FUSE

Fungal Systematics and Evolution

VOLUME 13
JUNE 2024
PAGES 183–440

doi.org/10.3114/fuse.2024.13.11

Fungal Planet description sheets: 1614–1696

P.W. Crous[1,2], Ž. Jurjević[3], S. Balashov[3], S. De la Peña-Lastra[4], A. Mateos[5], U. Pinruan[6], A. Rigueiro-Rodríguez[4], E.R. Osieck[7], A. Altés[8], P. Czachura[9], F. Esteve-Raventós[8], S. Gunaseelan[10], M. Kaliyaperumal[10], E. Larsson[11], J.J. Luangsa-ard[6], G. Moreno[8], F. Pancorbo[12], M. Piątek[9], S. Sommai[6], S. Somrithipol[6], M. Asif[13], G. Delgado[14], A. Flakus[9], T. Illescas[15], K. Kezo[10], P. Khamsuntorn[6], A. Kubátová[16], R. Labuda[17], C. Lavoise[18], T. Lebel[19], P. Lueangjaroenkit[20,21], J.G. Maciá-Vicente[22], A. Paz[23], M. Saba[13], R.G. Shivas[24], Y.P. Tan[25], M.J. Wingfield[2], T. Aas[26], B. Abramczyk[27], A.M. Ainsworth[28], A. Akulov[29], P. Alvarado[30], F. Armada[31], B. Assyov[32], R. Avchar[33], M. Avesani[34], J.L. Bezerra[35], J.D. Bhat[36], P. Bilański[37], D.S. Bily[38], F. Boccardo[39], F. Bozok[40], J.C. Campos[41], S. Chaimongkol[6,42], N. Chellappan[10], M.M. Costa[1], M. Dalecká[43,44], V. Darmostuk[9], V. Daskalopoulos[45], J. Dearnaley[24,46], B.T.M. Dentinger[47], N.I. De Silva[48], D. Dhotre[33], J.R. Carlavilla[8], C. Doungsa-ard[49], F. Dovana[50], A. Erhard[3], L.O. Ferro[51], S.C. Gallegos[52,53], C.E. Giles[54], G. Gore[55], M. Gorfer[56], F.E. Guard[57], S.-Å. Hanson[58], P. Haridev[59], R. Jankowiak[37], S.N. Jeffers[54], H. Kandemir[1], A. Karich[60], K. Kisło[61], L. Kiss[24], I. Krisai-Greilhuber[62], K.P.D. Latha[59], M. Lorenzini[63], S. Lumyong[48], P. Manimohan[59], J.L. Manjón[8], F. Maula[13], E. Mazur[9], N.L.S. Mesquita[64], K. Młynek[65], S. Mongkolsamrit[6], P. Morán[66], R. Murugadoss[10], M. Nagarajan[10], S. Nalumpang[67], W. Noisripoom[6], S. Nosalj[68], Q.S Novaes[64], M. Nowak[27], J. Pawłowska[27,69], M. Peiger[70], O.L. Pereira[71], A. Pinto[3], M. Plaza[72], E. Polemis[45], A. Polhorský[73], D.O. Ramos[71], M. Raza[74], M. Rivas-Ferreiro[28,66], P. Rodriguez-Flakus[9], M. Ruszkiewicz-Michalska[75], A. Sánchez[8], A. Santos[64], A. Schüller[76], P.A. Scott[77], İ. Şen[78], D. Shelke[79], L. Śliwa[9], H. Solheim[26], H. Sonawane[55], D. Strašiftáková[80], M. Stryjak-Bogacka[9], M. Sudsanguan[67], N. Suwannarach[48], L.M. Suz[28], K. Syme[81], H. Taşkın[82], D.S. Tennakoon[83], P. Tomka[84], N. Vaghefi[85], V. Vasan[10], J. Vauras[86], D. Wiktorowicz[27], M. Villarreal[8], A. Vizzini[87], M. Wrzosek[61], X. Yang[88], W. Yingkunchao[6,42], G. Zapparoli[34], G.I. Zervakis[45], J.Z. Groenewald[1]

Key words:
ITS nrDNA barcodes
LSU
new taxa
systematics

Abstract: Novel species of fungi described in this study include those from various countries as follows: **Australia**, *Baobabopsis sabindy* in leaves of *Eragrostis spartinoides*, *Cortinarius magentiguttatus* among deep leaf litter, *Laurobasidium azarandamiae* from uredinium of *Puccinia alyxiae* on *Alyxia buxifolia*, *Marasmius pseudoelegans* on well-rotted twigs and litter in mixed wet sclerophyll and subtropical rainforest. **Bolivia**, *Favolaschia luminosa* on twigs of *Byttneria hirsuta*, *Lecanora thorstenii* on bark, in savannas with shrubs and trees. **Brazil**, *Asterina costamaiae* on leaves of *Rourea bahiensis*, *Purimyces orchidacearum* (incl. *Purimyces gen. nov.*) as root endophyte on *Cattleya locatellii*. **Bulgaria**, *Monosporascus bulgaricus* and *Monosporascus europaeus* isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum*. **Finland**, *Inocybe undatolacera* on a lawn, near *Betula pendula*. **France**, *Inocybe querciphila* in humus of mixed forest. **Germany**, *Arrhenia oblongispora* on bare soil attached to debris of herbaceous plants and grasses. **Greece**, *Tuber aereum* under *Quercus coccifera* and *Acer sempervirens*. **India**, *Alfoldia lenyadriensis* from the gut of a *Platynotus* sp. beetle, *Fulvifomes subramanianii* on living *Albizzia amara*, *Inosperma pavithrum* on soil, *Phylloporia parvateya* on living *Lonicera* sp., *Tropicoporus maritimus* on living *Peltophorum pterocarpum*. **Indonesia**, *Elsinoe atypica* on leaf of *Eucalyptus pellita.* **Italy**, *Apiotrichum vineum* from grape wine, *Cuphopyllus praecox* among grass. **Madagascar**, *Pisolithus madagascariensis* on soil under *Intsia bijuga*. **Netherlands**, *Cytosporella calamagrostidis* and *Periconia calamagrostidicola* on old leaves of *Calamagrostis arenaria*, *Hyaloscypha caricicola* on leaves of *Carex* sp., *Neoniesslia phragmiticola* (incl. *Neoniesslia gen. nov.*) on leaf sheaths of standing dead culms of *Phragmites australis*, *Neptunomyces juncicola* on culms of *Juncus maritimus*, *Zenophaeosphaeria calamagrostidis* (incl. *Zenophaeosphaeria gen. nov.*) on culms of *Calamagrostis arenaria*. **Norway**, *Hausneria geniculata* (incl. *Hausneria gen. nov.*) from a gallery of *Dryocoetes alni* on *Alnus incana*. **Pakistan**, *Agrocybe auriolus* on leaf litter of *Eucalyptus camaldulensis*, *Rhodophana rubrodisca* in nutrient-rich loamy soil with *Morus alba*. **Poland**, *Cladosporium nubilum*

Citation: Crous PW, Jurjević Z, Balashov S, De la Peña-Lastra S, Mateos A, Pinruan U, Rigueiro-Rodríguez A, Osieck ER, Altés A, Czachura P, Esteve-Raventós F, Gunaseelan S, Kaliyaperumal M, Larsson E, Luangsa-ard JJ, Moreno G, Pancorbo F, Piątek M, Sommai S, Somrithipol S, Asif M, Delgado G, Flakus A, Illescas T, Kezo K, Khamsuntorn P, Kubátová A, Labuda R, Lavoise C, Lebel T, Lueangjaroenkit P, Maciá-Vicente JG, Paz A, Saba M, Shivas RG, Tan YP, Wingfield MJ, Aas T, Abramczyk B, Ainsworth AM, Akulov A, Alvarado P, Armada F, Assyov B, Avchar R, Avesani M, Bezerra JL, Bhat JD, Bilański P, Bily DS, Boccardo F, Bozok F, Campos JC, Chaimongkol S, Chellappan N, Costa MM, Dalecká M, Darmostuk V, Daskalopoulos V, Dearnaley J, Dentinger BTM, De Silva NI, Dhotre D, Carlavilla JR, Doungsa-ard C, Dovana F, Erhard A, Ferro LO, Gallegos SC, Giles CE, Gore G, Gorfer M, Guard FE, Hanson S-A, Haridev P, Jankowiak R, Jeffers SN, Kandemir H, Karich A, Kisło K, Kiss L, Krisai-Greilhuber I, Latha KPD, Lorenzini M, Lumyong S, Manimohan P, Manjón JL, Maula F, Mazur E, Mesquita NLS, Młynek K, Mongkolsamrit S, Morán P, Murugadoss R, Nagarajan M, Nalumpang S, Noisripoom W, Nosalj S, Novaes QS, Nowak M, Pawłowska J, Peiger M, Pereira OL, Pinto A, Plaza M, Polemis E, Polhorský A, Ramos DO, Raza M, Rivas-Ferreiro M, Rodriguez-Flakus P, Ruszkiewicz-Michalska M, Sánchez A, Santos A, Schüller A, Scott PA, Şen İ, Shelke D, Śliwa L, Solheim H, Sonawane H, Strašiftáková D, Stryjak-Bogacka M, Sudsanguan M, Suwannarach N, Suz LM, Syme K, Taşkın H, Tennakoon DS, Tomka P, Vaghefi N, Vasan V, Vauras J, Wiktorowicz D, Villarreal M, Vizzini A, Wrzosek M, Yang X, Yingkunchao W, Zapparoli G, Zervakis GI, Groenewald JZ (2024). Fungal Planet description sheets: 1614–1696. *Fungal Systematics and Evolution* **13**: 183–440. doi: 10.3114/fuse.2024.13.11
Received: 15 March 2024; **Accepted:** 1 April 2024; **Effectively published online:** 28 June 2024
Corresponding editor: C.M. Visagie

Abstract: from hypersaline brine, *Entomortierella ferrotolerans* from soil at mines and postmining sites, *Pseudopezicula epiphylla* from sooty mould community on *Quercus robur*, *Quixadomyces sanctacrucensis* from resin of *Pinus sylvestris*, *Szafranskia beskidensis* (incl. *Szafranskia gen. nov.*) from resin of *Abies alba*. **Portugal**, *Ascocoryne laurisilvae* on degraded wood of *Laurus nobilis, Hygrocybe madeirensis* in laurel forests, *Hygrocybula terracocta* (incl. *Hygrocybula gen. nov.*) on mossy areas of laurel forests planted with *Cryptomeria japonica*. **Republic of Kenya**, *Penicillium gorferi* from a sterile chicken feather embedded in a soil sample. **Slovakia**, *Cerinomyces tatrensis* on bark of *Pinus mugo*, *Metapochonia simonovicovae* from soil. **South Africa**, *Acremonium agapanthi* on culms of *Agapanthus praecox*, *Alfaria elegiae* on culms of *Elegia ebracteata*, *Beaucarneamyces stellenboschensis* (incl. *Beaucarneamyces gen. nov.*) on dead leaves of *Beaucarnea stricta*, *Gardeniomyces kirstenboschensis* (incl. *Gardeniomyces gen. nov*.) rotting fruit of *Gardenia thunbergia*, *Knufia dianellae* on dead leaves of *Dianella caerulea*, *Lomaantha quercina* on twigs of *Quercus suber. Melanina restionis* on dead leaves of *Restio duthieae*, *Microdochium buffelskloofinum* on seeds of *Eragrostis cf. racemosa*, *Thamnochortomyces kirstenboschensis* (incl. *Thamnochortomyces gen. nov.*) on culms of *Thamnochortus fraternus*, *Tubeufia hagahagana* on leaves of *Hypoxis angustifolia*, *Wingfieldomyces cypericola* on dead leaves of *Cyperus papyrus*. **Spain**, *Geastrum federeri* in soil under *Quercus suber* and *Q. canariensis*, *Geastrum nadalii* in calcareous soil under *Juniperus*, *Quercus*, *Cupressus*, *Pinus* and *Robinia*, *Hygrocybe garajonayensis* in laurel forests, *Inocybe cistophila* on acidic soil under *Cistus ladanifer*, *Inocybe sabuligena* in a mixed *Quercus ilex* subsp. *ballota/Juniperus thurifera* open forest, *Mycena calongei* on mossy bark base of *Juniperus oxycedrus*, *Rhodophana ulmaria* on soil in *Ulmus minor* forest, *Tuber arriacaense* in soil under *Populus pyramidalis*, *Volvariella latispora* on grassy soils in a *Quercus ilex* ssp. *rotundifolia* stand. **Sweden**, *Inocybe iota* in alpine heath on calcareous soil. **Thailand**, *Craterellus maerimensis* and *Craterellus sanbuakwaiensis* on laterite and sandy soil, *Helicocollum samlanense* on scale insects, *Leptosporella cassiae* on dead twigs of *Cassia fistula*, *Oxydothis coperniciae* on dead leaf of *Copernicia alba*, *Russula mukdahanensis* on soil, *Trechispora sangria* on soil, *Trechispora sanpatongensis* on soil. **Türkiye**, *Amanita corylophila* in a plantation of *Corylus avellana*. **Ukraine**, *Pararthrophiala adonis* (incl. *Pararthrophiala gen. nov.*) on dead stems of *Adonis vernalis*. **USA**, *Cladorrhinum carnegieae* from *Carnegiea gigantea*, *Dematipyriformia americana* on swab from basement wall, *Dothiora americana* from outside air, *Dwiroopa aeria* from bedroom air, *Lithohypha cladosporioides* from hospital swab, *Macroconia verruculosa* on twig of *Ilex montana*, associated with black destroyed ascomycetous fungus and *Biatora* sp., *Periconia floridana* from outside air, *Phytophthora fagacearum* from necrotic leaves and shoots of *Fagus grandifolia*, *Queenslandipenidiella californica* on wood in crawlspace. Morphological and culture characteristics are supported by DNA barcodes.

[1]Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands
[2]Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa
[3]EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA
[4]University of Santiago de Compostela, Spain
[5]Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain
[6]Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand
[7]Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, The Netherlands
[8]Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain
[9]W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland
[10]Centre for Advanced Studies in Botany, University of Madras, Chennai, Tamil Nadu, 600 025, India
[11]Biological and Environmental Sciences, University of Gothenburg, and Gothenburg Global Biodiversity Centre, Box 463, SE40530 Göteborg, Sweden
[12]Sociedad Micológica de Madrid, Real Jardín Botánico. C/ Claudio Moyano 1, 28014 Madrid, Spain
[13]Department of Plant Sciences, Faculty of Biological Sciences, Quaid-i-Azam University, 45320, Islamabad, Pakistan
[14]Eurofins Built Environment, 6110 W. 34th St, Houston, TX 77092, USA
[15]C/ Buenos Aires 3, bajo 1, 14006 Córdoba, Spain
[16]Department of Botany, Faculty of Science, Culture Collection of Fungi (CCF), Charles University, Benátská 2, 128 00 Prague 2, Czech Republic
[17]Department for Farm Animals and Veterinary Public Health, Institute of Food Safety, Food Technology and Veterinary Public Health; Unit of Food Microbiology, University of Veterinary Medicine Vienna, Veterinaerplatz 1, 1210 Vienna, and Core Facility Bioactive Molecules: Screening and Analysis and Research Platform Bioactive Microbial Metabolites (BiMM), Konrad Lorenz Strasse 24, 3430 Tulln a.d. Donau, Austria
[18]Aptdo. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain
[19]State Herbarium of South Australia, Adelaide, South Australia, 5000 Australia
[20]Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand
[21]Biodiversity Center, Kasetsart University (BDCKU), Bangkok, Thailand
[22]Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands
[23]Aptdo. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain
[24]Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia
[25]Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park 4102, Queensland, Australia
[26]Norwegian Institute of Bioeconomy Research, P.O. Box 115, 1431 Ås, Norway
[27]Biology of Microorganisms Students' Society, Faculty of Biology, University of Warsaw, Miecznikowa 1, 02-096 Warsaw, Poland
[28]Royal Botanic Gardens, Kew, TW9 3AE, Richmond, UK
[29]Department of Mycology and Plant Resistance, V. N. Karazin Kharkiv National University, Maidan Svobody 4, 61022 Kharkiv, Ukraine
[30]ALVALAB, Dr. Fernando Bongera st. Severo Ochoa bldg. S1.04, 33006 Oviedo, Spain

[31]203 montée Saint-Mamert-le-Haut. F-38138 Les Côtes-d'Arey, France
[32]Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 2 Gagarin Str., 1113 Sofia, Bulgaria
[33]National Centre for Microbial Resource -National Centre for Cell Science, Pune - 411007, Maharashtra, India
[34]Department of Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy
[35]Programa de Pós-Graduação em Proteção Vegetal, Universidade Estadual de Santa Cruz, Bahia, Brazil
[36]Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 2455, Riyadh-11451, Saudi Arabia
[37]Department of Forest Ecosystems Protection, University of Agriculture in Krakow, Al. 29 Listopada 46, 31-425 Krakow, Poland
[38]Office of Plant Industry, Virginia Department of Agriculture and Consumer Services, 102 Governor St. 23219, Richmond, Virginia, USA
[39]Via Filippo Bettini 14/11, 16162, Genova, Italy
[40]Department of Biology, Faculty of Arts and Science, Osmaniye Korkut Ata University, 80000 Osmaniye, Türkiye
[41]Grupo Microscopía Sociedad Micológica Madrid, ETSIAAAB, Avda. Puerta de Hierro 2, 28040, Madrid, Spain
[42]Department of Biology, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Ladkrabang, Bangkok, Thailand
[43]Imaging Methods Core Facility at BIOCEV, Faculty of Science, Charles University, Průmyslová 595, 25242 Vestec u Prahy, Czech Republic
[44]Department of Genetics and Microbiology, Faculty of Science, Charles University, Viničná 5, 128 44 Prague 2, Czech Republic
[45]Department of Crop Science, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece
[46]School of Agriculture & Environmental Science, University of Southern Queensland, Toowoomba 4350, Queensland, Australia
[47]Natural History Museum of Utah & School of Biological Sciences, University of Utah, UT 84108, Salt Lake City, Utah, USA
[48]Faculty of Science, Department of Biology, Chiang Mai University, 50200, Chiang Mai, Thailand
[49]Plant Protection Research and Development Office, Department of Agriculture, Bangkok, Thailand
[50]Dipartimento di Bioscienze, Biotecnologie e Ambiente (DBBA), Campus Universitario "Ernesto Quagliariello", Università degli Studi di Bari "Aldo Moro", Via Orabona 4, 70125, Bari, Italy
[51]Centro de Ciências Biológicas, Universidade Federal de Pernambuco, Pernambuco, Brazil
[52]Herbario Nacional de Bolivia (LPB), Instituto de Ecología, Universidad Mayor de San Andrés, Campus Universitario Cota-Cota, calle 27, La Paz, Bolivia
[53]Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Grosse Steinstrasse 79/80, D-06108 Halle, Germany
[54]Department of Plant and Environmental Sciences, 214 Biosystems Research Complex 29631, Clemson, South Carolina, USA
[55]Research Centre in Botany Prof. Ramakrishna More Arts Commerce and Science College, Akurdi, Pune, affiliated to S.P.P University Pune
[56]Bioresources, Center for Health & Bioresources, AIT Austrian Institute of Technology GmbH, Konrad-Lorenz-Straße 24, 3430 Tulln an der Donau, Austria
[57]Maleny, Queensland, Australia
[58]Birkagatan 49, 256 55 Helsingborg, Sweden
[59]Department of Botany, University of Calicut, Kerala, 673 635, India
[60]Unit of Bio- and Environmental Sciences, TU Dresden, International Institute Zittau, Markt 23, 02763 Zittau, Germany
[61]Botanic Garden, Faculty of Biology, University of Warsaw, Aleje Ujazdowskie 4, 00-478 Warsaw, Poland
[62]Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Wien, Austria
[63]Unione Italiana Vini, Viale del Lavoro 8, 37135 Verona, Italy
[64]Departamento de Fitotecnia e Zootecnia, Universidade Estadual do Sudoeste da Bahia, Bahia, Brazil
[65]Faculty of Agrobioengineering and Animal Husbandry, University of Siedlce, Konarskiego 2, 08-110 Siedlce, Poland
[66]Centro de Investigación Mariña (CIM), Universidade de Vigo, 36310, Vigo, Spain
[67]Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai, Thailand
[68]Department of Soil Science, Faculty of Natural Sciences, Comenius University, Ilkovičová 6, 842 15 Bratislava, Slovakia
[69]Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, ul. Żwirki i Wigury 101, 02-086 Warsaw, Poland
[70]Research Station and Museum of TANAP, Tatra National Park Administration, Tatranská Lomnica 14066, 059 60 Vysoké Tatry, Slovakia
[71]Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-900, Viçosa, Minas Gerais, Brazil
[72]c/ La Angostura, 20. 11370 Los Barrios, Cádiz, Spain
[73]Pezinská 14, 90301 Senec, Slovakia
[74]Key Laboratory of Integrated Management on Crops in Northwestern Oasis, Ministry of Agriculture and Rural Affairs, Institute of Plant Protection, Xinjiang Academy of Agricultural Sciences, Urumqi, Xinjiang 830091, China
[75]Department of Algology and Mycology, Faculty of Biology and Environmental Protection, University of Lodz, Banacha 12/16, 90-237 Lodz, Poland
[76]Fungal Genetics and Genomics Laboratory, Department of Applied Genetics and Cell Biology, Institute of Microbial Genetics, University of Natural Resources and Life Sciences, Vienna (BOKU); Konrad Lorenz Strasse 24, 3430 Tulln a.d. Donau, Austria
[77]Friesner Herbarium, Department of Biological Sciences, Butler University, Indianapolis, IN 46208, USA
[78]Department of Biology, Faculty of Science, Muğla Sıtkı Koçman University, 48000 Muğla, Türkiye
[79]Department of Botany, Amruteshwar Arts Commerce and Science College, Vinzar, Pune, affiliated to S.P.P University Pune
[80]Slovak National Museum-Natural History Museum, Vajanského náb. 2, P.O.Box 13, 81006 Bratislava, Slovakia
[81]24 Offer St, Denmark, Western Australia, 6333 Australia
[82]Department of Horticulture, Faculty of Agriculture, Cukurova University, 01330 Adana, Türkiye
[83]Bioengineering and Technological Research Centre for Edible and Medicinal Fungi, Jiangxi Agricultural University, Nanchang 330045, China
[84]ul. 1. mája 2044/179, 03101 Liptovský Mikuláš, Slovakia
[85]School of Agriculture, Food and Ecosystem Sciences, University of Melbourne, Parkville 3010 Victoria, Australia
[86]Biological Collections of Åbo Akademi University, Herbarium, Biodiversity Unit, FI-20014 University of Turku, Finland
[87]Department of Life Sciences and Systems Biology, University of Torino, Viale P.A. Mattioli 25, 10125, Turin, Italy
[88]Department of Plant Industry, Clemson University, 511 Westinghouse Road 29670 Pendleton, South Carolina, USA

ACKNOWLEDGEMENTS

The work of P.W. Crous and colleagues benefitted from funding by the European Union's Horizon 2020 research and innovation program (RISE) under the Marie Skłodowska-Curie grant agreement No. 101008129, project acronym "Mycobiomics", and the Dutch NWO Roadmap grant agreement No. 2020/ENW/00901156, project "Netherlands Infrastructure for Ecosystem and Biodiversity Analysis – Authoritative and Rapid Identification System for Essential biodiversity information" (acronym NIEBA-ARISE). G. Gore and colleagues would like to thank G. Mane from Prof. Ramkrishna More Arts, Commerce and Science College, Pune, Maharashtra for his help with the microscopic images. This work was supported by the Department of Biotechnology (DBT), Government of India (grant no. BT/COORD.II/01/03/2016 (NCMR), under the project Establishment of Centre of Excellence for National Centre for Microbial Resource (NCMR). H. Taşkın, B. Assyov, F. Bozok and İ. Şen received support from the Bulgarian Academy of Sciences and the Scientific and Technological Research Council of Türkiye (Bilateral grant agreement between BAS and TÜBİTAK, project number 118Z640). They would also like to thank to A. Selam Küçük (Ordu, Türkiye) for conveying the locality of *A. corylophila.* A. Voitk is thanked for the detailed information of *Arrhenia* specimens. A. Mateos and colleagues thank the Instituto das Florestas e Conservação da Natureza authorities and guards (Licence 01/IFCN/2021 – BIO MAD). The authors would like to thank E. Beltrán Tejera and L. Quijada for the locations of some of the sampling areas. We would also like to thank R. Mahiques Santandreu for his invaluable help in nomenclatural aspects and in general any taxonomic aspect. S. De la Peña-Lastra and colleagues thank the Garajonay National Park authorities and guards (Licence number 369631). We would also like to thank D. Chavez for his help and company in the field sampling. S. De la Peña-Lastra and co-authors would like to thank Secretaria Regional do Ambiente e Alterações Climáticas Açores for the permission granted for the sampling (Licença nº 16/2021/DRAAC). To the ECOTOX group for co-funding the trip. We would like to thank S. Ruiz-Moyano for his assistance with certain phylogenetic tasks. S. De la Peña-Lastra and colleagues would like to thank M. Rodríguez and J.L. Rego for their collaboration in the treatment of the samples and their hospitality. S. De la Peña-Lastra and colleagues would like to thank C. Vila-Viçosa for his help in locating laurel forest areas in Portugal. A. Santos and co-authors thank the Municipal City Hall of Vitória da Conquista for permission and support to collect fungi in the Parque da Serra do Periperi, a fungal hotspot of the State of Bahia, Brazil. The authors express their gratitude to Fundação de Amparo à Pesquisa do Estado da Bahia (FAPESB), Fundação de Amparo à Ciência e Tecnologia do Estado de Pernambuco (FACEPE), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) for scholarships offered and to L.C. Maia for allowing examination of exsiccates in URM herbarium. M. Sudsanguan and co-authors express their appreciation to the Agricultural Research Development Agency (Public Organisation), Thailand for financial support of this research. A. Polhorský and D. Strašiftáková were supported by the Operational Program of Integrated Infrastructure, co-financed with the European Fund for Regional Development (EFRD) ITMS2014+313021W683: "DNA barcoding of Slovakia (SK-BOL), as a part of international initiative International Barcode of Life (iBOL)". M. Wrzosek and colleagues thank J. Nowakowska, from the Imaging Laboratory, Faculty of Biology, University of Warsaw, for help with TEM pictures. K. Syme and T. Lebel pay their respects to the traditional and spiritual custodians of the regions on which the collections were made – the Pibulmen and Menang Noongar custodians in south-west Western Australia, and the Peramangk, Kaurna and Ngarrindjeri in South Australia. Gratitude is expressed by K. Syme to her long-term foraying companion M. Hart, S. McMullan-Fisher for her help and encouragement, the Walpole-Nornalup National Parks Association, to Fungimap Australia (Inc.) and its generous donors for assistance with funding, and the Australian Biological Resources Study for support towards molecular work. Both authors also wish to thank curation staff at PERTH, MEL and AD for their assistance. U. Pinruan and colleagues were financially supported by the Platform Technology Management Section, National Center for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. M. Nowak and colleagues were financed from state budget funds granted by Polish Ministry of Education and Science as part of the program "Studenckie Koła Naukowe Tworzą Innowacje" (grant no SKN/SP/570335/2023). M. Nowak and colleagues thank M. Graniszewska and J. Audycki for assistance in taking photomicrographs. A. Flakus and co-authors thank N. Taboada and C.L. Lopez for field assistance, M. Espejo for taking the photographs showing the bioluminescence of basidiomata, and M. Piepenbring and A. Ronikier for helpful discussions. We are greatly indebted to our colleagues and all staff of the Santiago de Chirca Biological Station and the Herbario Nacional de Bolivia, Instituto de Ecología, Universidad Mayor de San Andrés for their generous long-term cooperation and help with logistics. This research was financially supported by the German Research Foundation DFG (grant He 3041/23-1) and statutory funds of the W. Szafer Institute of Botany, Polish Academy of Sciences. M. Kaliyaperumal and S. Gunaseelan would like to acknowledge DST, SERB-EMR (EMR/2016/003078) for the financial assistance. D. Jayarama Bhat gratefully acknowledges the financial support provided under the Distinguished Scientist Fellowship Programme, King Saud University, Riyadh, Saudi Arabia. M. Kaliyaperumal, S. Gunaseelan and K. Kezo would like to thank N. Mathivanan, Director, Centre for Advanced Studies in Botany, University of Madras, Chennai, for providing laboratory facilities. S. Mongkolsamrit and colleagues were financially supported by the Platform Technology Management Section, National Centre for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. We thank A. Khonsanit for photo illustration and S. Jaiyen for identifying the insect hosts of *Helicocollum samlanense.* F. Pancorbo and colleagues acknowledge M.A. Ribes, E. Suárez, J. Vila for the loan of some collections for study. Y. Turégano and S. Camino have played an important role in the generation of *Inocybe* sequences. They also thank the entire team of the MycoSeq project (Société mycologique de France/CEFE) and especially F. Valade and J.M. Bellanger, for the molecular analyses carried out here for the FA4635, FA5280 and FA5362 collections. F. Esteve-Raventós and colleagues acknowledge P.-A. Moreau, M. Jeppson, N. Suberbielle and P. Hugot (Conservatoire Botanique National de Corse, Office de l'Environnement de la Corse, Corte) for their help during field work. F. Pancorbo and colleagues acknowledge P. Juste and M. Villarreal for the loan of some collections for study, Y. Turégano for generating some of the sequences and J. Rejos for his comments on soil and vegetation of the studied area. E. Larsson acknowledges the Swedish Taxonomy Initiative, SLU

Artdatabanken, Uppsala, Sweden. J. Vauras acknowledges the association Kuopion Luonnon Ystäväin Yhdistys r.y. K.P.D. Latha acknowledges the financial support (Grant No. SRG/2021/000676 dated 17.01.2022) from the Science and Engineering Research Board (SERB), Department of Science & Technology, Government of India (DST) under the Start-up Research Grant (SRG) scheme. The authors thank the authorities of the University of Calicut for providing facilities to conduct this study. L. Śliwa, A. Flakus and E. Mazur acknowledge all staff of the Herbario Nacional de Bolivia, Instituto de Ecología, Universidad Mayor de San Andrés, La Paz, for their generous long-term cooperation and P. Rodrigues-Flakus for making available material for the study. This study was supported by statutory funds from the W. Szafer Institute of Botany, Polish Academy of Sciences, the National Centre for Research and Development (under the LIDER Programme, project 92/L-1/09 in Poland), and also by the National Science Centre, Poland (project 2016/21/B/NZ8/02463). V. Darmostuk and P. Scott acknowledge the Great Smoky Mountains National Park for giving collection permit GRSN-22SCI-0001 and A. Akulov (Kharkiv, Ukraine) for assisting with a literature search. V. Darmostuk received additional support under statutory funds from the W. Szafer Institute of Botany, Polish Academy of Sciences. F.E. Guard and colleagues thank the Australian herbaria (MEL, AD and PERTH) for loans of collections and BRI for ongoing support and use of their collections. Thanks to J. Cooper for information, sequences and collections loan from New Zealand Fungarium (PDD). R. Labuda was supported by grants K3-G-2/026-2013 funded by the Lower Austria Science and Education Fund (NfB). Study of S. Nosalj was supported by Slovak National Agency – project VEGA (1/0194/21). G. Delgado is grateful to W. Colbert and S. Ward (Eurofins Built Environment) for continual encouragement and provision of laboratory facilities. J.G. Maciá-Vicente acknowledges support from the Landes-Offensive zur Entwicklung Wissenschaftlich-ökonomischer Exzellenz (LOEWE) of the state of Hesse within the framework of the Cluster for Integrative Fungal Research (IPF) of Goethe University Frankfurt. R. Labuda and co-authors thank V. Apondi Omondi and K. Kariuki Muli for helping in sample collections during A. Schüller's stay in Kenya. R. Labuda thanks W. Cherotich Maritim for help in isolation during her stay in BiMM-UFT Tulln (Austria) and M. Sulyok (IFA-BOKU Tulln) for performing metabolic profiling of the fungus, and C. Visagie for construction of phylogeny tree and valuable comments into the text. The authors acknowledge Imaging Methods Core Facility at BIOCEV, institution supported by the MEYS CR (LM2023050 Czech-BioImaging) and for their support and assistance in this work. This study of M. Rivas-Ferreiro and co-authors was supported by the Xunta de Galicia (ED431C 2020/05), Royal Botanic Gardens Kew and the University of Vigo. M. Rivas-Ferreiro is the recipient of a postgraduate FPU fellowship (FPU20/02280) from the Spanish Ministry of Education; the expedition to Madagascar was funded by the Kew-Rio Tinto Partnership Fund and Kew HLAA Fieldwork Fund. Many thanks to the Kew Madagascar Conservation Centre staff, Kew Fungarium staff and J. Piñeiro for their support in field sampling and laboratory work. The study of M. Piątek and co-authors was funded by the National Science Centre, Poland, under the project 2017/27/B/NZ9/02902. D.O. Ramos & O.L. Pereira are thankful to the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq-PROTAX 441384/2020-0), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Brazil (CAPES), finance code 001, and Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) for their financial support. The study of P. Czachura was funded by the National Science Centre, Poland, under the project 2019/35/N/NZ9/04173. U. Pinruan and colleagues were financially supported by the Platform Technology Management Section, National Center for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. N. Chellappan, V. Vasan, M. Nagarajan, R. Murugadoss, and M. Kaliyaperumal thank P. Palani, Director, Centre of Advanced Studies in Botany, University of Madras for the laboratory facilities. The authors acknowledge C. Janagar Dhas, Centre of Advanced Studies in Botany, University of Madras for assistance with photography. E. Polemis and colleagues were financially supported by the Hellenic Foundation for Research and Innovation (H.F.R.I.) under the "2nd Call for H.F.R.I. Research Projects to support Post-Doctoral Researchers" (Project Number: 1057). E. Papadopoulos is acknowledged for kindly providing truffle specimens used in this study. G. Moreno and colleagues express their gratitude to Á. Pueblas and N. Sánchez-Biezma of the Department of Drawing and Scientific Photography at the University of Alcalá for their help in the digital preparation of the photographs, and we are grateful to J. Rejos, curator of the AH herbarium, for his assistance with the specimens examined in the current study. M. Asif is thankful to A. Hassan for his assistance during field trips.

Fungal Planet 1614 MycoBank MB 852466

Agrocybe auriolus Asif, Saba & M. Raza, *sp. nov.*

Etymology: The epithet "*auriolus*" (Latin) refers to the golden colour of the pileus.

Classification: *Strophariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium to large. *Pileus* 1.9–3.2 cm diam, plane to convex, light golden (10YR8/4; Munsell 2009), rarely depressed from centre, umbo absent, surface smooth, dry, and shiny at young stage becoming dull with age, margins smooth to plicate, decurved becoming slightly uplifted with age. *Lamellae* light orange (10YR8/4) at the young stage becoming brownish grey (5YR4/1) with age, close, adnate, and uncinate, broad, edges even, margins become crisped or wavy with age, lamellulae present in three regularly arranged tiers of different lengths, alternating with lamellae. *Stipe* 3–7.5 × 0.3–0.6 cm, yellowish orange (7.5YR7/8) near pileus light brownish grey (7.5YR7/1) towards the base, becoming white (2.5Y8/1) at base, centrally attached, unequal, slightly broad near pileus becoming narrow from middle and the again become broad towards the base, mostly curved from lower half, become yellowish orange (10YR8/8) on bruising, cylindrical, solid, context thick, surface fibrous, dry and dull, base slightly bulbous with rhizomorphs. *Annulus* absent. *Volva* absent. *Smell* and *taste* are not recorded. *Basidiospores* (50/2/2) (6.3–)6.7–8.5(–9.1) × (3.8–)4.3–5.4(–5.9) µm, avl × avw = 7.6 × 4.8 µm; Q = 1.3–1.8; Qav = 1.6; ellipsoid, ovoid to obvoid or, rarely lemon-shaped, thick-walled, smooth, germ pore present, hyaline in 5 % KOH. *Basidia* (13–)15.4–18.7(–19.6) × (5.4–)6–8.2(–9) µm, avl × avw = 17 × 7.2 µm, broadly clavate, frequently two-spored, thick-walled, hyaline in 5 % KOH, congophilous. *Cheilocystidia* (7.9–)13.6–19.4(–23.1) × (5.7–)7–10(–12.6) µm, avl × avw = 17 × 8.4 µm, lageniform to broadly lageniform, thick-walled, no internal content present. *Pleurocystidia* (15.7–)16.3–21.4(–27) × (7.1–)7.5–10.2(–11.8) µm, avl × avw = 19.3 × 9 µm, cylindrical, utriform with median constriction, thin-walled, hyaline in 5 % KOH, tiny oil droplets present. *Pileipellis* a trichoderm, made up of long and regular hyphae with 1.6–3.7 µm diam, avw = 2.6 µm, hyaline, thin-walled, septate, smooth, rarely branched. *Pileocystidia* absent. *Stipitipellis* made up of long, narrow hyphae with 1.5–3.4 µm diam, avw = 2.5 µm, thick-walled, septate, rarely constricted at septa, parallelly arranged. *Caulocystidia* absent. *Clamp connections* are absent in all tissues.

Habitat: Saprotrophic, mostly solitary or in pairs, on fallen leaf debris in nutrient-rich loamy soil under *Eucalyptus camaldulensis*.

Typus: **Pakistan**, Punjab, Pirowal Reserve Forest, District Khanewal 30°34'N, 71°98'E, 136 m a.s.l., in nutrient-rich soil on fallen leaves of *Eucalyptus camaldulensis* (*Myrtaceae*), 27 Jul. 2022, *M. Asif*, SP33 (**holotype** LAH38158; ITS and LSU sequences GenBank PP431556 and PP431558).

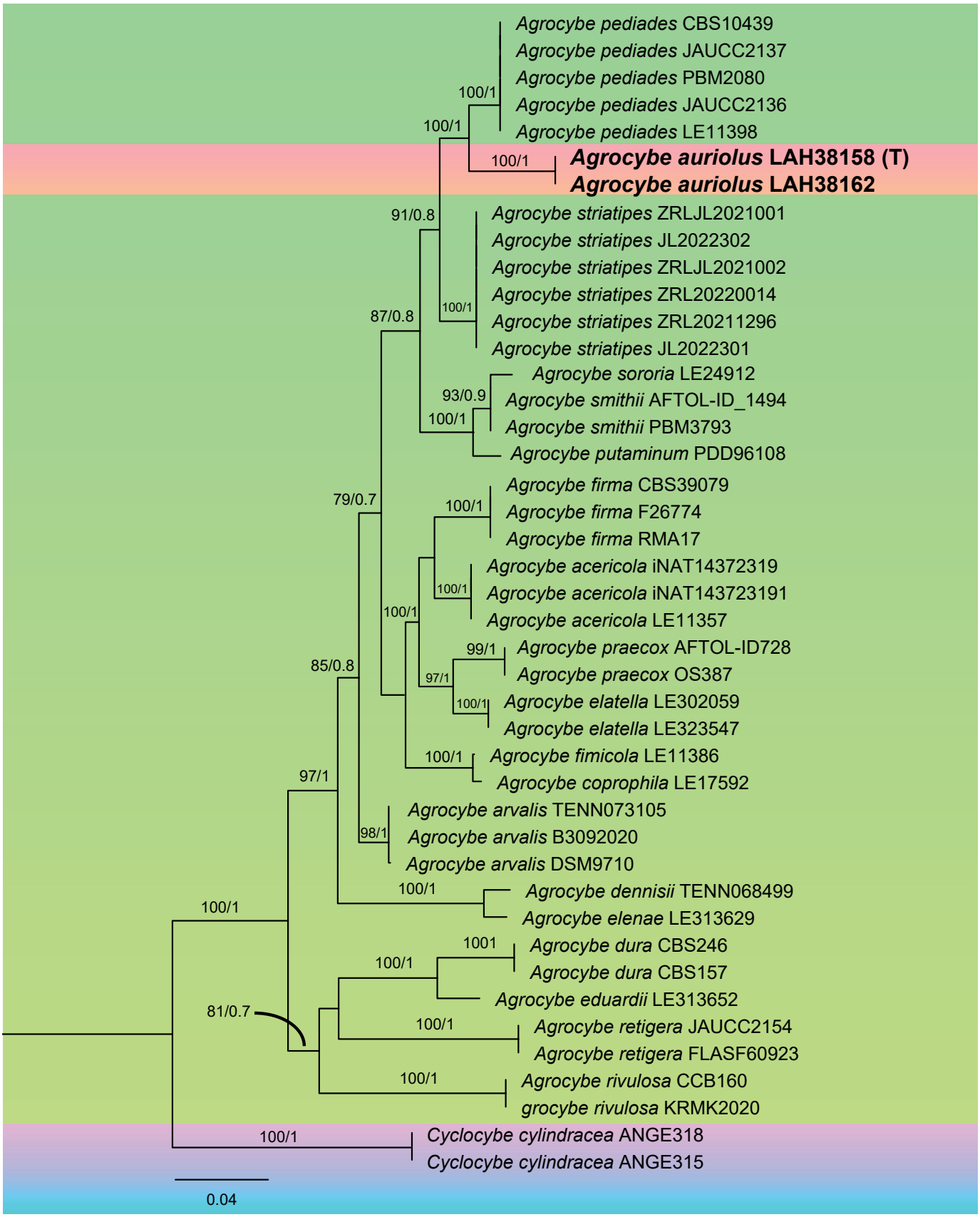
Colour illustrations: Pakistan, Punjab, District Khanewal, Pirowal Reserve Forest, in nutrient-rich soil on fallen leaves of *Eucalyptus camaldulensis* (photo credit Ali Hassan). Basidiospores in Congo red; basidiomata of *Agrocybe auriolus* in natural habitat; line drawings of basidia, basidiospores, cheilocystidia, pleurocystidia, pileipellis, and stipitipellis. Scale bars: basidiomata = 1 cm; all others = 5 µm.

Additional material examined: **Pakistan**, Punjab, Pirowal Reserve Forest, District Khanewal 30°34'N, 71°98'E, 136 m a.s.l., in nutrient-rich soil on fallen leaves of *E. camaldulensis*, 14 Aug. 2022, *M. Asif*, SP110 (LAH38162; ITS and LSU sequences GenBank PP431557 and PP431559).

Notes: Previously, only seven species of the genus *Agrocybe* were known from Pakistan (Ahmad *et al.* 1997, Aman *et al*. 2022) Here, we describe a new species named *A. auriolus*, growing on fallen leaves of *Eucalyptus camaldulensis* in nutrient-rich soil, and is characterized by its convex, golden coloured pileus with uplifted margins, broad and brownish grey lamellae, stipe becoming yellowish orange on handling, ovoid to lemon shaped basidiospores, two-spored, broadly clavate basidia, lageniform cheilocystidia, utriform pleurocystidia, pileipellis a trichoderm and absence of clamp connections.

In the phylogenetic analysis based on combined ITS-LSU sequences, *A. auriolus*, is found to be a close relative of *A. pediades* (LE11398) and *A. striatipes* (ZRLJL2021001) with a strong bootstrap support and Bayesian posterior probability value (100 % / 1). Apart from ITS and LSU sequences, *A. pediades* differs from *A. auriolus* due to its ochraceous, glabrous and applanate pileus, brown and ventricose lamellae, fragile stipe, ellipsoid and larger basidiospores (11–15 × 7–10.5 µm *vs* 6.3–9.1 × 3.8–5.9 µm in *A. auriolus*), four-spored basidia, cheilocystidia with capitate to subcapitate apex, absence of pleurocystidia, presence of pileocystidia, caulocystidia, and clamp connections (Niveiro *et al.* 2020). *Agrocybe striatipes* can be distinguished from *A. auriolus* due to a combination of morpho-anatomical characteristics such as yellowish ochraceous brown pileus with irregular surface, dark brown lamellae, stipe deeply striate-sulcate with somewhat fibril, globose to subglobose and slightly larger basidiospores, 8.1–10 × 5.2–6.9 µm *vs* 6.3–9.1 × 3.8–5.9 µm in *A. auriolus*), relatively larger ventricose cheilocystidia and pleurocystidia, pileipellis and stipitipellis composed of calvate elements and presence of clamp connections (Li *et al*. 2023).
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Agrocybe pediades* [voucher HBAU15142, GenBank MW855929; Identities = 624/671, (93 %), seven gaps (1 %)], and *Agrocybe* sp. [voucher SMY1, GenBank OL678094; Identities = 610/667 (90 %), 10 gaps (1 %)]. The closest hits using the **LSU** sequence are *Agrocybe* sp. [voucher LR-S1, GenBank OL614134; Identities = 939/1 011 (93 %), three gaps (0 %)], and *A. pediades* [voucher AH 40210, GenBank OL687128; Identities = 945/1 011 (92 %), two gaps (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.25507264 (Table).



Molecular phylogenetic tree inferred from the combined ITS-LSU sequence alignment. The evolutionary analysis was conducted using RAxML-HPC2 v. 8.1.11 on CIPRES, using Maximum Likelihood (ML) and Bayesian Inference (BI) methods (Stamatakis 2014). The tree was rooted to *Cyclocybe cylindracea* (ANGE315 & ANGE318). The new species is shown in **bold**. The alignment and tree are available in TreeBASE (study ID: S31182).

M. Asif & M. Saba, Department of Plant Sciences, Faculty of Biological Sciences, Quaid-i-Azam University, 45320, Islamabad, Pakistan; e-mail: m.asif@bs.qau.edu.pk & msaba@qau.edu.pk
M. Raza, Key Laboratory of Integrated Management on Crops in Northwestern Oasis, Ministry of Agriculture and Rural Affairs, Institute of Plant Protection, Xinjiang Academy of Agricultural Sciences, Urumqi, Xinjiang 830091, China; e-mail: mubasharraza73@yahoo.com

Fungal Planet 1615 MycoBank MB 850107

Alfoldia lenyadriensis G. Gore, R. Avchar, D. Shelke, H. Sonawane & D. Dhotre, ***sp. nov.***

Etymology: Name reflects Lenyadri, the place where this beetle was collected.

Classification:*Amorosiaceae*,*Pleosporales*,*Dothideomycetes.*

Mycelium consisting of branched, septate, subhyaline to pale brown, smooth-walled hyphae, 1.6–2.7 µm diam. Sparse black, short hyphae with intercalary chlamydospores of varying sizes (3–11.4 × 6–15.3 µm) were observed after 21 d of growth on Modified Melin-Norkrans (MMN) medium. The reverse colony morphology exhibited a darkish grey appearance. The optimum growth temperature range was 25–28 °C.

Culture characteristics: After 3 wk at 25 °C, the colony attained 52 mm diam on potato dextrose agar (PDA). The colony on PDA exhibited a fluffy, circular appearance, isabelline to greenish olivaceous in colour. The mycelium spread with a raised and entire margin. No sporulation was observed on PDA, malt extract agar, or water agar.

Habitat and distribution: *Alfoldia lenyadriensis* was isolated from the gut of a *Platynotus* sp. beetle feeding on organic waste in Pune, Maharashtra, India.

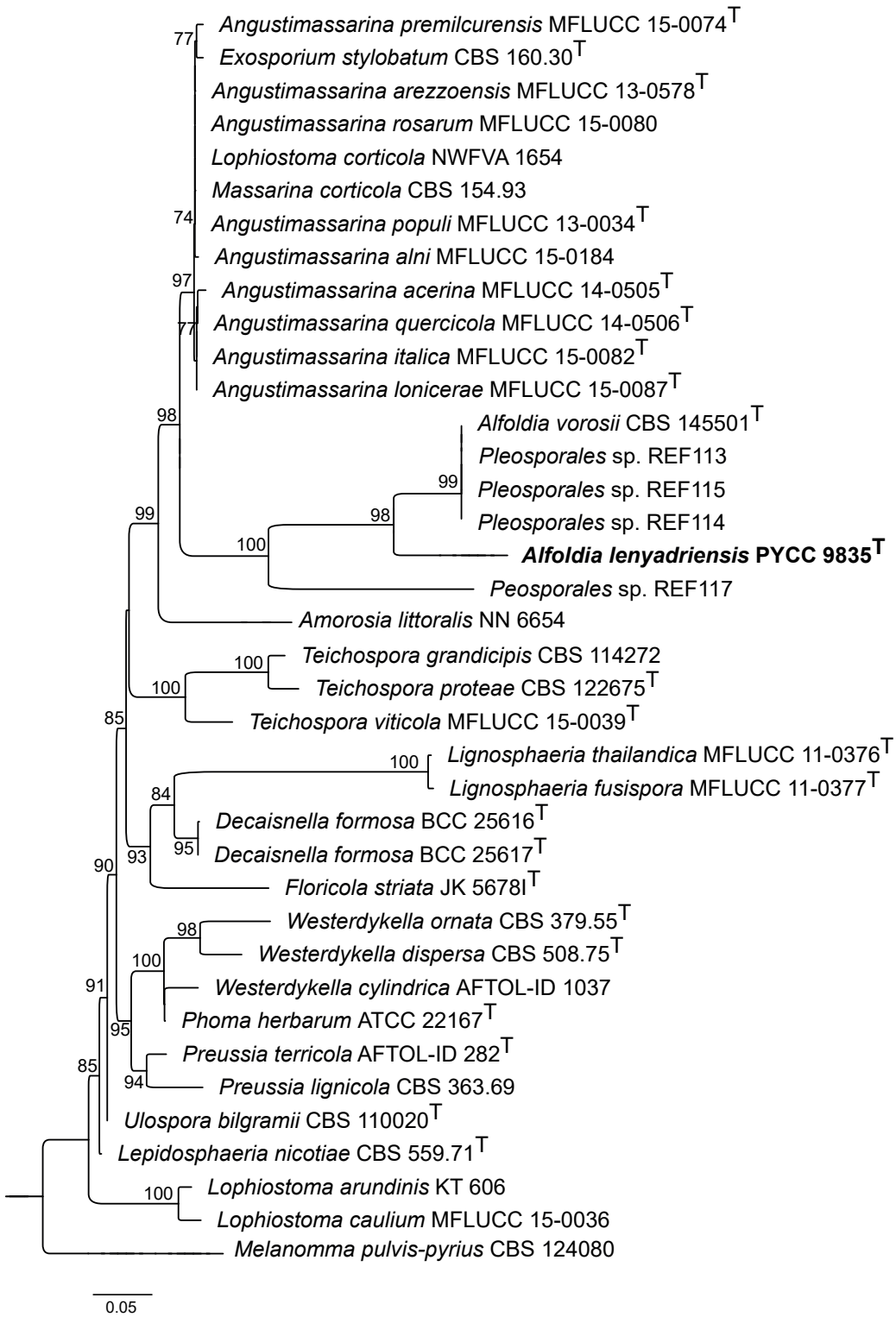
Typus: **India**, Maharashtra, Pune district, N19°22.338', E73°88.218' from the gut of *Platynotus* sp. beetle, 18 Aug. 2022, coll. *G. Gore* [**holotype** PYCC 9835 preserved in a metabolically inactive state at the Portuguese Yeast Culture Collection (PYCC) of the Caparica, Portugal; ITS, LSU, SSU, and *tef1* sequences GenBank OR451484, OR451485, OR520379, and OR475295]; *idem*., Microbial Culture Collection, (MCC), Pune India (MCC 9963).

Notes: The ascomycetous genus *Alfoldia* is a member of the family *Amorosiaceae* in the *Dothideomycetes*. *Alfoldia* is a monotypic genus, and *A. vorosii* represents the type specimen for this genus (Crous *et al.* 2019a). *Alfoldia vorosii* was isolated as a root endophyte associated with woody plants in semiarid grasslands (Crous *et al.* 2019a). *Pleosporales* species have been reported in various habitats as endophytes, epiphytes, parasites living on stems or leaves, hyperparasites on insects or fungi, saprobes of leaves, bark, or stems of dead plants, and animal dung (Kruys *et al.* 2006, Ruibal *et al.* 2009). Phylogenetic analysis, based on the sequences of the ITS nrDNA region, D1/D2 domain of the 28S nrRNA gene (LSU), SSU, and *tef1* gene, supported the recognition of a new species in the genus *Alfoldia* and positioned *A. lenyadriensis* near *A. vorosii* (Crous *et al.* 2019). *Alfoldia lenyadriensis* represents the second species within the genus *Alfoldia*. Additionally, this new species can be distinguished by differences in colony morphology, as well as the size and structure of chlamydospores. The colonies of *A. lenyadriensis* on PDA were isabelline to greenish olivaceous (21 D), whereas *A. vorosii* colonies appeared olivaceous grey to white. The new species produces black, intercalary chlamydospores on MMN medium, while *A. vorosii* does not produce chlamydospores.

Based on a megablast search of the NCBI GenBank nucleotide database, the closest hits using the **ITS** sequence of *Alfoldia lenyadriensis* (PYCC 9835) showed the highest similarity to *Alfoldia vorosii* [strain CBS 145501, GenBank NR_171211; Identities= 458/487 (94 %), three gaps (0 %)], *Pleosporales* sp. [strain REF113, GenBank JN859333; Identities = 440/498 (94 %), one gap (0 %)], *Pleosporales* sp. [strain REF114, GenBank JN859334; Identities = 440/504 (94 %), one gap (0 %)], *Pleosporales* sp. [strain REF115, GenBank JN859335; Identities = 440/513 (95 %), one gap (0 %)], and *Pleosporales* sp. [strain REF117, GenBank JN859337; Identities = 440/513 (95 %), one gap (0 %)]. Closest hits using the **LSU** sequence of *Alfoldia lenyadriensis* (PYCC 9835) are *Alfoldia vorosii* [strain CBS 145501, GenBank MK589354; Identities = 752/758 (99 %), one gap (0 %)], *Alfoldia vorosii* [strain REF113, GenBank MK589353; Identities = 752/758 (99 %), one gap (0 %)], and *Alfoldia vorosii* [strain REF117, GenBank MK589355; Identities = 752/758 (99 %), one gap (0 %)]. The closest hits using the **SSU** sequence of *Alfoldia lenyadriensis* (PYCC 9835) are *Lepidosphaeria nicotiae* [strain CBS 559.71, GenBank NG_061050.1; Identities = 690/695 (99 %), no gaps], *Massaria lantanae* [strain CBS 125592, GenBank NG_062387.1, Identities = 687/695 (99 %), no gaps] and *Massaria pyri* [strain CBS 125644, GenBank NG_062388.1, Identities = 685/695 (99 %), no gaps]. Closest hits using the ***tef1*** sequence of *Alfoldia lenyadriensis* (PYCC 9835) are *Alfoldia vorosii* [strain CBS 145501, GenBank MK599320; Identities = 722/733 (98 %), no gaps], *Alfoldia vorosii* [strain REF113, GenBank MK599319; Identities = 416/426 (98 %), no gaps], and *Alfoldia vorosii* [strain REF117, GenBank MK599321; Identities = 728/739 (98 %), no gaps].

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Type locality – agricultural waste in the field, Lenyadri (Chandipura), Maharashtra, India. The host (*Platynotus* sp.) of *Alfoldia lenyadriensis*; colony on PDA medium; septate hyphae of the strain MCC 9963. Chlamydospores on MMN medium. Scale bars: hypha = 10 µm; chlamydospores = 20 µm.



The placement of *Alfoldia lenyadriensis* using a maximum-likelihood (ML) analysis of the combined ITS nrDNA, D1/D2 domain of the 28S nrRNA gene, SSU, and *tef1* gene sequences employing the TN+F+G4 model in IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015). The scale bar indicates the expected number of substitutions per site. The numbers provided on branches are frequencies with which a given branch appeared in 1 000 bootstrap replications. The tree was rooted with *Melanomma pulvis-pyrius*. The new species proposed in the present study is highlighted and indicated in bold text.

G. Gore & H. Sonawane, Research Centre in Botany Prof. Ramakrishna More Arts Commerce and Science College, Akurdi, Pune, affiliated to S.P.P University Pune; e-mail: goreganesh001@gmail.com & amolsbr@gmail.com
R. Avchar & D. Dhotre, National Centre for Microbial Resource -National Centre for Cell Science, Pune - 411007, Maharashtra, India; e-mail: ramavchar@gmail.com & dheerajdhotre@gmail.com
D. Shelke, Department of Botany, Amruteshwar Arts Commerce and Science College, Vinzar, Pune, affiliated to S.P.P University Pune; e-mail: dpk.shelke1@gmail.com

Fungal Planet 1616 MycoBank MB 852624

Amanita corylophila Bozok, Taşkın, Şen & Assyov, *sp. nov.*

Etymology: From *Corylus* = hazel and phylos = friend (Latinised Greek), because of the apparent mycorrhizal host of the type collection.

Classification: *Amanitaceae*, *Agaricales*, *Agaricomycotina*.

Pileus up to 5 cm diam, campanulate when young, then convex to flat or depressed when mature, without umbo, striate approximately to 1/4 of the pileal radius; pileal surface initially light greyish brown, then dark greyish brown, paler, beige or cream at the striate marginal areas; universal velar remnants common on the pileal surface, initially whitish, ochraceous when touched or with age. *Stipe* up to 9 × 2.5 cm, cylindrical to narrowly clavate with slightly swollen base, exannulate, fragile, fibrillose-flocculose, whitish. *Volva* at the base of stipe up to 3.1 × 1.7 cm, type II (see Fraiture 1993), initially whitish on the outer and inner sides, then ochraceous on handling and with age. *Basidiospores* 8.3–9.8(–10.1) × 7.9–9.6(–9.9) µm, Q = 1–1.13, L_{av} = 9.2 µm, W_{av} = 8.8 µm, Q_{av} = 1.05 (n = 62), globose to subglobose, thin-walled, with a single large guttule or pluriguttulate, hyaline. *Basidia* 40.7–61 × 11.6–15.8 µm, generally 4-spored, but 3-spored also present rarely, clavate to elongate clavate, thin-walled, hyaline; sterigmata up to 6 µm. *Lamellar edge* sterile, marginal cells clavate, 33.2–46.4 × (8–)9.6–13.8 µm, thin-walled, hyaline. Lamellar trama 140–235 µm wide, colourless, mediostratum composed of cylindrical hyphae, 2.2–4.4 µm diam; hymenopodium of catenulate, inflated physaloidal cells, 8.6–14.9 × 5.2–8.5 µm; subhymenium branched. Pileipellis an ixocutis, 60–110 µm wide, gelatinized, composed of hyphae 2.3–4 µm wide, yellowish in KOH; tromboplerous hyphae present, 3.7–4.2 µm wide. Universal veil remnants on the pileus of undifferentiated hyphae 2.9–5.8 µm wide and abundant spherical or ovoid inflated elements, 34.1–80 × 11.3–29.4 µm; tromboplerous hyphae present, sometimes branched, straw yellow, 2.3–5.1 µm wide. Universal veil on the lower stipe (volva) composed of a single layer of 2.4–6.4(–9.5) µm wide, thin-walled, fragile, frequently branching undifferentiated filamentous hyphae; spherical or ovoid inflated elements common, 32.8–54.4(–62.2) × 16.2–40 µm; tromboplerous hyphae flexuous, straw yellow, rarely branched, 3.2–6.6 µm wide, thin-walled. Stipe context compact, longitudinally acrophysalidic, acrophysalides 59.3–118 × 16.4–29 µm, thin-walled, narrowly clavate to clavate; tromboplerous hyphae flexuous, 3.6–8 µm wide, straw yellow, thin-walled. Cottony context from stipe cavity composed of interwoven undifferentiated hyphae 3.4–6.6 µm wide; acrophysalides abundant, 40.7–109 × 24.1–53.9 µm, thin-walled; tromboplerous hyphae common, 5.2–12.3 µm wide, straw yellow, thin-walled, anastomosing tromboplerous hyphae present. *Clamp connections* not observed.

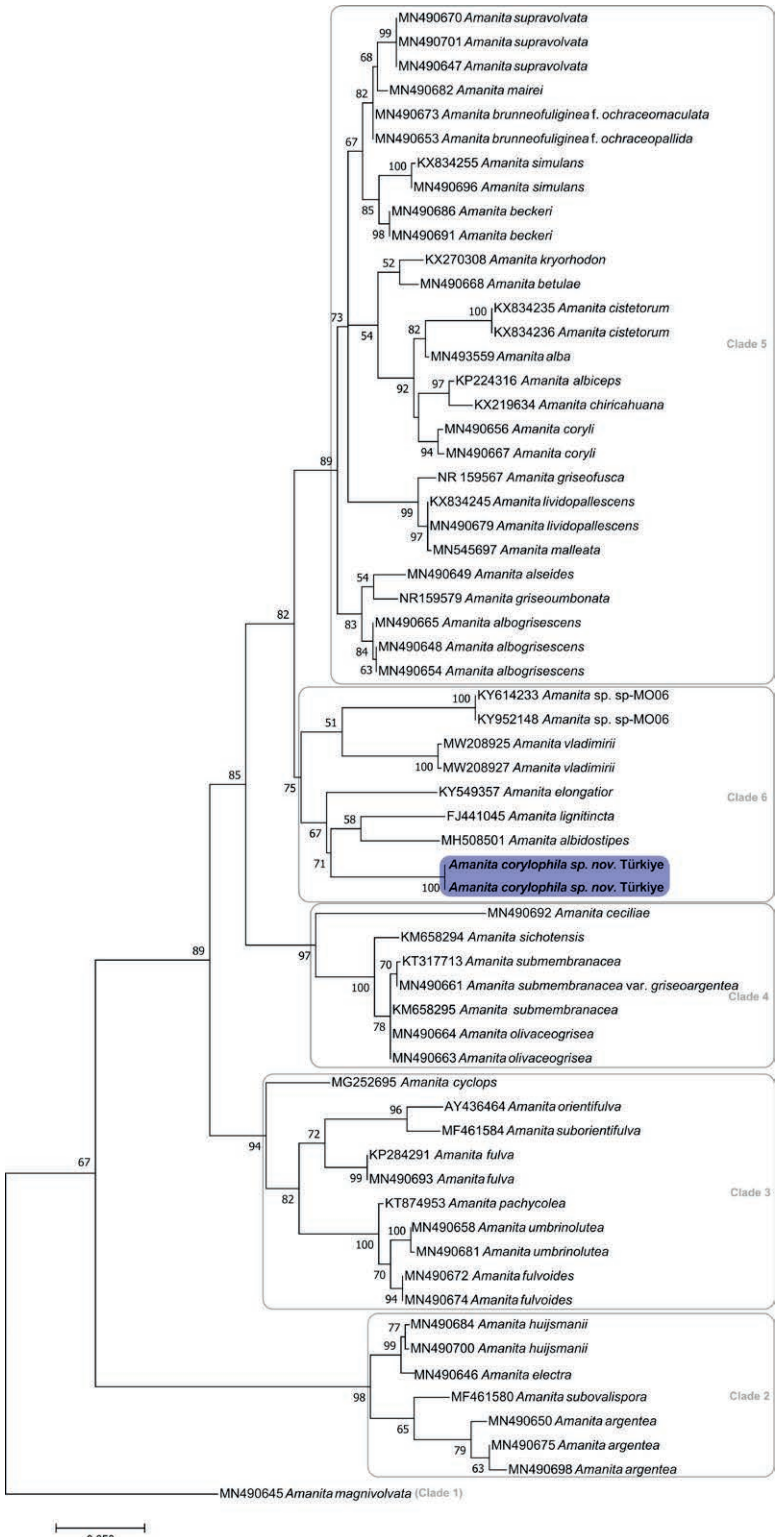
Habit, habitat and distribution: Known from Türkiye, where it appears scattered in August in a plantation of *Corylus avellana*.

Colour illustrations: Holotype collection area at Ordu province (Türkiye). Holotype collection FBozok1259 (top); isotype collection FBozok1322 (middle); basidiospores in Congo red (bottom; from holotype). Scale bar = 10 µm (basidiospores).

Typus: Türkiye, Ordu Province, Kumru Municipality, Duman street, 40°50'13.441"N, 37°15'10.08"E, c. 1 021 m a.s.l., in a plantation of Corylus avellana, 13 Aug. 2022, H. Taşkın & F. Bozok (holotype in Fungarium of Osmaniye Korkut Ata University: FBozok1259; ITS and tef1 sequences GenBank PP430369 and PP449042); (isotype in Fungarium of Osmaniye Korkut Ata University: FBozok1322; ITS, LSU, and tef1 sequences GenBank PP430370, PP434580, and PP449043).

