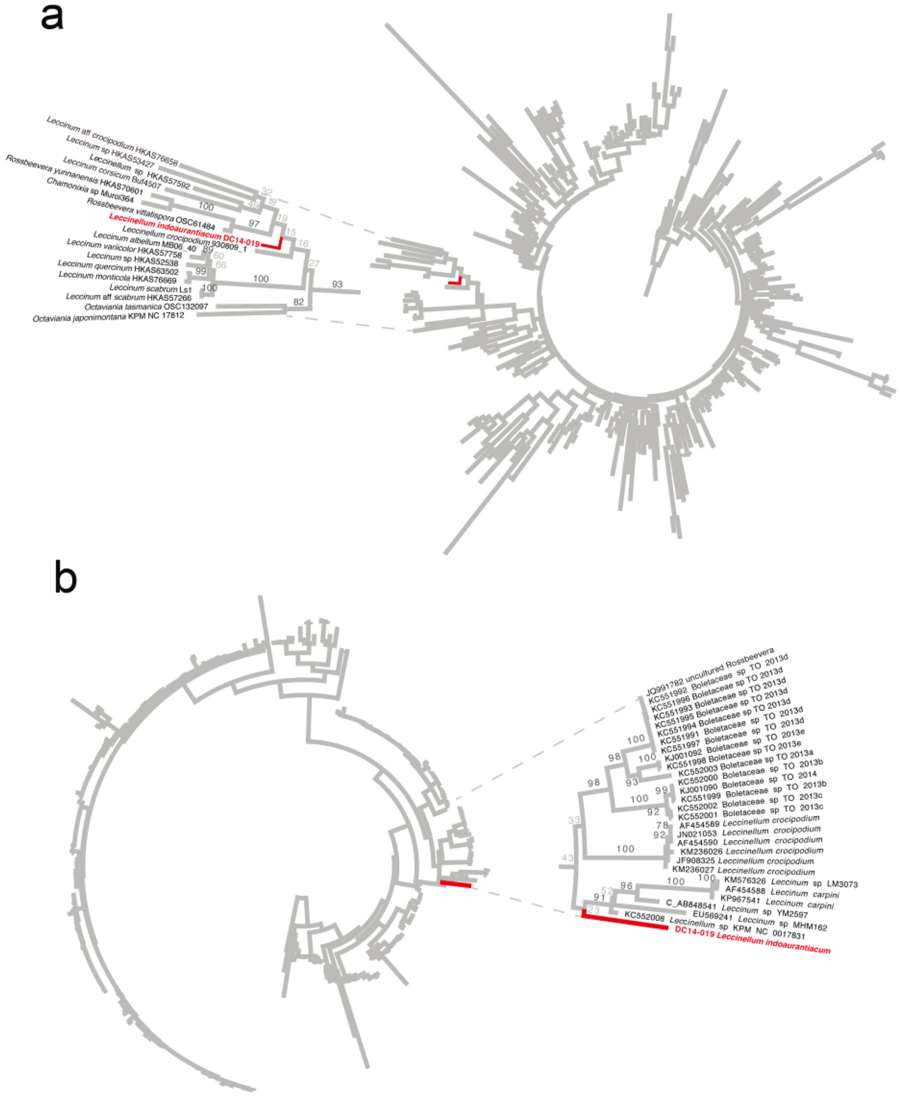


Fig. 125 Phylogenetic placement of the new species *Leccinellum indoaurantiacum* a Best maximum likelihood circle phylogram recovered using RAxML of an LSU dataset including the new species *Leccinellum indoaurantiacum* (DC 14-019) and the alignment of Wu et al. (2014). Tree is rooted with *Suillus* spp. (HKAS57622 and HKAS57748) following the topology of Wu et al. (2014). The clade containing *L. indoaurantiacum* is magnified to the left. Numbers on branches are percent nonparametric bootstraps b Best maximum likelihood circle phylogram recovered using RAxML of an ITS dataset including the new species *Leccinellum indoaurantiacum* (DC14-019) and related leccinoid taxa. Tree is rooted with *Harrya chromapes* following the topology of Wu et al. (2014). The clade containing *L. indoaurantiacum* is magnified to the right. Numbers on branches are percent nonparametric bootstraps.

337. *Leccinellum indoaurantiacum* D. Chakr., K. Das, A. Baghela, S.K. Singh & Dentinger, ***sp. nov.***

Index Fungorum number: IF 551569, *Facesoffungi number*: FoF 02049, Figs 126, 127

Etymology: Named after leccinoid specimens (collected from India) with an orange pileus like in *Leccinum aurantiacum* (Bull.) Gray.

Holotypus: D. Chakraborty & K. Das DC 14-019 (H).

Diagnosis: Distinguished from the Chinese species *Boletus sinoaurantiacus* M. Zang & R.H. Petersen by its context (pileus and stipe) that quickly becomes pinkish white to light pink on exposure and presence of encrusted hymenial cystidia.

Pileus 22–45 mm. diam.; hemisphaerical to convex; surface irregularly ridged and wavy, slightly glutinous in young fruitbodies, reddish orange (7B8) gradually paler (4A8) towards margin, orange to deep orange or light yellow to yellowish orange (5A7–8/ 4A5–6), turning deep orange to reddish orange (5–7A8) with KOH; margin entire with narrow sterile flap of tissue. *Pore surface* slightly depressed near stipe, pastel yellow (2A4) to lemon yellow, unchanging when bruised; pore 2–3/mm, rounded, compound. Tube 11 mm long, adnate-sinuate, light yellow (1A4), unchanging when bruised. *Stipe* 80–105 ×10–13 mm, central, often curved, with white basal mycelia, surface longitudinally striate-lacerate to squamulose or scabrate, with brownish yellow (5–6C8) squamules on yellowish background (2–3A4–5). *Context* solid in pileus and stipe; context (pileus and stipe) pale yellow (1A3), soon becoming distinctly pinkish white to light pink when exposed. Pileus context turning deep yellow (4A8) with KOH, reddish grey (12D2) with $FeSO_4$ but, unchanging with guiacol. Stipe context turning reddish grey (12D2) with $FeSO_4$, unchanging with KOH and guiacol. *Odour* and *taste* indistinct.

Basidiospores 13.6–**16.2**–19 × 5.8–**6.4**–7 *µm* (n = 20, Q = 2.19–**2.52**–2.92), oblong to subfusoid, inequilateral, smooth under light microscope, olive brown. *Basidia* 33–53 × 11–16 *µm*, 4-spored, clavate to subclavate; sterigmata 4–7 ×1–1.5 *µm*. *Hymenial cystidia* 27–75 × 8.5–12 *µm*, common, subcylindrical, subfusiform to subappendiculate, content insignificant, often encrusted, incrustations distinct, mainly located in concentric zones on neck. *Tube edge* fertile. *Hymenophoral trama* intermediate type. *Pileipellis* 110–150 *µm* thick, ixotrichoderm, composed of erect septate hyphae, sometimes slightly interwoven; terminal cells 10–42 × 7–16 *µm*, cylindrical to subfusoid to fusoid or ventricose, subclavate to clavate or rarely irregular, content slightly dense. *Stipitipellis* 100–130 *µm* thick, fertile, composed of hyphae, basidia and cystidia; caulocystidia 47–85 × 10–21 *µm*, subfusoid, fusoid, ventricose, ventricose-rostrate to appendiculate; caulobasidia similar to tube basidia but less in number. *Clamp connections* absent in all tissues.

Habitat and distribution: Under *Betula* sp. in Memainchu and Kyangnosla areas, humid subalpine mixed (broadleaf and coniferous) forests dominated by species of *Abies*, *Betula* and *Acer*. (*Pseudotsuga*, *Tsuga*, *Abies*). Producing basidiomata in the rainy season. Uncommon, Found in East district of Sikkim (India).

Material examined: INDIA, Sikkim, East district, Memainchu area, 2 August 2014, D. Chakraborty & K. Das, DC 14-019 (**holotype**, CAL; isotype, AMH); *ibid.*, East district, Kyangnosla alpine sanctuary, 7 August 2014, D. Chakraborty & K. Das, DC 14-030, (CAL); *ibid*., East district, Memainchu area, 4 July 2015, D. Chakraborty, DC 15-007, (CAL).

Notes: LSU sequence data from the holotype (DC 14-019) was added to a dataset consisting of all LSU used in Wu et al. (2014). Multiple sequence alignment was achieved using the Practical Alignment using Sate and TrAnsitivity (PASTA) algorithm (Mirarab et al. 2014). The resulting alignment was used for maximum likelihood analysis implemented in RAxML v8.1.17 (Stamatakis 2006, Ott et al. 2007) using a GTRGAMMA model and branch support assessed using rapid bootstrapping set to terminate automatically based on the MRE criterion. The LSU sequence of DC 14-019 was strongly supported (93% bootstrap) in a clade with *Leccinellum*, *Rossbeevera*, *Chamonixia*, *Octaviania*, and *Leccinum* (Fig. 125a). The ITS sequence from the holotype (DC14-019) was combined with sequences from related taxa downloaded from GenBank (Benson et al. 2013). Relevant GenBank sequences were downloaded following queries using search terms including the target taxon followed by “AND internal transcribed spacer”, with model organisms excluded, including *Octaviania* (75 sequences), *Chamonixia* (21 sequences), *Rossbeevera* (92 sequences), and *Leccinum* (178 sequences). After adding the sequence of DC14-019 and removing duplicate sequences, the final dataset consisted of 367 sequences. One sequence (AB848541) was on the complementary strand and was corrected before alignment. Multiple sequence alignment was achieved using the Practical Alignment using Sate and TrAnsitivity (PASTA) algorithm (Mirarab et al. 2014). The resulting alignment was used for maximum likelihood analysis implemented in RAxML v8.1.17 (Stamatakis 2006, Ott et al. 2007) using a GTRGAMMA model and branch support assessed using rapid bootstrapping set to terminate automatically based on the MRE criterion. The sequence of DC 14-019 was weakly supported (43% bootstrap) with a clade composed of *Leccinellum crocipodium*, *L. carpini*, *L.* spp., and unnamed sequences (Fig. 125b). Although support was weak, the sequence clearly did not cluster with *Leccinum* s.s., and so we have provisionally included it within *Leccinellum* due to its putative phylogenetic affinities with other member of this genus.

Leccinellum indoaurantiacum is characterized by yellow-orange to orange-red typically hemisphaerical or convex pileus, yellow unchanging pore surface, striate squamulose to scabrate stipe with white basel mycelia, context quickly becoming pinkish white to light pink on exposure and presence of encrusted hymenial cystidia. In the field *Boletus sinoaurantiacus* M. Zang & R.H. Petersen appears to be similar with the present species but, the earlier grows on considerably lower altitudinal zone (1550–1680 m) and can be separated from the latter by showing unchanging context (pileus/stipe) and absence of encrusted hymenial cystidia. Moreover, the association of *B. sinoaurantiacus* with the members of *Fagaceae* is quite distinct (Zang et al. 2001).

Two other superficially similar species with an orange red pileus, *Leccinum aurantiacum* (Bull.) Gray (reported from North America) and *L. insigne* A.H. Sm., Thiers & Watling (reported from North America and also from India), may also create confusion with *Leccinellum indoaurantiacum*. However, the context of the *Leccinum* species are distinctly different, showing other colour reactions: context white initially becoming intermediate pinkish to wine-red then finally purple gray to blackish on exposure and pale blue with $FeSO_4$ in *L. aurantiacum*; context white initially becoming purplish gray and then blackish without any intermediate reddening on exposure and bluish with $FeSO_4$ in *L. insigne* (Bessette et al. 2010, Das & Chakraborty 2014). Moreover, *L. aurantiacum* has larger basidiomata (pileus 50–205 mm, stipe 100–160 × 20 mm) and a pore surface that becomes brownish on bruising. Similarly, in *L. insigne*, basidiomata are more robust (pileus up to 15 cm diam., stipe 7–12 × 1–2 cm) with smaller (11–16 × 4–5 *µm*) spores.

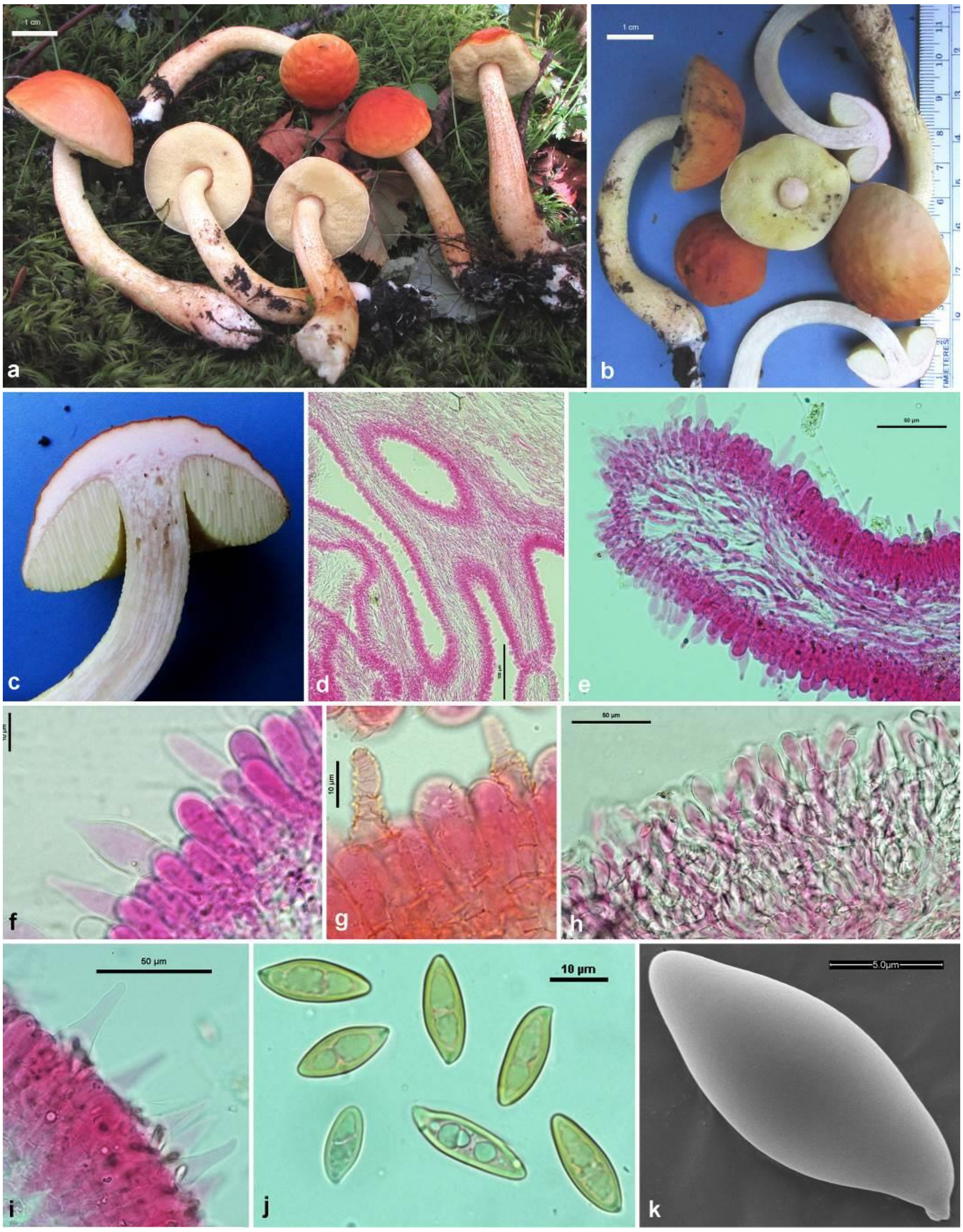


Fig. 126 ***Leccinellum indoaurantiacum*** (**holotype**) **a**, **b** Fresh basidiomata **c** Pink context on exposure **d** Tube trama **e** Tube edge **f** Basidia **g** Hymenial cystidia **h** Transverse section through pileipellis **i** Caulocystidia **j** Basidiospores **k** SEM image of a basidiospore. Scale bars: a, b = 1 cm, d = 100 *µm*, e, h, i = 50 *µm*, f, g, j = 10 *µm*, k = 5 *µm*.

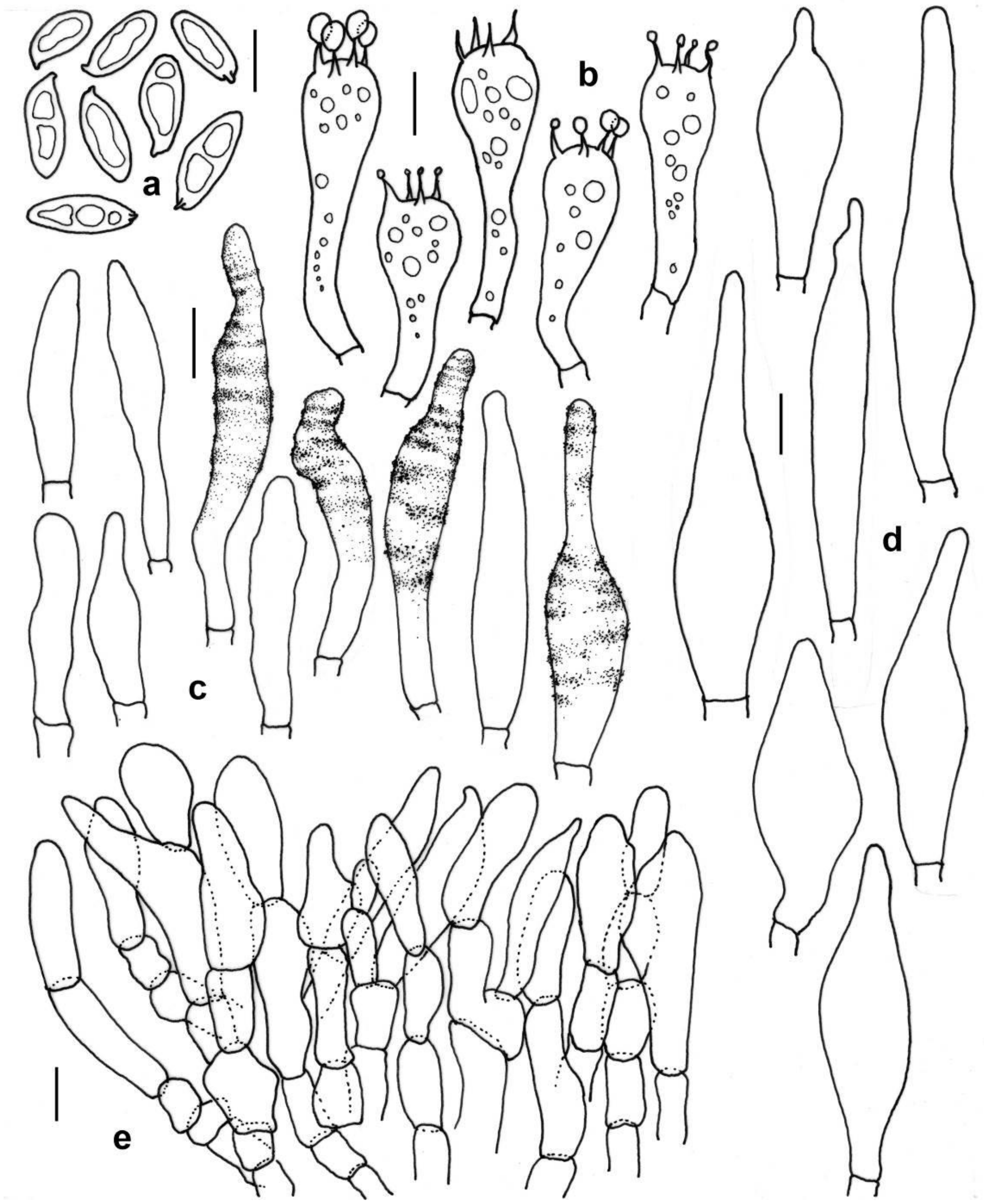


Fig. 127 ***Leccinellum indoaurantiacum*** (**holotype**) **a** Basidiospores **b** Basidia **c** Hymenial cystidia **d** Caulocystidia **e** Transverse section through pileipellis. Scale bars: a–e = 10 *µm*.

Polyporales **genus,** ***incertae sedis***

Galzinia Bourdot

Galzinia is a small genus of corticiod fungi typified with *G. pedicellata* Bourdot. The genus currently comprises nine species (Biodin and Gills 1990, Index fungorum 2016), but the boundaries of the genus is not well-defined and its taxonomy needs to be revised. In our *Galzinia* type studies (unpublished), we noticed that several types are in poor condition. Morphologically, *Galzinia* is mainly characterized by cylindrical to urniform basidia sometimes with internal repetition, and allantoid basidiospores (Bernicchia and Gorjón 2010). Except for *G. incrustans* (Höhn. & Litsch.) Parmasto, most of the other species produce scanty basidiomes which are difficult to see. The generic type *G. pedicellata* is not yet sequenced; the species is known only from very few collections and our attemps to get sequence data from this species have failed until now. *Galzinia incrustans* is the only member of the genus sequenced, and nests in the order *Corticiales*, within the family *Corticiaceae* (Ghobad-Nejhad et al. 2010).

338. *Galzinia longibasidia* Hallenb., Mycotaxon 11(2): 454, 1980.

MycoBank number: MB 112942, *Facesoffungi number*: FoF 02050

This is a little know species described by Hallenberg (1980) from Iran, and is characterized by its long basidia and relatively large, subcylindrical basidiospores. Here, we obtained ITS and LSU sequence data from the holotype material of *G. longibasidia*. Blast searches at NCBI shows the new sequences as close to *Phanerochaete* P. Karst. and *Phlebia* Fr. spp., with the highest similarity to uncultured and insuffficently identified isolates. *Galzinia* is shown to be a polyphyletic genus, and *G. longibasidia* is nested within *Polyporales* but its closest relatives could be verified via thorough phylogentic analyses of *Polyporales*, mainly the phlebioid clade.

Material examined: IRAN, Golestan Province, Gorgan, Golestan National Park, on a fallen branch of a deciduous tree, 4.V.1978, Hallenberg NH2417 (GB, **holotype**).

Leptocorticium Hjortstam & Ryvarden

The corticioid genus *Leptocorticium* was typified with *L. cyatheae* (S. Ito & S. Imai) Hjortstam & Ryvarden and is characterized by monomitic hyphal system with clamps, dendrohyphidia, subulate leptocystidia, and fusiform to navicular basidiospores (Bernicchia and Gorjón 2010). The genus currently contains seven species and was recently discussed by Gorjón and Saitta (2014). Because no sequecne data is avaliable from the type, the phylogenetic position of the genus is not clear. Based on morphology, Larsson (2007) proposed that the genus may belong to the order *Corticiales*. *Leptocorticium tenellum* is the first member of the genus for which we present sequence level data.

Russulales* genus, *incertae sedis

339. *Leptocorticium tenellum* Nakasone, Mycol. Progr. 4(3): 253, 2005.

MycoBank number: MB 341582, *Facesoffungi number*: FoF 02051

The species was recently re-described by Hallenberg (2012) who studied its type and reported some new material he collected in Chile; from one of those material we could obtain ITS and LSU sequence data. A megablast search of GenBank nucleotide database at NCBI (as of 20 November 2015) using the new LSU showed that the best hits were isolates of *Aleurodiscus* Rabenh. ex J. Schröt. spp. and *Lentinellus ursinus* (Fr.) Kühner. Blast searches of the new ITS (only 392 bp recovered) showed the best three hits to be *Lentinellus subargillaceus* (Kauffman) R.H. Petersen, and *L. tridentinus* (Sacc. & P. Syd.) Singer, with 99% over 41% query coverage. Therefore, *Leptocorticium tenellum* is shown to be a member of the order *Russulales*.

Material examined: CHILE, Los Lagos, Parque Nacional Puyehue, Trail Los Rapidos, Circuito, 40° 44' 01.4" S, 72° 18' 44.1" W, elev. 496 m, on bamboo, 22.II.2010, Hallenberg (GB NH16311, **reference specimen designate here**).

Hymenochaetales

Hymenochaetaceae

Hymenochaetaceae, belonging to *Hymenochaetales*, is one of the most important families in Basidiomycota. This family accommodates some serious forest pathogens (Cui et al. 2015) and important medicinal species (Zhou et al. 2016a). In the last two decades, molecular phylogeny extremely improved the knowledge of *Hymenochaetaceae* at the generic level. At least seven genera were newly erected (Niemelä et al. 2001, Dai 2010, Rajchenberg et al. 2015, Zhou 2015a, Zhou et al. 2016a) and some old genus names were also reused (Dai 2010). Meanwhile, studies on global diversity of certain genera in *Hymenochaetaceae* extremely increased known species number (Zhou 2015b, Zhou and Dai 2012, Zhou et al. 2016a, b). However, there are still some undescribed species that need to be introduced. The phylogenetic tree for *Fomitiporia* is presented in Fig. 130.

Fomitiporia Murril

Fomitiporia is characterized by pileate to resupinate basidiomata, hymenial setae present in some species, dextrinoid basidiospores, and a dimitic hyphal system through all the basidioma (Decock et al. 2007). The genus has about 40 species described, many of those have been collected on live tree hosts, suggesting some levels of host-specificity (Amalfi et al. 2012; Dai et al. 2008). Historically, due to low morphological variation, several taxa represent morphological complexes of cryptic species, thus the phylogenetic reconstructions based on molecular data have been playing a crucial role in the discovery of unknown lineages (Decock et al. 2007; Vlasák and Kout 2011). Neotropical region presents a high diversity unknown (Amalfi and Decock, 2013; Amalfi et al. 2014), mainly because there are many areas without records of collections. Two new pileate species of *Fomitiporia* from south Brazil are described in this study. The phylogenetic tree for *Fomitiporia* is presented in Fig. 128.

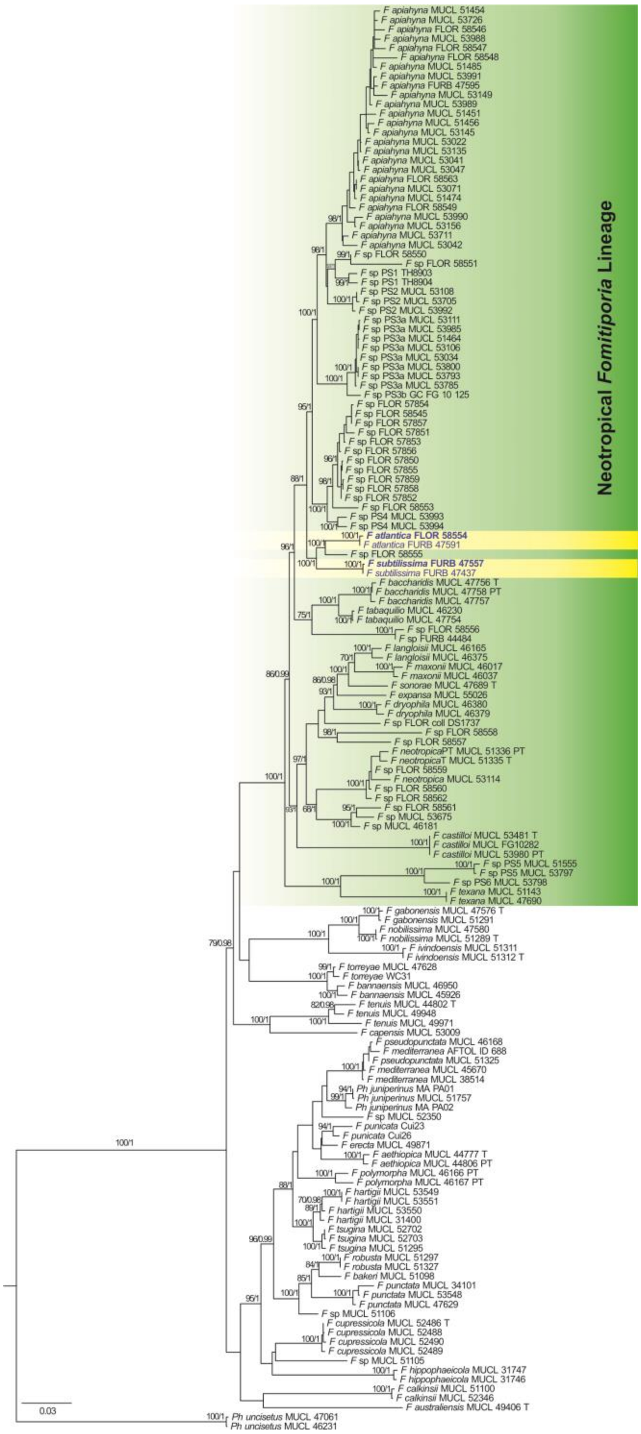


Fig. 128 Phylogram generated from Maximum Likelihood (RAxML) analysis based on combined nrLSU, nrITS, EF and RPB2 sequence data of *Fomitiporia*. Maximum Likelihood bootstrap support values greater than 70 % and Bayesian posterior probalities (BPP) greater than 0.98 are indicated above and below the nodes (BS/BPP). In the BI analysis average standard deviation of split frequencies = 0.005 and the bootstopping criteria of RAxML indicated 204 pseudoreplications as sufficient to access the internal branch support. New taxa are in blue and species for which obtained sequences are based on type material have names in bold. The tree is rooted with *Phellinus uncisetus*.

340. *Fomitiporia atlantica* Alves-Silva, Reck & Drechsler-Santos, ***sp. nov.***

Index Fungorum number: IF 551915, *Facesoffungi number*: FoF 01831, Fig. 129

Etymology: referring to the vegetacional type where the fungus was found, the Atlantic forest.

Holotype: FLOR 58554.

Basidiomata perennial, pileate, sessile and mostly broadly attached, semicircular, solitary to imbricate, then with the different pilei fusing, with a nodulous aspect when emerging from the wood, obtriquetrous to obungulate, also triquetous, projecting 12.5–51 mm, 21–66 mm wide and 20–82 mm thick at the base, woody consistency when dried; *pileus* glabrous, concentrically zonated with multiple narrow bands, slightly sulcate, faintly cracked when old, dull, when fresh pilear surface greyish brown 11E3, violet brown11F4 to dark brown [7 F(6–8)], upon dried brown[6 E(5–8)]to olive brown [6 F(4-8)] when young [6 E(5–8)], becoming dark brown [6 F(5–8)]; *margin* finely velutinous, round, folded, thick, 3.5–19 mm thickness, sterile, olive brown [6 F(4–8)], yellowish brown to brown [5 DEF(6–8)]; *pore surface* light greyish brown (5D8) when young, greyish brown to cinnamon; *pores* rounded to angular, 6–8 (–9) per mm, (60–) 70–110 (–120) *µm* diam. (mean = 89 *µm*); *dissepiments* entire, (30–) 40–120 *µm* (mean = 67 *µm*) thick; *tubes* distinct to mostly indistinctly stratified, with several layers (up to 15 layers in the oldest basidioma), those interleaved with context layers usually thicker (up to five times), individual tube layers relatively thin, sometimes difficult to distinguish, up to 2 mm tall, brown [5 EF (4–5)] to grayish brown (5E3), the older layers filled with whitish mycelium; *context* simple, up to 20 mm thick, concentrically zonate, sometimes constituted by extremely thin black lines (invisible to the unaided eye) that made the separation between growth layers of the context, with dense texture and woody consistency, golden to brownish yellow [5 BC (7–8)], with a distinct dark line at the surface, which is dark brown when young, becoming black, sometimes with a resinous aspect. *Hyphal system* dimitic in all parts; *generative hyphae* simple septate, hyaline to pale yellow, sparingly branched, 2–3 *µm* diam; *skeletal hyphae* golden brown to reddish brown, unbranched, thick-walled, rarely with local swelling up to 8 *µm*, in the context 4–5(–5.5) *µm* diam., the lumen 1.5–3 *µm* wide, in the hymenophoral trama 4–5(–6) *µm* diam., the lumen 1.5–3(–4) *µm* wide. *Hymenium*: *hymenial setae* absent, other sterile elements presents (as basidioles), hyaline, thin-walled; *basidia* subglobose to globose, hyaline, tetrasporic, 9–11 × 7–8 (mean = 9.5 × 8 *µm*) Q = 1–1.3 *µm* (meanQ = 1.18 *µm*); *basidiospores* subglobose, globose to obovoid, with the wider portion displaced towards the apex,(4.5–) 5–5.5 (–6) × 4–5.5 *µm* (mean = 5.1 × 4.8 *µm*) Q = 1–1.25 *µm* (meanQ = 1.08 *µm*) (*n* = 40), hyaline, strong to weakly dextrinoid, cyanophilous, thick-walled, smooth.

Material examined: BRAZIL, Santa Catarina, Blumenau, Parque Natural Municipal São Francisco de Assis, 26°55'17"S 49°04'18"W, on dead cut tree, 21 November 2014, G. Alves-Silva 640, (FLOR 58554, **holotype**); *Ibid*., on dead standing trunk, 15 September 2015, F. Bittencourt 507 (FURB 47591).

Notes: *Fomitiporia atlantica* is mainly characterized by the nodulose aspect of basidiomata with thick-rounded margin and darkness aspect of basidiomata when fresh, the narrowly zonated pilear surface, the zonation of the context (with variable presence of concentric thin black lines invisible to the unaided eye) and by the irregular layers of tubes (Fig. 2i); microscopically, the new species presents dimitic hyphal system and globose, subglobose to obovoid basidiospores with variable dextrinoid reaction. *Fomitiporia atlantica* shares with *F. castilloi* Decock & Amalfi the nodulous basidiomata (better observed in young specimens). However, *F. castilloi* is described by Amalfi and Decock (2013) from French Guiana as presenting distinct hymenial setae and slightly larger basidiospores in range and average (6.2 × 5.2 *µm*), besides having a wider pilear zonation as well as an azonated context. *Fomitiporia gabonensis* Amalfi & Decock also presents imbricate basidiomata and variable dextrinoid basidiospores. Nevertheless, *F. gabonensis* was described by Amalfi et al. (2010) from Africa (Gabon) as presenting smaller basidiospores (4.7 × 4.1 *µm*) and acute thinner margin. Besides the morphological evidences, *F. atlantica* is also supported by molecular results. The phylogenetic analysis (Fig. 128) showed the two specimens clustered together in a strong supported clade (BS = 100, BPP = 1). *Fomitiporia atlantica* forms a more inclusive clade with other two species, *F. subtilissima* (described below) and another undescribed species from Brazil (FLOR 58555). This clade displays nested vicinity to *F. apiahyna sensu lato* clade (Amalfi et al. 2014), appearing as a sister clade of this lineage. *Fomitiporia atlantica* differs from *F. apiahyna* (Speg.) Robledo, Decock & Rajchenb. *sensu* Amalfi and Decock (2013) mainly by its slightly smaller basidiospores (*F. apiahyna* = 5.9 × 5.1 *µm*) and pileus slightly sulcate and cracked, conspicuous features in *F. apiahyna*.

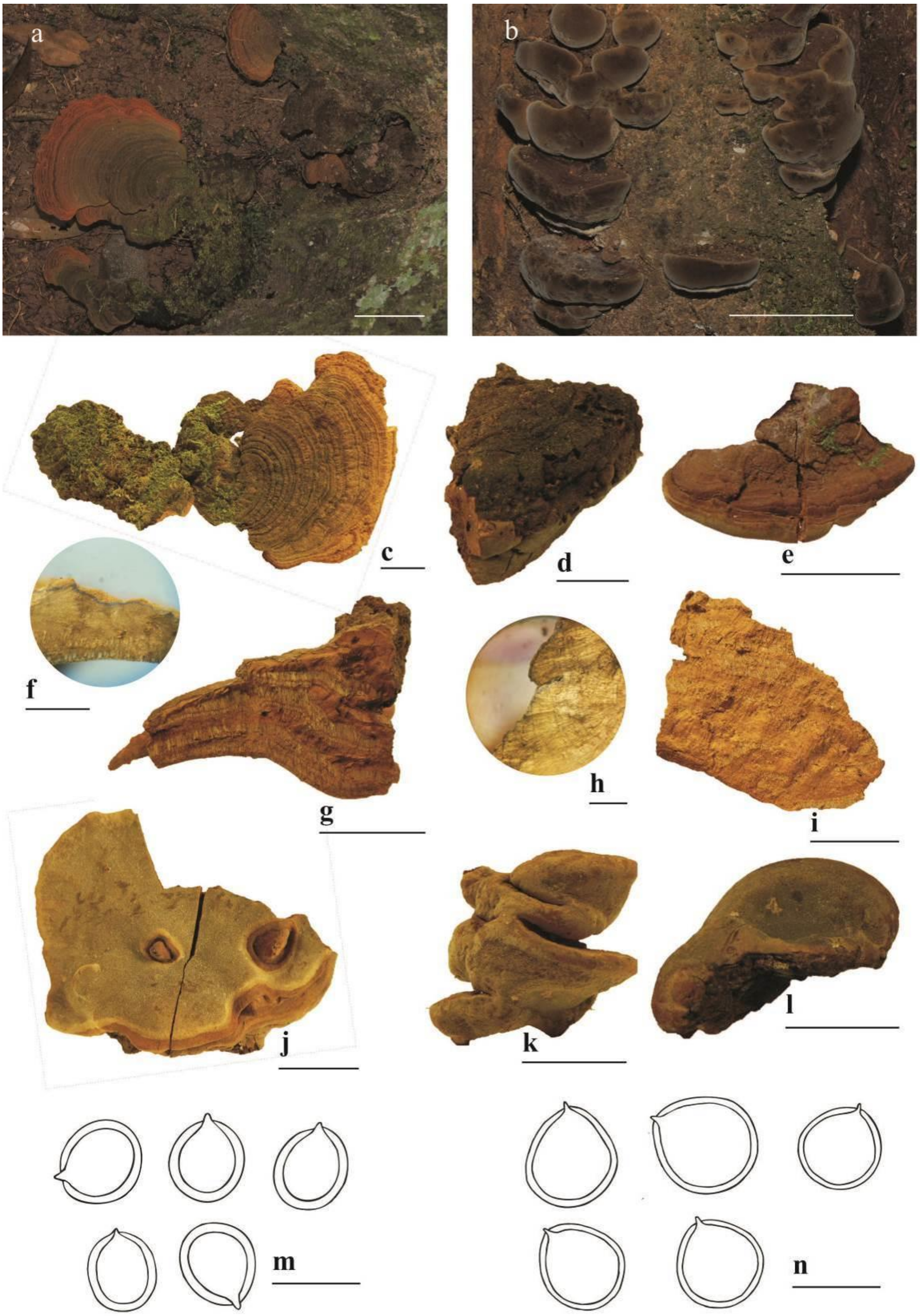


Fig. 129 ***Fomitiporia subtilissima*** (FURB 47437) **a** Basidiomata *in situ* **c** Abmenial surface showing the concentric zonation and spathulate aspect of basidioma. ***Fomitiporia subtilissima*** (**holotype**) **f**, **g** Details of context and tubes **f** Black line at the surface **g** Context and tube layers **j** Hymenophoral surface **m** Basidiospores. ***Fomitiporia atlantica*** (FURB 47591) **b**

Darkness aspect of basidiomata *in situ* **e** Abhymenial surface **h** Black line at the surface **k** Nodulous basidioma **l** Hymenophoral surface **n** Basidiospores. ***Fomitiporia atlantica*** (**holotype**) **d** Detail of slightly cracked abhymenial surface **i** Context and tube layers. Scale bars: a, b = 50 mm, c–e, g and i, l = 20 mm, f, h = 2 mm, m, n = 5 *µm*.