Notes: When the sequence from the holotype of *Amanita corylophila* is compared with the sequences in the GenBank database, the ITS gene region is similar to the sequences of *Amanita* sp. "*obconicobasis*" (MZ831862), *Amanita arctica* (ON059325) and *Amanita constricta* (HQ650724) at rates of 92.23 % (40 indels difference), 92.18 (47 indels difference) and 92.13 % (42 indels difference), respectively. Further on the sequence of the ITS region of *A. corylophila* differs by 39 bases from the sequence (MN490667) of the holotype of *A. coryli*. In our phylogenetic analyses *A. corylophila* nests in Clade 6 of section *Vaginatae* as defined in Ševčíková *et al*. (2021). The closest European species of this clade is *Amanita vladimirii*. *Amanita corylophila* however is aptly distinguished from the latter by the friable general veil, disrupting in numerous patches on the pileal surface and forming an ample and easily disintegrating volva at the stipe base, composed of a single layer with numerous sphaerocysts entangled by undifferentiated hyphae. The general veil in *A. vladimirii* does not leave remnants on the pileal surface and forms a well-developed volva, usually of type IV of Fraiture (1993), which is distinctly 3-layered (Ševčíková *et al*. 2021). The two species seem to share notable ochraceous bruising of the general veil (Ševčíková *et al*. 2021), but such was not noted for two other species residing in Clade 6, namely *A. albidostipes* and *A. lignitincta*, which also differ by the microarchitecture of the volva (Cui *et al.* 2018). Among the European species of section *Vaginatae*, *A. coryli* was described as strictly associated with *Corylus* (Neville & Poumarat 2009), although it is now known that it may occur also with other hosts (Hanss & Moreau 2020, Bozok *et al*. 2023). This species is not closely related to the fungus described here and is member of Clade 5 of Hanss & Moreau (2020). Although *A. corylophila* and *A. coryli* share some macroscopic characters, including the colour of the pileus and remnants of the general veil that may stain ochraceous, the vaginate, not crumbly volva of *A. coryli,* with an external layer composed predominantly of filamentose hyphae (Neville & Poumarat 2009), should be enough to distinguish those two species. Due to the staining of the veil on damage and the sacciform volva *A. corylophila* must be compared to *A. sponsa*, although they are not closely related. This recently described and still poorly known, but can be distinguished on account of its semi-membranaceous volva, which has an external jellified stratum (Hanss & Moreau 2022). The exact host range of *A. corylophila* is not precisely known, and although the new species is so far documented only with *Corylus,* further studies may show that it could link to different hosts as seen in other European species of section *Vaginatae*.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Microscopic characters of *A. corylophila*).



Maximum Likelihood (ML) analysis based on the Kimura 2-parameter model (Kimura 1980) of ITS sequences of *Amanita corylophila* and related species of the genus *Amanita* selected from the GenBank database. Bootstrap support values are given next to the branches. The sequences of the new species are shown in bold turquoise colour. The highest log-likelihood of the tree is -5830.62. Neighbour-Joining and BioNJ algorithms and the topology with superior log likelihood value were used to obtain the initial tree(s) for the heuristic search. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 62 nucleotide sequences and a total of 758 positions in the final dataset. Evolutionary analyses were conducted in MEGA v. 7 (Kumar *et al.* 2016).

F. Bozok, Department of Biology, Faculty of Arts and Science, Osmaniye Korkut Ata University, 80000 Osmaniye, Türkiye; e-mail: fbozok@osmaniye.edu.tr
H. Taşkın, Department of Horticulture, Faculty of Agriculture, Cukurova University, 01330 Adana, Türkiye; e-mail: hatirataskin1@gmail.com
İ. Şen, Department of Biology, Faculty of Science, Muğla Sıtkı Koçman University, 48000 Muğla, Türkiye; e-mail: frapesle@gmail.com
B. Assyov, Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 2 Gagarin Str., 1113 Sofia, Bulgaria; e-mail: contact@boletales.com

Fungal Planet 1617 MycoBank MB 851222

Apiotrichum vineum Zapparoli, Avesani & Lorenzini, *sp. nov.*

Etymology: Name refers to grape wine, from which the ex-type strain was isolated.

Classification: *Trichosporonaceae*, *Trichosporonales*, *Tremellomycetes*.

On yeast mould (YM) agar after 1 wk at 25 °C, vegetative cells are subglobose (3–11 × 3–5.5 µm), ellipsoidal, ovoid, elongate, pseudohyphae, true hyphae and arthroconidia (4–11 × 2–3.5 µm) are formed. On malt extract agar (MEA) after 1 wk cells are subglobose (3–8.5 × 3–5 µm), ellipsoidal, ovoid, elongate, pseudohyphae, true hyphae and arthroconidia (4.5–10 × 2–3.5 µm) are formed. On corn meal agar (CMA) after 1 wk cells are subglobose (3–5.5 × 2–4.5 µm), ellipsoidal, ovoid, pseudohyphae, true hyphae and arthroconidia (4–7.5 × 2–3 µm) are formed.

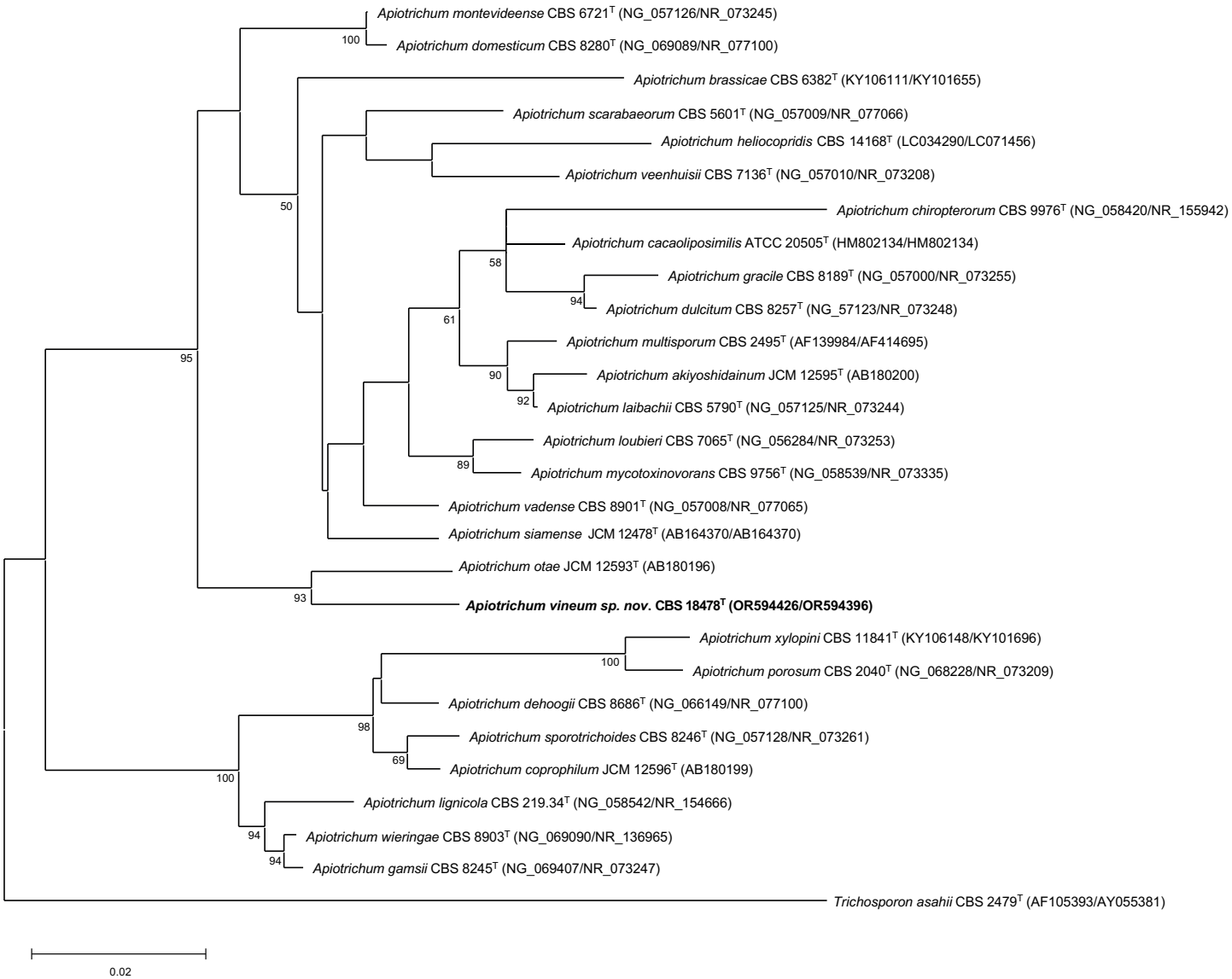
Culture characteristics: On YM agar, colonies creamy whitish to yellowish, round with a moderate convex elevation, wrinkled, fimbriate margin, 5–9 mm diam, after 1 wk at 25 °C. On MEA, colonies creamy yellowish to pale brown, round with convex elevation, wrinkled to cerebriform, fimbriate margin, 4–5 mm diam after 1 wk at 25 °C. On CMA, colonies whitish, flat, fimbriate margin, 2 mm diam after 2 wk at 25 °C.

Typus: **Italy**, Verona, 45°26’18”N, 10°59’30”E, from grape wine, Apr. 2022, *M. Lorenzini* (**holotype** CBS 18478, preserved as a metabolically inactive culture; ITS and LSU sequences GenBank OR594396 and OR594426).

Notes: Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Apiotrichum otae* [strain CBS 9977, GenBank NR_155943; Identities = 490/511 (96 %), five gaps (0 %)], *Apiotrichum vadense* [strain CBS 8901, GenBank NR_077065; Identities = 482/509 (95 %), five gaps (0 %)], and *Apiotrichum mycotoxinovorans* [strain CBS 10094, GenBank KY105750; Identities = 482/510 (95 %), six gaps (1 %)]. Closest hits using the **LSU** sequence are *Apiotrichum otae* [strain JCM 12593, GenBank AB180196; Identities = 611/628 (97 %), 11 gaps (1 %)], *Apiotrichum montevideense* [strain CBS 8605, GenBank KY106139; Identities = 604/627 (96 %), 11 gaps (1 %)], *Apiotrichum siamense* [GenBank AB164370; Identities = 604/627 (96 %), 11 gaps (1 %)], and *Apiotrichum scarabaeorum* [strain A1MYC-3, GenBank ON838571; Identities = 603/627 (96 %), 12 gaps (1 %)]. The presented multilocus phylogenetic tree places *A. vineum* as a novel species, closely related to *A. otae* (Takashima *et al.* 2020).

Apiotrichum vineum differs biochemically from *A. otae* by raffinose (positive), melibiose (positive), L-arabinose (positive), L-rhamnose (positive), citrate (latent) and D-arabinose (weak and latent) assimilation (Takashima *et al*. 2020). *Apiotrichum* has already been isolated from grape wine and other alcoholic fermented beverages (Chen *et al.* 2022, Wei *et al.* 2022a). The isolation of *A. vineum* CBS 18478 from wine corroborates the ability of these yeasts to survive in substrates containing ethanol, which can be used as an important carbon source.

Colour illustrations: Italy, Verona, laboratory of Unione Italiana Vini. Colonies on yeast mould agar at 10 d; yeast cells and hyphae; hyphae with blastoconidium; arthroconidia (left). Scale bars: colony = 1 cm; all others = 10 µm.



Maximum likelihood tree obtained by phylogenetic analysis of the combined LSU and ITS sequences from *Apiotrichum vineum* and the other *Apiotrichum* species. Analysis was conducted in MEGA v. 11 software employing T92+G+I model (Takamura *et al*. 2021) with 1 000 bootstrap re-samplings. Bootstrap support values (BS > 60 %) are shown at the nodes. *Trichosporon ashaii* CBS 2479^{T} was used as outgroup. This analysis involved 28 nucleotide sequences, with a total of 920 positions in the final dataset. The novel taxon is indicated in **bold**. The alignments and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.24943185).

G. Zapparoli, Department of Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy; e-mail: giacomo.zapparoli@univr.it
M. Avesani, Department of Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy; e-mail: michele.avesani@univr.it
M. Lorenzini, Unione Italiana Vini, Viale del Lavoro 8, 37135 Verona, Italy; e-mail: lorenzini.marilinda@gmail.com

Fungal Planet 1618 MycoBank MB 852591

Arrhenia oblongispora Karich, Krisai & S.-Å. Hanson, *sp. nov.*

Etymology: Named after its comparatively long and slender spores, within the species of the acerosa-complex.

Classification: *Lichenomphaliaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata pleurotoid. *Pileus* 6–20 mm wide, 1–2 mm thick, when fresh light brown to cream coloured and translucently striate with slightly darker brownish striation, hygrophanous, becoming light grey when drying, glabrous, finely white pubescent at point of attachment, margin somewhat undulating. *Lamellae* normally developed, slightly thickish, not to somewhat anastomosing, concolourous to pileus. *Stipe* lateral and reduced, up to 4 mm long, 1–2 mm wide, concolourous to pileus, slightly to distinct tomentose at the base. *Smell* inconspicuous; *taste* unknown. *Spore print* white. *Basidia* 4-spored. *Spores* (n = 67, 3 collections, 5 basidiomata): (7–)8.5–10.5(–11) × 3.5–4.5(–5) µm (av. 8.5–9.6 × 3.9–4.3 µm), Q = 1.9–2.7(–2.9), Q_{AV} = 2.3–2.4, oblong dacryoid to pyriform and sometimes distinctly constricted centrally, with a prominent apiculus. *Hymenophoral trama* subirregular, consisting of 4–8 µm wide hyphae, not incrusted. *Pileipellis* a cutis of (sub)parallel 4–6 µm wide hyphae. *Pileitrama* consisting of 4–10 µm wide hyphae. *Pileipellis* and *pileitrama* hyphae not incrusted. *Cystidia* absent. *Clamp connections* abundant in all tissues.

Sociability, habitat and distribution: Basidiomata growing solitary or in small clusters on the debris of herbaceous plants and grasses, on bare soil attached to debris of herbaceous plants and grasses or on older dung of herbivores (horse) in unimproved grassland on neutral to calcareous soil. Known from Germany and Sweden.

Typus: **Germany**, Lückendorf, "Birkwiese", 50°49.54'N, 14°45.43'E, 470 m a.s.l., on bare soil attached to plant debris in semi-natural orchard meadow on neutral to acidic soil, 14 Oct. 2023, *A. Karich* (**holotype** GLM-F137902; ITS and LSU sequences GenBank PP463916 and PP471049).

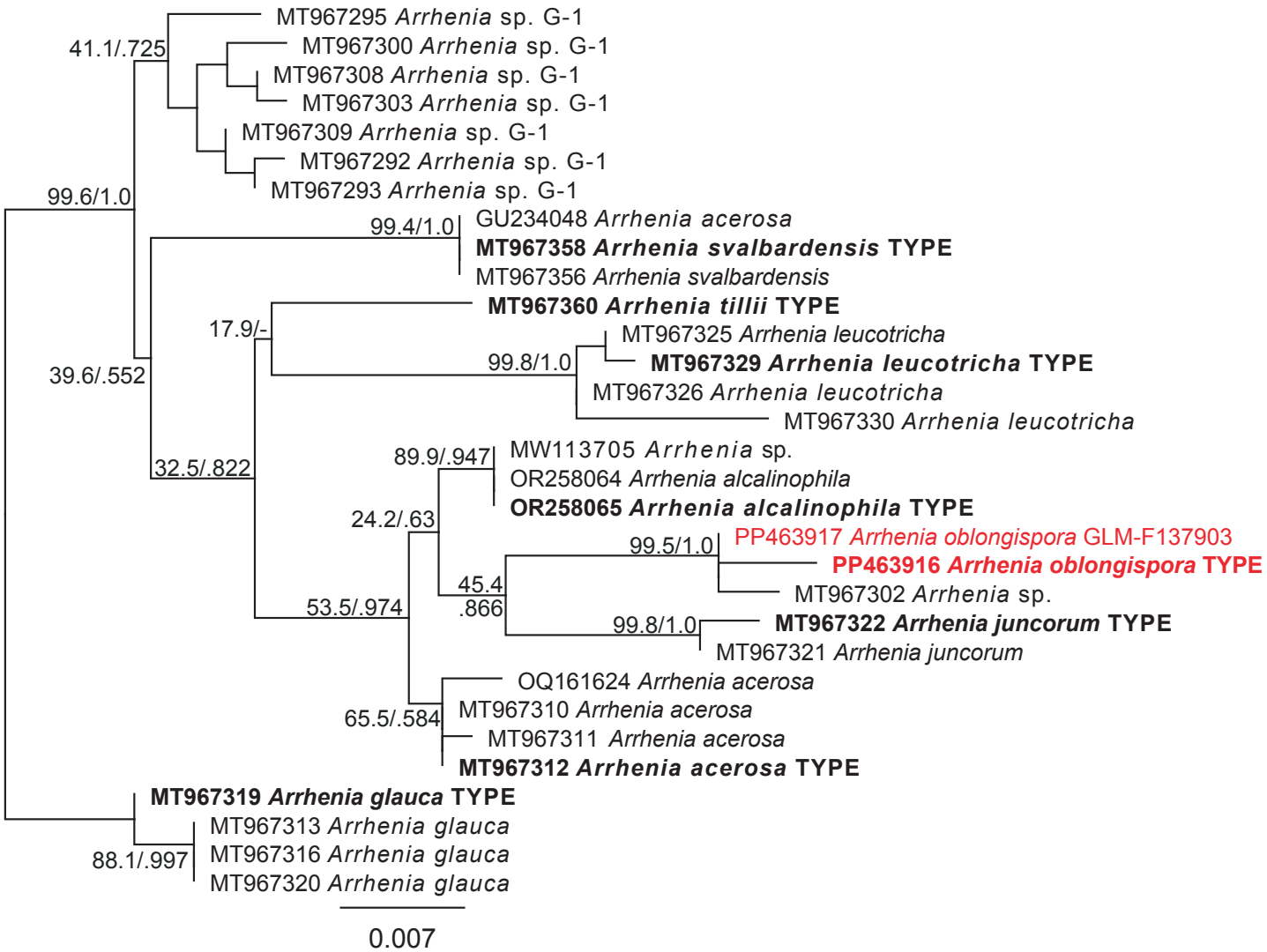
Additional materials examined: **Germany**, Dolgelin, 52°29.93'N, 14°26.29'E, 40 m a.s.l., on plant debris in a semi-arid meadow over calcareous soil, 19 Oct. 2023, *A. Karich* (GLM-F137903; ITS and LSU sequences GenBank PP463917 and PP471050). **Sweden**, Scania, Maglehem parish, Björshus, Äskebjär, 55°46.00'N, 14°6.74'E, 90 m a.s.l., in a calciphilous dry calciphilous dry meadow, on old horse dung, 27 Oct. 2001, 27 Oct. 2001, *S.-Å. Hanson* (SAH2001-315; ITS sequence GenBank MT967302).

Notes: Voitk *et al.* (2020b) investigated pleurotoid and omphalinoid species of the *Arrhenia acerosa*-complex. While some species were already described by Voitk *et al.* (2020b), others remained undescribed due to insufficient data. Recently, two additional *Arrhenia* species of the acerosa-complex were published, both representing species groups predicted by Voitk *et al*. (2020b), namely *Arrhenia similis* and *A. alcalinophila* (Crous *et al.* 2023a, b).

Arrhenia oblongispora represents the taxon referred to as AC-4 in Voitk *et al.* (2020b) that was a singleton based on a Swedish specimen growing in a calciphilous dry meadow. Two recently collected specimens of the same taxon from unimproved grasslands in Germany confirm its separate phylogenetic position within the acerosa-complex (see phylogenetic tree).

Arrhenia oblongispora can be distinguished from *A. acerosa s.str.* by longer spores and by a higher spore Q-value. Macroscopically, it is distinguishable by paler basidiomata and a different substrate preference (debris of herbaceous plants and grasses over woody debris, Voitk *et al.* 2020b). *Arrhenia glauca*, another pleurotoid species of the acerosa-complex with pale basidiomata, has shorter and wider spores and 2-spored basidia. *Arrhenia juncorum* and *A. leucotricha* can macroscopically be very close to *A. oblongispora* but prefer wetlands and have shorter spores. The spore Q-values in specimens of *A. oblongispora* are max. 2.8–2.9 and range on average from 2.3 to 2.4, which is usually the upper limit of Q-values in pleurotoid species of the acerosa complex: *A. acerosa* Q = 1.4–2.5; *A. glauca* Q = 1.4–1.9; *A. juncorum* Q = 1.6–2.4; *A. leucotricha* Q = 1.8–2.4; *A. subglobisemen* Q = 1.1–1.3; *A. similis* 1.2–1.4; *A. svalbardensis* Q = 1.3–2.3; *A. tillii* Q = 1.4–1.6 (Krisai-Greilhuber & Noordeloos 1998, Voitk *et al.* 2020b, Crous *et al.* 2023b).

Colour illustrations: Orchard meadow at the holotype location in Lückendorf, Germany. Basidiomata of GLM-F137903 (photo A. Karich); line drawings of spores and 4-spored basidia from holotype (drawing A. Karich). Scale bars: basidiomata = 1 cm; spores and basidia = 10 µm.



Maximum Likelihood tree obtained by analysis of newly generated ITS sequences from *A. oblongispora* (red) and related *Arrhenia* sequences of the acerosa-complex. Type specimens in **bold**. Phylogenetic analysis performed in Geneious Prime v. 2023.0.4 using the ClustalOmega algorithm for alignment (611 bp in the final dataset) and PhyML with 1 000 bootstrap repeats to build the tree. The alignment and tree were deposited in figshare.com (doi: 10.6084/m9.figshare.25295575).

A. Karich, Unit of Bio- and Environmental Sciences, TU Dresden, International Institute Zittau, Markt 23, 02763 Zittau, Germany;
e-mail: alexander.karich@tu-dresden.de
I. Krisai-Greilhuber, Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Wien, Austria;
e-mail: irmgard.greilhuber@univie.ac.at
S.-Å. Hanson, Birkagatan 49, 256 55 Helsingborg, Sweden; e-mail: monica.hanson@telia.com

Fungal Planet 1619 MycoBank MB 852459

Ascocoryne laurisilvae A. Mateos & De la Peña-Lastra, *sp. nov.*

Etymology: The specific epithet refers to the ecosystem where it was found, evergreen laurel forest, commonly called "laurisilvae".

Classification: *Gelatinodiscaceae*, *Helotiales*, *Leotiomycetes*.

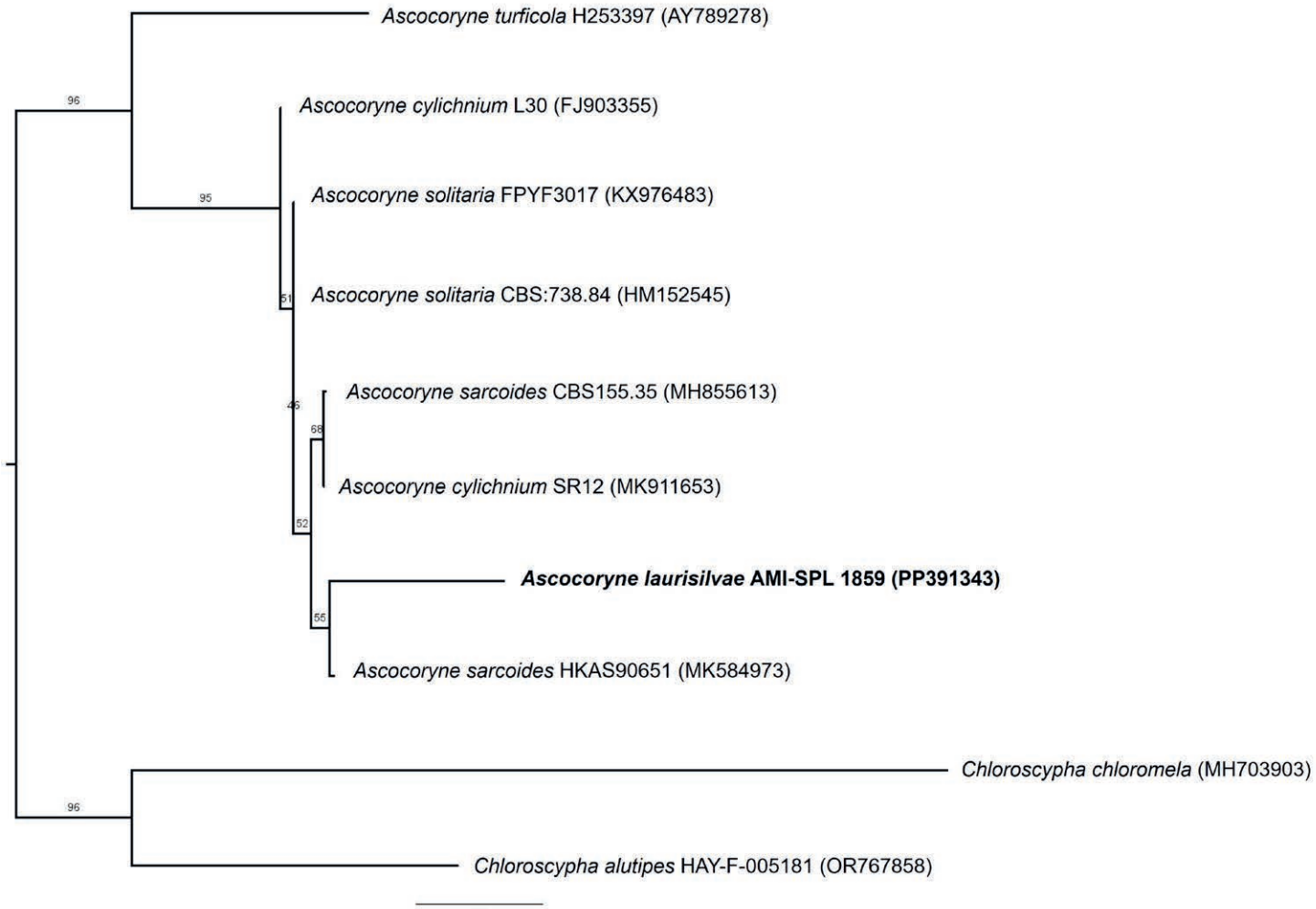
Conidiomata cerebriform, sessile, 8 mm high, 8 mm wide at base, consisting of globose or obtuse cupuliform elements, 1 mm diam, vesiculously grouped in 3–5 lobes, forming a cluster of up to 50 units, gelatinous, smooth, shiny, translucent, milky-white (Ség. 680; Séguy 1936), pale pink, cream-pink (Ség. 5, 20) or pale violet (Ség. 610). Immature conidiomata are whiter and more translucent. *Context* homogeneous, *taste* and *smell* indistinct. Mature conidiomata as they age become an amorphous mass, the lobes collapse and turn dark blackish brown. They develop on wood together with corticial fungi and next to their congener *Ascocoryne sarcoides*. *Asexual morph*: *Conidiophores* sometimes simple, composed of many straight conidiophores, in unbranched columns, but in others branched 2–3 times, often similar to those of *Penicillium*, forming more or less complex systems. *Conidiophore* with cylindrical, thick-walled, basal cells, 15–18 × 3–5 µm. *Branchlets and metulae* claviform, 10–13 × 2.3–3.5 µm. *Phialides* 5.5–13 µm long and 1.6–1.8 µm wide, cylindrical, usually straight, with a conidiogenous opening 1–1.5 µm wide and without obvious collarets or periclinal thickening. *Conidia* (2.9–)3.2–*3.5*–3.7(–3.9) × (2.2–)2.5–*2.8*–3.1(–3.2) µm; Q = (1.1–)1.12–*1.2*–1.3(–1.4); N = 50; Ve = 14 µm^3, subglobose or ovoid, with a guttule occupying 70 % of their interior, some with an inconspicuous apiculum. *Sexual morph* immature, only a few spores, 17–19 × 4–4.2 µm, fusoid, 1-septate, one end rounded, the other acute.

Habitat and distribution: In Atlantic laurel forest, on degraded and very damp wood of *Laurus nobilis*. Currently known only from the type location in north Portugal.

Typus: Portugal, Viana do Castelo, Arcos de Valdevez, Cabreiro, Parque Nacional da Peneda-Gerês, N41°57'16.0", W8°24'27.3", 150 m a.s.l., gregarious on degraded and very damp wood of *Laurus nobilis* (*Lauraceae*), 17 Feb. 2023, *A. Mateos* & *S. De la Peña-Lastra* (holotype AMI-SPL1859; ITS and LSU sequences GenBank PP391343 and PP386697).

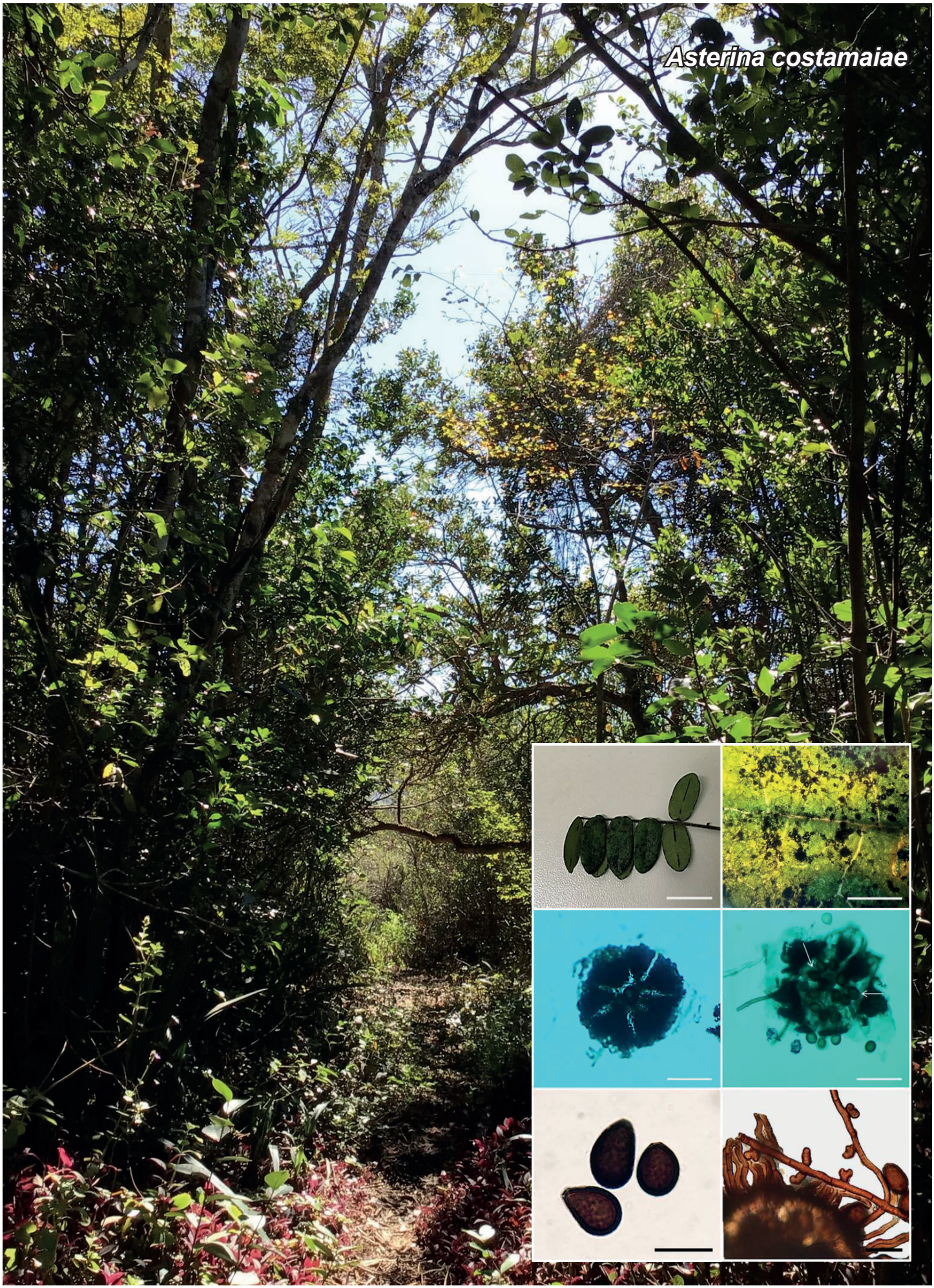
Notes: The genus *Ascocoryne* was established by Groves & Wilson (1967), and includes both sexual and asexual morphs, and the same name must be used for both, according to Art. 57.2 of the ICN (Johnston *et al.* 2014). The genus is currently comprised of eight species (Index Fungorum) with a worldwide distribution; it is characterised by sporodochial asexual morphs that are similar in colour and consistency to apothecia, predominantly violet, purple, pink or pale colours and gelatinous texture. *Ascocoryne laurisilvae* resembles *Tremella fibulifera* morphologically at first sight although it is distinct because *A. laurisilvae* has auricularioid and not globose forms. It differs from *A. cylichnium* which has two types of conidia, some (2.0–)2.3–4.0(–5.0) × (1.3–)1.5–2.8 µm, ovoid in shape and others more allantoid or rod-shaped conidia, 3.5–7.0 × 0.8–1.2(–1.5) µm in size (ITS 90.94 % match); differs from *A. sarcoides* with ovoid conidia, 2.0–3.0 × (0.8–)1.2–1.6 and allantoid conidia, 3.0–6.0(–7.5) × 0.8–1.4(–1.9) (Roll-Hansen & Roll-Hansen 1979, Quijada *et al.* 2017) (ITS 90.77 % match). *Ascocoryne albida* has allantoid conidia (3–3.5 × 1–1.2 µm) (Korf & Candoussau 1974, Cannon 2020, Hall & Cannon 2021). *Ascocoryne trichophora* has much smaller conidia, 1.5–2 × 1.0–1.5 µm, subglobose to ellipsoidal (Seifert 1989). *Ascocoryne striata* and *A. turficola* have no known asexual morph (Kučera & Lizoň 2005, Cannon 2016) as do *A. javanica* and *A. lilacina* (Fries 1821, Penzig & Saccardo 1904).

Colour illustrations: Portugal, Viana do Castelo, Arcos de Valdevez, Cabreiro, Parque Nacional da Peneda-Gerês, forest of *Laurus nobilis*, where the holotype of *Ascocoryne laurisilvae* was collected. Left column: conidiomata in upper photo correspond with the holotype AMI-SPL1859; the bottom photo corresponds with conidia and ascospores (in H_2O). Right: conidiophores (in H_2O). Scale bars: conidiomata detail (right) = 1 mm; general conidiomata (left) = 10 mm; all others = 10 µm.



The most probable maximum likelihood (ML) tree obtained from the ITS (GenBank accession numbers in brackets) alignment showing on the branches the ML bootstrap (ML-bs) support values calculated with IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015). ML-bs ≥ 70 % were considered significant.

A. Mateos, Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain; e-mail: amateosiz1@gmail.com
S. De la Peña-Lastra, University of Santiago de Compostela, Spain; e-mail: saul.delapena@gmail.com
A. Rigueiro-Rodríguez, University of Santiago de Compostela, Spain; e-mail: antonio.rigueiro@usc.es



Fungal Planet 1620 MycoBank MB 849527

Asterina costamaiae A. Santos, N.L.S. Mesquita & J.L. Bezerra, *sp. nov.*

Etymology: In honour of Dr Leonor Costa Maia, an outstanding Brazilian mycologist who has significantly contributed to the knowledge of Brazilian fungal biodiversity.

Classification: *Asterinaceae*, *Asterinales*, *Dothideomycetes.*

Colonies black, circular, isolated to confluent, flat, growing on the abaxial and adaxial surface of leaflets and on the petioles of leaves. *Mycelium* superficial formed by brown, septate, hyphopodiate, flexuous to substraight, oppositely branched at 45° angles. *Hyphopodia* unicellular, cylindrical, lobed or irregular shaped, opposite, unilateral or alternate, 8–10 × 5–9 µm. *Ascomata* absent. *Pycnothyria*, orbicular, flattened, dark brown, 80–110 µm diam, with upper wall formed by radiating rectangular cells, opening by stellar dehiscence, with fimbriated margins. *Conidiogenous cells* unicellular, formed under the upper wall of the pycnothyrium. *Pycnothyriospores* unicellular, oval to pear-shaped, brown, smooth-walled, 17–26 × 14–17 µm.

Typus: **Brazil**, Bahia, on leaves of *Rourea bahiensis* (*Connaraceae*), Serra do Periperi, 14°49'52.87"S, 40°50'1.46"W, Aug. 2023, coll. *A. Santos* (**holotype** URM 95349; ITS sequence GenBank OR815599).

Notes: In December 2020, black colonies were observed growing on *Rourea bahiensis* plants in Serra do Periperi in the municipality of Vitória da Conquista, Bahia, Brazil. Microscopic analysis of the structures showed scutellate pycnothyria and hyphae, hyphopodia and pycnothyriospores typical of the genus *Asterina* of the *Asterinaceae* family. The species *Asterostomella roureae* was reported on *Rourea erecta* (Petrak 1958), in the Philippines. *Asterostomella* is presently regarded as a synonym of *Asterina* (Müller & Arx 1962, Hongsanan *et al.* 2014). A co-type of Petrak´s species was found in Herbarium Camille Torrend - URM (Maia & Gibertoni 2022), Universidade Federal de Pernambuco. Microscopic slides from *A. roureae* (URM 4678) were compared with slides prepared from the *Asterina* species collected on *R. bahiensis*.

Asterostomella roureae and *Asterina costamaiae* are different in size of their main structures as shown in The table below. Phylogenetically, *Asterina costamaiae* is a neighbour of *A. neomangiferae* (MFLU 210038) collected as an epiphytic on leaves of *Mangifera indica* in Thailand (Marasinghe *et al.* 2022). This species is also the closest relevant hit using the ITS sequence based on a megablast of NCBIs GenBank nucleotide database (strain MFLU 210038, GenBank MZ225576; Identities = 405/476 (85 %), 23 gaps (4 %)).

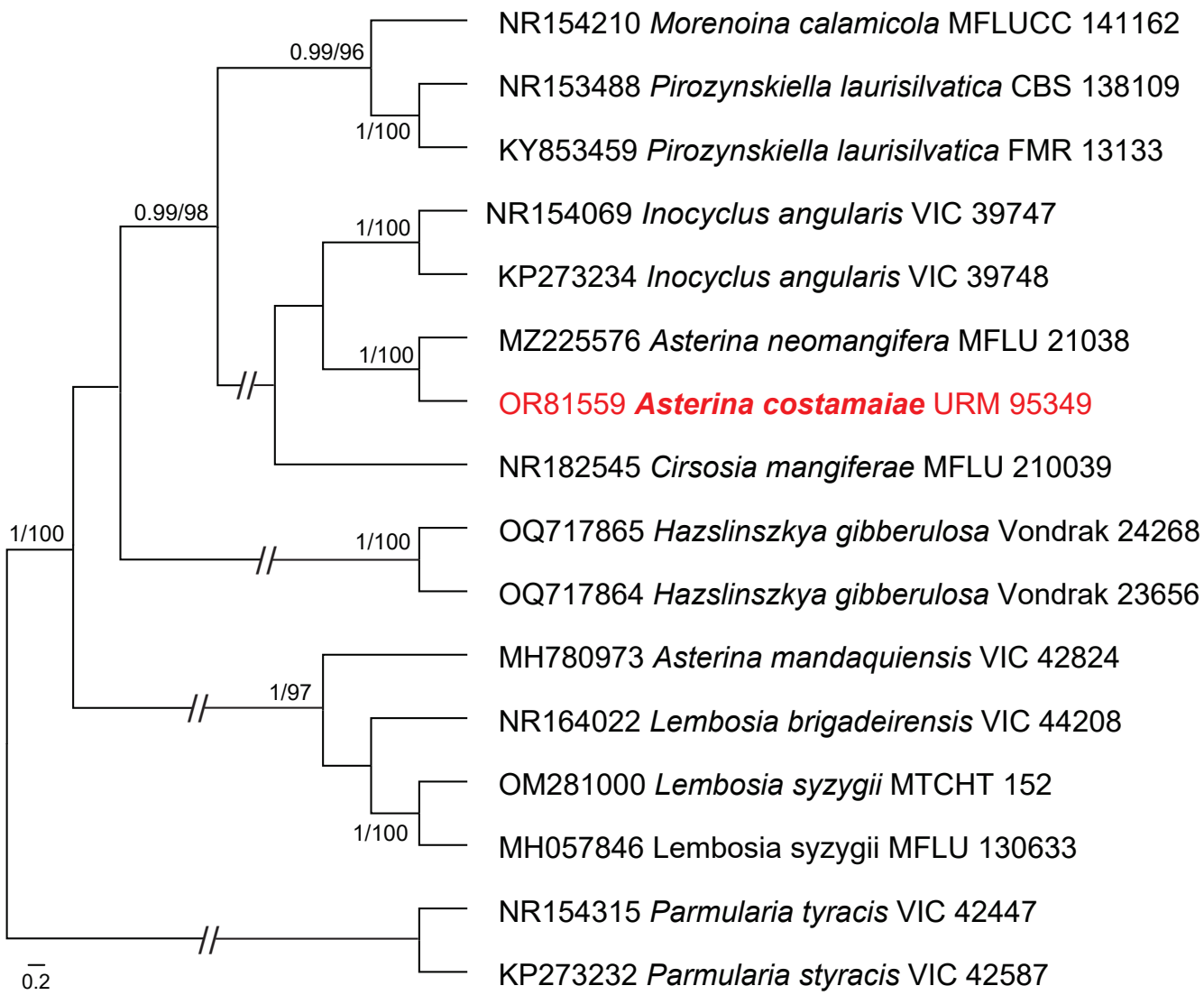
Comparison between *Asterina* (=*Asterostomella*) species found on *Rourea*.

Species	Pycnothyria (µm)	Pycnidiospores (µm)		Hyphopodia (µm)	
	Diameter	Length	Width	Length	Width
Asterostomella roureae (Petrak 1958)	56.34–98.81 (78.47)*	15.04–18.71 (17.06)	8.87–13.78 (11.91)	6.74–7.76 (7.25)	5.05–5.81 (5.33)
Asterina costamaiae (this paper)	88–125 (109.6)**	17–26 (20.7)	14–17 (15.1)	8–10 (8.55)	5–9 (6.65)

*Average value obtained from 10 measurements.

**Average value obtained from 40 measurements.

Colour illustrations. *Rourea bahiensis* located at Serra do Periperi, Brazil. *Asterina costamaiae* on *Rourea bahiensis* with colonies on adaxial surface of the leaves; closer view of the colonies; pycnothyrium showing stelar dehiscence; mature and immature pycnothyriospores (arrows); magnified pycnothyriospores; hyphopodia. Scale bars: leaves = 1.5 cm; colonies = 1 mm; pycnothyrium = 50 µm; pycnidiospores and hyphopodia = 20 µm.



Bayesian inference (BI) tree obtained by a phylogenetic analysis of the sequences of ITS nrDNA conducted in MrBayes on XSEDE and Maximum Likelihood (ML) analysis in RAxML in the CIPRES science gateway (Miller *et al.* 2010). The substitution model GTR+G was used for the alignment in the BI and GTR+G+I in the ML. Bayesian posterior probability and Maximum Likelihood bootstrap support values are indicated at the nodes. The new species is indicated in red. *Parmularia styracis* (VIC42447 and VIC42587) was used as outgroup. Some branches were shortened to facilitate layout.

A. Santos, N.L.S. Mesquita & Q.S Novaes, Departamento de Fitotecnia e Zootecnia, Universidade Estadual do Sudoeste da Bahia, Bahia, Brasil; e-mail: arminioo@uesb.edu.br, nasonmesquita@yahoo.com & quelmo@gmail.com
L.O. Ferro, Centro de Ciências Biológicas, Universidade Federal de Pernambuco, Pernambuco, Brasil; e-mail: layanne.ferro93@gmail.com
J.L. Bezerra, Programa de Pós-Graduação em Proteção Vegetal, Universidade Estadual de Santa Cruz, Bahia, Brasil; e-mail: jlulabezerra@hotmail.com

Fungal Planet 1621 MycoBank MB 851117

Baobabopsis sabindy Sudsanguan, R.G. Shivas & Y.P. Tan, ***sp. nov***.

Etymology: Named for a meeting place where surveys are planned, and projects discussed.

Classification: *Peronosporaceae*, *Peronsporales*, *Oomycota*.

Sexual morph (*oogonia*) in leaf blades of *Eragrostis spartinoides* that split into tangled vascular strands up to 15 cm long. *Oogonia* golden brown, sub-globose, 28–40 µm diam (n = 25); wall (exosporium) 3–10 µm thick, uneven with several low domed rounded warts; warts 3–4 µm high. *Oospores* one per oogonium, globose to subglobose, 21–25 µm in diam (n = 25), adnate with oogonial wall; *wall* (endosporium) 2–3 µm thick, pale golden brown, even, smooth.

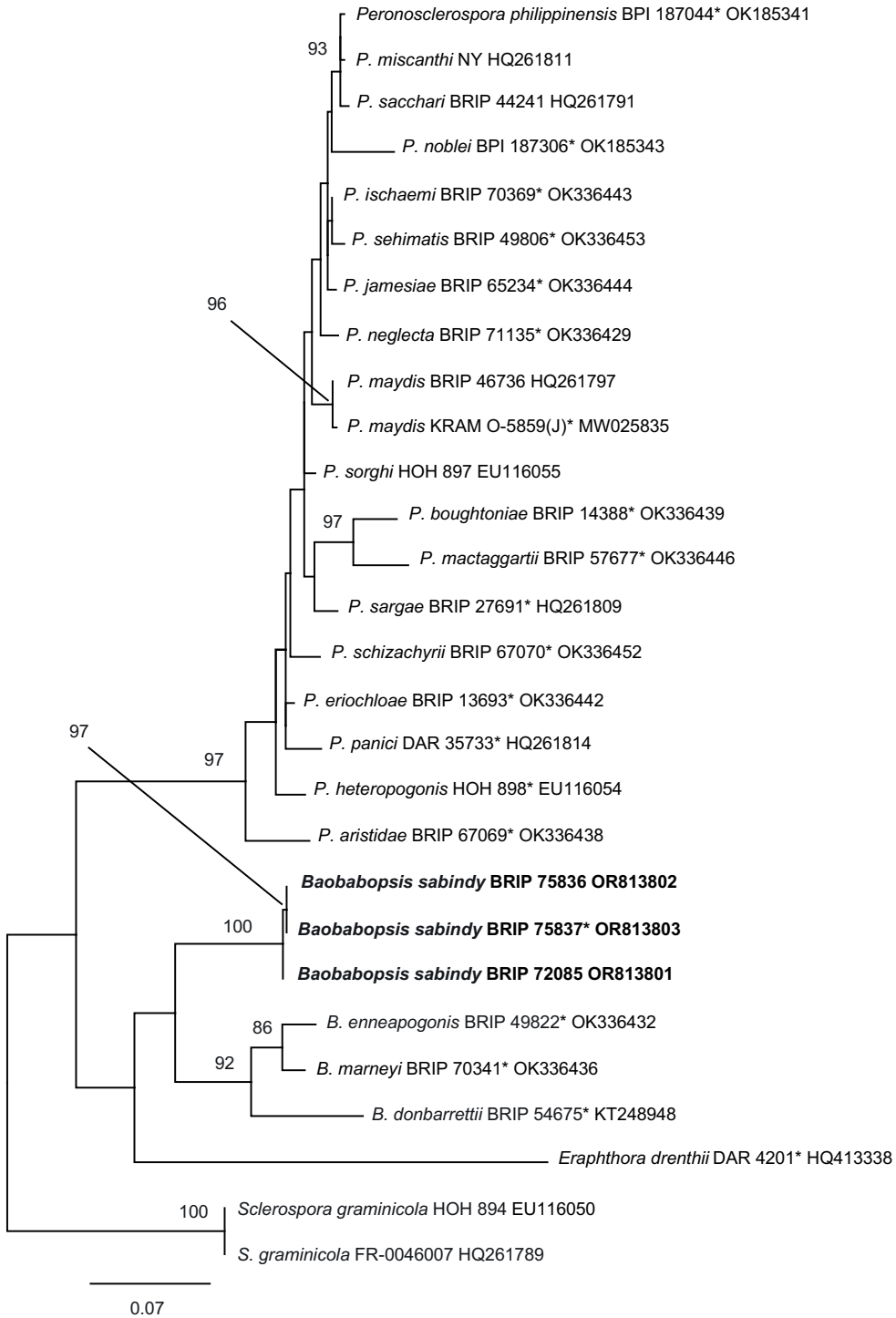
Typus: **Australia**, Queensland, Silver Valley Road, in leaves of *Eragrostis spartinoides* (*Poaceae*), 23 Apr. 2023, *M. Sudsanguan, Y.P. Tan, M.D.E. Shivas & R.G. Shivas* (**holotype** BRIP 75837a; *cox2* sequence GenBank OR813803).

Additional materials examined: **Australia**, Queensland, Teewah, in leaves of *Eragrostis* sp., 8 Dec. 2020, *L.S. Shuey & A.R. McTaggart* (specimen BRIP 72085a; *cox2* sequence GenBank OR813801); Queensland, Silver Valley Road, in leaves of *Schizachyrium fragile* (*Poaceae*), 23 Apr. 2023, *M. Sudsanguan, Y.P. Tan, M.D.E. Shivas & R.G. Shivas* (specimen BRIP 75836a; *cox2* sequence GenBank OR813802).

Notes: Based on a BLASTn search of NCBIs GenBank nucleotide database, the closest relevant hits using the *cox2* sequence are *Baobabopsis donbarrettii* [specimen BRIP 54675a; GenBank KT248948; Identities 412/469 (88 %), no gaps], *B. enneapogonis* [specimen BRIP 49822a; GenBank OK336432; Identities 422/469 (90 %), no gaps], and *B. marneyi* [specimen BRIP 7034a1; GenBank OK336436; Identities 422/469 (90 %), no gaps].

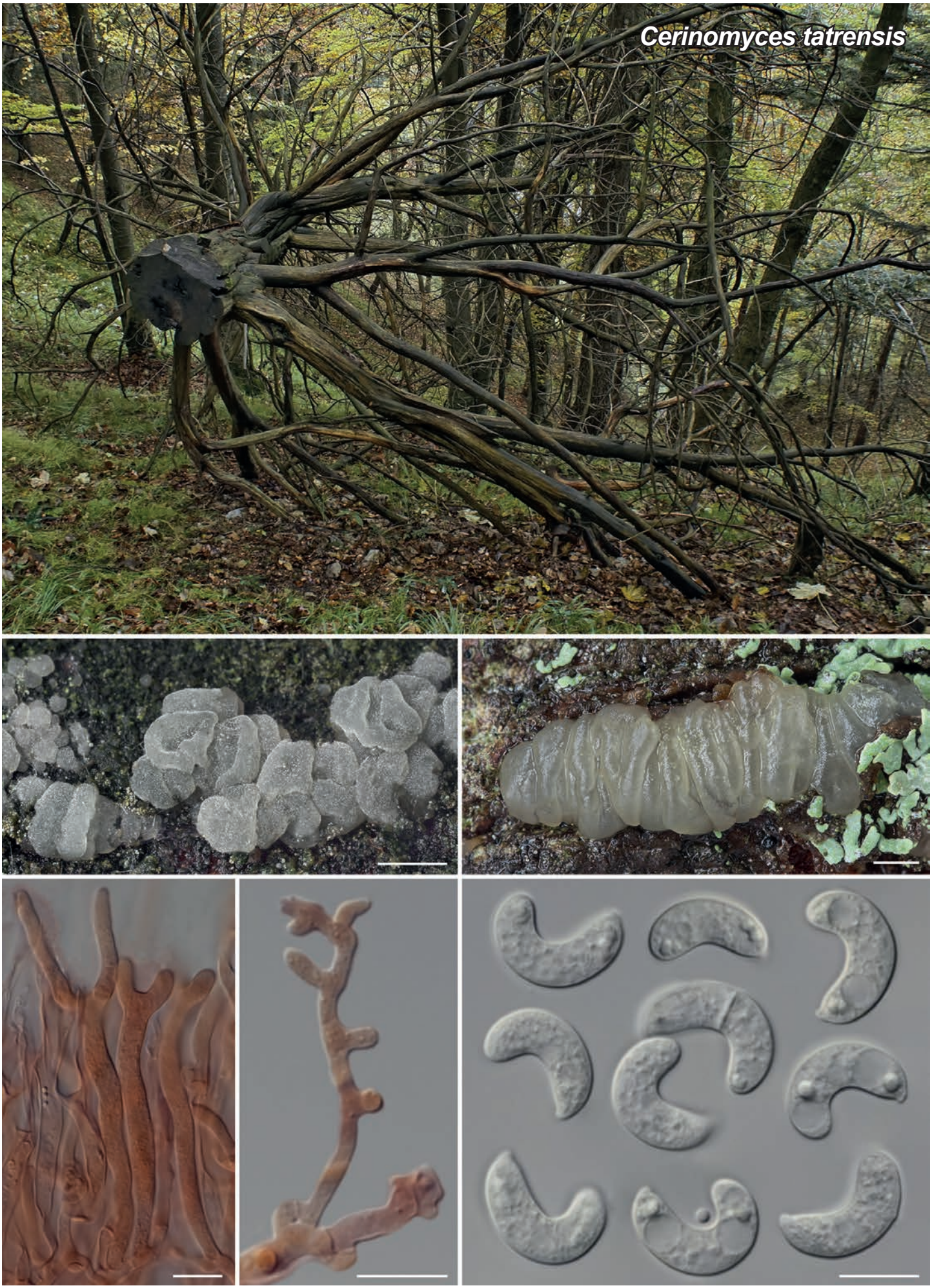
Baobabopsis sabindy was found on several plants of two unrelated genera of *Poaceae*, specifically *Eragrostis* (subfamily *Chloridoideae*) (BRIP 75837a) and *Schizachyrium* (subfamily *Panicoideae*) (BRIP 75836a). These grasses were growing at the same roadside location adjacent to open eucalypt woodland in northern Queensland. The plants had shredded leaf blades typical of downy mildew. Oospores were apparent and abundant in the shredded vascular tissues. The identity of the grasses was confirmed by occasional healthy flowering stems on diseased plants. A third specimen (BRIP 72085a) of *B. sabindy* was identified on *Eragrostis* sp. approx. 1 300 km distant in south-east Queensland.

Colour illustrations: Eucalypt woodland, Silver Valley Road, northern Queensland, Australia. *Baobabopsis sabindy* in leaves of *Eragrostis spartinoides*; oogonia. Scale bars: 1 cm, 100 µm, 100 µm, 10 µm.



Phylogenetic tree of selected *Baobabopsis*, *Eraphthora*, and *Peronosclerospora* species based on a maximum likelihood analysis of a *cox2* alignment. Analysis was performed on the Geneious Prime 2023 platform (Biomatters Ltd.) using RAxML v. 8.2.11 based on the GTR substitution model with gamma-distribution rate variation (Stamatakis 2014). RAxML bootstrap support values greater than 70 % are shown at the nodes. *Sclerospora graminicola* was used as the outgroup. Novel taxon is indicated in bold. Type specimens are marked with an asterisk (*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.10706185).

M. Sudsanguan & S. Nalumpang, Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai, Thailand; e-mail: s.manorat@gmail.com & sarunya.v@cmu.ac.th
C. Doungsa-ard, Plant Protection Research and Development Office, Department of Agriculture, Bangkok, Thailand; e-mail: chanintorn.dd@gmail.com;
R.G. Shivas, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: roger.shivas@unisq.edu.au
Y.P. Tan, Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park 4102, Queensland, Australia; e-mail: yupei.tan@daf.qld.gov.au



Fungal Planet 1622 MycoBank MB 852595

Cerinomyces tatrensis Polhorský, Peiger & Tomka, *sp. nov*.

Etymology: Named after its occurrence in Západné and Vysoké Tatry Mts.

Classification: *Cerinomycetaceae*, *Dacrymycetales*, *Dacrymycetes*.

Basidiocarps firmly-gelatinous, whitish, semitranslucent to pale yellow when fresh, dark brown when dry, scattered or densely gregarious, pulvinate when young, later centrally depressed, irregularly discoid, gyrose, often coalesced forming convoluted masses, sessile when growing on wood or with a short stipe and rooting when growing erumpent through bark, smooth or appearing pruinose from mature basidiospores, individual basidiocarps (0.3–)0.5–1.5(–2) mm diam when fresh. *Marginal hyphae* simple, not branched, not thickened. *Internal hyphae* (1.7–)2–3(–4.1) µm wide, thin- to slightly thick-walled, often branching, walls roughened, embedded in a gelatinous matrix, with low number of lipid bodies (LBs) clamp connections present, perforated or not. *Hymenium* composed of basidia intermixed with well-branched, cylindrical, dendroid hyphidia. *Hyphidia* with numerous (0–)5–15 branches or short nodules, infrequent, 35–70 µm long, (1.4–)1.6–2.3(–2.6) diam in the upper half, basal septum clamped. *Young basidia* cylindrical to narrowly clavate, often flexuous. *Mature basidia* 2-spored (very rarely 3-spored), (30–)43–58(–65) × (4.4–)4.7–5.6(–6) µm, sterigmata 19–43 µm long; with varying number of LBs and hyaline, non-refractive vacuolar bodies (VBs) – appearing granulose. *Basidiospores* approximate real length (15.8–)18–22(–24) × (4.5–)5–5.8(–6.5) µm, Q = (2.8–)3.3–4(–4.4), maximum diam (13.1–)14.4–16.6(–17.7) µm, cylindrical, (very) strongly curved (± semicircular), ends rounded to obtuse, thin-walled (walls ~ 0.2–0.3 µm wide), tardily forming one thin septum, strongly overmature spores up to three septa, hyaline, filled with small LBs, 0.2–0.5 µm diam, which sometimes coalesce into 1–2 larger LBs at each pole, 1–2.2 µm diam and with non-refractive VBs, 0.9–2 µm diam, that likewise coalesce into 1 large VB near each pole, 3.4–5 µm diam; uninucleate (sometimes 2 nuclei seen prior to septation), nucleus 1.2–2.8 µm diam; apical germination tube rarely observed. *Conidia* not seen.

Ecology: Currently known from near-natural montane Medio-European limestone mixed beech forest (*Fagus sylvatica*, *Picea abies*, *Pinus sylvestris*, *Abies alba*, *Taxus baccata*, *Acer pseudoplatanus*) and natural acidophilous Picea forest of the montane to alpine levels (*Vaccinio-Piceetea*) mixed with *Pinus cembra*, *Pinus mugo* and *Sorbus aucuparia*. natural alpine *Larix decidua* forest mixed with *Picea abies*, *Pinus cembra*, *Pinus mugo* and *Sorbus aucuparia*. Basidiocarps grow on dead decorticated trunks and branches, or on a bark of coniferous trees. *Cerinomyces tatrensis* was recorded on *Taxus baccata* and *Pinus mugo* in areas of its natural stands. Occurrence in human-influenced forests or on other coniferous tree species was not confirmed but is not excluded.

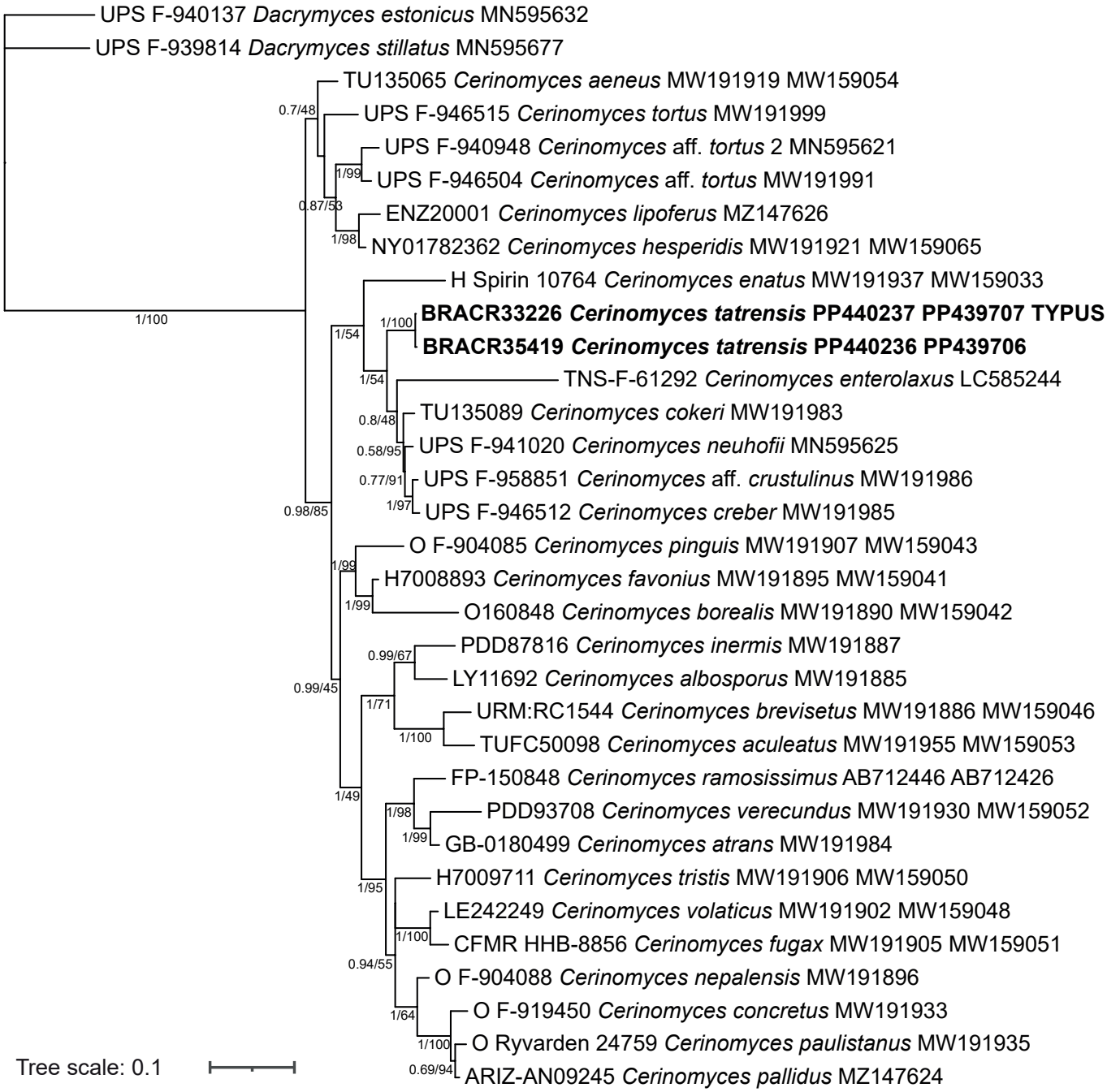
Typus: **Slovak Republic**, Žilina, Pribylina, Baranec (Západné Tatry Mts.), N49.1506°, E19.7739°, 1 580 m a.s.l., bark of *Pinus mugo* (*Pinaceae*), 18 Jul. 2020, *A. Polhorský* (**holotype** BRA CR33226; ITS and LSU sequences GenBank PP440237 and PP439707).

Additional material examined: **Slovak Republic**, Žilina, Liptovské Matiašovce, Suchá dolina – Huňová (Západné Tatry Mts.), N49.193° E19.603°, 1 070 m a.s.l., rotting trunk of *Taxus baccata* (*Taxaceae*), 7 May 2017, *M. Peiger* (BRA CR35419; ITS and LSU sequences GenBank PP440236 and PP439706); *ibid*., 8 Nov. 2017 (TNP 7/2023/1–BM–405). ; Prešov, Lysá Poľana, Bielovodská dolina (Vysoké Tatry Mts.), N49.184° E20.11734°, 1 417 a.s.l., lying, rotting, decorticated branch of *Pinus mugo*, 5 Jun. 2024, A. Polhorský (BRA CR40201)..

Notes: Due to the measurement difficulty of strongly curved spores, two methods of determining basidiospore length were applied. Approximate real length indicates the length of segmented, curved line through the middle of the spore from one end to another (excluding the hilar appendix) and maximum diameter reflects the distance from two furthest points of the basidiospore.

Phylogenetically *C. tatrensis* belongs to the *C. enatus* clade, which species form similarly gelatinous, pustulate and coalescing basidiocarps, but is readily distinguished by its strongly curved basidiospores. Remarkably similar spore morphology is found in *C. curvisporus*, known only from the type locality in Southeast China on *Pinus densata* wood. Its strongly curved basidiospores are however larger, up to 20.4 µm, in their maximum diameter. Moreover, this species lacks dendroid hyphidia and differs in arid, resupinate basidiocarps with hyphal pegs and presumably belongs to the *C. albosporus* group (Maekawa & Zang 1997, Savchenko *et al*. 2021). Genetic data is not available for this species, however macro- and micromorphology is sufficient to distinguish it from *C. tatrensis*. Basidiospores of the genus *Cerinomyces* are typically cylindrical to curved-cylindrical, however none to the degree of *C. curvisporus* and *C. tatrensis*. Furthermore, basidiospores of these two species belong to the largest in the genus.

Colour illustrations: Taxus baccata old rotting decorticated trunk. Basidiocarps; mature and young basidia; branched hyphidium; living spores. Scale bars: basidiocarps = 1 mm; microstructures = 10 µm.



The phylogenetic tree based on a Maximum Likelihood (ML) analysis from the combined ITS/LSU sequence alignment. Analyses were done on the Phylosuite v. 1.2.3 platform (Zhang *et al.* 2020). The alignment was performed with MAFFT v. 7 (Katoh & Standley 2013) and manually checked and trimmed. The ML and Bayesian Inference phylogenies were inferred using IQ-TREE v. 2 (Minh *et al*. 2020) under the models automatically selected by IQ-TREE for 5 000 ultrafast (Minh *et al.* 2013) bootstraps. Bootstrap support values and Bayesian posterior probabilities are given at the nodes. *Dacrymyces stillatus* and *D. estonicus* were used as an outgroup. The novel taxon is indicated in **bold**. The scale bar on the tree indicates the expected number of changes per site. The alignment and tree were deposited in figshare.com (doi: 10.6084/m9.figshare.25354750).

A. Polhorský, Pezinská 14, 90301 Senec, Slovakia; e-mail: polhorsky.adam@gmail.com
M. Peiger, Research Station and Museum of TANAP, Tatra National Park Administration, Tatranská Lomnica 14066, 059 60 Vysoké Tatry, Slovakia; e-mail: maros.peiger@tanap.sk
P. Tomka, ul. 1. mája 2044/179, 03101 Liptovský Mikuláš, Slovakia; e-mail: palonahuby@gmail.com
D. Strašiftáková, Slovak National Museum-Natural History Museum, Vajanského náb. 2, P.O. Box 13, 81006 Bratislava, Slovakia; e-mail: dana.strasiftakova@snm.sk

Fungal Planet 1623 MycoBank MB853139

Cladosporium nubilum Wrzosek, Kisło, Ruszk.-Mich. & Młynek, *sp. nov.*

Etymology: Latin *nubilum* – cloudy. The name refers to the atypical, cloudy, irregular, three-dimensional shape of sterile cultures that seem to "float" above the medium surface.

Classification: *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes*.

Asexual morph. Mycelium formed by rounded and slightly elongated meristematic cells, often with swellings and constrictions, packed in three-dimensional clusters and stromatic-like aggregations. *Hyphae* toruloid. Young cells produced according to the meristematic growth scheme: the emerging "buds" enlarge and rupture the coating visible at the bottom of the mother cell. Cells olivaceous and smooth when young and dividing; with aging, the walls thicken and turn black and rough as become covered by an amorphous, unevenly thick coating. Septa vertical, horizontal, and oblique. Cells (5.7–)8–10(–12.7) µm long (mean 9.24, SD: 1.44), and (5.7–)7.5–10(–11) µm wide (mean 8.25, SD: 1.13), with translucent lipid globules of diverse size. No *conidiogenous cells* and *conidial formation* observed. *Sexual morph* undetermined.

Culture characteristics: Colonies soft, loosely, pinpoint attached to the medium, erumpent, three-dimensional, cauliflower-like, higher than wider, 1.2 cm diam after 14 d at 18 °C; on malt extract agar (MEA) upper part dark olivaceous to almost black and the bottom light coloured, colourless to light beige, surface with glassy shine; reverse olivaceous blackish.

Typus: **Poland**, Radzyń Podlaski, N51°46'29", E22°35'49", isolated from hypersaline brine, 10 Jun. 2020, *K. Młynek* (**holotype** WA0000074608, preserved as metabolically inactive culture, culture ex-type CBS 150747; ITS, SSU, *act*, and *tef1* sequences GenBank OR539697.1, OR539698.1, OR557574.1, and OR557575.1).

Notes: The original conditions of *C. nubilum* growth (brine, up to 18 % of salt) support the assumption that it is a xerophilic, halotolerant species with an unusual type of growth (meristematic) for *Cladosporium*, resulting from the adaptation to an extreme habitat. It grows on standard media, both supplemented and free from NaCl and/or sucrose.

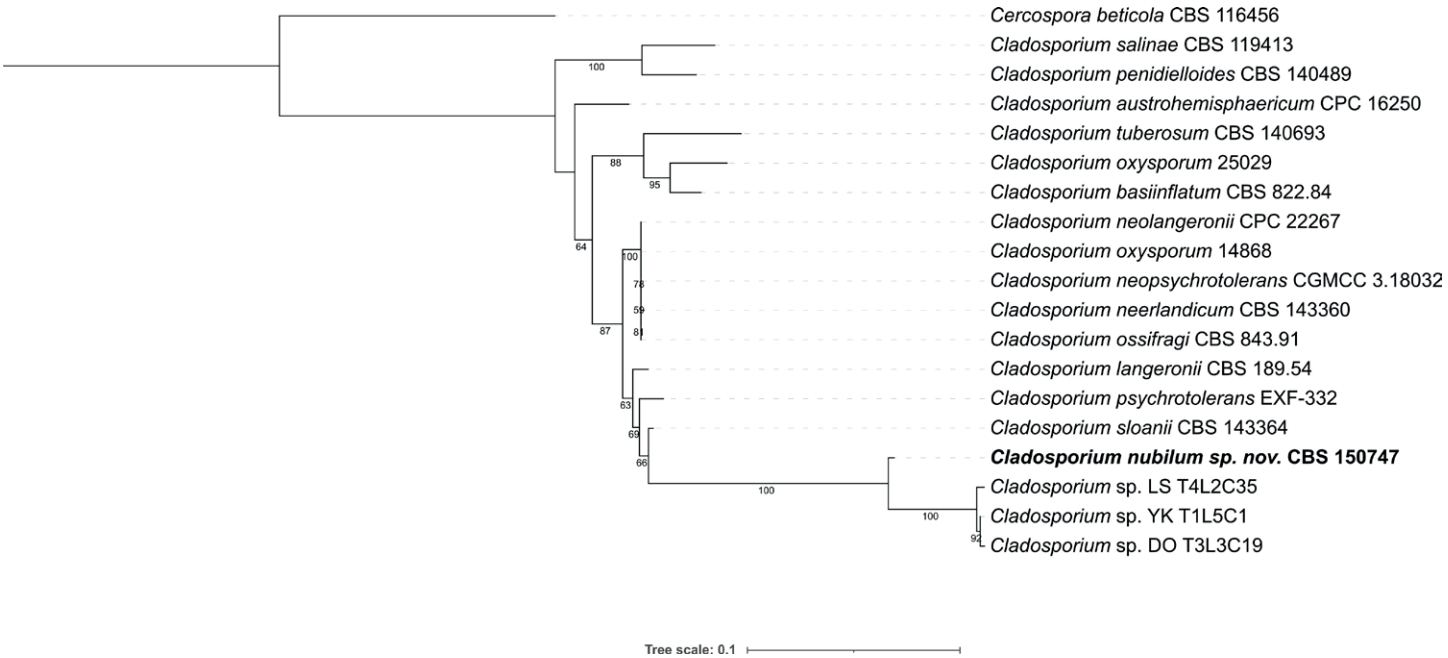
Cladosporium nubilum differs from other cladosporioid fungi by lacking typical hyphae and both micro- and macronematous reproduction structures. The dissemination occurs by single cells liberated from clusters or by cluster fragmentation and scattering. Neither conidiogenous cells, conidial scars, nor conidia were observed in the original material and subsequent cultures. The morphology of *C. nubilum* is highly similar to extremophilic, rock-dwelling species of the genus *Cryomyces* (Selbmann *et al.* 2005) and *Saxomyces* (Selbmann *et al*. 2014) or *Sarcinomyces* (Seifert *et al*. 2011), but our molecular data (ITS, SSU, *tef1* and *act* sequences) do not confirm such affinity.

According to molecular data, the group of species closely related to *C. nubilum* includes several endophytic strains of undescribed *Cladosporium* species (*e.g*., strains LS T4L2C35, YK T1L5C1, DO T3L3C19) from *Populus trichocarpa,* and three extremophilic species, *e.g*., *C. sloanii, C. langeronii,* and *C. psychrotolerans*. *Cladosporium sloanii,* produces typical conidiophores, ramoconidia, and conidia in chains but also forms substrate mycelium in the form of short chains of melanised cells (Bensch *et al.* 2018), which resemble mycelium of *C. nubilum.* However, *C. sloanii* differs from *C. nubilum* in most colony characters (velvety, with narrow, whitish, feathery, and crenate margin, and aerial mycelium up to 2 mm high, with several very small exudates). *Cladosporium langeronii* produces cells arranged like a starting stroma, but mycelium is mainly composed of elongated hyphae (Bensch *et al.* 2012, 2018). Few features shared by *C. nubilum* and *C. sloanii* include the halotolerancy and slow growth [on dichloran-glycerol agar (DG18): 8–9 mm diam in 14 d at 25 °C]. However, *C. sloanii* is known from a single isolate unable to grow on media standard for *Cladosporium* identification, and it is referred to as an obligately xerophilic species developing on substrates with low water activity (Bensch *et al*. 2018). In contrast, *C. nubilum* grows only slightly worse on standard media while it originally grew on the cheese skin and container walls, among salt crystals and other organic and inorganic deposits in a Polish cheese factory.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence are *Cladosporium* sp. [strain FP-027-A2, GenBank MH102092.1; Identities 549/552 (99 %), one gap], and *C. sloanii* [culture DTO:130-D5, GenBank MF473253.1; Identities 549/552 (99 %), one gap]. The closest hits using the **SSU** sequence are *Cladosporium perangustum* [isolate SICAUCC 20-0007, GenBank MT427737.1; Identities 558/558 (100 %), no gaps], and *Cladosporium* sp. [isolate SICAUCC 20-0009, GenBank MT427736.1; Identities 558/558 (100 %), no gaps]. The closest hits using the ***act*** sequence are *C. sloanii* [culture DTO:130-D5, GenBank MF474103.1; Identities 135/136 (99 %), no gaps], and *C. psychrotolerans* [isolate MUT:2579, GenBank MG832120.1; Identities 131/136 (96 %), no gaps]. The closest hits using the ***tef1*** sequence are *Aureobasidium thailandense* [strain CU 26, GenBank EU719352.1; Identities 518/536 (97 %), no gaps], *Cladosporium* sp. [isolate DO T3L3C19, GenBank MN054856.1; 516/536 (96 %), no gaps], *Cladosporium* sp. [isolate LS T4L2C35, GenBank MN054849.1; 515/536 (96 %), no gaps], and *Cladosporium* sp. [isolate YK T1L5C1, GenBank MN054857.1 514/536 (96 %), no gaps]. The surprising similarity of the *tef1* sequences of *C. nubilum* and *A. thailandense* can be caused by its misidentification (see also polyphyletic tree in Peterson *et al*. 2013). All other sequences with higher than 93 % similarity values belong to the known *Cladosporium* species.

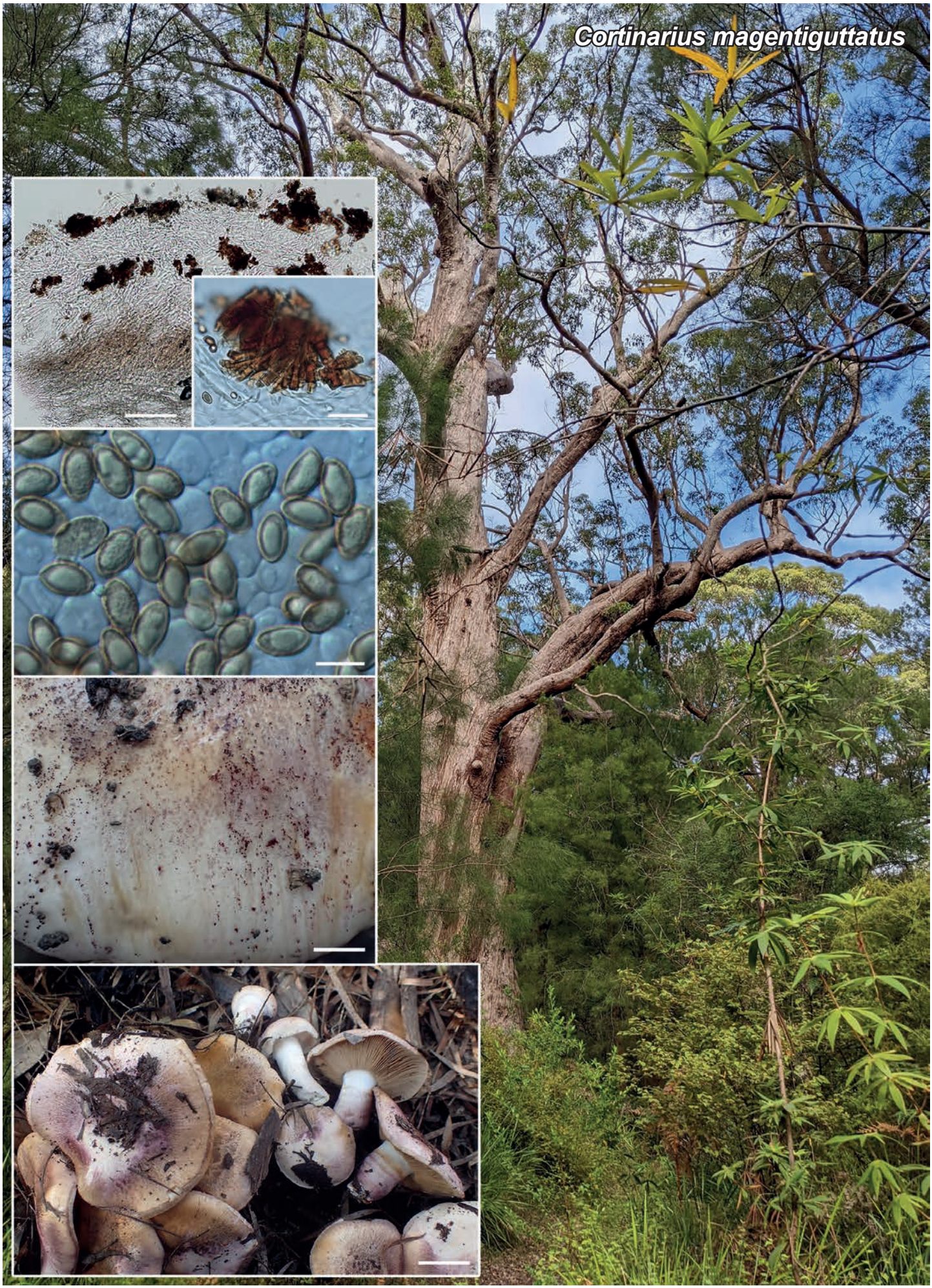
Supplementary material: doi: https://doi.org/10.6084/m9.figshare.24680514.v1

Colour illustrations: Sampling site at the production line in a cheese factory with brine (containing up to 18 % of salt), Poland. Colonies growing on the MEA; stromatic-like aggregations of growing and dividing cells; toruloid hypha with lipid globules (stained with Sudan III). Scale bars = 10 µm.



Maximum likelihood phylogenetic tree calculated using three loci: ITS, *tef1* and *act*, showing the position of *C. nubilum* (**bold** font) within the clade. *Cercospora beticola* was used as an outgroup. The sequences were aligned using the MUSCLE algorithm (Edgar 2004) implemented in SeaView v. 5.0.5 software (Galtier *et al.* 1996). Non-conserved positions were removed using Gblocks v. 0.81 (Castresana 2000). Concatenation of sequences from all four regions was performed using FasconCAT v. 1.0 (Kück & Meusemann 2010). Evolutionary models were determined using ModelTest-NG v. 0.1.7 (Darriba *et al*. 2020) separately for each nucleotide position in the codon of the *tef1* and *act* regions and for the whole ITS. Subsequently, maximum likelihood trees with 1 000 bootstrap replications were constructed using RaxML-NG v. 1.2.0 (Kozlov *et al.* 2019), and both analyses were executed on the CIPRES gateway (Miller *et al.* 2010) for support values. The tree and alignment were deposited in figshare (doi: 10.6084/m9.figshare.24680514) and TreeBASE (study S31024).

M. Wrzosek & K. Kisło, Botanic Garden, Faculty of Biology, University of Warsaw, Aleje Ujazdowskie 4, 00-478 Warsaw, Poland; e-mail: ma.wrzosek@uw.edu.pl & k.kislo@uw.edu.pl
K. Młynek, Faculty of Agrobioengineering and Animal Husbandry, University of Siedlce, Konarskiego 2, 08-110 Siedlce, Poland; e-mail: krzysztof.mlynek@uph.edu.pl
M. Ruszkiewicz-Michalska, Department of Algology and Mycology, Faculty of Biology and Environmental Protection, University of Lodz, Banacha 12/16, 90-237 Lodz, Poland; e-mail: malgorzata.ruszkiewicz@biol.uni.lodz.pl



Fungal Planet 1624 MycoBank MB 851804

Cortinarius magentiguttatus Syme & T. Lebel, *sp. nov.*

Etymology: Named in reference to the fine magenta-coloured particles and shards scattered across the pileus and lower stipe of the pale sporocarps, *magenteus* (L. for the colour magenta or red-purple), "*guttatus*" (L. for spotted or speckled).

Classification: *Cortinariaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata tricholomatoid habit, gregarious, sometimes caespitose, often in large groups, never solitary. *Pileus* 35–75 mm diam, broadly convex, becoming planoconvex then reflexed, margin finely inrolled, becoming plane, with a fine line of cortina (partial veil) strands forming a visible line around the edge as the pileus expands, or sometimes cortina remnants appendiculate, hanging down from pileus margin; pale tan to cream with scattered purple, mauve-lilac and faint orange patches or tinges, sometimes appearing almost white when remaining under leaf litter, becoming patchy pale apricot to pale yellowish brown in age and exposure; slightly viscid but drying with a fine, sandpapery feel, due to minute radiating lines of violet to rose magenta (11B4, 11D4, 12B4, 12C5, Kornerup & Wanscher 1967) particles or shards becoming dark and dull brown toward the margin, which appear more visible on exposure to sunlight. *Context* up to 12 mm thick, white, unchanging, firm, solid. *Lamellae* adnexed or adnate, narrow, very close, up to 10–13 mm long × 3–8 mm deep with one tier of lamellules, margin and face smooth, white to cream initially, remaining pale as pileus expands, then slowly becoming light rust (5C6). *Stipe* 25–58 mm long × 5–16 mm diam, stout, central, terete, tapering neatly at base or very slightly bulbous at base; surface dry to slightly viscid, longitudinally fibrillose, white above the cortina remnants, purple, magenta-lilac and orange-yellow at base and partially up length of stipe, at times forming jagged bands in the same colours (mauve lilac and orange-yellow), appearing glandular dotted below cortina from minute loose, violet to rose magenta (11B4, 11D4, 12B4, 12C5) particles or shards similar to pileus (most obvious in young buttons); context firm, solid, white and unchanging. *Basal mycelium* white. *Cortina* white, fine fragile, apparent in young sporocarps, breaking as the pileus expands to form a fine annulus approximately 2/3 up the stipe; universal veil white, leaving a basal ring of fine remnants as the pileus expands. *Odour* none or faintly floral. *Spore print* yellowish brown (5D6-7). *Spores* 7.5–10(–10.5) × 5–6.5(–7) µm, (mean 9.11 × 5.92, Q_m = 1.45), amygdaliform, rusty brown in 3 % KOH, very finely verrucose, ornamentation less than 0.5 µm high. *Basidia* 23–33 × 8–10 µm, clavate, hyaline, tetrasporic. *Pleuromacrocystidia*, *pleuropseudocystidia* and *cheilomacrocystidia* absent. *Hymenophoral trama* composed of parallel hyaline hyphae 4–7 µm diam. *Subhymenium* consisting of irregular cells, sub-gelatinised, 4–9 µm diam. *Pileipellis* duplex. A patchy outer gelatinised layer 15–25 µm wide, of loosely interwoven, hyaline, partially gelatinised, thin-walled narrow hyphae, 2–4 µm diam, overlying a 200–300 µm wide *epicutis*, of loosely interwoven hyaline hyphae 2–4 µm diam and rare sinuous encrusted hyphae, 4–6 µm diam, with hyphal tips occasionally upright; *hypocutis* 50–90 µm wide, of densely packed, magenta (H_2O) to golden brown (3 % KOH) pigmented, non-gelatinised, interwoven irregularly shaped hyphae, 4–8 µm diam. Scattered shards or aggregations 50–140 × 50–100 µm, of magenta (H_2O) to dark brown (3 % KOH) pigmented, thick-walled, septate hyphae, 6–12 µm diam, in shortish lengths 11–32 µm long or small irregular sheets 11–45 × 10–32 µm, occurring in outer gelatinised layer and into epicutis and also in stipitipellis; *context* 400–1100 µm wide, of parallel to somewhat interwoven, hyaline, non-gelatinised, hyphae 4–7 µm diam, intermixed with abundant irregularly shaped, hyaline inflated elements 8–30 × 5–20 µm. *Partial veil* of subparallel to somewhat interwoven, thin-walled, hyaline hyphae 2–5 µm broad. *Clamps* are medallion or keyhole type, occurring in all tissues.

Habit, habitat and distribution: Gregarious in large groupings of medium sized sporocarps, sporulating in deep leaf litter. Currently known from long undisturbed eucalypt forest and woodlands in southern Western Australia and South Australia.

Typus: **Australia**, Walpole, Walpole-Nornalup National Park, Bibbulmun Track east of Gulley Road towards Douglas Hill, 8 May 2018, *K. Syme, D. Edmonds & J. Wall*, KS2968 (**holotype** PERTH 9624236, **isotype** AD 293967; ITS and LSU sequences GenBank PP151603 and PP151609).

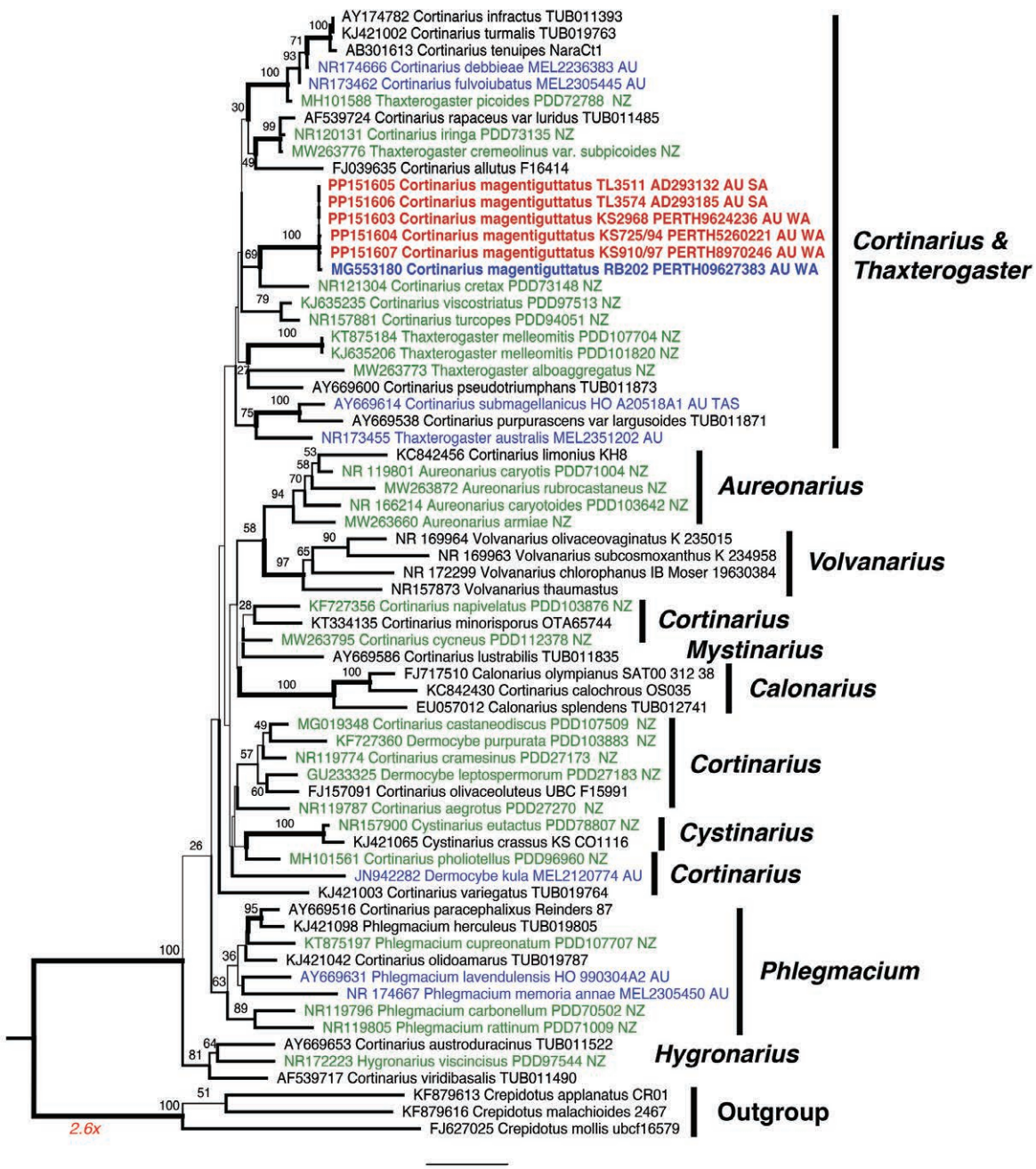
Additional materials examined: **Australia**, Western Australia, Denmark, William Bay National Park near the Ranger's residence, 7 Jun. 1994, *K. Syme & M. Hart*, KS725/94 (PERTH 5260221; ITS and LSU sequences GenBank PP151604 and PP151610; Denmark, west of Sunny Glen Road, 31 May 1997, *K. Syme, S. Ellis, & the Pedro family*, KS910/97 (PERTH 8970246; ITS and LSU sequences GenBank PP151607 and PP151612); Mountain Road, Walpole Fire Mosaic Study Grid 16, 6 Jun. 2011, *R. Robinson, K. Syme & P. Anderson*, RB202 WFM555 (PERTH 09627383; ITS sequence GenBank MG553180); South Australia, Springmount Conservation Park, main walking track, approximately 600 m from car park, 17 Jun. 2022, *T. Lebel*, TL3511 (AD 293132; ITS and LSU sequences GenBank PP151605 and PP151608); Adelaide Hills, Mylor Conservation Park, upper Heysen track off Whitehead Rd, along edge of track in leaf litter, 4 Jun. 2023, *T. Lebel*, TL3574 (AD 293185; ITS and LSU sequences GenBank PP151606 and PP151611.

Notes: *Cortinarius magentiguttatus* differs from other pale coloured cortinarioid species in having scattered purple, mauve-lilac and faint orange patches or tinges scattered over the pileus and bands of the same colour on the stipe from below the cortina to the base. In addition, the minute particles and shards of violet-rose magenta in radiating lines over the pileus and the stipe below the cortina appear to be unique. These shards of pigment survive drying and are most obvious on the margin of the pileus and the stipe base in younger basidiomata. The pigment does not dissolve in 3 % KOH.

Colour illustrations: Long unburnt *Eucalyptus* forest dominated by *E. jacksonii* and *E. diversicolor*, Walpole-Nornalup National Park, Walpole, Western Australia, Australia, holotype site. Basidiomata; violet-magenta rose pigmented shards on pileus; microscopic elements: ornamented basidiospores; pellis cross-section showing loosely interwoven epicutis and magenta pigmented hypocutis, with scattered aggregations of magenta shards; inset- close up of pigmented shards. Scale bars: basidiomata = 20 mm; pileus = 5 mm; spores = 10 µm; pileipellis = 100 µm; inset = 20 µm.

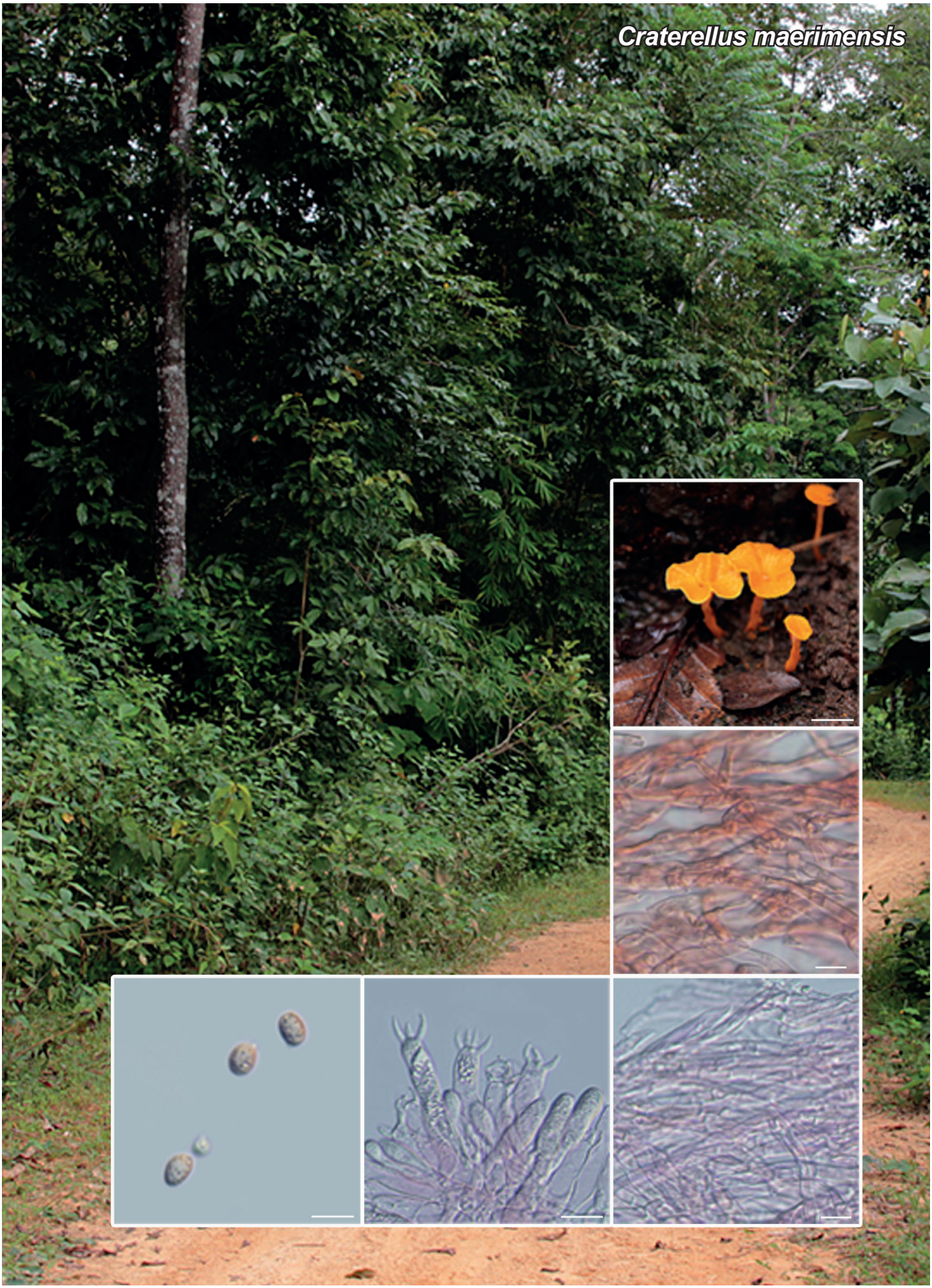
The gregarious mass sporulation (15–20 sporocarps in a cluster) of medium-sized colourful sporocarps is unusual enough that we would expect there to be more observations and herbarium collections. The sometimes pale pileus (when not exposed) and initially pale lamellae, may cause some confusion with *C. austroalbidus*. However, that species has a curry smell, remains whitish even in age, and may have a lilac apex to the stipe that *C. magentiguttatus* lacks.

Cortinarius magentiguttatus is a distinctive species (BS support 100 %) that has no apparent close relatives based on barcode ITS-LSU DNA data. While there is no support for any phylogenetic relationship, a well-supported clade including *Thaxterogaster picoides* from New Zealand, *Cortinarius debbiae* and *C. fulvoiubatus* from Australia (New South Wales and Tasmania respectively), and *T. turmalis* from Europe often appears as the next closest clade in any analyses we have conducted. Recent phylogenetic and phylogenomic investigations have changed our understanding of relationships within this morphologically diverse genus and resulted in the distinction of 10 genera (Soop *et al*. 2019, Liimatainen *et al.* 2022). For the moment we retain the species under the genus name *Cortinarius*, rather than placing in *Thaxterogaster*, until further genes can be obtained and analysed.



Bayesian (Mr Bayes v. 3.2.6) 50 % majority-rule consensus tree obtained from the ITS-LSU-nrDNA for a selection of cortinarioid species. Bold lines indicate PP support >0.95. Bold red text indicates sequences generated for this study, *C. magentiguttatus sp. nov.*

K. Syme, 24 Offer St, Denmark, Western Australia, 6333 Australia; e-mail: katrinasyme@gmail.com
T. Lebel, State Herbarium of South Australia, Adelaide, South Australia, 5000 Australia; e-mail: Teresa.Lebel@sa.gov.au



Fungal Planet 1625 MycoBank MB 847929

Craterellus maerimensis Khamsuntorn, Pinruan, & Luangsa-ard, *sp. nov.*

Etymology: Refers to the location where the fungus was collected, Mae Rim district, Chiang Mai Province, Thailand.

Classification: *Hydnaceae*, *Cantharellales*, *Agaricomycetes.*

Basidiomata small, thin, 17–30 mm high, cantharelloid. *Pileus* 2–17 mm diam, infundibuliform when young becoming convex to plano-convex with a shallow depression at centre, umbilicate; surface brilliant orange yellow (23B; The Royal Horticultural Society 2015). *Hymenophore* continuous over lower side, decurrent, pale orange, down to the stipe in some specimens, smooth, forming a demarcating zone with stipe. *Stipe* insertion central, cylindrical, 8–20 × 0.5–2 mm, solid, surface strong orange (25A–B; RHS 2015). *Context* fleshy, concolourous with pileus. *Odour* and *taste* not observed. *Spore print* not observed. *Basidiospores* (7.5–)8–11.3 × 6.3–8.8(–9.5) µm, Q = 1.10–1.50, Qm = 1.29 (n = 50). hyaline, smooth surface, globose to subglobose shaped, *Basidia* 60–83 × 7.5–10 µm, hyaline, subcylindrical, clavate, thick-walled, with large guttules or with finely granulose contents, 2–4 sterigmata, 3–5.5(–7.5) µm long, stout, incurved. *Basidioles* abundant, cylindrical with finely granulose contents. *Hymenial cystidia* absent. *Subhymenium* 125–150 µm. *Pileus trama* 300–400 µm. *Pileipellis* hyaline to brown, branch septate, 3.8–11.3 µm wide. *Stipitipellis* composed of interwoven hyphae, hyaline to pale brown, branched, septate, 2.5–7.5 µm wide. *Clamp connections* absent in all tissues.

Habitat and known distribution: On laterite and sandy soil at Ban Saluang Nok Community Forest, Mae Rim district, Chiang Mai Province, Thailand.

Typus: **Thailand**, Chiang Mai Province, Mae Rim district, on soil, 26 Aug. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (**holotype** BBH 49161; ITS and LSU sequences GenBank OK073898 and OK067673).

Additional material examined: **Thailand**, Chiang Mai Province, Mae Rim district, on soil, 26 Aug. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (BBH 47881; ITS and LSU sequences GenBank OK073900 and OK067672).

Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence of the type collection has the closest GenBank BLAST match (94.59 %) with a sequence identified as *Craterellus calyculus* from the USA (GenBank MK607596) and similar sequences identified to species of *C. carolinensis* (94.59 %) from Canada (GenBank KY654712). The **LSU** sequence of the type collection has the closest GenBank BLAST match (96.19 %) with a sequence identified as *C. albostrigosus* from India (GenBank MG593194), and *C. albidus* (95.59 %) from India (GenBank MT921162).

As observed in *C. sanbuakwaiensis* (this study, FP 1626), the phylogenetic analyses reveal that *C. maerimensis* is included in the clade comprising *C. badiogriseus*, *C. calyculus*, *C. carolinensis*, *C. hesleri*, *C. indicus*, *C. inusitatus*, *C. parvogriseus* and *C. shoreae* with strong support values (85 %MP, 90 %ML and 1.00 PP). *Craterellus maerimensis* is phylogenetically closely related to *C. albostrigosus* and *C. sanbuakwaiensis*. However, the basidiomata of *Craterellus albostrigosus* are chocolate brown or brownish grey to greyish brown whereas those of *C. maerimensis* and *C. sanbuakwaiensis* are orange-yellow. *Craterellus maerimensis* differs from *C. sanbuakwaiensis* in having a larger basidiomata and basidia. Additionally, the basidial wall of *C. maerimensis* is thicker than that of *C. sanbuakwaiensis*.

For phylogenetic tree, see *Craterellus sanbuakwaiensis* (FP 1626).

Colour illustrations: The mixed deciduous forest, Mae Rim district, Chiang Mai Province, Thailand, where the holotype was collected. Right top: Basidiomata of BBH 49161; pileipellis; stipitipellis; basidia; basidiospores. Scale bars: basidiomata = 10 mm; all others = 10 µm.

P. Khamsuntorn, U. Pinruan & J.J. Luangsa-ard, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: phongsawat.kha@ncr.nstda.or.th, umpawa.pin@biotec.or.th & & jajen@biotec.or.th

Fungal Planet 1626 MycoBank MB 847928

Craterellus sanbuakwaiensis Sommai, Somrith., Khamsuntorn & Pinruan, *sp. nov.*

Etymology: Refers to the location where the fungus was collected, San Buak Wai Community Forest, Mae Rim district, Chiang Mai Province, Thailand.

Classification: *Hydnaceae*, *Cantharellales*, *Agaricomycetes*

Basidiomata small, thin, 10–17 mm high, cantharelloid. *Pileus* 2–8 mm diam, infundibuliform when young becoming convex to plano-convex with a shallow depression at centre, umbilicate; surface vivid orange yellow (21A–B; The Royal Horticultural Society 2015) when moist, becoming brownish yellow when dried. *Hymenophore* continuous over lower side, decurrent, pale orange, down to the stipe in some specimens, smooth, forming a demarcating zone with stipe. *Stipe* insertion central, cylindrical, 8–15 × 0.5–1 mm, solid, surface vivid orange yellow (21A–B; RBS 2015). *Context* fleshy, concolourous with pileus. *Odour* and *taste* not observed. *Spore print* not observed. *Basidiospores* (6.25–)7.5–10 × 5–7 µm, Q = 1.14–2.00, Q_m = 1.42 (n = 50), hyaline, smooth surface, ovoid or globose to subglobose. *Basidia* 35–50 × 5–7.5 µm, hyaline, subcylindrical, clavate, thin-walled, with large guttules or with finely granulose contents, 2–4 sterigmata, 3.7–5 µm long, stout, incurved. *Basidioles* abundant, cylindrical with finely granulose contents. *Hymenial cystidia* absent. *Subhymenium* 112.5–125 µm. *Pileus trama* 250–300 µm, pale brown to brown, branched, septate, 2.5–10 µm wide. *Stipitipellis* composed of interwoven hyphae, hyaline to pale brown, branch, septate, 3.8–7.5 µm wide. *Clamp connections* absent in all tissues.

Habitat and known distribution: On laterite and sandy soil at San Buak Wai Community Forest, Mae Rim district, Chiang Mai Province, Thailand.

Typus: **Thailand**, Chiang Mai Province, Mae Rim district, on soil, 26 Aug. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (**holotype** BBH 49162; ITS and LSU sequences GenBank OK073899 and OK067674).

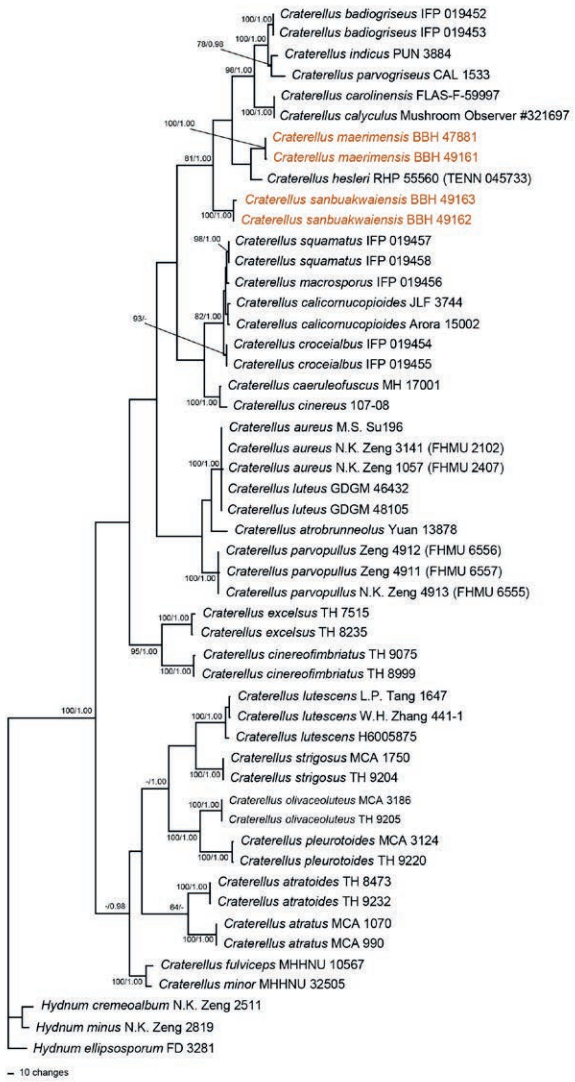
Additional material examined: **Thailand**, Chiang Mai Province, Mae Rim district, on soil, 26 Aug. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (BBH 49163; ITS and LSU sequences GenBank OK073901 and OK067675).

Colour illustrations: The mixed deciduous forest, Mae Rim district, Chiang Mai Province, Thailand, where the holotype was collected. Left top: Basidiomata of BBH 49162. Left centre: Pileipellis. Left bottom: Stipitipellis. Centre bottom: Basidia. Right bottom: Basidiospores. Scale bars: basidiomata = 10 mm; all other microscopic structures = 10 µm.).

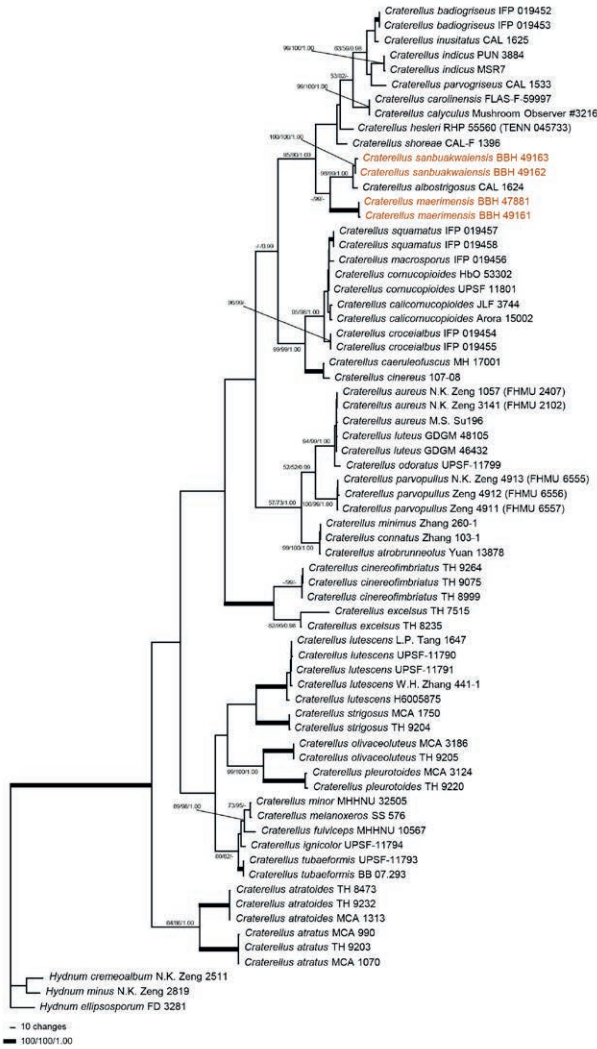
Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence of the type collection has the closest GenBank BLAST match (91.52 %) with a sequence identified as unidentified *Craterellus* from Thailand (GenBank MF589901) and similar sequences identified to species of *C. carolinensis* (87.22 %) from Canada (GenBank ON943343). The **nrLSU** sequence of the type collection has the closest GenBank BLAST match (97.43 %) with a sequence identified as *C. albostrigosus* from India (GenBank MG593194), *C. inusitatus* (95.63%) from India (GenBank MG593195) and *C. albidus* from China (GenBank MT921162)

The phylogenetic analyses reveal that *Craterellus sanbuakwaiensis* is included in the clade comprising *C. badiogriseus*, *C. calyculus*, *C. carolinensis*, *C. hesleri*, *C. indicus*, *C. inusitatus*, *C. maerimensis*, *C. parvogriseus* and *C. shoreae* with strong support values (85 % MP, 90% ML and 1.00 PP). All species in this clade possess the identical characteristic of lacking a clamp connection. In the clade, *C. sanbuakwaiensis* formed a highly supported sister group to *C. albostrigosus* (98 % MP, 99 % ML and 1.00 PP). However, these two species have a distinct colour of basidiomata. *Craterellus sanbuakwaiensis* has vivid orange-yellow basidiomata when moist that become brownish yellow when dried whereas the basidiomata of *C. albostrigosus* (Bijeesh *et al.* 2018) are chocolate brown or brownish grey to greyish brown when moist that become brownish orange to mouse grey when dried. *Craterellus albostrigosus* has strigose hairs with pointed to slightly curved tips which are not present in *C. sanbuakwaiensis*. Furthermore, *C. sanbuakwaiensi* has longer stipes than the stipes of *C. albostrigosus*. Micro-morphologically, the basidia and basidiospores of *C. albostrigosus* are larger than those of *C. sanbuakwaiensis* (48–72 × 6.5–9 µm of basidia and 8–11.5 × 6–8 µm of basidiospores in *C. albostrigosus vs* 35–50 × 5–7.5 µm of basidia and 6.3–10 × 5–7 µm of basidiospores in *C. sanbuakwaiensis*).

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



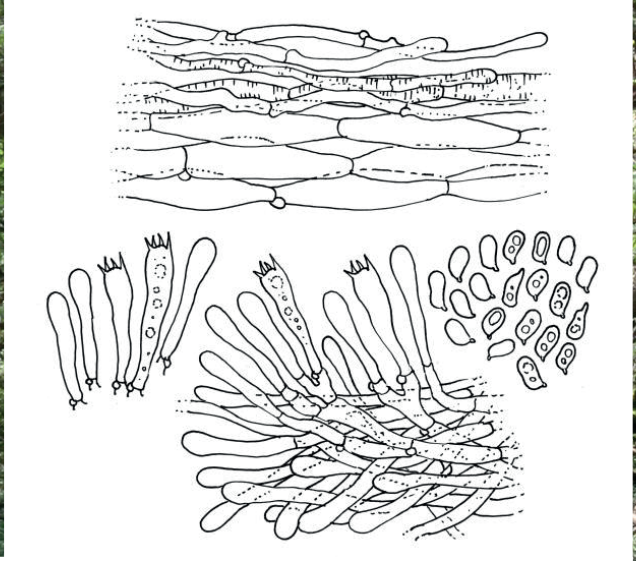
Maximum Parsimony Tree based on ITS sequence data. Numbers left of branches correspond to bootstrap support in parsimony analysis; numbers right of branches are bootstrap support values from Maximum Likelihood analysis.



Maximum Parsimony Tree based on combined ITS and LSU sequences data. Numbers left of branches correspond to bootstrap support in parsimony analysis; numbers right of branches are bootstrap support values from Maximum Likelihood analysis. Bold lines in the tree represent 100 % bootstrap (BSMP/BSML) and 1.00 posterior probability (BPP).

S. Sommai, S. Somrithipol, P. Khamsuntorn & U. Pinruan, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: sujinda.som@biotec.or.th, sayanh@biotec.or.th, phongsawat.kha@ncr.nstda.or.th & umpawa.pin@biotec.or.th

Cuphopyllus praecox



Fungal Planet 1627 MycoBank MB 852616

Cuphopyllus praecox Boccardo, Dovana & Vizzini, *sp. nov.*

Etymology: The species epithet derives from the Latin adjective *praecox*, early, and refers to its spring growth.

Classification: *Cuphophyllaceae*, *Agaricales*, *Agaricomycetes.*

Pileus 15–30 mm diam, initially convex, semi-globose or slightly truncated-conical, then flattened and with a depressed centre when old; margin at first entire, then clearly wavy and crenulated, often fissured when dry; surface slimy when moist, silky and entirely covered with fine radial fibrils which are more evident when dry, clearly hygrophanous; clearly striated up to the centre and tending to crack along radial lines, in dry weather; brownish grey, paler at the margin which sometimes shows yellowish-cream hues, increasingly darker in the centre which often appears blackish-brown even in dry conditions. *Lamellae* decurrent to strongly decurrent, arcuate, thick and distant (lamellae that reach the stipe = 25–30), interspaced with lamellulae; whitish, in strong contrast with the pileus and stipe colour; edge often eroded and cracked, sometimes faintly coloured brown. *Stipe* 20–50 × 1–4 mm, slender, cylindrical, often curved and tapering towards the base, hollow, waxy, pale grey, sometimes with faint lilac hues at apex, paler towards the base, smooth, weakly pruinose at the apex; easily fractureable, it tends to streak weakly longitudinally in dry weather. *Context* thin, white to greyish, smell indistinct, taste mild. *Spore print* whitish. *Basidiospores* (5.5–)6.6–*7.6*–8.6(–10.0) × (3.0–)3.4–*3.9*–4.5(–5.0) µm, Q = (1.46–)1.68–*1.97*–2.25(–2.76), smooth, hyaline, cylindrical to larmiform, often with weak median constriction, hilar appendix evident, often oblique, multiguttulate, non-amyloid, non-dextrinoid. *Basidia* 38–40(–50) × 6–7(–8) µm, clavate, 4-spored, rarely 2-spored, sterigmata up to 5 µm long; basidium-to-spore length ratio = 5.4–7.1. *Hymenial cystidia* absent. *Hymenophoral trama* subregular to interwoven, made up of cylindrical hyphae, 20–60 × 5–8 µm. *Pilepellis* an ixocutis with cylindrical hyphae, 50–100 × 3–4 µm, some ascending hyphae with rounded apex present; *subcutis* consisting of elements that are swollen in the middle part, 40–80 × (5–)8–13 µm; greyish-brown intracellular and encrusting zig-zag-shaped wall pigments observed. *Stipitipellis* a xerocutis consisting of elongated cylindrical hyphae like those of the pileipellis with greyish brown intra- and extracellular encrusting pigment. *Clamp connections* present in all pseudotissues.

Habit, habitat and distribution: Gregarious, sometimes loosely cespitose, on basic soil (limestone flysch), in meadow environments or at the edge of paths between patches of mixed broad-leaved trees with a predominance of *Ostrya carpinifolia*, *Acer italicus* and *Prunus avium*, on bare ground or among decaying leaves, with presence of lichens (*Cladonia* spp.) and mosses; fruiting in spring. So far known only from the type locality, Liguria, Italy.

Colour illustrations: Sassello, Italy, deciduous forest. *Cuphopyllus praecox* basidiomata in habitat; microscopy drawing: basidia, spores, hymenophoral trama and hymenium, and pileipellis (holotype GDOR 4881). Scale bars = 10 µm.

Typus: **Italy**, Ligura, Loc. Verlia, Sassello (SV), 44°28’18”N, 8°29’36”E, 433 m a.s.l., among the grass, 23 May 2020, *F. Boccardo* (**holotype** GDOR 4881; ITS, LSU and *rpb1* sequences GenBank PP410365, PP406894 and PP419032).

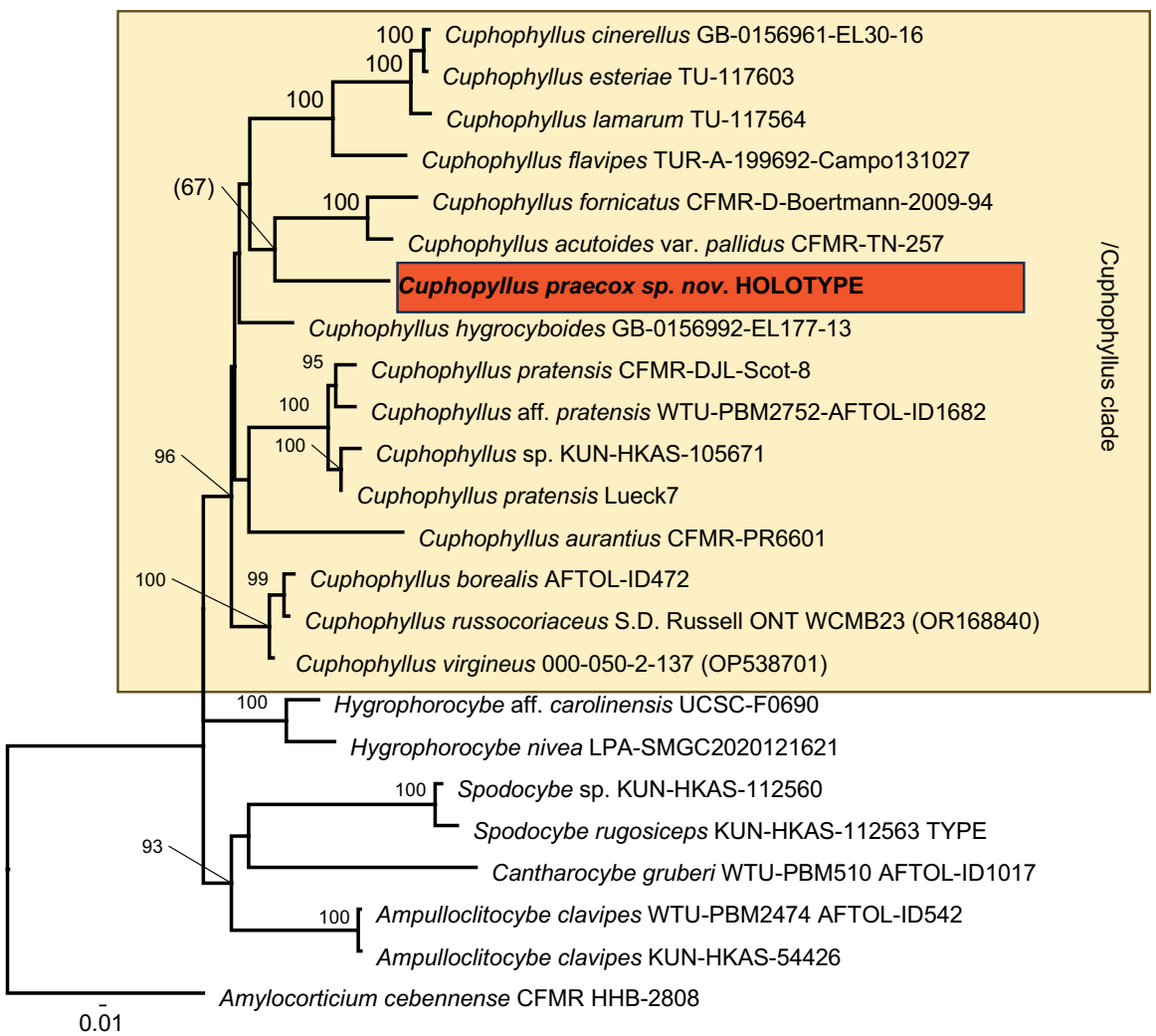
Additional materials examined: **Italy**, Ligura, Loc. Verlia, Sassello (SV), 44°28’18”N, 8°29’36”E, 433 m a.s.l., among the grass, 30 May 2020, *F. Boccardo* (GDOR 4883); *ibid*., 29 May 2021 (GDOR 45110).

Notes: *Cuphophyllus* is a genus, within the *Cuphophyllaceae* (*Hygrophorineae*, *Agaricales*), forming clitocyboid to omphalinoid (rarely mycenoid) basidiomes with thick and usually long decurrent lamellae, white spore print, a subregular to interwoven hymenophoral trama with or without a regular or subregular central strand; hyaline, smooth, non-amyloid basidiospores, very long basidia relative to spore length (usually 7–8, rarely 5–6 times spore length), and clamp connections present at least at the base of the basidia (Bon 1984b, 1990, Boertmann 2010, Lodge *et al.* 2014, Voitk *et al*. 2020a). The typically interwoven hymenophoral trama, together with the long basidium-to-spore ratio are diagnostic characters to distinguish *Cuphophyllus* from the other genera of the suborder *Hygrophorineae*.

Cuphopyllus praecox is circumscribed by a unique combination of features such as a *Camarophyllopsis*/*Hodophilus*-like appearance, a brownish grey viscid pileus, cylindrical to larmiform, often medially constricted spores, and by growing in spring. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hit using the **ITS** sequence had highest similarity to *Cuphophyllus virgineus* [voucher 000-050_2_137, GenBank OP538701; Identities = 369/451 (82 %), 32 gaps (7 %)]. *Cuphophyllus virgineus* is clearly distinct by entirely white basidiomes (pileus pinkish buff in its var. *ochraceopallidus*), non-constricted spores and by growing in autumn (Bon 1984a, 1990, Boertmann 2010). In our phylogenetic analysis *C. praecox* nested in the /Cuphophyllus clade (ML-BS = 95 %), and it is related to the clade that includes *C. acutoides* var. *pallidus* and *C. fornicatus* but with poor statistical support (ML-BS = 67 %). Morphologically, among the grey/brown-capped species of *Cuphophyllus*, all growing in late summer-autumn, *Cuphophyllus lacmus* is distinguished by more robust basidiomes with a medium-sized pileus (25–60 mm diam) which lacks fibrils and is not long radially striated when dry, greyish lamellae, and broadly ellipsoid to subglobose spores (Bon 1984a, 1990, Boertmann 2010). *Cuphophyllus colemannianus* (= *C. subradiatus ss. auct*.) characteristic species of northern Europe, may present a similarly entirely striated pileus, but its surface is typically orange-brown, reddish brown, sometimes with violet hues, the stipe is whitish and concolourous with the lamellae, and the spores are ovoid to broadly ellipsoid, not constricted (Bon 1984a, 1990, Boertmann 2010). *Cuphophyllus radiatus* shares with *C. praecox* a small pileus (15–25 mm diam) translucently striate up to the centre, a grey stipe sometimes with weak violaceous tinges and spores with a large, obtuse hilar appendix (apiculus) but it differs in an often umbonate dry pileus, pale brown, reddish brown, dark brown when moist, and wider, 4.5–6(–6.5) µm, ellipsoid, ovoid or lacrimiform, not constricted spores (Arnolds 1989, Bon 1990). *Cuphophyllus cinerellus*, a small-sized (pileus 5–30 mm diam) arctic/alpine species, shows a pileus surface translucently striate

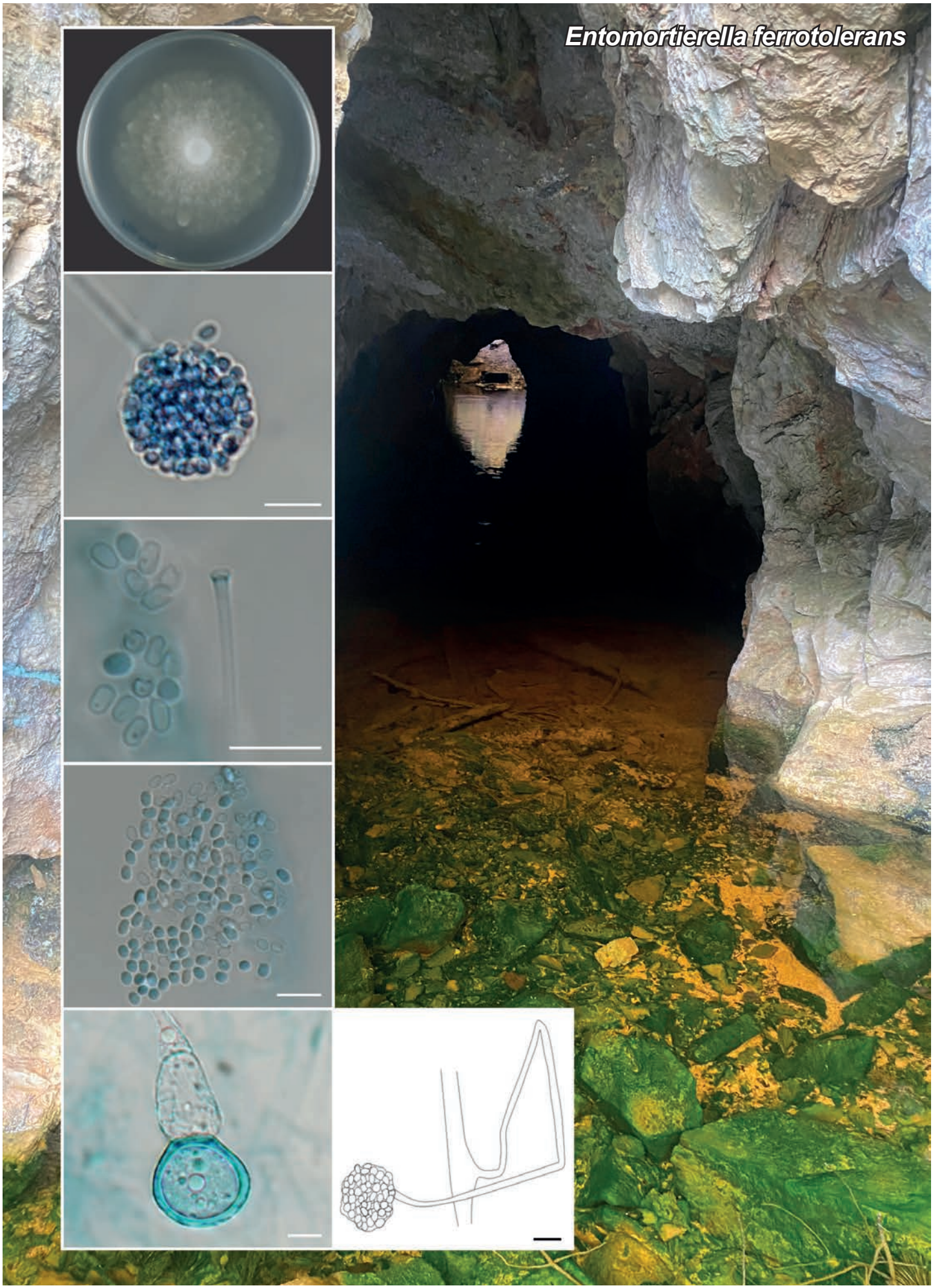
halfway to the centre when young but it is dry, first smooth, then often becoming minutely scaly, especially at the centre, fuscous to grey-brown, pale greyish brown, often with lilac hues, the stipe is white and concolourous with the lamellae, spores are ellipsoid to oblong, not constricted and wider than those of *C. praecox* (4–6 µm) (Kühner 1977, Bon 1984a, 1990, Borgen & Arnolds 2004, Boertmann 2010, Voitk *et al.* 2020a). The recently described *C. esteriae*, an arctic-alpine species so far known from eastern North America, is distinguished by a small pileus (4–32 mm diam.), grey to dark greyish brown with violet tinges, light to dark brownish violet grey lamellae, a light brownish grey stipe but which may be somewhat yellowish at the base, larger broadly elliptical, elliptical and occasionally subglobose or pip-shaped, not constricted spores, (6–)6.5–7.5(–10.5) × (4–)5–6(–6.5), and shorter than 40 µm basidia (*viz*. 22–40 × 6–8 µm) (Voitk *et al.* 2020a).

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



Most likely tree of the Maximum Likelihood analysis of *Cuphophyllaceae* species [some sequences retrieved from the dataset used in Vizzini *et al*. (2024) and other sequences from GenBank] inferred from the ITS/LSU/*rpb1*/*rpb2*/*tef1* regions generated by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016) using 1 000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS) ≥ 70 % are shown above branches. Voucher numbers and GenBank accession numbers are indicated in the table (see supplementary material). The tree was rooted to *Amylocorticium cebennense* (CFMR HHB-2808) and *Cuphopyllus praecox* is highlighted with **bold** font. The alignment and tree were deposited in TreeBASE (study S31214).

F. Dovana, Dipartimento di Bioscienze, Biotecnologie e Ambiente (DBBA), Campus Universitario "Ernesto Quagliariello", Università degli Studi di Bari "Aldo Moro", Via Orabona 4, 70125, Bari, Italy; e-mail: francesco.dovana@uniba.it
F. Boccardo, Via Filippo Bettini 14/11, 16162, Genova, Italy; e-mail: micete@libero.it
A. Vizzini, Department of Life Sciences and Systems Biology, University of Torino, Viale P.A. Mattioli 25, 10125, Turin, Italy; e-mail: alfredo.vizzini@unito.it



Fungal Planet 1628 MycoBank MB 852633

Entomortierella ferrotolerans B. Abramczyk & M. Nowak, ***sp. nov.***

Etymology: Latin for the word "iron tolerant", as all known representatives were isolated from iron-rich soil.

Classification: *Mortierellaceae*, *Mortierellales*, *Mortierellomycetes*.

Hyphae aseptate, hyaline, 5–6 µm wide, sparse rhizoid, forming substrate mycelium cords. *Gemmae* absent. Two types of *sporangiophores* 100–200 µm for unbranched and up to 300 µm branched. *Sporangiophores* are 3–5 µm wide at base and tapering down to 1–3 µm. *Sporangia* multispored, spherical, approximately 19 ± 3 µm, after spore liberation with pronounced collarette, columella absent. *Sporangiospores* smooth-walled, hyaline, 2.5–4 µm × 1.6–2.7 µm, variable in shape: oval and ellipsoidal but also globose, subglobose and broadly ellipsoidal. *Zygospores* smooth-walled, 28 µm diam. No *chlamydospores* observed.