341. ***Fomitiporia subtilissima*** Alves-Silva, Reck, & Drechsler-Santos, ***sp. nov.***

Index Fungorum number: IF 551916, *Facesoffungi number*: FoF 01832, Fig. 129

Etymology: referring to the relatively thin basidiomata.

Holotype: FURB 47557.

Basidiomata perennial, pileate; sessile, subdimidiate to pseudostipitate, the pseudostipe formed by successive deposited layers, single or with distinct pilei developing from the same point, semicircular, flabelliform to slightly spathulate, aplanate to convex, in section and near the base slightly obtriquetrous, projecting 18–162 mm, 17–96 mm wide and 6–40 mm thick at the base, soft, woody consistency; *pileus* glabrous,concentrically zonated with multiple narrow bands, moderately sulcate, light brown [6 D(5–8)], brownish orange [6 C(7–8)] to brown [6 E(5–8)], becoming dark brown [6 F(5–8)] to black; *margin* acute to obtuse, sterile, light brown [5 D(6–8)] to yellowish brown [6 E(5–8)]; *pore surface* grayish brown [6 F(3)] to cinnamon, near the base the newest tube layer presents an wider sterile yellowish brown [5 D(6–8)] margin (up to 2 mm), contrasting with the precedent layer recovered by brown [6 E(6–8)]context; *pores* rounded to angular, (4–) 5–9 per mm, (70–) 80–131 (–170) *µm* diam. (mean = 107 *µm*); *dissepiments* entire, 30–76 (–100) *µm* (mean = 45 *µm*) thick; *tubes* distinctly stratified, up to 9 layers, individual layers 0.3–3 mm thick, with context among it, up to 2 mm thick, greyish brown [6 F(3–4)] to brown [6 E (6–8)], but the youngest (active) layer greyish brown (6E4) to cinnamon, the older layers filled with whitish mycelium; *context* simple, concentrically zonate, up to 6mm thick, with soft and hard to woody consistency, light golden brown to light brownish yellow [5 BC (7–8)], with a distinct dark line at the surface. *Hyphal system* dimitic in all parts; *generative hyphae* simple septate, hyaline to pale yellow, mildly branched, 1.5–2 (–2.5) *µm* diam; *skeletal hyphae* golden brown to reddish brown, unbranched, thick-walled, occasionally with constrictions uncompleted becoming local swellings up to 8 *µm* diam., in the context 3–5 *µm* diam., the lumen 1–3 *µm* wide, in the hymenophoral trama 3.5–4.5 *µm* diam., the lumen 1–3 *µm* wide. *Hymenium*: *hymenial setae* absent, other sterile elements presents (as basidioles), hyaline, thin-walled; *basidia* subglobose to globose**,** hyaline, tetrasporic**,** 9–10 × 7–9 (mean = 9.2 × 8.1 *µm*) Q = 1–1.3 *µm* (meanQ = 1.14 *µm*); *basidiospores* subglobose, globose to obovoid, the wider portion displaced towards the apex, 4–5 × 4–4.5(–5) *µm* (mean = 4.5 × 4 *µm*) Q = 1–1.25 *µm* (meanQ = 1.13 *µm*) (*n* = 40), hyaline, slightly to moderately dextrinoid and cyanophilous, thick-walled and smooth.

Material examined: BRAZIL, Santa Catarina, Blumenau, Parque Natural Municipal São Francisco de Assis, 26°55'17"S 49°04'18"W, growing on dead root of living *Sloanea guianensis* (Aubl.) Benth. (*Elaeocarpaceae*), 28 July 2015, F. Bittencourt 493 (FURB 47557, **holotype**, isotype in FLOR); *Ibid*., in the base of a living unidentified angiosperm, 13 May 2015, F. Bittencourt 428 (FURB 47437).

Notes: The flabelliform to spathulate, thin and aplanate basidiomata, with the presence of a pseudostipe, and the narrow concentrically zonated and sulcate abhymenial surface characterizes this species as unique in the genus. The pseudostipe is explained by its successive depositing forward tube layers that do not cover the precedent layer near the base. Besides, *F. subtilissima* has slightly to moderately dextrinoid basidiospores, which are relatively small when compared with other *Fomitiporia* species. Due to its macroscopic features, *F. subtilissima* resembles some *Phylloporia* species, but this genus is characterized by monomitic hyphal system and IKI- basidiospores. Variably dextrinoid small basidiospores are also found in *F. gabonensis* and *F. ivindoensis* Decock, Amalfi & Yombiyeni (Amalfi et al. 2010), both described from Gabon, Africa. *Fomitiporia gabonensis* has thick, obtriquetrous and broadly attached basidiomata, while *F. ivindoensis* has cushion-shaped to aplanate basidiomata, but they do not have pseudostipe. The morphologic and molecular data (BS = 100, BPP = 1) high support the new species. The phylogenetic analysis (Fig. 128) recovered *F. subtilissima* in a clade nested with *F. atlantica* and another undescribed species from Brazil.

***Inonotus* P. Karst.**

Inonotus, typified by *I. hispidus* (Bull.) P. Karst., is one of the largest genera within the *Hymenochaetaceae*; in a wide sense, this genus, accommodating more than 100 species, is distinct from other genera in *Hymenochaetaceae* by its annual, non-stipitate or rarely laterally stipitate basidiocarps, poroid hymenophores and a monomitic hyphal system (Ryvarden 2005). According to phylogenetic results, four narrowly defined genera segregated from *Inonotus* sensu lato, viz. *Inocutis* Fiasson & Niemelä, *Inonotopsis* Parmasto, *Mensularia* Lázaro Ibiza, *Onnia* P. Karst., are accepted, whereas some species with perennial basidiocarps and/or a dimitic hyphal system were also transferred to *Inonotus* (Wagner and Fischer 2002, Dai 2010, Wu et al. 2012, Vlasák et al. 2013). Recently, Zhou (2015a) introduced a monotypic genus *Cylindrosporus* L.W. Zhou & Y.C. Dai for species previously belonging to *Inonotus*, while Zhou et al. (2016a) segregated *Sanghuangporus* Sheng H. Wu, L.W. Zhou & Y.C. Dai and *Tropicoporus* L.W. Zhou, Y.C. Dai & Sheng H. Wu from *Inonotus* and proposed that the remain species in *Inonotus* still have polyphyletic origins (Zhou et al. 2016a). Herein, a new species of *Inonotus* is described from Chiang Mai, Thailand.

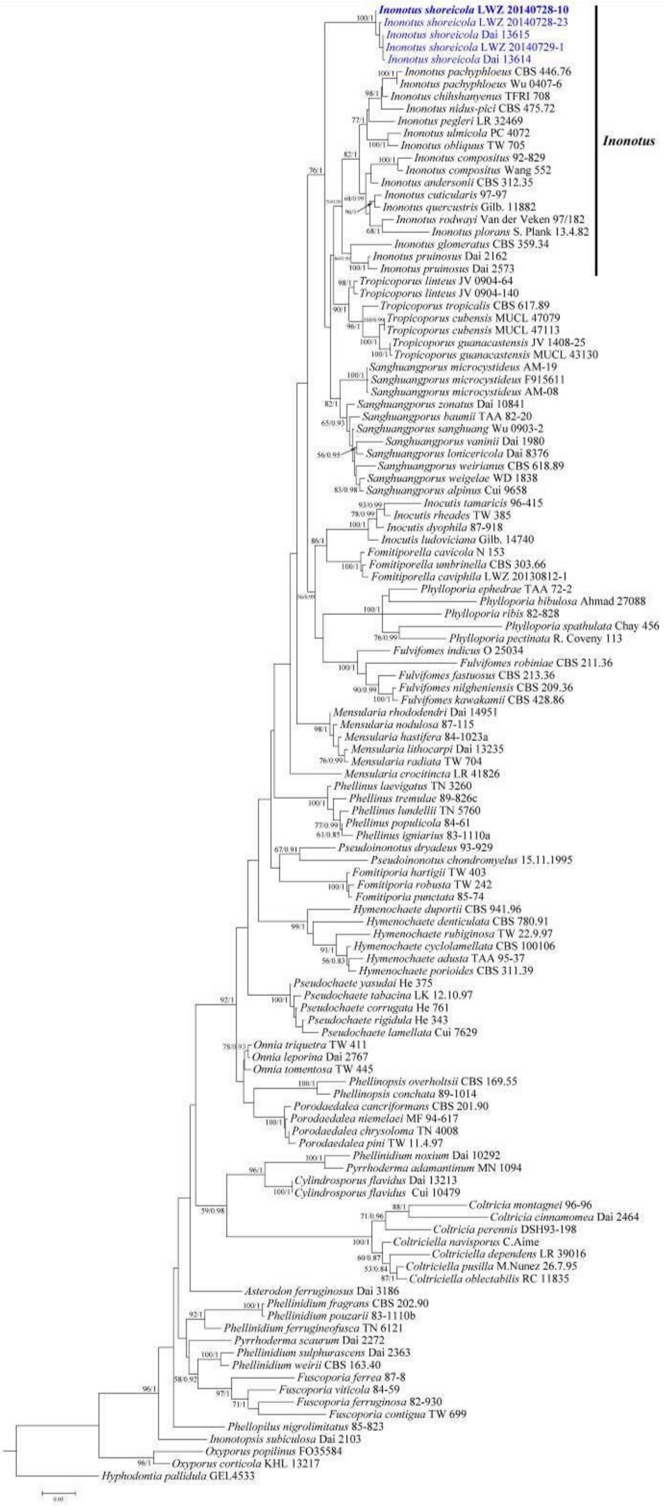


Fig. 130 Phylogenetic position of *Inonotus shoreicola* inferred from nLSU sequence data. Topology is from maximum likelihood (raxmlGUI 1.2) analysis, and the statistical values simultaneously above 50% for bootstrap values and 0.80 for Bayesian posterior probabilities are indicated at the nodes. New taxa are in blue and species for which obtained sequences are based on type material have names in bold.

342. *Inonotus shoreicola* L.W. Zhou, Y.C. Dai & Vlasák, *sp. nov.*

Index Fungorum number: IF 551555, *Facesoffungi number*: FoF 02052, Fig. 131

Etymology: refers to the host genus *Shorea*.

Holotypus: LWZ 20140728-10 (IFP)

Basidiocarps perennial, sessile, single, ungulate, woody hard, without Odour and taste when dry. *Pileus* dimidiate, projecting up to 7 cm, 20 cm wide and 8 cm thick at base. *Pileal surface* pale mouse-grey to vinaceous grey, radially cracked, concentrically zonate and sulcate; *margin* obtuse, ash-grey. *Pore surface* dark brown, slightly glancing; *sterile margin* distinct, yellowish brown, up to 5 mm; *pores* circular to angular, 7 per mm; *dissepiments* thin, entire. *Context* dark brown, woody hard, up to 4 mm. *Tubes* yellowish brown, woody hard, tube layers distinctly stratified, annual layer about 5 mm long; *white mycelial strands* present in old tubes.

Hyphal system monomitic; *generative hyphae* simple septate; *tissue* darkening but otherwise unchanged in KOH. *Contextual generative hyphae* yellowish, thick-walled with a wide lumen, rarely branched, simple septate, interwoven, acyanophilous, 1–2.5 *µm* in diam. *Tramal generative hyphae* yellowish, slightly thick- to thick-walled with a wide lumen, occasionally branched, simple septate, parallel along the tubes, acyanophilous, 2–3 *µm* in diam. *Hyphoidsetae* absent; *hymenialsetae* occasionally present, subulate to ventricose, dark brown, thick-walled, sharp pointed, sometimes with an elongated base, 15–38 × 8–20 *µm*; *cystidia* and *cystidioles* absent; *basidia* and *basidioles* not seen; *rhomboid crystals* present in hymenium.

Basidiospores broadly ellipsoid, yellowish, slightly thick-walled, neither amyloid nor dextrinoid, cyanophilous, (4.4–)4.6–5.1(–5.4) × (3.2–)3.5–3.9(–4) *µm*, L = 4.86 *µm*, W = 3.75 *µm*, Q = 1.29–1.3 (n = 60/2).

Material examined: THAILAND, Chiang Mai Province, Sri Lanna National Park, Mae Taeng Forests, on living tree of *Shorea*, 28 July 2014, LWZ 20140728-10 (IFP, **holotype)**, LWZ 20140728-23 (IFP); *Ibid*., 21 October 2013, Dai 13614 (BJFC), Dai 13615 (BJFC), 29 July 2014, LWZ 20140729-1 (IFP).

Notes: Zhou *et al*. (2016a) identified three clades within *Inonotus* and also several species of *Inonotus* outside the three clades. The clade, including the generic type *Inonotus hispidus,* was considered to be *Inonotus sensu stricto,* while the other two clades were introduced as new genera *Sanghuangporus* and *Tropicoporus*; the species outside any clade were also accommodated in *Inonotus sensu stricto* for they have key characters of *Inonotus* (Zhou et al. 2016a). The current phylogeny (Fig. 130) shows that *Inonotus shoreicola* is close to *Inonotus sensu stricto*, *Sanghuangporus* and *Tropicoporus*. Moreover, *Inonotus shoreicola* fits well with the morphological concept of *Inonotus sensu* Dai (2010). Therefore, we place species in *Inonotus*.

Inonotus shoreicola resembles the pileate members of *Sanghuangporus* and *Tropicoporus* in its perennial basidiocarps, cracked pileal surfaces and colored basidiospores; however, these two genera are distinguished by having dimitic hyphal system at least in trama (Zhou et al. 2016a), while *Inonotus shoreicola* has a monomitic hyphal system in both context and trama. *Inonotus pachyphloeus* (Pat.) T. Wagner & M. Fisch. also has perennial basidiocarps and a monomitic hyphal system as *I. shoreicola*, but differs in the presence of hyphoid setae (Fidalgo 1968, Dai 2010).

Some pileate species of *Fomitiporia* Murrill, such as *F. hartigii* (Allesch. & Schnabl) Fiasson & Niemelä and *F. robusta* (P. Karst.) Fiasson & Niemelä, also have cracked pileal surfaces (Dai 2010), which make them similar to *I. shoreicola* especially in the field. However, in micromorphology, *Fomitiporia* is characterized by a dimitic hyphal system and hyaline, dextrinoid basidiospores (Dai 2010).

Inonotus shoreae (Wakef.) Ryvarden, originally described from India, also inhabits *Shorea* like *I. shoreicola*, and is a serious parasite on roots and butts of *Shorea* (Sharma 1995). These two species could be easily differentiated in the field: *I. shoreae* has annual basidiocarps with much larger pores (2–4 per mm, Sharma 1995). Moreover, *Inonotus shoreae* has shorter basidiospores (3.5–5 × 2.5–3 *µm*) than *I. shoreicola* (Sharma 1995). It is noteworthy that *I. shoreicola* is relatively common and has been considered to be a medicinal fungus in Thailand (Fig. 131).

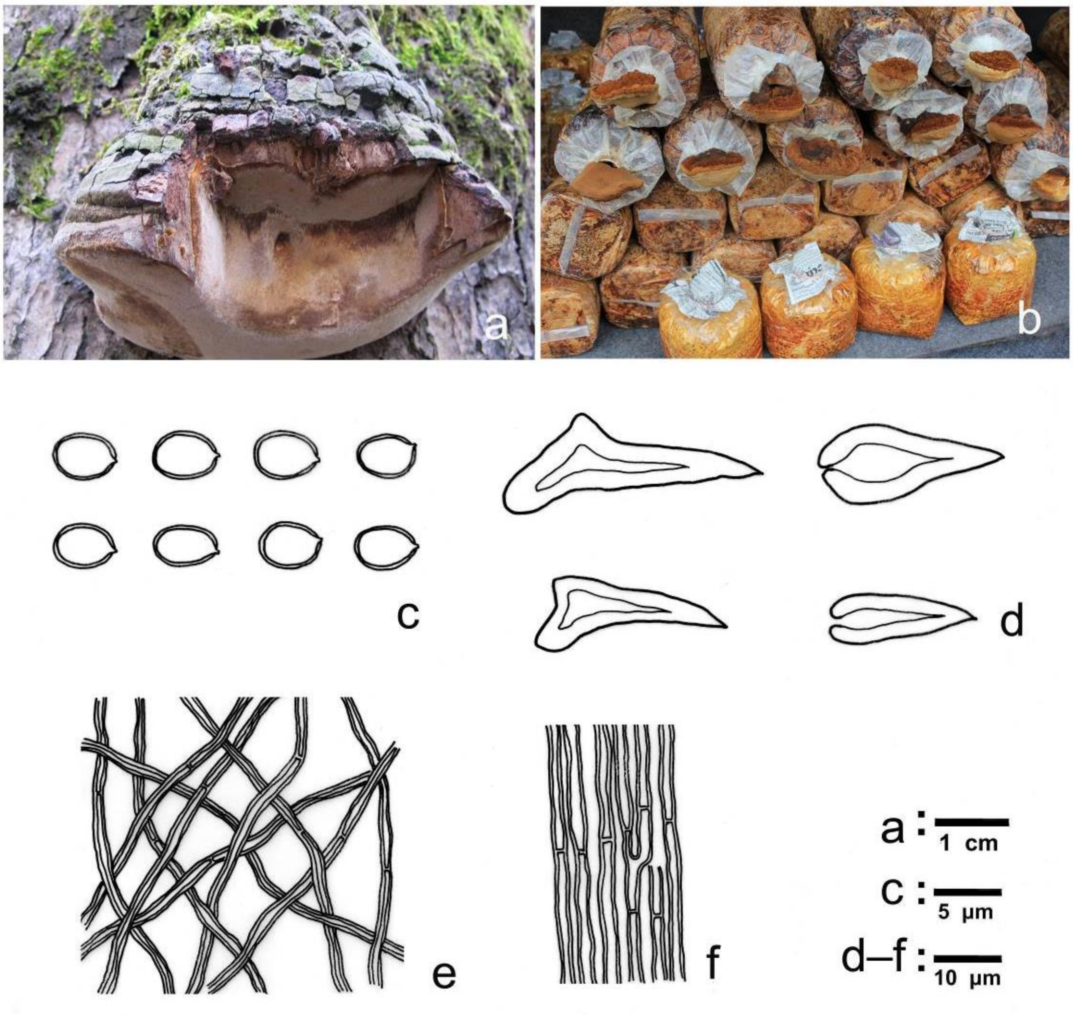


Fig. 131 ***Inonotus shoreicola*** **a** Basidiocarps *in situ* **(holotype)** **b** Cultivations **c** Basidiospores **d** Hymenial setae **e** Hyphae from trama **f** Hyphae from context.

Polyporales

Ganodermataceae

Ganoderma P. Karst

The genus *Ganoderma* was established by Karsten (1881) with *Ganoderma lucidum* (W.Curt:Fr.) as the only species (Moncalvo and Ryvarden 1997). *Ganoderma* species are distributed all over the world, in tropical and temperate regions, although usually found in subtropical and tropical regions, since it can withstand \hot and humid conditions (Pilotti 2004). *Ganoderma* species are not classified as edible mushrooms, as the fruiting bodies are always thick, corky and tough and do not have the fleshy texture characteristic of true edible mushrooms (Singh et al. 2013). *Ganoderma* has long been regarded as one of the most important medicinal fungi worldwide (Paterson 2006), and laccate species of *Ganoderma*, have been used as medicinal fungi in traditional Chinese medicine for over two millennia (Anon 1955). China is very rich in *Ganoderma* species, with at least 80 species names (Zhao and Zhang 2000; Wang et al. 2009a; Cao et al. 2012, 2013), although part of them are synonyms. *Ganoderma* P. Karst. (*Ganodermataceae*, *Polyporales*) is characterized by its double-walled basidiospores with interwall pillars, bears an apical umbo, often shrunk, and the apex appears then truncate (Li et al. 2013c). The taxonomy of the genus is, however, poorly circumscribed, not universally accepted, and has been described as being in a state of chaos (Ryvarden 1991). The objective of the present study is to introduce a new *Ganoderma* sp.with a description from Hainan Province, China and compare it with similar taxa.

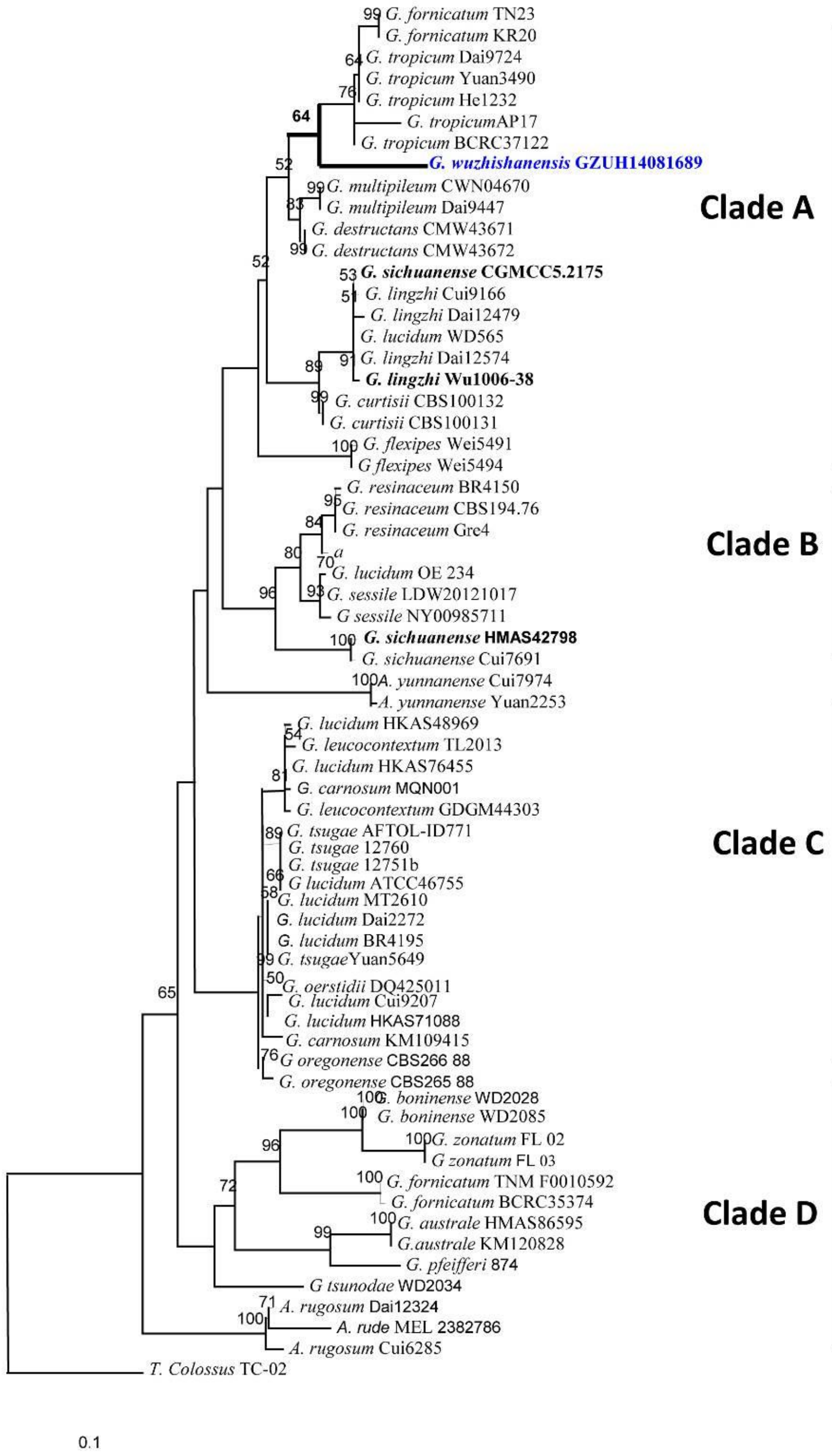


Fig. **132** Phylogram generated from Maximum likelihood (RAxML) analysis based on ITS and RPB2 sequence data. Maximum likelihood bootstrap support values greater than 50% are indicated above the nodes, new species is in red and ex-type specimens in bold. The tree is rooted with *Tomophagus colossus*.

343. ***Ganoderma wuzhishanensis*** T.C. Wen, K. Hapuarachchi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 551681, *Facesoffungi number*: FoF 00915, Fig. 133

Etymology: refers to the type collecting site “Wuzshishan Mountain”, Hainan, China

Holotype: GACP 14081689

Basidiocarp annual, sessile, woody, Pileus 3–5.5 × 1–3 cm, up to 1.5 cm thick at the base, suborbicular, plano convex, sub applante. Upper surface; hard, several layers thick, deep buff (460) to leaf brown (489), crust overlies the pithy context, not cracking, containing fibrous pithy context, strongly laccate, no concentrically sulcate zones, no differentiated zones. radially rugose, margin soft or with numerous undulations and irregularities, 5 mm thick, rounded and concolorous with the pileus. Lower surface light straw (384) basidiospores. *Pore surface* light straw (384), tubes up to 0.7 mm long in total, middle buff (359) to middle brown (411), pores circular or sub circular or isodiametric. *Context* up to 1.5 cm thick, dry, triplex, lower layer; golden brown (414), fibrous/pithy, composed of coarse loose fibrils, soft, middle layer; red oxide (446), upper layer: dark camouflage red (436), woody, not cracking, composed of tightly interwoven, finer fibrils, dulling when cut, trimitic hyphal system, generative hyphae; 0.8 –2(–3) *µm* ($\bar{x}$=1.4, n = 30) in width, thin walled, colourless, hyaline, Skeletal hyphae; (–2)3–3.5(–4) *µm* ($\bar{x}$= 3, n = 40) in width, Golden brown (414) to Light brown (320) in 5% KOH, dextrinoid, thick walled, ligative hyphae; (–0.5)1– 2(–3) *µm* ($\bar{x}$=1.8, n = 40) in width, Dark camouflage red (436), 2) to Light brown (320), thick walled, branched, intertwined the skeletal hyphae. *Basidiospores* 7–9 (–10) × (–3)4–6 *µm* ($\bar{x}$= 8.4 × 5, n = 30, Q = 1.3–2.7, **Q** = 1.7, with myxosporium). 5– 7 (–8) × (–2)3–4 *µm* ($\bar{x}$= 6.2 × 3.3, n = 30, Q = 1.43–3.18, **Q** = 1.99, without myxosporium), elongate, Dark camouflage red (436) to Light brown (320), eusporium bearing fine, short and distinct echinulae, overlaid by a hyaline myxosporium, bitunicate. *Cuticle* hymeniodermiformic, Light brown (320), composed of apically acanthus like branched cells, dextrinoid.

Habitat and distribution: On a decaying wood log, accompanied in humus rich soil with over heavily rotted litter in forest,.mossy coniferous forests, producing basidiomata from late summer to late autumn, only found in Hainan Province, China.

Material examined: CHINA, Hainan Province, Wuzhishan Mountain, Coniferous rainforest, 18°"N 110 "E, elev. 1350 m, 16 August 2014, collector T.C Wen, (GACP14081689, **holotype**).

Notes: *Ganoderma wuzhishanensis* is a new member of Genus *Ganoderma* (Fig. 132) and it clustered with *G. multi-pileum* Hou, which is characterized by two kinds of pilei, one from the stalk with some of the stipes and pilei growing together, and the other growing from the lower pilei; a thin crust, composed of enlarged and bulbous ends of hyphae, 16.5 × 2–6 *µm*; and basidiospores 8–9 × 4 *µm*, ovoid, truncate, with numerous and minute echinulae 4–6 *µm* (Wang et al. 2009a). *Ganoderma wuzhishanensis* is morphologically similar to *Ganoderma tropicum* (Jungh.) Bres. which is characterized by its laccate surface, large spores (distinctly larger than for most species in the *G. lucidum*–complex), 11–14 × 7.5–10 *µm* and the slightly small pileus size, deep buff (460) to leaf brown (489) pileus colour, grow as invidual but live as a group, without concentrically sulcate zones, small tube size, triplex context, basidiospores 7–9 × 4–6 *µm*, elongate, dark camouflage red (436) to light brown

(320) and bitunicate. The species is currently only known from the type locality, Wuzshishan Mountain, Hainan, China.

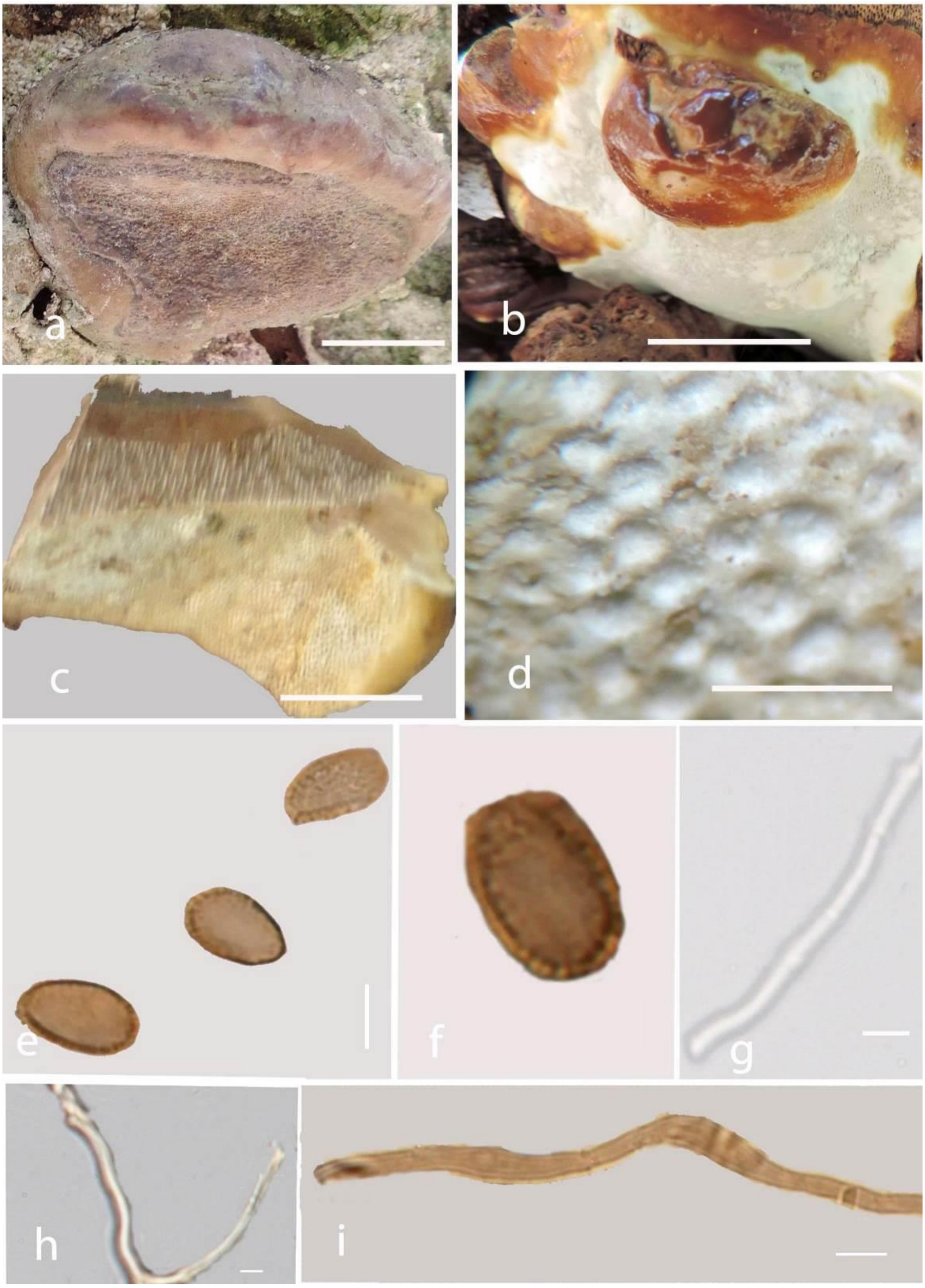


Fig. 133 ***Ganoderma wuzhishanensis*** (**holotype**) **a** Upper surface **b** Lower surface **c** Cutting surface **d** Pores in the lower surface **e**–**f** Spores **g** Vegetative hyphae **h** Skeletal hyphae **i** Ligative hyphae. Scale bars: a–c = 1 cm, d = 0.5 cm, f =10 μm, g–i = 5 μm.

Polyporales genus, *incertae sedis*

Dentocorticium (Parmasto) M.J. Larsen & Gilb.

The genus *Dentocorticium*, typified with *D. ussuricum*, currently comprises seven species of corticioid fungi with resupinate, smooth to dentate hymenophore, monomitic hyphal system with clamps, and smooth, non-amyloid basidiospores. The species possess dendrohyphidia (dendrophyses) and lack cystidia (Boidin and Gilles 1998, Duhem and Michel 2009).

344. ***Dentocorticium ussuricum*** (Parmasto) M.J. Larsen & Gilb., Norw. Jl Bot. 21(3): 226, 1974.

MycoBank number: MB 312868

We studied the type material of *D. ussuricum* and obtained ITS sequence of an authentic material conforming to the type, to deduce the relationships of the type of the genus. A megablast search of GenBank nucleotide database at NCBI (as of 16 November 2015) using the new ITS showed that the best hits were isolates of *Dentocorticium sulphurellum* (Peck) M.J. Larsen & Gilb. with 95–96% identity over 98% query coverage, followed by isolates of *Trametes* Fr. spp. According to Binder et al. (2013), *Trametes* and *Dentocorticium sulphurellum* reside in the core polyporoid clade (*Polyporaceae*, *Polyporales*). Here, the position of generic type *D. ussuricum* within the family *Polyporaceae*, and congeneric relationship of *D. sulphurellum* with *D. ussuricum* are established.

Material examined: RUSSIA, Primorsk, Insula Petrova, on *Actinidia arguta*, 1 September 1961, leg. A. Raitviir (TAA 42424, **holoype**). CHINA, Jilin Province, Antu County, Erdaobaihe, south of Erdaocun town, ca. 30 km from Erdaocun towards Changbaishan Mountain and Lake; forest mainly with *Abies*, *Picea*, *Larix*, *Acer* spp., also *Betula*, *Populus*, *Tilia amurensis*, and *Pinus*; 42.205 Lat., 128.165 Long., elev. ca. 1100 m; on hanging branch of cf. *Acer*, 3 cm in diam.; 11 September 2011; Ghobad-Nejhad 2465 (Ghobad-Nejhad ref. collection, and BJFC).

Polyporaceae

Lentinus

Lentinus (Fr.) Quel is a cosmopolitan genus with an estimated 63 species (Kirk et al. 2008) and 629 records under the name of *Lentinus* in the index fungorum (Index Fungorum 2016) and, species are able to survive over a wide temperature range, are abundant in boreal, temperate and tropical regions (Corner 1981; Pegler 1983; Karunarathna et al. 2011). The phylogenetic tree for *Lentinus* is presented in Fig. 134.

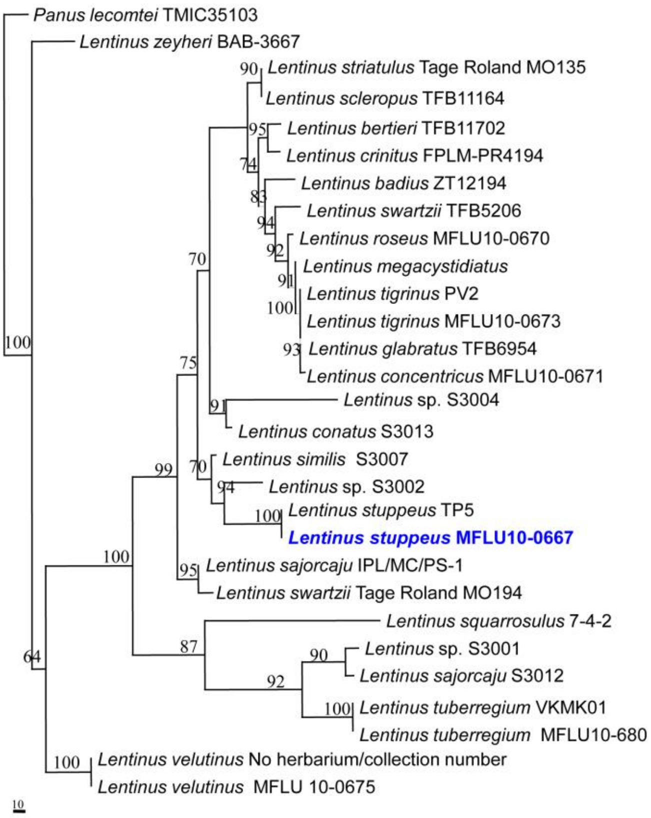


Fig. 134 Phylogeny of *Lentinus stuppeus* and related species in the genus based on nrITS sequences, inferred by maximum likelihood (ML) analysis. Numbers at internodes refer to confidence estimates based on 100 rapid ML bootstraps (only those >50 are indicated). *Lentinus stuppeus* from Thailand is in blue. *Leucoagaricus barssii* and *Leucoagaricus leucothites* are outgroup taxa.

345. ***Lentinus stuppeus*** Klotzsch [as 'stuppens'], Linnaea 8(4): 480, 1833.

≡ *Pocillaria stuppea* (Klotzsch) Kuntze [as 'stupea'], Revis. gen. pl. (Leipzig) 2: 866, 1891.

≡ *Panus stuppeus* (Klotzsch) Pegler & R.W. Rayner [as 'stupeus'], Kew Bull. 23(3): 385, 1969.