Culture characteristics: Colonies on potato dextrose agar (PDA), after 7 d at 18 °C in the dark: irregular flat undulated, reaching up to 53 mm diam, white. On malt extract agar (MEA) colonies circular, raised with slightly undulated edges; on Sabouraud dextrose agar (SDA) circular raised entirely; on water agar (WA) colonies circular flat with slightly undulated edges, whitish. Garlic-like odour detected on all media.

Habitat and distribution: Mines and postmining sites in Poland, Germany, USA, with high Fe concentration.

Typus: **Poland**, Rudawy Janowickie, Wieściszowice, 50°8280'N, 15°9740'E, bank of Żółte Jeziorko (Yellow Lake), soil, 25 Sep. 2018, *B. Abramczyk* (**holotype** WA135233, culture ex-type CBS 151316; ITS and LSU sequences GenBank OQ344505 and PP430714).

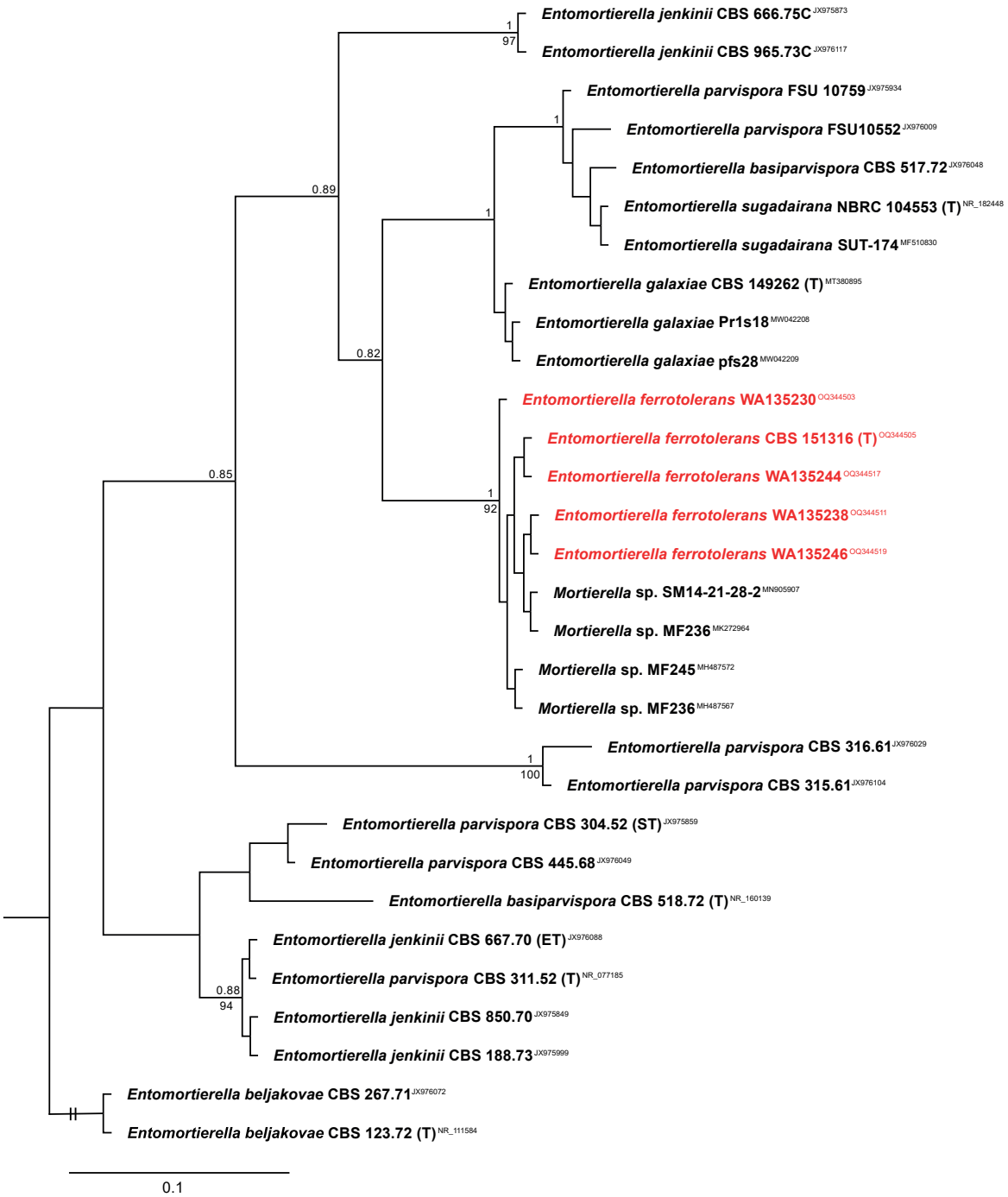
Additional materials examined: **Poland**, Rudawy Janowickie, Wieściszowice, 50°8280'N, 15°9740'E, bank of Żółte Jeziorko, soil, 25 Sep. 2018, *B. Abramczyk* (WA135238; ITS and LSU sequences GenBank OQ344511 and PP430715); *ibid*., (WA135244; ITS and LSU sequences GenBank OQ344517 and PP430716); Rudawy Janowickie, Wieściszowice, 50°8232'N, 15°9718'E, bank of Niebieskie Jeziorko, soil, Sep. 2018, *B. Abramczyk* (WA135230; ITS and LSU sequence GenBank OQ344503 and PP430718).

Notes: Phylogenetic analysis of ITS sequences of WA135233 and all other strains used in this study reveals a well-supported clade corresponding to a distinct new species within the *Entomortierella parvispora* complex (*sensu* Telagathoti *et al*. 2022). *Entomortierella ferrotolerans* seems to be closely related to *E. galaxiae* and *E. sugadairana*. However, the bootstrap support and Bayesian posterior probability for this clade is low. Moreover, the spores of *E. ferrotolerans* are smaller and more elongated than those of *E. sugadairana.* Additionally, sporangiophores of *E. ferrotolerans* are shorter and lack rhizoids. The species differs from *E. galaxiae* by complete reduction of columellae and bigger size of spores.

Based on morphological observations and key to *Entomortierella parvispora* complex provided by Telagathoti *et al*. (2022), the closest species to *E. ferrotolerans* is *E. basiparvispora*. However, *E. ferrotolerans* exhibits dense sporulation on MEA medium compared to moderate by *E. basiparvispora*. Sporangiophores are shorter and thinner in *E. ferrotolerans* than in *E. basiparvispora*, and are not always branched, and when branched not necessarily basitonously. Sporangiophores are also arising from aerial mycelium compared to arising from substratum in *E. basiparvispora*. Sporangiospores in both species are hyaline but in *E. basiparvispora* are globose and subglobose when in *E. ferrotolerans* vary in shape and are generally smaller. Sporangia are smaller in *E. ferrotolerans*. Both lack chlamydospores.

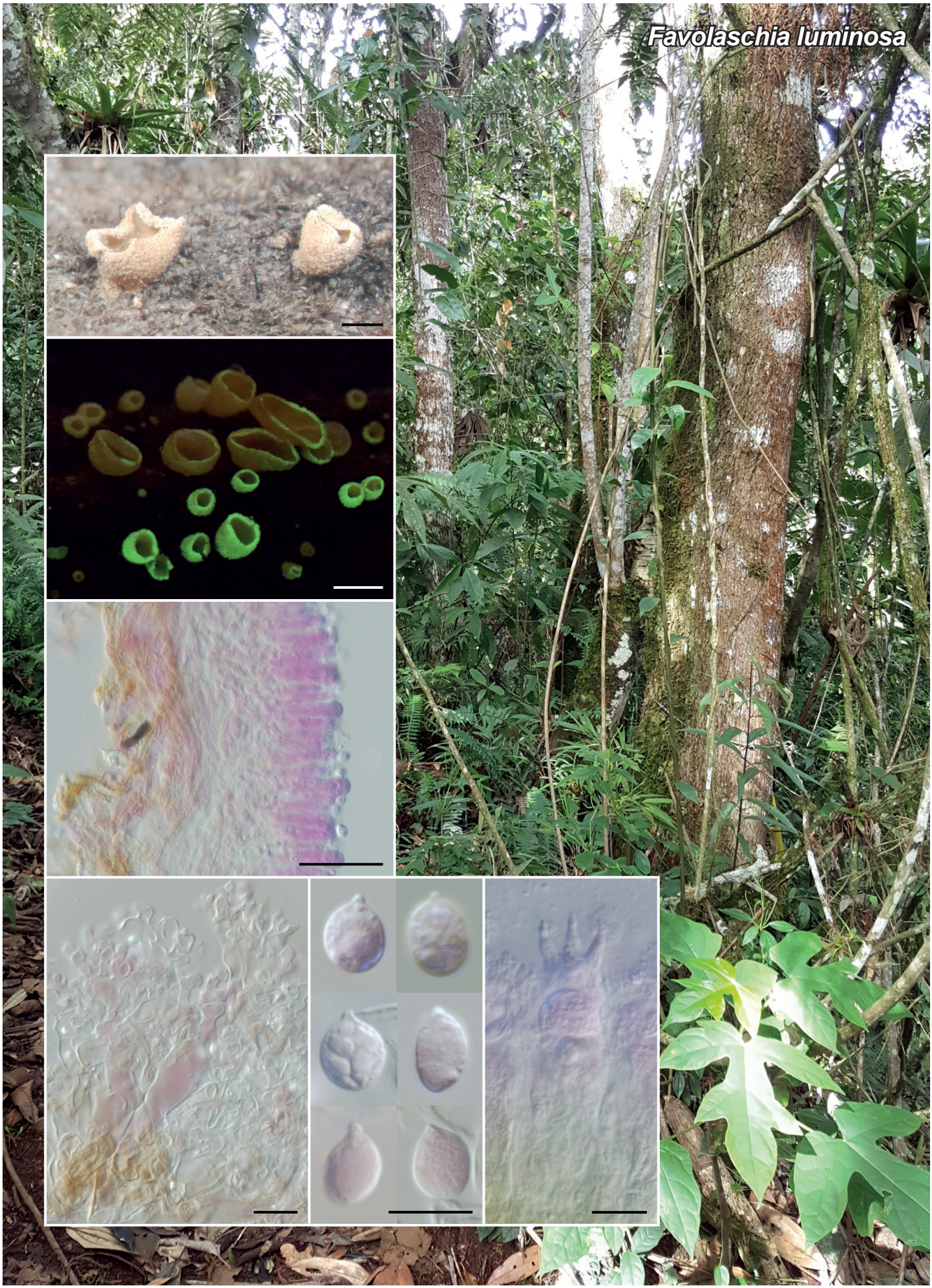
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to unknown isolates of *Mortierella* (strain SM14-21-28-2, GenBank MN905907; Identities = 100 %; strain MF238, GenBank MH487568.1; Identities = 99.82 %; strain MF233, GenBank H487566.1; Identities = 99.82 %). All these sequences represent *Mortierellaceae* isolates from soil containing a high iron concentration (Burow *et al.* 2019, Held *et al*. 2020).

Colour illustrations: Żółte Jeziorko (Yellow Lake) in Wieściszowice, Poland. Seven-day-old colony sporulating on PDA; sporangium; sporangiophore tip with collarette; spores; zygospore; drawing of sporangiophore. Scale bars = 10 µm.



Bayesian inference tree of *Entomortierella parvispora* complex based on ITS rDNA sequences showing the placement of *Entomortierella ferrotolerans sp. nov*. (in red) as a separate clade within the complex. Bootstrap support data (> 60 %) for each clade is shown below the branches. Bayesian posterior probability (> 0.8) for each clade is shown above the branches. Scale bar = 0.1 substitution/site. Alignment length: 583 bp (github.com/rainbowmycelium/alignments). Sequences were aligned using the MAFFT algorithm (Katoh & Standley 2013) and trimmed with trimAl using the automated1 algorithm (Capella-Gutierrez 2009). RAxML-NG (Kozlov *et al.* 2019) was used for maximum likelihood tree calculation and MrBayes v. 3.2.6 (Ronquist *et al.* 2012) for Bayesian inference. Nucleotide substitution models used for Maximum Likelihood: TPM3uf+I+G4, for Bayesian inference: GTR+I+G4.

M. Nowak, B. Abramczyk & D. Wiktorowicz, Biology of Microorganisms Students' Society, Faculty of Biology, University of Warsaw, Miecznikowa 1, 02-096 Warsaw, Poland; e-mail: me.nowak6@student.uw.edu.pl, b.abramczyk2@student.uw.edu.pl & d.wiktorowicz@student.uw.edu.pl
J. Pawłowska, Biology of Microorganisms Students' Society, Faculty of Biology, University of Warsaw, Miecznikowa 1, 02-096 Warsaw, Poland, and Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, ul. Żwirki i Wigury 101, 02-086 Warsaw, Poland; e-mail: julia.z.pawlowska@uw.edu.pl



Fungal Planet 1629 MycoBank MB 852894

Favolaschia luminosa Flakus, Gallegos & Rodr. Flakus, *sp. nov.*

Etymology: The epithet refers to the bioluminescent capacity of the new species.

Classification: *Mycenaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata cupulate, (0.5–)1.1–1.5(–2.0) × (0.3–)1.0–1.6 (–2.0) mm (measured when dry), astipitate to shortly stipitate, attached centrally to slightly eccentrically, pale beige to pale yellowish brown (fresh) with slight orangish tinge (when dry), external surface dull, pruinose to rough, usually frosted at the edge and on the upper external surface; margin rounded to irregular, slightly involute. *Hymenophore* smooth, pale beige. *Basidiospores* (7–)9–10(–12) × (5–)6–8(–10) µm (n = 30), broadly ellipsoid, smooth, thin-walled, multi-guttulate or with a single large droplet, faintly amyloid. *Basidia* 35–43× 6–12 µm, clavate to broadly clavate, 4-spored. *Basidioles* subcylindric to clavate. *Hymenial* and *cortical gloeocystidia* and *acanthocystidia* not observed. *Subhymenium* of short-celled hyphae. *Pileopellis* of long-celled, thin-walled, branched, interwoven, irregularly inflated, clamped, 4–15 µm wide hyphae, sometimes irregularly constricted at the septum, cells smooth to strongly encrusted or ornamented, hyaline or with encrusting golden-yellow pigment (K+ reddish orange), sometimes with waved walls; inner cortical layer cutis with few gleoporouse hyphae; terminal cells erect to suberect, branched and diverticulate at the end. *Pileocystidia* observed on the edge and the upper external surface of the basidiomata, hyaline, thin-walled, frequently branched and strongly diverticulate. *Trama* of rather long-celled, thin-walled, non-incrusted, non-gelatinous, clamped, interwoven hyphae, 3–5 µm wide.

Habit, habitat and distribution: *Favolaschia luminosa* is known from three localities where its populations are growing on twigs of *Byttneria hirsuta* (*Malvaceae*) in the tropical Yungas montane forest developed on the north-eastern slopes of the Andes, in secondary vegetation between 1 925 and 2 200 m a.s.l. in Bolivia.

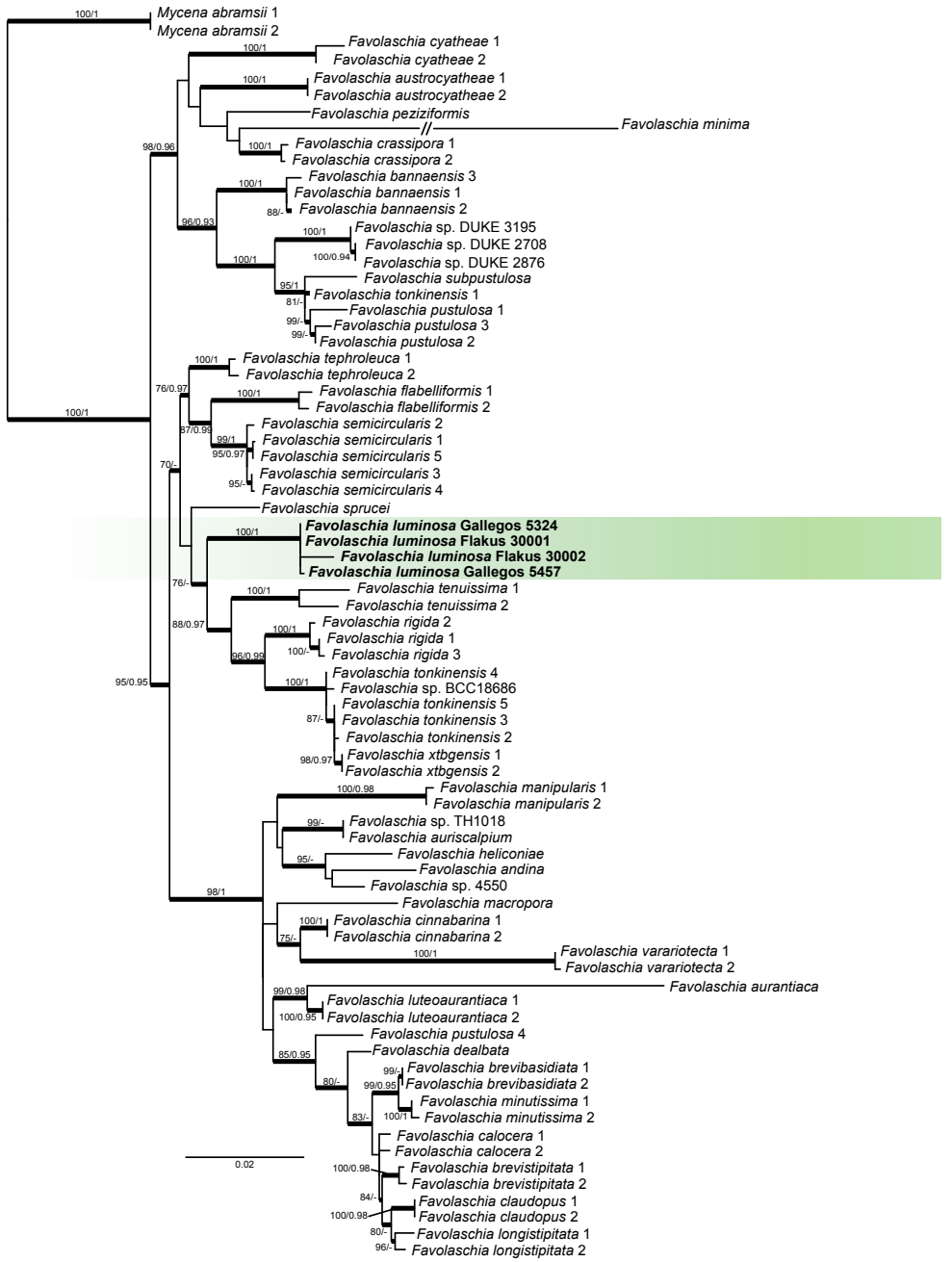
Typus: **Bolivia**, La Paz department, Sud Yungas province, near Pataloa village, 16°24’09.77”S, 67°34’14.84”W, 2 200 m a.s.l., Yungas montane forest, on twigs of *Byttneria hirsuta* (*Malvaceae*), 29 Apr. 2021, leg. *S. Gallegos*, 5324 (**holotype** KRAM F-59991, **isotype** LPB; ITS and LSU sequences GenBank PP488378 and PP488382).

Colour illustrations: The tropical Yungas montane forest, Sud Yungas province, Bolivia (photo credit A. Flakus). A habit of dry basidiomata; fresh basidiomata producing faint greenish bioluminescence on a natural substratum (photo credit M. Espejo); cross-section of the basidioma edge; diverticulate pileocystidia; basidiospores; basidium [all from holotype; stained with Phloxin (1 % in water) after pre-treatment with KOH (5 %)]. Scale bars: habit = 500 µm; bioluminescence = 1 000 µm; cross-section = 50 µm; all others = 10 µm.

Additional materials examined: **Bolivia**, La Paz department, Sud Yungas province, near Condormayu village, 16°24’21.96”S, 67°33’29.6”W, 1 925 m a.s.l., Yungas montane secondary forest, on twigs of *B. hirsuta*, 3 Aug. 2021, *S. Gallegos*, 5457 (KRAM-F 59992, LPB; ITS and LSU sequences GenBank PP488379 and PP488383); Pataloa, near Santiago de Chirca Biological Station, 16°24’03.15”S, 67°34’22.21”W, 2 179 m, Yungas montane forest, on twigs of *B. hirsuta*, 12 Jan. 2020, *A. Flakus,* 30002*, S. Gallegos & P. Rodriguez-Flakus* (KRAM-F 59993, LPB; ITS and LSU sequences GenBank PP488377 and PP488381); *ibid*., *A. Flakus,* 30001*, S. Gallegos & P. Rodriguez-Flakus* (KRAM-F 59994, LPB; ITS and LSU sequences GenBank PP488376 and PP488380).

Notes: The genus *Favolaschia* is saprobic and distributed worldwide, with especially high diversity reported from the Neotropics (Singer 1974, Gillen *et al*. 2012). Although *Favolaschia* is characterised by mushroom-like poroid basidiocarps, several species have a tendency to reduce the number of pores in hymenophores. One of the best examples of species with a reduced hymenophore, consisting of 2–6 pores only, is *Favolachia macropora* described from the decaying stem of a bamboo in Panama (Gillen *et al*. 2012). The newly introduced *F. luminosa* is the first cyphelloid member of the genus which has basidiomata reduced to a single pore. It grows on twigs of *Byttneria hirsuta* in the Bolivian montane forest and is characterised by small, cupulate basidomata of pale beige to pale yellowish (with slight orangish tinge when dry) colour, broadly ellipsoid basidiospores, lack of hymenial and cortical gloeocystidia and acanthocystidia, and presence of diverticulate pileocystidia. *Favolaschia luminosa* is known to produce faint greenish bioluminescence on the edge and outside portion of basidiomata. There are three additional bioluminescent species in this genus (*F. manipularis*, *F. peziziformis*, *F. xtbgensis*) which strongly differ in morphology (Corner 1954, Bodensteiner *et al.* 2004, Audrey *et al*. 2015, Nimalrathna *et al*. 2022). Our Maximum Likelihood inference based on multiple loci supports the phylogenetic placement of *Favolaschia luminosa* within the genus *Favolaschia*, despite its unusual morphology. It forms a clade together with *F. flabelliformis*, *F. rigida*, *F. semicircularis*, *F. tenuissima*, *F. tephroleuca*, *F. tonkinensis* and *F. xtbgensis*, described from China, and *F. sprucei* known from South America (Gillen *et al*. 2012, Nimalrathna *et al*. 2022, Zang *et al*. 2023). Although the generic placement of the new species is strongly supported in our analyses its phylogenetic relationships within the genus *Favolaschia* need further studies including more loci and several still not sequenced species. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Favolaschia* sp. QZ-2023a (voucher Dai 26131, GenBank OR855972; Identities = 95.63 %, no gaps). The closest hit using the **LSU** sequence is *Favolaschia* sp. QZ-2023a (voucher Dai 26115, GenBank OR575906; Identities = 99 %, no gaps).

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



Maximum Likelihood (ML) phylogenetic placement of *Favolaschia luminosa* within *Favolaschia* generated of a concatenated ITS, LSU, SSU, mtSSU and *TEF* dataset. *Mycena abramsii* sequences were used as the outgroup. The novelty described here is highlighted in green with a **bold** font, and bootstrap support values ≥ 70 % and/or Bayesian posterior probabilities ≥ 0.95 are represented by thickened branches. The ML analyses were carried out in each single-locus alignment using IQ-TREE v. 2.1.2 (Nguyen *et al.* 2015, Chernomor *et al.* 2016) to detect potential conflicts. We performed 1 000 ultrafast bootstrap replicates to estimate branch support amongst the five loci which later were concatenated to a single alignment. Alignment has 76 sequences with 3 641 characters, 655 distinct patterns, 361 parsimony-informative, 150 singleton sites, 3 130 constant sites. We performed 1 000 replicates under the best-fitting substitution model determined by the ModelFinder Plus as implemented in IQ-TREE (Kalyaanamoorthy *et al.* 2017). The selected models for each partition of the analysis were as follows: TPM2u+F+G4 for ITS1, K2P for 5.8S, TNe+I+G4 for ITS2 and the three codon positions of *TEF*, TPM2u+F+I+G4 for LSU, K2P+I for SSU, and TPM3u+F+I for mtSSU. The best-fit model according to BIC in our partitioned per each locus dataset (gene partitioned -s + -m TEST + -m TESTMERGE + -bb). Bayesian Inference (BI) of the phylogenetic relationships was calculated using the Markov Chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012), using the partitions and substitution models obtained. Two independent parallel runs were started each with four incrementally heated (0.15) chains. This MCMC was allowed to run for 40 million generations, sampling every 1 000th tree and discarding the first 50 % of the sampled tree as a burn-in factor. The NCBI accession numbers of each sequence used in these analyses are provided in a supplementary file and the concatenated matrix was deposited at figshare.com (doi: 10.6084/m9.figshare.25419265).

A. Flakus & P. Rodriguez-Flakus, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland; e-mail: a.flakus@botany.pl & p.rodriguez@botany.pl

S.C. Gallegos, Herbario Nacional de Bolivia (LPB), Instituto de Ecología, Universidad Mayor de San Andrés, Campus Universitario Cota-Cota, calle 27, La Paz, Bolivia; Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Grosse Steinstrasse 79/80, D-06108 Halle, Germany; e-mail: silvia.gallegos.a@gmail.com

Fungal Planet 1630 MycoBank MB 852461

Fulvifomes subramanianii S. Gunaseelan, & M. Kaliyaperumal, *sp. nov.*

Etymology: Named after the Indian mycologist C.V. Subramanian for pioneering Hymenochaetoid taxonomic studies in India.

Classification: *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiomata perennial, solitary, applanate, broadly attached to substrate, hard, woody when dry. *Pilei* applanate, projecting up to 18 cm in length, 13 cm in width and 8 cm near the attachment. *Pileal surface* zonate, radially cracked, with brownish grey scales (6E3; Kornerup & Wanscher 1978), deeply sulcate, weakly rimose, brown (6E5) to dark brown (6F5). *Margin* brown (6E8), obtuse, finely velutinate. *Pore surface* brown (6E6) to dark brown (6F5), pores round, 5–7 per mm. *Context* brown (6D7), homogeneous up to 0.8 cm. *Tube layer* light brown (6D6), stratified up to 3 cm, each stratum up to 0.4 cm long. Hyphal system: mono-dimitic; tissue darkening but otherwise unchanged in KOH. *Context* generative hyphae hyaline to yellowish brown, thin to thick-walled with a narrow to wide lumen, occasionally branched and septate, 2.6–4.8 µm wide; skeletal hyphae rare, light brown, thick-walled with narrow lumen, unbranched, 2.3–4.6 µm wide. *Trama* generative hyphae hyaline to golden brown, thin to thick-walled, rarely branched and septate, 2.3–4.6 µm in diam; skeletal hyphae golden yellow, thick-walled with a narrow lumen, unbranched, aseptate, 2–4.3 µm wide. *Cystidioles* and *Setae* absent. *Basidioles* clavate, 5–17 × 3–5.5 µm; *Basidia* clavate to broadly clavate, 5–16 × 3.8–6 µm. *Basidiospores* smooth, thick-walled, globose to subglobose, pale yellow to golden yellow in water, turning golden brown to brown in KOH, acyanophilous, inamyloid, non-dextrinoid, (4.8–)5.1–6.7(–6.9) × (4.6–)4.8–6.2(–6.5) µm, L = 5.8 µm, W = 5.65 µm, Q = 1.07 (Q range 1–1.1) (n = 50/2).

Typus: **India**, Tamil Nadu, Thiruvannamalai district, 12°17'84.10"N, 78°85'02.34"E, on living *Albizzia amara* (*Fabaceae*), 3 Feb. 2018, *K. Malarvizhi*, SKM-PRF20 (**holotype** MUBL 4019; ITS and LSU sequences GenBank OM912446 and OM909045).

Additional material examined: **India**, Tamil Nadu, Thiruvannamalai district, 12°17'86.98"N, 78°85'03.14"E, on living *A. amara*, 3 Feb. 2018, *G. Sugantha* (**paratype** SKM-PRF15; ITS and LSU sequences GenBank OM912447 and OM909042).

Notes: The Maximum Likelihood (ML) and Bayesian Inference (BI) analyses revealed that *F. subramanianii* formed a distinct lineage (100 % ML, 1.0 BI) from other Asian *Fulvifomes* spp. (*viz. F. aurantiacus*, *F. jawadhuvensis*, *F. karaiensis*, *F. malaiyanurensis*, *F. maritimus*, *F. natarajanii*, *F. pannensis* and *F. thiruvannamalaiensis*).

Colour illustrations: Holotype collection area, India. Habitat; pilear surface; transverse section of basidiomata (arrows indicating stratified tube layer); microscope illustrations and *camera lucida* drawing of holotype: tramal hyphae, contextual hyphae; basidioles; basidia and basidiospores: basidiospore in water; basidiospore in cotton blue; basidiospore in KOH; basidiospore in Melzer's reagent. Scale bars: macromorphology = 5 cm; micromorphology = 5 µm.

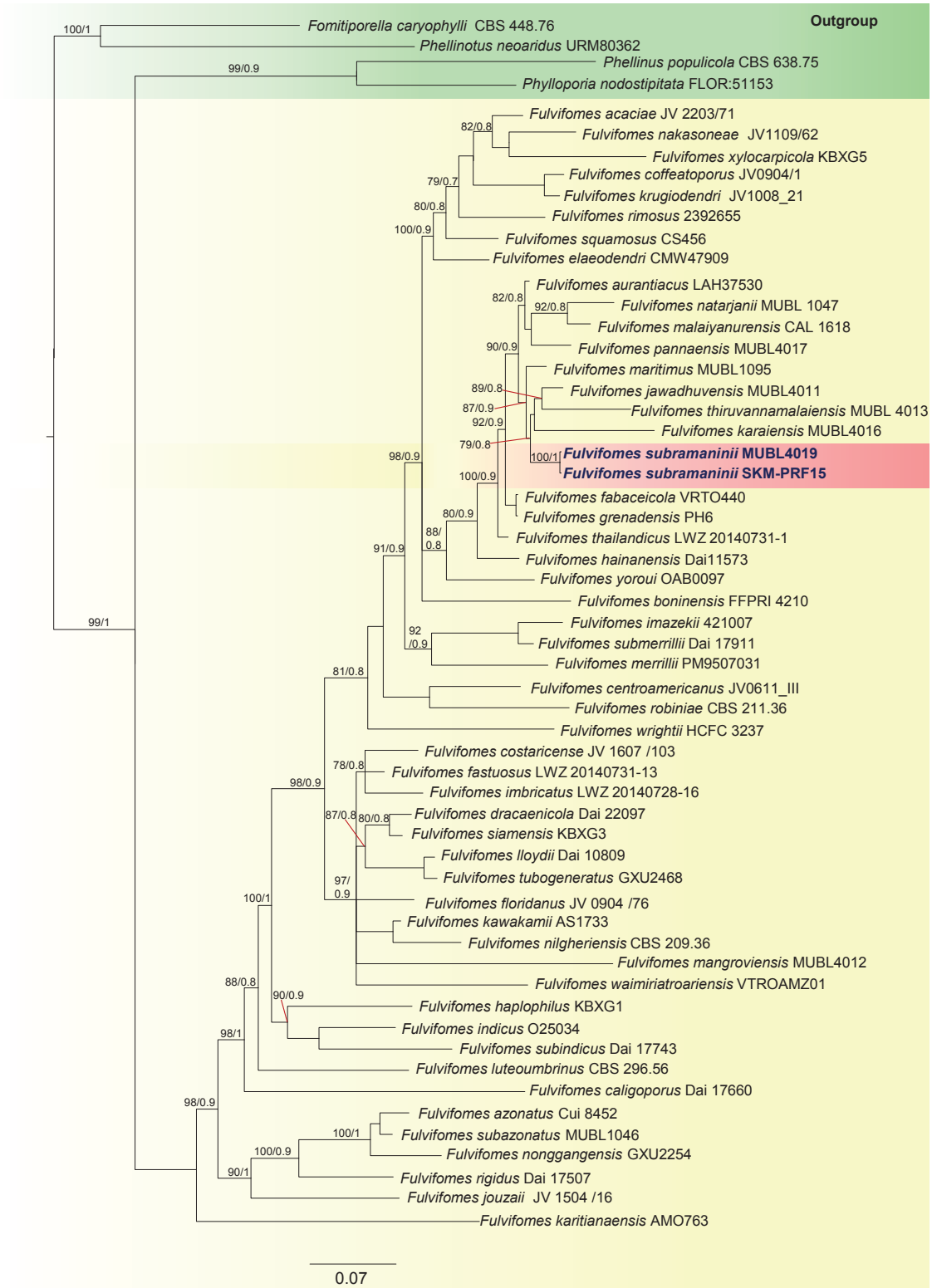
Fulvifomes subramanianii formed a well-resolved sister clade to *F. jawadhuvensis, F. karaiensis*, *F. maritimus* and *F. thiruvannamalaiensis* (87 % ML, 0.9 BI). *Fulvifomes subramanianii* differs from *F. karaiensis*, by having a zonate, radially cracked, sulcate pilear surface with smaller pores (5–7 / mm), absence of cystidioles and smaller basidiospores (4.8–6.9 × 4.6–6.5 µm). In *F. karaiensis* the basidiome has a weakly zonate pileal surface, with a few cracks appearing on maturity, larger pores (4–5 / mm), the presence of fusoid cystidoles and smaller basidiospores (5.2–6.2 × 4.7–5.7 µm) (Senanayake *et al*. 2023). *Fulvifomes subramanianii* and *F. thiruvannamalaiensis* resemble each other in a cracked basidiome, obtuse margin, and stratified tubes. However, the former differs in the absence of cystidioles and basidiospore size (54.8–6.9 × 4.6–6.5 µm) (Jayawardena *et al*. 2022). Likewise, *F. subramanianii* and other species from our previous reports, namely, *F. jawadhuvensis F. malaiyanurensis*, *F. maritimus, F. natarajanii* and *F. pannaensis* are similar in zonate basidiomes with an obtuse margin without cystidioles, but *F. subramanianii* significantly differs in the morpho-microtaxonomic characters (Jayawardena *et al*. 2022, Crous *et al.* 2023a, Senanayake *et al.* 2023).

Fulvifomes subramanianii differs from *F. aurantiacus* described from Pakistan by having brownish grey scales in its pilear surface with larger basidiospores (4.8–6.9 × 4.6–6.5 µm), whereas the latter has pileate to substipitate basidiocarps, zonate orange brown to yellow ocher pileal surface with a dull surface and smaller basidiospore size (4.9–6.7 × 3.75—5.8 µm) (Fatima *et al.* 2023).

Fulvifomes subramanianii significantly differs from other Asian and Neo-tropical collections and forms a distinct lineage in phylogenetic analyses.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phellinus* sp. [strain YD-2015 isolate KP27, GenBank KP658587; Identities = 615/626 (98 %) two gaps (0 %)], *Phellinus* sp. [strain YD-2015 isolate KP44, GenBank KP658601; Identities = 614/626 (98 %), two gaps (0 %)], and *Fulvifomes grenadensis* [strain JRF74, GenBank MH048097; Identities = 613/626 (98 %), three gaps (0 %)]. Closest hits using the **LSU** sequence are *Fulvifomes thailandicus* [strain IFP LWZ 20140731-1, GenBank NG_068761; Identities = 875/881 (99 %), no gaps], *Phellinus robiniae* [strain CBS 211.36, GenBank AY059038; Identities = 875/882 (99 %), one gap 1/882 (0 %)], and *Fulvifomes jawadhuvensis* [strain SKM-JMR5, GenBank MW048886; Identities = 868/873 (99 %), no gaps].

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



Phylogenetic tree inferred from ITS+LSU sequences of *Fulvifomes subramanianii* (MUBL4019 and SKM-PRF 15) and related species rooted with *Fomitiporella caryophylli* (CBS 448.76) and *Phellinotus neoaridus* (URM80362). The maximum likelihood analysis was performed using MEGA v. X (Kumar *et al*. 2018) and the same data were used for Bayesian analysis using MrBayes v. 3.2.7 (Ronquist *et al.* 2012). Branches are labelled with maximum likelihood bootstrap support (ML) and Bayesian posterior probabilities values (BPP). Novel species is in **bold**. The alignment and tree are available from TreeBASE (study ID: 31187).

S. Gunaseelan, M. Kaliyaperumal & K. Kezo, Centre for Advanced Studies in Botany, University of Madras, Chennai, Tamil Nadu, India-600 025;
e-mail: suganthagunseelan@gmail.com, malar.kaliyaperumal@gmail.com & z.kezh.kezo@gmail.com
J.D. Bhat, Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 2455, Riyadh-11451, Saudi Arabia;
e-mail: bhatdj@gmail.com

Fungal Planet 1631 MycoBank MB 853201

Geastrum federeri A. Paz & C. Lavoise, *sp. nov*.

Etymology: The epithet *federeri* is dedicated to the great Swiss tennis player Roger Federer, the best on the grass court in the history of tennis, for his achievements in this sport, as a sign of admiration for his career and his person.

Classification: *Geastraceae*, *Geastrales*, *Phallomycetidae*, *Agaricomycetes*, *Agaricomycotina.*

Basidiomata hypogeous, indehiscent, 0.8–2.6 × 0.6–2.3 cm diam, subglobose, slightly depressed at the top, with mycelial base, and without pedicel, apophysis and peristome. *Peridium* thick, 2.5–3.2 mm, non-hygrometric, 3-layered, with exoperidium, mesoperidium and endoperidium. *Exoperidium* not fissuring at maturity into a characteristic star-like structure, fibrous, leathery, often detached from mesoperidium, yellowish to light brown in cross section, turning red in Lugol's solution, 95–122 µm thick, two-layered, the outer stratum with incrustations, detaching in patches, composed of 3.1–7.4 µm wide skeletal hyphae and rhizomorphs with bipyramidal crystals inside, stratum formed by thick-walled 0.4–0.9 µm wide. *Mesoperidium* thick, 275–305 µm, pale yellowish cream in colour, with purplish-purple reflections, compact, persistent, not reacting with Lugol's solution, with plectenchymatous structure, intricate, formed by elongated hyphae with very sinuous septa, measuring on average of 4.2 × 9.5 µm¸ with thin walls, which widen slightly towards the gleba. *Endoperidium* very thin (maximum two rows of cells), absent in some areas, formed by subglobose cells, interspersed with other more elongated elements. *Gleba* initially white, compact, changing to dark brown, powdery mass, with a robust, club-shaped columella, with a rounded apex, which penetrates a third of the height of the gleba. *Capillitium* formed by abundant straight hyphae with 0.65 µm thick walls, without crystals. *Basidia* narrowly ellipsoid to subcylindrical or more or less lageniform, 19–26 × 4.5–7.1 µm, with 5–8 short sterigmata. *Basidiospores* globose, 4.1–4.8 µm diam, greenish yellow when young, brownish at maturity, with reticulate ornamentation, formed by intense greenish yellowish ridges, reaching a height up to 5 µm, joining at the bases to form a network with alveoli very irregular in shape and size.

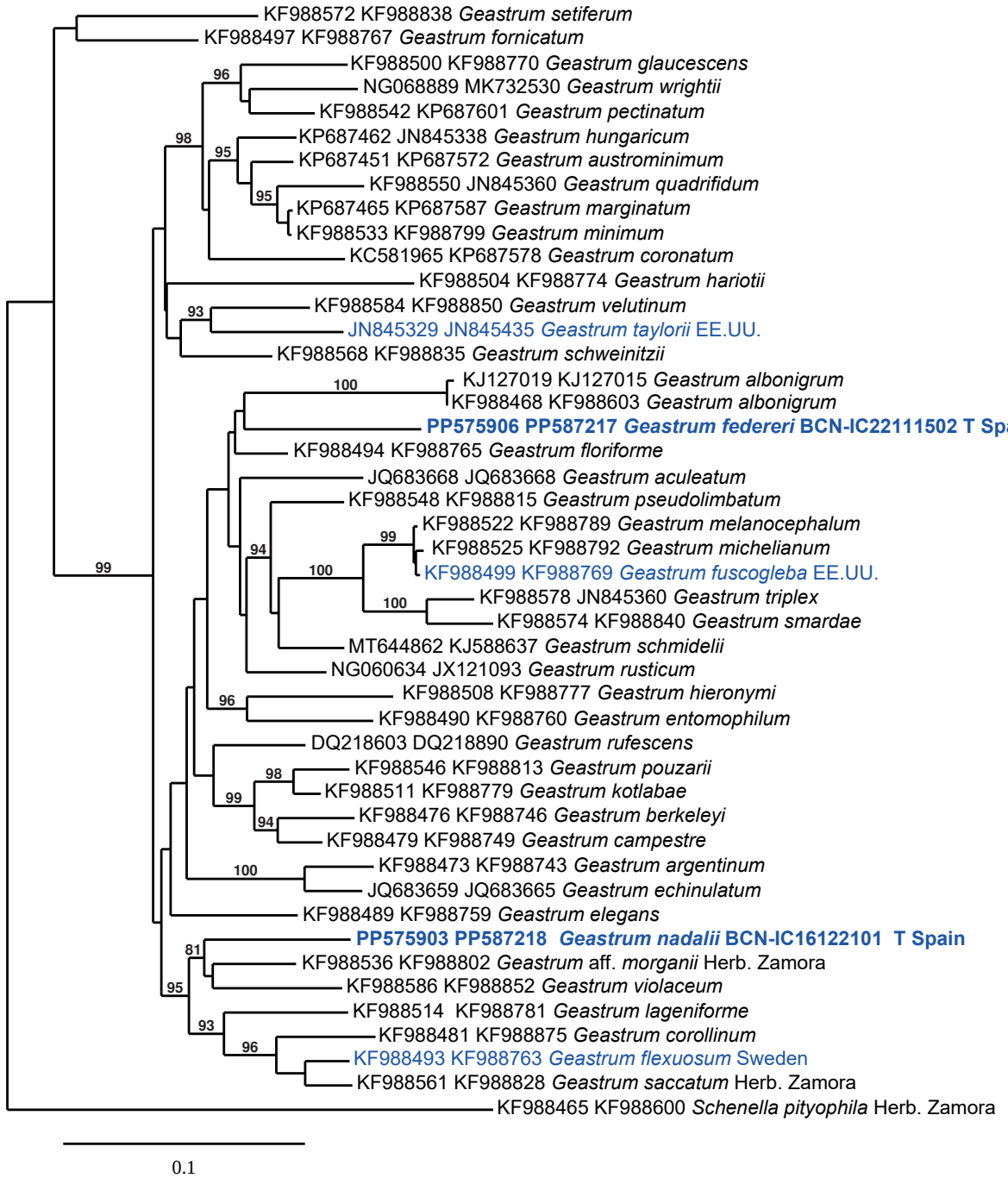
Habitat and distribution: Solitary to gregarious among plant remains, under *Quercus* with little presence of *Pinus,* near a stream, on siliceous soil, occurring in autumn. Species so far only known from the type locality in Spain.

Typus: **Spain**, Andalucia, Cádiz, Los Barrios, Valdeinfierno, 36°13'45.76"N, 9°35'40.93"W, 174 m a.s.l., under *Quercus suber* and *Q. canariensis*, with little presence of *Pinus* sp., siliceous soil, 22 Nov. 2015, *A. Paz & C. Lavoise* (**holotype** BCN-IC22111502, **isotype** IC22111502; ITS, LSU, *ATP6*, *TEF1* and *RPB1* sequences GenBank PP575904; PP575906; PP587217).

Additional material studied: **Spain**, Andalucia, Cádiz, Los Barrios, Valdeinfierno, 36°13'45.76"N, 9°35'40.93"W, 174 m a.s.l., under *Quercus suber* and *Quercus canariensis*, on siliceous soil, 17 Sep. 2018, *A. Paz & C. Lavoise* (**paratype** IC17091801, GenBank PP575905).

Notes: Phylogenetic studies reveal that *G. federeri* has the epigeous *G. albonigrum* as a sister species, the latter belonging to *Geastrum* sect. *Exaerolata* De Toni (1887), but we will need to study more collections to be able to confirm if *G. federeri* also belongs to this section. It differs from *G. nadalii* (*Geastrum* sect. *Corollina*) to which the similarly indehiscent species *G. flexuosum* also belongs, but the latter has also been placed in subsect. *Marginata* (Zamora *et al.* 2014). Morphologically, *G. federeri* differs from *G. albonigrum* by the indehiscent exoperidium and the lack of peristome, which in *G. albonigrum* is divided into lacinias, in a radial arrangement, which gives them a star-like shape, and has a peristome. Morphologically *G. federeri* differs from other indehiscent species of the genus *Geastrum* by the mesoperidium with purple reflections, formed by elongated hyphae with very sinuous septa, creating a plectenchymatous, intricate structure, and reticulate basidiospores, while in *G. flexuosum*, *G. fuscogleba*, *G. taylorii* and *G. bushnellii* the mesoperidium is dirty white, without purple reflections, formed by globose or isodiametric cells, creating a pseudoparenchymatous structure, the spores are globose and are ornamented with isolated warts, although in *G. flexuosum* they can unite to form crests and in *G. bushnellii* the ornamentation is furrowed near the apicule.

Colour illustrations: Spain, Andalucia, Cadiz, Los Barrios, Valdeinfierno, where the type specimen was collected. Mature basidiomata; organization of peridium hyphae (exoperidium, mesoperidium and endoperidium); basidiospores under light microscope. All images are of the holotype. Scale bars: peridium = 100 µm; basidiospores = 5 µm.



Combined *Geastrum* phylogeny based on LSU and *ATP6*. The alignments were done with ClustalW checked in BioEdit Sequence Alignment Editor 7.2.5 (12/11/2013) and then ran at "Méthodes et Algorithmes pour la Bio informatique LIRMM", phylogeny.fr. One click mode. Phylogenetic tree obtained from the maximum likelihood analysis. Numbers above branches are maximum likelihood bootstrap (MLbs), bootstrap support values (≥ 50 %) are given above the branches. Adobe Acrobat Pro software was used to edit the final tree. Indehiscent species are indicated in blue text and new species are indicated in **bold** text, T = type strain. *Schenella pityophila* was included as an outgroup.

A. Paz, Aptdo. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain; e-mail: ita-paz@hotmail.com
C. Lavoise, Aptdo. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain; e-mail: c.lavoise@free.fr

Fungal Planet 1632 MycoBank MB 853204

Geastrum nadalii A. Paz, C. Lavoise, P. Chautrand, M. Slavova, P.P. Daniëls & C. Rojo, *sp. nov.*

Etymology: The epithet *nadalii* is dedicated to the great Spanish tennis player Rafael Nadal, the best on clay court in the history of tennis, for his achievement and sign of admiration for his career and his person.

Classification: *Geastraceae*, *Geastrales*, *Phallomycetidae*, *Agaricomycetes*, *Agaricomycotina.*

Basidiomata hypogeous, indehiscent, 1.3–3.2 × 0.9–2.8 cm in diam, subglobose, slightly depressed at the top, with mycelial base and without pedicel, apophysis and peristome. Peridium 4.5–6.2 mm thick, non-hygrometric, 3-layered, with exoperidium, mesoperidium and endoperidium. *Exoperidium* not fissuring at maturity into a characteristic star-like structure, not in ray with fissures, thin, fibrous, and leathery, adherent to mesoperidium, yellowish in cross section, turning red in Lugol's solution, 92.5–115.5 µm thick, two-layered; the outer stratum with incrustations, detaching in patches, composed of 3.1–7.4 µm wide skeletal hyphae and rhizomorphs with bipyramidal crystals inside, stratum formed by thick-walled, 0.5–2.0 µm wide, generative hyphae. *Mesoperidium* very thick, 1 265.1–1 347.2 µm wide, whitish to cream, compact, persistent, not reacting with Lugol's solution, with pseudoparenchymatous structure, formed by thin-walled, subglobose to slightly elongated elements, measuring on average 7.4 × 10.8 µm, Q = 0.69, widening closer to the gleba. *Endoperidium* 28.4–52.9 µm thick, reddish-brown, fragile, formed by elongated cells, measuring on average 9.5 × 20.2 µm, with brown walls and intermingling with septate hyphae, forming a fragile inner layer. *Gleba* initially white coloured, compact, changing to dark brown, powdery mass with a robust columella with rounded apex, intruding up to ½ of the gleba. *Capillitium* formed by abundant straight hyphae with 0.81 µm thick walls; surface with crystalline incrustations of large bipyramidal crystals. *Basidia* narrowly ellipsoid to subcylindrical or more or less lageniform, 18–29 × 4.7–6.5 µm, with 5–8 short sterigmata. *Basidiospores* globose, 4.7–5.3 µm diam, with a slightly prominent apiculus, brown coloured with darker ornamentation formed by warts 0.36–0.51 µm high and 0.70–1.31 µm thick at the base, isolated or grouped fasciculate, with somewhat labyrinthiform pattern.

Habitat and distribution: Solitary to gregarious growth among plant remains; under *Juniperus*, *Quercus*, *Cupressus*, *Pinus* and *Robinia*, in calcareous soil, in winter. So far known from Spain, France, Italy and Bulgaria.

Typus: **Spain**, Castilla y León, Burgos, Mecerreyes, 42°06'16.71"N, 3°33'18.26"W, 1 080 m a.s.l., under *Juniperus thurifera* and *Quercus ilex*, in calcareous soil, 16 Dec. 2021, *A. Paz & C. Lavoise* (**holotype** BCN-IC16122101, **isotype** IC16122101; ITS, LSU, *ATP6*, *TEF1* and *RPB1* sequences GenBank PP575901; PP575903; PP587218).

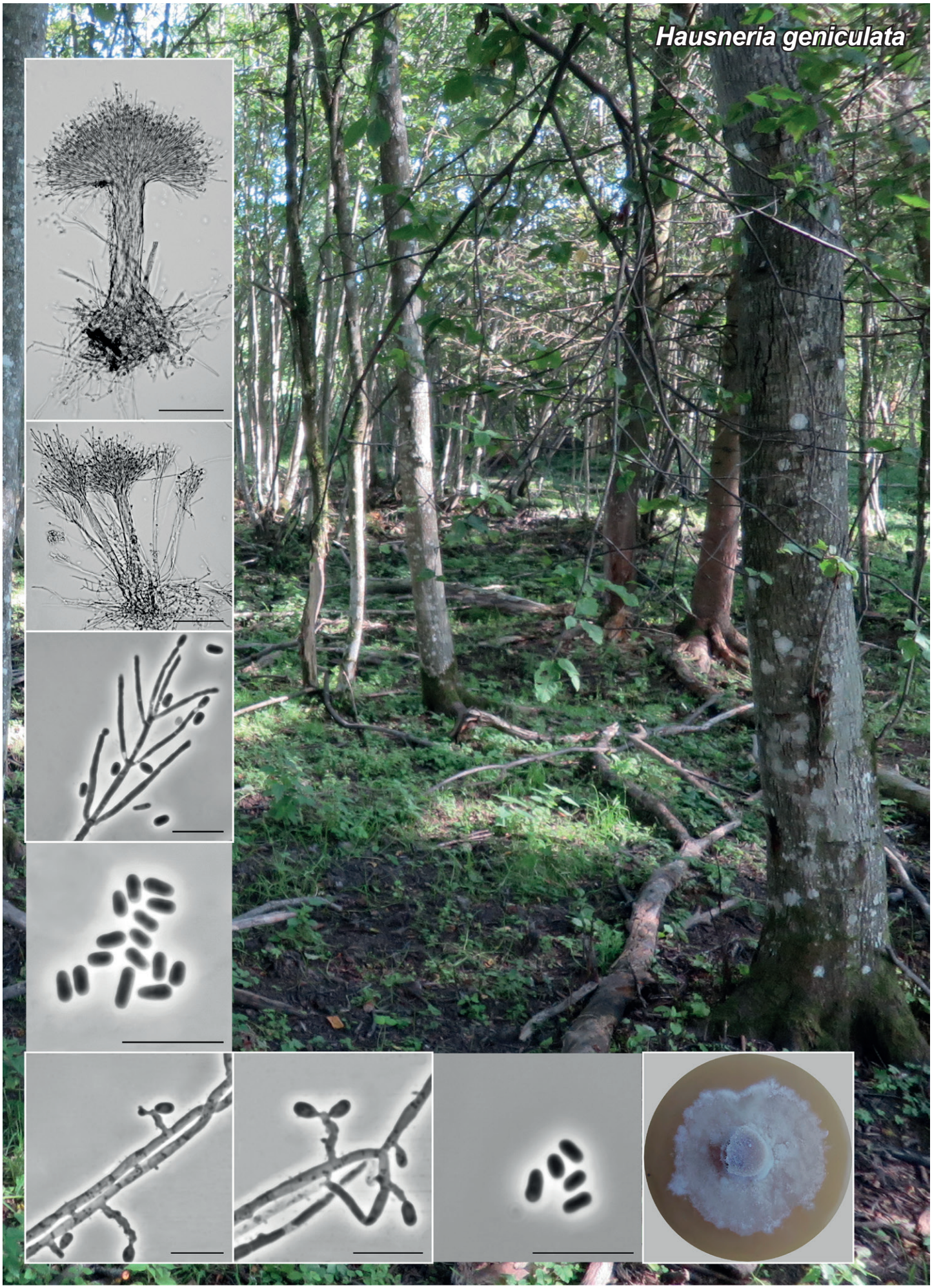
*Additional materials studied (**paratypes**)*: **Bulgaria**, Blagoevgrad province, north of Kresna town, 41°43'51.46"N, 23°09'12.97"E, 195 m a.s.l., under *Juniperus excelsa*, 27 Nov. 2021, *M. Slavova* (SOMF30876); Burgas province, west of Sozopol town, in the vicinity of Gradina camping site, 42°25'00.17"N, 27°38'44.92"E, *ca*. 10 m a.s.l., under *Cupressus*, 11 Dec. 2020, *M. Slavova* (SOMF30877). **France**, Ronce-les-Bains, La Tremblade, Forêt de La Coubre, 45°47'22.33"N, 1°10'17.39"W, 14 m a.s.l., dune forest of *Pinus pinaster*, *Quercus ilex*, *Robinia pseudoacacia*, on calcareous sandy soil, 20 Jan. 2014, *P. Chautrand* (IC07091506, GenBank PP575902). **Italy**, *s. l.*, *s. d.*, *S. Franco* (IC21011701). **Spain**, Castilla y León, Burgos, Burgos, Hortigüela, Valleconde, 42°3'16"N, 3°28´12"W, 973 m a.s.l., under *Quercus ilex* subsp. *ballota* and *Juniperus* sp., 3 Jan. 2016, leg. *P. Daniëls & C. Rojo* (Daniëls 3395); Mecerreyes, 42°06'16.71"N, 3°33'18.26"W, 1 080 m a.s.l., under *Juniperus thurifera*, *Quercus ilex* and *Pinus nigra,* calcareous soil, 8 Dec. 2014, *A. Paz & C. Lavoise* (IC08121428).

Notes: *Geastrum nadalii* is a member of *Geastrum* sect. *Corollina* to which the similarly indehiscent species *G. flexuosum* also belongs, but the latter is placed in subsect. *Marginata* (Zamora *et al.* 2014), within the complex group of *G. saccatum,* while *G. nadalii* belongs to subsect. *Plicostomata*, having as phylogenetically sister species the epigeous *G. morganii* and *G. violaceum* (see the phylogenetic tree provided for *G. federeri* elsewhere in this study). Morphologically, *G. nadalii* is characterised by having rhizomorphs with bipyramidal crystals, slightly felted surface of basidiomata, a two-layered exoperidium, which remains attached to the mesoperidium and not in ray with fissures, a mesoperidium consisting of subglobose to slightly elongated cells, a well-defined endoperidium, and basidiospores ornamented with isolated or grouped fasciculate warts forming a labyrinthiform pattern. *Geastrum flexuosum* has an easily separable exoperidium, a mesoperidium formed by isodiametric cells; it lacks endoperidium and has basidiospores ornamented by fused warts that form crests, oriented toward the apicule. *Geastrum fuscogleba* may have or lack endoperidium, and has slightly larger basidiospores, ornamented with isolated warts. *Geastrum taylorii* has rhizomorphs with slender, prism-shaped crystals, smooth surface of basidiomata, and smaller basidiospores ornamented with isolated warts. *Geastrum bushnellii* is characterised by having small basidiomata, capillitium absent or poorly developed, gleba initially arranged in chambers, and the ornamentation of the basidiospores is somewhat furrowed near the apicule, the sequence deposited in GenBank by Hosaka & Spatafora (DQ218895) indicates that it is a close species to *G. taylorii*. Morphologically *G. nadalii* differs from the epigeous sister species by having indehiscent exoperidium, without a peristome, pedicel and apophysis. *Geastrum morganii* and *G. violaceum* have peridium fissured in rays of radial arrangement, which gives them a star-like shape. They also have peristome and pedicel and in addition, the basidiospores of the latter are smaller.

For phylogenetic tree, see *G. federeri* (FP 1631).

Colour illustrations: Spain, Castilla and León, Burgos, Mecerreyes, where the type specimens were collected. Mature basidiomata; organisation of peridium hyphae (exoperidium, mesoperidium and endoperidium); basidiospores under light microscope. All images are from the holotype. Scale bars: peridium = 100 µm; basidiospores = 5 µm.

A. Paz, Aptdo. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain; e-mail: ita-paz@hotmail.com
C. Lavoise, Apt. Post Office No. 6, 17455, Caldes de Malavella, Girona, Spain; e-mail:c.lavoise@free.fr



Fungal Planet 1633

MycoBank MB 852544

Hausneria Jankowiak & Solheim, *gen. nov.*

Etymology: Named for Prof. George Hausner, in recognition of the leading role that he has played in taxonomy and molecular evolution of fungi, including species of *Ophiostomatales*.

Classification: *Ophiostomataceae*, *Ophiostomatales*, *Sordariomycetes*.

Mycelium consisting of subhyaline to pale green, smooth, branched, septate hyphae. *Conidiophores* dimorphic, macronematous, mononematous and synnematous. *Mononematous conidiophores* reduced to conidiogenous cells, simple, flexuous, often geniculate, unbranched, hyaline; *conidiogenous cells* polyblastic, sympodial with scars and denticles; *conidia* hyaline, 1-celled, obovoid to broadly ellipsoid, often curved. *Synnematous conidiophores* densely or loosely compacted, stipes hyaline, without rhizoid-like structures; *conidiogenous cells* hyaline annellidic; *conidia* 1-celled, hyaline, oblong to obovoid.

Type species: *Hausneria geniculata* Jankowiak & Solheim

MycoBank MB 852545

Hausneria geniculata Jankowiak & Solheim, *sp. nov.*

Etymology: The epithet *geniculata* (Latin) derives from the Latin *geniculatus* - geniculate, bent like a knee, refers to the geniculate mononematous conidiophores.

Sexual morph not observed. *Conidiophores* dimorphic, macronematous, mononematous and synnematous. *Synnematous conidiophores* (pesotum-like asexual morph) single or in groups, arising from the agar and aerial mycelium, (22–)110–184.5(–233) µm long with the capitulum. *Stipes* hyaline, (11.5–)65–126.5(–184) µm long, (3.5–)12–31(–48) µm wide at the apex, and (2–)11.5–34(–44.5) µm wide at the base. *Rhizoids* absent at the base. Conidiophores produced in the divergent capitulum with 2–3 series of branches, densely or loosely compacted. *Conidiogenous cells* annellated, (12.5–)15–23.5(–30.5) × 0.5–1.5 µm with 2–4 (mostly 3) conidiogenous cells per branch point, often one cell grows up below branch point. *Conidia* aseptate, hyaline, 1-celled, oblong, obovoid (2–)2.5–3.5(–4) × 1–2 µm; in a terminal mucilaginous mass, cream (4A3; Kornerup & Wanscher 1978), becoming greyish yellow (2B5) with age. *Mononematous conidiophores* reduced to *conidiogenous cells*, unbranched, straight to flexuous, often geniculate or with an irregular zigzag appearance, hyaline, polyblastic, sympodial with scars and denticles, (1.5–)4–14.5(–23) × 0.5–1.5 µm. *Conidia* hyaline, 1-celled, obovoid to broadly ellipsoid, often curved, (2.5–)3–4(–5) × 1–2 µm.

Cultural characteristics: Colonies with optimal growth at 25 °C on 2 % MEA, reaching 14 mm (± 0.12 mm) diam in 14 d and 22 mm (± 0.23 mm) diam in 28 d, with a radial growth rate of 0.05 mm/d. Colonies brownish grey (5C2), margin undulate to serrated. Reverse greyish yellow (4B4). Hyphae submerged in agar with aerial mycelium, subhyaline to pale green (30A3), smooth, (0.5–)1–1.5(–2) µm wide.

Cardinal temperature for growth: Minimum 5 °C, optimum 25 °C, maximum 30 °C.

Colour illustrations: Alnus incana trees infested by *Dryocoetes alni*, Nes, Norway. Synnematous conidiophores (pesotum-like asexual morph): conidiogenous apparatus; conidiogenous cells; conidia; mononematous conidiophores; conidia; colony on MEA after 28 d. Scale bars: two top photos in column = 50 µm; all others = 10 µm.

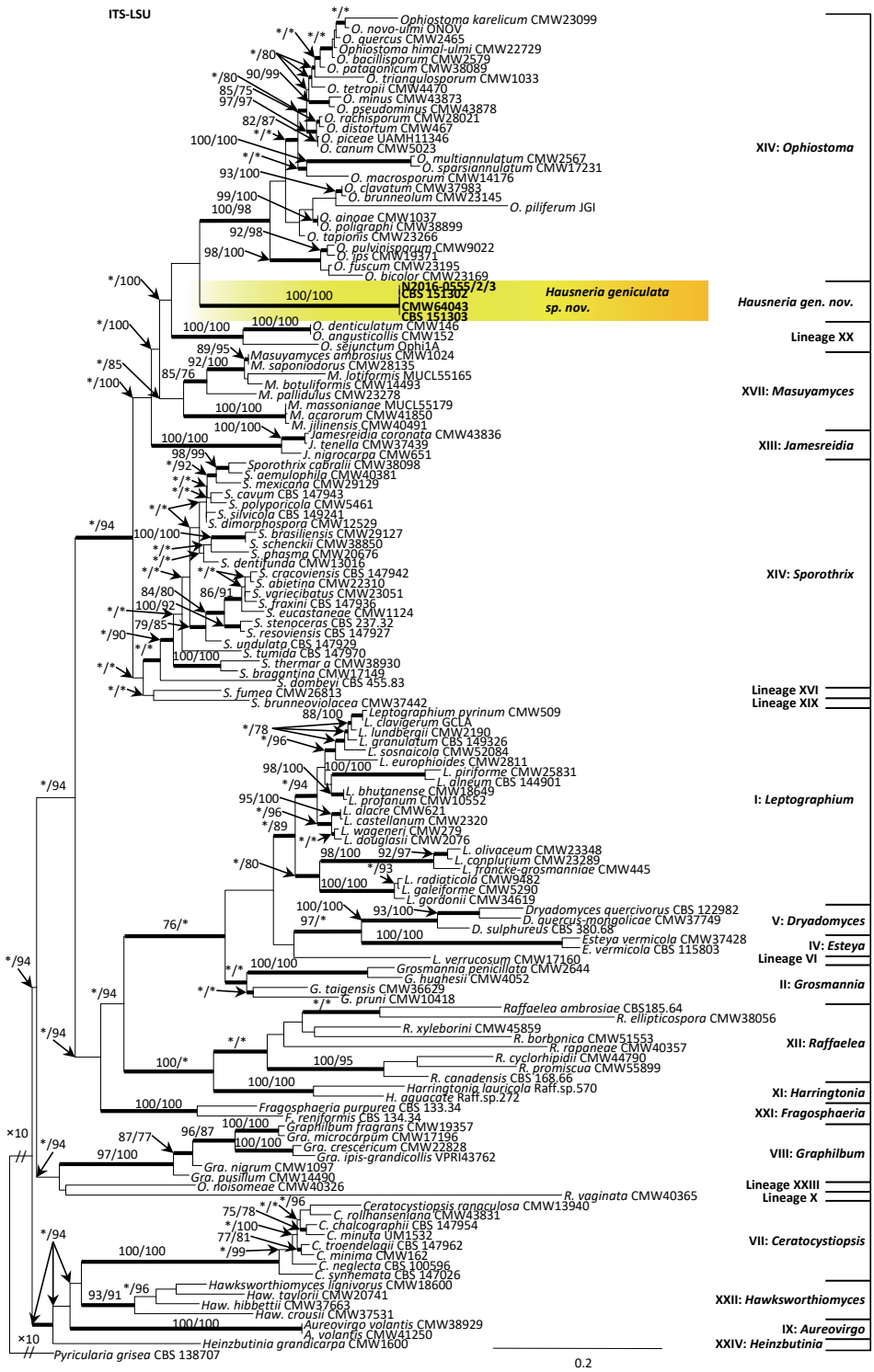
Typus: **Norway**, south-eastern Norway, Nes, isolated from a gallery of *Dryocoetes alni* on *Alnus incana*, Feb. 2016, *T. Aas & P. Aas* (**holotype** O-F-270960, culture ex-type CBS 151303 = CMW 64044; ITS-LSU, *CAL, TEF1*, and *TUB2* sequences GenBank PP410007, PP400434, PP400438, and PP400442).

Additional materials examined: **Norway**, northern Norway, Kvæfjord, isolated from a gallery of *Dryocoetes alni* on *Alnus incana*, Jun. 2015, *H. Solheim & L. Evje* (O-F-270961, culture CBS 151302 = CMW 64042; ITS-LSU, *CAL*, *TEF1*, and *TUB2* sequences GenBank PP410009, PP400436, PP400440, and PP400444).

Notes: Similar to members of the *Ophiostomatales*, *Hausneria* is associated with bark beetles, mostly with *Dryocoetes alni* and rarely with *Trypodendron domesticum* on *Alnus incana*. Analyses of the ITS and LSU regions showed that the ex-type isolate of *H. geniculata* together with the three other isolates formed a well-supported lineage distinct from all known genera and smaller lineages remains inconclusive in the *Ophiostomatales*, and sister to a lineage formed by members of the genus *Ophiostoma* (de Beer *et al.* 2022). *Hausneria* is a new genus in the family *Ophiostomataceae* characterised by production of two types of conidiophores: mononematous reduced to conidiogenous cells with scars and denticles, and synnematous with hyaline stipe. Members of the *Ophiostomatales* are known to be dimorphic and produce various asexual morphs in culture: hyalorhinocladiella-like, leptographium-like, pesotum-like, raffaelea-like, and sporothrix-like. Similar to members of *Graphilbum*, *Masuyamyces* and *Ophiostoma*, *H. geniculata* forms a typical pesotum-like asexual morph. Mononematous conidiophores formed by *H. geniculata* possess morphological features hyalorhinocladiella-like (conidiogenous cells with scars) as well as sporothrix-like (conidiogenous cells with denticles) asexual morphs. In contrast to other ophiostomatalean fungi, conidiogenous cells of *H. geniculata* are geniculate, with obvious and numerous scars resulting in an irregular zigzag appearance.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sporothrix cf. inflata* 2 [strain KFL1111N16DBRJ, GenBank MH740958; Identities = 574/693 (83 %), 64 gaps (9 %)], *Sporothrix cavum* [strain 42215aDRJ, GenBank MF782813; Identities = 575/695 (83 %), 64 gaps (9 %)] and *Sporothrix silvicola* [strain KFL5So, GenBank OP594841; Identities = 561/680

(83 %), 65 gaps (9 %)]. Closest hits using the **LSU** sequence are *Ophiostomataceae* sp. [strain JH14668, GenBank MN384641; Identities = 813/825 (96 %), no gaps], *Ophiostoma pallidulum* [strain VPRI43846, GenBank MW046139; Identities = 853/889 (96 %), two gaps (0 %)], and *Ophiostoma saponiodorum* [strain CBS 128125, GenBank MH877992; Identities = 838/874 (96 %), two gaps (0 %)]. Closest hits using the ***TUB2*** sequence had highest similarity to *Sporothrix* sp. [strain FMR 9338, GenBank FN547385; Identities = 313/387 (81 %), 19 gaps (4 %)] and *Sporothrix brunneoviolacea* [strain KFL64PFDb, GenBank OP588971; Identities = 312/387 (81 %), 18 gaps (4 %)]. Closest hits using the ***TEF1-α*** sequence had highest similarity to *Ophiostoma fasciatum* [strain VPRI43845, GenBank MW066416; Identities = 459/485 (95 %), one gap (0 %)], *Ophiostoma pallidulum* [strain VPRI43846, GenBank MW066427; Identities = 459/486 (94 %), two gaps (0 %)], and *Ophiostoma angusticollis* [strain VPRI43765, GenBank MW066415; Identities = 454/483 (94 %), no gaps]. Closest hits using the ***CAL*** sequence had highest similarity to *Ophiostoma fasciatum* [strain VPRI43845, GenBank MW075131; Identities = 255/293 (87 %), 20 gaps (6 %)], *Ceratocystiopsis chalcographii* [strain CBS 147955, GenBank OL310005; Identities = 255/296 (86 %), 14 gaps (4 %)] and *Jamesreidia coronata* [strain CBS 497.77, GenBank KX590786; Identities = 252/293 (86 %), 14 gaps (4 %)].



Phylogram from Maximum Likelihood (ML) analyses of the combined datasets of ITS and LSU for the *Ophiostomatales* carried out with PhyML v. 3.0 (Guindon *et al.* 2010) using the GTR+I+G model. Maximum Parsimony (MP) analyses were performed using PAUP v. 4.0b10 (Swofford 2003) while Bayesian Inference (BI) analyses using Markov Chain Monte Carlo (MCMC) methods were carried out with MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). The bootstrap support values (≥ 75 % for ML and MP analyses) are presented at nodes as follows: ML/MP. **Bold** branches indicate posterior probabilities ≥ 0.95 obtained from BI analyses. * indicates bootstrap support values < 75 %. The tree is drawn to scale (see bar) with branch lengths indicating the expected number of substitutions per site. *Pyricularia grisea* was used as outgroup taxon. Two additional strains of *H. geniculata* (NIBIO 2016-0555/2/3 and CMW 64043= NIBIO 2015-1555/2/3/2) obtained from *D. alni* on *A. incana* in Norway and deposited in Norwegian Institute of Bioeconomy Research (NIBIO) were included in the phylogenetic analysis. GenBank accession numbers for reference sequences used in the phylogenetic tree are given in De Beer *et al.* (2022). Alignment and tree are deposited in TreeBASE (ID: S31192).

R. Jankowiak & P. Bilański, Department of Forest Ecosystems Protection, University of Agriculture in Krakow, Al. 29 Listopada 46, 31-425 Krakow, Poland; e-mail: r.jankowiak@urk.edu.pl & piotr.bilanski@urk.edu.pl

H. Solheim & T. Aas, Norwegian Institute of Bioeconomy Research, P.O. Box 115, 1431 Ås, Norway; e-mail: halvor.solheim@nibio.no & aastruls@gmail.com

Fungal Planet 1634 MycoBank MB 852708

Helicocollum samlanense Mongkols., Noisrip. & Luangsa-ard, *sp. nov.*

Etymology: Refers to the locality where the type specimen was found, Namtok Samlan National Park.

Classification: *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

Stromata pulvinate or tomentose to planar, in various shades of cream, white or grey, 2–5 mm diam. *Perithecia* pseudo-immersed, sparsely packed on mycelium covering the insect, ovoid, 200–250 × 120–180 µm. *Asci* cylindrical, 8-spored, up to 100–150 × 8–15 µm, with caps 3–7 µm thick. *Ascospores* hyaline, whole, septate, 80–120 × 1.5–3 µm, remaining whole after discharge.

Culture characteristics: Colonies on potato dextrose agar (PDA) slow-growing, *ca*. 0.5 cm diam in 30 d at 25 °C, strong orange yellow (N163C; Royal Horticultural Society 2015), consisting of densely packed, partly submersed, and somewhat stromatic cells and felt-like aerial mycelium. *Conidiogenous cells* mono-or polyphialidic, arising from hyphae laterally from hyphae, entire phialides 25–60 × 2–5, slightly helical necks present, 1–1.5 µm wide. *Conidial* masses orange yellow (4A8). *Conidia* cylindrical, 1-septate, smooth-walled, (8–)10–14(–15) × 2–5 µm.

Typus: **Thailand**, Saraburi Province, Namtok Samlan National Park (Phra Buddha Chai), 14°26'26.68"N, 100°57'34.66"E, on scale insect **(***Hemiptera*, *Coccidae*), underside of bamboo leaves, 24 Dec. 2022, *J.J. Luangsa-ard, K. Tasanathai & S. Mongkolsamrit* (**holotype** BBH 49714, culture ex-type SM02407 = BCC 96785; LSU and *tef1* sequences GenBank PP447259 and PP453598).

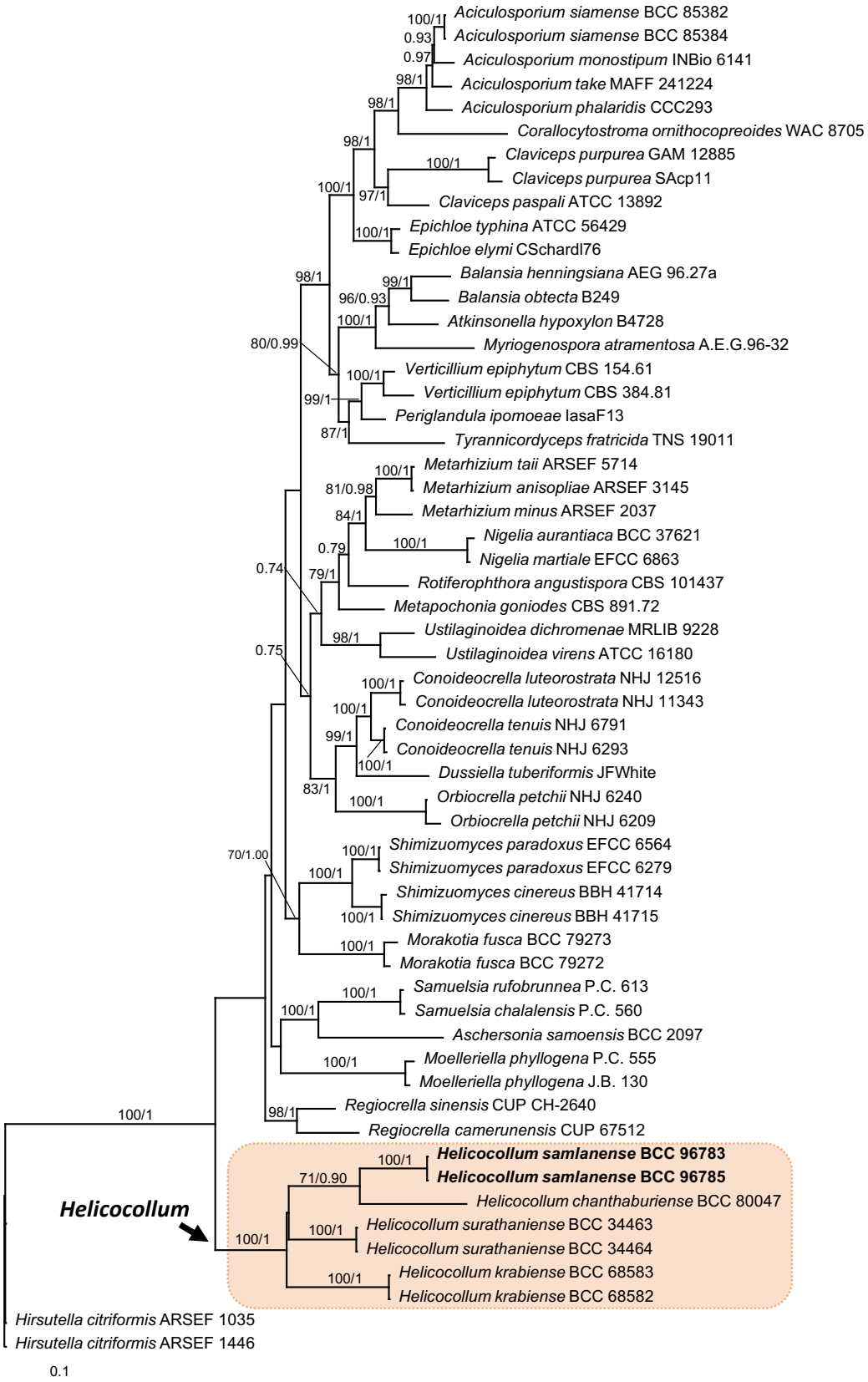
Additional materials examined: **Thailand**, Saraburi Province, Namtok Samlan National Park (Phra Buddha Chai), 14°26'26.68"N, 100°57'34.66"E, on scale insect (*Hemiptera*, *Coccidae*), underside of bamboo leaves, 24 Dec. 2022, *J.J. Luangsa-ard, K. Tasanathai & S. Mongkolsamrit* (BBH 49712, culture SM02405 = BCC 96783; LSU and *tef1* sequences GenBank PP447258 and PP453597); *ibid*., (BBH 49713, culture SM02406 = BCC 96784).

Notes: *Helicocollum*, a genus introduced by Luangsa-ard *et al.* (2018), currently includes three recognised species: *H. chanthaburiense*, *H. krabiense* and *H. surathaniense* (www.indexfungorum.org, accessed 6 March 2024). The identification of these species was based on the observation of their asexual morph, where phialides that taper into long, helical necks were produced, seen in both natural specimens and colonies on PDA. They are commonly found in association with scale insect nymphs (*Hemiptera*). *Helicocollum krabiense* and *H. surathaniense* exhibit a preference for the undersides of monocot (bamboo) leaves, while *H. chanthaburiense* is found on the undersides of dicot (*Durio zibethinus*) leaves. The macromorphologies observed in natural samples of *H. samlanense* produce pseudo-immersed perithecia, found on bamboo leaves covering scale insects (*Hemiptera*, *Coccidae*). Importantly, these characteristics differ significantly from those of entomopathogenic fungi associated with scale insects or whiteflies (*Hemiptera*) identified in Thailand. Our phylogenetic analyses strongly support the placement of *H. samlanense* within the genus *Helicocollum*, forming a sister lineage with *H. chanthaburiense*. This discovery marks the first observation of the sexual reproduction of *Helicocollum*, representing a significant record in our understanding of this genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **LSU** sequence had highest similarity to *Helicocollum krabiense* [strain BCC71374, GenBank KT222327; Identities = 754/787 (96 %), 10 gaps (1 %)], *Helicocollum krabiense* [strain BCC71373, GenBank KT222326; Identities = 754/787 (96 %), 10 gaps (1 %)] and *Helicocollum krabiense* [strain BCC71372, GenBank KT222325; Identities = 754/787 (96 %), 10 gaps (1 %)]. Closest hits using the ***tef1*** sequence are *Helicocollum surathaniense* [strain BCC34463, GenBank KT222336; Identities = 852/887 (96 %), no gaps], *Helicocollum krabiense* [strain BCC68582, GenBank KT222338; Identities = 822/890 (92 %), three gaps (0 %)] and *Metarhizium khaoyaiense* [strain BCC 14290, GenBank KJ398797; Identities = 865/962 (90 %), two gaps, (0 %)].

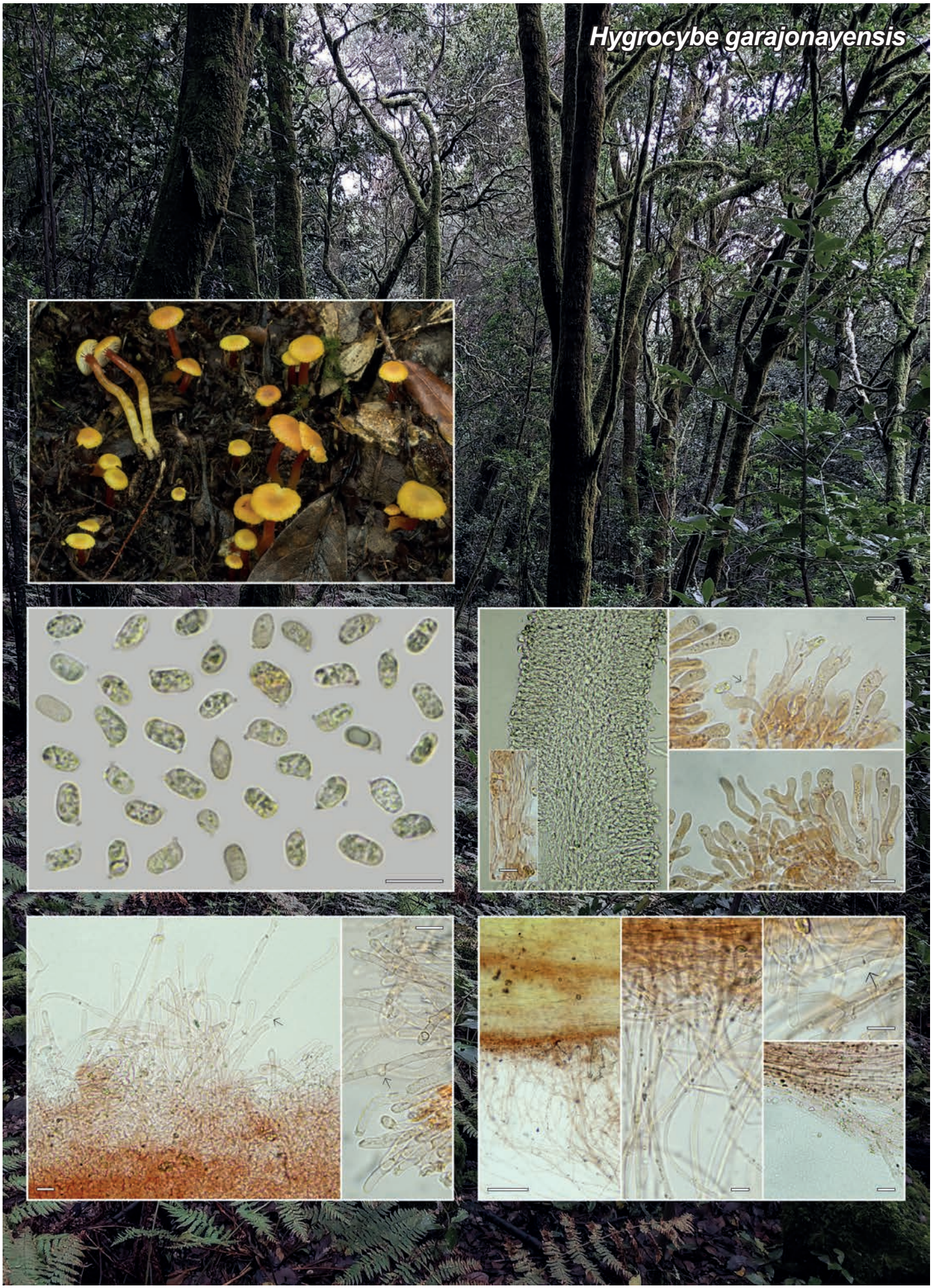
Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Background photo of forest in Thailand. Fungi on hosts; perithecia; ascus; whole-ascospore; culture on PDA (obverse and reverse); phialide on PDA; conidia and immature conidia (red arrows) on PDA. Scale bars: fungi on insect host = 1 mm; perithecia = 120 µm; ascus = 50 µm; ascospore = 20 µm; colonies on PDA = 5 mm; phialides and conidia = 10 µm.



Phylogenetic tree derived from Maximum likelihood (ML) analysis based on a combined dataset comprising LSU, *tef1* and *rpb1* sequences. The data was analysed using Maximum likelihood (ML) and Bayesian inference (BI). The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) on XSEDE in the CIPRES portal (www.phylo.org). Bayesian inference was calculated with MrBayes v. 3.2 (Ronquist *et al*. 2012), with 5 M generations and MrModeltest v. 2.2 (Nylander 2004) under the GTR+I+G model. Numbers at the significant nodes represent maximum likelihood bootstrap and Bayesian posterior probabilities MLB/BPP.

S. Mongkolsamrit, W. Noisripoom & J.J. Luangsa-ard, BIOTEC, National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: suchada@biotec.or.th, wasana.noi@biotec.or.th & jajen@biotec.or.th



Fungal Planet 1635 MycoBank MB 852457

Hygrocybe garajonayensis De la Peña-Lastra, A. Mateos & Illescas, *sp. nov.*

Etymology: The epithet refers to the place where it was found (Parque Nacional de Garajonay, La Gomera, Canary Islands, Spain).

Classification: *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

Pileus 5–12 mm diam, hemispherical, campanulate when young, then flattened in centre, with incurved margin, margin crenulate, striate on two-thirds of the radius, rugulose to magnifying glass especially in centre, viscid, orange light yellowish (Ség. 214; Séguy 1936), yellowed orange, lighter yellow at margin (Ség. 241) and darker ochraceous in centre (Ség. 211), which may be somewhat greyish. *Lamellae* separate, L = 16–18, with lamellulae (l = 1–3), arched, adnate, subdecurrent, thick, whitish-creamy. *Stipe* 12–32 × 0.9–1.8 mm, slender, central, cylindrical, widening downwards, with somewhat narrowed base, smooth, straight to curved or somewhat flexuous, translucent, viscid, fistulous, carmine red (Ség. 167) or scarlet red (Ség. 166) in the upper third, orange yellowish (Ség. 214) in the transition to the lower part, hidden by the substratum, which is canary yellow (Ség. 241), whitish at the base. *Context* exiguous, yellowish, no discernible *odour*, *taste* indistinct. *Basidiospores* (4.5–)6.1–*6.7*–7.5(–8.4) × (3.0–)3.3–*3.8*–4.3(–4.9) µm, Q = (1.3–)1.6–*1.8*–2.0(–2.1); n = 50; Ve = 51 µm^3, ellipsoidal, broadly ellipsoidal, cylindrical to oblong, amygdaliform, some rare constricted in the centre or phaseoliform, non-amyloid, hyaline, with oily content and rarely with a large guttule. *Basidia* (27.9–)28.3–*31.2*–37(–37.5) × (4.9–)5.2–*6.3*–7.3(–7.4) µm, predominantly 4-spored, claviform, with sterigmata 3.5–6.3 µm high, with basal fibulae. *Lamellar edge* subregular, with subcylindrical-subellipsoid hyphae, 20–60 × 4–10 µm, with fibulae. *Pileipellis* in ixotrichodermia, with elements 30–60 × 4–8 µm, mixed with filiform elements with rounded or claviform ends, 3–5.5 µm in diameter and 50–150 µm long. *Stipitipellis* in ixocutis with hyphae 3–4.2 µm thick, in some areas with ixotrichodermia of filiform elements with rounded or acute and claviform terminations 2–5 µm in diameter and 160–280 µm long, crystals present. *Clamp-connections* present in all tissues.

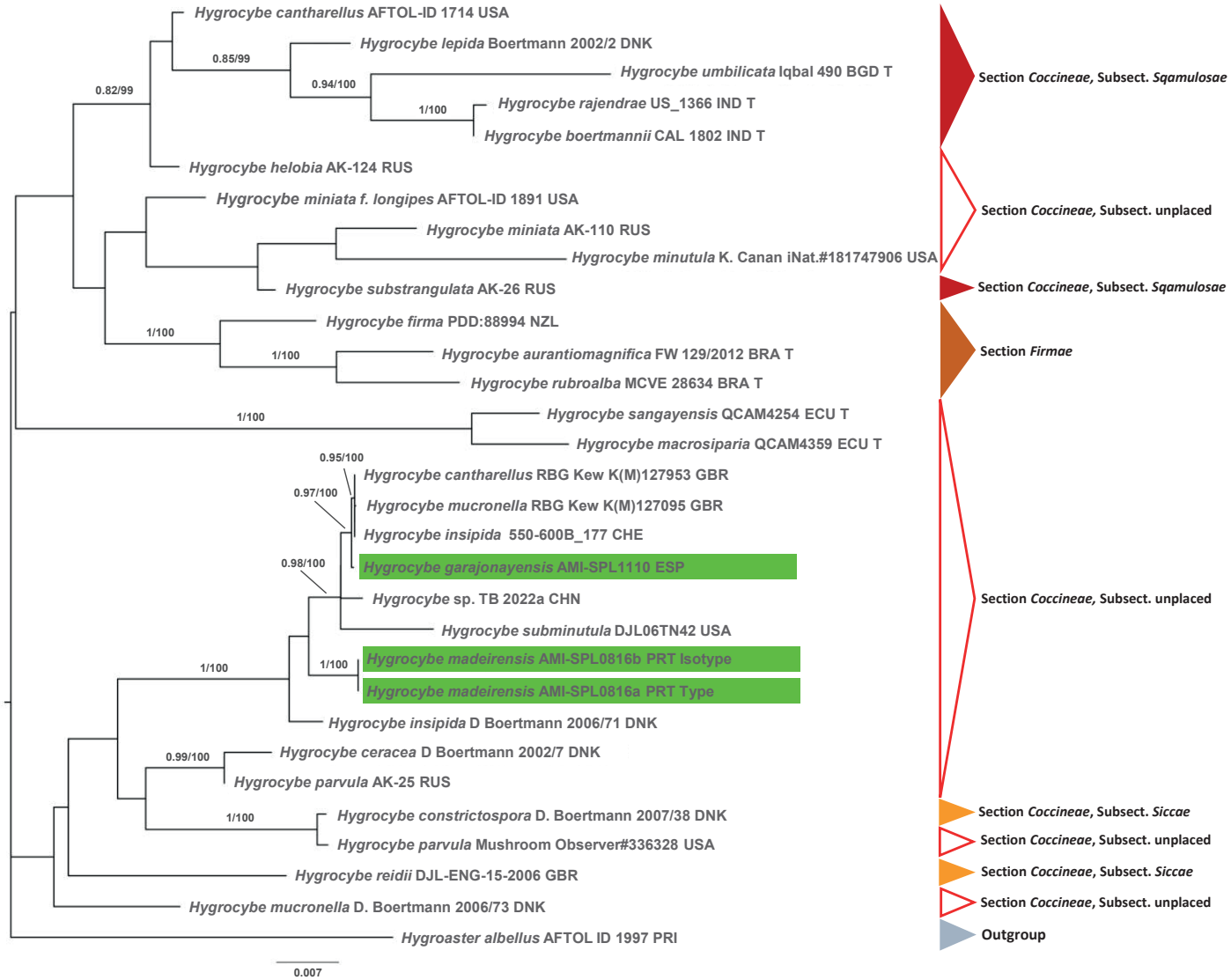
Distribution: Currently known only from the type location in the Canary Islands.

Typus: **Spain**, Canary Islands, Santa Cruz de Tenerife, La Gomera, Parque Nacional de Garajonay, N28°06'37.3", W17°14'54.5", 1 470 m a.s.l., gregarious in laurel forests, 5 Dec. 2021, *A. Mateos* & *S. De la Peña-Lastra* (**holotype** AMI-SPL1110; ITS and LSU sequences GenBank PP409982 and PP409984).

Colour illustrations: Spain, Canarias, La Gomera, P.N. Garajonay, laurel forest, where the holotype of *Hygrocybe garajonayensis* was collected. Top, basidiomata correspond with the holotype. Right column: hymenophoral trama (left RC) and lamellar edge con basidia and immature basidia (two pictures on the right RC), and the bottom photo is stipitipellis (four pictures RC). Left column: upper photo corresponds to basidiospores (H_2O, RC); and the bottom photo is pileipellis (two pictures RC). Scale bars: stipitipellis (left) = 100 µm; all others = 10 µm.

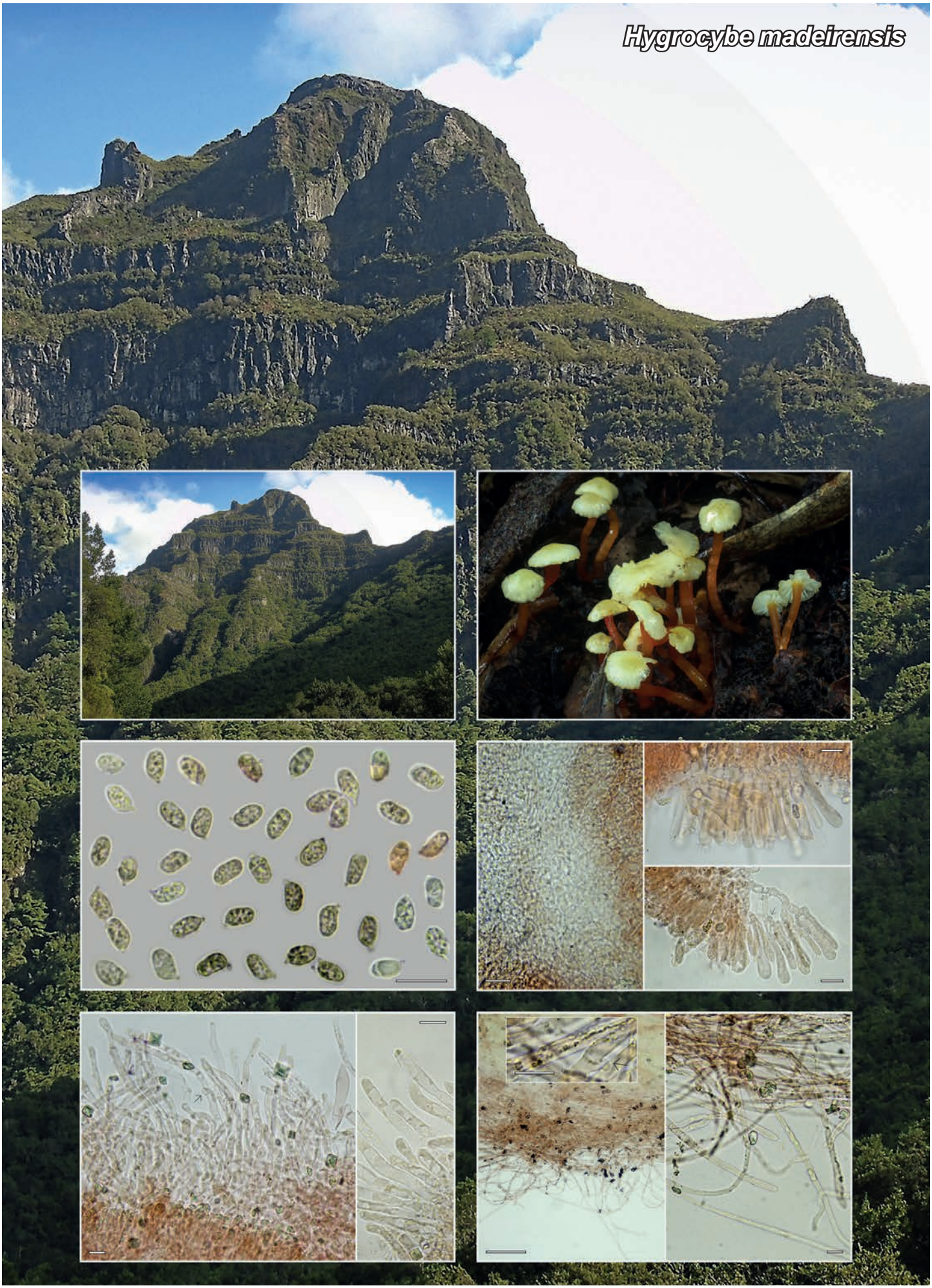
Notes: *Hygrocybe garajonayensis* is characterised by very small basidiomata, among the smallest of all species in the genus, slimy on the pileus and stipe when wet, striated and crenulate on the pileus, orange yellowish in colour, pale cream-coloured adnate-subdecurrent lamellae, flexuous stipe reddish carmine in the upper part, tending to lighten to yellow towards the base, ellipsoid to oblong spores of small size; therefore found in section *Coccineae*. In this section we have the species most similar morphologically and phylogenetically to *H. garajonayensis*, with which we will compare it. *Hygrocybe subminutula* and *H. parvula* are two North American species, also small in size and with equally small spores, but with a different colour combination in the pileus, which is also not so crenulate striated, more decurrent lamellae, especially in *H. parvula*, the stipe of *H. subminutula* is orange red and not carmine red or scarlet like *H. garajonayensis*, but that of *H. parvula* varies from "citron yellow" to "amber yellow", the latter being similar to our species, the spores of these two species being more constricted (Hesler & Smith 1963, Bon 1990, Landry & Labbé 2023). Other related species are *Hygrocybe insipida*, larger, with a cherry-red or scarlet pileus when young and only transparently striated, not crenulate, also the spores are larger; *Hygrocybe ceracea* larger, pileus not very viscous or ceraceous, only somewhat transparently striated, somewhat orange yellow, lamellae chrome yellow, not so pale, spores more constricted, caulocutis in cutis, not in ixocutis; *Hygrocybe constrictospora* with non-viscous pileus, somewhat transparently striated, scarlet, dry stipe, spores constricted, pileipellis and stipitipellis in cutis; *Hygrocybe reidii* with non- or slightly slimy pileus, yellow-orange lamellae, dry stipe and orange at apex, pileipellis and stipitipellis in cutis; *Hygrocybe mucronella* is different because of scarlet pileus, orange lamellae and stipe, spores strongly constricted; *Hygrocybe cantharellus* is distinct by its umbilicate, tomentose and dry pileus, very decurrent lamellae, dry stipe, with larger spores, pileipellis in trichodermia and stipitipellis in cutis (Candusso 1997, Boertmann 2010). Phylogenetically, *H. garajonayensis* is part of a fully supported subclade (0.87/100 %) that is part of a large, poorly supported clade whose taxa would be integrated into section *Coccineae*, subsection *Siccae* and subsect. *unplaced* (Lodge *et al.* 2014), with *H. mucronella* and *H. reidii* as the outermost species. A subclade derived from that of *H. garajonayensis* collects three sequences diversely interpreted as *H. insipida* (98.9 % affinity at ITS level), *H. cantharellus* (98.7 %) and *H. mucronella* (97.9 %), constituting a possible close taxon. At the ITS+LSU level, the sequences deposited as *Hygrocybe* sp. TB-2022a (GenBank ON117845 and ON062057) show 96.7 % affinity in the matching fragment of both species.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



The most probable maximum likelihood (ML) tree obtained from the ITS + LSU (GenBank accession numbers in supplementary table) alignment showing on the branches the ML bootstrap (ML-bs) support values and Bayesian posterior probability (BPP) values (ML-bs/BPP) considered significant (ML-bs ≥ 80 % and BPP values ≥ 95 %), calculated with IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015) and MrBayes v. 3.2 (Ronquist *et al.* 2012), respectively. The novel species is highlighted in green. Sequences from type material are indicated with a T.

S. De la Peña-Lastra, University of Santiago de Compostela, Spain; e-mail: saul.delapena@gmail.com
A. Mateos, Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain; e-mail: amateosiz1@gmail.com
T. Illescas, C/ Buenos Aires 3, bajo 1, 14006 Córdoba, Spain; e-mail: tillescas2@gmail.com
A. Rigueiro-Rodríguez, University of Santiago de Compostela, Spain; e-mail: antonio.rigueiro@usc.es



Fungal Planet 1636 MycoBank MB 852458

Hygrocybe madeirensis A. Mateos, De la Peña-Lastra & Illescas, *sp. nov.*

Etymology: The epithet refers to the place where it was found (Madeira, Portugal).

Classification: *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

Pileus 4–9 mm diam, hemispherical, campanulate, somewhat obtuse umbonate when young, then flattened in centre or rarely somewhat depressed, margin incurved at first, margin somewhat crenulate, smooth, hygrophanous, viscid, striated by transparency, cream, pale yellowish (Ség. 265; Séguy 1936), ochraceous greenish (Ség. 335) in centre and margin. *Lamellae* separate, L = 13–15, with lamellulae (l = 1–2), adnate, arcuate-decurrent, ventricose, whitish creamy. *Stipe* 14–23 × 0.7–1.5 mm, slender, central, cylindrical, subequal, straight to curved or generally flexuous, smooth, translucent, very viscid, fistulous, carmine red (Ség. 167), orange, pale vermillion (Ség. 196, 181) throughout. *Context* exiguous, concolorous to surface, no discernible *odour*, *taste* indistinct. *Basidiospores* (4.8–)5.8–*6.2*–6.6(–6.9) × (2.9–)3.1–*3.5*–3.8(–4.0) µm, Q = (1.4–)1.6–*1.8*–2.0(–2.1); n = 50; Ve = 39 µm^3, ellipsoidal, subcylindrical, very rarely constricted in the centre, smooth, non-amyloid, thin-walled, hyaline, with granular/oleaginous contents and rarely with a large guttule. *Basidia* 21.3–*27*–29.9(–33.2) × 4.5–6.0 µm, tetrasporic, claviform, with sterigmata 3.5–6.5 µm high, with basal fibulae. *Lamellar edge* subregular, confused or intertwined, with more or less inflated elements, 20–70 µm long. *Pileipellis* in ixotrichodermia, with rounded or claviform terminations 4–5.5 µm in diameter and up to 150 µm long, with abundant fibulae, frequent crystals. *Stipitipellis* is a mixture, consisting of an ixotrichodermia with filiform hyphae 2–4.5 µm with rounded terminations, 45–110 µm long and an ixocutis; with abundant crystals. *Clamp-connections* present in all tissues.

Distribution: Currently known only from the type location in the centre of Madeira.

Typus: **Portugal**, Madeira, Chão dos Louros, N32°45'37.1", W17°00'58.5", 820 m a.s.l., gregarious in laurel forests, 19 Nov. 2021, *A. Mateos* & *S. De la Peña-Lastra* (**holotype** AMI-SPL816a; ITS2 and LSU sequences GenBank PP407500 and PP409983); *idem*., (**isotype** AMI-SPL816b; ITS2 sequence GenBank PP409981).

Colour illustrations: Portugal, Madeira, Chão dos Louros, laurel forest, where the holotype of *Hygrocybe madeirensis* was collected. Right column: basidiomata in upper photo correspond with the holotype; middle photo corresponds with: hymenophoral trama (left RC) and lamellar edge con basidia and immature basidia (two pictures on the right RC), and the bottom photo is stipitipellis (three pictures RC). Left column: in middle photo corresponds to basidiospores (H_2O, RC); and the bottom photo is pileipellis (two pictures RC). Scale bars: stipitipellis (left) = 100 µm; all others = 10 µm.

Notes: *Hygrocybe madeirensis* is a member of the subgenus *Pseudohygrocybe* sect. *Coccineae*, having a very small size, the smallest known in the genus, with abundant viscosity on the pileus and especially on the stipe, pileus slightly striated by transparency and crenulate margin, pale yellowish and ochraceous greenish in the centre, lamellae adnate decurrent whitish-creamy, stipe flexuous, translucent, reddish-carmine or orange throughout, spores ellipsoid or subcylindrical, very inconstricted, very small, pilleipellis in ixotrichodermia and caulocutis with ixotrichodermia and ixocutis. Its sister species, *Hygrocybe garajonayensis* (see FP 1635), is very similar morphologically and closely related phylogenetically, but distinguished by the colour of the pileus, orange pale yellowish, by the colour of the stipe, scarlet red in the upper third, orange yellowish in the lower part, whitish at the base, and the somewhat larger spores. *Hygrocybe subminutula* is distinguished by the colour of the bright red pileus which turns yellow, with red persisting in the centre, the stipe is red, which also turns yellow at maturity and pale at the base, and the spores are more phaseolate and constricted (Hesler & Smith 1963, Bon 1990, Landry & Labbé 2023). *Hygrocybe parvula* is less slimy, with variable but more vivid yellow pileus than *H. madeirensis*, which is paler, as well as the stipe with variegated yellow but not red, larger spores [5–7(–8.5) × 3.5–5] (Hesler & Smith 1963, Landry & Labbé 2023). The larger *Hygrocybe insipida* has a cherry red pileus and larger spores (Candusso 1997, Boertmann 2010). Other phylogenetically close species such as *H. ceracea, H. constrictospora, H. reidii* or *H. mucronella*, besides their larger size, have obvious differences with *H. madeirensis*. From a phylogenetic point of view, *H. madeirensis* belongs to a subclade with complete support (1/100 %), sister to the subclade that includes *H. garajonayensis*. The phylogenetically most closely related species is *H. garajonayensis* itself (93.2 % affinity in the matching fragment of the combined ITS2 and LSU sequences of both holotypes); on the other hand, the sequences deposited as *Hygrocybe* sp. TB-2022a (GenBank ON117845 and ON062057) and *H. ceracea* Boertmann 2002/7 (GenBank KF291108 and KF291109) have, respectively, 92.8 % and 85.8 % affinity with the matching fragments of the sequences of the holotype of *H. madeirensis* (ITS2+LSU). Finally, at the LSU level, the holotype of *H. madeirensis* shows an affinity of 94.6 % with the sequence of *H. parvula* AK-25 (GenBank KF291189).

For phylogenetic tree, see *Hygrocybe garajonayensis* (FP 1635).

A. Mateos, Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain; e-mail: amateosiz1@gmail.com
S. De la Peña-Lastra, University of Santiago de Compostela, Spain; e-mail: saul.delapena@gmail.com
T. Illescas, C/ Buenos Aires 3, bajo 1, 14006 Córdoba, Spain; e-mail: tillescas2@gmail.com
A. Rigueiro-Rodríguez, University of Santiago de Compostela, Spain; e-mail: antonio.rigueiro@usc.es

Fungal Planet 1637

MycoBank MB 852409

Hygrocybula De la Peña-Lastra, Mateos & Plaza, *gen. nov.*

Etymology: Epithet reflects its macro- and microscopic similarity to *Hygrocyboides* fungi and its small size.

Classification: *Hygrophoraceae*, *Agaricales*, *Agaricomycetes.*

Pileus conical mammillate, somewhat brightly coloured, dry coating. *Lamellae* spaced, thick, adnate. *Stipe* fusiform, pruinose at apex, yellowish. *Flesh* of watery texture, *smell* and *taste* indistinct. *Spores* smooth, not amyloid, with thin, easily collapsible membrane and internally guttulate. *Basidia* elongate tetrasporic. *Lamellar edge* confuse, low-fertile, with *cheilocystidia* present. *Pleurocystidia* absent. *Pileipellis* in cutis. *Clamp connections* present. *Ecology* gregarious, mycorrhizal, on conifer humus with laurel forest.

Type species: *Hygrocybula terracocta* De la Peña-Lastra & Mateos

Notes: The new genus *Hygrocybula* forms a well-supported clade within *Hygrophoraceae* in combined ITS, LSU, SSU, *RPB2* and *TEF1* phylogenetic trees (see Supplementary material). Also based on a megablast search of NCBIs GenBank nucleotide database, the closest hits indicated consistent placement of *Hygrocybula* in the family *Hygrophoraceae* close to genera such as *Cuphophyllus*.

MycoBank MB 852415

Hygrocybula terracocta De la Peña-Lastra & Mateos, *sp. nov.*

Etymology: The epithet refers to the colour "terracotta", namely reddish or orange brown.

Pileus 12–16 mm wide, conical, then campanulate and finally spreading, with pronounced mamelon, broad and obtuse or small, sometimes umbilicate or depressed at maturity, with involute margin, sometimes fissured; cuticle granular, hygrophanous, pruinose, terracotta or reddish-brown, (Ség. 152, 172; Séguy 1936), darker vinous (Ség. 43) in centre, ochre-tobacco when desiccated (Ség. 174). *Lamellae* somewhat appressed, L = 30–34, with abundant lamellulae (1 L = 1–3 lam), adnate, ascending, thick, pruinose, with concolorous, or somewhat paler, eroded, brownish, or brownish pinkish laminar edge (Ség. 154, 164). Stipe 20–26 × 2–3 mm, uniformly cylindrical, but usually broadened at the apex (–5 mm) and very narrowed at the base, fusiform, sometimes somewhat eccentric, straight or sinuous, terete, fibrillose-sedose, pale pruinose at the apex, reddish brown above, ochraceous elsewhere, more yellowish towards the base. *Context* fistulous on the stipe, sparse on the pileus, pale beige, light fungal *odour* and sweet *taste*, somewhat astringent. *Spores* (3.2–)3.5–*4.1*–4.8(–5.2) × (2.5–)2.8–*3.4*–4.2(–4.7) µm; Q = (1–)1.1–*1.2*–1.4(–1.5); N = 70; Vm = 26 µm^3, smooth, subglobose, ovoid, sometimes ellipsoid or lacrymoid, with thick rounded, sometimes elongate apiculum, usually with a large oily guttule, sometimes with granular vacuolar contents, inamyloid, somewhat dextrinoid, thin-walled, easily collapsible. *Basidia* (19.6–)22.4–*24.5*–27.8(–29) × (4.5–)4.8–*5*–6.3(–6.7) µm, tetrasporic, claviform, with sterigmata 2.4–5 µm high. *Lamellar edge* sparsely fertile, *cheilocystidia* clustered in zones, sparse, (13–)15.5–*23.8*–26.9 × (2.2–)3.5–*4.5*–5.7 µm, claviform, cylindrical and fusiform, sometimes bifid. *Pleurocystidia* absent. *Hymenophoral trama* confused, hyphae 3–5.5 µm wide, with abundant fibulae, woof elements (20.6–)24.8–*33.3*–45.9(–46.1) × (7.3–)7.5–*9.3*–10.3(–10.9) µm, vermiform, fusiform or cylindrical. *Pileipellis* in a cutis of cylindrical or fusiform hyphae, 2.6–8 µm wide in the suprapellis and 8–10(–25) µm wide in the mediopellis, pileus trama is filamentous and fuzzy; with yellowish intracellular pigment, with abundant fibulae. *Stipitipellis* is a cutis of parallel, cylindrical, smooth hyphae, 4–9 µm wide. *Caulocystidia* numerous at apex of stipitate, clustered, (15.7–)20.5–*22.7*–25.4(–28.5) × 4.3–*5*–6.1(–6.2) µm, cylindrical and fusiform. *Clamp connections* present in all tissues.

Habitat and distribution: Gregarious, in more or less numerous groups growing on mossy areas of laurel forest areas planted with *Cryptomeria japonica*. Known from one island (São Miguel, Azores, Portugal).

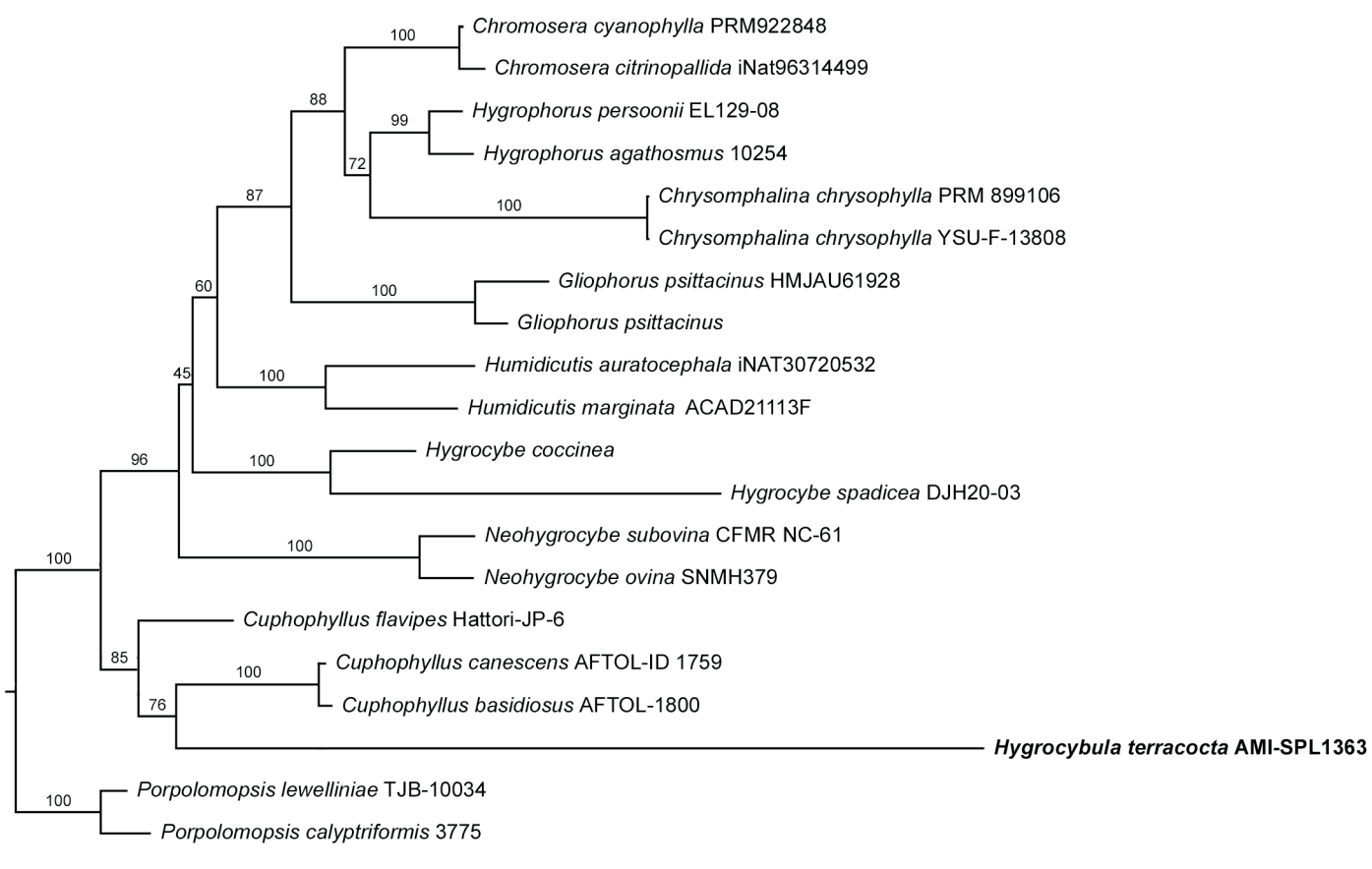
Typus: **Portugal**, Azores, São Miguel, M1038, 9630-186 Nordeste, N37°47'59.7", W25°10'01.9", 560 m a.s.l., gregarious growing on mossy areas of laurel forest areas planted with *Cryptomeria japonica*, 10 Oct. 2022, *S. De la Peña-Lastra* & *Aira Rego* (**holotype** AMI-SPL1363; ITS, SSU, and LSU sequences GenBank PP391595, PP391344, and PP391596).

Notes: *Hygrocybula terracocta* is characterised by its small size, mammillate conical habit, dry cuticle, terracotta coloured pileus and ochraceous stipe, spaced, rather thick and adnate lamellae, context with watery texture, elongate basidia, non-amyloid, smooth, subglobose, ovoid spores, intermingled lamellar edge, cheilocystidia (pseudocystidia) present, epicutis formed by a

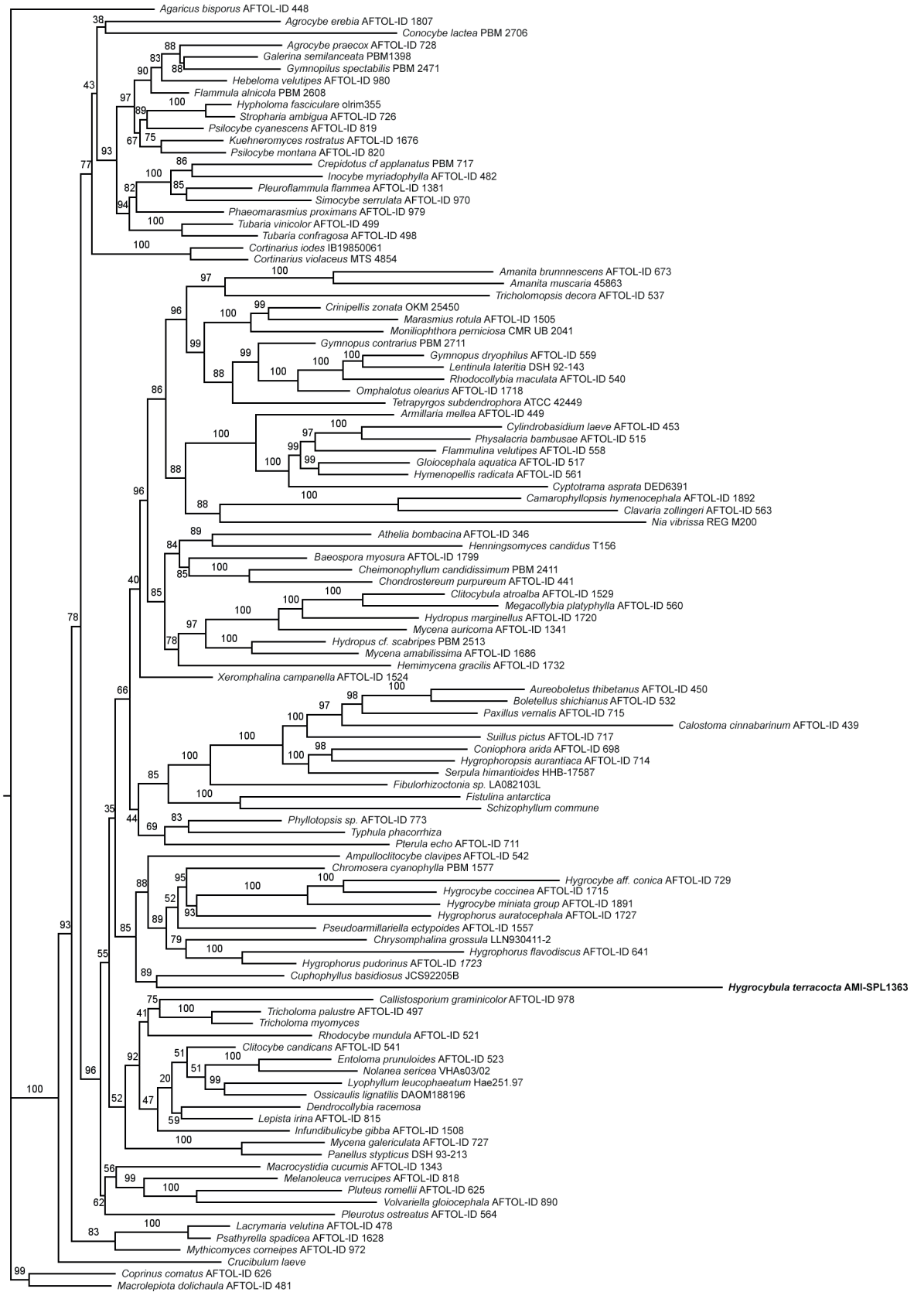
Colour illustrations: Portugal, Azores, São Miguel, laurel forests planted with *Cryptomeria japonica*, place where the holotype of *Hygrocybula terracocta* was collected. Right column: basidiomata in upper photo correspond with the holotype; middle photo corresponds with cheilocystidia, and the bottom photo is caulocystidia and stipitipellis trama, detail with crozier. Left column: in upper photo basidiospores (right *IKI 2, left *H_2O); middle photo corresponds with: lamellar edge, basidia and edge elements; the bottom photo is pileipellis (left two pictures (*H_2O), epicutis and subcutis with crozier (right *H_2O). * = living. Scale bars = 10 µm.

cutis, not hymeniform, not ixocutis, with caulocystidia on the upper part of the stipe. Many of these characters are common to the tribe *Hygrocybeae* (Bon 1990) and in particular to the genera *Hygrocybe* or *Cuphophyllus*; however, there are some that are exclusive to the new genus *Hygrocybula*, such as the presence of cheilocystidia on the lamellar edge and caulocystidia at the apex of the stipe. This new genus and species contribute to delimit the *Cuphophyllus canescens-C. basidiosus* clade reported in the systematic of Lodge *et al*. (2014). The phylogenetically closest species (*C. canescens* 89.86 % and *C. basidiosus* 89.73 %) are also those with morphological similarities in some aspects, especially microscopically, they differ from *H. terracocta: C. basidiosus* has a larger pileus (up to 4 cm), greyish colours, many more lamellulae, more robust stipe (2.5–5 cm long, 3–10 mm thick at the apex), similar but somewhat larger spores [4–5.5(–6) × 3–4. 5 µm], and absence of cystidia on the laminar edge and caulocutis (Hesler & Smith 1963, Landry & Labbé 2023). *Cuphophyllus canescens*, is larger, with a silky-fibrillose pileus, pale greyish colour and violet tones when young, adnate to decurrent greyish lamellae, polymorphous spores similar to *H. terracocta*, somewhat larger in size 4–5.5(–6) ´ 4–4.5 µm (Hesler & Smith 1963). *Cuphophyllus atlanticus*, a sister species of *C. canescens* has the same differences with *H. terracocta* (Jordal & Larsson 2021). Further away is *Cuphophyllus flavipes* with macro morphology more like the above and very different from *H. terracocta*, and with larger spores and pileipellis wich an ixocutis (Boertmann 2010). *Cuphophyllus pratensis* has a somewhat similar pileus, brownish orange, but its basidiomata are large, with decurrent lamellae, larger spores and no cystidia.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Tables).



The most probable maximum likelihood (ML) tree obtained from the ITS + LSU (GenBank accession numbers in supplementary Table 2) alignment showing on the branches the ML bootstrap (ML-bs) support values calculated with IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015). UltraFast method has been used for Maximum likelihood bootstrap with support values from 1 000 replicates and ≥ 95 % were considered significant.



The most probable maximum likelihood (ML) tree obtained from the ITS+LSU+SSU+*RPB2*+*TEF1* (GenBank accession numbers in supplementary Table 1) alignment showing on the branches the ML bootstrap (ML-bs) support values calculated with IQ-TREE v. 2.1.3 (Nguyen *et al*. 2015). UltraFast method has been used for Maximum likelihood bootstrap with support values from 1 000 replicates and ≥ 95 % were considered significant.

S. De la Peña-Lastra, University of Santiago de Compostela, Spain; e-mail: saul.delapena@gmail.com
A. Mateos, Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain; e-mail: amateosiz1@gmail.com
M. Plaza, c/ La Angostura, 20. 11370 Los Barrios, Cádiz, Spain; e-mail: manpc58@gmail.com
A. Rigueiro-Rodríguez, University of Santiago de Compostela, Spain; e-mail: antonio.rigueiro@usc.es

Fungal Planet 1638 MycoBank MB 850270

Inocybe cistophila Pancorbo, Esteve-Rav., & Armada, *sp. nov.*

Etymology: Name derives from Latin plant name "*Cistus*", and "*-philus*", from Greek *-philos*, which means loving, friendly, dear, or related to.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata agaricoid and stipitate. *Pileus* 10–30(–40) mm, at first hemispherical, conico-convex to campanulate-convex, soon convex to plano-convex, clearly umbonate to subumbonate in young stages, broadly umbonate with age; margin inflexed, often irregular or wavy, fissurate; colour brown to chestnut brown, often darker at the centre, sometimes mixed with a purplish to wine purplish component (Mu 7.5YR 4/4-8, 5/4-6); surface dry, fibrillose to finely squamulose, in the centre felty to squamose (depending on age and environmental conditions), in old specimens radially fibrose only at extreme margin, not or hardly hygrophanous. Velipellis visible in young specimens, especially in the centre, very fugacious, when present it appears as a white arachnoid patch or sparse remains. *Lamellae* moderately crowded (L = 35–45); l = (0–)1(–2), 3.5–4 mm wide, adnexed to narrowly adnate, ventricose, initially whitish, becoming pale grey to clay-coloured, often showing a rosaceous carmine reflection, then pale brown ochraceous with a rosaceous reflection, edge whitish to paler than the sides, finely crenulate. *Stipe* 10–40(–50) × (2.5–)4–8(–10) mm, straight or curved towards the base, sometimes compressed or flattened, cylindrical to slightly enlarged downwards or clavate; colour initially dirty white due to the fibrillose sheath, soon revealing the brownish to reddish brown background similar to the pileus colour, usually mixed with purplish, lilac or violet, shades; surface densely cottony white, distinctly fibrillose along the entire surface when young, mimicking the darker background. *Cortina* present in young specimens. *Context* fibrous, whitish at pileus and stipe base, wine purplish to purplish lilaceous at the stipe cortex, with a similar colour to the stipe surface (but exceptionally purplish to violet shades absent in some specimens, *e.g.*, FA 4635, FA 5280). *Smell* spermatic to weakly spermatic, occasionally with a honey-like reflection. *Macrochemical reactions*: null with KOH and TL4 anywhere in the basidiome (surface or flesh). *Spores* (7.7–)8.8–*10.0*–11.5(–12.5) × (4.5–)4.8–*5.5*–6.5(–7.0) µm, Q: (1.4–)1.6–*1.8*–2.1(–2.3) (n = 390 / N = 8), narrowly amygdaliform or subamygdaliform, smooth; apex ogival to slightly truncate, in some cases with a small pore. *Basidia* (24.1–)26.1–*29.5*–34.1(–36.6) × (7.0–)7.6–*9.4*–11.0(–11.9) µm; Q: (2.4–)2.5–*3.1*–4.0(–4.4) (n = 60 / N = 3), 4-spored, rarely 2-spored, cylindrical to clavate, sterigmata 3–5 µm long. *Lamellar edge* practically sterile, composed of numerous protruding hyaline cheilocystidia mixed with abundant mostly hyaline clavate to piriform paracystidia, often yellowish pigmented with age. *Pleurocystidia* abundant, (54.4–)57.0–*68.1*–77.8(–80.0) × (10.0–)11.8–*14.1*–16.7(–19.5) µm, Q: (2.8–)4.0–*4.8*–5.8(–6.5), (n = 124/ N = 5), lageniform to more or less cylindrical or fusiform, most frequently provided with a distinctly long neck, more rarely shorter and stubby claviform vesiculate with a short neck, vesiculate, rather often with sinuose, undate walls, sometimes with subcapitate or capitate apex; walls (0.8–)0.9–*1.3*–1.8(–2.1) µm thick, yellowish (+, ++, but not too bright) in aqueous ammonia solutions. *Cheilocystidia* (34.0–)44.3–*63.0*–77.9(–113.0) × (10.3–)10.7–*14*.0–18.8(–23.0) µm, Q: (3.2–)3.6–4.8–5.8(–6.3) (n = 125 / N = 8), similar in size and shape to pleurocystidia. *Stipitipellis* a cutis of parallel hyphae 2.5–14 µm wide, with parietal to encrusting dark yellow pigment. *Caulocystidia* only at the stipe apex, weakly crystalline or not, accompanied by numerous hairs with brown-encrusting pigment, shape of caulocystidia cylindrical to lageniform, sometimes with subcapitate apex (*e.g.*, 80 × 13 µm). *Pileipellis* a cutis formed by parallel fusiform cells, 1–3 µm wide, over a layer of parallel hyphae up to 12 µm wide, with yellow to dark yellow or reddish encrusting "zebra-like" pigment; hipocutis with broader hyphae –15 µm, paler and often tapering at the ends. *Clamp connections* abundant.

Habitat and distribution: Species of different *Cistaceae* are always present in all our collections. They constitute the main shrub component of the macchia on the Meso-Mediterranean forests in the Iberian Peninsula, where *I. cistophila* is found. These ecosystems mainly consist of pure or mixed thickets developing in acid-to-basic soils, often with sandy texture, and forming the undergrowth of diverse *Pinus* or *Quercus* forests. A collection in GenBank from southern Italy (Cosenza), determined as *I. rufula* (GenBank JF908248), most likely corresponds to *I. cistophila*. This new species is known from Spain and Italy so far but, according to habitat preferences, it is most probably present also in southern Portugal.

Typus: **Spain**, Castilla-La Mancha, Ciudad Real, El Viso del Marqués, La Calabaza, 38°28'32"N, 3°34'55"W, 835 m a.s.l., under *Cistus ladanifer*, in acidic soil, 6 Dec. 2014, *F. Pancorbo & M.A. Ribes* (**holotype** AH 56407, **isotype** FP14120602; ITS and LSU sequences GenBank OR644709 and OR637407).

Additional materials examined: **Spain**, Andalucía, Granada, Dílar, Cuesta Blanca, 37°03'45"N, 3°34'04"W, 930–1 000 m a.s.l., macchia of diverse *Cistaceae* in a mixed forest of *Pinus pinaster*, *P. halepensis*, *P. sylvestris* and *Quercus ilex* subsp. *ballota*, 16 Nov. 2018, *F. Armada & M.J. Díaz de Haro* (FA 4635; ITS sequence GenBank OR644714); *ibid.*, 15 Nov. 2019, *F. Armada* (FA 5280; ITS sequence GenBank OR644715); *ibid.*, 3 Dec. 2019, *F. Armada* (FA 5379); *ibid*., 16 Dec. 2020 (FA 5718); Granada, Víznar, El Portugués, 37°13'33"N, 3°32'13"W, 1 150 m a.s.l., macchia with diverse *Cistaceae*, *Quercus ilex* subsp. *ballota* and some *Pinus halepensis*, 1 Dec. 2019, *F. Armada & M.J. Díaz de Haro* (FA 5362; ITS sequence GenBank OR644716); Aragón, Teruel, Bronchales, El Estepar, 40°32'46"N, 1°34'33"W, 1 450 m a.s.l., *Cistus laurifolius* thicket in acidic soil, 12 May 2016, *E. Suárez* (AH 46591, duplicate HHTSG No. 1503; ITS sequence GenBank OR644712); Castilla-La Mancha, Ciudad Real, El Viso del Marqués, La Calabaza, 38°28'32"N, 3°34'55"W, 835 m a.s.l., under *Cistus ladanifer*, in acidic soil, 6 Dec. 2014, *F. Pancorbo & M.A. Ribes* (AH 56408; ITS and LSU sequences GenBank OR644708 and OR637408); *ibid*., Valle de Los Perales, 38°28'40"N, 3°36'27"W, 890 m a.s.l., under *Cistus ladanifer*, in acidic soil, 8 Dec. 2014, *M.A. Ribes* (AH 58559); Guadalajara, Tamajón, Sacedoncillo, 40°59'31.17"N,

Colour illustrations: *Inocybe cistophila* habitat in El Viso del Marqués, Spain; *Cistus ladanifer*, *Quercus rotundifolia, Pinus pinea* forest in acidic, sandy soil. *In situ* basidiomata of the holotype (AH 56407); photos of basidiospores; pleurocystidia; cheilocystidia; caulocystidioid hairs on stipe apex. Scale bars: basidiomata = 2 mm; cystidia = 50 µm; spores = 10 µm.