Facesoffungi number: FoF 02054, Fig. 135

Basidiomes very small to medium. *Pileus* 1–5.5 cm in diam., coriaceous, deeply umbilicate to deeply infundibuliform; margin inflexed, entire, thin at first reflexed, surface mahogany red, dark purplish brown to almost black, dry, densly villose, covered with curled, hispid, fibrillose hairs up to 7–8 mm long, glabrescent and finely rimose at the centre; margin strongly and persistently involute, densely pilose. *Lamellae* short decurrent, usually with some anastomosing at the stipe apex, pale yellowish buff, narrow, up to 3–4 mm wide, moderately crowded, with 4–5 tiers of lamellulae, edge strongly denticulate. *Stipe* 1.5–4.5 cm × 2–4.5 mm, central, rarely lateral, cylindrical, slender, solid, expanding above, surface dull yellowish brown, often with deeply purple tints, covered by cinnamon brown tomentum at the apex, elsewhere with small, blackish, apprised squamules becoming hispid at the base; context 2–3 mm, white to dull white in color, fibrous, consisting of a dimitic hyphal system with generative and skeletal hyphae. *Generative hyphae* 2–4 *µm* diam., hyaline, very thin walled, frequently branched, with prominent clamp connexions. *Skeletal hyphae* 3–7 *µm* diam., hyaline with a thickened wall, with wide dichotomous branching. *Spore print* cream color. *Basidiospores* (Fig. 135a) 6–9 × 2.3–3.4 *µm* [n = 30, (7.5 × 2.8 *µm*), Q = 2.78], cylindric, hyaline, thin walled. *Basidia* (Fig. 135b) 20–24 × 5–6.5 *µm*, clavate, bearing 4 sterigmata. Lamella-edge sterile. *Cheilocystidia* (Fig. 135c) 16–36 × 4–8 *µm*, sinuous clavate, hyaline, thin-walled. Hyphal pegs abundant. *Hymenophoral trama* hyaline, irregular, similar to context. Subhymenial layer narrow. *Pileipellis* an epicutis, with reddish brown walls. *Hairs* comprising fascicles of unbranched hyphae, with thickened, pigmented wall.

Habitat: On dead wood, in clusters, in rain forest dominated by *Castanopsis armata*, and *Lithocarpus* sp.

Material examined: THAILAND, Chiang Mai Prov., Mae Taeng Dist., Ban Pha Deng village, N19°17.123’ E 98°44. 009’, elev. 900 m, rainforest dominated by *Castanopsis armata and Pinus kesiya*. 18 June 2013, (MFLU 10–0667, **reference specimen designate here**).

Distribution: Ghana, Nigeria, West Cameroons, Zaire Republic, Uganda, Kenya, Madagascar, Mauritius, Zimbabwe, South Africa (Pegler 1986), new record to Thailand (this study).

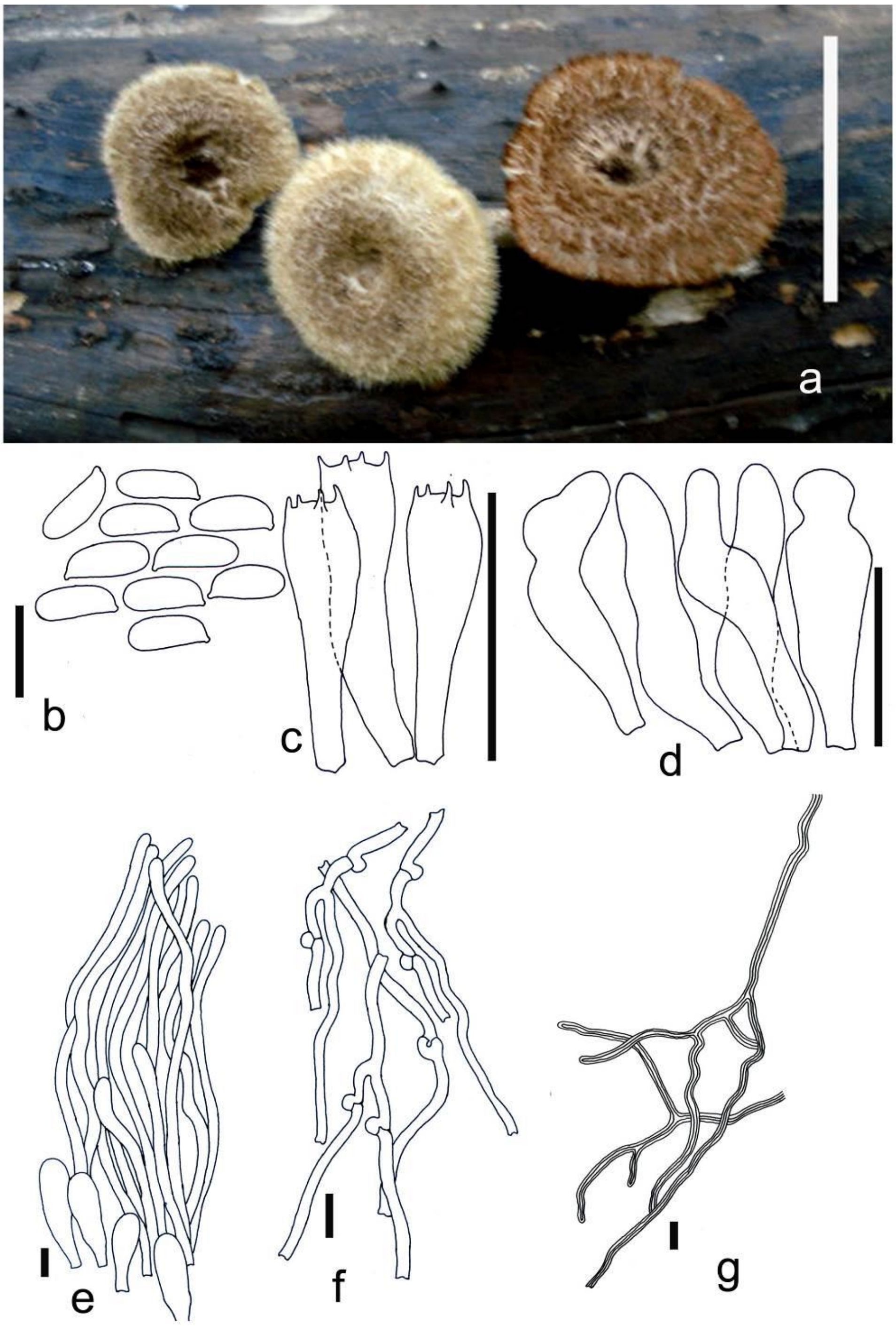


Fig. 135 ***Lentinus stuppeus*** (MFLU 10–0667, **reference specimen**) **a** Basidiocarps **b** Basidiospores **c** Basidia **d** Cheilocystidia **e** Hyphal pegs **f** Generative hyphae **g** Skeletal hyphae. Scale bars: a = 5 cm, b = 10 μm, c–g = 20 μm.

Russulales

Bondarzewiaceae

Bondarzewia

Bondarzewia Singer was established by Singer (1940) based on *B. mesenterica* (Schaeff.) Kreisel, originally described from *Abies* in Germany. It is a remarkable genus because the species usually have huge and imbricate basidiocarps. Some species are edible and medicinal mushrooms (Dai et al. 2009), while others are pathogens on their host trees (Dai et al. 2007). The genus is characterized by an annual growth habit, pileate basidiocarps with poroid hymenophores and it is morphologically a polypore genus. However, it has strongly amyloid and ornamented basidiospores and phylogenetic analysis showed that it belongs to *Russulales* (Larsson and Larsson 2003). The phylogenetic tree is presented in Fig. 136.

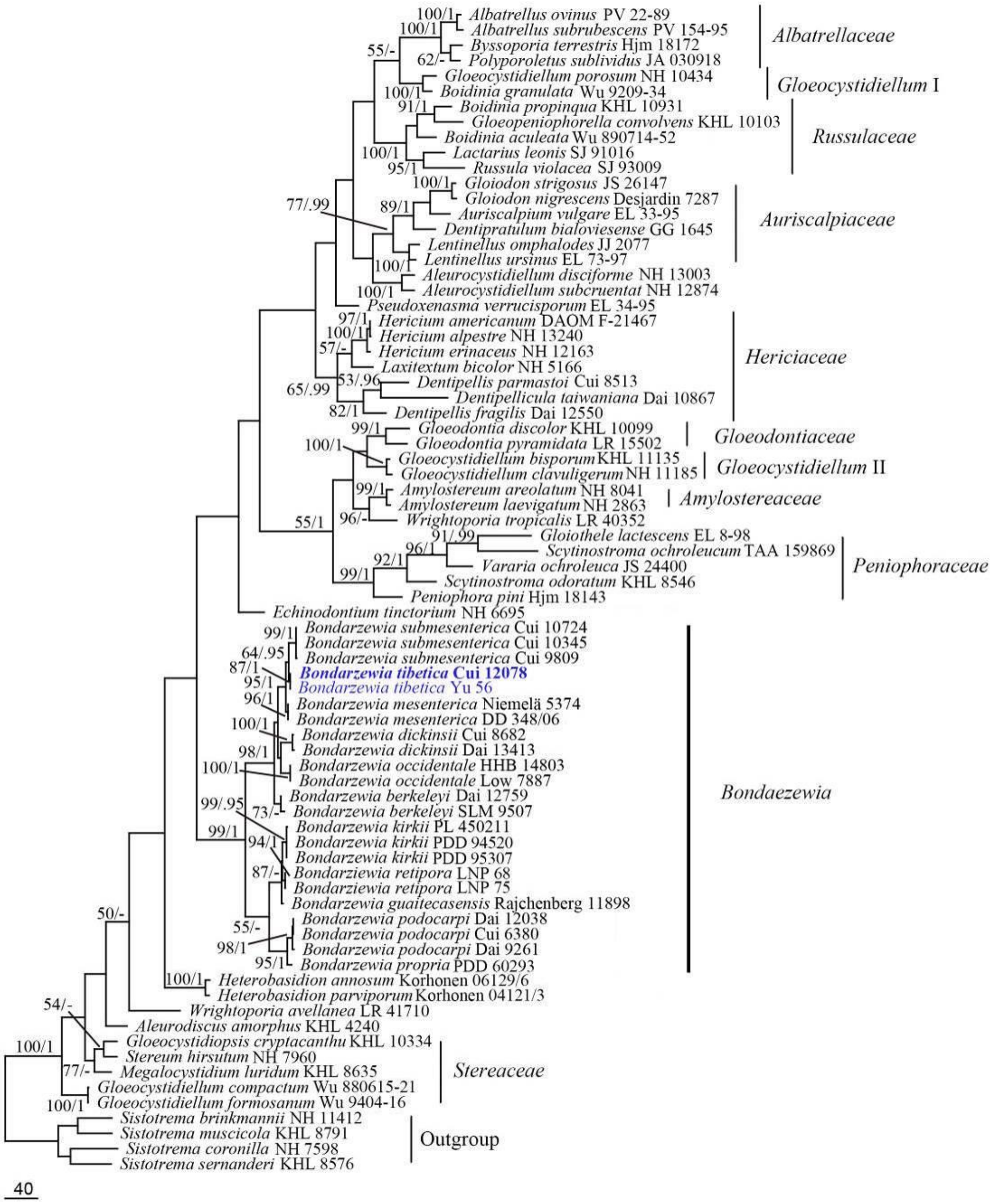


Fig. 136 Phylogeny of species in *Bondarzewia* and related species generated by maximum likelihood based on ITS+nLSU sequence data. Branches are labeled with bootstrap

proportions (before the slash markers) higher than 50% and Bayesian posterior probabilities (after the slash markers) more than 0.95. New taxa are in blue and ex-type specimens in bold.

346. ***Bondarzewia tibetica*** B.K. Cui, J. Song & Jia J. Chen, ***sp. nov.***

MycoBank number: MB 815274, *Facesoffungi number*: FoF 02055, Figs 137, 138

Etymology: tibetica (Lat.), referring to the locality of the type specimen.

Holotype: BJFC 016992

Basidiocarps annual, pileate, broadly attached to the substrate, imbricate, soft corky and watery when fresh, becoming fragile upon drying; *pileus* fan-shaped, projecting up to 16 cm long, 25 cm wide and 2 cm thick; *pileal surface* cream to orange brown when fresh, olivaceous buff to deep olive when dry, azonate, glabrous; *margin* white when fresh, becoming deep olive when dry; *pore surface* white to cream when fresh, becoming cream to buff when dry; *pores* irregular to angular, 1–3 per mm, mostly 1 per mm; *dissepiments* thin, entire to slightly lacerate; *context* white when fresh, up to 0.8 cm thick; *tubes* concolorous with the pore surface, up to 1.2 mm long. *Hyphal system* dimitic; *generative hyphae* simple septate; skeletal hyphae IKI–, CB–; *tissues* unchanged in KOH. *Contextual generative hyphae* seldom, hyaline, thick-walled, simple septate, 4–8 *µm* in diam; *contextual skeletal hyphae* dominant, hyaline, thick-walled with a narrow to wide lumen, rarely branched, flexuous, interwoven, 4–10 *µm* in diam. *Tramal generative hyphae* dominant, hyaline, slightly thick-walled to thick-walled, simple septate and numerous branched, 2–3.5 *µm* in diam; *tramal skeletal hyphae* rarely, hyaline, thick-walled with a narrow to wide lumen, rarely branched, flexuous, interwoven, 2–4 *µm* in diam. *Cystidia* and *cystidioles* absent; *basidia* clavate, with a simple basal septum and four sterigmata, 35–58 × 9–11 *µm*; *basidioles* in shape similar to basidia, but distinctly shorter. *Basidiospores* subglobose, hyaline, thick-walled, with obvious ridges, strongly amyloid, CB+, (5.5–)5.8–7 × 5–6.5(–6.8) *µm*, L = 6.4 *µm*, W = 5.8 *µm*. *Ridges* of spores blunt, up to 1 *µm* long.

Type of rot: White rot.

Material examined: CHINA: Xizang Autonomous Region (Tibet), Milin County, Nanyigou Park, on fallen trunk of *Picea*, 16 Sep 2014, Cui 12078 (**holotype**, BJFC 016992); *ibid*, Linzhi County, Bayi, on fallen trunk of *Picea*, 16 Aug 2004, Yu 56 (**paratype**, IFP 000968); Milin County, Nanyigou Park, on fallen trunk of *Picea*, 16 Sep 2014, Cui 12079 (**paratype**, BJFC 016993).

Notes: *Bondarzewia tibetica* is found on *Picea* in Xizang Autonomous Region of China. It is characterized by its cream to orange brown pileal surface, white to cream pore surface, small pores, a dimitic hyphal system, and large basidiospores with blunt spines. *Bondarzewia dickinsii* (Berk.) Jia J. Chen, B.K. Cui & Y.C. Dai, *B. occidentalis* Jia J. Chen, B.K. Cui & Y.C. Dai and *B. podocarpi* Y.C. Dai & B.K. Cui are morphologically similar to *B. tibetica*; they all produce similar pileal surface and pore surface; however, *B. dickinsii* is different by producing a monomitic hyphal system and sharp basidiospore spines; *B. occidentalis* is separated by its larger basidiospores and pores; *B. podocarpi* is different by producing sharp basidiospore spines (Chen et al. 2016; Dai et al. 2010). Phylogenetically, all species of *Bondarzewia* formed a monophyletic lineage belonging to *Russulales* (Fig. 136).

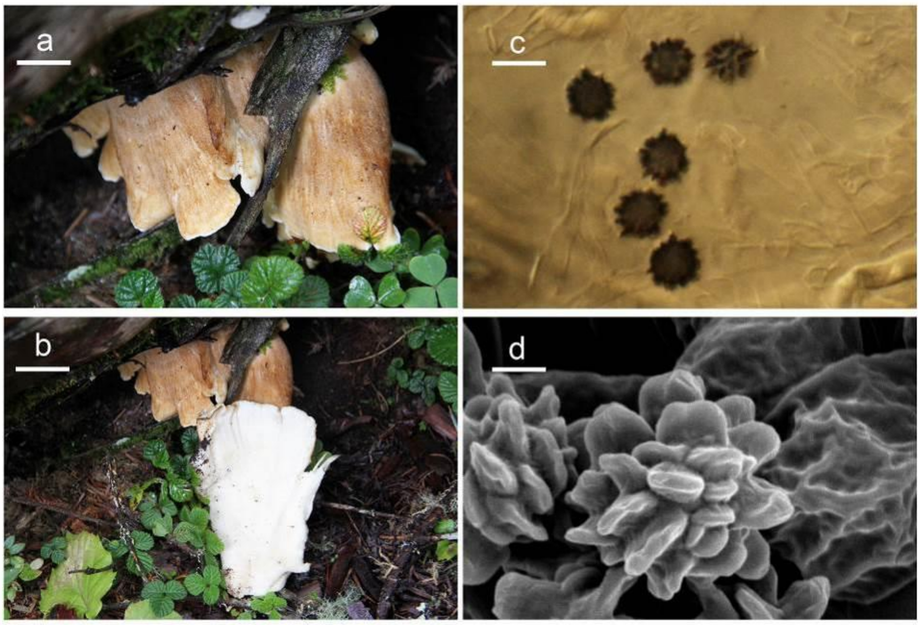


Fig. 137 ***Bondarzewia tibetica*** (**holotypes**) **a, b** Basidiocarps **c, d** Basidiospores. Scale bars: a, b = 1 cm, c = 7 *µm*, d = 2 *µm*.

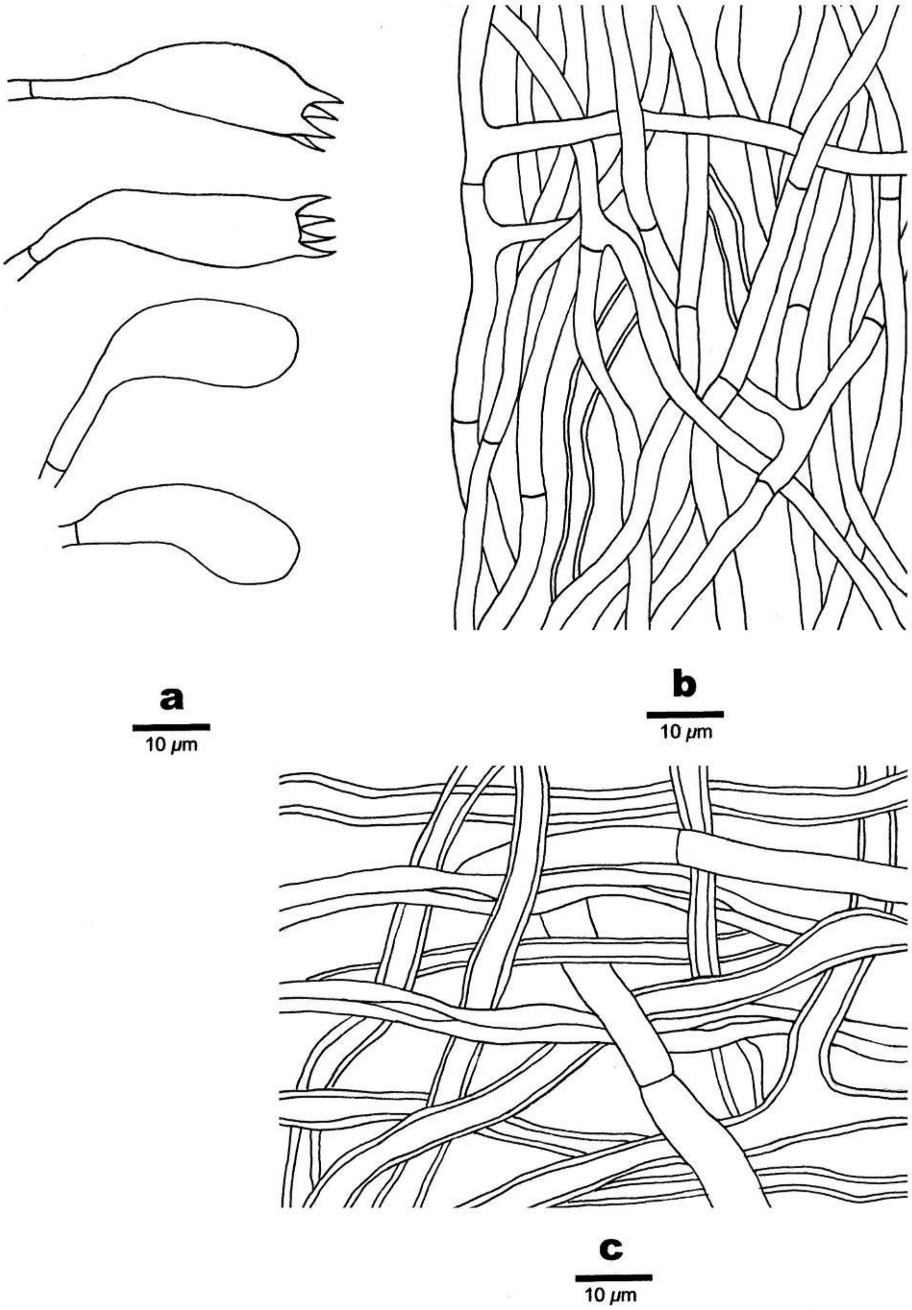


Fig. 138 ***Bondarzewia tibetica*** (**holotype**) **a** Basidia and basidioles **b** Hyphae from trama **c** Hyphae from context. Scale bars: a–c = 10 μm.

Russulaceae

Within the *Russulales* order, members of the *Russulaceae* family display a large diversity in sporophore morphology. Sporophores range from resupinate to agaricoid, pleurotoid or sequestrate types, with hymenophores that can be poroid or lamellate (Miller et al. 2006). The vast majority of the known species are mainly agaricoid and belong to the genera *Lactifluus* (Pers.) Roussel, *Lactarius* Pers., *Multi-furca* Buyck & V. Hofstetter and *Russula* Pers. (Buyck et al. 2008, Buyck et al. 2010). These genera are all ectomycorrhizal and have representatives in Thailand. Next to these genera, the

Russulaceae family also contains three mainly corticoid genera: *Boidinia* Stalpers & Hjortstam, *Gloeopeniophorella* Rick and *Pseudoxenasma* K.H. Larss. & Hjortstam (Larsson and Larsson 2003, Miller et al. 2006).

Lactifluus

The ectomycorrhizal genus *Lactifluus* is the smallest of the two milkcap genera (*Russulaceae*). The genus is mainly distributed in the tropics and is well-represented in Thailand (Le et al. 2007; Stubbe et al. 2010; Van de Putte et al. 2010; De Crop et al. 2014). In a recent study (De Crop et al. subm.), the genus is revised and four subgenera are proposed: *L*. subg. *Lactariopsis*, *L*. subg. *Rugati*, *L*. subg. *Gymnocarpi* and *L*. subg. *Lactifluus*. The two species from Thailand that are presented here belong to *L*. subg. *Lactariopsis* and *L*. subg. *Rugati*. The phylogenetic tree is presented in Fig.139.

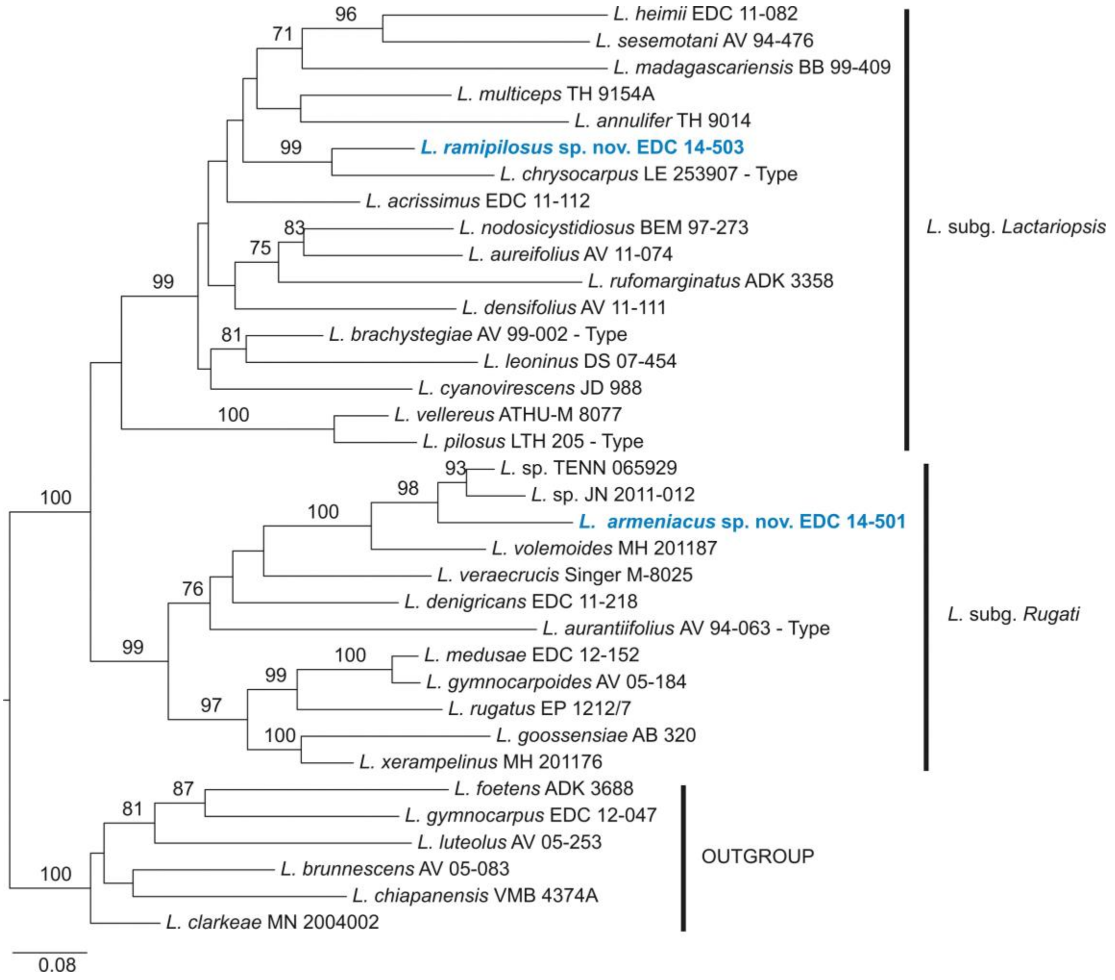


Fig. 139 Maximum likelihood tree of *Lactifluus* subg. *Lactariopsis* and *L*. subg. *Rugati*, based on ITS-LSU sequence data. Maximum likelihood bootstrap values >70 are shown. New taxa are in blue and species for which obtained sequences are based on type material have names in bold.

347. *Lactifluus armeniacus* De Crop & Verbeken, ***sp. nov.***

MycoBank number: MB 815137, *Facesoffungi number*: FoF 02056, Figs 140, 141

Etymology: Referring to the apricot-coloured basidiocarps.

Holotype: MFLU E. De Crop 14–501

Diagnosis: A medium-sized, warm apricot-coloured species which is microscopically characterized by septated lamprocystidia, low ornamented spores and a lampropalisade as pileipellis structure, with small to medium-sized, thick-walled hairs in the suprapellis and a thick layer of sphaerical cells in the subpellis.

Pileus 69–72 mm diam., planoconvex with central depression to slightly infundibuliform; margin sometimes slightly striate, sometimes concentrically wrinkled; edge rather irregular, sometimes crenulate or locally undulate; surface chamois leather-like, locally wrinkled but smooth in the centre, pruinose, bright orange(as 5B5/6, but more yellow), unicolourous. *Lamellae* adnate with decurrent tooth to subdecurrent, distant (2L + 1l / cm – 4L + 3l / cm), bright orange to yellow (4A3 to 4/5A4), very broad, rather thick and brittle, slightly intervenose; edge entire and concolourous. *Stipe* 27–28 × 11–18 mm, cylindrical to slightly tapering downwards, sometimes curved, centrally attached to pileus; surface very soft, pruinose and finely striate, concolourous with pileus (bright orange 5B5/6 with a more yellowish tinge). *Context* solid and quite firm, white, unchanging; taste sweet, mild; smell not distinctive. *Latex* abundant, white, unchanging; taste sweet.

Basidiospores broadly ellipsoid, sometimes subglobose, sometimes ellipsoid, 6.4–7.7–9 × 5.1–6.2–6.7 *µm* (n = 20, Q = 1.11–1.24–1.41); ornamentation amyloid, forming an almost complete reticulum, composed of very low warts connected by fine ridges, up to 0.2 *µm* high; plage inamyloid. *Basidia* 4-spored, sometimes 2-spored, 59–71 × 8–9 *µm*, cylindric to subclavate, with refringent to slightly thickened walls; content guttate to granular. *Pleurolamprocystidia* abundant, slightly emergent up to 17 *µm*, cylindrical, septate, 50–80 × 4–8 *µm*, with slightly thickened walls (<1 *µm*). *Pleuropseudocystidia* very scarce, 7–9 *µm*, cylindrical, mostly collapsed at apex; content granular. *Lamellae-edge* sterile; completely composed of cheilolamprocystidia which are 41–45 × 4–7 *µm*, cylindrical, septate, thick-walled. *Hymenophoral trama* cellular, with abundant lactifers and sphaerocytes. *Pileipellis* a lampropalisade; elements of the suprapellis 28–64 × 3–5 *µm*, cylindrical, obtuse, thick-walled; subpellis 132–174 *µm* thick, sphaerical cells 9–22 *µm* diam., with thickened wall. *Stipitipellis* hymeniderm; elements of the suprapellis 15–26 × 5–11 *µm*, cylindrical to clavate, sometimes with strong congophilous content, thick-walled.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng district, Baan Tapa (22km marker along road 1095), N19°7'45" E98°46'1", alt. 766.8 m, on soil in mixed forest, with *Dipterocarpus* sp., *Castanopsis* sp., *Lithocarpus* sp. and *Quercus* sp., 31 July 2014, E. De Crop 14–501 (**holotype** in MFLU, **isotype** in GENT).

Fig. 140 a *Lactifluus armeniacus* (holotype) b *Lactifluus ramipilosus* (holotype)

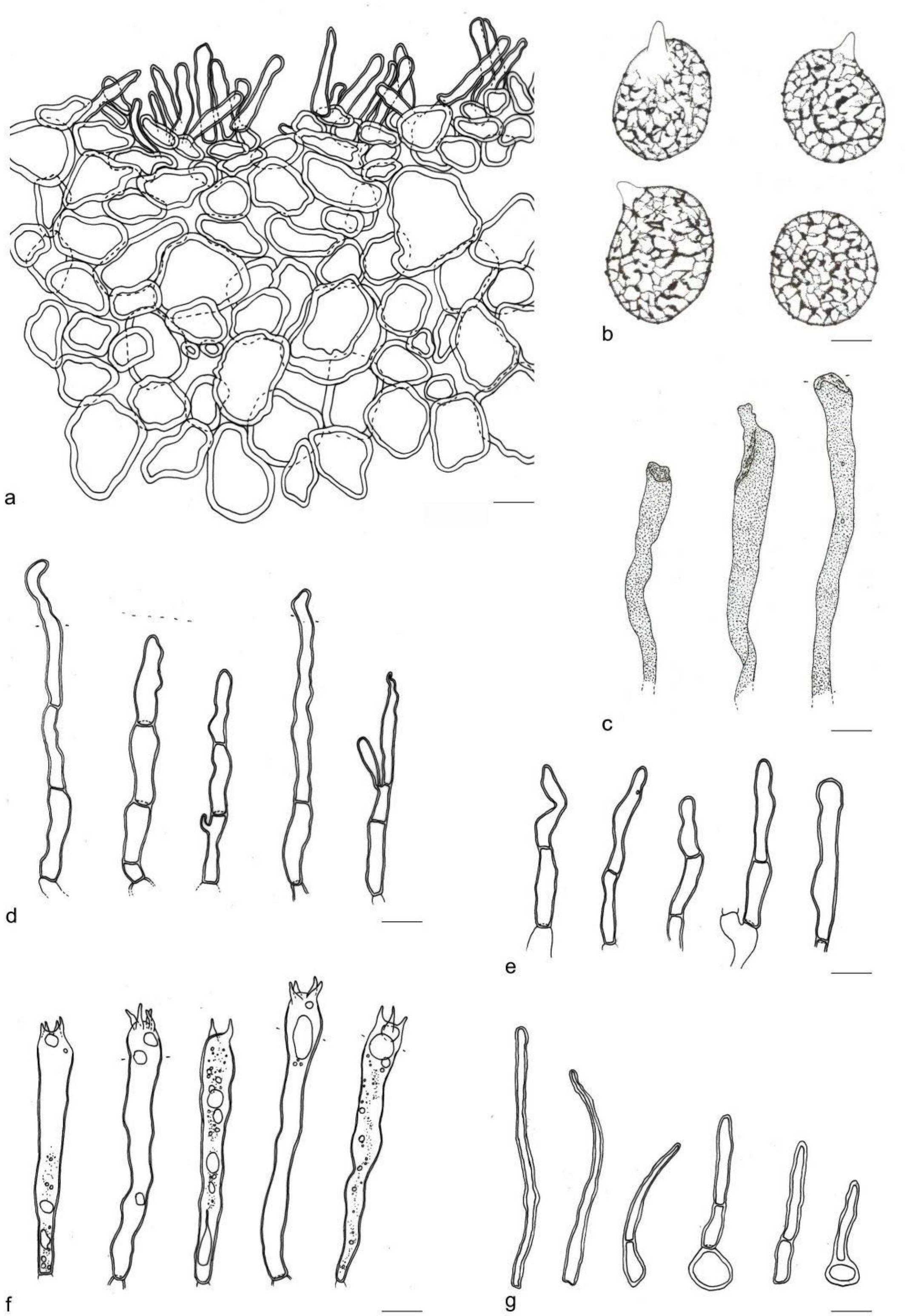


Fig. 141 ***Lactifluus armeniacus*** (**holotype**) **a** Section through pileipellis **b** Basidiospores **c** pleuropseudocystidia **d** Pleurolamprocystidia **e** Marginal cells **f** Bsidia **g** Terminal elements of the pileipellis. Scale bars: a–g = 10 μm.

348. ***Lactifluus ramipilosus*** Verbeken & De Crop, ***sp. nov.***

MycoBank number: MB 815138, *Facesoffungi number*: FoF 02057, Figs 140, 142

Etymology: with branched (rami-) hairs (-pilosus), referring to the striking hairs in the pileipellis structure.

Holotypus: MFLU E. De Crop 14–503

Diagnosis: A medium-sized, warm yellowish orange species which is microscopically characterized by the very lowly and indistinctly ornamented spores, the absence of true cystidia and ramified thick-walled hairs in the pileipellis structure.

Pileus 55 mm diam., convex to planoconvex with undeep depression in the center; surface soft, chamois-leather like and pruinose, almost smooth but slightly irregular, yellowish orange (5A3-4A4); margin entire, straight to slightly deflexed. *Stipe* 25 × 17 mm, strongly tapering downwards; surface pale yellow (4A2), slightly paler towards the lamellae, very finely fibrillose. *Lamellae* broadly adnate to decurrent, up to 4 mm broad, medium thick, brittle, yellow (4A3). *Context* whitish yellow. *Latex* not observed.

Spores 5.6–*7.2*–8.9(9.1) × 5.5–6.2–7.2(7.3) *µm*, Q = 1.03–1.16–1.32, broadly ellipsoid, sometimes subglobose; ornamentation amyloid but very low and weakly developed, composed of low and irregular warts that are often connected by very fine ridges forming a partial reticulum; plage mostly not amyloid, but sometimes with a very weak central amyloid spot. *Basidia* 4-spored, with some rare 2-spored basidia present, 45–55 × 8–10 *µm*, subcylindrical to subclavate, with guttate contents. *True cystidia* absent. *Pleuropseudocystidia* abundant, not emergent to slightly but distinctly abundant, 6–8 *µm* diam., cylindric but often swollen at the apex, with rounded apex, with needle-like to granular content. *Hymenophoral trama* mixed with some hyphae present but especially abundant sphaerocytes of up to 25 *µm* diam., with abundant lactifers. *Subhymenium* cellular. *Lamellar edge* sterile; marginal cells 15–28 × 6–8 *µm*, subclavate to irregular, mostly hyaline, sometimes with refringent walls, sometimes with slightly needle-like content. *Pileipellis* lamprotrichoderm-like, composed of a layer of hyphae with 3-5 *µm* diam., which are mainly horizontally arranged and often terminating in remarkable thick-walled hairs which are pericline to oblique; hairs thick-walled, 35–125 × 3–5 *µm*, often branched, sometimes septate, sometimes tapering near paex, sometimes with rounded apex.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng district, Baan Tapa (22km marker along road 1095), N19°8'0" E98°46'15", alt. 829.6 m, on soil in mixed forest, with *Dipterocarpus* sp., *Castanopsis* sp., *Lithocarpus* sp. and *Quercus* sp., 31 July 2014, E. De Crop 14–503 (**holotype** in MFLU, **isotype** in GENT)

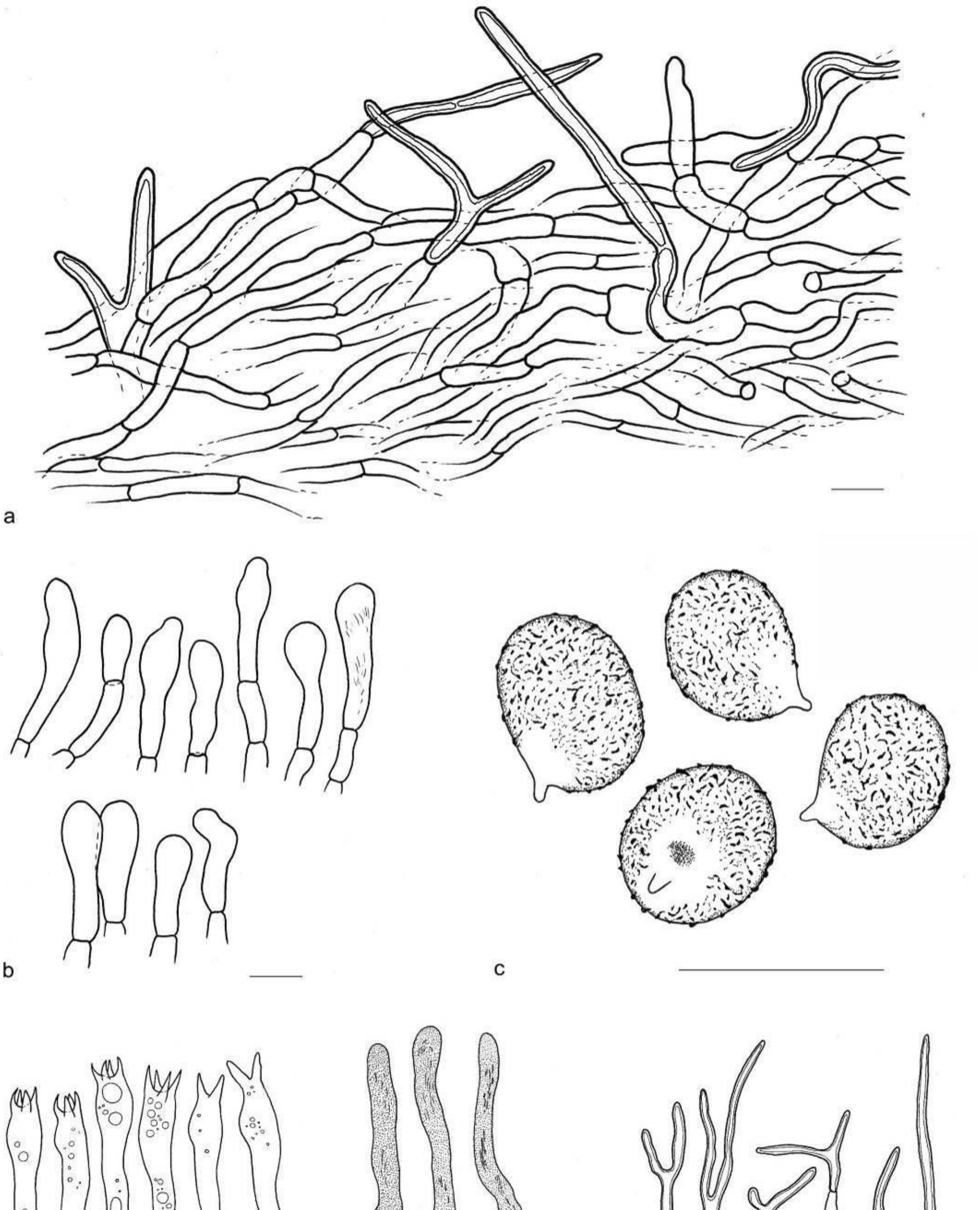


Fig. 142 ***Lactifluus ramipilosus*** (**holotype**) **a** Section through pileipellis **b** Marginal cells **c** Basidiospores **d** Basidia **e** Pleuropseudocystidia **f** Terminal elements of the pileipellis. Scale bars: a–f = 10 *µm*.