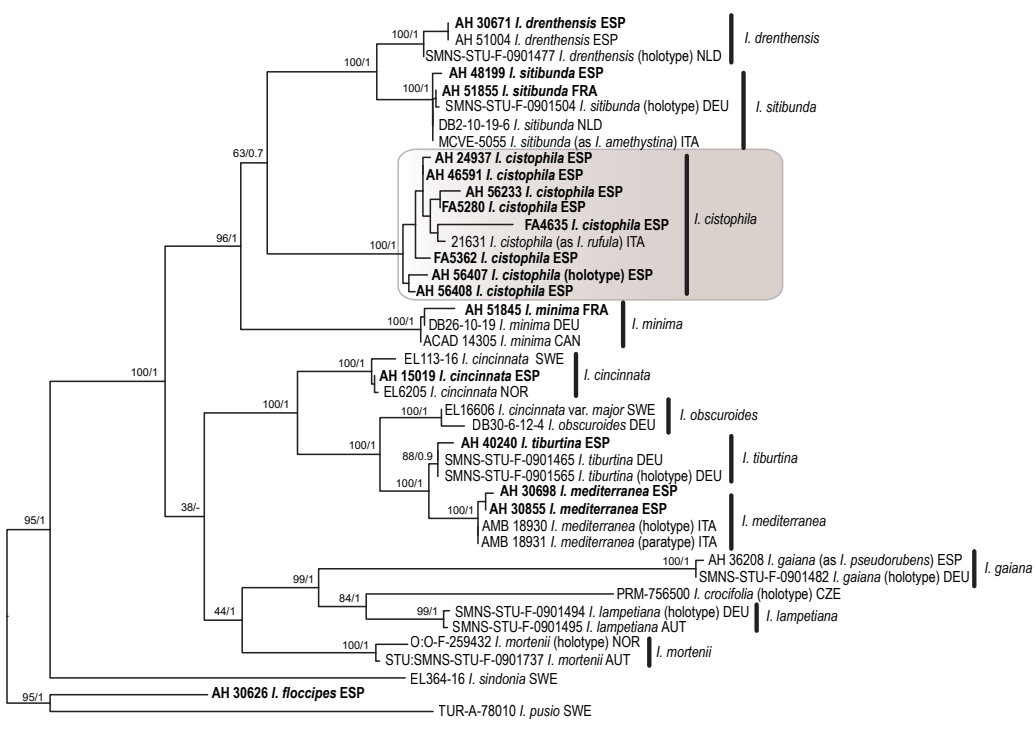
3°13'9.29"W, 1 005 m a.s.l., in *Cistus ladanifer* thicket with some *Pinus pinaster* trees nearby, on acidic and sandy soil, 2 Nov. 2022, *A. Altés & F. Esteve-Raventós* (AH 56233; ITS sequence GenBank OR644713); Catalonia, Girona, Roses, Mas de la Torre del Sastre, 42°14'52"N, 3°12'50"E, 170 m a.s.l., in a *Cistus monspeliensis* thicket, in acidic soil, 25 Jan. 1999, *J. Vila & X. Llimona* (AH 24937, duplicate Herb. J. Vila No. 990125-47; ITS sequence GenBank OR644711).

Notes: Colour codes are taken from Munsell (1994), terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe cistophila* is a typical Mediterranean species, which thrives in xerophytic forests and scrublands, establishing ectomycorrhizal associations with various *Cistaceae* in soils with a sandy component. Its morphological characteristics place it in the clade Cincinnata (Bandini *et al.* 2021, 2022a), due to the basidiomata with a fibrillose to squamose pileus, the presence of lilac to purplish tones in the basidiomata (especially visible in the stipe apex of young specimens) and the elongated cystidia with a fuso-lageniform to lanceolate morphology, whose walls take on an intense yellow colour in the presence of alkaline media.

Both *Inocybe drenthensis* and *I. sitibunda*, two species recently described by Bandini *et al.* (2021) in continental Europe, are phylogenetically very close. They clearly differ in the ITS, but also in their more continental habitat and distribution (although this character is not always delimiting) and their slightly broader and shortest spores. Cystidia of *I. cistophila* usually have a very elongated, often wavy, thin-walled distinct neck. *Inocybe minima* Peck, originally described from North America but also present in Europe, has smaller spores, and different cystidia with often a subcapitate apex (Bandini *et al*. 2021).

Within the Cincinnata group (see phylogenetic tree), the Cincinnata clade includes species (*I. cincinnata*, *I. obscuroides*, *I. gracillima*, *I. tiburtina*, *I. mediterranea*) with brownish incrustations on the lamellar edge (brown pigmented cheilocystidia), and on the stipe fibrils (often with a brownish scaly, tabby appearance), and spores with a marked tendency towards citriform morphology, often with a papillate apex (Bandini *et al*. 2021, Marchetti *et al*. 2021). In our ITS/LSU phylogenetic analysis, *I. cistophila* grouped in a fully-supported clade (ML-BS 100 %, BPP 1) with *I. sitibunda* and *I. drenthensis*. Comparison of ITS sequences showed that the *I. cistophila* holotype sequence (GenBank OR644709) has 641/750 (85 %) identity and 73 gaps with the *I. sitibunda* holotype sequence (GenBank MW845918), 639/751 (85 %) identity and 73 gaps with the *I. drenthensis* holotype sequence (GenBank MW845869).

Supplementary material: doi: 10.6084/m9.figshare.24307204 (Table).



Most likely tree of the Maximum Likelihood analysis of smooth-spored species of *Inocybe* inferred from the ITS and LSU regions generated by IQ-TREE web server (Trifinopoulos *et al.* 2016) using 1 000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS) ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.95 are shown on the branches and ordered as ML-BS/BPP. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers are indicated for all species retrieved from GenBank (see table) and generated in this study, as well as country ISO alpha3 code abbreviations. The tree was rooted to *Inocybe floccipes* (AH 30626) and *Inocybe pusio* (TUR-A-78010). The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site. The alignments were deposited in FigShare (doi: 10.6084/m9.figshare.24307204).

F. Pancorbo, Sociedad Micológica de Madrid, Real Jardín Botánico. C/ Claudio Moyano 1, 28014 Madrid, Spain; e-mail: fermin@socmicolmadrid.org
F. Esteve-Raventós, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: fernando.esteve@uah.es
F. Armada, 203 montée Saint-Mamert-le-Haut. F-38138 Les Côtes-d'Arey, France; e-mail: paco38@wanadoo.fr
A. Altés, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: alberto.altes@uah.es

Fungal Planet 1639 MycoBank MB 852639

Inocybe iota E. Larss., *sp. nov.*

Etymology: Refers to the habitus, the tiny, small basidiomata.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

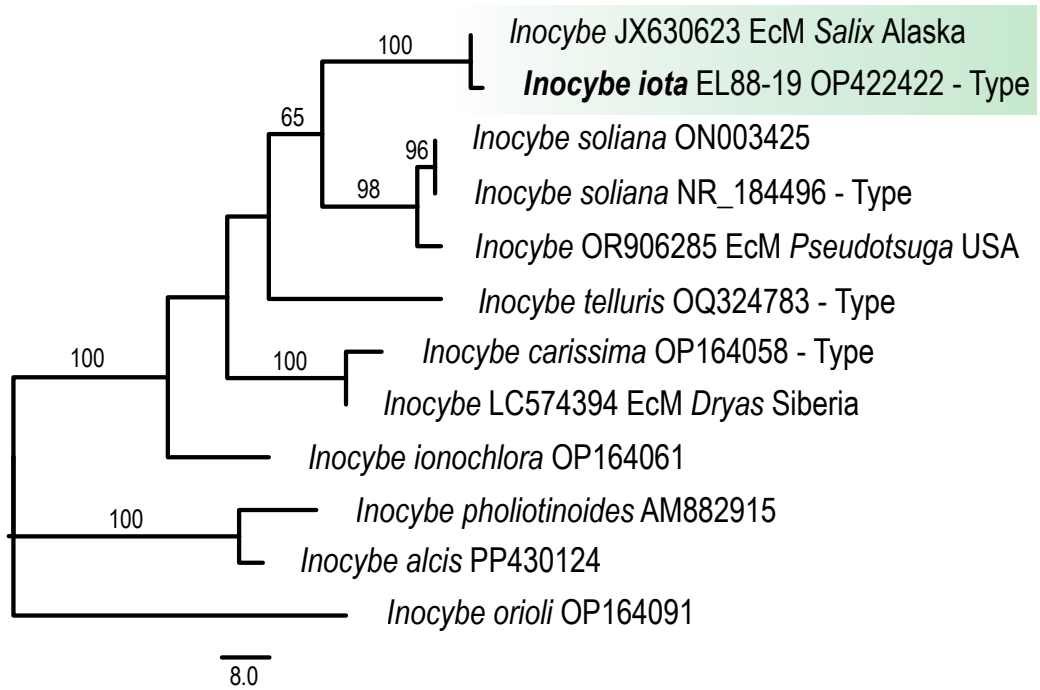
Pileus 6–14 mm diam, as young hemisphaerical to campanulate, becoming plano-convex, without pronounced umbo, margin slightly decurved to straight, dry, disc fibrillose to depressed scaly, margin coarsely fibrillose to finely scaly, rimulose, rather uniformly pale yellow-ochraceous brown. *Cortina* not present, velipellis fugacious. *Lamellae* subdistant, interspersed with lamellulae, L = 20–30, adnexed to almost free, first pale whitish to cream, later pale ochraceous brown, edge pale fimbriate to concolourous. *Stipe* 8–15 × 2–4 mm, equal, slightly clavate to subbulbous base, solid, first pale buff, later with a pale ochraceous tone, pruinose over the entire length. *Context* pale buff. *Smell* weakly spermatic. *Basidiospores* (8.4–)9.7–*9.9*–10.1(–11.9) × (5.6–)6.4–*6.6*–7.2(–8.0) µm, n = 82, Q = 1.36–1.58, Q av. = 1.55, smooth, ellipsoid, ovoid to subamygdaliform, with rounded apex and a small apiculus, rather thick-walled, pale ochraceous brown. *Basidia* 26–*30*–33 × 9–*10*–12 µm, n = 25, clavate, 4-spored, a few 2-spored, hyaline, some with yellowish brown content, sterigmata 4.2–5.6 µm long. *Pleurocystidia* 46–*63*–85 × 9–*12*–20 µm, Q mean = 5.1, n = 50, fusiform to sublageniform, with a pedicel or truncate, crystalliferous at apex, thick-walled, up to 4 µm, yellow in KOH solution. *Cheilocystidia* 44–*48*–57 × 10–*14*–17 µm, n = 25, similar to pleurocystidia, but more variable and on average shorter, thick-walled, yellow, mixed with hyaline pyriform to globose paracystidia 17–*27*–31 × 11–*16*–20 µm, n = 22. *Caulocystidia* over the entire length, less dense in the lower part, at apex similar to pleurocystidia but on average shorter, crystalliferous and thick-walled, 40–*49*–60 × 10–*12*–15 µm, n = 20, intermixed with thin-walled clavate to pyriform paracystidia, 26–*32*–45 × 10–*12*–15 µm, n = 20, at the base thin-walled, hyaline, more or less without crystals, 54–*74*–90 × 17–*21*–25 µm, n = 20, and with clusters of caulocytidoid hairs 45–*60*–110 × 5–*8*–12 µm, n = 10. *Stipetipellis* a cutis of cylindrical parallel hyphae 3–5 µm wide, encrusted with pale yellowish-brown pigments, subpellis with inflated interwoven hyaline hyphae 8–20 µm wide. *Pileipellis* a cutis of cylindrical to inflated hyphae with 8–10 µm wide, encrusted with yellowish brown pigments, subpellis with inflated interwoven hyaline hyphae 10–20 µm wide. *Clamp connections* frequent.

Ecology and distribution: So far only known from one collection originating from Sweden and the alpine zone in reindeer grazed area, likely associated with *Dryas octopetala* and *Salix reticulata* on calcareous ground. Blast search of NCBI's GenBank nucleotide database and the UNITE database gave 100 % match with one ITS sequence (JX630623) isolated from ectomycorrhiza of *Salix arctica* in Fairbanks, Alaska, suggesting the species to have a wide distribution in the arctic and alpine zones, but seems to be rare.

Typus: **Sweden**, Åsele lappmark, Vilhelmina, Frimhtstjahke, 65°14'46.55"N, 14°24'5.90"E, 996 m a.s.l., in alpine heath on calcareous ground, among mosses and herbs associated with *Dryas octopetala*, *Salix reticulata* and *Bistorta vivipara*, 22 Aug. 2019, *E. Larsson 88-19* (**holotype** GB-0207680; ITS-LSU sequence GenBank PP422422).

Notes: *Inocybe iota* is a tiny, rather indistinct species, easily overlooked and likely also rare. Our single collection originates from the alpine zone on calcareous ground sporulating close to *Dryas octopetala* and *Salix reticulata*. The first association when collecting it was with the small alpine species *I. egenula* that has a similar habit and ecology (Favre 1955). However, the pileus of *I. iota* is a bit more coarsely fibrillose and it differ in micromorphology by having smooth spores and caulocystidial hairs at the base of the stipe. The presence of smooth ellipsoid spores and caulocystidia over the entire length of the stipe suggests it belongs in sect. *Spendentes*, and a Blast search of the ITS in NCBIs GenBank show about 92 % similarity with the described species *I. carissima* and *I. telluris*, and about 90 % with *I. soliana* and *I. ionochlora*. *Inocybe iota* has a deviating ITS sequence but seems to be related to these other species that also have a complete pruinose stipe and fusiform thick-walled cystidia that become strongly yellow in KOH solution. These are lowland forest species found in other ecosystems than *I. iota* but can also be separated by other measurements of the cystidia and spores. A similar species genetically more distantly related to *I. iota* that occur in the alpine zone is *I. alcis*. It differs by the dark ochraceous brown pileus and has on average longer pleurocystida and a higher Q value of the spores (Bandini *et al.* 2022a, c, 2023).

Colour illustrations: Inocybe iota habitat in the alpine zone from the type locality in Frimhtsjahke, Åsele lappmark, Sweden. *In situ* basidiomata of the holotype (GB-0207680); photos of the hymenium with pleurocystidia, cheilocystidia, caulocystidia with paracystidia, caulocystidial hairs and basidiospores. Scale bars: pleurocystidia, cheilocystidia, caulocystidia, caulocystidial hairs = 20 µm; spores = 10 µm.



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. iota* among its closest relatives. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Inocybe iota* is marked with a green box and the holotype indicated in **bold**.

E. Larsson, Biological and Environmental Sciences, University of Gothenburg, and Gothenburg Global Biodiversity Centre, Box 463, SE40530 Göteborg, Sweden; e-mail: ellen.larsson@bioenv.gu.se

Fungal Planet 1640 MycoBank MB 851886

Inocybe querciphila Esteve-Rav., Pancorbo & E. Larss., *sp. nov.*

Etymology: The name is derived from the Latin plant name "*Quercus*" and "*-philus*", referring to its ectomycorrhizal relationship with this plant.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata agaricoid and stipitate. *Pileus* 10–20(–25) mm, at first campanulate to hemispherical, later campanulate-convex, to broadly convex, distinctly umbonate, umbo prominent, broad and obtuse with age; margin straight to deflexed, sometimes wavy, entire to crenulate; colour variable depending on hydration, from orange-ochraceous to fulvous orange, cinnamon, sienna to fulvous brown, sometimes chocolate brown (Mu 7.5YR 6/6-8, 5/3-8, 4/4-6); surface dry, often slightly glossy, smooth and radially fibrillose in young stages, often very finely squamulose towards the centre with age, sometimes broken in a delicate tessellate appearance, in old specimens radially fibrose only at margin, hygrophanous to subhygrophanous depending on soil moisture and ambient humidity, not striate. Velipellis not visible at any stage of development. *Lamellae* moderately crowded (L = 42–48); l = 1(–2), 2–4 mm wide, adnexed to narrowly adnate, ventricose, initially whitish, becoming cream to pale ochraceous, ochraceous brown to light tobacco-brown when mature, edge whitish to paler than the sides, finely crenulate. *Stipe* 25–40(–45) × (2.5–)3–4 mm, slender, straight or often curved to sinuate towards the base, cylindrical to hardly enlarged at the base; colour initially dirty white to light ochraceous or buff with slight pink reflection, clearly pinkish to pink reddish at the apex; surface smooth to finely fibrillose at the lower part, sometimes longitudinally striated, clearly floccose towards the apex (upper third), sparsely to indistinctly floccose at the middle. *Cortina* not seen, even in young specimens. *Context* fibrous, concolourous with the surface, slightly pinkish at the stipe apex. *Smell* subspermatic to lightly herbaceous. *Spores* (6.6–)7.2–*7.9*–8.6(–9.3) × (4.1–)4.4–*4.8*–5.2(–5.7) µm, Q: (1.38–)1.47–*1.60*–1.80(–1.95) (n = 249 / N = 2), ellipsoid to ovoid, smooth; with rounded apex. *Basidia* (21.9–)23.7–*26.9*–30.3(–31.3) × (6.4–)6.9–*8.1*–9.2(–9.7) µm; Q: (2.29–)2.75–*3.30*–3.78(–3.95) (n = 63 / N = 2), 4-spored, rarely 2-spored, cylindrical to clavate, sterigmata 3–4 µm long. *Lamellar edge* sterile, composed of numerous protruding cheilocystidia surrounded at the base by ellipsoid to isodiametric subhymenial cells, mixed with hyaline, claviform paracystidia. *Pleurocystidia* (31.5–)35.3–*45.3*–55.1(–58.5) × (10.2–)10.5–*13.7*–17.1(–23.5) µm, Q: (1.75–)2.25–*3.30*–4.62(–4.97), (n = 135 / N = 2), fusiform to sublageniform, most frequently provided with a short pedicel, bearing crystals at apex, sometimes also microcrystals; walls (0.95–)1.09–*1.30*–1.51(–1.57) µm thick, reaching up to 2 µm at the apex, pale yellowish in aqueous ammonia solutions. *Cheilocystidia* (36.6–)39.2–*45.1*–53.7(–59.5) × (10.8–)11.1–*14.6*–18.8(–19.9) µm, Q: (1.94–)2.28–*3.10*–4.05(–4.77) (n = 64 / N = 2), variable in shape, mostly (sub)lageniform to subfusiform. *Stipitipellis* a cutis of parallel hyphae 3.4–6.8 µm wide, with parietal to encrusting yellowish pigment. *Caulocystidia* present in the upper part of the stipe, (36.5–)40.4–*55.1*–68(–73.9) × (10.1–)10.8–*13.6*–17.5(–18.1) µm, Q: (2.56–)3.08–*4.10*–5.52(–6.43) (n = 42 / N = 2), reaching up to the middle of the stipe, although scattered, similar to hymenial cystidia but more slender, often in clusters with cauloparacystidia. *Clamp connections* abundant.

Habitat & distribution: The holotype and one paratype come from the same locality in Corsica, near Corte, in the mesomediterranean bioclimatic floor with a subhumid to humid ombroclimate (Delbosc *et al.* 2021), in a mixed *Quercus* forest (*Q. suber*, *Q. ilex*, *Q. pubescens*) with macchia scrub. The Swedish collection belongs to the Fennoscandian nemoral zone (Moen 1999) and was collected in a moist temperate deciduous forest under *Quercus* and *Fagus*. Judging by the geographical distance at which the collections were found, we assume that it is probably widespread in both continental and Atlantic nemoral areas of Europe but has probably been overlooked because of its banal appearance. BLAST search of NCBI's GenBank nucleotide database and the UNITE database gave no additional data and information.

Typus: **France**, Corsica, Corte, Saint-Jean, Maison San Giovanni, 42°17'38.22"N, 9°10'11.38"E, 419 m a.s.l., in humus of mixed forest of *Quercus suber, Q. ilex* and *Q. pubescens,* with *Arbutus unedo* and some sparse *Pinus pinaster*, with undergrowth of *Cistus monspeliensis,* in acidic soil, 8 Nov. 2019, *A. Altés, F. Pancorbo, F. Esteve-Raventós & G. Moreno* (**holotype** AH 51897; ITS and LSU sequences GenBank PP262644 and PP262643).

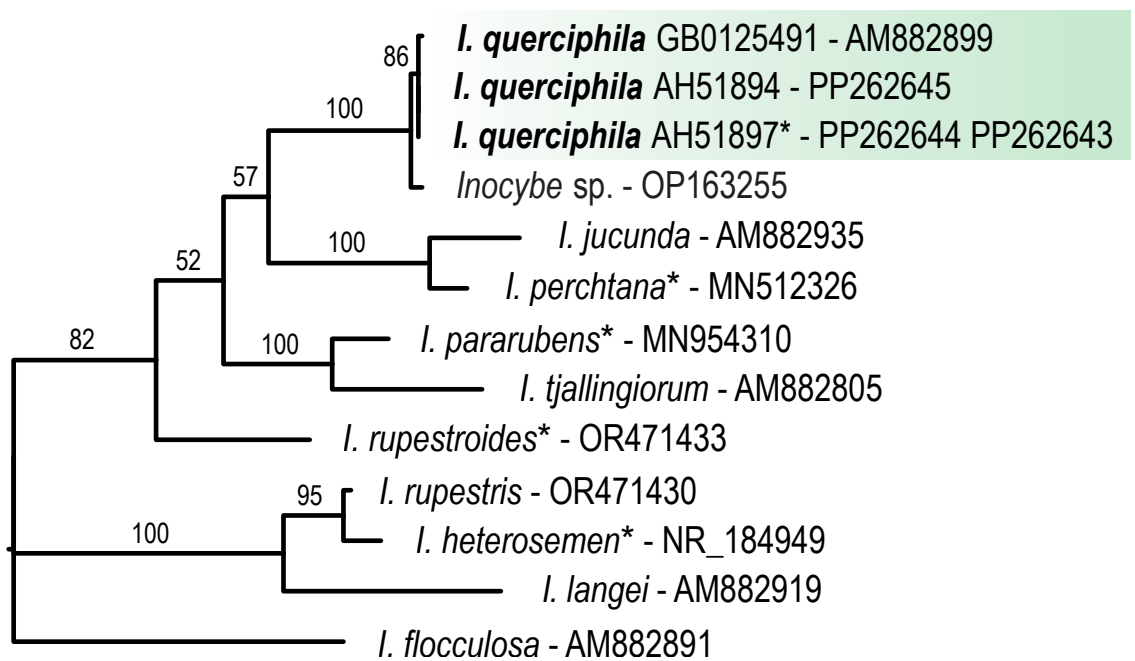
Additional materials examined. **France**, Corsica, Corte, Saint-Jean, Maison San Giovanni, 42°17'39.54"N, 9°10'10.40"E, 419 m a.s.l., in humus of mixed forest of *Quercus suber, Q. ilex* and *Q. pubescens, with Arbutus unedo* and some sparse *Pinus pinaster*, with undergrowth of *Cistus monspeliensis,* in acidic soil, 8 Nov. 2019, *A. Altés, F. Pancorbo, F. Esteve-Raventós & G. Moreno* (AH 51894; ITS-LSU sequence GenBank PP262645). **Sweden**, Skåne, Dalby, Dalby Norreskog Nature Reserve, 55°40'45.08"N, 13°20'38.76"E, 85 m a.s.l., in deciduous graced forest and meadows with *Quercus robur*, *Fagus sylvatica* and *Corylus avellana*, on acidic soil, 15 Sep. 1988, *S. Jacobsson*, SJ88053 (GB-0125491; ITS-LSU sequence GenBank AM882899, as *Inocybe cf. tenebrosa*).

Notes: Colour codes are taken from Munsell (1994), the terminology follows Vellinga (1988) and Kuyper (1986). In phylogenetic and morphological characters *I. querciphila* is a very distinctive species because of the distribution of its caulocystidia, the pinkish tones of the stipe and the small ovoid-ellipsoid spores. According to the practical taxonomic treatment of Bon (1997), the presence of caulocystidia in the basal part of the stipe, which is not bulbous and shows pinkish tones, would place *I. querciphila* in section *Splendentes* Sing. subsection *Subbrunneinae*. However, like *I. querciphila*, some species in this section have very scattered or apparently absent

Colour illustrations: Inocybe querciphila habitat in Saint Jean, Corte, Corsica. *In situ* basidiomata of the holotype (AH 51897); photos of basidiospores SEM, MO; pleurocystidia; cheilocystidia; caulocystidia on upper third of the stipe. Scale bars: basidiomata = 1 cm; cystidia = 50 µm; spores (MO) = 10 µm; spores (SEM) = 2 µm.

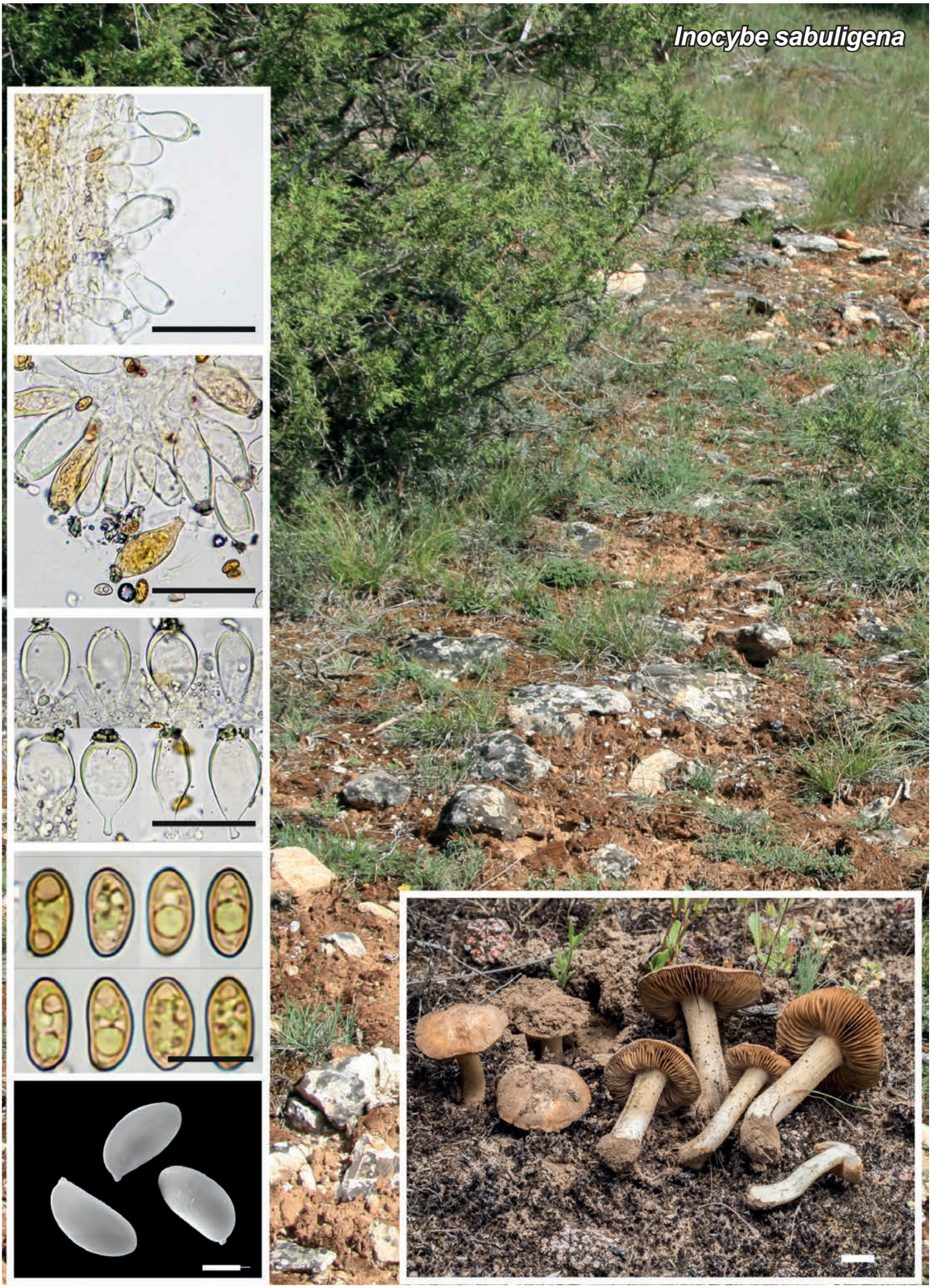
caulocystidia on the lower half of the stipe and could therefore be placed in section *Tardae*. A representative example of this case is *I. furfurea*, which sometimes shows caulocystidia only in the upper zone, and whose cystidia of cylindrical morphology make it clearly recognisable (Kühner 1955, Bandini *et al.* 2020).

Recently, some species have been described in which the caulocystidia are scattered or widely dispersed towards the base or apparently absent. This is the case of *Inocybe rivierana* and *I. beatifica*, which differ in the morphology of their cystidia and spores, and in the absence of distinct pink stipe colours; both are also phylogenetically very distant (Bandini *et al.* 2021). A similar case is that of *I. agroterae*, recently described from central Europe in *Picea* and *Salix* forests, with very elongate cystidia (Bandini *et al.* 2022b). *Inocybe querciphila* could also be reminiscent of *I. tjallingiorum* (= *I. subporospora*), whose stipe develops characteristic orange-brown tones, the caulocystidia are numerous along the entire stipe and the morphology of the cystidia is different (Kuyper 1986, Larsson *et al.* 2014, Bandini *et al.* 2021). Finally, the macroscopic appearance of *I. suecica* is somewhat reminiscent of that of *I. querciphila*, although it differs in having a stipe without pinkish tones, completely covered with caulocystidia, spores with a more amygdaloid morphology and a preference for calcareous soils (Vauras & Larsson 2016). In BLAST, all the species mentioned above show very clear phylogenetic differences.



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. querciphila* among its closest relatives. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Inocybe querciphila* is marked with a green box and the holotype indicated with an asterisk (*).

F. Esteve-Raventós, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: fernando.esteve@uah.es
F. Pancorbo, Sociedad Micológica de Madrid, Real Jardín Botánico. C/ Claudio Moyano 1, 28014 Madrid, Spain; e-mail: fermin@socmicolmadrid.org
A. Altés, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: alberto.altes@uah.es
E. Larsson, Biological and Environmental Sciences, University of Gothenburg, and Gothenburg Global Biodiversity Centre, Box 463, SE 40530, Göteborg, Sweden; e-mail: ellen.larsson@bioenv.gu.se



Fungal Planet 1641 MycoBank MB 851873

Inocybe sabuligena Esteve-Rav. & Pancorbo, *sp. nov.*

Etymology: Name derives from Latin "sabulum" and "geno/gigno", which means "originating in the sand".

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata agaricoid and stipitate, robust in appearance. *Pileus* 20–45(–50) mm, at first hemispherical, then plano-convex, finally applanate, sometimes with a slightly depressed centre, not or shallowly and broadly umbonate; margin straight to inflexed, often irregular or wavy, exceptionally reflexed with age; generally uniform in colour, cream, stramineous, buff ochre, sienna-buff to orange-ochraceous (Mu 10YR 7/3-6, 6/8); surface dry, finely fibrillose to tomentose in some specimens, matt, sometimes radially fibrose only at extreme margin, not hygrophanous. Velipellis distinct in young specimens, especially in the centre, often rather persistent as an arachnoid whitish patch, typically agglutinating sandy soil debris. *Lamellae* crowded to moderately crowded (L = 48–56); l = 1–2(–3), 4–7 mm wide, adnexed to narrowly adnate, ventricose, long time pale, initially whitish, becoming pale grey to clay-yellowish or "tobacco-brown" (reminding *Hebeloma spp*.), in some cases showing a rosaceous reflection, then pale brown ochraceous, finally orange ochraceous to orange yellow, edge white, fimbriate to finely crenulate. *Stipe* 20–40(–45) × 5–10 mm, firm, straight or curved towards the base, cylindrical, not enlarged towards the often rounded base, but sometimes tapering into a shortly sub-radicant base; colour initially white to dirty white, often unchanging but in some specimens turning yellowish-brown to dark greyish-brown, either spontaneously or in damaged spots, especially at the base; surface uniform or sometimes longitudinally stripped, densely whitish pruinose in upper half, becoming sparsely pruinose towards the lower half. *Cortina* absent. *Context* fibrous, whitish to pale ochraceous at pileus and stipe base. Smell fungoid, not particular. *Spores* (8.0–)9.1–*10.3*–11.7(–12.7) × (4.5–)4.8–*5.6*–6.3(–6.9) µm, Q: (1.45–)1.61–*1.80*–2.07(–2.29) (n = 288 / N = 3), smooth, narrowly ellipsoidal, ellipsoidal, very rarely subamygdaliform; apex rounded. *Basidia* 25.1–*28.9*–32.6(–32.7) × (7.9–)8.1–*9.4*–10.3(–10.8) µm; Q: 2.62–*3.00*–3.44(–3.64) (n = 19 / N = 1), 4-spored, rarely 2-spored, cylindrical to clavate, sterigmata 3–4 µm long. *Lamellar edge* sterile, composed of numerous protruding cheilocystidia mixed with hyaline, slightly thick-walled claviform paracystidia. *Pleurocystidia* (29.8–)35.1–*43.6*–54.7(–57.8) × (12.5–)15.0–*20.2*–25.3(–28.6) µm, Q: (1.57–)1.66–*2.20*–2.89(–3.21), (n = 85/ N = 3), globose to subglobose to utriform or subclavate to subfusiform, often provided with a short pedicel, and bearing crystal at apex; walls (1.56–)1.70–*2.10*–2.81(–2.91) µm thick, reaching up to 4 µm at the apex, yellowish in aqueous ammonia solutions. *Cheilocystidia* (23.7–)30.8–*41.2*–56.6(–70) × (9.5–)12.7–*16.8*–23.3(–29.4) µm, Q: (1.76–)1.90–*2.50*–3.39(–4.46) (n = 153 / N = 3), variable in shape, subcylindrical, subfusiform, sublageniform, utriform, subglobose, sometimes with subcapitate or capitate apex, often with a brownish-ochre to yellowish content. *Stipitipellis* a cutis of parallel hyphae 2.8–7.4 µm wide, with parietal to encrusting yellowish pigment. *Caulocystidia* present in the upper part of the stipe, more rarified in the lower half, similar in size and shape to hymenial cystidia in clusters with cauloparacystidia. *Clamp connections* abundant.

Habitat and distribution: Until now, it has only been found in Spain during the spring season in different localities, always within the Mediterranean biogeographic region. It grows on very sandy soils, slightly acidic or neutral, resulting from the washing away of calcareous rocks (calcarenites). The collections come from typical Mediterranean holm oak (*Quercus ilex* subsp. *ballota*) forests with *Cistaceae* undergrowth ('rockroses'), such as various species of *Helianthemum* and *Fumana*, with which it probably forms an ectomycorrhizal association. The basidiomata have a semi-hypogeous growth and typically appear by lifting the sandy soil, which often remains attached to the pileus.

Typus: **Spain**, Castilla-La Mancha, Guadalajara, Tamajón, Ermita de los Enebrales, 41°00'59"N, 3°15'11"W, 1 053 m a.s.l., near diverse *Cistaceae* (*Fumana* spp., *Helianthemum* spp.), in a mixed *Quercus ilex* subsp. *ballota/Juniperus thurifera* open forest, in slightly acidic sandy areas on calcareous soils (calcarenites), 14 Jun. 2018, *M. Villareal, M. Lizárraga, F. Pancorbo, F. Esteve-Raventós & G. Moreno* (**holotype** AH 48210, **isotype** FP18061405; ITS-LSU sequence GenBank PP262648).

Additional materials examined: **Spain**, Andalucía, Granada, Orce, in mixed forest of *Pinus halepensis* and *Quercus ilex* subsp. *ballota* in calcareous soil, 1 May 2004, *B. Moreno & E. Pulido* (AH 30872); Castilla-León, Segovia, Sepúlveda, Castrillo de Sepúlveda, 41°19'41"N, 3°46'19"W, 1 097 m a.s.l. in *Quercus ilex* subsp. *ballota* in sandy spots (calcarenites) in calcareous soil, 7 Apr. 2002, *P. Juste* (AH 29940, duplicate in *P. Juste* No. B-1826; ITS sequence GenBank PP262646); Castilla-La Mancha, Ciudad Real, Manzanares, Sierra de Siles, 38°53'25"N, 3°30'44"W, 714 m a.s.l. in *Quercus ilex* subsp. *ballota* forest with *Populus alba, P. nigra* and *Ulmus minor* nearby in sandy spots in calcareous soils, 30 Apr. 2000, *F. García & P. Juste* (AH 26806, duplicate in *P. Juste* No. B-1693; ITS-LSU sequence GenBank PP262647); Guadalajara, Tamajón, Ermita de los Enebrales, 41°0.5'82"N, 3°15'15.7"W, 1 048 m a.s.l. near diverse *Cistaceae* (*Fumana* spp., *Helianthemum* spp.), in a mixed *Quercus ilex* subsp. *ballota/Juniperus thurifera* open forest, in slightly acidic sandy areas on calcareous soils (calcarenites), 14 Jun. 2018, *M. Villareal, M. Lizárraga, F. Pancorbo, F. Esteve-Raventós & G. Moreno* (AH 49106; ITS1 and ITS2-LSU sequences GenBank PP262649 and PP262650).

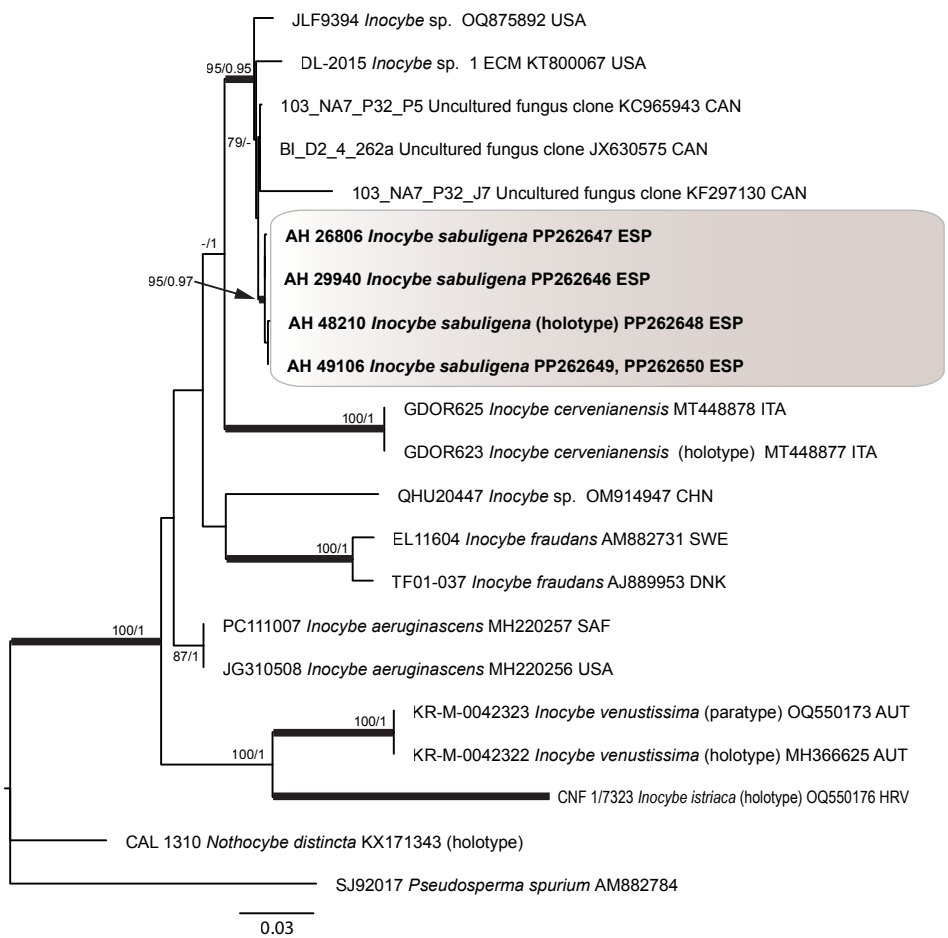
Notes: Colour codes are taken from Munsell (1994), terminology follows Vellinga (1988) and Kuyper (1986). In our analysis, *Inocybe cervenianensis* appears to be the most phylogenetically related European species (ITS 86.6 % of similarity in BLAST). This species shares a similar habitat with *I. sabuligena,* in Mediterranean *Quercus ilex* forests, but its morphological differences are obvious: a marginate bulb, the brownish reddish colour of the stipe, the amygdaloid spores and the quite different cystidia, from ventricose-lageniform to fusiform

Colour illustrations: *Inocybe sabuligena* habitat in Tamajón, Spain, the type locality. *In situ* basidiomata of the holotype (AH 48210); photos of basidiospores (SEM, MO); pleurocystidia; cheilocystidia; caulocydia in the upper part of the stipe. Scale bars: basidiomata = 20 mm; cystidia = 50 µm; spores (MO) = 10 µm; spores (SEM) = 2 µm.

(Dovana *et al*. 2021). In sandy soils, both coastal and inland, *Inocybe fulvida* var. *subserotina* (Bon 1984b, LIP!) and *I. pruinosa* (with a neotype designated by Kuyper 1986 in L!) may resemble *I. sabuligena* in colour and appearance, but their larger fusiform cystidia and spores, which in *I. pruinosa* are sometimes irregular or subangular in outline, clearly separate them. Both taxa are not related phylogenetically to *I. sabuligena*, according to the sequences deposited in GenBank with these names or as *I. inodora* (considered by Kuyper 1986 as contaxic).

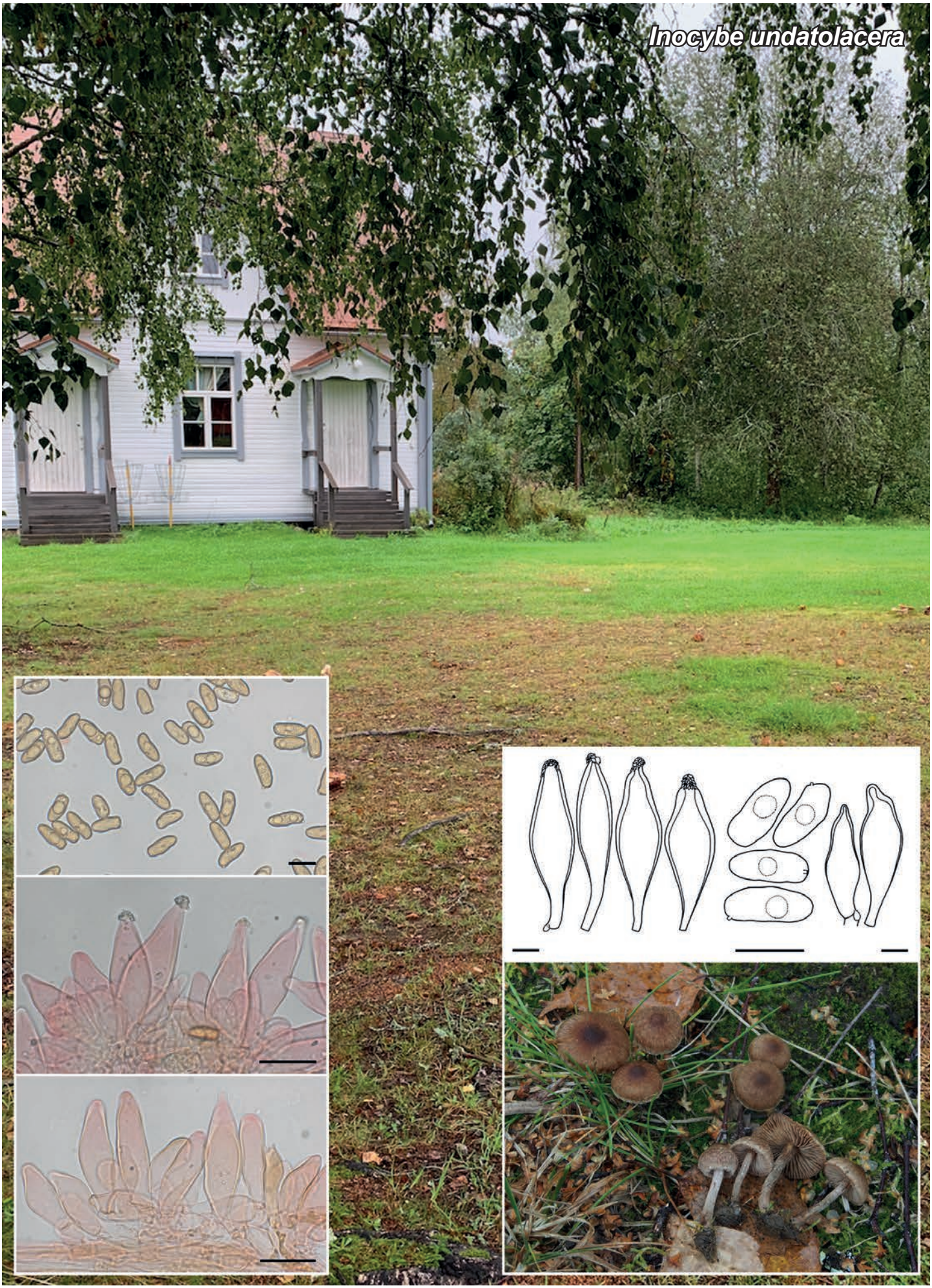
In the phylogenetic analysis, three mycorrhizal sequences deposited in GenBank appear close to *I. sabuligena* (KC965943, JX630575 and KF297130, ITS 97–97.5 % similarity in BLAST). The three come from Arctic Canada, found in *Dryas integrifolia* mats (Timling *et al*. 2012, Timling *et al.* 2014); similarly, two sequences in the GenBank nucleotide database, one from ectomycorrhizae of *Pinus ponderosa* in the Pacific Northwest, Oregon, USA and one from an observation in iNaturalist (García *et al*. 2016, and Frank https://www.inaturalist.org/observations/87790532), appear also close to *I. sabuligena* (GenBank KT800067 and OQ875892 respectively) with 95.5–96 % ITS similarity in BLAST. Both may represent two distinct species and differ manifestly in ecological and phytogeographic patterns.

Apart from its morphological and ecological features, it is very particular in *I. sabuligena* its spring fruiting season and the sub-hypogeous growth, with basidiomata rising from the sandy soil as they develop. In some collections certain specimens show a slight darkening of the context and surface of the stipe, and this brownish pigment is also evident in the contents of some hymenial elements, such as the cystidia.



Most likely tree of the Maximum Likelihood analysis of smooth-spored species of Inocybe inferred from the ITS and LSU regions generated by IQ-TREE web server (Trifinopoulos *et al.* 2016) using 1 000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS) ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.95 are shown on the branches and ordered as ML-BS/BPP. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. The tree was rooted to *Nothocybe distincta* (CAL 1310) and *Pseudosperma spurium* (SJ92017). The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site. The alignments were deposited in FigShare (doi: 10.6084/m9.figshare.25144571)

F. Pancorbo, Sociedad Micológica de Madrid, Real Jardín Botánico. C/ Claudio Moyano 1, 28014 Madrid, Spain; e-mail: fermin@socmicolmadrid.org
F. Esteve-Raventós, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: fernando.esteve@uah.es
A. Altés, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: alberto.altes@uah.es
G. Moreno, Universidad de Alcalá, Facultad de Ciencias, Departamento de Ciencias de la Vida (Botánica). 28805 Alcalá de Henares, Madrid, Spain; e-mail: gabriel.moreno@uah.es



Fungal Planet 1642 MycoBank MB 852594

Inocybe undatolacera Vauras & E. Larss., *sp. nov.*

Etymology: Refers to the angular and undulate outline of the spores and that it belongs in the *I. lacera* group.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 7–35 mm diam, as young hemispherical to campanulate, later becoming convex to expanded, mainly with low umbo, margin at first inflexed, soon deflexed, then straight, colour around centre mostly dark brown, blackish brown, red-brown, outwards brown to grey brown, at margin sometimes whitish grey or pale brown all over, velipellis not seen, subtomentose-smooth around centre, towards margin coarsely woolly-fibrillose to subsquamulose. *Cortina* pale greyish, rather abundant in young basidiomata. *Lamellae* moderately crowded, interspersed with lamellulae, up to 4 mm broad, often ventricose, narrowly adnate to adnate, first pale beige, later grey brown, edge fimbriate, pale. *Stipe* 13–40 × 1.5–4 mm, equal, base often widened, often curved, solid, first pale with a greyish to brownish tone and at the base brown, later brownish, red brown to blackish brown, at apex narrowly white-pruinose, downwards longitudinally strongly and often coarsely silvery-white-fibrillose. *Context* in pileus whitish, watery grey to pale brown, in stipe whitish, watery brown to dark brown. *Smell* rather faint, acidulous. *Basidiospores* (10.5–)11.1–*12.5*–14.2(–15.1) × (4.6–)4.8–*5.3*–5.9(–6.1) µm, Q = (1.85–)2.15–2.55(–2.75), Q mean = 2.37, n = 120, subboletoid, minimally angular, often truncate, often with conspicuous suprahilar depression, pale yellow brown. *Basidia* (20–)22–*25*–30(–31) × (8–)9–*10*–11 µm, n = 40, subclavate to clavate, mainly 4-spored. *Pleurocystidia* (44–)50–*59*–70(–78) × (10–)13–*17*–20(–23) µm, Q mean = 3.5, n = 140, mainly fusiform, some mucronate, mainly pedicellate, often crystalliferous at apex, crystals rather small and dense, thick-walled, wall to 2 µm thick, pale yellowish. *Cheilocystidia* (30–)37–*49*–56(–60) × (10–)13–*16*–20(–30) µm, n = 41, mainly fusiform but variable, some mucronate, mainly hyaline. *Paracystidia* (12–)14–*18*–22(–26) × 8–*10*–12(–13) µm, n = 30, oval, pyriform to clavate, rather scarce. *Caulocystidia* only at extreme apex of stipe, (30–)36–*46*–58(–62) × (10–)11–*14*–18(–20) µm, n = 60, mainly fusiform, *cauloparacystidia* (12–)14–*19*–24 × 7–*9*–10 µm, n = 26, scarce. *Clamp connections* frequent.

Ecology and distribution: The species occurs from the nemoral zone to subalpine forests, in the northern boreal zone often growing on sandy soil with *Betula* spp. on lawns and at roadsides, fruiting from mid-June to late September. Known from Finland, Sweden and Norway. Blast search of NCBIs GenBank and the UNITE database recovered no additional data.

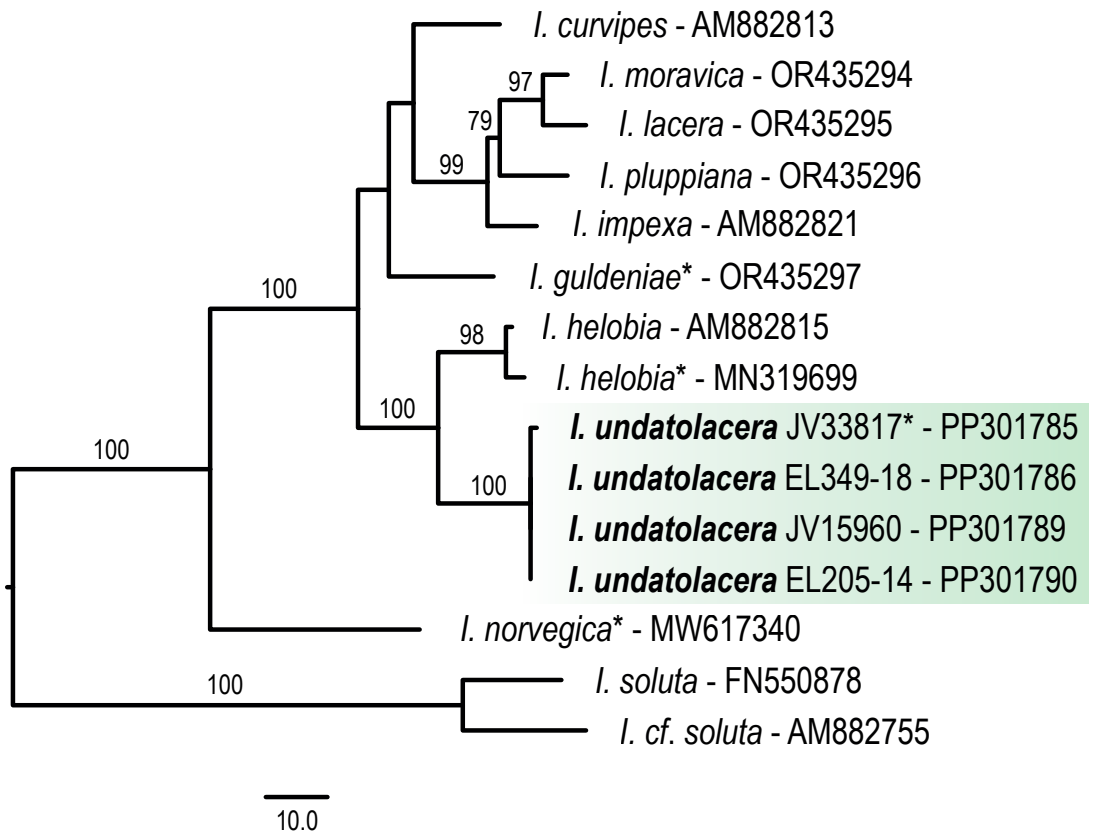
Colour illustrations: *Inocybe undatolacera* habitat from type locality in Ikaalinen, Finland, yard lawn with *Betula pendula*. *In situ* basidiomata of the holotype (TUR-A 216820); photos of pleuro-, caulo-, cheilocystidia and basidiospores; drawing of pleurocystidia (left), basidiospores, caulocystidia (right). Scale bars: spores and drawing = 10 µm; pleuro-, caulo- and cheilocystidia = 20 µm.

Typus: **Finland**, Satakunta, Ikaalinen, Karttu, Koivikko, WGS84: 61.7801, 23.0259, *ca*. 96 m a.s.l., worn lawn, near *Betula pendula*, together with *Inocybe moravica* and *I. humilis*, 5 Sep. 2023, *J. Vauras*, JV33817 (**holotype** TUR-A 216820, **isotype** GB-0207679; ITS-LSU sequence GenBank PP301785).

Additional materials examined: **Finland**, Etelä-Häme, Hämeenlinna, Hattelmala, lawn, near *Betula*, 19 Jun. 2014, *M. Lahti,* ML8/14, TUR-A 203074; Juupajoki, Hyytiälä Forestry Field Station, lawn, near *Betula*, 24 Aug. 2004, *J. Vauras*, JV21846 (TUR-A 171009); Jyväskylä, Korpilahti, Ristisuo, 22 Aug. 1988 *R. Storbacka* (TUR-A 171493); Tammela, Saloinen, margin of sandy road, *Pinus sylvestris*, *Picea abies*, *Betula*, *Salix*, 7 Jul. 2000, *J. Issakainen & J. Vauras*, JV15960 (TUR-A 175911); Etelä-Savo, Savitaipale, church village, church yard, lawn, *Betula*, *Picea abies*, *Quercus robur*, 20 Aug. 1987, *J. Vauras*, JV2805 (TUR-A 144279); Savonlinna, Punkaharju, Laukansaari, lawn, *Betula*, 21 Sep. 2004, *J. Vauras*, JV22379 (TUR 166180); Kittilän Lappi, Kolari, Lappea, sandy road bank, *Pinus sylvestris*, 11 Jul. 2000, *J. Vauras*, JV16018 (TUR-A 144253); Perä-Pohjanmaa, Tervola, Peura, Raemäki, *Betula pendula*, *Salix* spp., along roadside, 25 Aug. 2012, *E. Larsson*, EL145-12 (GB-0207678, TUR-A 216884; ITS-LSU sequence GenBank PP301787); Pohjois-Karjala, Nurmes, Raesärkät, old sand-pit area, margin of sandy road, *Pinus sylvestris*, *Betula*, *Alnus incana*, 25 Aug. 2023, *J. Vauras*, JV33809 (TUR-A 216821); Pohjois-Savo, Kuopio, Puijo, Antikkalanrinne, forest margin, *Alnus incana*, *Salix*, *Beula*, *Picea abies*, 12 Aug. 2011 *K. Kokkonen*, KK153/11 (TUR-A 195003); Siilinjärvi, Toivala, deciduous forest, 6 Aug. 1979, *J. Vauras*, JV465 (TUR-A 175397); Suonenjoki, Jauhomäki, sandy road margin, *Alnus incana*, *Betula*, *Salix*, *Picea abies*, 15 Aug. 2005, *J. Vauras*, JV23102 (TUR-A 171011); Uusimaa, Helsinki, Malmi cemetery, lawn, *Quercus robur*, 1 Sep. 1994, *I. Kytövuori*, IK94-126; H. Varsinais-Suomi, Koski Tl., Hongisto, yard of cottage, *Betula, Picea abies,* 18 Aug. 2007, *M.-L. & P. Heinonen*, PH243-2007 (TUR 191363); Parainen, Ersby, moist mixed forest, *Salix*, *Betula*, *Picea abies*, *Pinus sylvestris*, 18 Jul. 1986, *J. Vauras*, JV2070 (TUR-A 175393); Salo, Halikko, Piintilä, old sand-pit, *Picea abies*, *Pinus sylvestris*, *Betula*, *Salix*, 1 Jul. 2000, *M.-L. & P. Heinonen*, PH551-2000, (TUR 136994); Turku, Ruissalo, deciduous forest, 24 Jul. 1978, *J. Vauras*, JV334 (TUR-A 175466). **Norway**, Møre og Romsdal, Skolde, Reiakvam, *Picea abies*, 17 Aug. 2006, *P. Larsen*, PL-2006 (TUR-A 177116); Vestfold, Hof, Eidsfoss, road margin, ditch, 30 Aug. 2003, *J. Vauras*, JV20248 (TUR-A 151446). **Sweden**, Bohuslän, Håby. Lammö, *Quercus, Corylus*, *Tilia,* on calcareous soil, 29 Sep. 2014, *E. Larsson*, EL205-12 (GB-0207682; ITS-LSU sequence GenBank PP301790); Lycksele lappmark, Tärna, Hemavan, Atoklimpen, subalpine area, *Betula pubescens*, *Salix* spp., 27 Jul. 2014, *E. Larsson*, EL29-14 (GB-0207677, TUR-A 216885; ITS-LSU sequence GenBank PP301791); Västergötland, Stora Lundby, Gråbo grustäkt, *Betula pendula*, *Salix* spp., on gravely soil, 20 Sep. 2018, *E. Larsson*, EL157-16 (GB-0207676, TUR-A 216886; ITS-LSU sequence GenBank PP301786).

Notes: *Inocybe undatolacera* belongs in the *I. lacera* group that earlier was treated as a smooth-spored species (Kuyper 1986, Stangl 1989), but molecular phylogenetic analyses show that it is closely related with species in section Cortinatae (*e.g*. Ryberg *et al*. 2010). It is characterised by the rather small and slender basidiomata, mostly with rather dark pileus centre, and in micromorphology by the rather pale, long and minimally angular spores, fusiform pleurocystidia which are often mucronate and with small crystals tightly at apex. It is similar to *I. helobia*, that is also rather small and slender, but has broader and darker spores

and grows with *Salix* in moist localities. Also *I. lacera* has long and narrow spores but more regular. *Inocybe pluppiana* has minimally angular and shorter spores (av. Q = 2.1), on average shorter pleurocystidia, a pileus with darker centre and larger basidiomata (Bandini *et al.* 2020). Blast search of the ITS in NCBIs GenBank show 96.5 % similarity with *I. helobia*, that comes out as the sister species to *I. undatolacera.*



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. undatolacera* within the *I. lacera* group. Heuristic searches with 1 000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1 000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Inocybe undatolacera* is marked in **bold** and a green box, the holotype indicated with *.

J. Vauras, Biological Collections of Åbo Akademi University, Herbarium, Biodiversity Unit, FI-20014 University of Turku, Finland; e-mail: jukvau@utu.fi
E. Larsson, Biological and Environmental Sciences, University of Gothenburg, and Gothenburg Global Biodiversity Centre, Box 463, SE40530 Göteborg, Sweden; e-mail: ellen.larsson@bioenv.gu.se

Fungal Planet 1643 MycoBank MB 851852

Inosperma pavithrum K.P.D. Latha & P. Haridev, *sp. nov.*

Etymology: Name derived from the Sanskrit adjective *pavithr* (sacred), refers to the occurrence of the species in a traditional sacred grove.

Classification: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps small to medium-sized. *Pileus* 18–73 mm diam, paraboloid or hemispherical when young, becoming convex or plano-convex with a broad umbo at the centre surrounded by a shallow depression with age; surface deep orange (5A6; Kornerup & Wanscher 1978) at the centre, pale orange (5A3) elsewhere when young, becoming dark brown (6E5) on and around the umbo, greyish orange (6B3) elsewhere at maturity, appressed-fibrillose all over, radially rimose exposing paler tissue beneath towards the margin at maturity; margin incurved when young, becoming straight at maturity, rarely reflexed, wavy, occasionally fissile. *Lamellae* adnexed or narrowly adnate, crowded, initially white, becoming brownish orange (6C4) at maturity, up to 4 mm wide, with lamellulae in 2–3 tiers; edge entire to the naked eye, finely fimbriate under a lens, concolourous with the sides. *Stipe* 34–90 × 3–10 mm, central or slightly eccentric, terete or rarely compressed, initially equal, becoming equal or slightly tapering towards the apex at maturity, rarely flexuous, cartilaginous, stuffed; surface white to orange white (6A2) when young, becoming greyish orange (6B3) all over with age, appressed-fibrillose all over, pruinose towards the apex; base subbulbous to bulbous with a white mycelium. *Context* soft, up to 3 mm wide, orange grey (6B2). *Odour* and *taste* not distinctive. *Basidiospores* 9–11 × 6–8 (9.9 ± 0.7 × 6.6 ± 0.7) µm, Q = 1.3–1.8, Qm = 1.5, smooth, ellipsoid or ovoid in frontal view, amygdaliform or amygdaliform with an acute apex in side view, thick-walled, pale yellowish brown. *Basidia* 18–26 × 8–11 µm, cylindrical or clavate, thin-walled, hyaline or occasionally filled with pale yellowish contents and collapsed (necrobasidia), 2- or 4-spored; sterigmata up to 3 µm long. *Pleurocystidia* absent. *Lamella-edge* sterile with clusters of cheilocystidia. *Cheilocystidia* 25–39 × 11–20 µm, abundant, versiform: obovoid, clavate, broadly clavate or obpyriform, thin- to slightly thick-walled, hyaline or with amorphous contents all over, especially at the apex. *Lamellar trama* subregular; hyphae 6–22 µm wide, thin-walled, hyaline. *Pileipellis* a cutis; hyphae 5–16 µm wide, slightly thick-walled, with a yellowish brown wall pigment. *Pileus trama* subregular; hyphae 6–28 µm wide, thin-walled, hyaline or with a pale yellowish plasmatic pigment. *Stipitipellis* a cutis disrupted by caulocystidia confined to the stipe apex; hyphae 5–15 µm wide, thin- to slightly thick-walled, with a pale yellowish brown wall pigment. *Caulocystidia* 25–85 × 9–15 µm, scarce, cylindrical or clavate, occasionally septate, thin- to slightly thick-walled, hyaline. *Oleiferous hyphae* present in all trama. *Clamp connections* observed on all hyphae.

Colour illustrations: Iringol Kavu sacred grove, the type locality in Kerala State, India. Basidiocarps; basidiocarp showing lamellae; basidiospores; basidium; cheilocystidia; pileipellis; stipitipellis; caulocystidium. Scale bars: basidiocarps = 10 mm; basidiospores, basidium, cheilocystidia, caulocystidium = 10 µm, pileipellis = 40 µm; stipitipellis = 20 µm.

Habit, habitat and distribution: On the ground, near *Hopea ponga* (*Dipterocarpaceae*) trees, gregarious, often as large, discrete clusters. Known only from the type locality in Kerala State, India.

Typus: **India**, Kerala State, Ernakulam District, Perumbavoor, Iringol Kavu sacred grove, 10°06'30.9"N, 76°30'01.3"E, 31 Aug. 2022, *P. Haridev* [**holotype** DKP-SERB65 (CALI); ITS, LSU, and *rpb2* sequences GenBank PP350421, PP192110, and PP209642].

Notes: Small to medium-sized basidiocarps, a brown-tinted, fibrillose-rimose pileus with a straight or reflexed margin; adnexed, brownish orange lamellae; a fibrillose stipe with a pruinose apex; smooth basidiospores; a sterile lamella-edge; versiform cheilocystidia with yellowish amorphous contents; a cutis-type pileipellis and a cutis-type stipitipellis with caulocystidia restricted to the stipe apex are the characteristic features of *Inosperma pavithrum*.