Russula

Russula is a genus of high species diversity with a comprehensive wide distribution from frigid to tropical forests (Kundsen and Borgen 1982; Singer 1986; Buyck 1989; Buyck et al. 1996; Miller et al. 2012). *Russula* is evidenced from ITS, nLSU and rpb2 to be a monophyletic genus (Buyck et al. 2008, 2010), but it contains stipitate epigeous, hypogeous, and pleurotoid-formed fruiting bodies (Buyck and Hoyak 1999; Miller et al. 2001; Larsson and Larsson 2003; Lebel and Tonkin 2007). Nine subgenera have been introduced in *Russula* based on morphological characteristics, such as taste of fruiting bodies, colour of spore print, shape of pileipellis hyphal extremities, existence of lamellulae, dermatocystidia and primordial hyphae (Romagnesi 1967, 1985, 1987), and phylogenetic data is needed in classification (Eberhardt 2002; Li and Wen 2009; Li 2014, Li et al. 2015a). A total of 22 *Russula* taxa have been described from China and the adjacent Himalayan Mountain in recent years (Das et al. 2005, 2006a, 2006b, 2010, 2013, 2014; Wang et al. 2009b; Li et al. 2011, 2012, 2013a, 2013b, 2015a, 2015b). Two taxa are newly described from Tibet Plateau based on morphological characters and phylogenetic analyses. The phylogenetic tree for *Russula* is presented in Fig. 143.

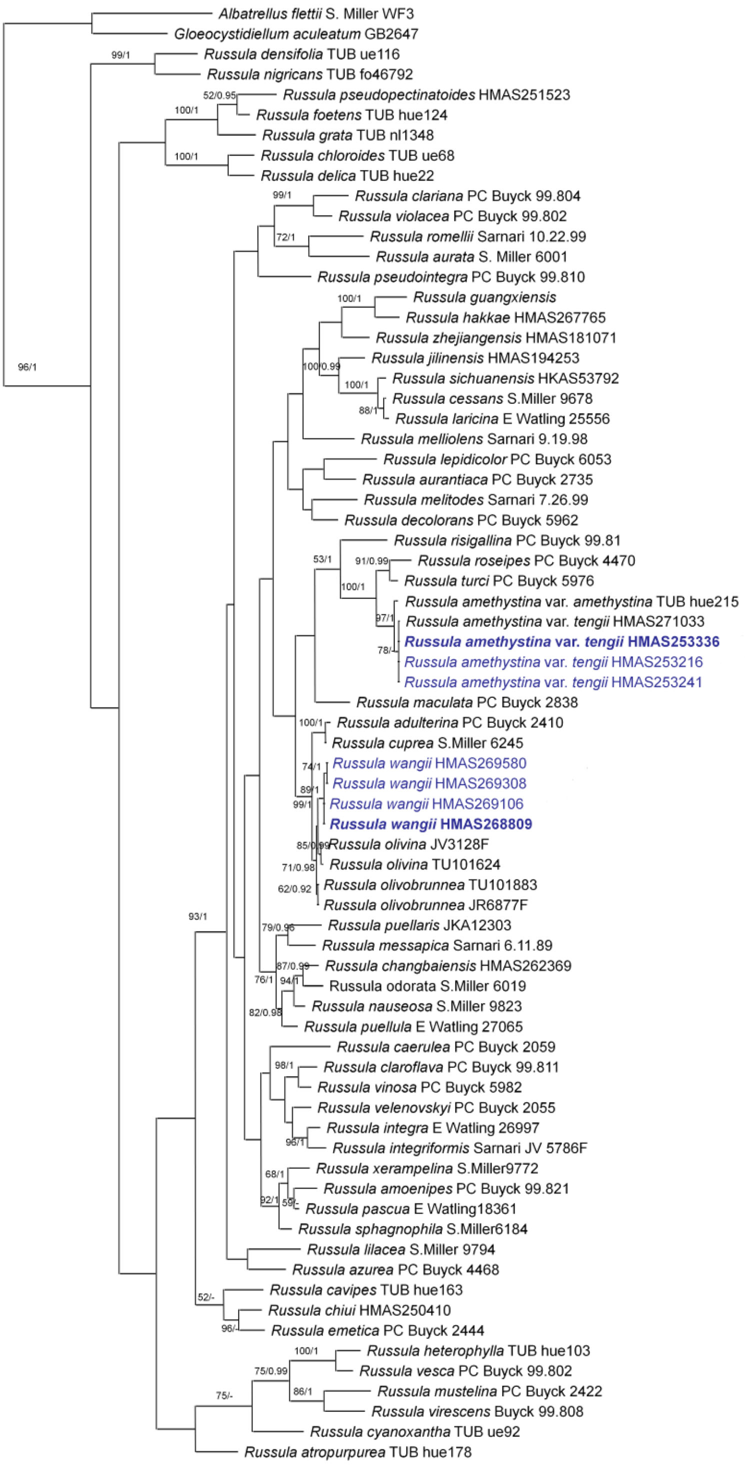


Fig. 143 Phylogram generated from maximum parsimony (PAUP* v.4.01) analysis based on ITS sequence data of *Russula*. Sequences used in this study have been sampled from previous studies to represent the major phylogenetic clades of *Russula* (Eberhardt 2002; Miller and Buyck 2002). Maximum parsimony bootstrap support values above 50% and Bayesian posterior probabilities greater than 0.9 are indicated above or below the nodes (BS/PP), new taxa are shown in blue. Holotype are shown in bold and blue.

349. *Russula amethystina* subsp. *tengii* G.J. Li, H.A. Wen & R.L. Zhao, ***subsp. nov.***

Fungal Names number: FN 570231, *Facesoffungi number*: FoF 02058, Fig. 144.

Etymology: named after Prof. S.C. Teng, in honor of his contribution to the taxonomy of *Russula*.

Holotype: HMAS 253336

Basidiomata small- to medium-sized. *Pileus* 43–52 mm in diam., hemispheric when young, plano-convex, expanding to applanate when mature, rarely center slightly depressed with age, not striate, sometimes cracked, slightly viscid when wet, peeling 1/4–1/3 from the edge, lilac to vinous tinged with intermixed with brown vinous tinged with Brownish Vinaceous (XXXIX5‴b), Light Russet-Vinaceous (XXXIX1‴d) to Haematite Red (XXXIX5″m), reddish tinge of Pompeian Red (XIII3′i) in center, Dark Vinaceous-Brown (XXXIX5‴k) and Vinaceous-Brown (XXXIX5‴i) intermixed with Pale Brownish Drab (XLV5⁗d) towards the margin when dry. *Lamellae* slightly subfree, 2–5 mm in height, 13–16 pieces per cm in the edge, rarely forked near the stipe or in the middle, interveined, with ocherous, yellowish tinged with Light Ochraceous-Salmon (XV13′b), Light Ochraceous-Buff (XV15′d) to Ochraceous-Buff (XV15′b); lamellulae absent. *Stipe* 5.5–6.8 × 0.9–1.5 cm, subcylindrical, surface dry, rugulose longitudinally, dull, without annulus, slightly attenuate upwards, White (LIII), a tinge of Pale Yellow–Orange (III15f) when injured and dry, stuffed first, becoming hollow when old. *Context* up to 1–2 mm at the center of the pileus, White (LIII), fragile, with iodoform Odour; taste mild. *Spore print* Ocher (Romagnesi IIId–IVa).

Basidiospores [100/10/8] 7.4–8.7 (–9.2) × 6.2–7.5 (–8) *µm*, Q = (1.06–) 1.10–1.28 (–1.34), (**Q** = 1.20 ± 0.06), hyaline, mostly broadly ellipsoid, rarely subglobose or ellipsoid; ornamentation cristulate to subreticulate, composed of amyloid warts that linked as small crests and ridges, forming a nearly complete to complete network, rarely intermixed with isolated verrucae, warts 0.5–0.8 *µm* in height; suprahilar area distinctly amyloid. *Basidia* 30–40 × 7–10 *µm*, 4-spored, sterigmata 3–6 *µm* long, hyaline, sometimes yellowish in KOH, subclavate to clavate, rarely cylindrical. *Pleuroystidia* scattered, 55–100 × 8–13 *µm*, distinctly projecting 20–60 *µm* beyond the basidia, subfusoid to subcylindrical, sometimes clavate to subclavate, apex obtuse, thin–walled, contents rare, granular to crystal, weakly gray in sulphovanillin (SV). *Cheilocystidia* not observed; lamellar edge sterile. *Subhymenium* a cellular layer 20–35 *µm* thick composed of inflated cells 7–13 *µm* in diam., hyaline, sometimes pale yellowish in KOH. *Pileipellis* composed of epipellis and subpellis; epipellis a trichoderm 125–150 *µm* thick, composed of thin-walled, cylindrical hyaline hyphae 3–6 *µm* wide; primordial hyphae 4–7 *µm* wide, with heteromorphous-opalescent inclusions and acid-resistant incrustations, septate, clavate to cylindrical, apex obtuse; subpellis a cutis 100–120 *µm* thick, composed of gelatinized, interweaved hyaline hyphae 2–6 *µm* wide, pileocystidia not observed. *Stipitipellis* a cutis, composed of filamentous hyphae 3–6 *µm* in diam., interweaved with inflated cells 10–15 *µm* in diam., hyaline, some hyphae pale yellow in KOH; caulocystidia absent. *Clamp connections and lacticiferous hyphae* absent from all tissues.

Habit and habitat. Single or small groups in coniferous forest (dominated by e.g. *Pinus densata* var. *pygmaea, P. yunnanensis, Picea likiangensis* var. *likiangensis* and *P. likiangensis* var. *linzhiensis*) at 2000–3500 m altitude. *Distribution*. China (Xizang and Yunnan). *Season*. July and August.

Material examined: CHINA, Yunnan Province, Lijiang City, Yulong County, Lijiang Alpine Botanic Garden, N27°05' E100°10', elevation 3447 m., 17 July 2014, collector Guojie Li and Yaning Wang, 14252 (HMAS 253336, **holotype**); *Ibid*., elevation 3258 m., collector Guojie Li and Yun Yu, 14075 (HMAS 271033); *Ibid*., elevation 3471 m., collector Guojie Li and Mingjun Zhao, 14188 (HMAS 271034); *Ibid*., elevation 3274 m., collector Guojie Li and Shuhua Jiang, 14088 (HMAS 271161); *Ibid*., collector Guojie Li and Yunlong Li, 14187 (HMAS 271048); Chuxiong City, Nanhua County, Zixishan Forest Park, N25°01' E101°32', elevation 2134 m., 20 August 2013, collector Weilai Lu, Tiezheng Wei and Zhenping Yang, 354 (HMAS 252864); Xizang Autonomous Region, Nyingchi Prefecture, Mainling County, roadside of National Road 318 to Nang County, N29°12' E94°11', elevation 2994 m., 12 August 2013, collector Tiezheng Wei, Xiaoyong Liu, Jianyun Zhuang and Tian zhou Li, 3701 (HMAS 253216); *Ibid*., 3698 (HMAS 253241).

Notes: The combination of a violet-tinged pileus without olive green, bluish gray or entirely yellow tinges, deep yellow spore print, pileipellis with primordial hyphae, absence of pileocystidia, and coniferous habitat assign this taxon into *Russula amethystina* Quél. of *Russula* subgenus *Incrustatula* Romagn, *Russula* section *Amethystinae* Romagn. (Romagnesi 1987). The phylogenetic result (Fig. 143) also supports the placement (BS 97% and PP 1.00). These suggest *R. amethystina* subsp. *tengii* is very closely related to *R. amethystina* subsp. *amethystina*, which however, has easily distinguishable higher basidiospore ornamentation composed of mostly isolated. (Romagnesi 1967; Sarnari 2005; Kränzlin 2005). Because the basidiospore of *R. amethystina* subsp. *tengii* is almost the same as that of *R. turci* Bres., the morphological distinction between the two closely related species is becoming blurred. Yet it is clear in the distinction among *R. amethystina*, *R. turci*, and *R. roseipes* Secr. ex Bres. phylogenetic analyses. The high phylogenetic BS/PP values and the only obvious morphological difference effectively supported that *R. amethystina* subsp. *tengii* is a subspecies of *R. amethystine* (Fig. 143).

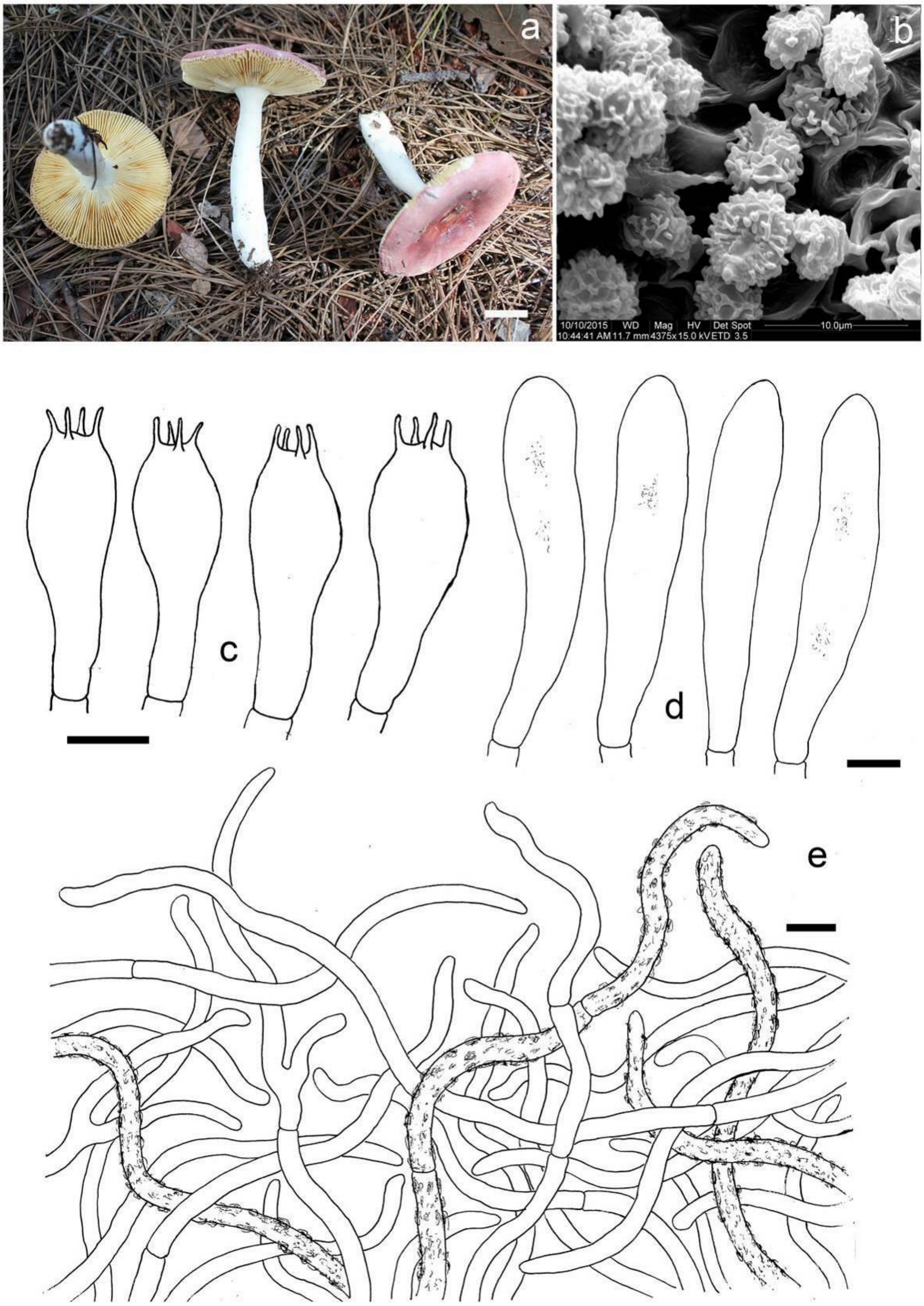


Fig. 144 Basidiocarps and microcharacters of ***Russula amethystina* subsp. *tengii*** (**holotype**) **a** Basidiocarps **b** Basidiospores **c** Basidia **d** Pleurocystidia **e** Epipellis. Scale bars: a = 1 cm, b–e = 10 *μm*.

350. *Russula wangii* G.J. Li, H.A. Wen & R.L. Zhao, ***sp. nov.***

Fungal Names number: FN 570232, *Facesoffungi number*: FoF 02059, Fig. 145.

Etymology: named after Prof. Y.C. Wang, in honor of his contribution to the study of fungi from China.

Holotype: HMAS 268809

Basidiomata small- to medium-sized. *Pileus* 38–56 mm in diam., hemispheric when young, plano-convex, expanding to applanate when mature, rarely center slightly depressed with age, not striate, sometimes cracked, viscid when wet, peeling 1/3–1/2 from the edge, brownish vinous to violet tinged with Pecan Brown (XXXVIII11″i) to Cacao Brown (XXXVIII9″i), intermixed with darker tinge of Walnut Brown (XXXVIII9″k) to Rood's Brown (XXXVIII11″k) in center, sometimes completely Dark Bull Bluish Violet (X57m), Prussian Red (XXVII5″k) and Dark Indian Red (XXVII3″m) intermixed with Deep Cortinthian Red (XXVII3″i) towards the margin when dry. *Lamellae* slightly subfree, 2–5 mm in height, 13–17 pieces per cm in the edge, not forked, interveined, with ocherous, yellowish tinged with Salmon Buff (XIV11′d), Salmon Colour (XIV9′d) to Apricot Buff (XIV11′b); lamellulae absent. *Stipe* 4.4–6.5 × 0.8–1.7 cm, subcylindrical, surface dry, rugulose longitudinally, dull, without annulus, slightly attenuate upwards, White (LIII), a tinge of Pale Yellow–Orange (III15f) when injured and dry, stuffed first, becoming hollow when old. *Context* up to 3 mm at the center of the pileus, White (LIII), fragile, no distinct Odour; taste acrid. *Spore print* Yellow (Romagnesi IVd–IVe).

Basidiospores [100/10/7] (6.3–) 6.8–8.2 × 7–8 (–8.5) *µm*, Q = (1.06–) 1.13–1.30 (–1.34), (**Q** = 1.38 ± 0.06), hyaline, broadly ellipsoid to ellipsoid, rarely subglobose; ornamentation cristulate to subreticulate, composed of amyloid warts that linked as small crests and ridges, forming a nearly complete network, often intermixed with isolated verrucae, warts 0.5–1 *µm* in height; suprahilar area amyloid. *Basidia* 30–40 × 8–10 *µm*, mostly with four sterigmata 4–7 *µm* long, hyaline, sometimes yellowish in KOH, subclavate to clavate, rarely cylindrical. *Pleuroystidia* scattered, 60–80 × 8–13 *µm*, projecting 20–55 *µm* beyond the basidia, subfusoid to subcylindrical, sometimes clavate to subclavate, apex obtuse, often with a moniliformto papillate appendage, thin–walled, contents granular to crystal, blackish gray in SV. *Cheilocystidia* not observed; lamellar edge sterile. *Subhymenium* a cellular layer 20–35 *µm* thick composed of inflated cells 7–13 *µm* in diam., hyaline, sometimes pale yellowish in KOH. *Pileipellis* composed of epipellis and subpellis; epipellis a trichoderm 125–150 *µm* thick, composed of thin-walled, diverticulate, cylindrical hyaline hyphae 3–6 *µm* wide; pileocystidia 6–8 *µm* wide with refractive contents blackened in SV, abundant, septate, diverticulate, clavate to cylindrical, apex obtuse, sometimes inflated; subpellis a cutis 100–150 *µm* thick, composed of gelatinized, interweaved hyaline hyphae 2–6 *µm* wide. *Stipitipellis* a cutis, composed of filamentous hyphae 3–5 *µm* in diam., interweaved with inflated cells 15–25 *µm* in diam., hyaline, some hyphae yellowish to pale ocher in KOH; caulocystidia absent. *Clamp connections and lacticiferous hyphae* absent from all tissues.

Habit and habitat. Single or scattered in coniferous forest (dominated by e.g. *Pinus densata* var. *pygmaea*, *P. yunnanensis, Picea purpurea* and *P. likiangensis* var.

balfouriana) at 3000–4000 m altitude. *Distribution*. China (Qinghai and Sichuan). *Season*. July and August.

Material examined: CHINA, Sichuan Province, Garzê Autonomous Prefecture, Dawo County, Geka Township, Geka Village, N30°59' E101°08', elevation 3471 m., 12 August 2013, collector Weilai Lu, Lan Jiang and Guojie Li, 13279 (HMAS 268809, **holotype**); *Ibid*., 13278 (HMAS 268808); Zamtang County, N32°19' E100°59', elevation 3930 m., 28 July 2013, collector Binbin Li, Xiaoying Li and Ruiheng Yang, 180 (HMAS 269580); Ngawa Tibetan Qiang Autonomous Prefecture, Ngawa County, N32°53' E101°42', elevation 3457 m., 24 July 2013, collector Binbin Li, Xiaoying Li and Ruiheng Yang, 48 (HMAS 269308); Qinghai Province, Golog Autonomous Prefecture, Baima County, Hongjungou, N32°57' E100°42', elevation 3516 m., 26 July 2013, collector Binbin Li, Xiaoying Li and Ruiheng Yang, 197-1 (HMAS 269106); *Ibid*., 243 (HMAS 269398); *Ibid*., 383 (HMAS 269143).

Notes: The violet tinged pileus, acrid tasted context, yellow spore print, sulphoaldehyde sensitive pileocystidia, diverticulate epicutis hyphal ends and pileocystidia clearly place *R. wangii* within *Russula* section *Urentinae* Maire ss. str. of *Russula* subgenus *Insidiosula* Romagn. Ten species, *R. adulterina* Secr., *R. cristata* Romagn., *R. cuprea* J.E. Lange, *R. cupreoaffinis* Sarnari, *R. cupreola* Sarnari, *R. firmula* Jul. Schäff., *R. gigasperma* Romagn. ex Romagn., *R. juniperina* Ubaldi, *R. subcristulata* Romagn., *R. transiens* (Singer) Romagn. and *R. urens* Romell, have been recognized in *Russula* section *Urentinae*. *Russula adulterina* differs in larger basidospores 7.5–12 × 7–9.5 *µm* with higher ornamentations composed of isolated warts up to 1.6–2 *µm*, and non-diverticulate pileocystidia (Romagnesi 1967). *Russula cristata* can be distinguished from *R. wangii* in brownish grey staining context, lower basidiospore ornamentations up to 0.75 *µm*, nonseptate and non-diverticulate pileocystidia (Romagnesi 1967). *Russula cuprea* discriminates from *R. wangii* in larger basidospores 8.5–12 × 6.7–8.5 *µm* with higher ornamentations composed of isolated warts up to 1.5 *µm* (Romagnesi 1967; Sarnari 1998). *Russula cupreoaffinis* differs in larger basidiospores variable pileus colors, larger basidiospores 7.7–10 × 6.2–7.4 *µm*, and habitat of broad-leaved forest dominated by *Quercus* spp. (Sarnari 1998). *Russula cupreola* can be distinguished from *R. wangii* in longer and wider basidia 42–64 × 10.5–14 *µm*, longer and wider pleurocystidia 60–100 × 9–16 *µm*, and habitat of alpine dwarf shrubs associated with *Salix herbacea* and *S. reticulata* (Sarnari 1998). *Russula firmula* discriminate from *R. wangii* in larger basidospores 8–10.5 × 6.8–8.4 *µm* with ornamentations composed of mostly isolated warts, and non-diverticulate pileocystidia (Romagnesi 1967; Sarnari 1998). *Russula gigasperma* is different from *R. wangii* in larger basidospores 10–12 × 8–10 *µm* with higher ornamentations composed of isolated warts up to 1.4 *µm*, and habitat of hardwood forest (Romagnesi 1967; Sarnari 1998). *Russula juniperina* discriminates from *R. wangii* in brightly red pileus, larger basidiospores 8–11 × 7.2–9 *µm*, and habitat of broad-leaved forest dominated by *Quercus ilex* or *Q. pubescens* (Sarnari 1998). *Russula subcristulata* can be distinguished from *R. wangii* in in longer basidia 42–57 × 9–12 *µm*, longer and wider pleurocystidia 65–105 × 10–15.7 *µm*, nonseptate and non-diverticulate pileocystidia (Romagnesi 1967). *Russula transiens* differs in larger basidiospores 7.5–10 × 6.7–10 *µm* with ornamentations up to 1.25 *µm*, and non-diverticulate pileocystidia (Romagnesi 1967; Sarnari 1998). *Russula urens* discriminate from *R*. *wangii* in large green to yellowish green tinged pileus up to 12 cm with strongly tuberculate-striated margin (Sarnari 1998). *Russula olivina* Ruots. & Vauras from *Russula* section *Laricinae* Romagn. of *Russula* subgenus *Tenellula* Romagn. and *R*. *olivobrunnea* Ruots. & Vauras from *Russula* section *Integroidinae* Romagn. of *Russula* subgenus *Polychromidia* Romagn., cluster together with *R*. *wangii* by support of BS 71% and PP 0.98 in phylogenetic tree. However, *R*. *olivina* differs in larger basidospores 9–11.2 × 7.2–9.5 *µm* with higher ornamentations composed of isolated warts up to 1.5 *µm*, longer and wider basidia 37–71 × 13–20 *µm*, and longer and wider pleurocystidia 65–105 × 10–19 *µm*. *Russula olivobrunnea* can be distinguished from *R*. *wangii* in larger basidospores 9–12.8 × 7.4–10.4 *µm* with higher ornamentations composed of isolated warts up to 1.6 *µm*, longer and wider basidia 37–58 × 9–15 *µm*, and longer, wider pleurocystidia 45–98 × 9–15.5 *µm*, and non-diverticulate pileocystidia (Sarnari 2005).

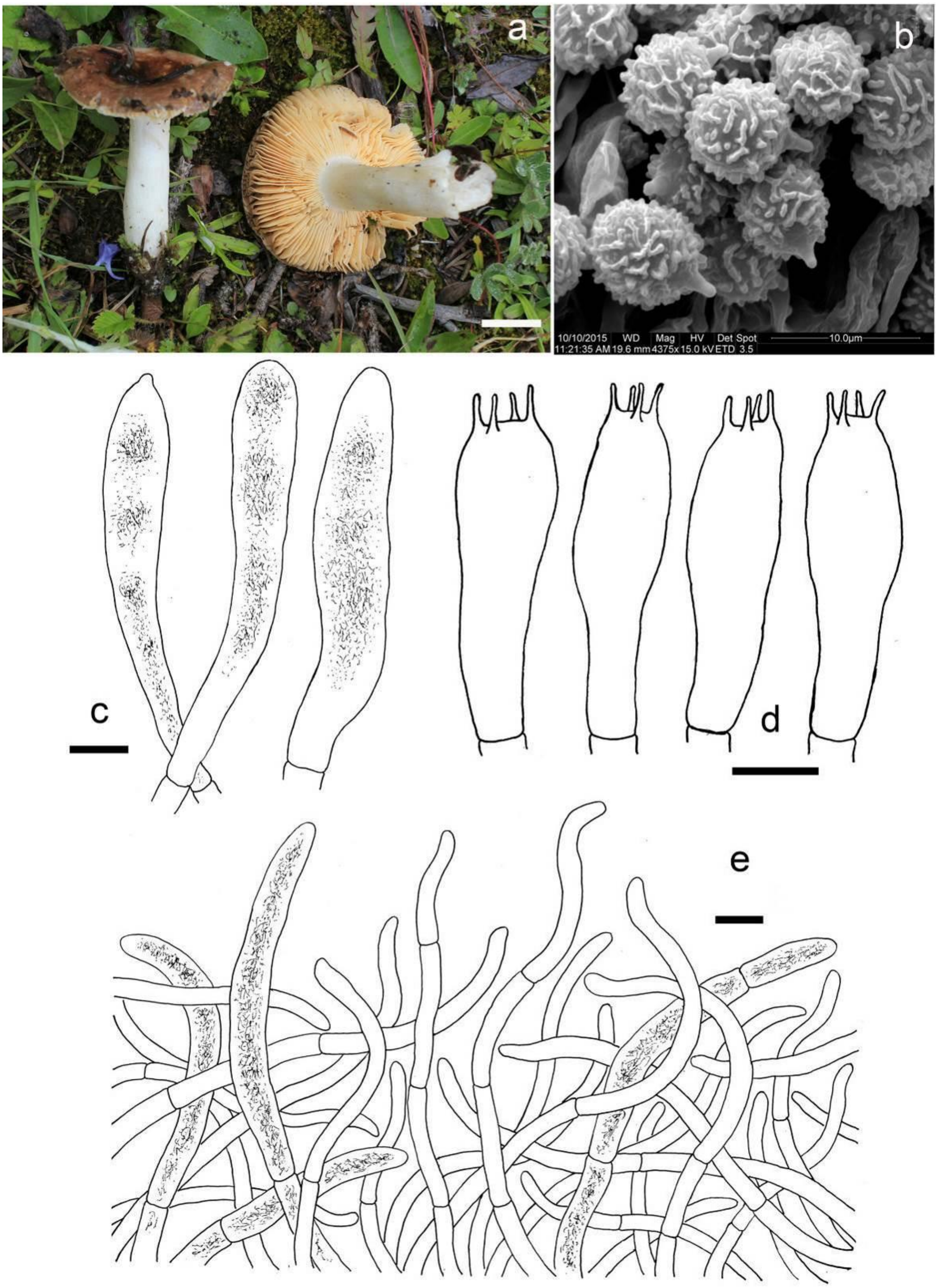


Fig. 145 Basidiocarps and microcharacters of ***Russula wangii*** (**holotype**) **a** Basidiocarps **b** Basidiospores **c** Pleurocystidia **d** Basidia **e** Epipellis. Scale bars: a = 1 cm, b–e =10 μm.

Contributions to *Neocallimastigomycota*

Neocallimastigales

Neocallimastigaceae

Neocallimastigomycota or anaerobic fungi represent a special group of microorganisms inhabiting the digestive tract ecosystem of large mammalian herbivores, including ruminants and non-ruminants. Anaerobic fungi release a broad range of polysaccharide-degrading enzymes that, to date, are among the most effective reported for the breakdown of plant material. Their active role in the degradation of plant structural material has simulated considerable worldwide interest both in terms of their place in fungal evolution and in their potential for industrial exploitation. The phylogeny of the *Neocallimastigomycota* is illustrated in Figs 146, 147.

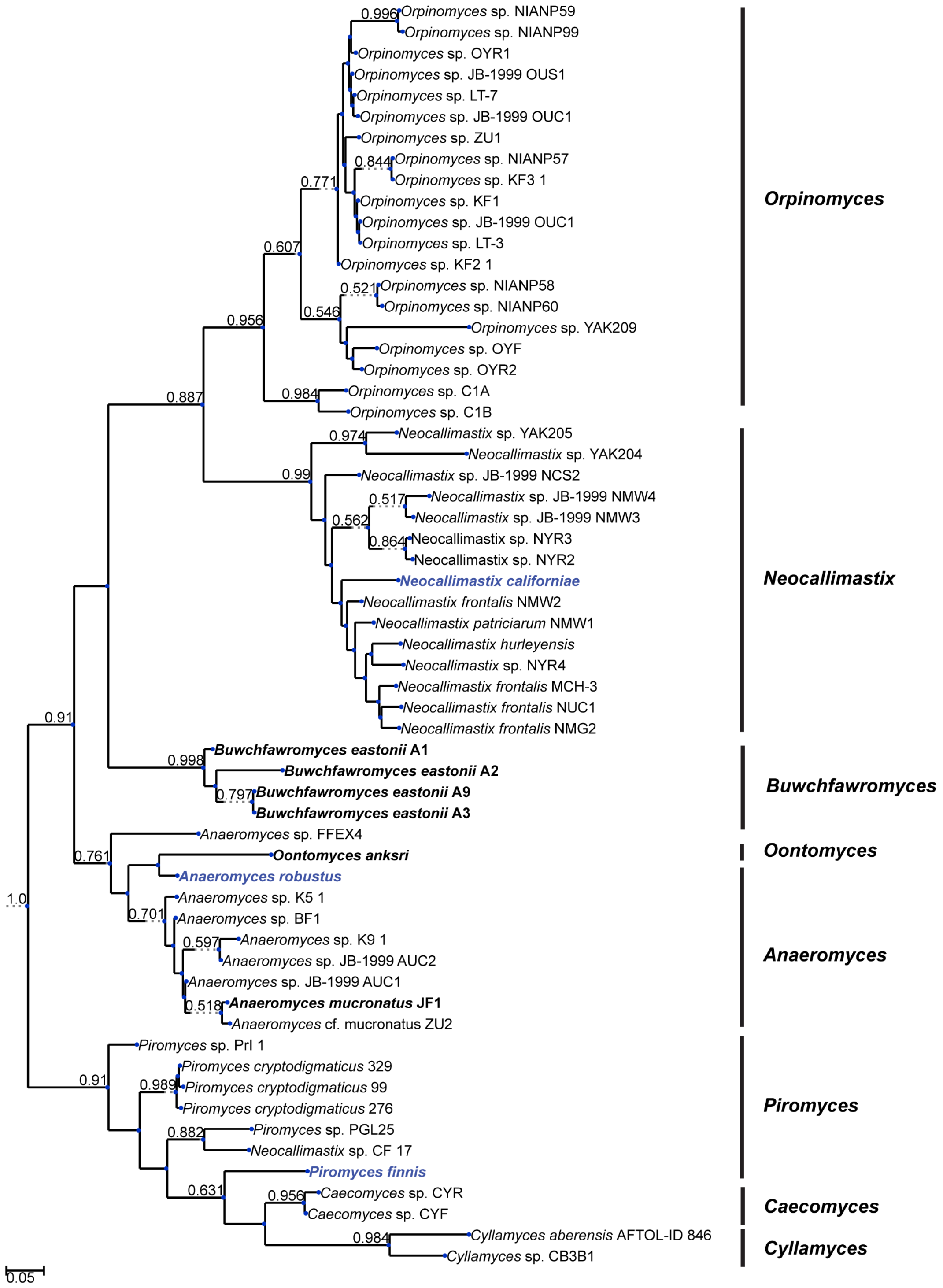


Fig. 146 Molecular phylogeny generated by maximum likelihood analysis of ITS1 sequence data from the *Neocallimastigomycota*. Representative species from all known eight genera (indicated) are shown. Bootstrap values above 50% are indicated above each branch. Ex-types (reference strains) are bolded and new isolates are indicated in blue.

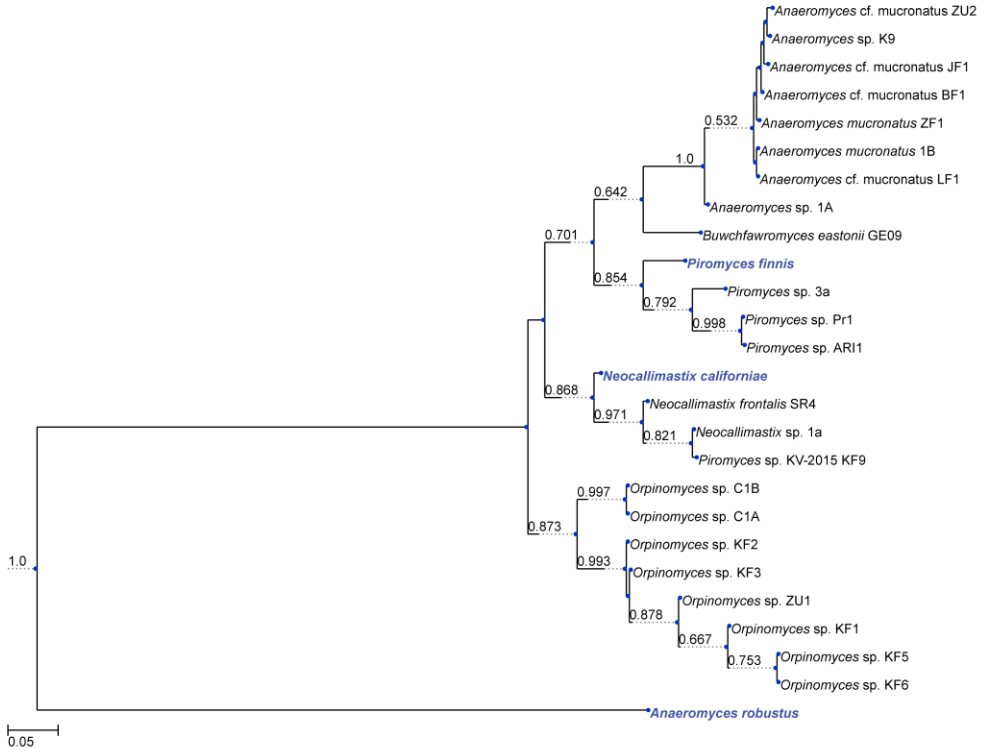


Fig. 147 Molecular phylogeny generated by maximum likelihood analysis of partial large subunit (28S) ribosomal DNA sequence data from the *Neocallimastigomycota*. Bootstrap values above 50% are indicated above each branch. New isolates are indicated in with a filled shape.

Anaeromyces Breton et al.

The genus *Anaeromyces* was described using morphological characteristics by Breton *et al*. (1991). Following isolation of *Anaeromyces mucronatus* from the rumen of a cow. The type culture, *Anaeromyces mucronatus* (NR_111156.1) was obtained from faeces of an American bison by Fliegerova *et al*. (2004). This group isolated a number of different polycentric fungi belonging to the genera *Orpinomyces* and *Anaeromyces*. These two genera are morphologically very similar, but Fliegerová et al. (2004) used molecular methods (analysis of ITS1 fragments) in addition to morphology to distinguish between them. From a descriptive perspective, the genus *Anaeromyces* contains species of strictly anaerobic fungi, which are characterized by a polycentric thallus, a polynuclear rhizomycelium of extensively branched hyphae, zoosporangia that are sometimes mucronate with an acuminate apex and uniflagellated zoospores. The rhizomycelium contains hyphae that can be tubular and uniform or very wide, sometimes with constrictions. Sporangia can develop intercalary as swellings in hypha or on sporangiophores. Some cultures fail to produce mature sporangia and zoospores are rarely seen making classification by molecular means the only sure way of assigning them to the genus.

351. ***Anaeromyces robustus*** O'Malley, Theodorou & Henske, ***sp. nov.***

Index Fungorum number: IF 551676, *Facesoffungi number*: FoF 02060, Fig. 148

Etymology: The specific epithet refers to the physical similarities between some fungal zoosporangia and the tails of gray whales (*Eschrichtius robustus*) that travel the Californian coast near where the fungus was isolated.

Holotype: *Anaeromyces* sp. S4 (O'Malley Lab, University of California, Santa Barbara, NCBI Taxon ID: 1642509), JMRC:SF:12178.

An obligate anaerobic fungus isolated from the feces of a sheep (*Ovisaries*) at the Santa Barabara Zoo (www.sbzoo.org) in 2013. The species is polycentric, producing many zoosporangia per fungal thallus and therefore has an indeterminate (infinite) life cycle. The fungus exhibits exogenous zoosporangial development (i.e., the encysted zoospore does not retain the nucleus, which can migrate and by mitosis populate the developing zoosporangium and the rhizomycelium). The zoosporangia are typically club-shaped (≥ 50 *μm* long × 30 *μm* wide at their widest point). Occasionally they fuse to form a shape like a whale's tail. Upon maturity, each zoosporangium can liberate ≥ 60 zoospores. The rhizomycelium does contain nuclei (as seen under DAPI staining) and is highly branched and tapering. The zoosporangium is typically attached to the rhizomycelium via one or several main rhizoids and is capable of vegetative reproduction by fragmentation. Free swimming zoospores are typically sphearical (ca. 10 *μm* diam.) and the species is characterized by the presence of several posteriorly directed flagella that are in length up to 3–fold the diam. of the zoospore. When swimming the flagella beat together as if they were a single flagellum and thus propel the zoospore forward in a spiral or helical motion.

The reference culture is maintained by continual passage at the University of California, Santa Barbara (S4, JMRC:SF:12178, **holotype**), and under cryopreservation in repositories at the O'Malley Lab, University of California, Santa Barbara, and University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany (Jena Microbial Resource Collection JMRC: SF: 012178 – **ex-type**). Fixed glutaraldehyde preparations are also kept by the O'Malley Lab.

The internal transcribed spacer regions of the ribosomal RNA were amplified with primers JB206/JB205 (Tuckwell et al. 2005). Phylogenetic analysis of the ITS1 regions of several cultured anaerobic fungal specimens spanning all 8 known genera, firmly place S4 within *Anaeromyces* as a distinct, previously unclassified species comparable in age to the type culture *A. mucronatus* JF1 (Fig. 146). The partial 28s rRNA sequence of *A. robustus*, however, appears as a unique outgroup, perhaps due to its incompleteness (Fig. 147). The ~72 Mbp genome has been sequenced by the US Department of Energy's Joint Genome Institute (JGI). The genome will be made available at Mycocosm in 2016 (http://genome.jgi.doe.gov/Anasp1/Anasp1.home.html) and aid in the discovery of novel biomass degrading enzymes that may be engineered or heterologously expressed for the production of lignocellulosic biofuels and other value added chemicals. Furthermore, the genome will enable future –OMICs based characterization of these organisms, including insight into their unique organelles and biomass-degrading enzyme complexes.

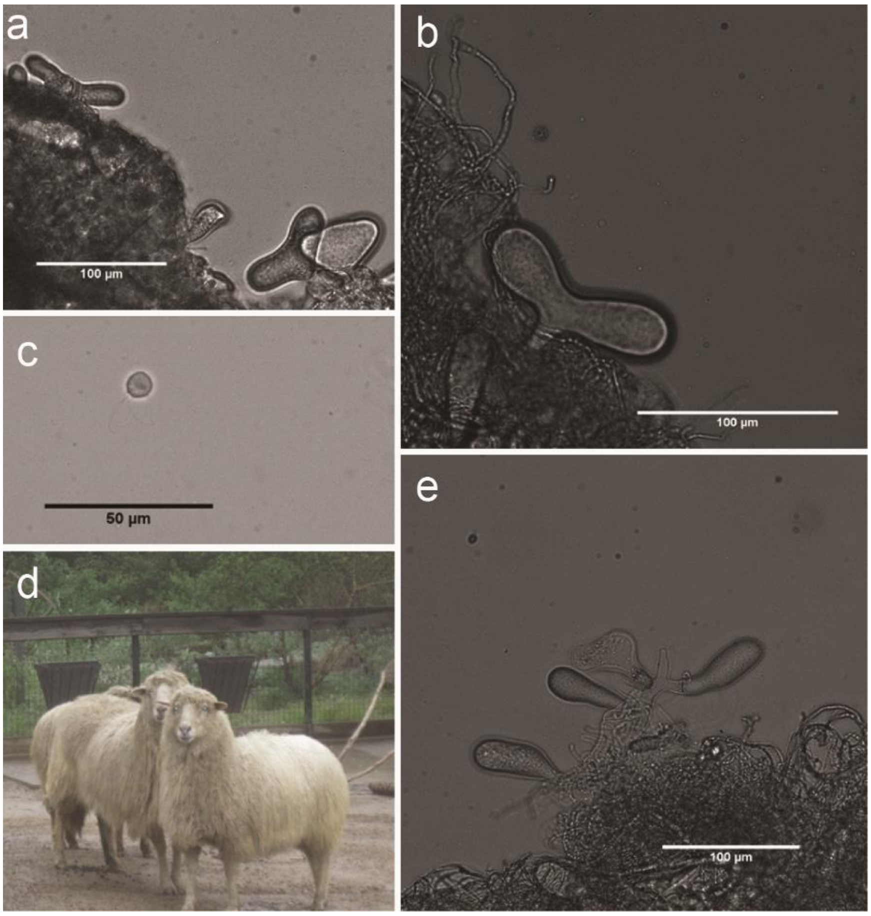


Fig. 148 ***Aneromyces robustus*** (**holotype**) **a** Multiple sporangia of *A. robustus* displaying a range of morphologies **b** A whale-tale shaped sporangia, which inspired the name of this species, with a single zoospore **c** A zoospore with multiple flagella visible **d** Navajo-Churro sheep host from which the species was isolated **e** Multiple sporangia demonstrating club-like morphology, with several sharing the same mycelial structure.

Neocallimastix Vávra & Joyon ex I.B. Heath

The genus *Neocallimastix* was described by Vavra and Joyon (1912). At that time, the propensity for nutritional microbiologists to work with rumen fluid and discard rumen solids meant that the solids-associated vegetative stage of the fungus was not recognized. The zoospores of the fungus evident in rumen fluid were therefore mistakenly identified as polyflagellated protozoans. The correct identification of these zoospores by Orpin's pioneering studies showed that the 'flagellates' were liberated from a benthic, vegetative stage of a 'chytrid-like' fungus (Orpin 1975). Soon after his initial observations, chitin was identified in the fungal cell walls and by 1989 a new classification had emerged to accommodate these obligately anaerobic (oxygen intolerant) fungi (Orpin 1977a, b; Barr 1989). Anaerobic fungi from this genera are among the most studied of all the anaerobic fungi. Numerous isolates have been obtained and at least three species, *N. frontalis*, *N. patriciarum* and *N. hurleyensis* have been classified (Heath et al. 1983; Orpin and Munn 1986; Webb and Theodorou 1991). The original classification of these species used classical taxonomy whereby morphological characteristics were used to identify the genus and zoospore ultrastructure was used for the species recognition. Brookman *et al*. (2000) under took a molecular characterization of the gut fungi based on ribosomal ITS1 and 18S rRNA. Their analysis revealed that *N. hurleyensis* and *N. frontalis* were very similar, but that they differed from *N. patriciarum*. From a morphological perspective the genus *Neocallimastix* contains species of strictly anaerobic fungi characterized by a monocentricthallus, which consists of a network of branched, tapering rhizoids devoid of nuclei. The zoosporangia are variable, often oval or sphaerical in shape supported on a sporangiophore developed from one or more main rhizoids. As the life cycle of a monocentric fungus is determinate (finite), each thallus (the rhizoidal network) supports just one zoosporangium. Zoospores are uninucleate, and either monoflagellated or often polyflagellated.

352. ***Neocallimastix californiae*** O'Malley, Theodorou & Solomon, ***sp. nov.***

Index Fungorum number: IF 551675, *Facesoffungi number*: FoF 02061, Fig. 149

Etymology: The specific epithet refers to the state of California where the fungus was isolated.

Holotype: *Neocallimastix* sp. G1 (O'Malley Lab, University of California, Santa Barbara, NCBI Taxon ID: 1550276), JMRC:SF:12176.

An obligate anaerobic fungus isolated from the feaces of a goat (*Capra aegagrushircus*) housed at the Santa Barbara Zoo (www.sbzoo.org) in 2013. The species is monocentric and has a determinate (finite) life cycle. The fungus exhibits endogenous zoosporangial development (i.e., the encysted zoospore retains the nucleus). The encysted zoospore germinates to form a rhizoidal system and a single typically sphaerical zoosporangium (≥ 120 *µm* diam.) that on maturity liberates ≥ 100 zoospores. The rhizoidal system is devoid of nuclei (as seen under DAPI staining) and is highly branched and tapering. The zoosporangium is typically attached to the rhizoidal system via one main rhizoid or sporangiophore. A septum is often visible in mature zoosporangia, separating the zoosporangium from the sporangiophore. Free swimming zoospores are typically sphaerical (ca. 10 *µm* diam.) and the species is characterized by the presence of ca. 16 or more posteriorly directed flagella that are in length up to 3–fold the diam. of the zoospore. When swimming the flagella beat together as if they were a single flagellum and thus propel the zoospore forward in a spiral or helical motion.

The reference culture is maintained by continual passage at the University of California, Santa Barbara (G1, JMRC:SF:12176, **holotype**), and under cryopreservation in repositories at the O'Malley Lab, University of California, Santa Barbara, and University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany (Jena Microbial Resource Collection JMRC: SF: 012176 – **ex-type**). Fixed glutaraldehyde preparations are also kept by the O'Malley Lab.

The internal transcribed spacer regions of the ribosomal RNA were amplified with primers JB206/JB205 (Tuckwell et al. 2005). Phylogenetic analysis of the ITS1 regions of several cultured anaerobic fungal specimens spanning all eight known genera and partial 28s reads, firmly place G1 in the genus *Neocallimastix* as a distinct, previously unclassified sister species to established cultures such as *N. frontalis* (Figs 146, 147). The ~190 Mbp genome has also been sequenced by the US Department of Energy's Joint Genome Institute (JGI) to reveal that G1 is a polyploid organism. The genome will be made available at Mycocosm in 2016 (http://genome.jgi.doe.gov/programs/fungi/index.jsf).

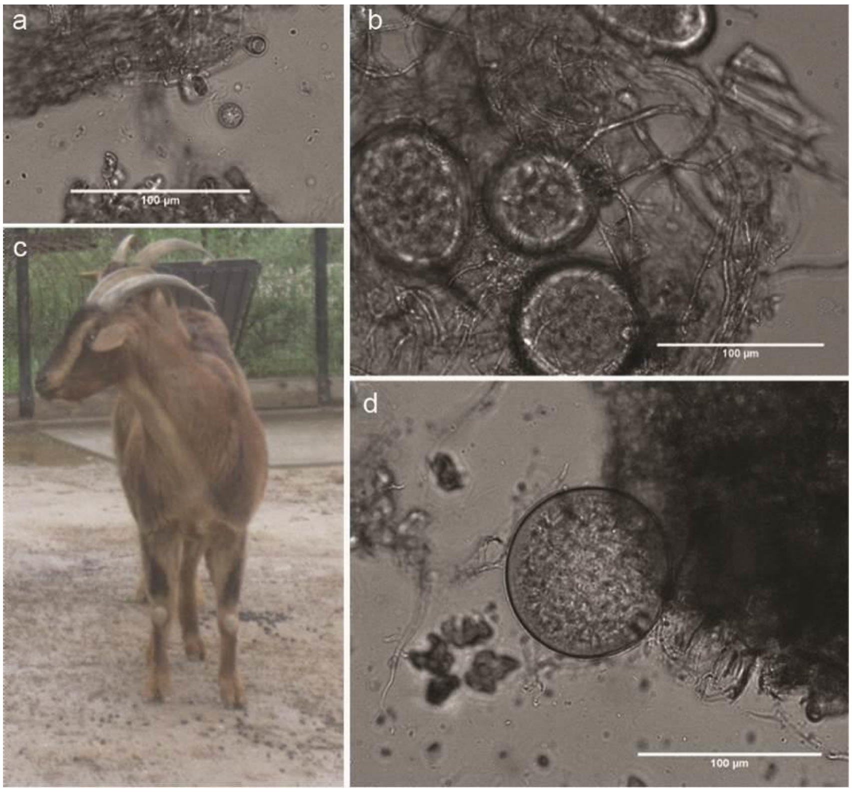


Fig. 149 ***Neocallimastix californiae*** (**holotype**) **a** Sphearical zoospores with multiple flagella which are splayed out **b** Multiple sporangia, demonstrating the predominantly sphearical to ovoid structure **c** Goat host from which *N. californiae* was isolated **d** Large sphearical sporangia that is characteristic of this species.

Piromyces J.J. Gold et al.

Monoflagellated protozoans found in the rumen were assigned to the genus *Piromonas* (Liebetanz 1910; Braune 1913). Orpin concluded that these flagellated cells were in fact zoospores of anaerobic fungi (Orpin 1977a). Orpin retained the generic name on the assumption that the fungi he isolated from the sheep rumen were the same as Liebetanz's 'protozoans' (Liebetanz 1910). However, Gold *et al*. (1988) questioned this assumption because Liebetanz's isolates were anteriorly flagellated, obtained nutrition by phagocytosis and divided by binary fission, whereas Orpin's isolates were posteriorly flagellated, rhizoid producing saprobes that did not undergo binary fission. For these reasons, and to stress fungal affinity, *Piromonas* was renamed *Piromyces* (Gold et al. 1988). *Piromyces* appears the most heterogeneous genus among anaerobic fungi, covering up to eight species. Species of *Piromyces* isolated to date include *P. communis*, *P. mae*, *P. dumbonica*, *P. rhizinflata*, *P. minutus*, *P. spiralis*, *P. citronii*, *P. polycephalus* and *P. cryptodigmaticus* (Gold et al. 1988; Li et al. 1990; Breton et al. 1991; Ho et al. 1993a, 1993b; Gaillard-Martinie et al. 1995; Chen et al. 2002; Fliegerová et al. 2010). While some of these species appear to have morphologically distinct characteristics, relationships with each other and indeed with other gut fungal genera remains unclear. Just one named but uncultured species (*P. cryptodigmaticus* GQ850355.1, GQ850368.1, and GQ850318.1) has been categorized according to their molecular characteristics (Fliegerová et al. 2010). *Piromyces* sp. E2 Teunissen et al. (1991) has been sequenced by the JGI and sequence data is available on request. From a morphological perspective the genus *Piromyces* contains species of strictly anaerobic fungi characterized by a monocentricthallus, which consists of a network of branched, tapering rhizoids devoid of nuclei. The zoosporangia are variable, sphearical, oval or club-shaped and are supported by a sporangiophore, which develops from one or more rhizoids. As the life cycle of the monocentric fungi is determinate (finite), each thallus (the rhizoidal network) supports just one zoosporangium. Zoospores are uninucleate, sometimes bi- or quadri-flagellate (Gruninger et al. 2014). The phylogenetic relatedness of the rhizoidal genera with monoflagellated zoospores (*Piromyces* and *Anaeromyces*) is unclear and as observed by Brookman et al. (2000), it seems likely that the genus *Piromyces* is polyphyletic and in need of reappraisal.

353. *Piromyces finnis* O'Malley, Haitjema & Gilmore, ***sp. nov.***

Index Fungorum number: IF 551677, *Facesoffungi number*: FoF 02062, Fig. 150

Etymology:*"*"*Piromyces* of Finn"/"Finn's *Piromyces.''*The specific epithet refers to the animal host, a horse named "Huckleberry Finn", from which the fungus was isolated.

Holotype: *Piromyces* sp. finn (O'Malley Lab, University of California, Santa Barbara, NCBI Taxon ID: 1577477), JMRC:SF:12177.

An obligate anaerobic fungus isolated in 2011 at MIT from the feaces of the award-wining show jumping horse Huckleberry Finn, owned by Susan Huyett of Concord, MA. The species is monocentric and has a determinate (finite) life cycle. The fungus exhibits endogenous zoosporangial development (i.e., the encysted zoospore retains the nucleus). The encysted zoospore geminates to form a rhizoidal system and a single oval or club shaped zoosporangium ($\geq$ 100 μm long and 30–60 μm wide), which on maturity liberates $\geq$ 100 zoospores. The rhizoidal system is devoid of nuclei (as seen under DAPI staining) and is highly branched and tapering. The zoosporangium is typically attached to the rhizoidal system via one main rhizoid or sporangiophore. A septum is often visible in mature zoosporangia, separating the zoosporangium from the sporangiophore. Free swimming zoospores are typically sphearical (ca. 10 μm diam.) and the species is characterized by the presence of a single posteriorly directed flagella that is in length up to 3–fold the diam. of the zoospore. When swimming the flagella beats posteriorly and thus propel the zoospore forward in a spiral or helical motion.

The reference culture is maintained by continually passage at the University of California, Santa Barbara (JMRC:SF:12177, **holotype**), and under cryopreservation in repositories at the University of Jena and Leibniz Institute for Natural Product

Research and Infection Biology, Jena, Germany (Jena Microbial Resource Collection JMRC:SF:012177, **ex-type**). Fixed glutaraldehyde preparations are also kept by the O'Malley Lab.

The internal transcribed spacer regions of the ribosomal RNA were amplified with primers JB206/JB205 (Tuckwell et al. 2005). Phylogenetic analysis of the ITS1 regions of several cultured anaerobic fungal specimens spanning all eight known genera and partial 28s reads, firmly place Finn within the *Piromyces* as a distinct, previously unclassified species (Figs 146, 147). The ~56 Mbp genome has been sequenced by the US Department of Energy's Joint Genome Institute (JGI). The genome will be available at Mycocosm in 2016 (http://genome.jgi.doe.gov/Pirfi3/Pirfi3.home.html).

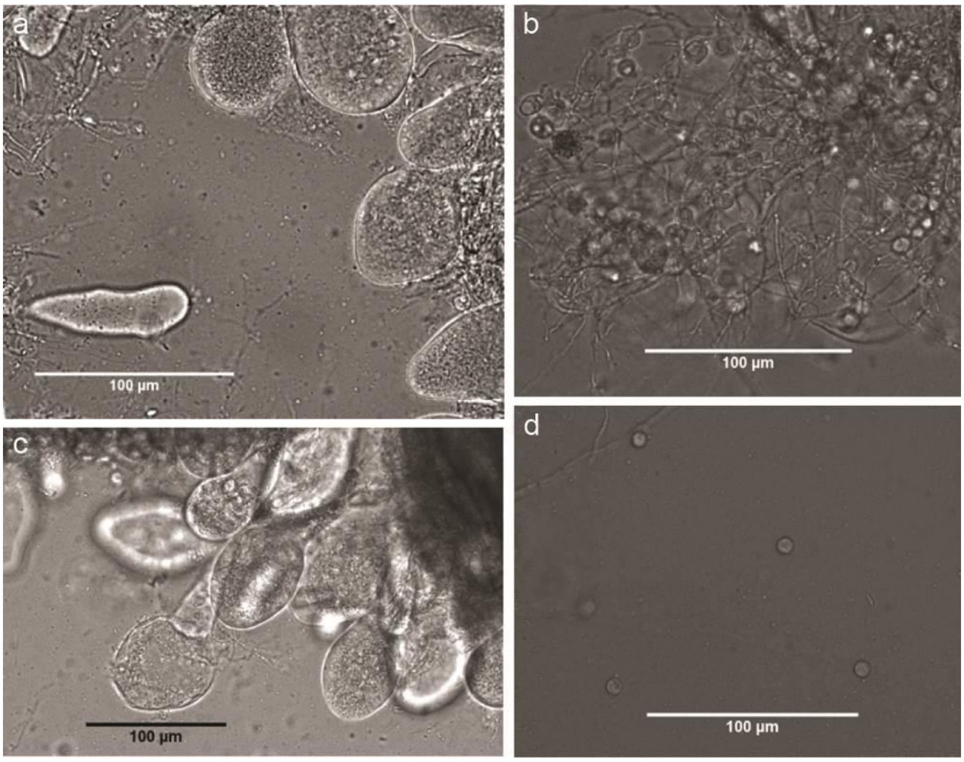


Fig. 150 ***Piromyces finnis*** (**holotype**) **a** Multiple sporangia of *P*. *finnis* exhibiting a range of morphological features from club-like to ovoid **b** A group of young sporangia, not much larger than zoospores beginning to form **c** Mature zoosporangia **d** Several zoospores of *P*. *finnis*.

Contribution to *Oomycota*

The *Oomycota* are a highly diverse group of heterotrophic fungal-like eukaryotes that are placed within the kingdom Straminipila, in the supergroup SAR (Adl et al. 2012). The major components of their cell walls are cellulose and β-1,3-glucans and unlike fungal cell walls, only small amounts of chitin are present in some species (Kamoun 2003, Rossman and Palm 2006). They reproduce asexually by heterokont biflagellate zoospores (Hardham 2009) and when sexuality is present, by forming in most cases oogonia and antheridia that mate, producing thick-walled oospores

(Judelson 2009). They are cosmopolitan and ubiquitous, playing key roles in a wide range of ecosystems as saprotrophs and parasites of a variety of host organisms such as algae, oomycetes, fungi, plants, invertebrates and vertebrates (Marano et al. 2014). They were informally classified into two lineages or “galaxies”, the “peronosporaleans” and the “saprolegnialeans” until recently when Beakes et al. (2014) have designated these lineages as classes, the *Peronosporomycetes* and *Saprolegniomycetes* in the phylum *Oomycota*.

Peronosporales

Pythiaceae

Phytophthora de Bary

Phytophthora includes mainly ecologically and economically important plant pathogens (e.g. Kroon et al. 2004; Brasier et al. 2005; Balci et al. 2007), but also species that have not been yet associated with disease (Hansen et al. 2012) and that are abundantly distributed in forested streams (Reeser et al. 2011). The genus is currently subdivided into 10 well-recognized ITS clades (Kroon et al. 2012), plus the novel lineage represented by *P. stricta* (Yang et al. 2014a). Multi-gene phylogenies have shown that most of the 10 clades are monophyletic, except the Clades 4 and 9 (Blair et al. 2008). Clade 9 is the most rapidly expanding, with most of its species recently described (Hong et al. 2010, 2012; Naher et al. 2011; Rea et al. 2011; Yang and Hong, 2013; Yang et al. 2014a, b). Members of this clade generally produce non-papillate and non-caducous zoosporangia. A well-defined subclade of species within Clade 9 have a relatively high-temperature optima, ca. 30–32°C, and are able to tolerate up to 40°C (Yang et al. 2014a). In this contribution, we describe two new species for the *Phytophthora* ITS Clade 9, which both fall into this high-temperature optima subclade (Fig. 151).

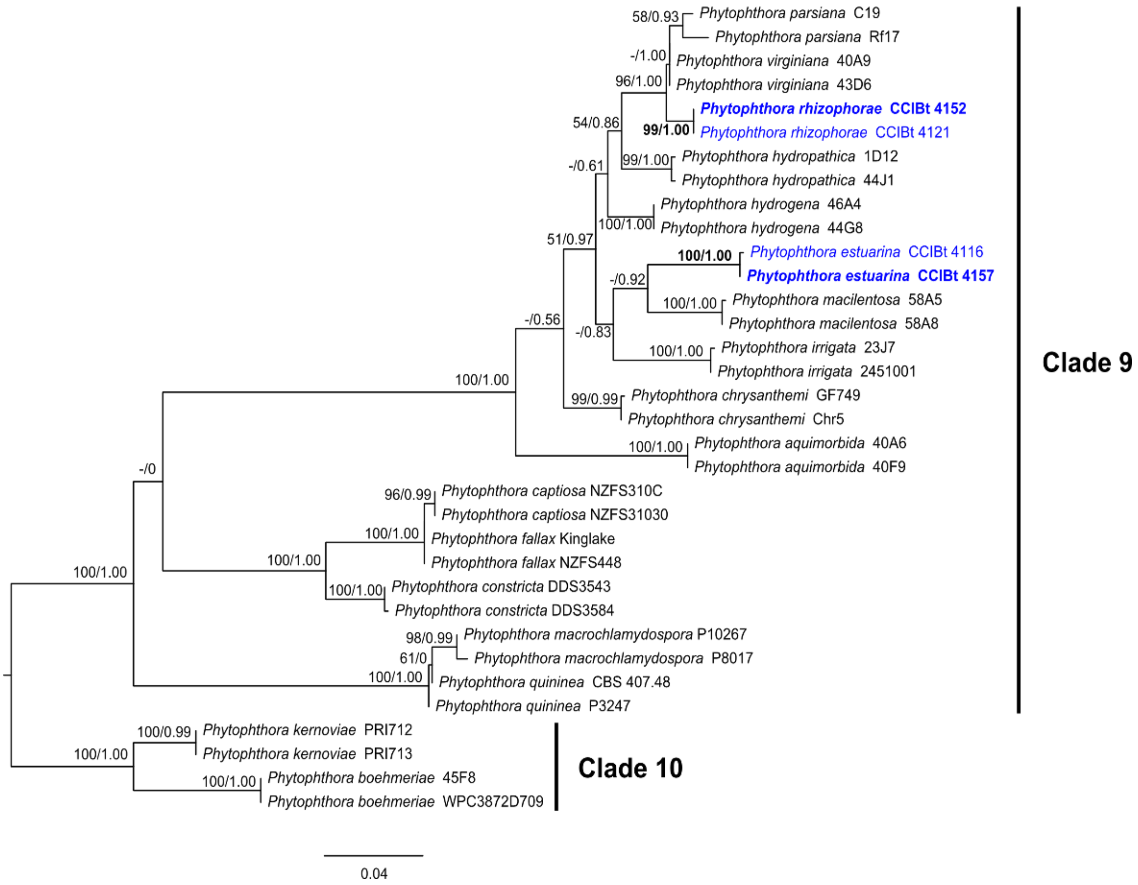


Fig. 151 Phylogram generated from Maximum likelihood (ML) analysis (PhyML 3.1, Guindon & Gascuel 2003) based on entire ITS rDNA sequences showing the phylogenetic placement of *Phytophthora rhizophorae* and *P. estuarina* within *Phytophthora* Clade 9. ML bootstrap support values < 50% are marked with (-). Clades that do not appear in the Bayesian analysis are indicated with a zero. Bayesian posterior probability values (MrBayes 3.2, Ronquist et al. 2012) > 0.50 are labelled numerically. Scale bar indicates the average number of substitutions per site. New taxa are in blue and species for which obtained sequences are based on type material have names in bold.

354. ***Phytophthora estuarina*** Marano, A.L. Jesus & Pires-Zottar., ***sp. nov.***

Index Fungorum number: IF 551608, *Facesoffungi number*: FoF 01275, Fig. 152

Etymology: "estuarina" refers to the estuarine habitat in where this species was isolated.

Holotype: SP 466380

Mycelium well-developed on PYGs, aerial mycelium scanty, hyaline, branched, aseptate, hyphae 3.75–5 *µm* thick (av. 4.85 *µm*); *hyphal swellings* sphaerical, globose, tubular to irregular. *Zoosporangiophores* undifferentiated of the vegetative hyphae, long, simple or sympodially branched, bearing one terminal zoosporangium. *Zoosporangia* produced abundantly in water cultures, non-caducous, semipapillate or apapillate, ovoid to obpyriform, 55–83 × 43–63 *µm* (av. 77 × 54 *µm*), internally proliferating in both a nested and extended way; secondary lateral zoosporangia regularly formed; transparent lens-shaped plug material prior to zoospore differentiation; wall rough after zoospore discharge; *basal-plug* present. *Zoospores* formed inside the zoosporangium and discharged by an elongate, vase-shaped, and semi-persistent vesicle, 33–80 *µm* long when expanded, through which zoospores swim away; encysted zoospores 7.5–12.5 *µm* diam. (av. 10.1 *µm*). The vesicle shrinks completely in length and width in up to 1 hour after zoospore release. *Chlamydospores* and *sexual structures* not observed. Gametangia not produced in single culture or when paired with tester strains of *P. capsici* A1 (CBS 111334) and A2 (CBS 370.72). Auto-sterile when the isolates were paired with each other. Radial growth rates on PYGs (photoperiod: 12 h) at near the optimum temperature (30°C) = 12 ± 1 mm/d (n = 10); at near the maximum temperature (35°C) = 2 ± 1 mm/d (n = 10); no growth during five days at 40ºC and even after subsequent incubation at room temperature (~20°C).

Culture characteristics: colonies cottony, with scanty aerial mycelium and no defined growth pattern on PYGs.

Material examined: BRAZIL, São Paulo, Cananéia, “Parque Estadual da Ilha do Cardoso” (PEIC), 25°03’05’’–25°18’18’’S; 47°53’48’’–48°05’42’’W, Perequê river (salinity 1.3%), from leaves of *Laguncularia racemosa* onto PYGs medium, 27 Feb 2013, A.L. Jesus, C.L.A. Pires-Zottarelli & A.V. Marano (SP 466380, **holotype**), **ex-types** CCIBt 4157, MMBF 14/15; *Ibid*., permanent shallow lagoon (salinity 2.8%), from leaves of *Rhizophora mangle*, on *Sorghum* sp. seeds, 30 Aug 2012 A.L. Jesus, C.L.A. Pires-Zottarelli & A.V. Marano (SP 466372, **paratype**), **ex-paratypes** CCIBt 4116, MMBF 06/15.

Notes: The isolates of *P. rhizophorae* and *P. estuarina* were recovered from mangrove swamps, which exhibited salinity concentrations between 0.8–2.8% and, therefore, the habitat of the ITS Clade 9 members is expanded to include estuaries. Both *P. rhizophorae* and *P. estuarina* appear as well-delimited species and along with ten other species, they consistently form a high temperature-tolerant subclade within Clade 9, supported by strong bootstrap (100%) in our ITS phylogeny (Fig. 151). *Phytophthora rhizophorae* is phylogenetically related with *P. virginiana* and *P. parsiana*, while *P. estuarina* appear as closely related to *P. macilentosa* and *P. irrigata* in our ITS phylogeny. The two new species share the presence of ovoid to obpyriform, apapillate and non-caducous zoosporangia, which are terminal and internally proliferating in both a nested and extended way (Figs 152 and 153). These characteristics appear to be common to most members of Clade 9. *Phytophthora estuarina* has additionally semi-papillate zoosporangia, a characteristic that is present in a few species from this clade, such as *P. constricta* (Rea et al. 2011). During zoospore discharge, it develops an elongate and semi-persistent vesicle, which completely retracts in length and width in up to 1 h after zoospore release and acquires a characteristic morphology after shrinkage (Fig. 153). The zoosporangia have wrinkled walls after zoospore release and the shrunken vesicle remains constricted at the apex of the zoosporangium. This process of vesicle development is peculiar and has not been previously reported for *Phytophthora* species.

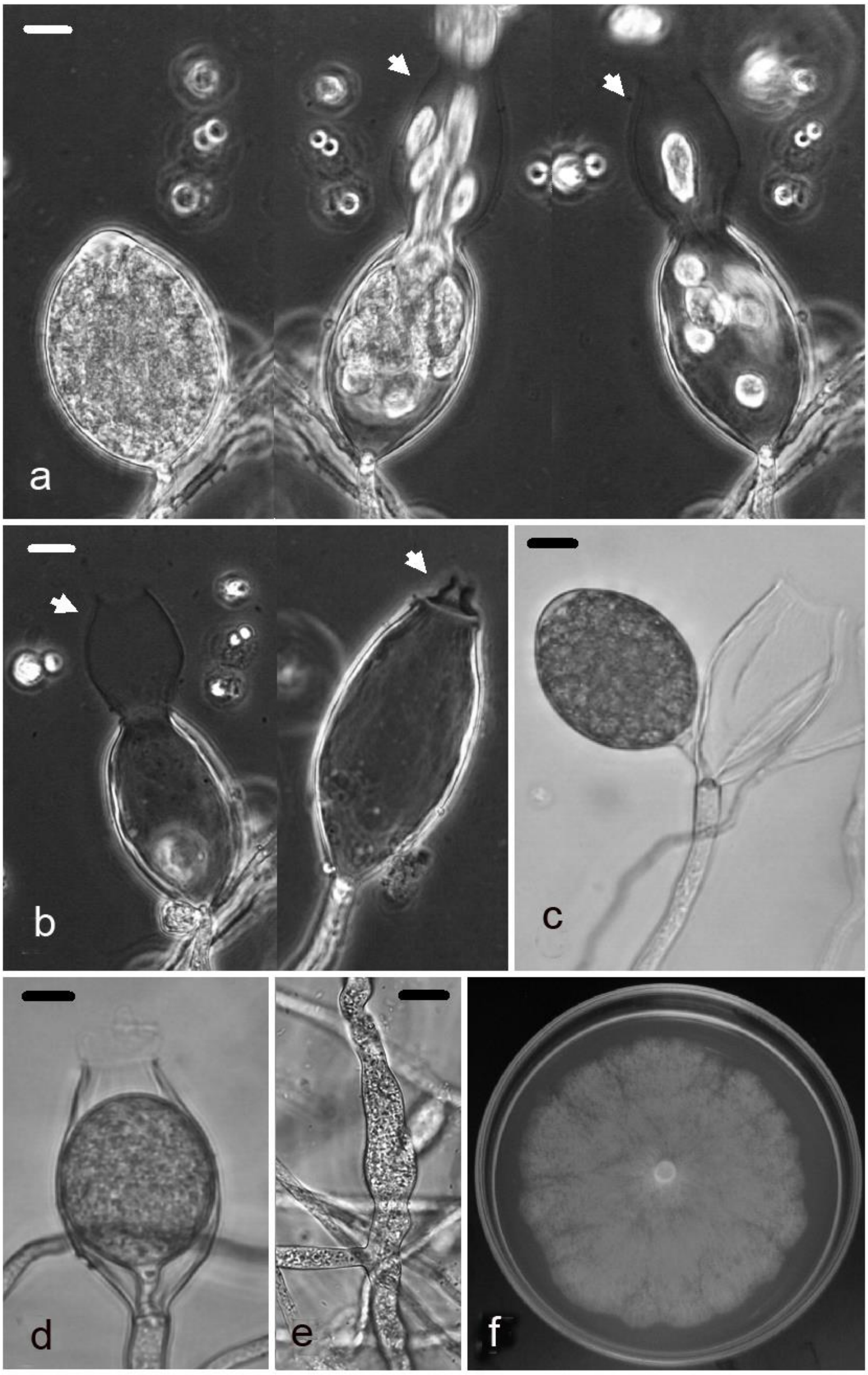


Fig. 152 ***Phytophthora estuarina*** (**holotype**) **a, b** Zoospore differentiation inside the zoosporangium and discharge of zoospores through an elongate semi-persistent vesicle After shrinkage, the vesicle acquires a characteristic morphology (arrows) **c** Secondary lateral zoosporangium and empty zoosporangium with characteristic rough walls after zoospore discharge **d** Internal proliferation of the zoosporangium **e** Hyphal swellings **f** Colony with scanty aerial mycelium and no defined growth pattern onto PYGs culture medium (CCIBt 4116). Scale bars: a–e = 10 *µm*.

355. *Phytophthora rhizophorae* Pires-Zottar., A.L. Jesus & Marano, ***sp. nov.***

Index Fungorum number: IF 551607, *Facesoffungi number*: FoF 01274, Fig. 153

Etymology: "*rhizophorae*" refers to *Rhizophora mangle*, the substrate from where this species was isolated.

Holotype: SP 466375

Mycelium well-developed on PYGs, aerial mycelium scanty, hyaline, branched, non-septate, hyphae 3.5–6.3 *µm* thick (av. 5.1 *µm*); *hyphal swellings* sphearical, globose, tubular, obpyriform to irregular. *Zoosporangiophores* undifferentiated from the vegetative hyphae, long, simple, bearing one terminal zoosporangium. *Zoosporangia* internally proliferating, ovoid to obpyriphorm, non-papillate to semi-papillate, non-deciduous, 35–58 × 20–45 *µm* (av. 45–32 *µm*); *basal-plug* present. *Zoospores* formed inside the zoosporangia and discharged by a globose vesicle; encysted zoospores 7.5–12.5 *µm* diam. (av. 9.3 *µm*). *Chlamydospores* and *sexual structures* absent. Gametangia not produced in single culture or when paired with tester strains of *P. capsici* A1 (CBS 111334) and A2 (CBS 370.72). Auto-sterile when the isolates were paired with each other. Radial growth rates on PYGs (photoperiod: 12 hs) at near the optimum temperature (30°C) = 14 ± 2 mm/d (n = 10); at near the maximum temperature (35°C) = 7 ± 2 mm/d (n = 10); no growth was observed during five days at 40ºC but the growth was reactivated after subsequent incubation at room temperature (~20°C).

Culture characteristics: colonies petaloid on PYGs.

Material examined: BRAZIL, São Paulo, Cananéia, "Parque Estadual da Ilha do Cardoso" (PEIC), 25°03'05''–25°18'18''S; 47°53'48''–48°05'42''W, Perequê river (salinity 0.8%), from leaves of *Rhizophora mangle*, on *Sorghum* sp. seeds, 30 Aug 2012, A.L. Jesus, C.L.A. Pires-Zottarelli & A.V. Marano (SP 466375, **holotype**), **ex-holotypes** CCIBt 4152, MMBF 09/15; *Idem* (SP 466374, **paratype**), ex-paratypes CCIBt 4121, MMBF 08/15.