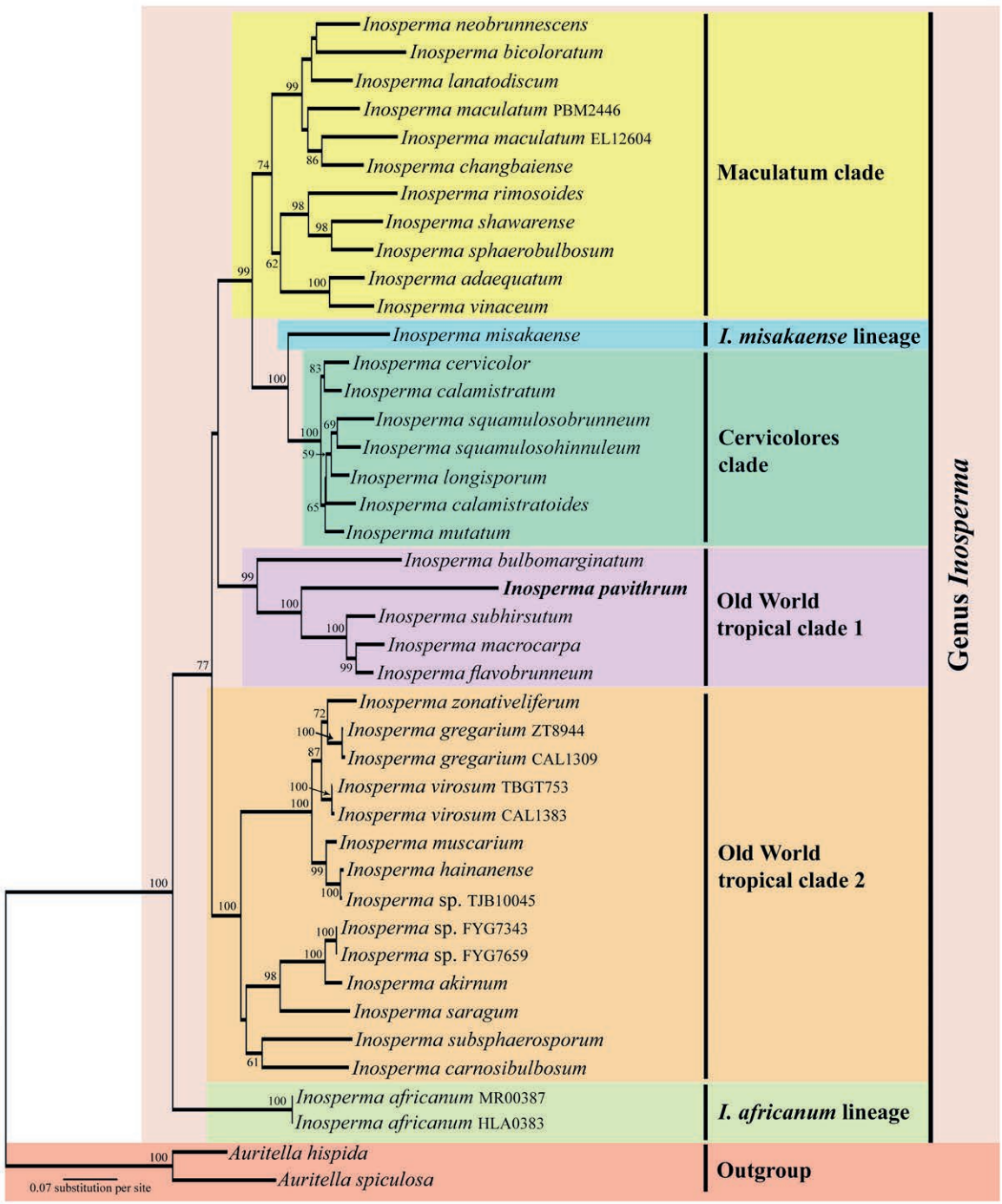
Inosperma akirnum, a species originally described as *Inocybe akirna* from Kerala, India (Latha & Manimohan 2017), seems to be close to *I. pavithrum* in having somewhat similar colour of the basidiocarps, a fibrillose-rimose pileus with a fissile margin, similar-coloured lamellae with a fimbriate edge, an appressed-fibrillose stipe and cutis-type pilei- and stipitipellis. However, *I. akirnum* has slightly smaller basidiocarps (pileus 22–55 mm; stipe 29–66 × 4–6 mm), somewhat smaller basidiospores (7–8.5 × 5–5.5 µm), the absence of necrobasidia, a heterogeneous lamella-edge, larger cheilocystidia (19–65 × 6–8 µm) and a stipitipellis devoid of caulocystidia.

Inosperma flavobrunneum, a species described from Benin (Africa) (Aïgnon *et al.* 2021), is similar to *I. pavithrum* in having a fibrillose stipe with a pruinose apex and a slightly swollen to almost bulbous base, similar size (9.2–11.2 × 5.7–7 µm) and shape of basidiospores, similar-sized (23–41 × 7–10 µm) cheilocystidia and cutis-type pilei- and stipitipellis. However, *I. flavobrunneum* differs from *I. pavithrum* in having smaller basidiocarps (pileus 8.5–15 mm; stipe 15–23 × 0.5–1 mm), vinaceous, emarginate-decurrent lamellae, slightly larger basidia (24–40 × 6–14 µm) and smaller caulocystidia (22–63 × 8–13 µm).

Inosperma macrocarpa, an African species (Aïgnon *et al*. 2023), resembles *I. pavithrum* in having a plano-convex to convex pileus with a fibrillose surface, adnexed lamellae with a comparable colour, a fibrillose stipe with a slightly bulbous base, similar size (8–10.5 × 5–6.6 µm) and shape of basidiospores, similar-sized (26–35 × 6–15 µm) cheilocystidia, a cutis-type pileipellis and a cutis-type stipitipellis with caulocystidia confined to the stipe apex. However, *I. macrocarpa* can be distinguished from *I. pavithrum* by its yellowish-white pileus, odour and taste reminiscent of almonds and smaller (15– 33 × 6–11 µm), utriform caulocystidia.

The distinct status of the ITS (626 bp), the LSU (694 bp) and the *rpb2* (658 bp) sequences generated from *I. pavithrum* was confirmed in BLASTn searches. No close hits with zero e-values were obtained using the ITS sequence. The closest hit using the LSU sequence was *I. flavobrunneum* (GenBank MN097891) with 95 % identity. *Inosperma macrocarpa* (GenBank OQ435245) resulted as the closest hit using the *rpb2* sequence with 93 % identity. The Maximum Likelihood (ML) phylogram constructed based on the combined data matrix of ITS, LSU, and *rpb2*

sequences revealed a clade representing the genus *Inosperma* with maximum bootstrap support (100 % BS). Within this clade, *I. pavithrum* clustered with *I. subhirsutum*, *I. macrocarpa* and *I. flavobrunneum* in the Old-World tropical clade 1. Remarkably, *I. pavithrum* formed a lineage distinct from the above three species with full bootstrap support (100 % BS).



A Maximum Likelihood (ML) phylogram was constructed for *I. pavithrum* based on the combined data matrix of ITS, LSU and *rpb2* sequences. Individual data matrices of ITS, LSU and *rpb2* were prepared and aligned using the MAFFT web tool (https://mafft.cbrc.jp/alignment/server/) with default settings. Manual tweaking was done with the help of AliView v. 1.23 (Larsson 2014). Manually aligned data matrices were concatenated using SeaView v. 4.7 (Gouy *et al.* 2010). The concatenated data matrix was partitioned into five sections: (1) ITS, (2) LSU, (3) *rpb2* first codon positions, (4) *rpb2* second codon positions, (5) *rpb2* third codon positions. The final data matrix comprised 2 640 nucleotide positions of 42 sequences including the outgroups (*Auritella hispida* and *A. spiculosa*). The phylogenetic analysis was executed in RAxML-HPC2 (v. 8.2.10) (Stamatakis 2014) with GTRGAMMA nucleotide substitution model and 1 000 rapid ML bootstrap (BS) replicates following the recommendations in the user manual. The analysis was performed on the XSEDE platform, implemented in the CIPRES Science Gateway web server (Miller *et al.* 2010). ML bootstrap values ≥ 50 % are indicated at the nodes. All the clades/lineages recovered in the larger clade Inosperma were colour-coded and the newly described species is designated in bold within the Old-World tropical clade 1. The alignment and tree are publicly accessible in FigShare (doi: 10.6084/m9.figshare.25256992).

K.P.D. Latha, P. Haridev & P. Manimohan, Department of Botany, University of Calicut, Kerala, 673 635, India; e-mail: deepnocybe@gmail.com, haridev95444@gmail.com & pmanimohan@gmail.com

Fungal Planet 1644 MycoBank MB 852432

Laurobasidium azarandamiae L. Kiss, Vaghefi, R.G. Shivas & Y.P. Tan, *sp. nov.*

Etymology: Named after Azar Andami (1926–1984), a physician and bacteriologist noted for her contributions to the development of the cholera vaccine.

Classification: *Laurobasidiaceae*, *Exobasidiales*, *Exobasidiomycetes.*

Hyphae thin, 1–1.5 µm wide, septate, hyaline. *Conidiophores* reduced to hyphae, abundant, cylindrical, straight to flexuous, terminal, with one or two sterigmata 1–5 µm long. *Conidia* narrowly cylindrical to fusiform, straight, sometimes slightly curved or flexuous, 6–20 × 1–2.5 µm, aseptate, hyaline, rounded at apex and narrowly tapered at base, sometimes refractive at base, smooth, thin-walled, germinating to form hyphae or secondary conidia.

Culture characteristics: Colonies on potato dextrose agar (PDA) and MYPGA (malt 0.3 %, yeast 0.3 %, peptone 0.5 %, glucose 1 %, agar 1.5 %) after 14 d at 25 °C, matt white, flat, sometimes folded in the central part, circular, 5–15 mm diam, with a clear hyphal margin 1–2 mm wide; reverse pale buff (PDA) or buff tinged with salmon (MYPGA); on PDA after 10 wk at 25 °C, pale rosy buff with a white margin 2–4 mm wide, flat, folded, 15–35 mm diam, reverse salmon, paler towards the margin.

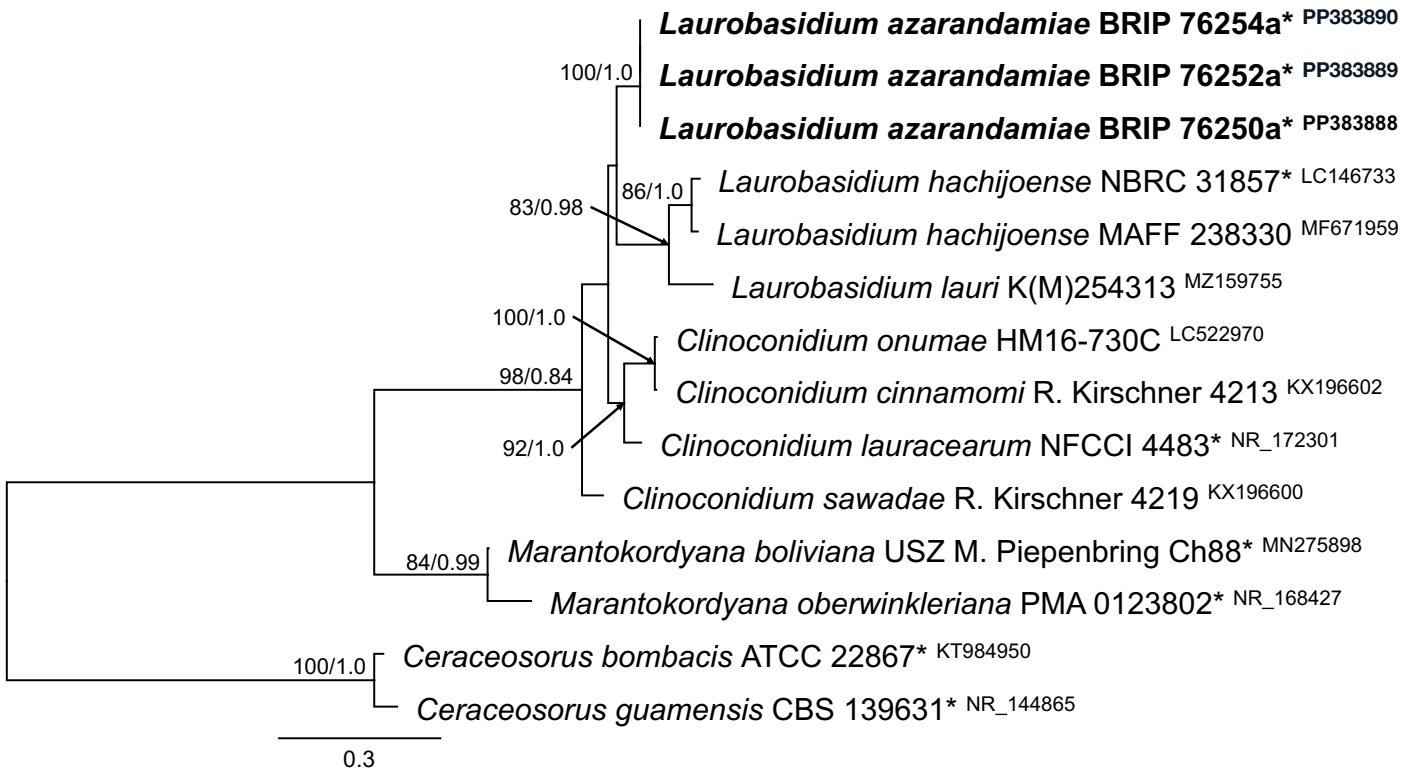
Typus: **Australia**, Victoria, Mornington Peninsula, from uredinium of *Puccinia alyxiae* on *Alyxia buxifolia* (*Apocynaceae*), 16 Sep. 2023, *N. Vaghefi & L. Kiss* (**holotype** preserved as a metabolically inactive culture BRIP 76250a; culture ex-type BRIP 76250a; ITS sequence GenBank PP383888).

Additional materials examined: **Australia**, Victoria, Mornington Peninsula, from uredinium of *Puccinia alyxiae* on *Alyxia buxifolia* (*Apocynaceae*), 16 Sep. 2023, *N. Vaghefi & L. Kiss* (culture BRIP 76252a; ITS sequence GenBank PP383889); *ibid*., from uredinium of *Puccinia alyxiae* on *Alyxia buxifolia* (*Apocynaceae*), 16 Sep. 2023, *N. Vaghefi & L. Kiss* (culture BRIP 76254a; ITS sequence GenBank PP383890).

Notes: *Laurobasidium azarandamiae* has colony characteristics, and conidial morphology on PDA similar to those given for a culture of *L. hachijoense* reported from Japan on *Cinnamomum pseudopedunculatum* (Shibata *et al.* 2021). *Laurobasidium hachijoense* was earlier proposed to accommodate *Exobasidium hachijoense* based on molecular, morphological, and biological data (Kakishima *et al.* 2017).

Based on a blastn search of the NCBI GenBank nucleotide database, the closest relevant hits with the ITS region are *Clinoconidium onumae* [strain HM16-730C; GenBank LC522970; Identities 349/386 (90 %), 12 gaps (3 %)], *C. sawadae* [voucher R. Kirschner 4219; GenBank KX196600; Identities 352/379 (93 %), 10 gaps (2 %)], and *L. hachijoense* [strain HM16-731C; GenBank LC521923; Identities 353/396 (89 %), 13 gaps (3 %)].

Colour illustrations: Alyxia buxifolia in the Mornington Peninsula, Victoria, Australia. *Laurobasidium azarandamiae* colony on PDA after 10 wk (upper surface and reverse); conidiophores and conidia; conidia, germinating conidia, conidium with sterigmata (top left corner). Scale bars: cultures = 1 cm; microscopic features = 10 µm.



Phylogenetic tree of selected *Cryptobasidiaceae* species based on maximum likelihood analysis of the ITS region. Analyses were performed on the Geneious Prime 2023 platform using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Huselsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Ceraceosorus bombacis* (ex-type strain ATCC 22867) and *C. guamensis* (ex-type strain CBS 139631) were used as the outgroup. GenBank accession numbers are indicated (superscript ITS). Novel taxon is indicated in **bold**. Ex-type strains indicated with asterisks (*). The alignment and phylogeny are publicly available as doi: 10.5281/zenodo.10703350.

L. Kiss, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: levente.kiss@unisq.edu.au
Y.P. Tan, Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park 4102, Queensland, Australia; e-mail: yupei.tan@daf.qld.gov.au
N. Vaghefi, School of Agriculture, Food and Ecosystem Science, University of Melbourne, Parkville 3010 Victoria, Australia; e-mail: vaghefin@unimelb.edu.au
R.G. Shivas, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: roger.shivas@unisq.edu.au

Fungal Planet 1645 MycoBank MB 852643

Lecanora thorstenii Śliwa, Flakus & Mazur, *sp. nov.*

Etymology: The newly discovered taxon is named in honour of Thorsten Lumbsch (Chicago, USA) in recognition of his significant contributions to lichenology, especially to the knowledge of the taxonomy of *Lecanora.*

Classification: *Lecanoromycetes*, *Lecanorales*, *Lecanoraceae.*

Thallus crustose, chalky white, conspicuous, thick, rimose, irregular in the outline, and epruinose; surface verruculose, without vegetative propagules; *prothallus* present, white, with filamentous structure; *photobiont* green, *Trebouxia*, abundant, photobiont layer 80–90 µm thick, continuous but uneven in some parts; *apothecia* abundant, scattered to loosely aggregated, sessile, 0.6–2.7 mm diam, circular, or partly angular, flexuose and pruinose, discs concave, white; *apothecium margin* concolourous with thallus, continuous, prominent; *amphithecium* 145–160 µm thick, without crystals; *amphithecial cortex* amorphous, well delimited, measure 105–110 µm thick; *parathecium* indistinct; *epihymenium* brown-olive (HCl–, K–, N+) with small crystals soluble in K, insoluble in N; *hymenium* hyaline, 100–110 µm high; *hypothecium* hyaline, 54–70 µm high; *subhymenium* indistinct; *paraphyses* simple to sparce branched, unthickened at the top; apical and basal parts measure 2.5 µm diam; *asci Lecanora*-type, oblong with 8 spores; *spores* simple, hyaline, broadly ellipsoid, 9.1–(9.7 ± 1.0)–10.9 length (L) × 5.2–(5.7 ± 0.5)–6.0 µm width (W), and spores ratio L/W = 1.7 µm (N = 40); *pycnidia* not seen. TLC (A and C solvents) revealed two chemotypes: i) atranorin, roccellic acid, rangiformic acid and protocetraric acid (*Rodriguez-Flakus* 3685, *Flakus* 28308), ii) atranorin, rangiformic acid and protocetraric acid (*Flakus* 26718).

Habit, habitat and distribution: *Lecanora thorstenii* grows on bark, in savannas with shrubs, trees also in disturbed areas.

Typus: **Bolivia**, La Paz department, Franz Tamayo province, between Apollo and Mapiri, 14°40’31”S, 68°25’05”W, 1 509 m a.s.l., on bark, savanna with shrubs and some trees, on bark of tree, 18 Nov. 2016, *Rozdriguez-Flakus* 3685 (**holotype** KRAM L 74771; **isotype** LPB; mycobiont ITS and mtSSU sequences GenBank PP447908 and PP447915).

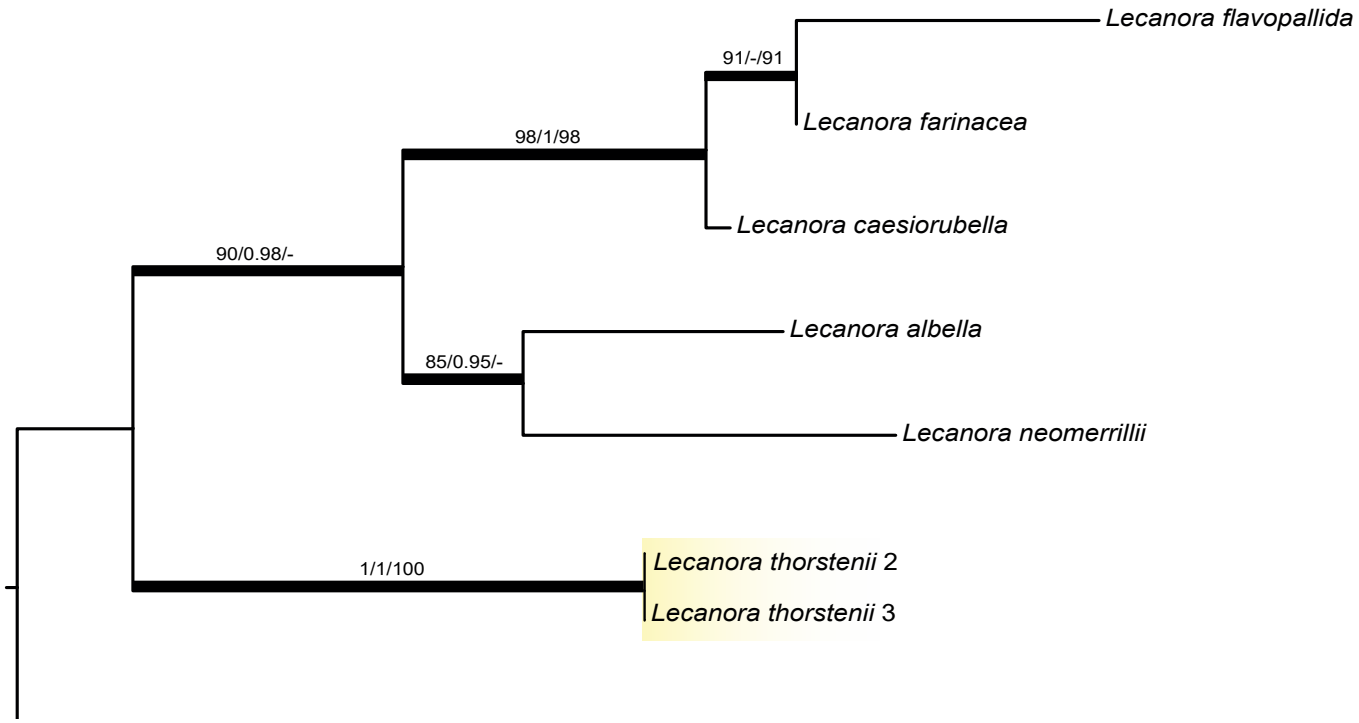
Colour illustrations: Bolivia, La Paz department, Franz Tamayo province, between Apollo and Mapiri, savanna with shrubs and some trees (locus classicus) (photo credit A. Flakus). Habitat of the new species (Rodriguez-Flakus 3685); cross-section of apothecium in polarised light (Rodriguez-Flakus 3685). Scale bars: thallus = 1 mm; apothecium = 100 µm.

Additional materials examined: **Bolivia**, La Paz department, Franz Tamay province, between Apollo and Mapiri, 14°40’31”S, 68°25’05”W, 1 509 m a.s.l., 18 Nov. 2016, *Flakus* 28308 (KRAM L 74772, LPB; mycobiont ITS and mtSSU sequences GenBank PP447909 and PP447914); Chuquisaca department, Luis Calvo province, Parque Nacional y Área Natural de Manejo Integrado Serranía del Iñao, close to Ticucha, between Tranqua and Monte Agudo, 19°39’50”S, 63°49’14”W, 1 022 m a.s.l., 18 Jul. 2015. *Flakus* 26718 (KRAM L 74773, LPB; LSU sequence GenBank PP447910).

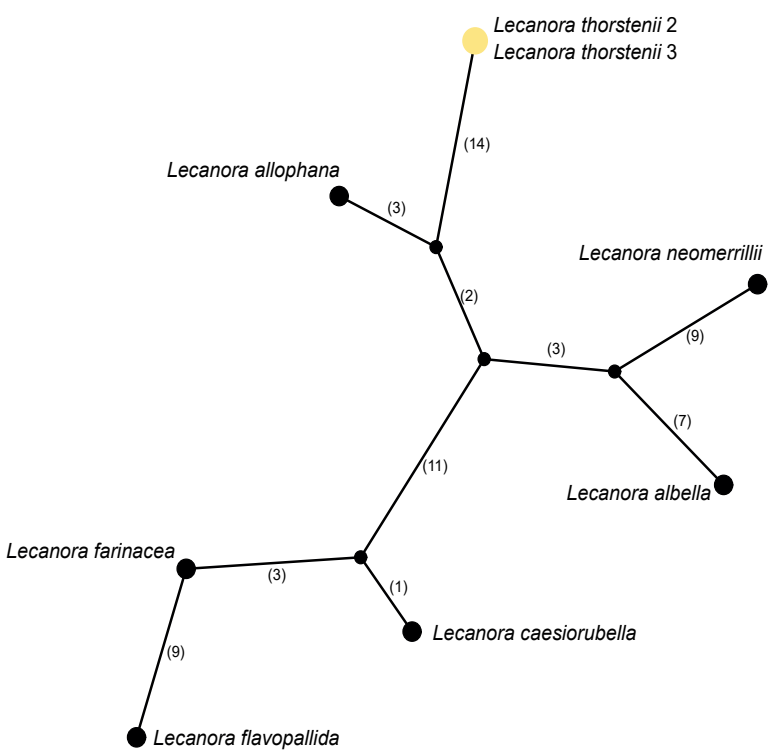
Notes: *Lecanora* (Acharius 1810) is the most speciose (including *ca*. 550 species) and widely distributed genus of lichen-forming fungi that belongs to the family *Lecanoraceae*. The genus consists of species that have lecanorine apothecia, crustose, and rarely lobate thallus containing green-algal photobionts of the genus *Trebouxia*. Its main characteristic features are hyaline, aseptate ascospores, and *Lecanora*-type asci (Lumbsch & Elix 2004). The exploration of crustose lichens in the tropics, particularly within the challenging genera like *Lecanora*, remains limited. Bolivia is known for its remarkable biodiversity, however, the number of recorded *Lecanora* species with 27 species reported, remains relatively low. The new species, *L. thorstenii* is a typical member of *Lecanora s. str*. Its distinguishing features are the colour of the thallus – chalky white, large apothecia and small spore size, and composition of secondary metabolites. It is corticolous and characterized by its geographical distribution and ecology. Concerning morphological similarities the species can be mainly confused with *L. albella*, *L. caesiorubella,* and *L. neomerrillii* (dos Santos *et al.* 2023). However, *L. thorstenii* can be distinguished by having a thicker amphithecial cortex and considerably smaller ascospores. Another characteristics feature of *L. thorstenii* is the presence of fatty acids, such as: roccellic acid which is not produced by similar *L. albella* and *L. caesiorubella*, and rangiformic acid distinguishing the new species from *L. neomerrillii*.

In the conducted phylogenetic analyses, *Lecanora thorstenii* is nested in the clade representing the *Lecanora albella* group incorporating the species: *L. albella*, *L. caesiorubella*, *L. farinacea,* and *L. flavopallida*. The phylogenetic position and species delimitation of *L. thorstenii* were confirmed on a broad phylogeny based on six loci, a phylogeny focusing on the *L. albella* group, based on ITS, and a network of haplotypes created from the nucleotide alignment. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the **mtSSU** sequence are *L. caesiorubella* [Flakus 29191, GenBank OL604127, Identities = 97 %, nine gaps (0 %)], *L. caesiorubella* [Flakus 27860, GenBank OL604081, Identities = 96 %, nine gaps (0 %)]; *Lecanora* sp. [Flakus 29594, GenBank OL604110, Identities = 94 %, 27 gaps (2 %)]. The closest hits using **ITS** sequence had the highest similarity to *Lecanoromycetes* sp. [ARIZ:NC1606, GenBank JQ761969, Identities = 86 %, 42 gaps (3 %)], *Lecanoromycetes* sp. [ARIZ:NC1605, GenBank JQ761970, Identities = 86 %, 42 gaps (3 %)], and *Lecanora subcavicola* [FR-0265493, GenBank MW257117, Identities = 85 %, 52 gaps (4 %)].

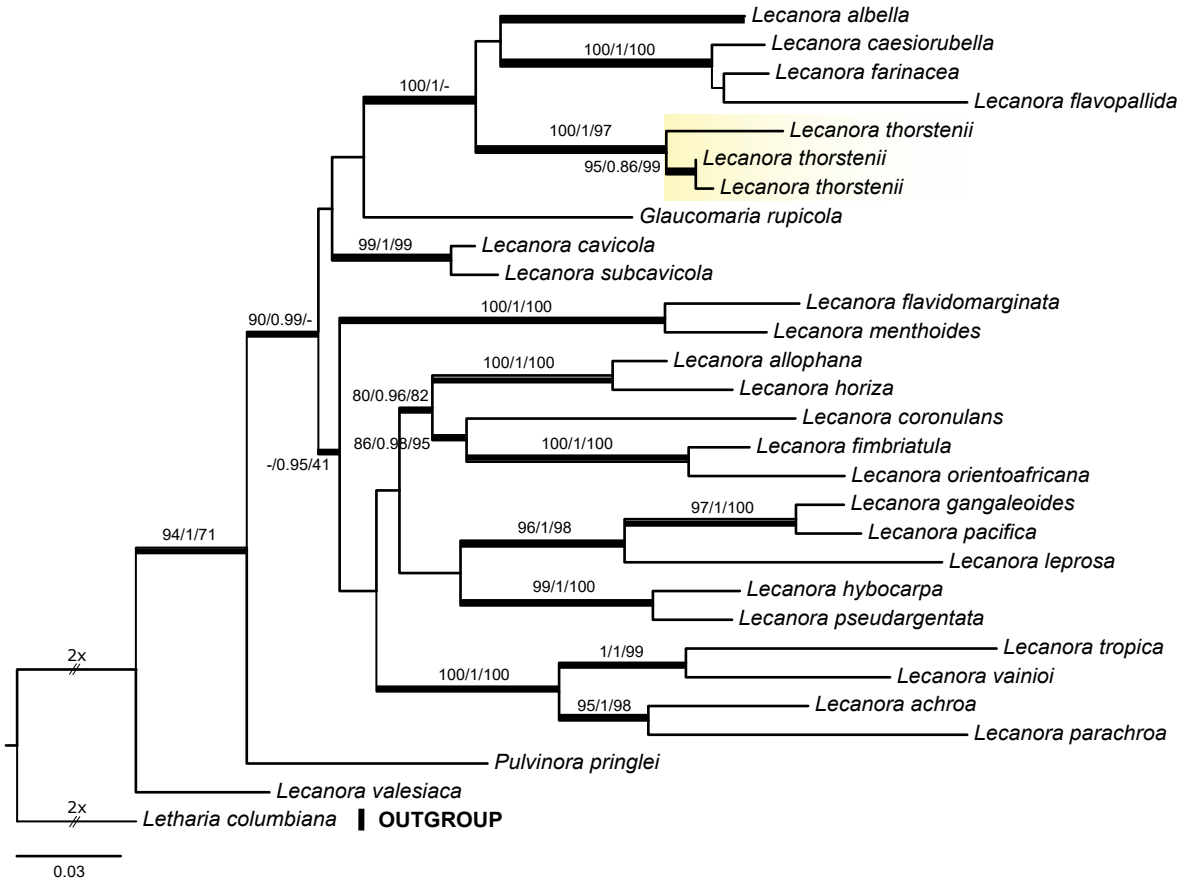
Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).



The relationships within *Lecanora albella* group were determined by analysing ITS. A maximum likelihood phylogenetic analysis using IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015, Chernomor *et al.* 2016) was executed on the CIVIB server (Trifinopoulos *et al.* 2016) to assess for any inconsistencies. The alignment was input for the SH aLRT test, aBayes and ultrafast bootstrap analysis. Bolded branches received the support of > 80 % of SH aLRT test, > 0.95 of aBayes analyses and bootstrap ≥ 95 % of UFBoot2 support. Phylogenetic reconstructions were based on 5 000 ultrafast bootstrap replicates to estimate branch support among all loci. A total of eight sequences were used in the dataset, two of them newly generated. Names correspond to those presented on phylogenetic tree. Clade representing new species is highlighted in yellow. The selected model for ITS partition is TIM2e+I. The alignment with the phylogenetic tree was deposited at figshare.com (doi: 10.6084/m9.figshare.25420876). All accession numbers of the sequences used in the alignment are provided in a supplementary file.



The present haplotype network was performed using PopART software with the TCS network option (Clement *et al*. 2002). Graph is showing the relationships between the ITS sequences of representatives from the *Lecanora albella* group. Names correspond to those presented on phylogenetic trees. Newly generated sequences are highlighted in **bold**. The mutational changes are depicted as numerical values in brackets near the lines connecting different haplotypes. The presented information aims to provide a comprehensive understanding of the genetic relationships between species.



The phylogenetic relationships of lecanoroid lichens were determined by analysing a combined dataset of six genetic loci (mtSSU, ITS, LSU, *rpb1*, *rpb2*, *mcm7*). Each locus alignment was employed as the input for a maximum likelihood phylogenetic analysis using IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015, Chernomor *et al.* 2016) executed on the CIVIB server (Trifinopoulos *et al*. 2016) to assess for any inconsistencies. The alignment was input for the SH aLRT test, aBayes and ultrafast bootstrap analysis. Bolded branches received the support of > 80 % of SH aLRT test, > 0.95 of aBayes analyses and bootstrap ≥ 95 % of UFBoot2 support. Phylogenetic reconstructions were based on 5 000 ultrafast bootstrap replicates to estimate branch support among all loci. A total of 97 sequences were used in the dataset including sequences representing various groups of lecanoroid lichens, a fourth of them newly generated. Clade representing new species is highlighted in yellow. The selected models for each partition of the analysis were as follows: HKY+F+I+G4 for mtSSU, TNe+G4 for ITS, TIM+F+I+G4 for LSU, TIM2e+G4 for *rpb1* and TNe+G4 *rpb2* and HKY+F+G4 for *mcm7*. The alignment with the phylogenetic tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25420876). All accession numbers of the sequences used in the alignment are provided in a supplementary file.

L. Śliwa, A. Flakus & E. Mazur, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland;
e-mail: l.sliwa@botany.pl, a.flakus@botany.pl & e.mazur@botany.pl

Fungal Planet 1646 MycoBank MB 852228

Leptosporella cassiae N.I. de Silva & S. Lumyong, *sp. nov.*

Etymology: Name refers to the host genus *Cassia* from which it was isolated.

Classification: *Leptosporellaceae*, *Chaetosphaeriales*, *Sordariomycetes*.

Ascomata solitary, aggregated, semi-immersed, subglobose, black, 200–300 µm diam, with central ostiole; wall of 5–7 layers of brown *textura angularis. Paraphyses* hyphae-like, hyaline, smooth, septate, unbranched, 2–3 µm diam. *Asci* unitunicate, 8-spored, cylindrical, with a short pedicel, subapical ring, 70–90 × 7–10 µm. *Ascospores* fasciculate, spiral, filiform, straight or curved, hyaline, aseptate, ends rounded, guttulate, smooth-walled, 55–70 × 2–3 µm.

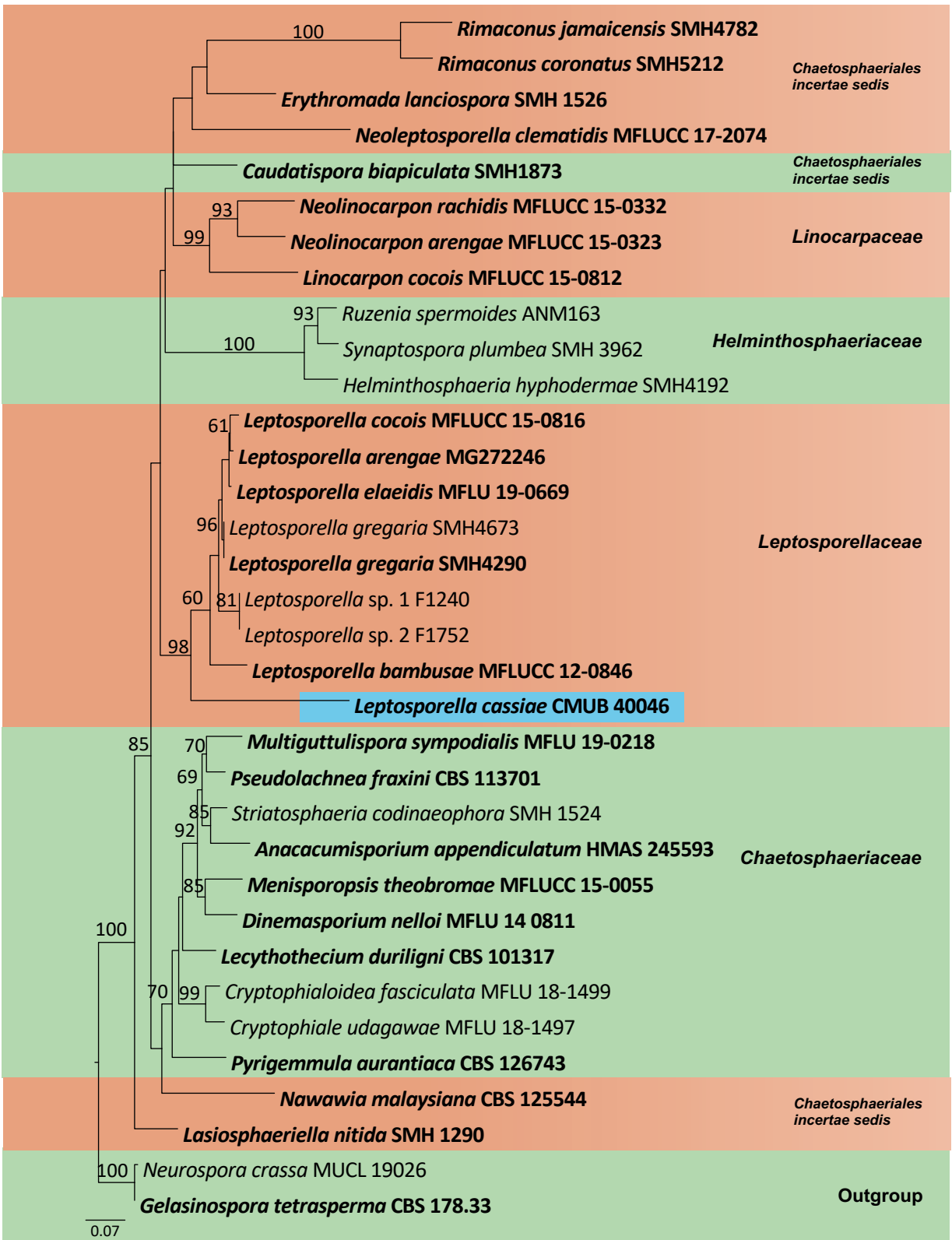
Typus: **Thailand**, Chiang Mai Province, on dead twigs of *Cassia fistula* (*Fabaceae*), 20 Aug. 2022, *N. I De Silva*, NID17 (**holotype** CMUB 40046; ITS sequence GenBank PP327424).

Notes: *Leptosporella* was established based on *L. gregaria* (Penzig & Saccardo 1897). This genus was placed in *Leptosporellaceae* (*Chaetosphaeriales*) based on morphology and phylogeny of combined ITS and LSU data (Konta *et al*. 2017). *Leptosporella* is characterised by solitary, superficial, black, subglobose, ostiolate ascomata, brown to black *textura angularis* cells of wall, hyaline, hypha-like, septate, paraphyses, 8-spored, unitunicate, cylindrical asci, fasciculate, filiform, straight or curved, hyaline or pale yellowish in mass, aseptate ascospores with or without polar mucilaginous appendages (Konta *et al*. 2017). *Leptosporella cassiae* clusters with *Leptosporella* species and formed a distinct lineage in the phylogenetic analysis. *Leptosporella cassiae* has an overlapping range of ascospore dimensions with *L. gregaria* (55–70 × 2.5–3 µm) (Konta *et al.* 2017). However, *Leptosporella cassiae* has guttulate aseptate ascospores, while *L. gregaria* has 7-septate ascospores (Konta *et al.* 2017). *Leptosporella cassiae* differ from *L. bambusae* in having smaller ascomata, asci and ascospores (*L. bambusae*: ascomata 500–850 µm diam; asci 100–195.5 × 9–13.5 µm; ascospores 130–175 × 2–3 µm; Dai *et al.* 2016). Nevertheless, *Leptosporella cocois* (99–156 × 2.5–4 µm) (Konta *et al.* 2017), *L. arengae* (108–132 × 2–3.5) (Konta *et al.* 2017), and *L. elaeidis* (124–136 × 2–4 µm) (Hongsanan *et al.* 2020) have larger ascospores than *Leptosporella cassiae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neoleptosporella camporesiana* [isolate Tak33, GenBank ON166827.1; Identities = 542/559 (97 %), four gaps (0 %)], *Neoleptosporella camporesiana* [strain RHP 132, GenBank MN699136.1; Identities = 484/509 (95 %), four gaps (0 %)], and *Neoleptosporella yunnanensis* [as *Neoleptosporella* sp. CFL-2021a; isolate KUMCC 21-0014, GenBank OL352056.1; Identities = 497/527 (94 %), 13 gaps (2 %)].

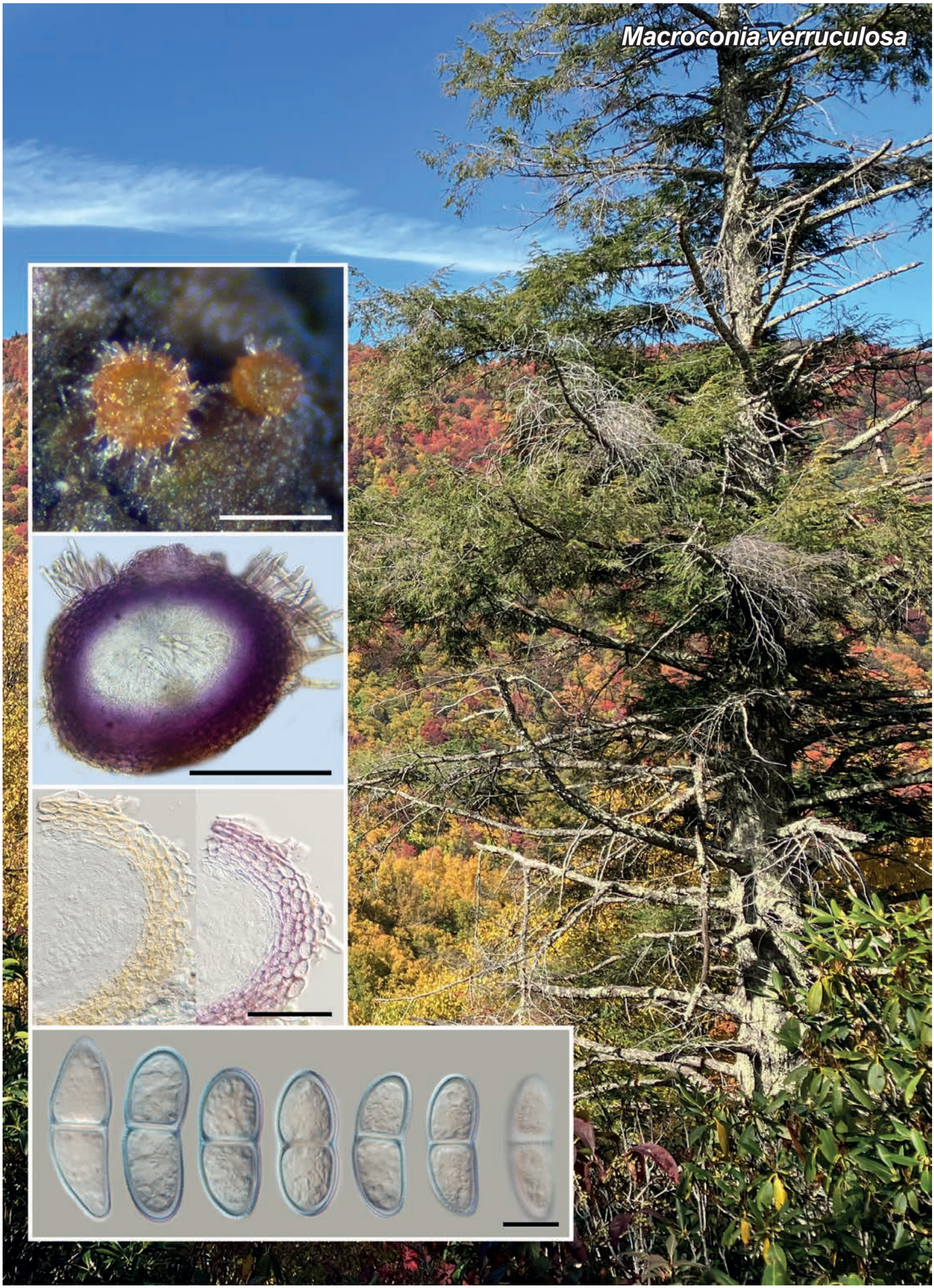
Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Collection place at Chiang Mai, Thailand from which *Leptosporella cassiae* was collected. Appearance of ascomata on host surface; section through ascoma; asci; ascospores. Scale bars: ascoma and section = 100 µm; asci and ascospores = 20 µm.



Phylogenetic analysis of *Leptosporella cassiae sp. nov*. inferred from a maximum likelihood (ML) analysis of ITS/LSU sequences. The analysis was performed with RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 1 000 bootstrap replicates. Bootstrap support values for ML greater than 60 % are indicated at the nodes. The tree is rooted with *Gelasinospora tetrasperma* (CBS 178.33) and *Neurospora crassa* (MUCL 19026). Ex-type strains are in **bold**. The novel species is indicated in a blue box. Scale bar on the tree indicates the expected number of changes per site. The matrix and the resulting tree have been deposited at TreeBASE (study ID: S31159).

N.I. De Silva & S. Lumyong, Faculty of Science, Department of Biology, Chiang Mai University, 50200, Chiang Mai, Thailand;
e-mail: nimaliindeewari_d@cmu.ac.th & scboi009@gmail.com



Fungal Planet 1647 MycoBank MB 852640

Macroconia verruculosa Darmostuk & P.A.Scott, *sp. nov.*

Etymology: Named after the verruculose surface of ascospores.

Classification: *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

Ascomata perithecioid, sessile, scattered, reddish-orange, subglobose, cupulate when dry, with a central ostiole, (180–)220–260(–270) µm diam (n = 15), covered by hyaline, thick-walled 2–3-septate setae with sometimes tapering apex; setae (52.2–)68.6–74.8(–120.4) × (6.2–)6.4–7.4(–8.2) µm (n = 20). Ascomatal wall 25–30 µm thick, with yellow pigment turning to violet in KOH, *textura angularis* in surface view, composed of two regions; outer region 20–25 µm thick, of thin-walled, angular to somewhat elongate cells, 9.5–15 × 2–2.5 µm; inner region 3–5 µm thick, of thin-walled, very narrow cells. *Asci* subcylindrical to clavate, with simple apex, (65–)75–85(–90) × (15.2–)16.0–17.5(–18.0) µm (n = 10), 8-spored. *Ascospores* uniseriate to biseriate in ascus, ellipsoid, verruculose, without perisporium, straight to slightly curved, hyaline, with round to slightly pointed ends, 1-septate, usually slightly constricted at the septum, (19.0–)25.0–29.2(–33.2) × (8.0–)9.2–10.8(–11.8) µm (n = 30). *Asexual morph* not observed.

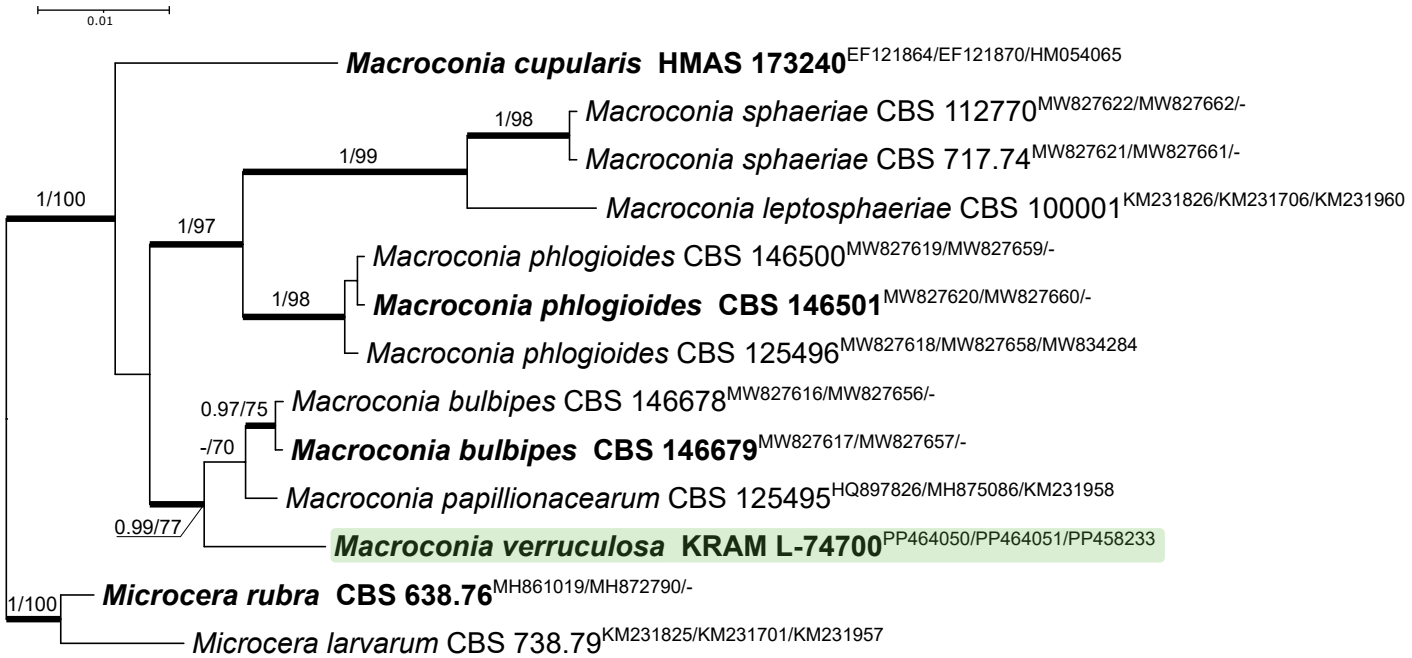
Habit, habitat and distribution: *Macroconia verruculosa* is known from the type locality in the Great Smoky Mountains National Park, where it grew on twigs of *Ilex montana* and is associated with black destroyed ascomycetous fungi and also overgrow the thallus of *Biatora* sp.

Typus: **USA**, North Carolina, Swain Co. Great Smoky Mountains National Park, Mount Sequoyah, 35.6746°N, 83.2868°W, 1 810 m a.s.l., open *Abies* forest, on twig of *Ilex montana*, associated with black destroyed ascomycetous fungus and *Biatora* sp. (*Ramalinaceae*), 5 Oct. 2022, *P. Scott 8401 & J. Hollinger* (**holotype** KRAM L-74700, **isotype** hb. P. Scott; ITS, LSU, and *tef1* sequences GenBank PP464050, PP464051, and PP458233).

Notes: The genus *Macroconia*, with the generic type *Macroconia leptosphaeriae*, comprises seven species associated with stromata of other ascomycetes on herbaceous plants or deciduous trees. These fungi are characterised by superficial orange to red ascomata, KOH + violet reaction of the ascomata wall, 1-septate ascospores and verticillate conidiophores producing large, multiseptate fusarioid macroconidia (Crous *et al.* 2021b). *Macroconia verruculosa* is morphologically similar to *M. papilionacearum* which was described on *Parodiella perisporioides* on leaves of dicotyledonous plants (Samuels *et al*. 1991, Gräfenhan *et al.* 2011). However, *Macroconia verruculosa* can be distinguished *M. papilionacearum* by somewhat larger verruculous ascospores, (19.0–)25.0–29.2(–33.2) × (8.0–)9.2–10.8(–11.8) µm [*vs* smooth-walled, 14–19(–28) × (5–)5.3–6.7(–8.8) µm in *M. papilionacearum*].

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Macroconia papilionacearum* [strain CBS 125495, GenBank MH863610; Identities = 97.26 %, two gaps (0 %)]. The closest hit using the **LSU** sequence is *M. papilionacearum* [strain CBS 125495, GenBank MH875086; Identities = 99.21 %, one gap (0 %)]. The closest hit using the ***tef1*** sequence is *Fusarium redolens* [strain CBS 743.97, GenBank MT010987; Identities = 91.1 %, two gaps (0 %)].

Colour illustrations: View from Gunter Fork Trail in the Great Smoky Mountains National Park, USA (photo credit P. Scott). Habits of the ascomata on the bark; cross-section of the ascoma (mounted in KOH); cross-section of the ascoma wall (right mounted in water, left in KOH); ascospores (mounted in water). Scale bars: habits = 250 µm; ascoma = 100 µm; ascoma wall 50 µm; ascospores = 10 µm.



Phylogenetic relationships of *Macroconia verruculosa* (highlighted with a coloured block and **bold** font) inferred from Bayesian Inference analysis (BI) of a combined ITS, LSU and *tef1* data set. *Microcera larvarum* and *M. rubra* were used as the outgroup. Bold branches represent either Bayesian posterior probabilities ≥ 0.97 and/or bootstrap support values ≥ 75 %. Maximum likelihood analyses were carried out using a heuristic search as implemented in IQ-TREE v. 2.1.2 on XSEDE (Nguyen *et al*. 2015) and 100 bootstrap interactions on 1 000 replicates to estimate branch support. Bayesian inference of the phylogenetic relationships was calculated using the Markov chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012). Culture or collection numbers and GenBank accession numbers (superscript; ITS/LSU/*tef1*) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The alignment and tree were deposited at figshare.com (https://doi.org/10.6084/m9.figshare.25288459).

V. Darmostuk, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland; e-mail: v.darmostuk@botany.pl
P.A. Scott, Friesner Herbarium, Department of Biological Sciences, Butler University, Indianapolis, IN 46208, USA; e-mail: lpbascott@gmail.com

Fungal Planet 1648 MycoBank MB 852546

Marasmius pseudoelegans F.E. Guard, T. Lebel & Dearnaley, *sp. nov.*

Etymology: The epithet *pseudo* is Greek for false or resembling and acknowledges this species' close morphological relationship to *Marasmius elegans.*

Classification: *Marasmiaceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata small, collybioid. *Pileus* 5–18(–25) mm, juvenile bluntly conical to hemispheric, mature basidiomes broadly convex to almost applanate, apricot (47; Royal Botanic Gardens, Edinburgh, 1969), rust (13), rusty tawny (14) to sienna (11), smooth to velvety surface, margin entire, slightly in-rolled. *Flesh* thin, white. *Lamellae* cream (2B–4D), non-marginate, free to adnexed, narrow, moderately crowded, ~26, and 4–5 tiers of lamellulae with multiple bifurcations. *Stipe* central, cartilaginous, 30–45 × 0.75–1.5 mm, cylindric, hollow, deep purplish chestnut (21) at the base, bay (19) mid- and upper shaft, pale cream (4D) at the apex, with cream to buff basal tuft of mycelium; glossy to pruinose surface. Juvenile stipe paler with brown restricted to base or lower shaft. *Spore print* white. *Basidiospores* 9.5–11.5 × 3.5–4 µm, Q = 2.30–3.02, (mean 10.5 ± 0.47 × 4.0 ± 0.19 µm, Q_m = 2.61, ± 0.16,) n = 50, smooth, inamyloid, narrowly ellipsoid. *Basidia* not seen. *Basidioles* clavate, fusiform 17–23 × 3.5–6 µm. *Cheilocystidia* common *Siccus*-type broom cells cylindric to clavate forming a sterile edge, main body 14–21 × 5–10 µm, with 6–9 refractive, slightly thick-walled, erect digits, 2.5–6 × 0.5–1 µm. *Pleurocystidia* absent. *Pileipellis* consists of a hymeniderm of *Siccus*-type broom cells, cylindric to broadly clavate, main body 14–21 × 4–8 µm, with 6–8 erect refractive digits, 2.5–8 × 0.5–1 µm. *Pileal trama* dextrinoid, hyphae 4–5 µm diam. *Caulocystidia* two types: i) common elongate *Siccus*-type broom cells, main body 8.5–24 × 6–8 µm, cylindric, at times geniculate, occasionally branched, to broadly clavate, thin to thick-walled, with 2–8 apical digits, (3.5–)10–15 × 1–3 µm; ii) uncommon subcylindrical, smooth, wavy in outline, obtuse cells 12–45 × 4–5 µm. *Stipe* trama consists of dextrinoid parallel hyphae, 4–7 µm diam. *Clamp connections* present in all tissues.

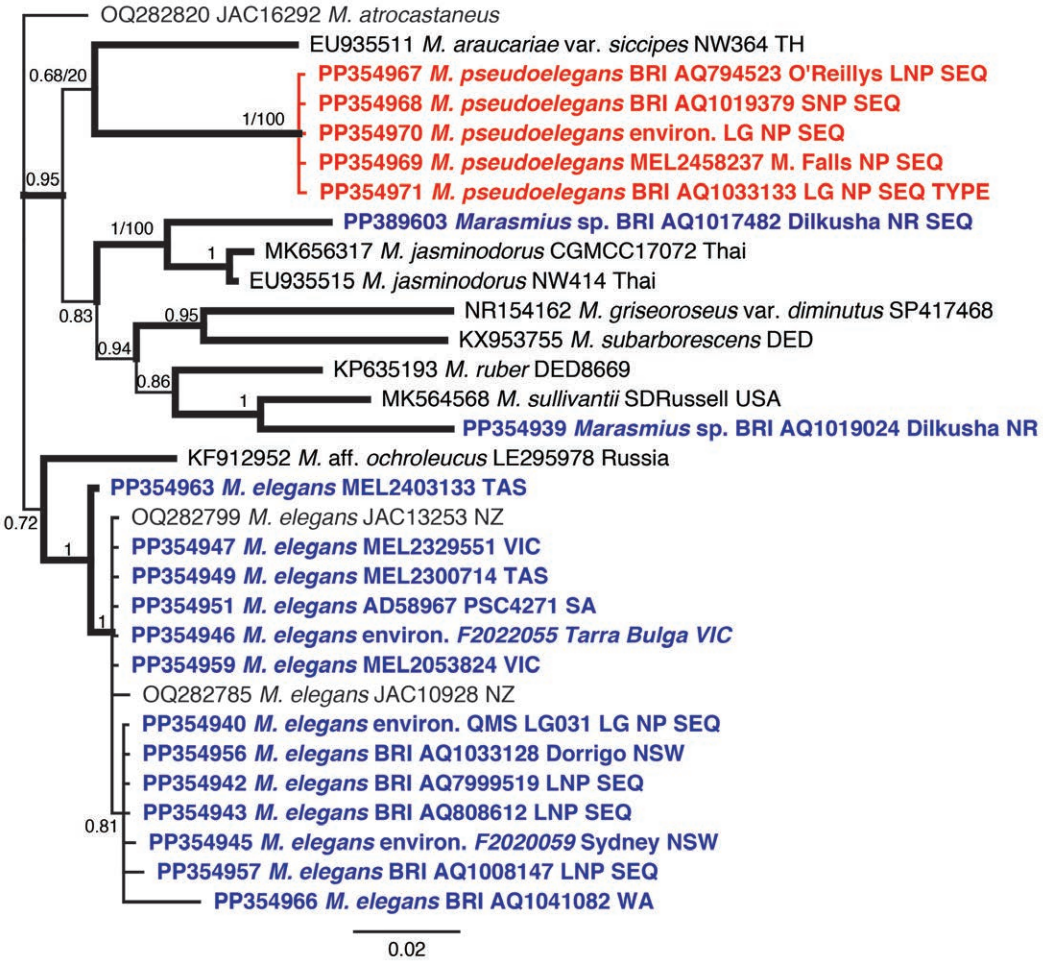
Habit, habitat and distribution: Usually gregarious, in leaf litter or well-rotted wood, an uncommon saprotroph of subtropical rainforest, palm forest and margins of wet sclerophyll forest. To date it has only been found in southeast Queensland in Lamington and Springbrook National Parks on the Qld-NSW border, Linda Garrett & Mapleton Falls National Parks and Maroochy Bushland Botanical Gardens in the Sunshine Coast hinterland.

Typus: **Australia**, Queensland, Linda Garrett National Park, S26°37'24.9", E152°50'51.4" on well-rotted twigs and litter in mixed wet sclerophyll and subtropical rainforest, 5 Mar. 2022, *W.G. Boatwright*, QMS2022-03-05 012 (**holotype** BRI AQ 1033133; ITS and LSU sequences GenBank PP354955 and PP354911).

Additional materials examined: **Australia**, Queensland, Springbrook National Park, Best of all Lookouts, 12 Feb. 2015, *J.C. Peuchmarin #2* (BRI AQ 1019379; ITS sequence GenBank PP354968); Mapleton Falls National Park, Linda Garrett Track, 21 Oct. 2018, *W.G. Boatwright WGB523* (MEL2458237; ITS and LSU sequences GenBank PP354969 and PP354933); Linda Garrett National Park, 4 Feb. 2023, *W.G. Boatwright F2023058* environmental sample (ITS and LSU sequences PP354970 and PP354908); Lamington National Park, O'Reillys, 5 Mar, 2003, *A. Young LNP957* (BRI AQ794523; ITS sequence GenBank PP354967).

Notes: *Marasmius pseudoelegans* is characterised by its small to medium orange-rusty smooth pileus, close gills with forking of lamellulae and brown stipe with pale apex. These characters, with cheilocystidia of *Siccus*-type broom cells and caulocystidia, in the absence of pleurocystidia, and a well-developed, non-collariate, non-instititious stipe place this species in section *Globulares* (*Globulares-Sicci* complex) subsect. *Leonini*, ser. *Luteoli* (Oliveira & Moncalvo 2020). Morphologically *M. pseudoelegans* is very similar to *M. elegans* which is widespread across southern Australia and New Zealand. The distribution of the two species coincides in southeast Queensland, where they occupy similar habitats. They are macroscopically indistinguishable as juveniles, but show some different characters as mature basidiomes, with common forking of lamellulae and dark stipe almost to apex in *M. pseudoelegans*, while these features are uncommon in *M. elegans.* Molecular analyses places *M. elegans* and *M. pseudoelegans* in the same series, though not as sister taxa. While a BLAST search shows them to be 95 % identical, both Bayesian and Maximum likelihood analyses show them to be distantly related. The closest species to *M. pseudoelegans*, with no support (PP 0.68, BS 20), is *M. araucariae* var. *siccipes* from Java and Thailand (Desjardin *et al.* 2000, Wannathes *et al.* 2009). We were unable to find any possible closer taxa in searches of literature or GenBank.

Colour illustrations: Complex notophyll vine forest Queensland, Australia, holotype site. Microscopy: caulocystidia - *Siccus*-type broom cells; line drawings: Upper row: pileipellis broom cells, basidioles, Middle row: cheilocystidia, basidiospores, Lower row: caulocystidia consisting of broom cells and smooth cells; basidiomata. Scale bars: basidiomata = 10 mm; caulocystidia and line drawings = 10 µm. Photos & illustration by F.E. Guard, habitat W.G. Boatwright.



Bayesian analysis of the ITS alignment. Analysis performed with MrBayes v. 3.2.6 (Heulsenbeck & Ronquist 2001) using substitution model GTR gamma, with MCMC settings of chain length 100 000 and burn-in length 10 000 in Geneious Prime v. 2023.2.1 (https://www.geneious.com). Posterior probability support values are indicated on the branches and thickened lines indicate support > 0.90. BS values are added where relevant for *M. pseudoelegans* and closest taxa. The outgroup was *M. atrocastaneus*. *Marasmius pseudoelegans sp. nov*. sequences are in red, blue text indicates other sequences generated for this study.

F.E. Guard, Maleny, Queensland, Australia; e-mail: franguard@icloud.com
T. Lebel, Botanic Gardens & State Herbarium, Hackney Road, Adelaide 5000, South Australia; e-mail: Teresa.Lebel@sa.gov.au
J. Dearnaley, School of Agriculture & Environmental Science, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: john.dearnaley@unisq.edu.au

Fungal Planet 1649 MycoBank MB 852093

Metapochonia simonovicovae S. Nosalj, Kubátová, Kandemir, M. Gorfer & Labuda, *sp. nov.*

Etymology: Latin, *simonovicovae*, named in honour of Alexandra Šimonovičová, Department of Soil Science, Faculty of Natural Sciences, Comenius University, Slovakia, an expert in soil microbiology and microbial remediation.