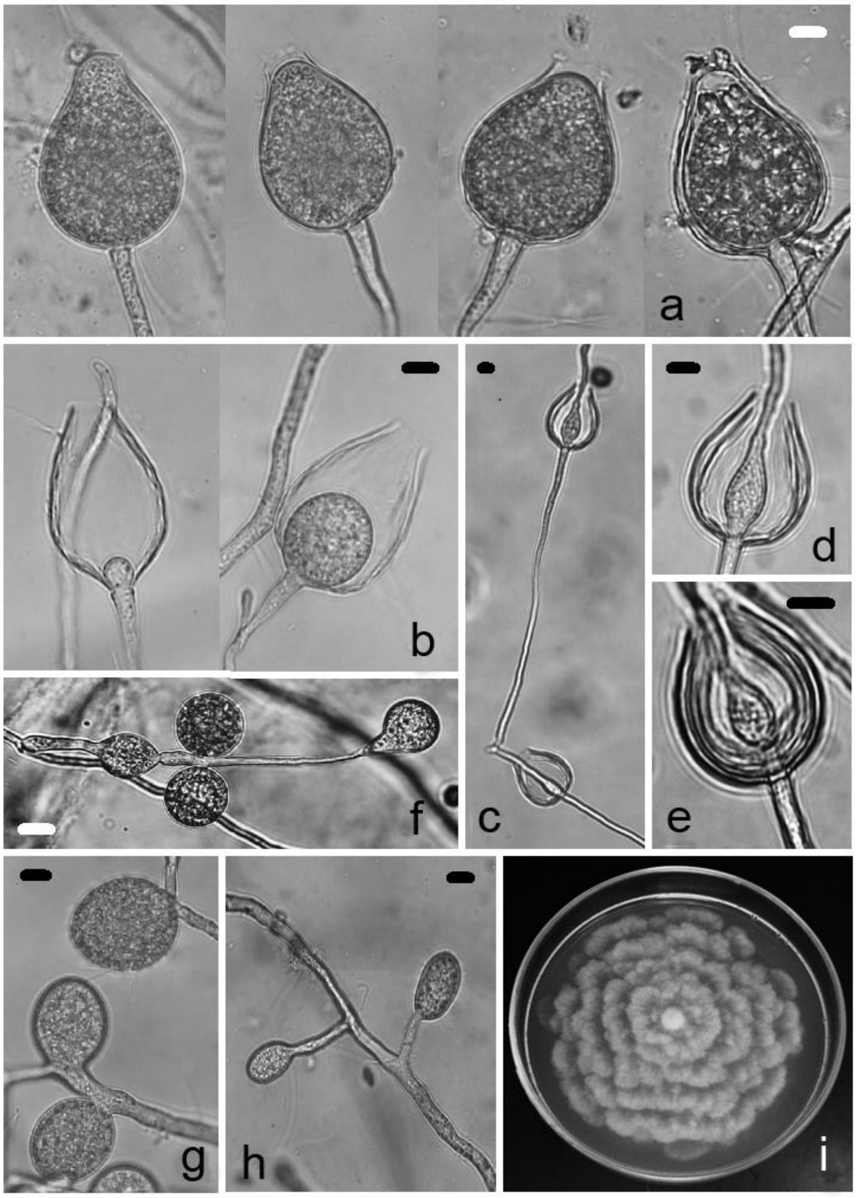


Fig. 153 ***Phytophthora rhizophorae*** (**holotype**) **a** Apapillate zoosporangia during different stages of zoospore differentiation **b, c** Empty zoosporangium with internal proliferation **c** General aspect of the zoosporangiophore with both nested and extended internal proliferation **d, e** Nested proliferation of the zoosporangium **f**–**h** Different morphologies of hyphal swellings **i** Petaloid colony pattern onto PYGs culture medium (CCIBt 4121). Scale bars: a–i = 10 *µm*.

Oomycota, incertae sedis

Salispina Marano, A.L. Jesus & Pires-Zottar., ***gen. nov.***

In the last few years, increasing molecular evidence has shown that the genus *Halophytophthora* (*Peronosporales*, *Oomycota*) as currently circumscribed is polyphyletic, being composed by an assemblage of species that belong to related peronosporalean genera, i.e. *Salisapilia*, *Phytophthora* and *Phytopythium*, and to yet undescribed genera (Marano et al. 2016). Several phylogenetic studies have shown that *Halophytophthora spinosa* falls into a new clade, commonly referred as “spinosa” clade, which appears to represent a basal lineage phylogenetically more closely related to *Sapromyces elongatus* (*Rhipidiales*) than to the “*Halophytophthora sensu stricto*” clade (Nakagiri 2002; Nakagiri and Izumi 2005; Beakes et al. 2014; Marano et al. 2014). Additional sequences of *Rhipidiales* are not available at GenBank to putatively test this hypothesis and place the members of this clade into a higher-level taxonomic category. Therefore, based on the phylogenetic analyses of the SSU (Fig. 154) and COI (Fig. 155) mtDNA regions we propose to establish *Salispina* gen. nov. in an *incertae sedis* order for accommodating *H. spinosa* var. *spinosa* and *H. spinosa* var. *lobata*, both elevated to species level, and the new species *S. intermedia*, until its relatedness with other members of the *Rhipidiales* and *Peronosporales* could be tested in a multi-gene phylogeny and its taxonomic placement confirmed.

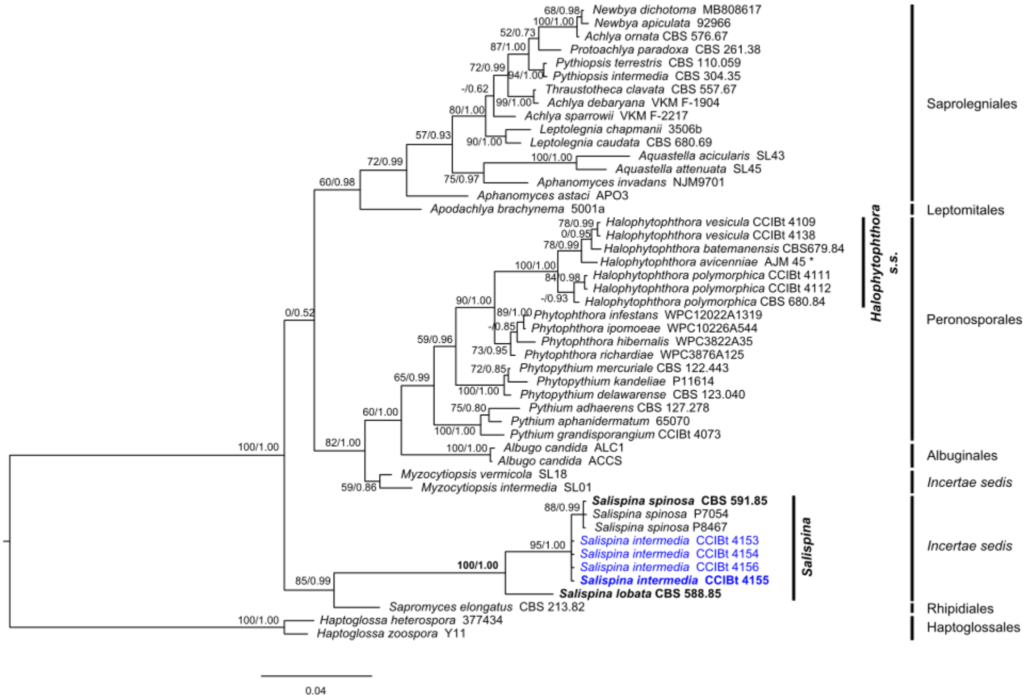


Fig. 154 Phylogram generated from Bayesian inference analysis (MrBayes 3.2, Ronquist et al. 2012) based on SSU rDNA sequences showing the phylogenetic placement of *Salispina* gen. nov. in a well-defined clade (indicated in bold). Maximum likelihood (ML) bootstrap support values (PhyML 3.1, Guindon and Gascuel 2003) < 50% are marked with (-). Clades that do not appear in the ML analysis are indicated with a zero. Bayesian posterior probability values > 0.50 are labelled numerically. Scale bar indicates the average number of substitutions per site. New taxa are in blue and ex-type strains are in bold.

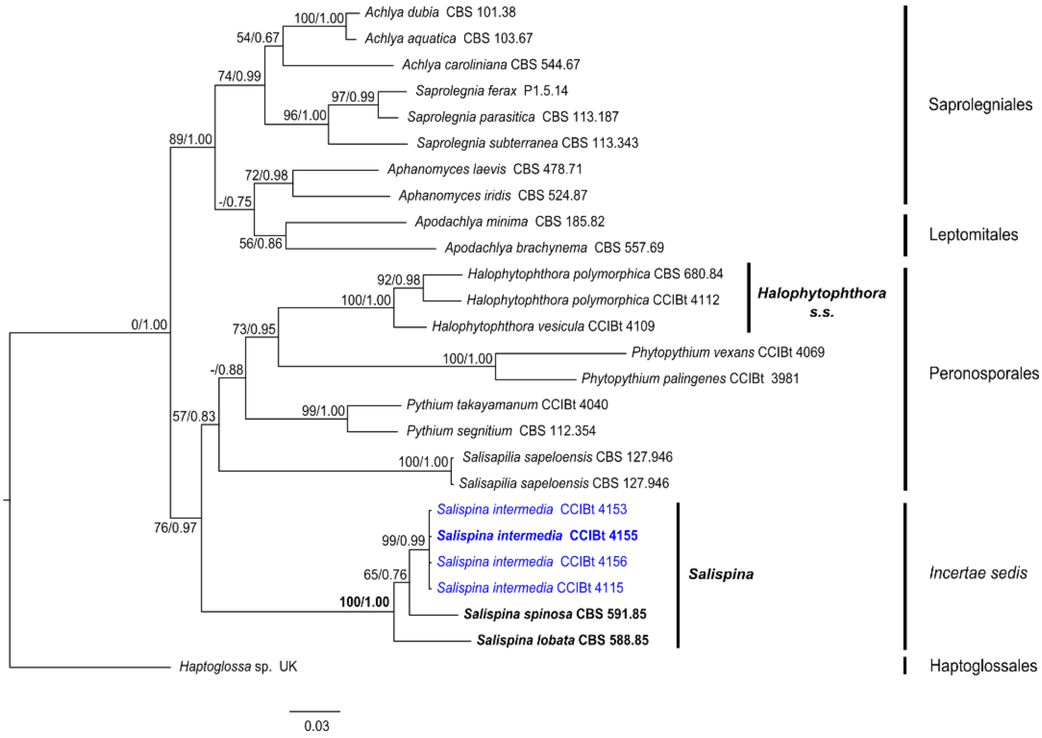


Fig. 155 Phylogram generated from Bayesian inference analysis (MrBayes 3.2, Ronquist et al. 2012) based on cytochrome oxidase I (COI mtDNA) sequences showing the phylogenetic placement of *Salispina* gen. nov. in a well-defined clade (indicated in bold). Maximum likelihood (ML) bootstrap support values (PhyML 3.1, Guindon & Gascuel 2003) < 50% are marked with (-). Clades that do not appear in the ML analysis are indicated with a zero. Bayesian posterior probability values > 0.60 are labelled numerically. Scale bar indicates the average number of substitutions per site. New taxa are in blue and ex-type strains in bold.

356. *Salispina* Marano, A.L. Jesus & Pires-Zottar., ***gen. nov.***

Index Fungorum number: IF 551605, *Facesoffungi number*: FoF 01276

Etymology: *salis* (salt) indicating its presence under saline conditions (estuarine and marine habitats), and *spina* (spine) because of the common presence of spines on the zoosporangia.

Type species: *Salispina intermedia* A.L. Jesus, Pires-Zottar. & Marano

Holotypus: SP 466378

Colonies petaloid, with scanty aerial mycelium on agar culture media; *mycelium* well-developed, hyaline, tortuous and highly branched, non-septate to few septate, hyphae irregular. *Zoosporangiophores* undifferentiated from the vegetative hyphae, long, simple, bearing one terminal zoosporangium. *Zoosporangia* with vacuolated protoplasm, sphaerical, globose, obovate, obpyriform, or elongated, thick-walled, from smooth to with spines showing variable degree of coverage on the zoosporangia; *basal-plug* hyaline, slightly below the zoosporangia. *Zoospore* release takes place through the formation of a persistent, short to long, dehiscence tube; vesicle absent. *Chlamydospores* absent. *Sexual reproduction* unknown.

Notes: *Salispina* forms a well-defined lineage phylogenetically distant from the *Halophytophthora s.s.* clade (Figs 154 and 155) and appears as closely related to

Sapromyces elongatus (Fig. 154; Nakagiri 2002; Nakagiri and Izumi 2005; Beakes et al. 2014; Marano et al. 2014). Fatty acid profiles evidenced that most members of the *Halophytophthora s.s.* clade produce both arachidonic (ARA) and eicosapentaenoic (EPA) acids while *Salispina spinosa* (*H. spinosa* var. *spinosa*) seems to be able to produce only ARA (Pang et al. 2015). Fell and Master (1975) observed that zoosporangial size and degree of spine coverage are nutritionally determined. Zoosporangia formed on a rich substrate are larger and completely covered with spines while those formed on poorer substrates are smaller and have only a few distal spines or are even smooth. The dehiscence tube appears to be hydrotropic, being its development conditioned by the presence of water (Fell and Master 1975).

357. *Salispina intermedia* A.L. Jesus, Pires-Zottar. & Marano, ***sp. nov.***

Index Fungorum number: IF 551603, *Facesoffungi number*: FoF 01277, Fig. 156

Etymology: "*intermedia*" refers to the presence of intermediate morphological features between *S. spinosa* and *S. lobata*.

Holotypus: SP 466378

Mycelium well-developed on PYGs, aerial mycelium scanty, hyaline, irregular, branched, few septate, hyphae 2.5–10 *µm* thick. *Zoosporangiophores* undifferentiated from the vegetative hyphae, long, simple, bearing one terminal zoosporangium, 6.25–12.5 *µm* (av. 9.8 *µm*). *Zoosporangia* of variable morphology, ranging from obovate, obpyriform, globose to elongate, thick-walled, 33–197 × 25–183 *µm* (av. 86 × 62 *µm*); with vacuolated content; smooth to spiny; spines with variable degree of coverage on the zoosporangium, from only one spine at the tip of the zoosporangium to completely spiny; spines (5–)7.5–35 *µm* long. (av. 17 *µm*); *basal plug* hyaline, 2.5–7.5 *µm* thick (av. 5.5 *µm*). *Zoospores* discharged through a persistent tube, long or short, 15–30 × (7.5–)12.5–15(–20) *µm* (av. 23 × 15 *µm*); *vesicle* absent; encysted zoospores, 6.3–12.5 *µm* diam. (av. 9 *µm*), germination by one germ tube. *Chlamydospores* absent. *Sexual reproduction* unknown.

Culture characteristics: colonies petaloid on PYGs; no growth on *Sorghum* sp. (L.) seeds.

Material examined: BRAZIL, São Paulo, Cananéia, "Parque Estadual da Ilha do Cardoso" (PEIC), 25°03'05''–25°18'18''S; 47°53'48''–48°05'42''W, Perequê river (salinity 2.2%), from leaves of *Rhizophora mangle*, 8 Nov 2012, A.L. Jesus, C.L.A. Pires-Zottarelli & A.V. Marano (SP 466378, **holotype**), ex-holotypes CCIBt 4155, MMBF 12/15; *Ibid*., Perequê river (salinity 0.8–2.8%), from leaves of *R. mangle* and *Laguncularia racemosa*, 30 Aug and 8 Nov 2012, 27 Feb and 5 Jun 2013, A.L. Jesus, C.L.A. Pires-Zottarelli & A.V. Marano (SP 466373, SP 466376, SP 466377, SP466379, **paratypes**), ex-paratypes CCIBt 4115 = MMBF 07/15, CCIBt 4153 = MMBF 10/15, CCIBt 4154 = MMBF 11/15, CCIBt 4156 = MMBF 13/15.

Notes: *Salispina intermedia* appears as morphologically and phylogenetically intermediate between *S. spinosa* CBS 591.85 (KT886057) and *S. lobata* CBS 588.85 (KT886056), Figs 154, 155 and 156. Its zoosporangial morphology resembles *S. spinosa*, although their zoosporangia are considerably larger than those observed for the ex-type cultures of *S. spinosa* (CBS 591.85) and *S. lobata* (CBS 588.85). Onto

PYGs, *S. intermedia* forms clusters of zoosporangia visible at naked eye. This species was particularly abundant and frequently recovered during spring (Nov) and summer (Feb) samplings, when water temperature was higher (25–28°C) than in the other samplings (18–22°C). We were not able of sequencing the ITS region of *Salispina* using the primers ITS4 and ITS6 (Cooke et al. 2000) and UN-up18S42 and UN-up28S22 (Robideau et al. 2011).

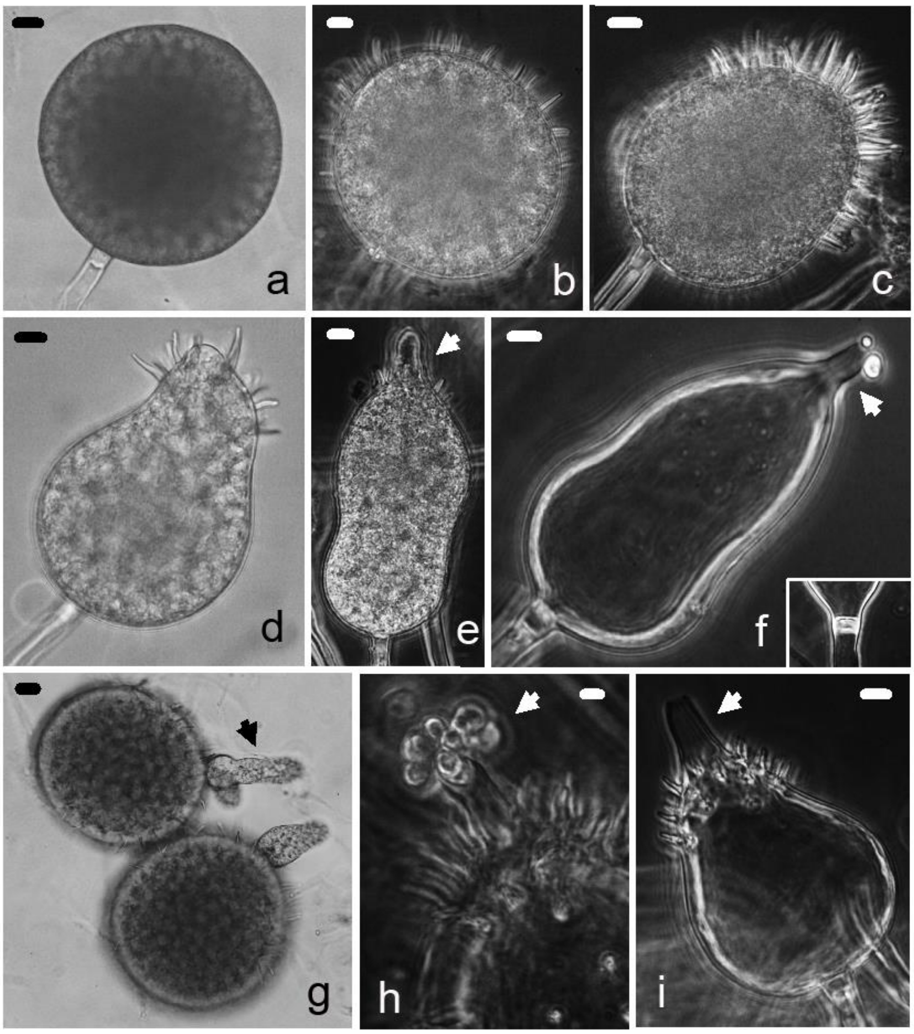


Fig. 156 ***Salispina intermedia*** (**holotype**) **a**–**d** Zoosporangia of different morphologies, from smooth (a) to with various degree of spines coverage (b–d) **e**–**i** Formation of a persistent tube through which zoospores swim away (no vesicle is formed) **f** Detail of the zoosporangial basal plug. Bars: a, h = 20 *µm*, b–g, i = 10 *µm*.

358. ***Salispina lobata*** (Fell & Master) A.L. Jesus, Marano & Pires-Zottar., ***comb. & stat. nov.***

Index Fungorum number: IF 551606

Basionym: *Phytophthora spinosa* var. *lobata* Fell & Master, Can. J. Bot. 53: 2919 (1975).

= *Halophytophthora spinosa* var. *lobata* (Fell & Master) H.H. Ho& S.C. Jong, Mycotaxon 36: 381 (1990).

Holotype: ATCC 28291 (Fell & Master 1975); ex-holotypes CBS 588.85, IFO 32592, IMI 33018.

Distribution: Malaysia, Seychelles, Singapore, Taiwan, Thailand, USA, Vietnam (Fell and Master 1975; Marano et al. 2012).

359. *Salispina spinosa* (Fell & Master) Marano, A.L. Jesus & Pires-Zottar., ***comb. & stat. nov.***

Index Fungorum number: IF 551604

Basionym: *Phytophthora spinosa* var. *spinosa* Fell & Master, Can. J. Bot. 53: 2917 (1975).

= *Halophytophthora spinosa* var. *spinosa* (Fell & Master) H.H. Ho& S.C. Jong, Mycotaxon 36: 381 (1990).

Holotype: ATCC 28294 (Fell & Master 1975); ex-holotypes CBS 591.85, IFO 32593, IMI 330187.

Distribution: Bahamas, Colombia, Grand Cayman, Haiti, Japan, Philippines, Thailand, The Netherlands Antilles, Trinidad and Tobago, USA (Fell and Master 1975; Marano et al. 2012).

Zygomycota

Mortierellales

Mortierellaceae

Mortierella Coem.

The genus *Mortierella*, the type of the order *Mortierellales*, was described in 1863 by Coemans and the first described species was *Mortierella polycephala*. The order *Mortierellales* is one of the largest basal fungal lineages. It is currently classified either within the subphylum *Mucoromycotina* (Hibbett et al. 2007) or within its own subphylum *Mortierellomycotina* (Hoffmann et al. 2011). Traditionally the genus *Mortierella* was divided into nine sections (Gams 1977). However, recent phylogenetic analyses do not support this classification. However some groups may be distinguished: '*selenospora* and *parvispora'*, *'verticillata-humilis'*, *'lignicola'*, *'mutabilis*, *globulifera* and *angusta'*, *'strangulata* and *wolfii'*, *'alpina* and *polycephala'*, *'gamsii'*. It was also shown that the genera *Dissophora*, *Gamsiella*, *Lobosporangium* and *Modicella* (Smith et al. 2013) are placed within the genus *Mortierella*. The morphology of *Mortierellales* is quite simplified and it seems to depend on culture condition, explaining the incompatibility between morphological and phylogenetic studies. The representatives of this group are mostly soil inhabiting saprotrophs (Wagner et al. 2013). The phylogenetic trees for *Mortierella* are presented in Figs 157, 158.

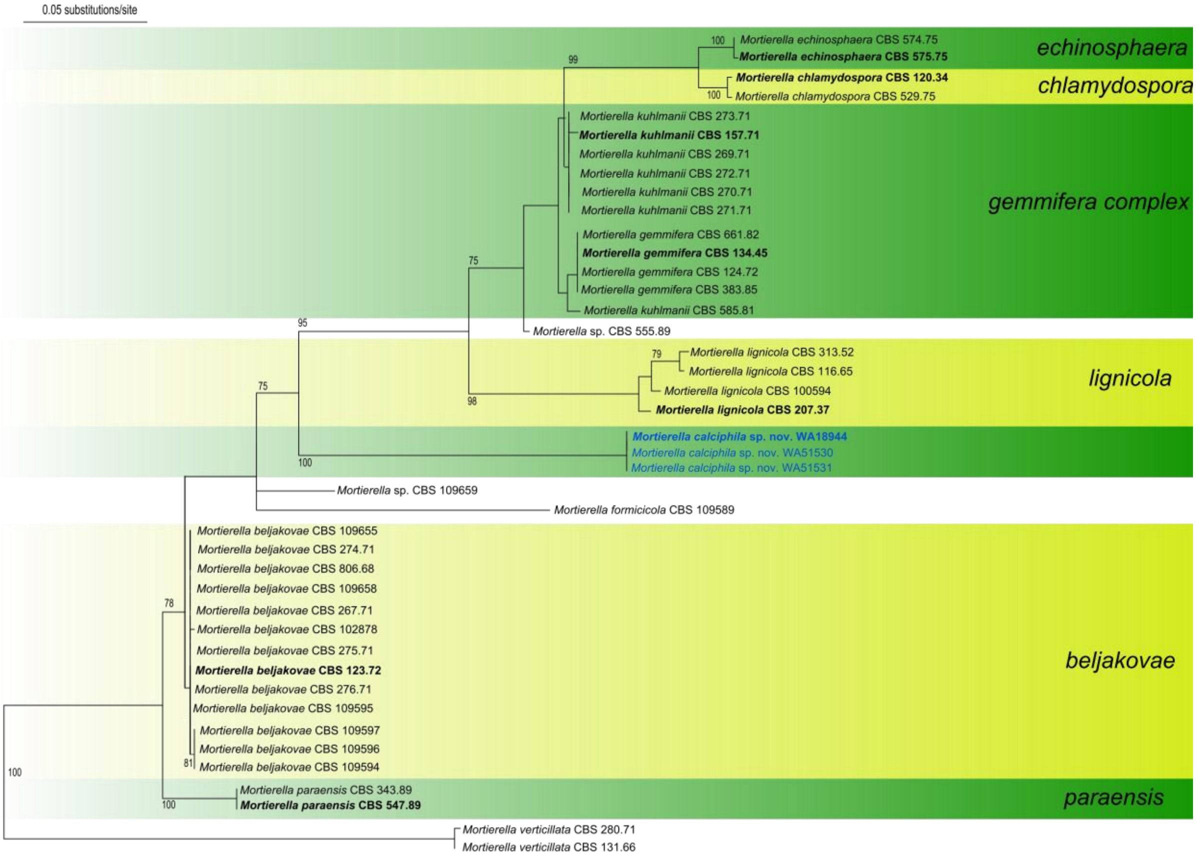


Fig. 157 Maximum likelihood analysis based on the ITS1-5.8S-ITS2 dataset for clade *lignicola* (as defined by Wagner et al. 2013). The phylogram is constructed from a muscle alignment of 616 nucleotides of 42 strains. Node support above 75% is given. New taxa are in blue and ex-type strains in bold.

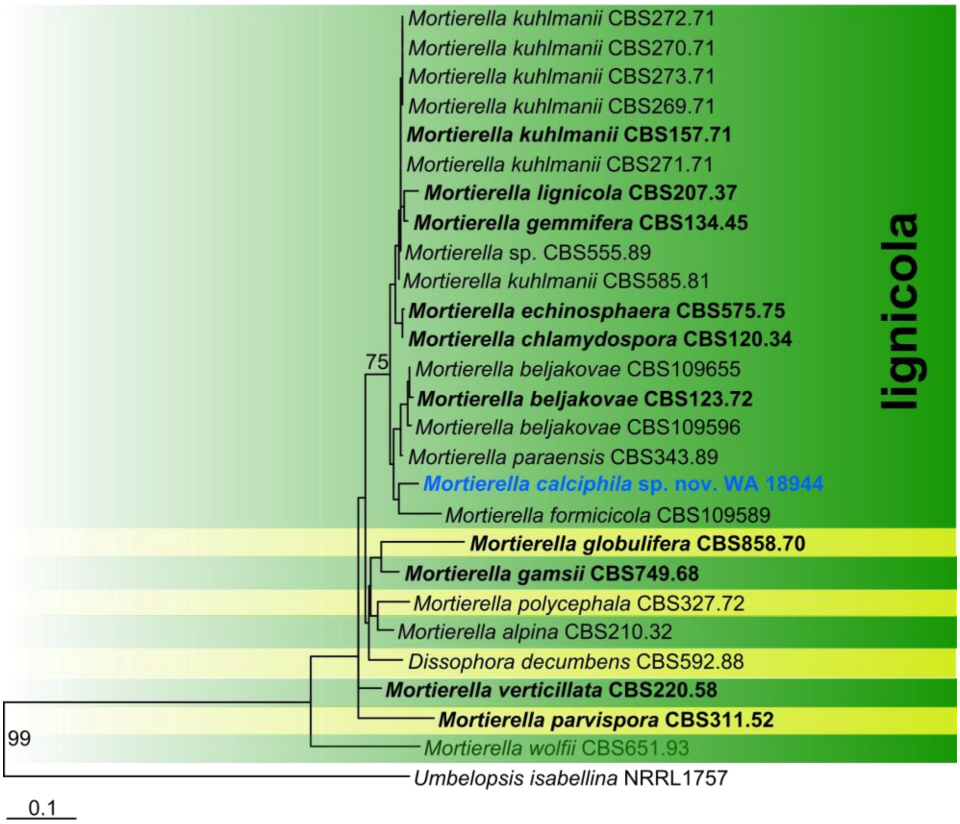


Fig. 158 Maximum likelihood analysis based on the D1/D2 domain of the large subunit (LSU, 28S) dataset for selected species of *Mortierellales*. The phylogram is constructed from a muscle alignment of 670 nucleotides of 27 strains. Node support above 75% is given. New taxa are in blue and ex-type strains in bold.

360. *Mortierella calciphila* Wrzosek, *sp. nov.*

MycoBank number: MB 814918, *Facesoffungi number*: FoF 02063, Figs 159, 160

Etymology: refers to the type of soil where the species was found (limestone soil)

Holotype: WA18944

Radiate colonies fast-growing (6–9 mm per day on PDA), without characteristic zonate growth nor garlic odour. *Sporangiophores* arising from the substratum with 2–4 (7) basal sympodial ramification or formed on aerial hyphae (then 0–1 ramification), slender, 2–3 *µm* under sporangium, 600–1400 *µm* long, without any cross wall. *Sporangia* (27–) 70 (–80) *µm* in diam., many-spored, with early deliquescent wall. *Columella* strongly reduced, without apophysis sometimes with tiny projection (up to 1 *µm*) on the top. *Spores* broadly ellipsoidal, smooth-walled, regular in shape (8–) 9 (–11) *µm* (SD = 0.8) × (6–) 7 (–9) *µm* (SD = 0.8). *Gemmae* abundantly produced in substratum or aerial hyphae, in chains or irregular clusters often connected by anastomosis, globose, hyaline to pale ochraceous (11–) 18 (–25) *µm* (SD = 3.44) in diam.

Habitat and distribution: humid soil in beech forest on limestone, Northern Poland

Material examined: POLAND, West Pomeranian Voivodeship, Polanów Forest District, Wapienny Las area ('forest on limestone soil'), 53º59'59.16 N, 16º42'47.75 E,elev. 110 m, 26 August 2015, collector Marta Wrzosek; **holotype** WA18944 (dried culture), ex-holotype CBS 140728 (lyophylised culture); ex type (living culture) is deposited in Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012173).

Notes: The phylogenetic analyses (Figs 157 and 158) show that this species belongs to group *lignicola* as defined by Wagner et al. (2013). However, the similarity of ITS sequence to any previously described taxa in this group is low: BS = 85% to *M. beljakovae*, BS = 84% to *M. paraensis*, BS = 83% to *M. formicicola*, BS = 81% to *M. gemmifera* and *M. kuhlmanii*.

The species is morphologically most similar to *Mortierella zychae* Linn., which is placed by Wagner et al. (2013) in Clade 7 grouping some species from former section "elongata" and to *M. parazychae* from Clade 5, containing *M. wolfii* and relatives. The most characteristic feature of this fungus is formation of gemmae in clusters, both in substrate and on aerial mycelium. Gams (1976) use the term "chlamydospores" for gemmae, what seems to be not always proper because the cell wall of these structures is very thin and it could be easily mechanically damaged. In young cultures of *M. calciphila* the clusters of gemmae are quite loose, regularly placed, and globose with enlargements. Sometimes they are arranged in chains with thin liaisons (Fig. 160c, d). The cross walls were observed sporadically. Large clusters, up to 0.8 mm diam. built by dense layers of gemmae, with very short liaison, and with numerous anastomosae could be observed in older cultures (Fig. 160e). The arrangement of the gemmae/chlamydospores in chains and clusters has been observed also in *M. zychae, M. parazychae, M. beljakowae, M. kuchlmanii* and others (Gams 1976). The gemmae of *M. calciphila* (as well as these of *M. parazychae*) are usually completely rounded, in contrast with *M. zychae* Linnem., where the gemmae outline merges gradually into the connecting hyphal parts (Gams 1976). We suggest that gemmae are organs of symbiotic associations with bacteria, which seem to be quite widespread among *Mortierellales*, rather than resting structures (Fujimura et al. 2014, Ogawa et al. 2012).

The sporangiophores of *M. calciphila* are more slender than in *M. beljakovae* and do not have an apophysis, nor collerate. The sporangiophores of *M. calciphila* are often larger than sporangiophores of *M. zychae* and others species of section "elongata". The spores of *M. calciphila* resemble those of *M. zychae,* but they are colourless and some granules in cytoplasm could be seen. They are much more regular than spores of *M. parazychae, M. beljakowae and M. kuhlmanii.*

The most closely related species to *M. calciphila* was *M. formicicola* D.S. Clark & W. Gams. The ITS and LSU sequences of that species were generated by Wagner et al. (2013) for phylogenetic studies, but the description of this fungus is not available and probably this species is not validly published.

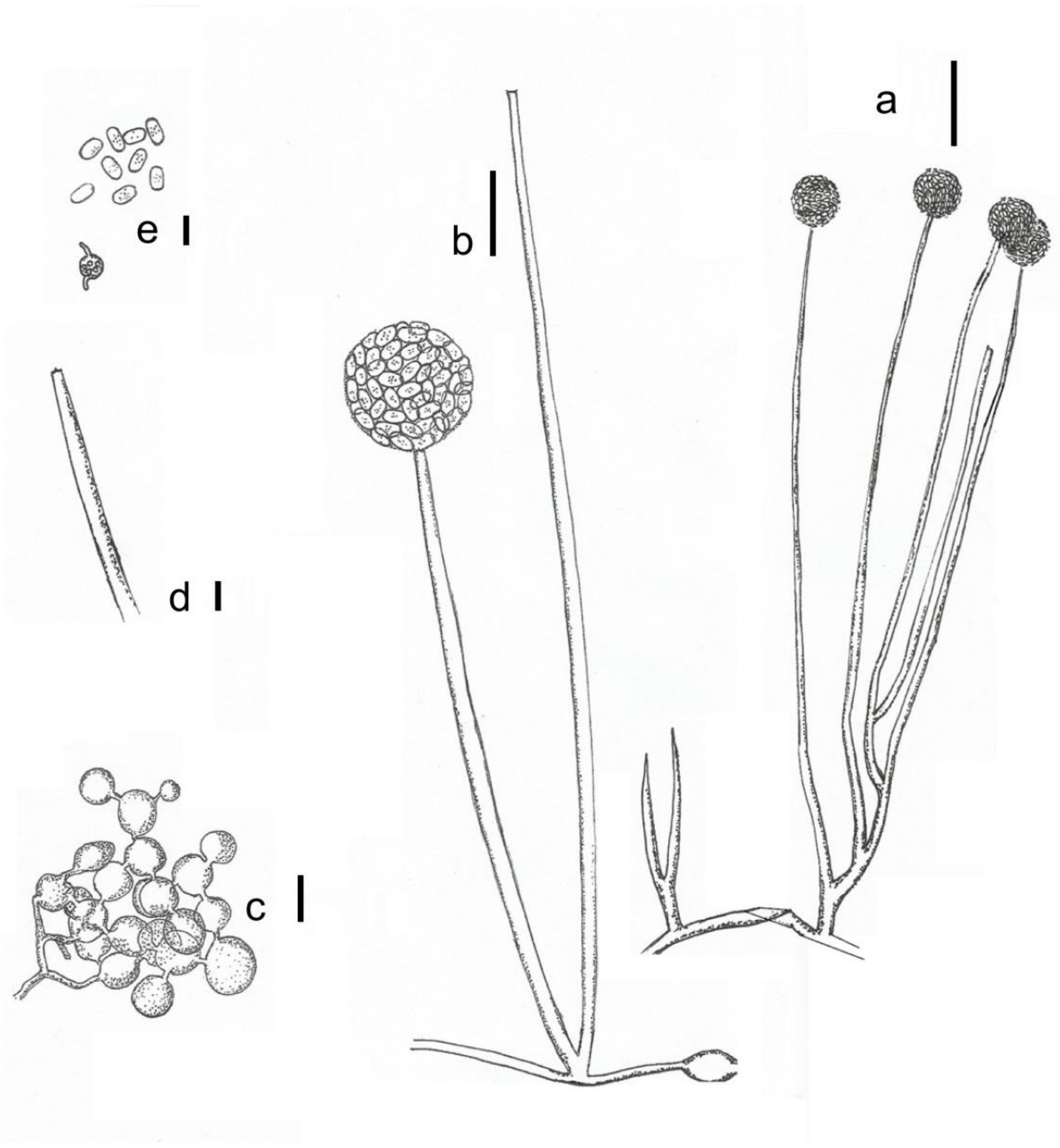


Fig. 159 ***Mortierella calciphila*** (**holotype**) **a** Branching sporophore emerging from substrate **b** Typical sporophore with sporangium on aerial mycelium **c** Loose cluster of young gemmae **d** Top of sporophore **e** Spores from sporangium, and germinating spore. Scale bars: a = 100 *µm*, b = 50 *µm*, c = 20 *µm*, d, e = 10 *µm*.

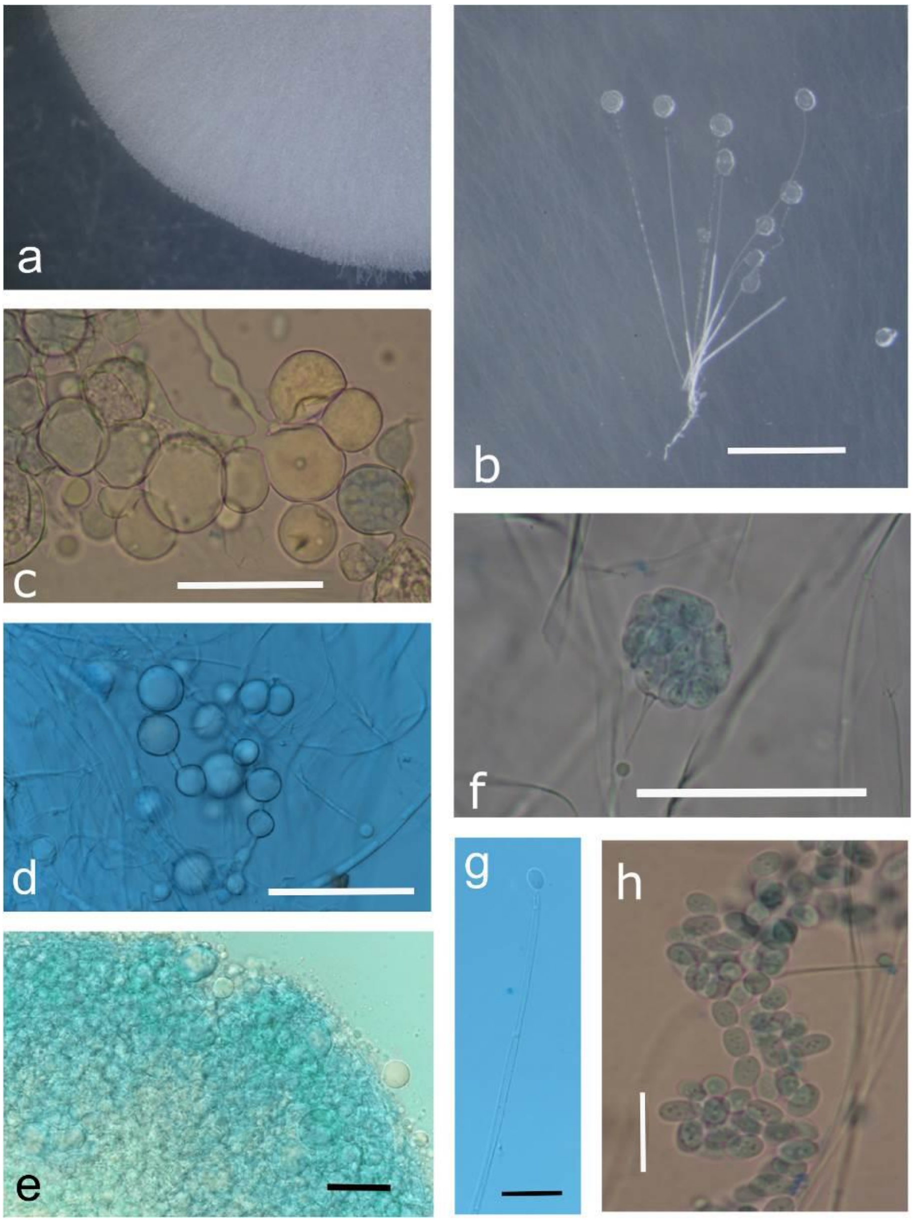


Fig. 160 ***Mortierella calciphila*** (**holotype**) **a** Type of growth (24 h colony) **b** Branching sporophore **c, d, e** Gemmae forming loose (c, d) or dense (e) clusters **f** Small sporangium formed on short sporophore emerging from aerial hyphae **g, h** Spores. Scale bars b = 500 *µm*, c–e = 20 *µm*, f = 50 *µm*, g, h = 20 *µm*.

Mucorales

Cunninghamellaceae

Absidia Tiegh.

The genus *Absidia* (*Cunninghamellaceae*, *Mucorales*) was originally described by van Tieghem (1876) with type species *A. reflexa* Tiegh. (Hesseltine and Ellis

1964). To the best of our knowledge, 21 species of *Absidia* have been reported thus far (Kirk et al. 2008).

The species belonging to this genus are characterized by the production of stolons and sporangiophores bearing pyriform columellate sporangia with deliquescent walls with a septum below the apophysis; the sporangiophores of *Absidia* never arise opposite the rhizoids as found in *Rhizopus* (Hesseltine and Ellis 1964). Species of *Absidia* typically exhibit rapid growth at temperatures ranging from 25^{o}C to 34^{o}C, although some species are able to grow at temperatures between 12^{o}C and 37°C (Hoffmann et al. 2007). They are frequently isolated from soil and dead or dying plant tissue (Hesseltine and Ellis 1964; Ho et al. 2004; Benny 2008). Several species of *Absidia* are implicated in diseases such as mucormycosis in humans and animals (Ribes et al. 2000; Santos 2003; Hoffmann and Voigt 2009; Alastruey-Izquierdo et al. 2010). Since first described, some species of *Absidia* have been transferred to other genera, for example, *Tieghemella* Berl. & De Toni, *Mycocladus* Beauverie, and *Proabsidia* Vuill. However, with the exception of *Lichtheimia*, all are regarded as synonyms of *Absidia* (Hesseltine and Ellis 1964; Schipper 1990; Kirk et al. 2008). Recently, Hoffmann et al. (2007) revised the classification of the genus based on physiological, phylogenetic, and morphological characteristics. They observed different growth patterns under different temperature conditions, and divided the species into three groups, namely, thermotolerant (species that exhibited optimum growth between 37^{o}C and 45^{o}C), mesophilic (species that exhibited optimum growth between 25^{o}C and 34^{o}C), and mycoparasitic (species that are potentially parasitic on other fungi within the order *Mucorales* and exhibit optimum growth below 30^{o}C). Although the identification of species based on morphological characteristics is important in traditional taxonomy, the delimitation of species of mucoralean fungi requires the addition of molecular data (O'Donnell et al. 2001; Hoffmann et al. 2013; Walther et al. 2013). In a previous study, a new species, *Absidia koreana* was reported from a soil sample from Dokdo island, Korea (Ariyawansa et al. 2015b). The phylogenetic tree for *Absidia* is presented in Fig. 161.

While evaluating the diversity of fungi of the order *Mucorales* isolated from a sample of rat dung from Gwangju, Korea a new species, based on morphological characteristics and multi-gene phylogenetic analyses, was isolated and is described here.

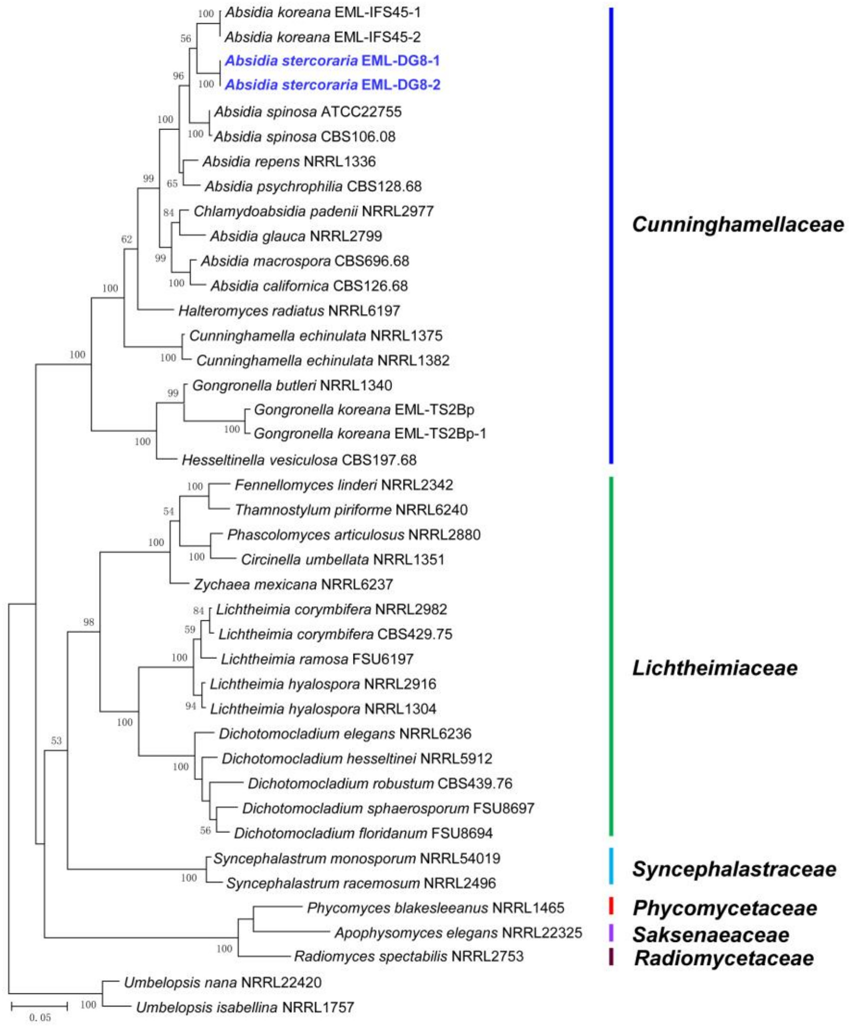


Fig. 161 Phylogenetic tree for *Absidia stercoraria* EML-DG8-1 and EML-DG8-2 and related species based on Maximum likelihood analysis of multi-genes including 18S and 28S rDNA, actin (Actin-1) and translation elongation factor (EF-1α). Sequences of *Umbelopsis nana* and *U. isabellina* were used as outgroups. Bootstrap support values >50% are indicated at the nodes. The *bar* indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold.

361. *Absidia stercoraria* Hyang B. Lee, H.S. Lee & T.T.T. Nguyen, *sp. nov.*

MycoBank number: MB 814409, *Facesoffungi number*: FoF 02064, Fig. 162

Etymology: *stercoraria*. Named for rat dung from which the species was first collected.

Holotype: EML-DG8-1, deposited at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, Korea. Living culture CNUFC-EML-DG8-1, in Chonnam National University Fungal Collection, Gwangju, Korea.

Colonies exhibit rapid growth on SMA attaining a diam. of 85–90 mm after 5 days at 25°C, initial colour white, later changing to grayish-white or smoky-gray, the reverse white and irregularly zonate. *Sporangiophores* are 4–6 *µm* wide and arise as

1–5 sporangiophores (average 2–3) per whorl from a single point on the stolons. *Sporangia* 19–30 × 20–31 *µm*, globose to pyriform, multi-spored, frequently with a bell-shaped apophysis. *Columellae* are 9–13 × 12–13.5 *µm*, hemisphaerical. *Collarette* appearing after sporangium maturation. *Sporangiospores* mostly short cylindrical, 4–5 × 2–3 *µm*. Zygospores not observed and rhizoids not well developed.

Notes: *Absidia stercoraria* is morphologically similar to *A. koreana*, but apparently differs from the related species by having a bell-shaped apophysis when cultivated on SMA, and by multi-gene sequence data. It is currently known from a single collection.

Material examined: REPUBLIC OF KOREA, Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Korea, from rat dung sample from Gwangju, Korea; EML-DG8-1 (ex-type) at Culture Collection of National Institute of Biological Resources (NIBR), Incheon, and preserved as glycerol stock at -80°C in the CNUFC; living culture(ex-type) deposited at Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012179) (ex-type).

The isolate was observed to grow over a wide range of temperatures with varying growth rates of 18 mm, 14 mm, and 13 mm per 24 hours on SMA, PDA and MEA, respectively. Optimal growth was observed around 25–27°C, slow growth was observed down to 20°C, and no growth above 35°C. *Absidia stercoraria* appears to be phylogenetically related to *A. koreana*, both clustering in the same clade together with other *Absidia* spp. within the family *Cunninghamellaceae* (Fig. 161).

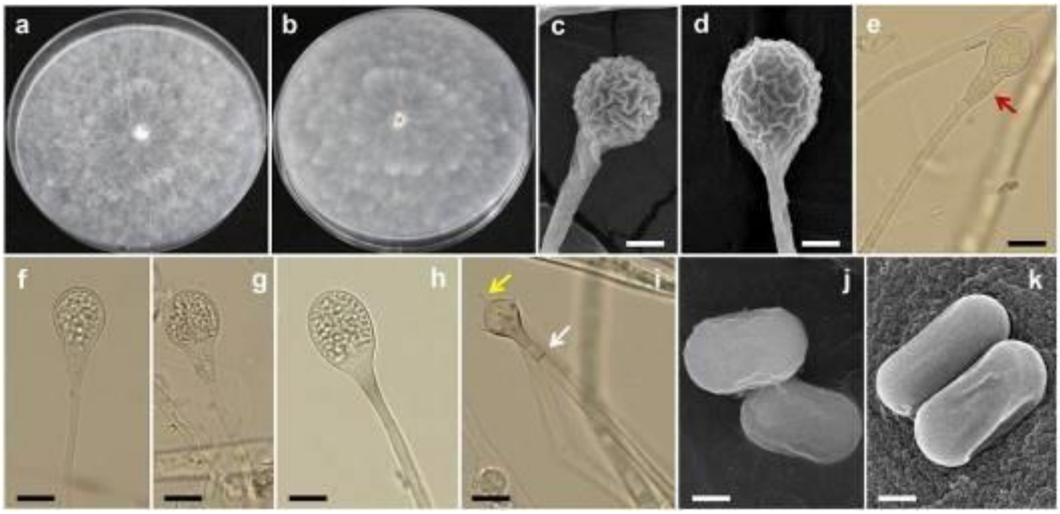


Fig. 162 ***Absidia stercoraria*** (**holotype**) **a**, **b** Colony in synthetic mucor agar (**a** obverse view, **b** reverse view) **c**, **d** Young sporangia with sporangial net wall **e** Young sporangium with a bell-shaped apophysis (*red arrow*) **f**, **g** Mature sporangia with bell-shaped apophysis **h** Mature sporangium without bell-shaped apophysis **i** Columellae with collarette and a single projection (*yellow arrow*), and septum (*white arrow*) below the apophysis **j, k** Rod-shaped sporangiospores. Scale bars: c, d = 10 *µm*, f–i = 20 *µm*, j, k = 5 *µm*.

Gongronella Ribaldi

Mucorales comprise ubiquitous, mostly saprotrophic organisms and are one of the most ancient groups of fungi. They can be easily isolated from soil, dung, water, stored grains, plants, as well as other fungi due to their rapid growth rate and ability to colonize and sporulate on diverse, carbohydrate-rich, terrestrial substrates (Benny 2008; O'Donnell et al. 2001). Some species are responsible for a number of opportunistic infections in immunocompromised humans and other mammals (Hoffmann et al. 2013). The genus *Gongronella* (*Cunninghamellaceae*, *Mucorales*) was established in 1952 by Ribaldi, for a single species, *Gongronella urceolifera* Ribaldi (Ribaldi 1952). The primary reason for introducing a separate genus to accommodate this species was its distinct urn-shaped apophyses and columellae. Three years later, based on the presence of an identical apophysis, Peyroneland Dal Vesco (1955) and Pici (1955) transferred *Absidiabutleri* Lendn. to *Gongronella*, both studies indicating that the type species, *G. urceolifera*, was identical to *G. butleri* (Lendn.) Peyronel & Dal Vesco. Hesseltine and Ellis (1961) added an additional species, *G. lacrispora* Hesselt. & J.J. Ellis, differing from *G. butleri* by forming circinate sporangia and teardrop-shaped sporangiospores. To date *Gongronella* includes only these two species: *G. butleri* and *G. lacrispora* (Kirk et al. 2008). Recently, Walther et al. (2013) showed that *Hesseltinella vesiculosa* H.P. Upadhyay and *Circinellala crymispora* Aramb. & Cabello belong to the *Gongronella* clade, but their morphological characteristics differ from those of the other species of *Gongronella*. In general, species of Gongronella grow slowly between 25ºC and 27ºC (Hesseltine and Ellis 1964) and are frequently found in soil (Hesseltine and Ellis 1961; Upadhyay 1969; Ho and Chen 1990). Several studies have reported that species of *Gongronella* have important biotechnological applications, such as the production of enzymes and antifungal proteins (Zhou et al. 2008; Wang et al. 2008; Wei et al. 2010). The taxonomy of *Gongronella* has been determined on the basis of morphological characteristics including the size and shape of sporangia, sporangiospores and columellae. Benny (1995) alluded to the limitations in the usage of morphological characters for species delineation in certain zygomycetes, and has suggested the use of molecular tools for solving existing controversies surrounding taxonomic classification. O’Donnell et al. (1998) also suggested that the traditional classification scheme for *Zygomycota* did not reflect the phylogenetic relationships among these taxa. Recently, molecular identification has been evaluated for *Mucorales*. O’Donnell et al. (2001) performed a comprehensive study of *Mucorales* with partial nucleotide sequences of nuclear 18S ribosomal RNA small subunit (SSU), nuclear large subunit 28S ribosomal RNA (LSU), and translation elongation factor-1α (EF-1*α*) gene exons. The phylogeny of *Mucorales* was also studied by White et al. (2006), who used the combined rRNA operon (18S + 28S + 5.8S gene) to infer relationships. In recent years, several studies based on multi-loci analysis (18S, 28S, EF-1α, actin, RNA polymerase II) have been conducted (Tanabe et al. 2003; Hoffmann et al. 2013; Walther et al. 2013). Different molecular targets have been used to characterize phylogenetic genera. In a previous study, a new species, *G. koreana*, isolated from forest soil from Jeonnam, Korea, was reported (Ariyawansa et al. 2015b). The phylogenetic trees are presented in Figs 163 and 164.

While evaluating the diversity of fungi of the order *Mucorales* isolated from a soil sample collected at Gwangan beach, Busan, Korea, an isolate showing morphological variation compared to other species of *Gongronella* was identified and, based on subsequent multi-gene phylogenetic analyses is described here as a new species.

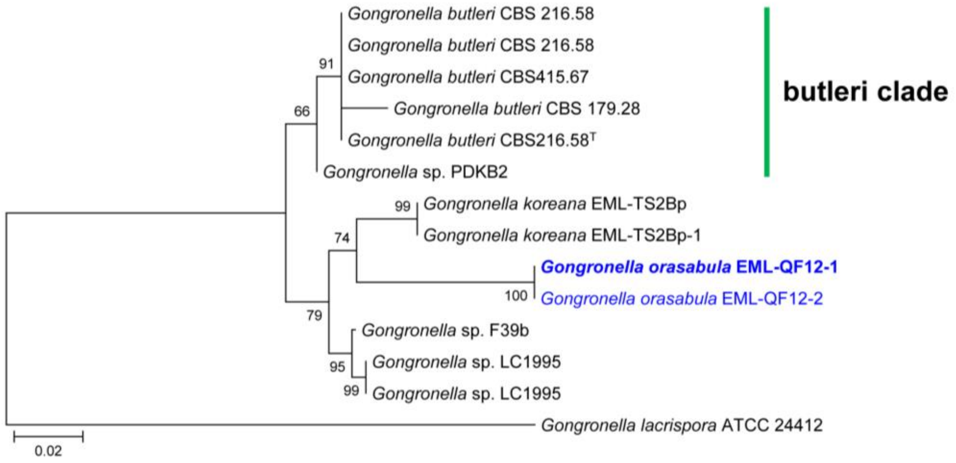


Fig. 163 Phylogenetic tree for *Gongronella orasabula* EML-QF12-1 and EML-QF12-2 based on Maximum likelihood analysis of ITS rDNA sequence. Sequences of *Gongronella lacrispora* was used as outgroup. Bootstrap support values >50% are indicated at the nodes. The bar indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold.

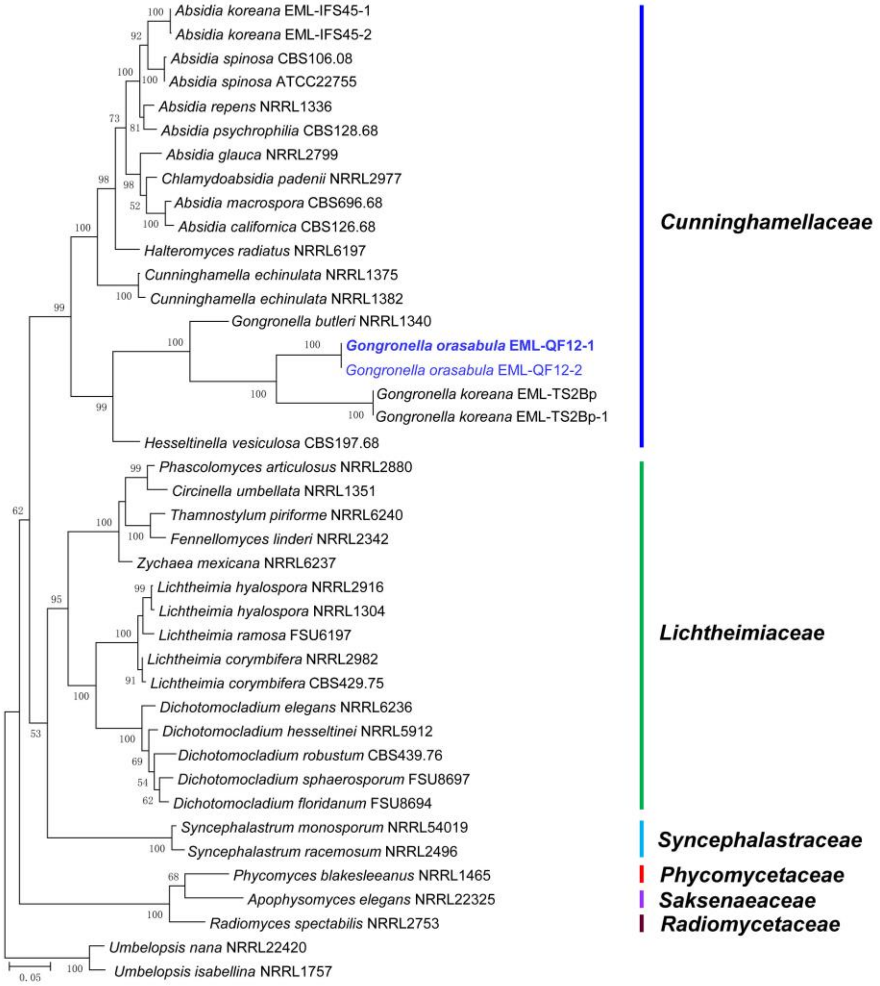


Fig. 164 Phylogenetic tree for *Gongronella orasabula* EML-QF12-1 and EML-QF12-2 and related species based on Maximum likelihood analysis of multi-genes including 18S and 28S rDNA, actin (Actin-1) and translation elongation factor (EF-1α). Sequences of *Umbelopsis nana* and *U. isabellina* were used as outgroups. Bootstrap support values >50% are indicated at the nodes. The *bar* indicates the number of substitutions per position.

362. *Gongronella orasabula* Hyang B. Lee, K. Voigt, P.M. Kirk & T.T.T. Nguyen, ***sp. nov.***

MycoBank number: MB 814447, *Facesoffungi number*: FoF 02065, Fig. 165

Etymology: *orasabula*. Referring to beach soil from which the species was first isolated (Busan, Korea).

Holotype: EML-QF12-1, deposited at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, Korea. Living culture CNUFC-EML-QF12-1, in Chonnam National University Fungal Collection (CNUFC), Gwangju, Korea.

Colonies exhibit fast growth on SMA attaining a diam. of 33–35 mm after 5 days at 25°C, initial colour white, later off-white, in reverse white with an irregular margin. *Sporangiophores* 35–200 × 2.5–4 *µm*, erect, either unbranched or with 2–3 branches. *Sporangia* 12–20 × 12.5–22 *µm*, globose to subglobose or calabash vase-shaped, multi-spored, with a thin wall having a purplish tinge and deliquescent at maturity. *Columellae* 2–3 × 3–4 *µm*, hemisphaerical, with a collarette. *Apophysis* of diverse shape, globose, subglobose to pyriform, 5–10 × 4.5–8.5 *µm*. *Sporangiospores* mostly bean-shaped, 2–3.5 × 2–2.5 *µm*. Chlamydospores absent in aerial mycelia. Zygospores not observed; rhizoids not well developed.

Notes: *Gongronella orasabula* is morphologically similar to *G. koreana*, but differs from related species by having larger and differently shaped sporangia. The apophysis is also larger, mainly globose, subglobose or pyriform or rarely long conical. Furthermore, the isolate has two septa below the apophysis.

Material examined: REPUBLIC OF KOREA, Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Korea, from a soil sample collected at Gwangan beach, Busan, Korea; EML-QF12-1 (**ex-type**) at Culture Collection of National Institute of Biological Resources (NIBR), Incheon, and preserved as glycerol stock at -80^{o}C in the CNUFC; living culture **(ex-type**) deposited at Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012180).

The isolate was observed to grow over a wide range of temperatures with varying growth rates of 7.3 mm, 6.7 mm, and 6 mm per 24 hours on SMA, PDA (potato dextrose agar), and MEA (malt extract agar), respectively. Optimal growth was observed at 27^{o}C, slow growth was observed at 20^{o}C, and no growth at 37^{o}C. *Gongronella orasabula* appears to be phylogenetically related to *G. koreana*, both clustering in the same clade together with *G. butleri* which is the type of the genus *Gongronella* (Figs 163, 164).

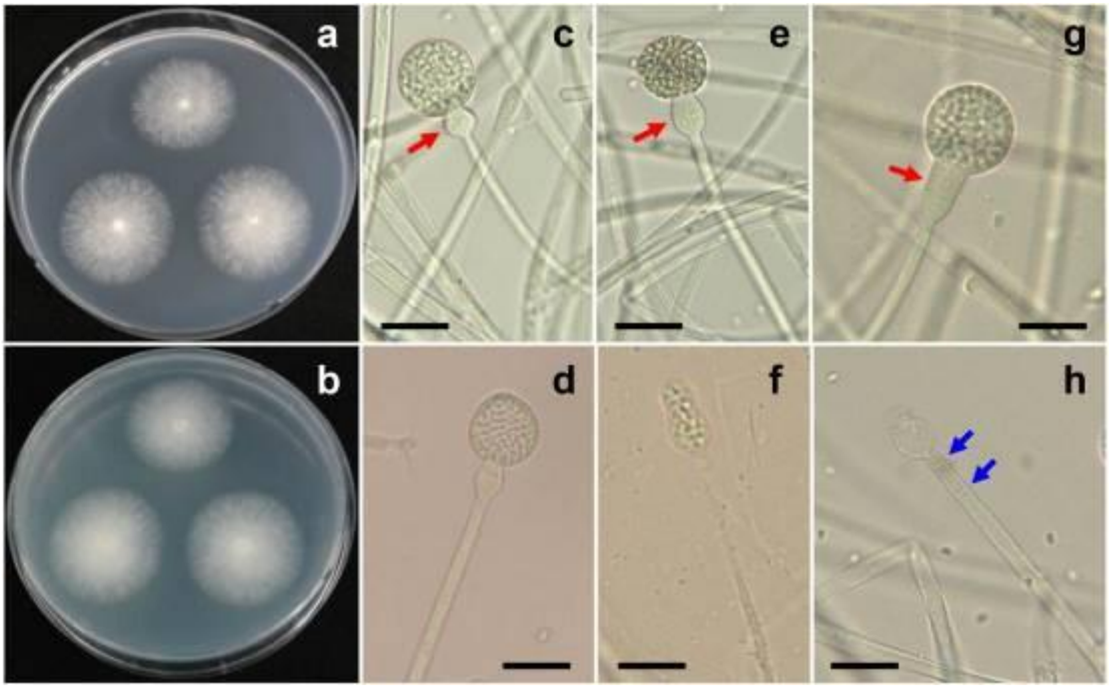


Fig. 165 ***Gongronella orasabula*** (**holotype**) **a**, **b** Colony in synthetic mucor agar (SMA) (**a** from above, **b** reverse view) **c**–**g** Mature sporangia with variously shaped apophysis (red

arrows) and sporangia **h** Columellae with collarette and two septa (blue arrows). Scale bars = 20 *μm*.

Mucor Fresen.

The *zygomycota* is an artificial grouping of related basal clades comprising the subphyla *Mortierellomycotina* Kerst. Hoffm. et al., *Mucoromycotina* Benny, *Kickxellomycotina* Benny and *Zoopagomycotina* Benny (Muszewska et al. 2014). The genus *Mucor* is the largest within the *Mucoromycotina* and includes more than 50 species several of which have important economical application, including the production of enzymes, fumaric acid, fatty acid, and also antifungal agents for plants (Dexter and Cooke 1984; Alves et al. 2002; Roa Engel et al. 2008). It is characterized by fast-growing colonies, simple or branched sporangiophores without basal rhizoids, non-apophysate sporangia, and zygospores which are borne from opposed suspensors, possess a thick pigmented and ornamented zygosporangium and are seldom produced (Schipper and Samson 1978; Benny 2013). This genera has a worldwide distribution, with most species described as saprobes commonly isolated from soil, stored grains, fruits, vegetables and the excrement of herbivores (Schoenlein-Crusius et al. 2006; Jacobs and Botha 2008; Santiago et al. 2011, 2013).

According to Álvarez et al. (2011) *Mucor* has the greatest number of described species among *Mucorales*. In a series of studies, Schipper (1973, 1975, 1976, 1978) monographed this genus and described 39 species, four varieties and 11 forms. Subsequently, 17 species have been proposed (Mehrotra and Mehrotra 1978; Mirza et al. 1979; Subrahamanyam 1983; Chen and Zheng 1986; Schipper and Samson 1994; Watanabe 1994; Zalar et al. 1997; Pei 2000; Alves et al. 2002; Jacobs and Botha 2008; Hermet et al. 2012; Madden et al. 2012).

Molecular studies have shown that *Mucor* is polyphyletic (O'Donnell et al. 2001; Kwasna et al. 2006; Jacobs and Botha 2008; Budziszewska and Piatkowska 2010; Álvarez et al. 2011). Based on phylogenetic relationships inferred from data of LSU and ITS regions (rDNA), and morphological characteristics, Walther et al. (2013) concluded that *Mucor* and *Backusella* Hesselt. & J.J. Ellis species represents a natural group characterized by transitorily recurved sporangiophores. Therefore, all *Mucor* species with this feature were transferred to *Backusella* [*B. grandis* (Schipper & Samson) G. Walther & de Hoog, *B. indica* (Baijal & B.S. Mehrotra) G. Walther & de Hoog, *B. oblongielliptica* (H. Nagan., Hirahara & Seshita ex Pidopl. & Milko) G. Walther & de Hoog, *B. oblongispora* (Naumov) G. Walther & de Hoog, *B. recurva* (E.E. Butler) G. Walther & de Hoog, *B. tuberculispora* (Schipper) G. Walther & de Hoog, and *B. variabilis* (A.K. Sarbhoy) G. Walther & de Hoog]. Considering that some of the characteristics traditionally used to separate *Zygorhynchus* Vuill. from *Mucor*, such as the unequal suspensors of the zygospores and the *Zygorhynchus* zygospore production pattern (two suspensors originating from the same hypha) do not represent synapomorphies of the genus *Zygorhynchus*, and seem to be convergent characters within *Mucor*, Walther et al. (2013) recombined all *Zygorhynchus* species in *Mucor* as follows: *M. exponens* (Burgeff) G. Walther & de Hoog, *M. fusiformis* G. Walther & de Hoog, *M. heterogamus* Vuill., *M. japonicus* (Komin.) G. Walther & de

Hoog, *M. megalocarpus* G. Walther & de Hoog, *M. moelleri* (Vuill.) Lendn. and *M. multiplex* (R.Y. Zheng) G. Walther & de Hoog. Non-thermophilic *Rhizomucor endophyticus* and *Circinella rigida* were reclassified as *M. endophyticus* (R.Y. Zheng & H. Jiang) J. Pawłowska & G. Walther and *M. durus* G. Walther & de Hoog, respectively.

Recently, molecular data have been used to evaluate mucoralean species (Hoffmann et al. 2013; Walther et al. 2013). During studies on the *Mucorales* from Brazil and Korea, taxa of *Mucor* that differs morphologically and molecularly from the other species was isolated and are thus described as new. The phylogenetic tree for *Mucor* are presented in Figs 166–169.

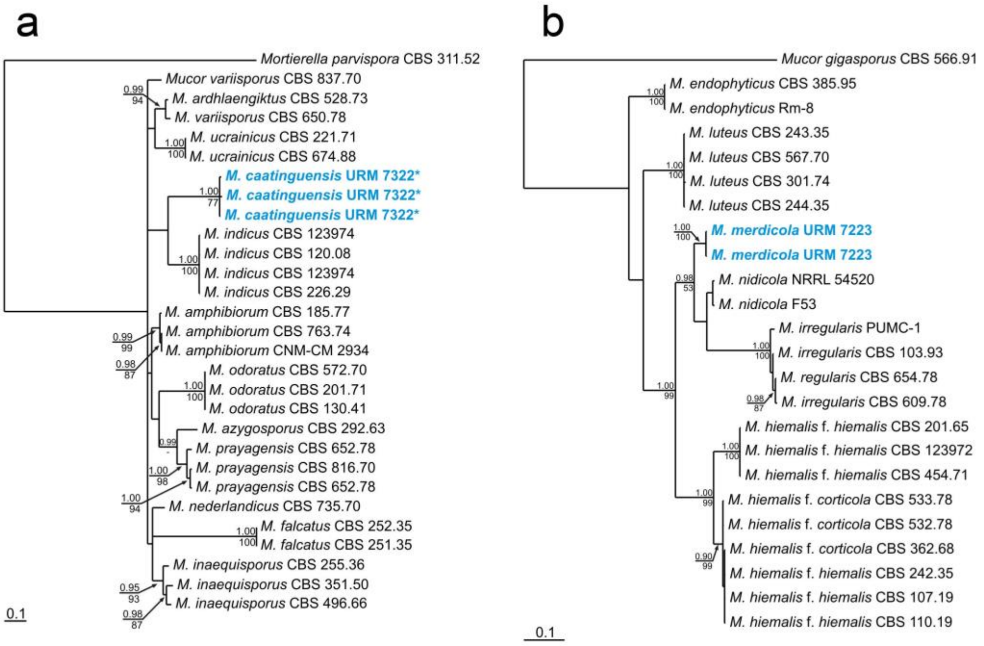


Fig. 166 Phylogenetic tree of *Mucor* constructed using the large subunit (LSU) rDNA sequence data. *Circinella* species were used as outgroup. Sequences are labeled with their database accession numbers. Support values are from Bayesian inference and maximum likelihood analyses (values above and below the branches, respectively). The sequences obtained in this study are annotated in blue.

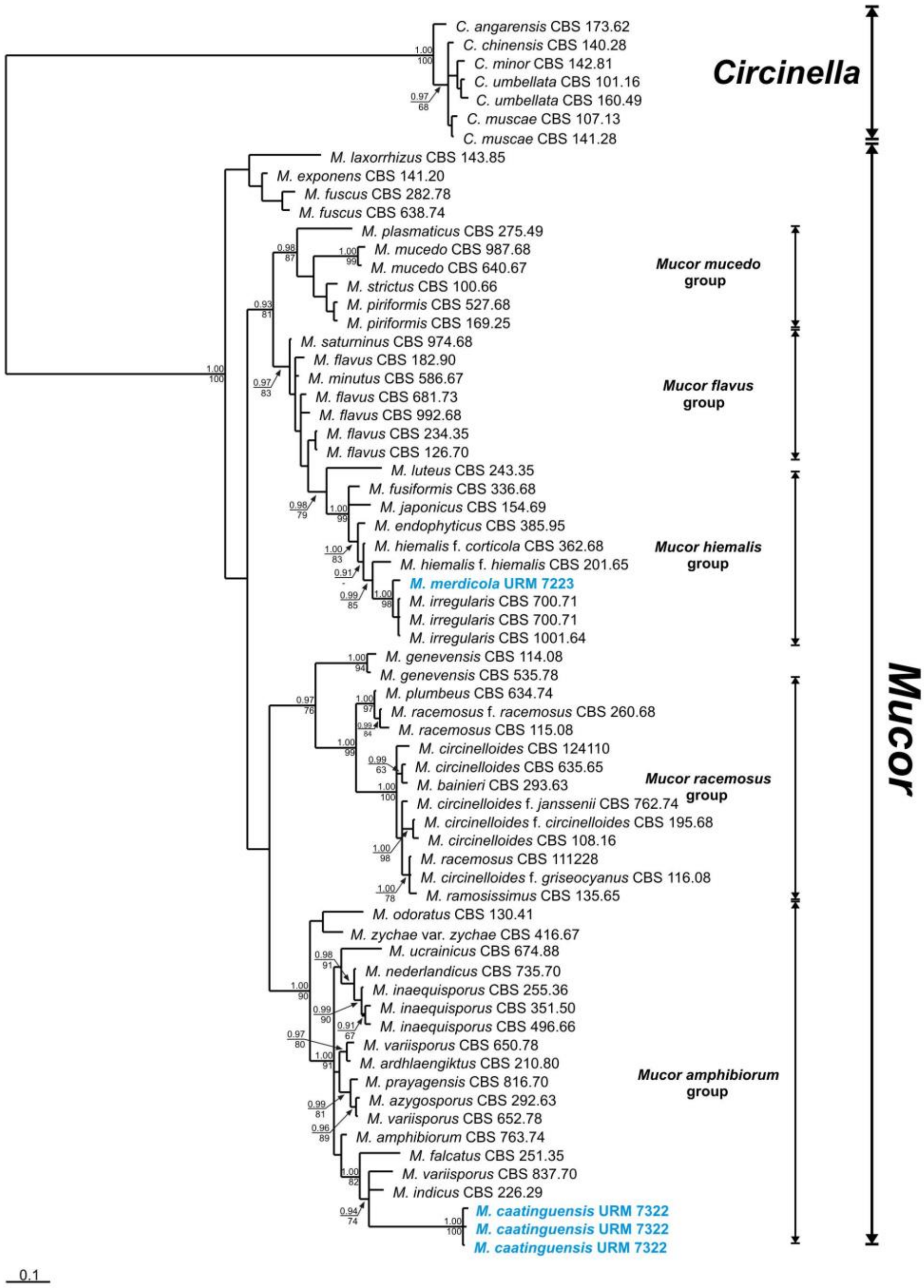


Fig. 167 Phylogenetic tree of *M. amphibiorum* group constructed using the ITS rDNA sequences. *Mortierella parvispora* was used as outgroup. b Phylogenetic tree of *Mucor hiemalis* group constructed using the ITS rDNA sequences. *Mucor gigasporus* was used as outgroup. Sequences are labeled with their database accession numbers. Support values are from Bayesian inference and maximum likelihood analyses (values above and below of the branches, respectively). Sequences with only ITS1 and 5.8s rDNA are marked with *. New taxa are in blue and ex-type strains in bold.

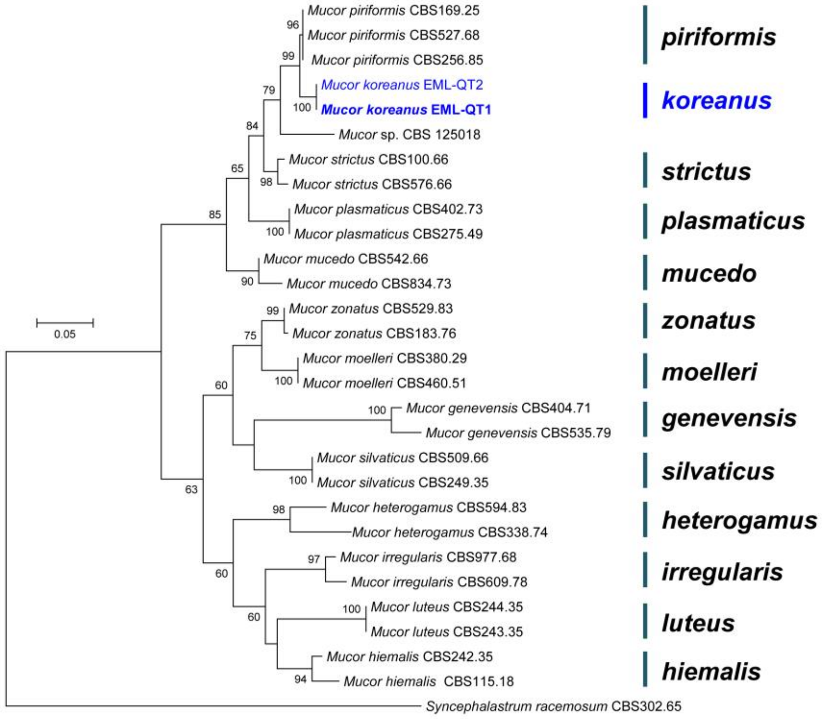


Fig. 168 Phylogenetic tree for *Mucor koreanus* EML-QT1 and EML-QT2 based on Maximum likelihood analysis of ITS rDNA sequence. Sequence of *Syncephalastrum racemosum* was used as outgroup. Bootstrap support values >50% are indicated at the nodes. The *bar* indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold.

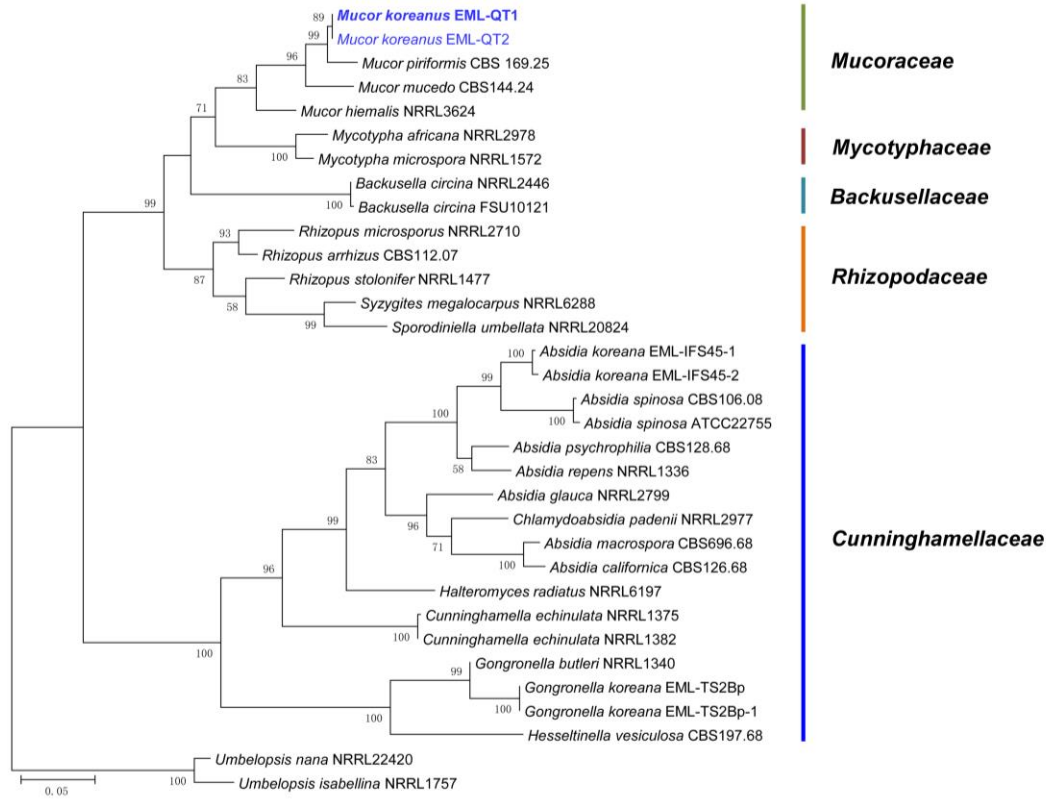


Fig. 169 Phylogenetic tree for *Mucor koreanus* sp. nov. EML-QT1 and EML-QT2 and related species based on Maximum likelihood analysis of multi-genes of 18S and 28S rDNA, actin (Actin-1) and translation elongation factor (EF-1α). Sequences of *Umbelopsis nana* and *U. isabellina* were used as outgroups. *Numbers* at the nodes indicate the bootstrap values (>50%) from 1000 replications. The *bar* indicates the number of substitutions per position.

363. *Mucor caatinguensis* A.L. Santiago, C.A. de Souza & D.X. Lima, ***sp. nov***.

Index Fungorum number: IF 551680, *Facesoffungi number*: FoF 01328, Fig. 170

Etymology: *caatinguensis*. Referring to the biome where the species was first isolated.

Holotype: URM 7322

Fast growing colonies, 9 cm diam. after 72 hours in MEA at 25 ºC, firstly white then turning cream with grey spots (MP 18A1), touching the plate lid in the central region. Reverse yellow (MP 10H2). Sterile mycelium abundant. *Sporangiophores* coenocytic, simple or slightly sympodially branched with long branches, (5–)7.5–15(–17) *µm* diam. with or without yellowish contents, slightly roughed-wall. Some sporangiophores show a globular swelling distant from the columellae. *Sporangia* first yellow then becoming light brown, globose, subglobose, 25–65 *µm* diam., subglobose to slightly flattened, 30–60 × 32–55 *µm* with a slightly echinulate wall. *Columellae* light gray, smooth-walled, globose, subglobose, (20–)2–45 (–60) *µm* in diam., ellipsoid, obovoid with a truncated base (mostly) and piriform (–25)30–60(–75) × (20–)27–45(–55) *µm*. *Collar* evident. *Columellae* cylindrical with or without a constriction in the central part, 24.5–35 × 30–55 *µm* where rarely observed. *Sporangiospores* hyaline, smooth-walled, regular in size and containing granules at each end, mostly ellipsoid, 5–6(–7) × 3–5 *µm* and cylindrical ellipsoid, 5–6 × 3–4 *µm*., some subglobose and globose, 3–5 *µm* diam. *Chlamydospores* abundant, globose, subglobose and doliform, sometimes produced in the sporangiophores. *Zygosporangia* not observed.

Material examined: BRAZIL, Buíque: Parque Nacional do Catimbau (8º31'55.8''S, 37º15'34.2''W), in soil samples. Soil, 11.III.2014, leg. C. Lira (URM 7322) and deposited in the Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012174).

Media and temperature tests: On MEA. At 10ºC – very limited growth (2 cm in diam. in 120 hours); total lack of reproductive structures. At 15ºC – low colonies (< 1 mm in height) with slow growth (4 cm in diam. after 120 hours); poor sporulation. At 20ºC – low colonies (<1mm diam.) with slow growth (5 cm in 120 hours); good sporulation. At 25ºC – better growth (9 cm in 72 hours); excellent sporulation. At 30ºC – good growth (8 cm in 72 hours); excellent sporulation. At 35ºC – better growth than at 15 and 20ºC (9 cm in 120 hours); rare sporangiophores production and poor sporulation. At 40ºC – lack of growth and sporulation. The growth of *M. caatinguensis* on PDA was slightly slower than on MEA at all tested temperatures. However, at 35ºC, on PDA, the production of reproductive structures was good, and the sporangiophores were more sympodially branched (up to seven times) than in at other temperatures. The columellae were mostly applanate and bizarrely shaped sporangiophores were also observed.

Notes: *Mucor caatinguensis* is distinguished from the other species of the genus as it simultaneously produces numerous chlamydospores in mycelia (sometimes in sporangiophores), unbranched or weakly branched sporangiophores, columellae and sporangiospores that are variable in shape and size. At first, *Mucor caatinguensis* could be confused with *M. silvaticus* Hagem because of the unbranched or weakly sympodially branched sporangiophores, the small size of the sporangia (up to 70 *µm* diam.) and by the production of cylindrical ellipsoid sporangiospores. However, colonies of *M. silvaticus* are pale olive gray, and it produces blackish brown sporangia (Schipper 1973), in contrast to the cream colonies of the new species, which show shows light brown sporangia. The former only produces sphaerical columellae, which are rarely ellipsoidal, never obovoid with a truncated base or piriform, as observed in *M. caatinguensis*. Additionally, the sporangiospores of *M. silvaticus* are 3.5–5.2 × 2.6–3.7 *µm*, smaller than the *M. caatinguensis* sporangiospores, and no chlamydospores where reported in *M. silvaticus*

The abundant production of chlamydospores, sometimes observed in sporangiophores, is also very common in *M. racemosus* f. *racemosus* Fresen. (Schipper 1976), although we did not observed these structures were not observed inside the columellae of *M. caatinguensis*. Nevertheless, the sporangiophores of *M. caatinguensis* are not as branched as those of *M. racemosus* f. *racemosus* which may be sympodially and monopodially branched. Additionally, the sporangiospores of *M.*

racemosus f. *racemosus* are broadly ellipsoidal to subglobose, and the colonies of *M. racemosus* f. *racemosus* are pale smoke gray, whereas the colonies of the new species are cream with grey spots.

Our molecular analysis (LSU and ITS rDNA, Figs 166, 167, respectively) showed that *M. caatinguensis* is genetically different from the other species of the genus, and placed the new species within the *M. amphibiorum* group, close to *M. indicus* Lendn. (Walther et al. 2013). In fact, the colour of both colonies of *M. indicus* and *M. caatinguensis* may be similar, but the sporangiophores of *M. indicus* are repeatedly sympodially branched (with long branches) and the columellae are mostly applanate and subglobose. We found repeatedly sympodial branches in *M. caatinguensis* at 35ºC on PDA. According to Schipper (1978), chlamydospores of *M. indicus* are also abundant in cultures grown in darkness at 20 ºC, but only in substrate hyphae, and the sporangiospores are ellipsoidal to globose.

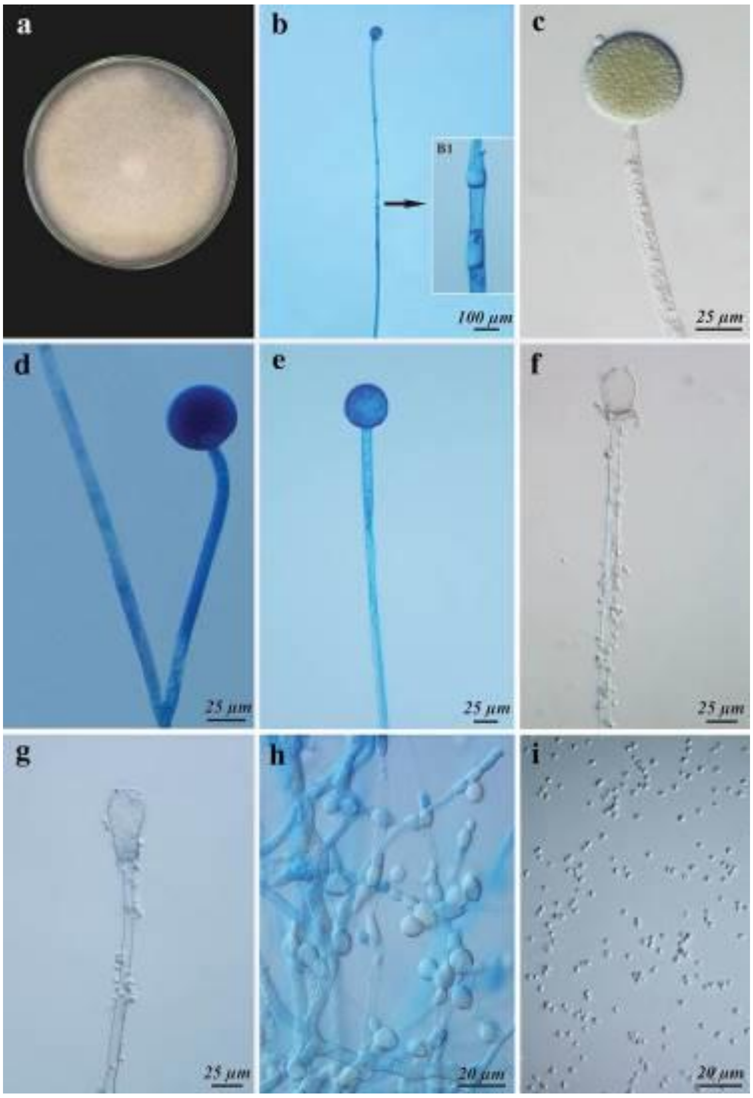


Fig. 170 ***Mucor caatinguensis*** (**holotype**) **a** Colony surface **b, b1** Simple sporangiophore with chlamydospores **c** Simple sporangiophore with sporangia **d** Sporangiophore branch **e–g**

Simple sporangiophores with columellae with different shapes **h** Chlamydospores **i** Sporangiospores.

364. ***Mucor koreanus*** Hyang B. Lee, S.J. Jeon & T.T.T. Nguyen, ***sp. nov.***

MycoBank number: MB 814424, *Facesoffungi number*: FoF 02066, Fig. 171

Etymology: *koreanus*. Referring to the country which from the species was first isolated (Korea).

Holotype: EML-QT1, deposited at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, Korea. Living culture CNUFC-EML-QT1, in Chonnam National University Fungal Collection, Gwangju, Korea.

Colonies growing fast on PDA, dark brown in the center, with a lighter margin, grayish-white in reverse, reaching 70–72 mm diam. at 23^{o}C after 2 days of incubation. *Sporangiophores* 21–44 *µm* wide, erect, unbranched or branched sympodially. *Sporangia* globose, subglobose, yellow to golden brown, multi-spored, reaching 129–159 × 137–165 *µm*; at maturity the sporangial wall fully deliquesces, leaving a small collar. *Columellae* globose, cylindrical-ellipsoidal, reniform or pyriform, 67–82 × 71–87 *µm*. *Sporangiospores* of diverse shape, ellipsoidal, globose, sometimes asymmetrically globose or bean-shaped, 9–14 × 6.5–11.5 *µm*. *Zygospores* not observed.

Notes: *Mucor koreanus* was similar in morphology and closely related to *M. piriformis* A. Fisch., but differs by larger sporangiospores, their different shapes, and colour of sporangia. Columellae are diverse in shape. Sometimes, the collar is not seen below the columellae. The sporangiospores have thick walls.

Material examined: REPUBLIC OF KOREA, Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Korea, from a tangerine fruit purchased from the grocery store in Korea; EML-QT1 (ex-type) at Culture Collection of National Institute of Biological Resources (NIBR), Incheon, Korea, and preserved as glycerol stock at –80^{o}C in the CNUFC; living culture (ex-type) deposited at Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012181).

The isolate was observed to grow over a wide range of temperatures with varying growth rates on PDA, MEA (malt extract agar), and CDA (czapek dox agar) of 35 mm, 17 mm and 28 mm per 24 hours, respectively. Optimal growth was observed around 20–23^{o}C, slow growth was observed at 5^{o}C, and no growth at 27^{o}C. *Mucor koreanus* appears to be phylogenetically related to *M. piriformis*, both clustering in the same clade together with *M. mucedo* which is the type of the genus *Mucor* (Figs. 168, 169).

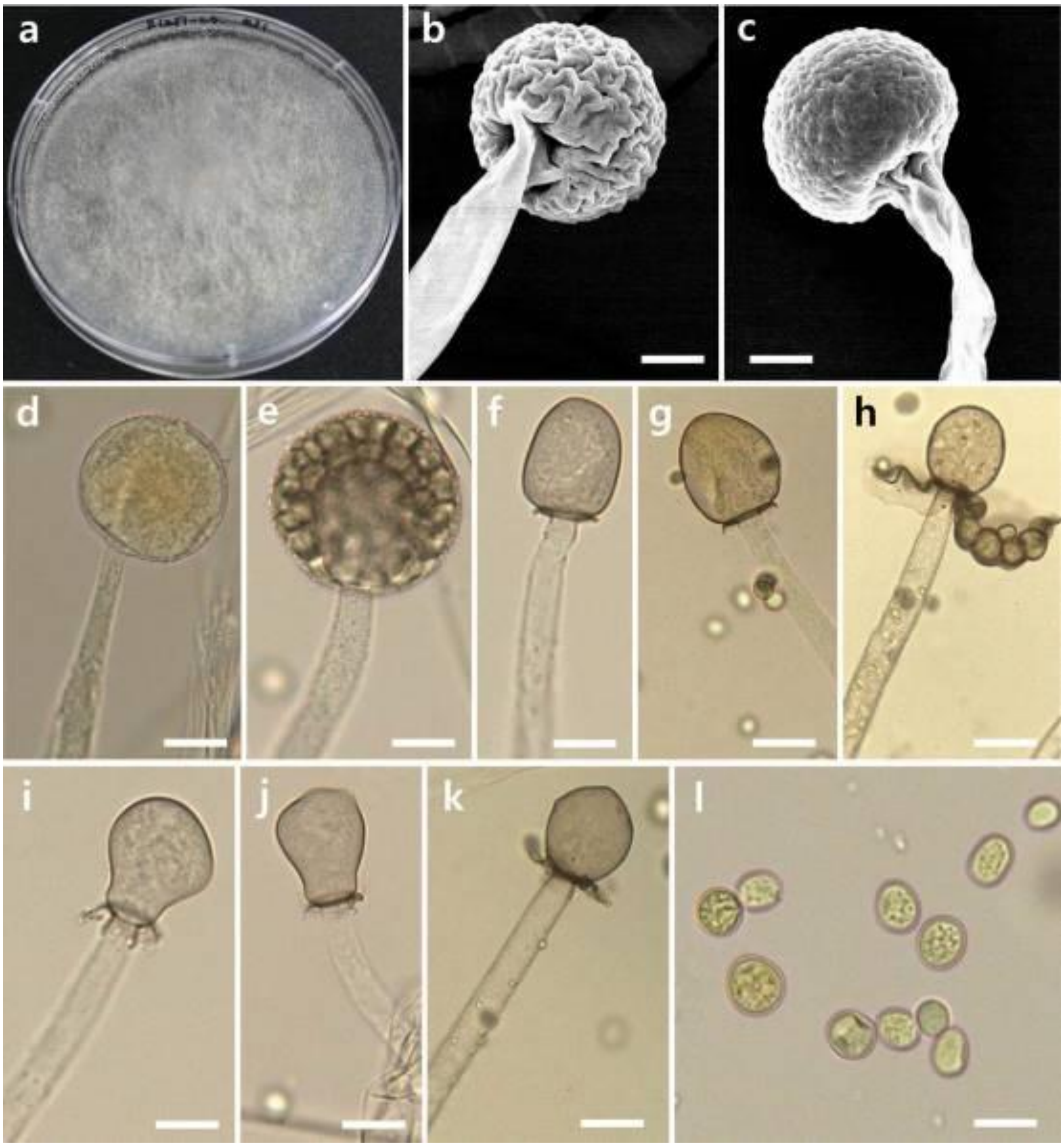


Fig. 171 ***Mucor koreanus*** (**holotype**) **a** Colony on potato dextrose agar **b**–**d** Young sporangia **e** Mature sporangium **f**–**k** Columellae with clear collar present at the apex of the sporangiophore **l** Sporangiospores. Scale bars: b, c = 50 *µm*, d–l = 20 *µm*.

365. ***Mucor merdicola*** C.A. de Souza & A.L. Santiago, ***sp. nov***.

Index Fungorum number: IF 551679, *Facesoffungi number*: FoF 01327, Fig. 172

Etymology: *merdicola*. Merda-dung, cola-dwelling.

Holotype: URM 7223

Colony initially white then becoming yellowish to cream (MP 19D1) with yellowish reverse (MP 11J6), reaching 9.5 cm in diam. and 9 mm in height after 4 days in MEA at 25ºC. *Sporangiophores* simple or repeatedly sympodially branched, erect, some slightly curved, arising from aerial hyphae (3–) 5–15.5 (–18) *µm* diam., hyaline, smooth walled, with or without yellowish contents. *Sporangia* globose (16–) 17.5–60 (–85) *µm* diam., initially yellow becoming greyish brown with diffluent wall, smooth-walled. *Columellae* globose (12.5–)15–45(–50) *µm*, subglobose and applanate (15–)20–29 × 30–34(–35) *µm*, hyaline or light to grey, smooth-walled; *collar* absent or little evident. *Sporangiospores* smooth-walled, hyaline, mostly ellipsoid to fusiform (2.5–)5–7 × 5–8.5(–10.5), but also ellipsoid 4–7.5 × 3–7.5(–10) *µm* or subglobose (2.5–)4–7.5(–8.5) *µm* diam., rarely globose. *Rhizoids* poorly developed. *Chlamydospores* globose, subglobose, doliform, some bizarre in shape. *Zygosporangia* not observed.

Media and temperature tests: On MEA. At 5ºC – lack of growth and sporulation. At 10ºC – slow growth colonies, reaching 5.9 cm in diam. after 168 hours; poor sporulation. At 15ºC – Slow growth (9 cm in 192 hours); good sporulation. At 20ºC – Better growth than at 10 and 15ºC (9 cm in 120 hours); good sporulation. At 25ºC – better growth (9 cm in 72 hours); excellent sporulation. Growth reasonably good at 30ºC (9 cm in 144 hours); good sporulation. At 35ºC – limited growth (3.3 cm in 168 hours); rare sporophores production and poor sporulation. At 40ºC – lack of growth and sporulation. The growth of *M. merdicola* on PDA was a slightly slower than on MEA at all tested temperatures.

Material examined: BRAZIL, Arcoverde: Instituto Agronômico de Pernambuco (IPA) (8°25'00"S; 37°04'00"W), in dung samples, *Bos taurus* L., breed Holandesa. Dung, 05.IX.2014, leg. C.A.F de Souza (URM 7223) and deposited in the Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012175).

Habitat: Dung.

Notes: *Mucor merdicola* is morphologically similar to *M. circinelloides* f. *circinelloides* Tiegh. The former is distinguished from *M. circinelloides* f. *circinelloides* as it produces globose, subglobose and applanate columellae, differing from the obovoid to ellipsoidal columellae of *M. circinelloides* f. *circinelloides* as described by Schipper (1976). The author describes globose columellae in *M. circinelloides* f. *circinelloides* only in the small sporangia. Additionally, *M. merdicola* presents sporangiospores smooth-walled, mostly ellipsoid to fusiform, 5–7 × 5–8.5 *µm*, but also ellipsoid, subglobose and rarely globose, whereas *M. circinelloides* f. *circinelloides* sporangiospores are only ellipsoidal, mostly 5.4 × 4 *µm* (Schipper, 1976). Our molecular analysis (ITS and LSU rDNA shown in Figs 166 and 167, respectively) revealed that *M. merdicola* is genetically different from the other species of the genus and placed the new species within the *M. hiemalis* group (Figs 166 and 167), in which species are characterized as producing tall sporangiophores that are weakly sympodially branched, and small sporangia that do not exceed 80 *µm* diam., while *M. merdicola* produces sporangiophores that are repeatedly sympodially branched, similar to the ones produced by the species from the *M. circinelloides* group (Fig. 4b).

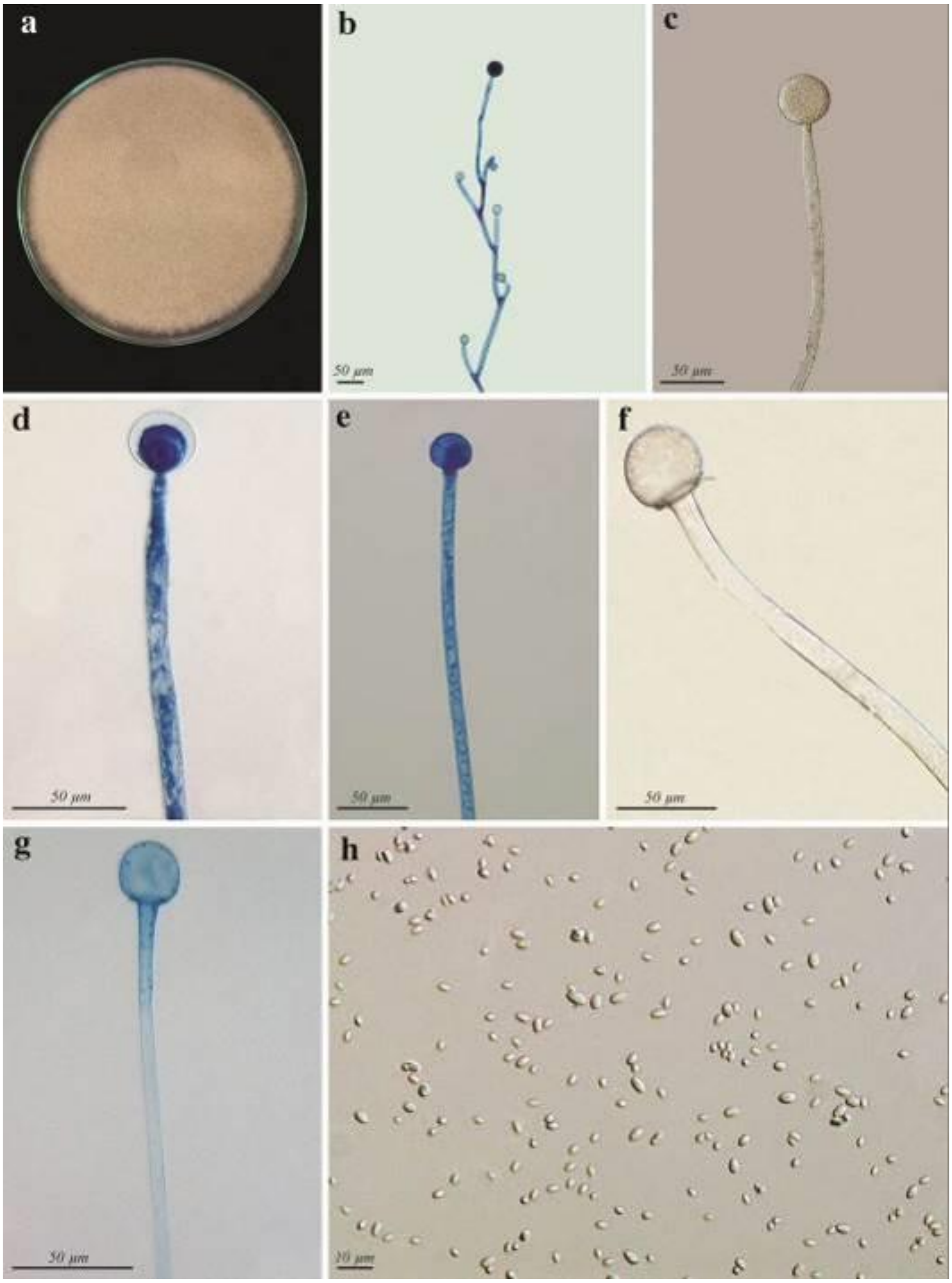


Fig. 172 ***Mucor merdicola*** (**holotype**) **a** Colony surface **b** A sympodially branched sporangiophore **c**, **d** Simple sporangiophores with sporangia **e**–**g** Simple sporangiophores with columellae with different shapes **h** Sporangiospores.

Rhizopus Ehrenb.

The classification system in the genus *Rhizopus* was previously revised based on physiological and morphological characteristics such as size of sporangia and sporangiophore and branching of rhizoids (Schipper 1984; Schipper and Stalpers 1984). Recently, however, molecular identification has been employed by analyses of rDNA ITS, small subunit (SSU), large subunit (LSU), actin (Actin-1) and translation elongation factor (EF-1α) genes (Abe et al. 2007, 2010; Hoffmann et al. 2013; Walther et al. 2013).

The genus *Rhizopus*, one of the genera of *Mucoromycotina*, includes many species that are often used as starters in food fermentation. In Asia especially, some species of *Rhizopus* are used to make Tempe, a fermented food based on soybeans (Schipper 1984; Schipper and Stalpers 1984). However, several species of *Rhizopus* are also implicated in diseases such as mucormycosis in humans and animals (Frye and Reinhardt 1993).

During a study on the *Mucorales* from a persimmon fruit in Korea, a species of *Rhizopus* was isolated that differs morphologically and molecularly from other species and is described here as new. The phylogenetic trees for *Rhizopus* are presented in Figs. 173, 174.

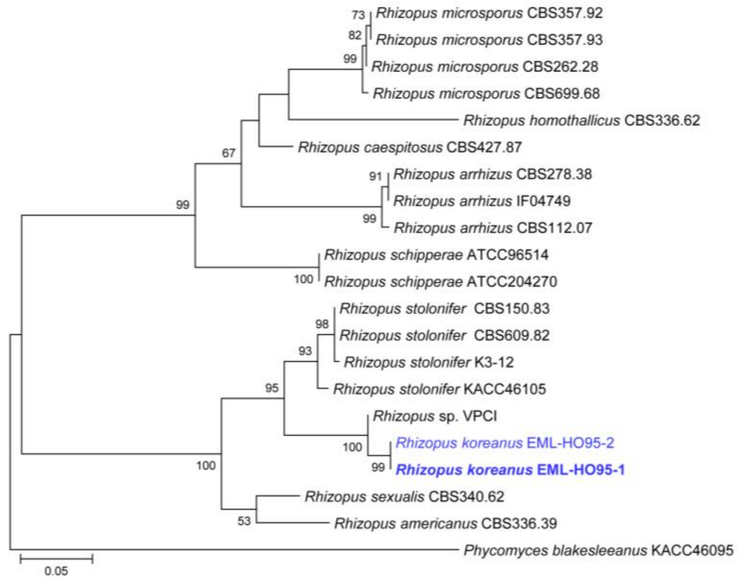


Fig. 173 Phylogenetic tree for *Rhizopus koreanus* EML-HO95-1 and EML-HO95-2 based on Maximum likelihood analysis of ITS rDNA sequence. Sequence of *Phycomyces blakesleeanus* was used as outgroup. Bootstrap support values >50% are indicated at the nodes. The *bar* indicates the number of substitutions per position. New taxa are in blue and ex-type strains in bold.

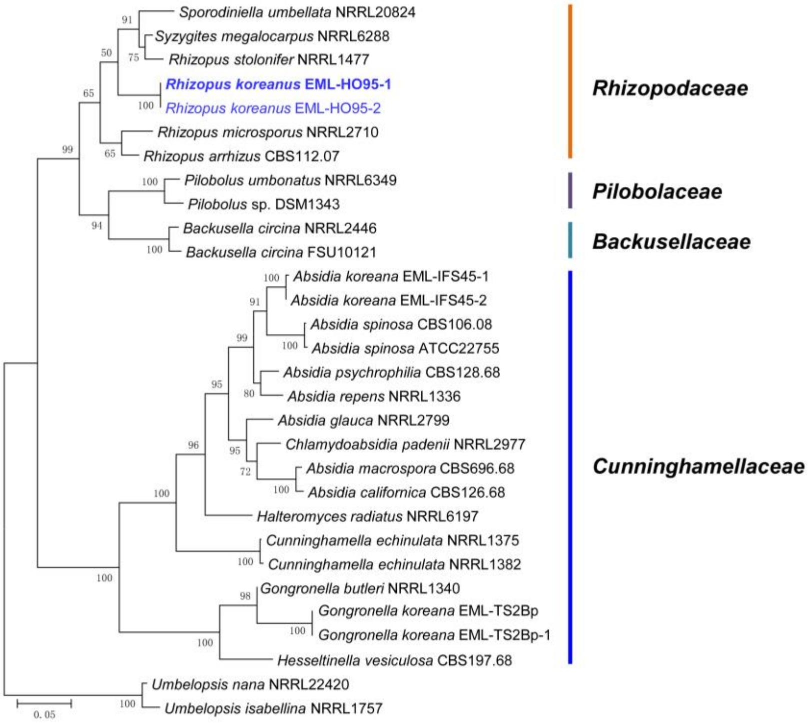


Fig. 174 Phylogenetic tree for *Rhizopus koreanus* EML-HO95-1 and EML-HO95-2 and related species based on Maximum likelihood analysis of multi-genes including 18S and 28S rDNA, actin (Actin-1) and elongation factor (EF-1α). Sequences of *Umbelopsis nana* and *U. isabellina* were used as outgroups. Bootstrap support values >50% are indicated at the nodes. The *bar* indicates the number of substitutions per position.

366. ***Rhizopus koreanus*** Hyang B. Lee & T.T.T. Nguyen, ***sp. nov.***

MycoBank number: *MB* 814406, *Facesoffungi number*: FoF 02067, Fig. 175

Etymology: *koreanus*. Referring to the country which from the species was first isolated (Korea).

Holotype: EML-HO95-1, deposited at the Environmental Microbiology Laboratory Fungarium, Chonnam National University, Gwangju, Korea, as dried fungal mass from culture (PDA), isolated from persimmon fruit, August 2014, by H.B. Lee. Living culture CNUFC-EML-HO95-1, in Chonnam National University Fungal Collection, Gwangju, Korea.

Colonies growing fast on PDA, reaching 73–77 mm diam. at 23ºC after 1 day of incubation, initially white, later grayish-black, reverse white, irregularly zonate. *Sporangia* globose to oval, reaching 88–215 × 84–193 (mean 123 × 126) *µm* in diam. *Columellae* 20–62 × 26–80 *µm*, conical, hemisphaerical or globose. *Sporangiospores* globose to ellipsoidal, sometimes asymmetrically ovoid, 12.5–17 × 14–19 (mean 14.6 × 15.4) *µm*. *Zygospores* are seldom observed in the artificial media.

Notes: *Rhizopus koreanus* is similar in morphology and closely related to *R. stolonifera* (Ehrenb.) Vuill., however the columellae were smaller, diverse in shape, reaching 20–61 × 26–79 *µm*, forming a separate clade as a new species in a phylogenetic tree.

Material examined: REPUBLIC OF KOREA, Division of Food Technology, Biotechnology & Agrochemistry, College of Agriculture & Life Sciences, Chonnam National University, Gwangju 61186, Korea, from a persimmon fruit purchased from the grocery store in Korea; EML-HO95-1 (ex-type) at Culture Collection of National Institute of Biological Resources (NIBR), Incheon, and preserved as glycerol stock at -80°C in the CNUFC; living culture (ex-type) deposited at Jena Microbial Resource Collection (University of Jena and Leibniz Institute for Natural Product Research and Infection Biology, Jena, Germany) (JMRC:SF:012182).

The isolate was observed to grow over a wide range of temperatures with varying growth rates on PDA, MEA (malt extract agar), and OA (oatmeal agar) of 74 mm, 52 mm, and 47 mm per 24 hours, respectively. Optimal growth was observed around 20–25°C, slow growth was observed at 5°C, and no growth at 35°C. *Rhizopus koreanus* appears to be phylogenetically related to *R. stolonifer* which is the type of the genus *Rhizopus* (Figs 173, 174).

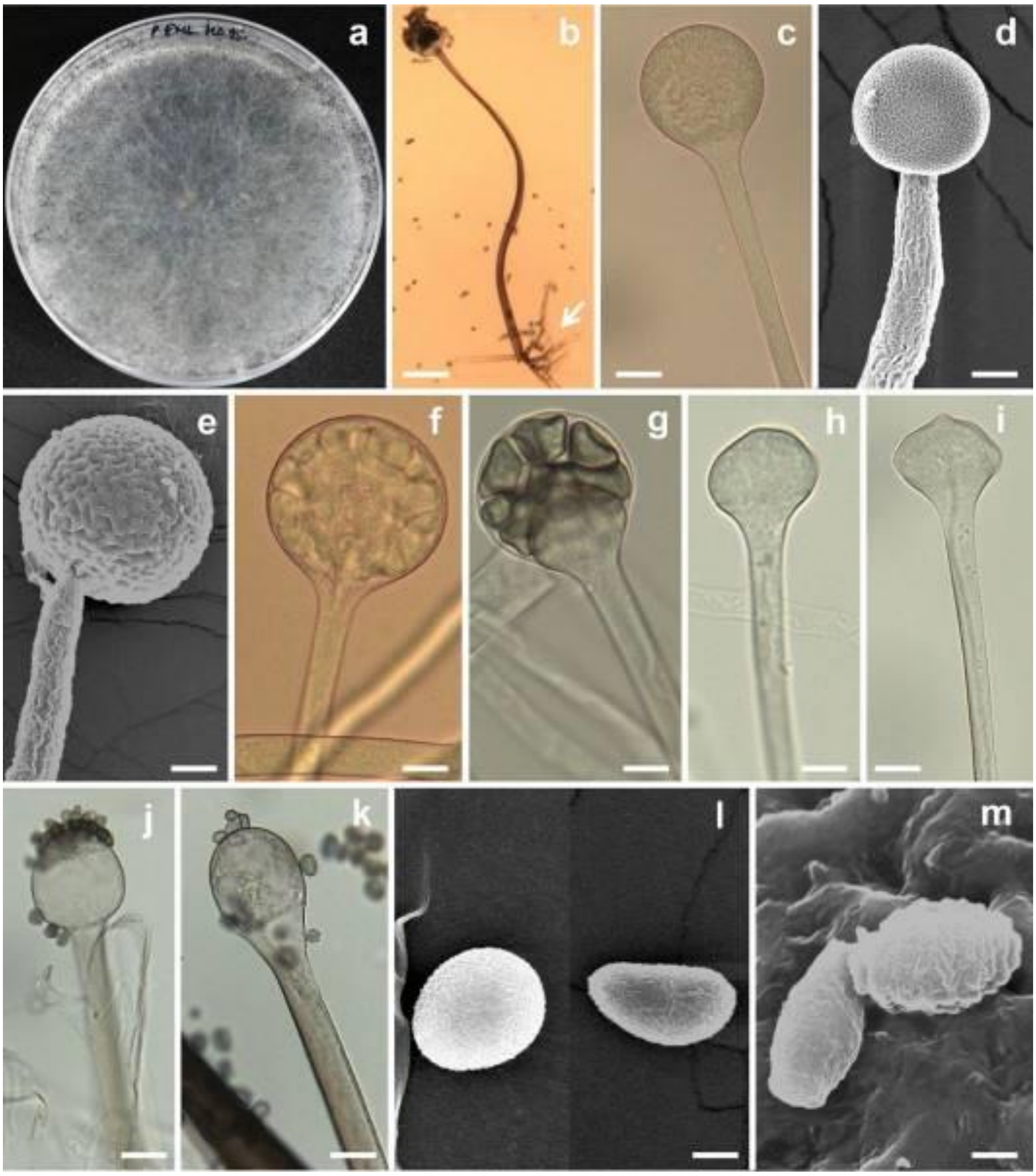


Fig. 175 ***Rhizopus koreanus*** (**holotype**) **a** Colony in potato dextrose agar **b** Rhizoids (white arrow) **c**–**e** Young sporangia **f**, **g** Mature sporangia **h**–**k** Different shapes of columella **l**, **m** Sporangiospores with asymmetrically oval to globose shapes. Scale bars: b = 200 *µm*, c–g = 50 *µm*, d, e = 50 *µm*, h–k = 20 *µm*, l = 30 *µm*, m = 5 *µm*.

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