Classification: *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes.*

Sexual morph not observed on any of the media used. *Asexual morph* on malt extract agar (MEA) and potato carrot agar (PCA) at 25 °C after 3 wk. *Vegetative hyphae* hyaline, smooth-walled and septate, (1.5–)2–3(–3.5) µm wide. *Conidiophores* usually up to 220–250 µm long, also longer (up to 800 µm long), stipe (1–)1.5–2(–2.5) µm wide, hyaline and smooth-walled, mostly unbranched, bearing a solitary or verticillate phialides (up to 2–4 per node), laterally (2–4 per node) and terminally in a whorl of 3–5(–7) phialides, of unequal length, the longest up to 50 µm. *Phialides* slender, subulate (awl-shaped), slightly but distinctly broader (swollen) from the base to the middle (1–1.5 µm), narrowing towards the slender neck (0.5–1 µm), hyaline and smooth-walled, rather variable in length, (12–)15–20(–26) µm long and 1–1.5 µm wide near the base (mean = 20.2 ± 3.0 × 1.2 ± 0.2 µm, n = 30). *Conidia* produced in globose false heads, smooth-walled, one-celled, mostly globose to ovoid usually with apiculate ends, (2.5–)3–3.5(–4.5) × (1.5–)2(–2.5) µm (mean = 3.0 ± 0.3 × 2.0 ± 0.1, n = 50), some also oblong, and slightly curved or bean-shaped to falcate with blunt ends, up to 5 µm long. The latter two types of conidia (oblong, falcate and curved) present especially at low temperatures (up to 20 °C, on PCA) or on MEA after 3–4 wk. *Chlamydospores* rather abundant, produced after 3–4 wk, aseptate, single or in pairs, intercalary or terminally, but more often forming irregular terminal chains or clusters of 3–5 cells, (5.5–)6–6.5(–7) µm (mean = 6.1 ± 0.45, n = 15), with prominent thick walls, smooth, dark coloured (melanised), submerged into agar (observed on MEA). Multicellular *dictyochlamydospores* observed after 3 mo on PCA, (17–)19–22(–25) µm (mean = 18.9 ± 2.3, n = 30).

Colour illustrations: Site at Banská Štiavnica, Slovakia - Šobov from Dystric Cambisol, where samples were collected. Colonies on SDA, PDA and MEA at 25 °C, after 3wk, a piece of horse hair colonised by the fungus at room temperature, after 3 wk (horse-hair baiting method); conidiophores with conidia, melanised chlamydospores, dictyochlamydospores. Scale bars: bottom left and right photos = 10 µm; all others = 5 µm.

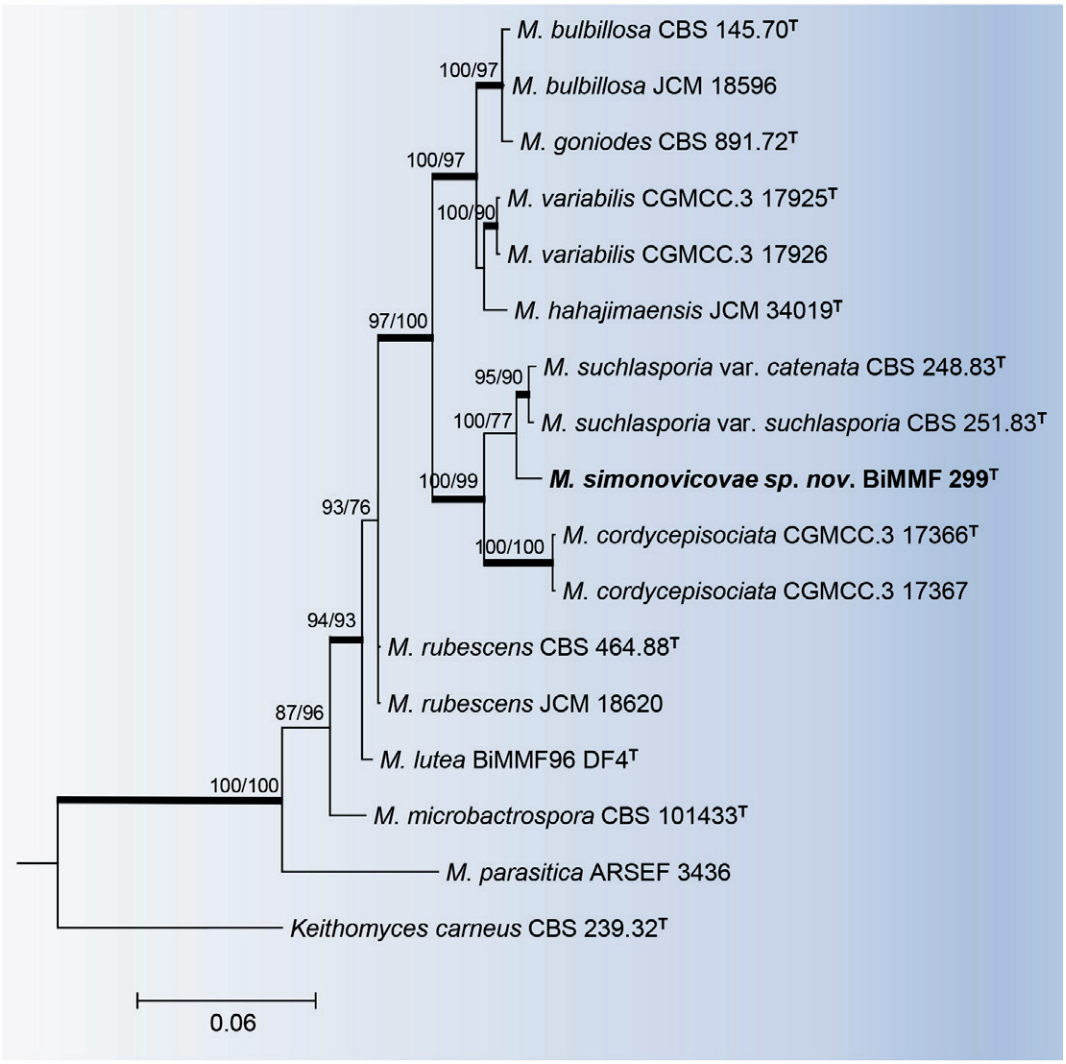
Culture characteristics (in darkness, 25 °C, 10 d): Colonies on **MEA** slow growing, 15–17 mm, yellow white, floccose aerial mycelium, strongly radially furcate and wrinkled, with crater-like center and subcentre areas, with slightly lobate margin, no exudate, reverse yellow orange, yellow pigment diffusing into the agar, odour indistinct. Colonies on sabouraud 4 % dextrose agar (**SDA)** slowly to moderately growing, 23–25 mm, slightly radially furcate (sulcate), yellow white, with white floccose aerial mycelium becoming yellow towards the colony centres, no exudate, reverse bright orange, yellow pigment diffusing into the agar, odour indistinct. Colonies on potato dextrose agar (**PDA)** slowly to moderately growing, 20–22 mm, similar to those on SDA. Colonies on oatmeal agar (**OA)** slow growing, 8–13 mm, umbonate, white, with pure white floccose aerial mycelium, no exudate, reverse bright yellow, yellow pigment diffusing into the agar, odour indistinct. Colonies on **PCA** slow growing, 15–17 mm, white, plane with loose pure white (hyaline) floccose aerial mycelium, no exudate, reverse yellow, yellow pigment diffusing into the agar odour indistinct.

Optimum temperature for growth after 10 d (see supplementary information), 18–25 °C (15–27 mm diam), reduced growth observed at 10–15 °C (5–17 mm diam), 27 °C (8–15 mm diam). *The minimum temperature* (microcolonies to 1 mm) is 6 °C, germination of conidia and microcolonies formation observed at 4 °C. *The maximum temperature* is 28 °C (microcolonies to 1 mm diam). *Sporulation* observed between 6 °C–27 °C. *Growth on MEA-CX 500* (with 500 µg/mL cycloheximide) 15–17 mm after 10 d at 20 °C. *Keratinolytic activity* moderate (see supplementary information), with hair attack intensity = 2 (cuticle and cortex attack with about 20 % destruction; boring hyphae present according to Marchisio *et al*. (1994).

Typus: **Slovak Republic**, Banská Štiavnica - Šobov, (approximate coordinates: 48°28’20.04”N, 18°54’25.23”E), a soil sample from Dystric Cambisol (Aric Toxic), Apr. 2022, coll. *A. Šimonovičová*, isol. *S. Nosalj,* May 2022 (**holotype** PRM 959949, ex-type culture BiMM-F299 = CCF 6700; ITS, LSU, *BenA*, and *tef1-α* sequences GenBank PP085431, PP085432, PP085550, and PP272031).

Notes: Based on a search of NCBI’s GenBank nucleotide database, the closest hit was *M. suchlasporia* var. *suchlasporia* culture CBS 251.83 using the **ITS** sequence [GenBank AJ292402.1; Identity = 563/567 (99 %)], using the ***BenA*** [GenBank: KJ398558.1; Identity = 372/382 (97 %)], and the ***tef1-α*** sequence [GenBank KJ398790.1; Identity = 732/751 (97 %)]. Phenotypically, *M. simonovicovae* can be readily distinguished from *M. suchlasporia* by its falcate conidia with blunt ends, melanised chlamydospores, bright orange reverse and yellow pigment production. Comparison of the key phenotypic characteristics of all accepted *Metapochonia* species is provided in the supplementary table (see supplementary material).

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Figures and Table).



Phylogeny of *Metapochonia* species based on combined ITS, LSU and *tef1-α* data. All sequences were aligned with MAFFT v. 7 with default settings. The best-fitting models for ITS, LSU, and *tef1-α* data were found to be K2P+G4, TNe, and TN+F+I, respectively, according to the Bayesian Information Criterion (BIC) in ModelFinder (Kalyaanamoorthy *et al.* 2017) on the IQ-TREE web server (Trifinopoulos *et al*. 2016). Phylogram was constructed using the maximum likelihood (ML) methods implemented in IQ-TREE web server as well as MRBAYES v. 3.2.7 (Ronquist & Huelsenbeck 2003) with default settings on the CIPRES portal (http://www.phylo.org/). *Keithomyces carneus* was used as outgroup. Phylogenetic trees were displayed and edited using TreeView v. 1.6.6 (Page 1996). The Bayesian probabilities (BP) above 0.9 and ML bootstrap values (BS) above 90 % are shown at the thickened nodes (BP/BS). The novel species is shown in **bold**. ᵀex-type species. The alignments and the tree are publicly available at figshare.com (doi:10.6084/m9.figshare.24972633). Host, country and GenBank accession number information of the strains used in the study are provided as supplementary information.

S. Nosalj, Department of Soil Science, Faculty of Natural Sciences, Comenius University, Ilkovičová 6, 842 15 Bratislava, Slovak Republic; e-mail: sanjanosalj@gmail.com

A. Kubátová, Department of Botany, Faculty of Science, Culture Collection of Fungi (CCF), Charles University, Benátská 2, 128 00 Prague 2, Czech Republic; e-mail: alena.kubatova@natur.cuni.cz

H. Kandemir, Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT, Utrecht, The Netherlands; e-mail: h.kandemir@wi.knaw.nl

M. Gorfer, Bioresources, Center for Health & Bioresources, AIT Austrian Institute of Technology GmbH, Konrad-Lorenz-Straße 24, 3430 Tulln an der Donau, Austria; e-mail: Markus.Gorfer@ait.ac.at

R. Labuda, Department for Farm Animals and Veterinary Public Health, Institute of Food Safety, Food Technology and Veterinary Public Health; Unit of Food Microbiology, University of Veterinary Medicine Vienna, Veterinaerplatz 1, 1210 Vienna, and Core Facility Bioactive Molecules: Screening and Analysis and Research Platform Bioactive Microbial Metabolites (BiMM), Konrad Lorenz Strasse 24, 3430 Tulln a.d. Donau, Austria; e-mail: roman.labuda@vetmeduni.ac.at

Fungal Planet 1650 MycoBank MB 853002

Monosporascus bulgaricus G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology: Named after Bulgaria, the country where the fungus originated from.

Classification: *Diatrypaceae*, *Xylariales*, *Sordariomycetes*.

Root endophyte isolated on culture media from surface-sterilised roots of living plants. *Mycelium* composed of branched, septate, smooth, hyaline, thin-walled hyphae, 1–3 µm wide, single or aggregated in tightly packed hyphal cords in older cultures, up to 51 µm wide.

Culture characteristics: Colonies on potato dextrose agar (PDA) fast growing, reaching 35–42 mm diam after 1 wk at 24 °C, velvety, somewhat cottony around the edges, dull white, mostly flat but slightly raised 1–2 mm at the centre, margin diffuse, reverse dull white. On malt extract agar (MEA) reaching 32–40 mm diam, velvety, white, cottony, umbonate and raised 2–3 mm at the centre, dull-white and with flat patches of scarce aerial mycelium all over the colonies or forming a concentric ring around the centre, margin irregular, reverse dull white. Cultures sterile.

Habitat and distribution: Root endophyte. Known so far from Bulgaria.

Typus: **Bulgaria**, Sofia Province, Dragoman Municipality, near Vladislavtsi, 42°54'31.9"N, 22°49'52.2"E, 617 m a.s.l., isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum* (*Brassicaceae*), 14 May 2013, coll. *T. Ali & S. Ploch*, isol. *K. Glynou*, P1916 (**holotype** permanently preserved in a metabolically inactive state CBS 151406, culture ex-type CBS 151406; ITS, LSU, and *tub2* sequences GenBank KT269184, PP454707, and PP460994).

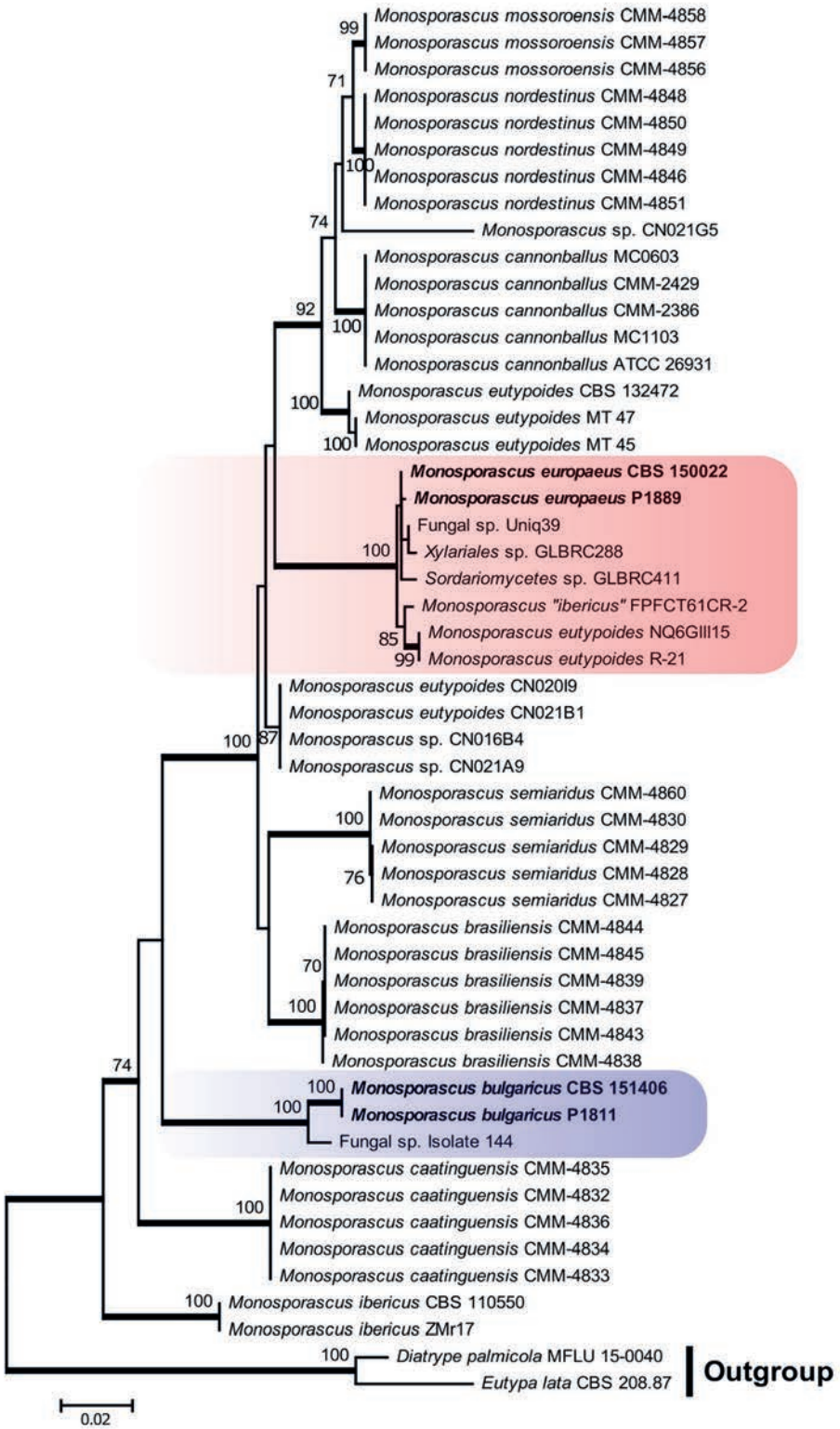
Additional material examined: **Bulgaria**, Sofia Province, Dragoman Municipality, near Vladislavtsi, 42°54'31.9"N, 22°49'52.2"E, 617 m a.s.l., isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum* (*Brassicaceae*), 14 May 2013, coll. *T. Ali & S. Ploch*, isol. *K. Glynou* (P1811; ITS sequence GenBank KT269083).

Notes: The diatrypaceous genus *Monosporascus* has been traditionally associated with plant-pathogenic species such as *M. cannonballus* or *M. eutypoides* causing root rot and vine decline of cucurbits worldwide, including crops such as melon and watermelon (Ben Salem *et al.* 2013). More recently, however, *Monosporascus* has shown to harbour a substantial diversity on other plant hosts *e.g.* on slightly decolourised roots of weeds prevalent in cucurbit growing fields of Brazil (Negreiros *et al.* 2019). Culturable, phylogenetic and phylogenomic studies also revealed that its members are ubiquitous root endophytes of different plant hosts in arid or semiarid ecosystems of the southwestern United States, and many *Monosporascus* isolates represent novel lineages still awaiting to be described (Robinson *et al*. 2020). Nevertheless, only 10 species of *Monosporascus* have been recognised so far according to the Index Fungorum database (https://www.indexfungorum.org). The new species introduced here, *M. bulgaricus*, was isolated during an extensive sampling for root endophytic fungi across Europe (Glynou *et al*. 2016). Phylogenetically, the two isolates of our fungus clustered together in a distinct and strongly supported lineage (100 % BS, 0.99 BPP) with a "Fungal sp. isolate 144" whose ITS sequence was available in GenBank. This is another root endophyte obtained from a grass species during studies of endophytic communities along altitudinal gradients in the Colorado Rocky Mountains, USA (Lyons *et al*. 2021). Their ITS sequences, however, differ in several indels and this isolate probably represent another novel taxon within the apparent hyperdiverse *Monosporascus*. They grouped sister to a large clade containing most described taxa including the generic type, *M. cannonballus*, and several other species such as *M. brasiliensis*, *M. caatinguensis* and *M. mossoroensis*. These are also root endophytes whose cultures were sterile on several different media and failed to produce the typical perithecial or cleistothecial ascomata of the genus containing asci with 1 to 6 spherical, smooth, reticulate or slightly granulose, brown to black ascospores (Negreiros *et al*. 2019). They were also distant from *M. ibericus*, another endophyte isolated from roots and stems of three halophytic hosts growing on saline soils in Spain (Collado *et al*. 2002), that produced ascomata on Potato Carrot Agar in contrast to *M. bulgaricus* whose strains remained sterile on MEA and PDA.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Fungal sp. [isolate 144, GenBank MT820097.1; Identities = 524/541 (97 %), five gaps (0 %)], *Monosporascus* sp. [strain CN021G5, GenBank ON074887.1; Identities = 416/453 (92 %), eight gaps (1 %)], and *Monosporascus* sp. [strain CN016B4, GenBank ON074821.1; Identities = 416/453 (92 %), nine gaps (1 %)]. Closest hits using the **LSU** sequence are *Eutypa* sp. [strain SMH3580, GenBank AY346280.1; Identities = 1 262/1 309 (96 %), three gaps (0 %)], *Diatrype disciformis* [isolate AFTOL-ID 927, GenBank DQ470964.1; Identities = 1 259/1 315 (96 %), one gap (0%)], and *Eutypa lata* [isolate AFTOL-ID 929, GenBank DQ836903.1; 1 252/1 308 (96 %), two gaps (0 %)]. Closest hits using the ***tub2*** sequence are *Monosporascus* sp. [isolate SCUA-Nem-KH34, GenBank MN635677.1; Identities = 401/435 (92 %), five gaps (1 %)], *Monosporascus brasiliensis* [isolate MBr20, GenBank MG725323.1; Identities = 396/430 (92 %), two gaps (0 %)], and *Monosporascus brasiliensis* [isolate MBr18, GenBank MG725322.1; Identities = 396/430 (92 %), two gaps (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Plant of *Microthlaspi perfoliatum* growing in Bulgaria. Colonies on PDA and MEA (after 1 wk at 24 °C) on surface view; hyphal cord; mycelium with hyphae. Scale bars = 5 µm.



Maximum likelihood phylogenetic tree obtained from the concatenated ITS, LSU and *tub2* sequences of *Monosporascus* (*Diatrypaceae*, *Sordariomycetes*) showing the affinities of *M. bulgaricus* and *M. europaeus* with other members of the genus. Dataset was built using closest hits from megablast searches in GenBank and additional sequences from Negreiros *et al*. (2019). Alignments were performed using MAFFT v. 7.520 on the online server (Katoh *et al.* 2019) and the final dataset included 1 925 positions, 528 from the ITS alignment, 683 from the LSU and 714 from the *tub2*. Phylogenetic relationships were inferred by Maximum likelihood and Bayesian Inference analyses using RAxML v. 8.2.12 (Stamatakis 2014) on the CIPRES Science Gateway server (Miller *et al.* 2010) and MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003), respectively. Settings followed Crous *et al*. (2021a) and the tree was rooted with the strains *Diatrype palmicola* MFLU 15-0040 and *Eutypa lata* CBS 208.87. Bootstrap support values ≥ 70% are shown at the nodes and Bayesian posterior probabilities ≥ 0.95 are indicated by thickened branches. Novel species are highlighted in colour boxes, a blue one for *M. bulgaricus* and a red one for *M. europaeus*, with new strains in **bold**. Alignment and trees are deposited in figshare.com (doi: 10.6084/m9.figshare.25395508).

G. Delgado, Eurofins Built Environment, 6110 W. 34th St, Houston, TX 77092, USA; e-mail: gregorio.delgado@et.eurofinsus.com
J.G. Maciá-Vicente, Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands; e-mail: j.maciavicente@nioo.knaw.nl

Fungal Planet 1651 MycoBank MB 852864

Monosporascus europaeus G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology: Named after Europe, the continent where the fungus was originally isolated.

Classification: *Diatrypaceae*, *Xylariales*, *Sordariomycetes*.

Root endophyte isolated on culture media from surface-sterilised roots of living plants. Mycelium composed of branched, septate, smooth, hyaline, thin-walled hyphae, 1.5–3 µm wide, sometimes wider 5–7 µm cells in chains are present, also pale brown to brown, thick-walled, smooth or finely verruculose, intercalary hyphae 2–4 µm wide are formed, single or in bundles and associated with the formation in old cultures of brown to dark brown, more or less compact, subspherical to irregular hyphal masses 11–33 µm diam made of coiled hyphae and resembling ascomatal initials.

Culture characteristics: Colonies on potato dextrose agar (PDA) fast growing, reaching 37–46 mm diam after 1 wk at 24 °C, flat and circular around a cream-coloured centre, somewhat cottony and white toward the edges, margin diffuse, reverse dull white. On malt extract agar (MEA) reaching 34–43 mm diam, cottony, white, with scarce aerial mycelium around the centre, margin diffuse, reverse dull white; abundant formation of radiated, compact bundles of colourless, acicular, needle-shaped crystals were observed on both PDA and MEA starting as early as the second week of incubation. Cultures sterile.

Habitat & distribution: Root endophyte. Known so far from Bulgaria and possibly China, Iraq and United States.

Typus: **Bulgaria**, Sofia Province, Dragoman Municipality, near Vladislavtsi, 42°54'31.9"N 22°49'52.2"E, 617 m a.s.l., isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum* (*Brassicaceae*), 14 May 2013, coll. *T. Ali & S. Ploch*, isol. *K. Glynou*, P1810 (**holotype** permanently preserved in a metabolically inactive state CBS 150022; culture ex-type CBS 150022; ITS, LSU, and *tub2* sequences GenBank KT269082, PP454705, and PP481183).

Additional material examined: **Bulgaria**, Sofia Province, Dragoman Municipality, near Vladislavtsi, 42°54'31.9"N 22°49'52.2"E, 617 m a.s.l., isolated from surface-sterilised, asymptomatic roots of *Microthlaspi perfoliatum* (*Brassicaceae*), 14 May 2013, coll. *T. Ali & S. Ploch*, isol. *K. Glynou* (P1889; ITS and LSU sequences GenBank KT269158 and PP454706).

Notes: Similar to other previously described taxa, *M. europaeus* was obtained during an extensive sampling for root endophytic fungi across Europe (Glynou *et al.* 2016). Surprisingly, the *M. perfoliatum* plant the fungus was isolated from was collected at the same location in Bulgaria, on the same day and same host species, but different plant individual, as *M. bulgaricus* described together in Fungal Planet 1650. Phylogenetically, however, they grouped distant in our ITS-LSU-*tub2* tree and strains of *M. europaeus* formed a clade sister to several species including the generic type, *M. cannonballus*, with no support, whereas *M. bulgaricus* represented an isolated lineage within the genus. Pairwise alignments of their individual ITS, LSU and *tub2* sequences also show several differences between them suggesting they are not conspecific. There are also visible differences between them in culture. Both species are fast growing in all media after 1 wk of incubation at 24 °C but colonies of *M. europaeus* on PDA are flat and circular around a cream-colored centre, scarcely cottony and white toward the edges, whereas those of *M. bulgaricus* are velvety, somewhat cottony around the edges and dull-white. On MEA, colonies of *M. europaeus* are cottony, white and with scarce aerial mycelium around the centre, whereas those of *M. bulgaricus* form a dull-white and flat concentric ring around the centre, which is umbonate, cottony and white. The two strains of our fungus clustered together in a strongly supported monophyletic group (100 % BS, 1 BPP) with six isolates represented in GenBank by their ITS sequences implying a possible wider distribution of *M. europaeus*. They are: "*Sordariomycetes* sp. GLBRC411" and "*Xylariales* sp. GLBRC288", two root endophytes isolated from *Panicum virgatum* (*Poaceae*) in Michigan, USA (da Costa et al. 2022) and "Fungal sp. Uniq39", another root-associated endophytic fungus obtained from a plant of *Bouteloua gracilis* (*Poaceae*) occurring in soils around a New Mexico uranium mine (Portman *et al.* 2023). The remaining three isolates are also root endophytes in plants of *Cucumis* spp. (*Cucurbitaceae*) or *Lycium barbarum* (*Solanaceae*) from China and Iraq (Chehri *et al*. 2010, Cheng *et al.* 2023) but they were annotated as *M. ibericus* or *M. eutypoides*. Their ITS sequences, however, are almost identical to those of *M. europaeus* and phylogenetic analyses suggest they might be conspecific. Cultures of *M. europaeus* remained sterile in all media but formation of hyphal structures resembling ascomata initials made of tightly packed, coiled hyphae were observed after long-term incubation on MEA. However, further development into protoascomata was not obtained.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sordariomycetes* sp. [isolate GLBRC411, GenBank OM106608.1; Identities = 523/525 (99 %), no gaps], Fungal sp. [isolate Uniq39, GenBank ON815415.1; Identities = 521/524 (99 %), two gaps (0 %)], and *Xylariales* sp. [isolate GLBRC288, GenBank OM106486.1; Identities = 533/537 (99 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Eutypa lata* [isolate AFTOL-ID 929, GenBank DQ836903.1; Identities = 1 290/1 322 (98 %), six gaps (0 %)], *Eutypa* sp. [strain SMH3580, GenBank AY346280.1; Identities = 1 289/1 323 (97 %), seven gaps (0 %)], and *Libertella blepharis* [isolate LBAg, GenBank AY621003.1; Identities = 1 313/1 348 (97 %), eight gaps (0 %)].

For phylogenetic tree, see *Monosporascus bulgaricus* (FP 1650).

Colour illustrations: Plant of *Microthlaspi perfoliatum* growing in Bulgaria. Colonies on PDA and MEA (after 1 wk at 24 °C) on surface view; mycelium with brown hyphae; ascoma initial. Scale bars: brown hyphae = 5 µm; ascoma initial = 10 µm.

G. Delgado, Eurofins Built Environment, 6110 W. 34th St, Houston, TX 77092, USA; e-mail: gregorio.delgado@eurofinset.com
J.G. Maciá-Vicente, Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands; e-mail: j.maciavicente@nioo.knaw.nl

Fungal Planet 1652 MycoBank MB 847924

Mycena calongei M. Villarreal & J.C. Campos, *sp. nov.*

Etymology: Dedicated to Dr Francisco de Diego Calonge (1938–2019), founder of the Sociedad Micológica de Madrid.

Classification: *Mycenaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps gregarious. *Pileus* 4–10 mm diam, hemispherical, then conical to parabolic, flattening to convex, becoming more or less plano-convex with or without a small central papilla, not depressed, pruinose, glabrescent, shallowly sulcate, more or less translucent-striate, very pale brown (MU10YR8/2; Munsell 1994), to pale grey (MU10YR7/2), sometimes dirty white (MU10YR8/1), the centre and striation greyish brown (MU10YR5/2) to brown (MU10YR5/3). *Context* very thin, whitish. *Odour* and *taste* indistinctive. *Lamellae* 13–18 reaching the stipe, lamellulae 1–3, well developed and fairly broad, ascending, the edge convex to subhorizontal, narrowly adnate to broadly adnate, up to 0.5 mm wide, decurrent with a very short tooth, initially white, pale brown, then pale grey brown, with pallid edge. *Stipe* 30–65 × 016–0.25 mm, thin, hollow, equal, terete, firm, pruinose, glabrescent, becoming shiny, curved to flexuous, watery white (MU10YR8/1) to watery pale brown (MU10YR8/4), becoming more whitish; sometimes brownish at the apex in old specimens; attached to the substratum by a whorl of radiating, flexuous, white mycelial fibrils. *Basidiospores* (6.4–)7.3–9(–10) × (3.5–)*4.1–4.8*(–5.7) µm; Q = (1.5–)*1.6–2.1*(–2.3); N = 100; Me = 8.1 × 4.5 µm; Qe = 1.8, pip-shaped, smooth, amyloid. *Basidia* 21–28 × 6–8 µm, clavate, 4–spored, rarely 2–spored, with plump sterigmata up to 4.5 µm long. *Cheilocystidia* 21–58 × 6–11 µm, forming a sterile band, lageniform, sublageniform, cylindrical or sometimes multiform, nearly smooth, frequently mucronate or furcated at the apex or provided with 2–5 short, straight excrescences, 1–6 × 0.5–1 µm. *Pleurocystidia* absent. *Lamellar trama* dextrinoid, reddish brown in Melzer's reagent. *Hyphae of the pileipellis* 5–10(–17) µm wide, densely covered with cylindrical, straight excrescences; terminal cells up to 40 × 15 µm, clavate to subcylindrical, covered with short, straight, cylindrical excrescences. *Hypodermium* of broad, cylindrical to subglobose, smooth cells 12–30 × 11–24 µm. *Hyphae of the cortical layer of the stipe* 2–5 µm wide, densely covered with cylindrical, sometimes more thorn-like, straight excrescences 1–6(–8) × 0.5–1 µm; terminal cells not differentiated. *Caulocystidia* absent. *Clamp connections* observed in all tissues.

Habitat and distribution: Gregarious in small clusters, on mossy bark base of *Juniperus oxycedrus* (*Cupressaceae*) in Mediterranean grove of evergreen oak forests.

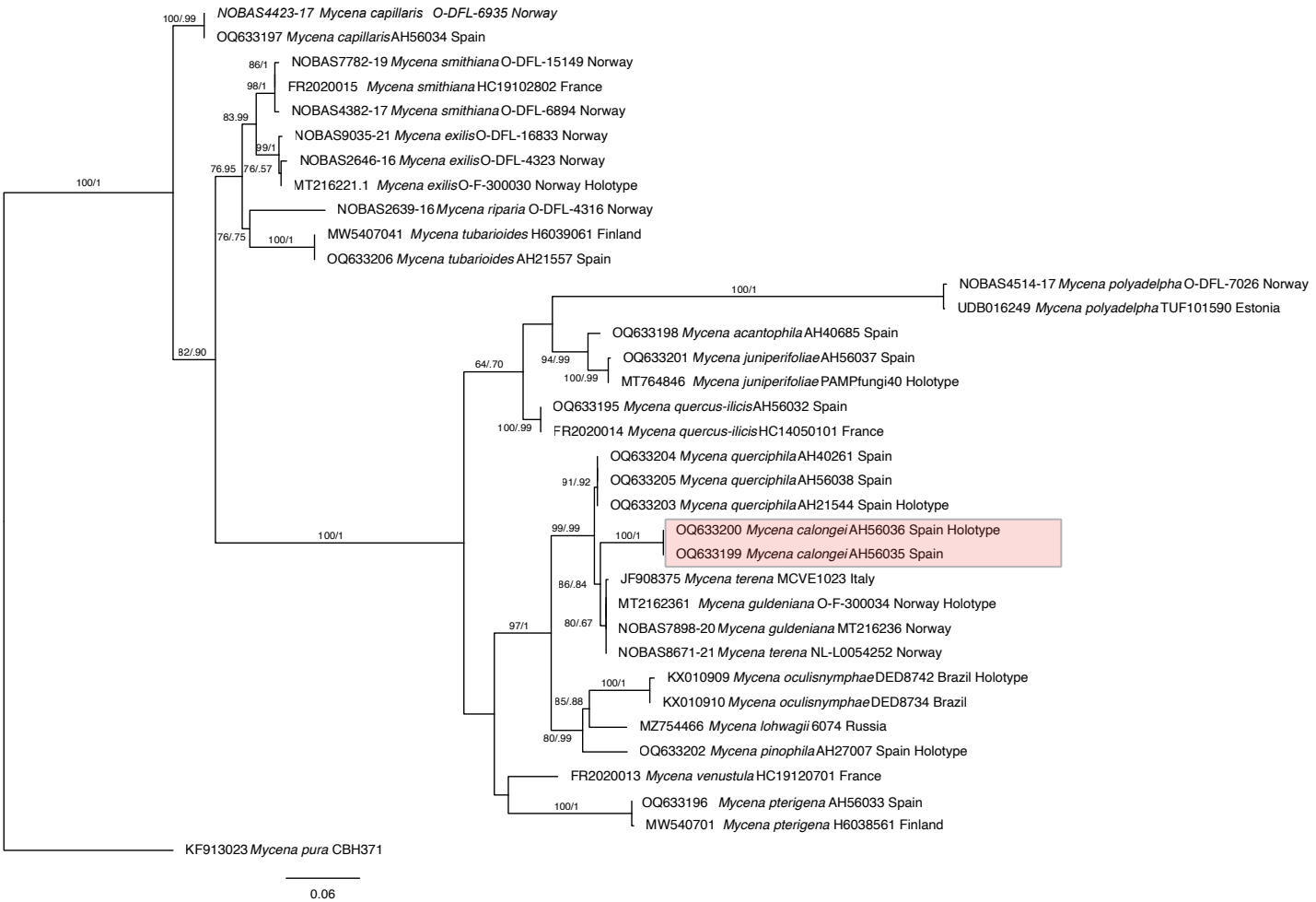
Typus: **Spain**, Madrid, Aldea del Fresno, Barranco de las Vacas, 40.312203, -4.204505, 465 m a.s.l., 5 Dec. 2020, *leg*. *J.C. Campos* & *M. Villarreal* (**holotype** AH56036; ITS sequence GenBank OQ633200).

Additional material examined: **Spain**, Madrid, Aldea del Fresno, Barranco de las Vacas, 40.312203, -4.204505, 465 m a.s.l., 26 Dec. 2022, *leg*. *M. Villarreal* (AH56035; ITS sequence GenBank OQ633199).

Notes: *Mycena calongei* belongs to monophyletic *M.* sect. *Polyadelphia.* It is characterised by its small size and gregarious basidiocarps fruiting at the base on mossy bark of *Juniperus oxycedrus*. The new species group with other smooth to nearly smooth cheilocystidiated species of the section and is very similar to the Mediterranean species *M. querciphila* (Esteve-Raventós & Villarreal 1997), which differs in having shorter cheilocystidia up to 33 µm and hyphae of the stipitipellis more sparsely ornamented with short excrescences 1–3 × 0.7–1 µm, and sporulating exclusively on *Quercus rotundifolia* and *Q. suber* dead leaves.

Based on the results of a blastn search of NCBIs GenBank nucleotide database using the ITS sequence, *M. calongei* differs from *Mycena querciphila* [voucher AH21544, GenBank OQ633203; Identities = 618/647 (96 %) three gaps (0 %)]. A phylogenetic analysis based on internal transcribed spacer sequences derived from two *M. calongei* collections clearly showed that they cluster together, being phylogenetically distinct from the closest species of *M.* sect. *Polyadelphia*.

Colour illustrations: Juniperus oxycedrus growing in Spain. Basidiocarps; basidium; cheilocystidia; hyphae of the pileipellis; terminal cells of the pileipellis; spores; hyphae of the stipitipellis. Scale bars: basidiocarps = 1 cm; all others = 10 µm.



Phylogenetic relationships in *Mycena* sect. *Polyadelphia* reconstructed from an unpartitioned ITS dataset. The Maximum Likelihood (ML) analyses were performed using IQ-TREE v. 2.2.0 (Nguyen *et al*. 2015). Branch support was assessed through 1000 replicates of standard non-parametric bootstrapping (Felsenstein 1985). The Bayesian Inference (BI) analyses were carried out in MrBayes v. 3.2.7 (Ronquist *et al*. 2012) and included two runs over 5 × 10^6 generations, with a sample frequency of 500 and a burn-in value of 25 %. The ML bootstrap support values and Bayesian posterior probabilities are indicated above the branches. Tree was drawn with FigTree v. 1.4.4 (Rambaut 2018) and edited with Inkscape. All tips are labelled with database accession number, taxon name, collection number and origin. *Mycena calongei* is marked in **bold** and the holotype is indicated. Scale bar on the tree indicates the expected number of changes per site. The tree was rooted to *Mycena pura* according to Lebeuf *et al*. (2023).

M. Villarreal, Dpto. Ciencias de la Vida (Botánica), Facultad de Ciencias, Universidad de Alcalá, 28805, Alcalá de Henares, Madrid, Spain;
e-mail: mvillarrmycena@gmail.com
J.C. Campos, Grupo Microscopía Sociedad Micológica Madrid, ETSIAAAB, Avda. Puerta de Hierro 2, 28040, Madrid, Spain;
e-mail: jucalactarius@gmail.com

Fungal Planet 1653 MycoBank MB 852092

Oxydothis coperniciae Tennakoon & N. Suwannarach, *sp. nov.*

Etymology: Named after the host genus from which it was collected, *Copernicia*.

Classification: *Oxydothidaceae*, *Xylariales*, *Sordariomycetes*.

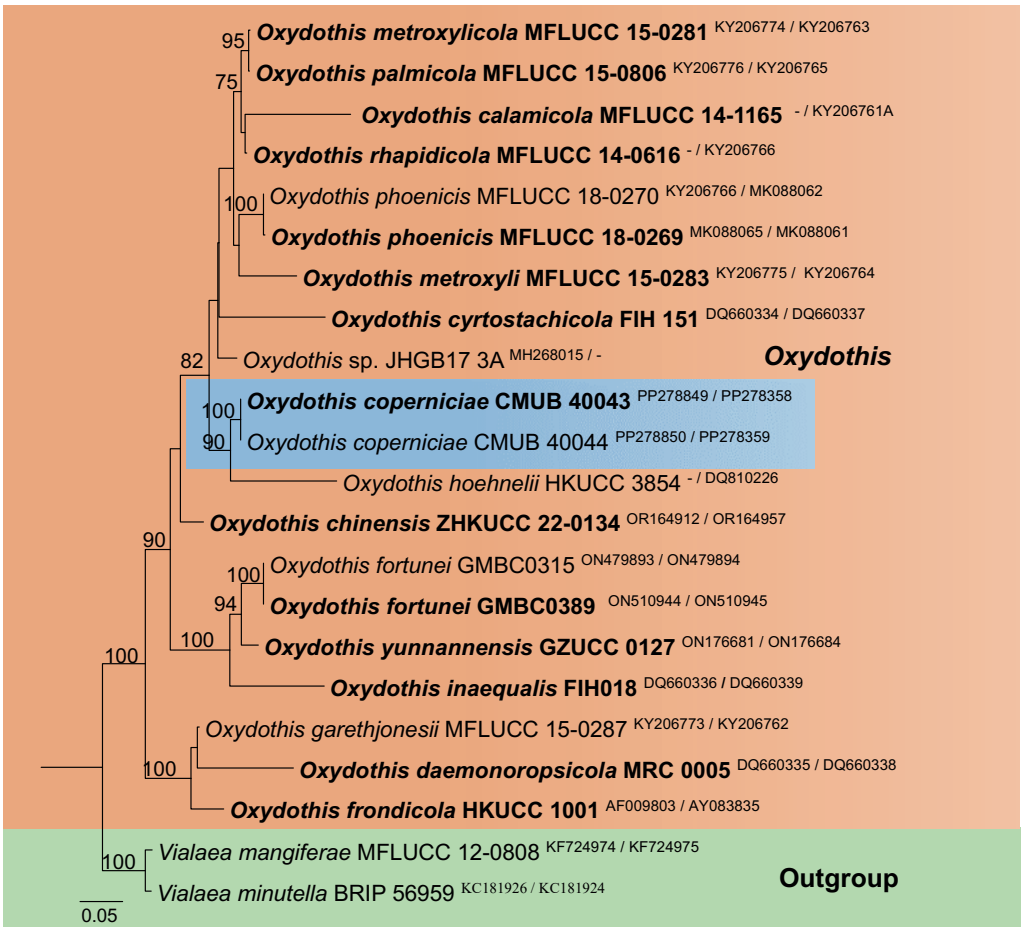
Ascomata forming under slightly raised blackened discs on the host surface, solitary or mostly clustered, sub-globose, unilocular to multilocular, dark brown to black, 130–200 µm diam, wall of 3–4 layers of brown, darkly pigmented cells of *textura angularis*. *Asci* 8-spored, fasciculate, unitunicate, cylindrical-clavate, short pedicellate, with a wedge-shaped, subapical ring, 130–160 × 10–12 µm. *Ascospores* 1–2-seriate, fusoid, curved, tapering gradually from the centre to the ends, one end subacute to acute, and mostly acute on the other end, swollen at the middle, hyaline, multi-guttulate, 40–50 × 7–8 µm.

Typus: **Thailand**, Chiang Rai Province, on dead leaf of *Copernicia alba* (*Arecaceae*), 15 Aug. 2020, *D.S. Tennakoon*, TMD016 (**holotype** CMUB 40043, **isotype** CMUB 40044; ITS and LSU sequences GenBank PP278849-PP278850 and PP278358–PP278359).

Notes: *Oxydothis* was introduced by Penzig & Saccardo (1897) to accommodate three species in the *Amphisphaeriaceae*, namely *O. grisea*, *O. nigricans* and *O. maculosa*. Subsequently, Konta *et al*. (2016) placed this genus in *Oxydothidaceae* (*Xylariales*). *Oxydothis* species have been reported as endophytes, pathogens and saprobes (Fröhlich & Hyde 1994, Konta *et al*. 2016, Tibpromma *et al*. 2018, Senanayake *et al*. 2023). Ascomata are mostly formed solitary or in clusters, as darkened, raised regions or dots on the surface of host (Konta *et al.* 2016, Senanayake *et al.* 2023). The phylogeny inferred from the ITS and LSU sequences demonstrated that the new species *O. coperniciae* nested in the *Oxydothis* clade and forms an independent lineage sister to *O. hoehnelii* with 90 % statistical support. *Oxydothis coperniciae* can be distinguished from *O. hoehnelii* in their smaller asci (130–160 × 10–12 µm *vs* 300 × 12–15 µm) and ascospores (40–50 × 7–8 µm *vs* 50–75 × 6–7 µm). In addition, *Oxydothis hoehnelii* has 1-septate ascospores, tapering from the central septum (both ends are mostly acute), whereas *O. coperniciae* has aseptate ascospores, which are tapering gradually from the centre to the ends, one end being subacute to acute, and the other mostly acute (Rehm 1913, Saccardo 1928, Hyde 1994).

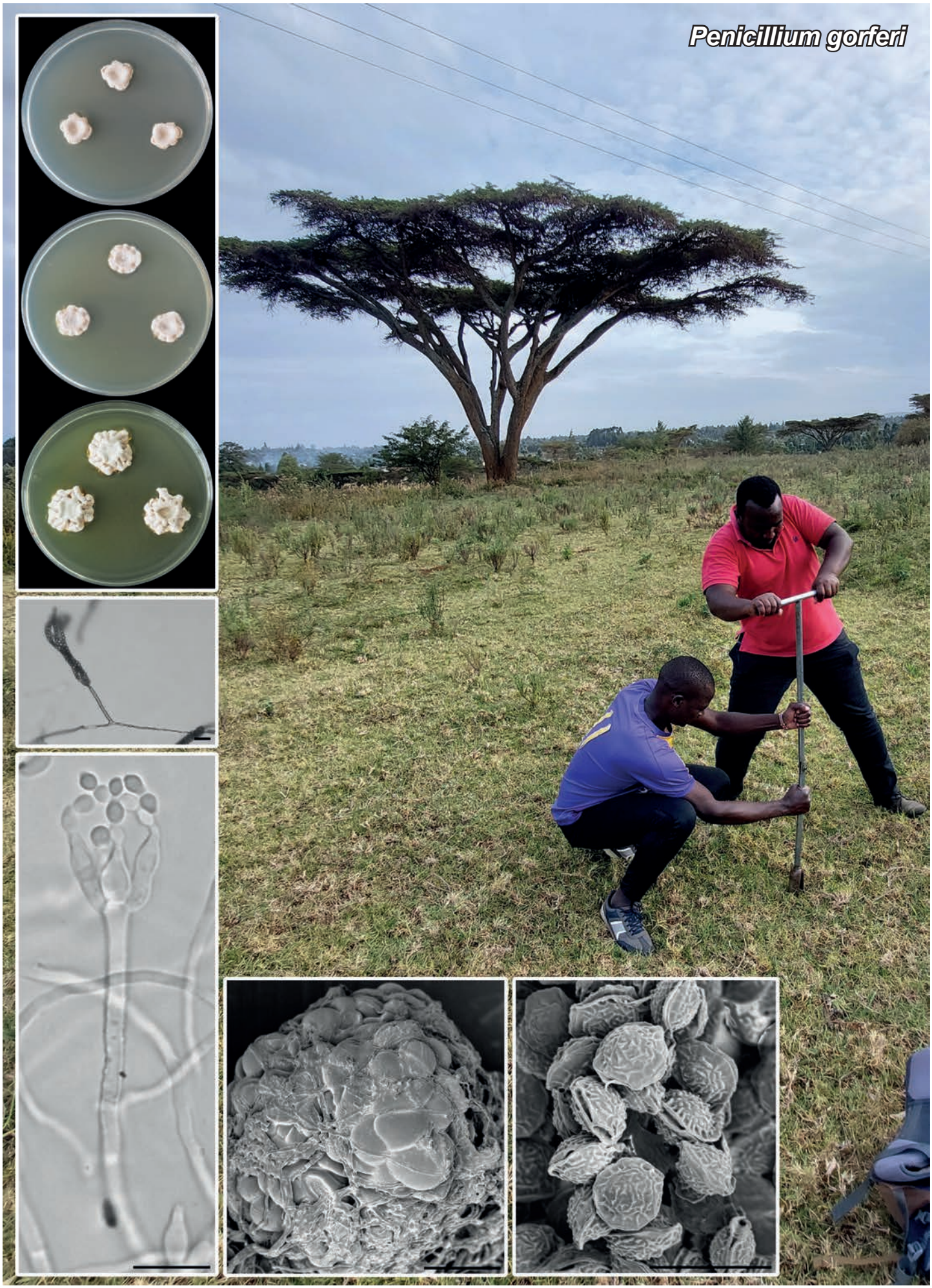
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Oxydothis phoenicis* [strain MFLUCC 18-0269, GenBank MK088065.1; Identities = 491/540 (91.06 %), seven gaps (1.2 %)], *O. cyrtostachicola* [strain MRC-007, GenBank DQ660334.1; Identities = 499/540 (92.43 %), 25 gaps (4.6 %)], *O. palmicola* [strain MFLUCC 15-0806, GenBank KY206776.1; Identities = 540/606 (89.2 %), 22 gaps (3.6 %)], and *O. metroxylicola* [strain MFLUCC 15-0281, GenBank NR_189794.1; Identities = 540/606 (89.2 %), 34 gaps (5.6 %)]. Closest hits using the **LSU** sequence are *O. garethjonesii* [strain MFLUCC 15-0287, GenBank NG_067548.1; Identities = 891/905 (98.48 %), one gap (0 %)], *O. frondicola* [strain HKUCC 1001, GenBank AY083835.1; Identities = 844/859 (98.24 %), no gaps], *Pseudotruncatella arezzoensis* [strain MFLUCC 14-0988, GenBank MG192317.1; Identities = 882/916 (96.25 %), one gap (0.1 %)], *O. chinensis* [strain ZHKUCC 22-0134, GenBank OR164957.1; Identities = 838/871 (96.13 %), two gaps (0.2 %)], and *O. metroxyli* [strain MFLUCC 15-0283, GenBank NG_241885.1; Identities = 1 156/1 201 (96.23 %), no gaps].

Colour illustrations: Holotype collection area in Chiang Rai, Thailand. Appearance of ascomata on dead leaf of *Copernicia alba*; vertical section of ascoma; asci; ascospores. Scale bars: section = 75 µm; asci = 50 µm; ascospores = 15 µm.



Phylogenetic analysis for *Oxydothis coperniciae* inferred from a maximum likelihood analysis of ITS/LSU sequences. The analysis was performed with RAxML v. 8.2.12 (Stamatakis 2014) using the rapid bootstrapping and search algorithm, with GTR+GAMMA nucleotide substitution model, and 1 000 bootstrap replicates. Maximum likelihood support values > 65 % are indicated on the branches. The tree is rooted with *Vialaea mangiferae* (MFLUCC12-0808) and *V. minutella* (BRIP 56959). Ex-type strains are in **bold**. The novel species is indicated in a blue box. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Scale bar on the tree indicates the expected number of changes per site. The matrix and the resulting tree have been deposited at TreeBASE (study ID: S31149).

D.S. Tennakoon, Bioengineering and Technological Research Centre for Edible and Medicinal Fungi, Jiangxi Agricultural University, Nanchang 330045, China; e-mail: danushkasandaruwanatm@gmail.com
N. Suwannarach, Faculty of Science, Department of Biology, Chiang Mai University, 50200, Chiang Mai, Thailand; e-mail: suwan.462@gmail.com



Fungal Planet 1654 MycoBank MB 851136

Penicillium gorferi Labuda, A. Schüller, M. Dalecká & Kubátová, *sp. nov.*

Etymology: Latin, *gorferi,* named in honour of Markus Gorfer from the Austrian Institute of Technology, an expert in fungal molecular ecology.

Classification: *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes.*

Cleistothecia produced on all media tested, after 3 wk, cream to light tan or yellowish brown, (40–)80–150(–250) µm; peridium sclerotioid, formed by polygonal thick-walled cells, at first hard, ripening within 8–12 wk. *Asci* born in short chains (3–6 per cluster) as terminal or lateral branches from ascogenous hyphae, 8-spored, 5–7.5 × 5–6.5 µm. *Ascospores* broadly lenticular from lateral view and globose from front view, hyaline to yellowish, (2.5–)3–3.5(–4) × 2–2.5(–3) µm (av. = 3.3 ± 0.2 × 2.2 ± 0.3 µm, n = 30), with two well separated equatorial ridges (crests), ± 0.5 µm wide, convex surface (valves) roughened, under scanning electron microscope (SEM) showing distinct reticulate pattern.

Conidiophores produced on SNA and WA at 25 °C after 5 wk in darkness, typically monoverticillate, born from surface or aerial hyphae; *stipes* (18–)25–45(–90) × 1.5—2 µm, hyaline, smooth-walled to coarsely rough or tuberculate, non-vesicular to slightly swollen tip, 2.5–3 µm; *phialides* flask-shaped (ampulliform), in verticils of 5–7, (4.5–)5.5–6.5(–8.5) × (1.5–)2–2.5(–3.5) µm, with short necks; *conidia* broadly ellipsoidal to subglobose, (1.5–)2(–2.5) (av. = 2.0 ± 0.2, n = 30), with smooth to finely roughened walls, produced in short to long, tangled chains, and after 7 wk forming false heads. *Sclerotia* absent.

Culture characteristics (in darkness, 25 °C, 7 d): Colonies on Czapek agar (CZ) 4–7 mm (11–13 mm after 14 d), convex, centrally plane or slightly crateriform, margins narrow, texture velutinous to floccose; aerial mycelium conspicuous, white at the margins, cream to light tan across the colonies; sporulation absent; exudate absent; reverse white to cream. Colonies on Czapek yeast extract agar (CYA) 7–9 mm (14–16 mm after 14 d), convex, up to 3 mm deep, centrally slightly umbonate to crateriform, at the margins strongly concentrically sulcate, margins narrow and slightly lobate, texture velutinous to floccose; aerial mycelium white to cream tan; sporulation absent; exudate present as minute clear droplets; reverse white to cream. Colonies on malt extract agar (MEA) 7–9 mm (14–16 mm after 14 d), similar as on CYA, cream tan, with more sulcate and lobate colonies; sporulation absent; exudate absent; reverse white to creamy. Colonies on yeast extract agar (YES) 12–14 mm (22–25 mm after 14 d), centrally strongly umbonate and crateriform, radially and concentrically deeply furcate, margins narrow and strongly lobate, texture velutinous to floccose; aerial mycelium white to cream tan; sporulation sparse, grey green to blue green; exudate absent; reverse cream. Colonies on creatine sucrose agar (CREA), weak growth, 8–10 mm (14–15 mm in after 14 d), acid not produced. Colonies on synthetic nutrient agar (SNA) after 5 wk, 15–18 mm, plane, white to tan centrally; sporulation sparse, scattered in central and subcentral areas; reverse white. Water agar (WA) after 5 wk similar as on SNA, 5–7 mm, translucent colonies, poor sporulation with conidiophores scattered mostly in subcentral areas; reverse white.

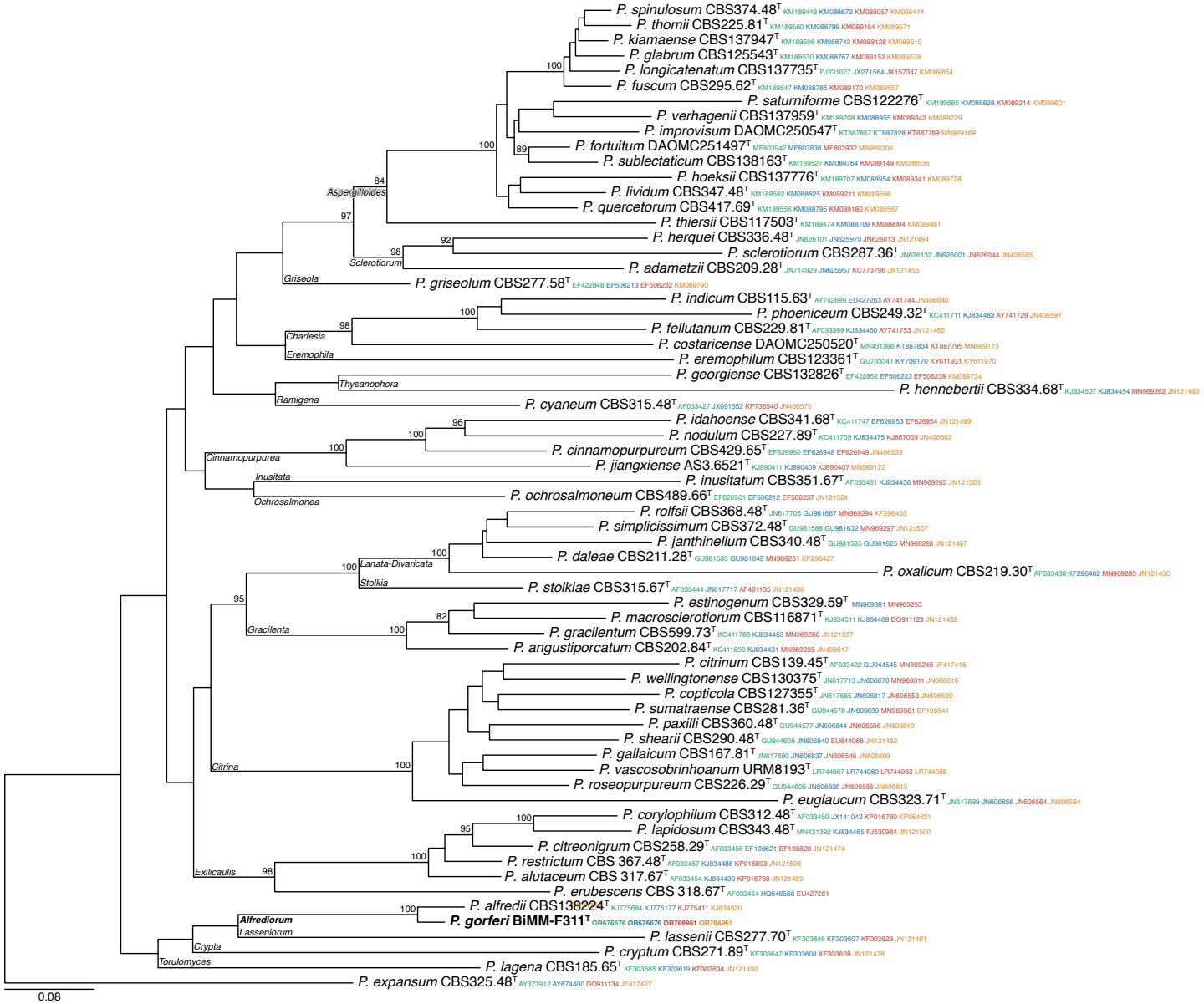
Colony diam (in mm, after 14 d): CYA at 37 °C no growth, at 33 °C germination, at 32 °C 2–4, at 30 °C 9–11, at 20 °C 5–6, at 10 °C microcolonies, at 6 °C no growth. MEA at 37 °C no growth, at 33 °C germination, at 32 °C 1–3, at 30 °C 5–10, at 20 °C 4–6, at 10 °C microcolonies, at 6 °C no growth.

Secondary metabolites: bilaid A, brevianamid F, NP 124, pyrenocin A, questiomycin, rugulusovin.

Typus: **Republic of Kenya**, Njoro, Egerton University campus (approximate coordinates: 0°22'09.3"S,, 35°55’24.2”E), from a sterile chicken feather embedded in a soil sample [top layer (20 cm)] close to the trunk of an *Acacia tortilis* tree, Feb. 2022, coll. *Andreas Schüller*, isol. *R. Labuda* [holotype PRM 959949 (dried culture in metabolically inactive state), culture ex-type BiMM-F311 = CCF 6700 = CBS 151105; ITS, *BenA*, *CaM*, *TEF*, and *RPB2* sequences GenBank OR676676, OR768960, OR768961, OR795058, and OR795059].

Notes: A multigene phylogeny resolves *P. gorferi* as the closest relative of *P. alfredii* in subgenus *Aspergilloides* section *Alfrediorum*. However, sequence similarities between *P. gorferi* and *P. alfredii* are low, with *BenA* differing by 38 bp, *CaM* by 24 bp, *RPB2* by 41 bp and ITS by 54 bp. Homology searches found no similar sequences in the NCBI and UNITE databases. Compared to *P. alfredii*, *P. gorferi* consistently produces cleistothecia, grows faster on CYA at 30 ºC (9–11 *vs* 5–6), generally sporulates poorer and produces broadly ellipsoid to subglobose (*vs* globose) and slightly smaller [(1.5–)2–2(–2.5) *vs* 2–2.5 µm) conidia (Visagie *et al*. 2014].

Colour illustrations: Site at the Egerton University campus, where Victor Apondi Omondi and Kelvin Kariuki Muli collected the soil sample. Colonies on CYA, MEA and YES; conidiophores with conidia; cleistothecium; ascospores. Scale bars: conidiophores with conidia = 10 µm; cleistothecium = 20 µm; ascospores = 5 µm.



Combined phylogeny of *BenA*, *CaM*, *RPB2* and ITS showing the relationship of *P. gorferi* with other *Penicillium* species classified in subgenus *Aspergilloides* representative of the sections and series defined by Houbraken *et al*. (2020). Aligned data sets (MAFT v. 7.450) were analysed using Maximum Likelihood (IQ-TREE v. 2.2.2.7). Bootstrap support values (≥ 80 %) are shown at branches. The new species is indicated by **bold** text, ^{T} = ex-type strain and GenBank accession numbers are shown in a smaller font next to the culture accession number (ITS = green, *BenA* = blue, *CaM* = red, *RPB2* = orange). The tree is rooted to *Penicillium expansum*.

M. Dalecká, Imaging Methods Core Facility at BIOCEV, Faculty of Science, Charles University, Průmyslová 595, 252 42 Vestec u Prahy, Czech Republic, and Department of Genetics and Microbiology, Faculty of Science, Charles University, Viničná 5, 128 44 Prague 2, Czech Republic; e-mail: marketa.dalecka@natur.cuni.cz

A. Kubátová, Department of Botany, Faculty of Science, Culture Collection of Fungi (CCF), Charles University, Benátská 2, 128 00 Prague 2, Czech Republic; e-mail: alena.kubatova@natur.cuni.cz

A. Schüller, Fungal Genetics and Genomics Laboratory, Department of Applied Genetics and Cell Biology, Institute of Microbial Genetics, University of Natural Resources and Life Sciences, Vienna (BOKU); Konrad Lorenz Strasse 24, 3430 Tulln a.d. Donau, Austria; e-mail: andi.schueller@gmx.at

R. Labuda, Unit of Food Microbiology, Department for Farm Animals and Veterinary Public Health, Institute of Food Safety, Food Technology and Veterinary Public Health, University of Veterinary Medicine Vienna, Veterinaerplatz 1, 1210 Vienna, and Research Platform Bioactive Microbial Metabolites (BiMM), Konrad Lorenz Strasse 24, 3430 Tulln a.d. Donau, Austria; e-mail: roman.labuda@vetmeduni.ac.at

Fungal Planet 1655 MycoBank MB 852808

Phylloporia parvateya M. Kaliyaperumal & S. Gunaseelan, *sp. nov.*

Etymology: "*parvateya*" in Sanskrit refers to "belonging to the mountain".

Classification: *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiome annual, sessile, pileate, applanate to imbricate, woody corky and without *odour* or *taste* when fresh, becoming hard corky and light in weight when dry. *Pilei* applanate, fused, single pileus projecting up to 3 cm long, 3.2 cm wide and 1.5 cm thick at the base. *Pileal surface* brown (6E8; Kornerup & Wanscher 1978) to dark brown (6F8), concentrically, narrowly zonate, tomentose with upper tomentum up to 1 mm thick, brown (6E8). *Margin* light brown (5D8) to brown (6E7), acute to obtuse, up to 3 mm in thick. *Pore surface* dark brown (6F8), with slightly velutinate, distinct sterile margin yellowish brown (5E8) to brown (6E8), up to 1 mm wide. *Pores* circular to angular, 7–10 per mm, dissepiments thin, entire. *Context* brown (6E7), up to 2 mm thick, duplex with a black line between tomentum and lower fibrous context. *Tubes* yellowish brown (5E8), up to 2 mm long. Hyphal system mono-dimitic; tissue darkening but otherwise unchanged in KOH. *Upper context* tomentum i.e. above the dark line has generative hyphae, pale yellowish to brown turning golden brown to rusty brown in KOH, thin to thick walled with a wide lumen, rarely branched, frequently septate, 1.8–5.2 µm wide. *Lower context* Generative hyphae hyaline to pale yellowish, slightly thin to thick walled with a wide lumen, frequently branched and septate, 1.5–2.7 µm wide. *Tubes* Generative hyphae hyaline to pale yellowish, thin to slightly thick walled, occasionally branched, frequently septate, 1.8–3 µm in wide; Skeletal hyphae golden yellow, thick walled with a narrow lumen, unbranched, aseptate, interwoven, 1.5–3 µm in wide. *Cystidia* and *Setae* absent. *Cystidioles* fucoid with tapering ends, 7–22 × 1.5–3 µm. *Basidioles* clavate to broadly clavate, 4.8–14 × 2.4–5.3 µm. *Basidia* clavate, with four sterigmata up to 3 µm long and a simple septum at the base, 5–12 × 3–6 µm. *Basidiospores* broadly ellipsoid to ellipsoid, hyaline to pale yellowish, thin to thick-walled, smooth, non-dextrinoid, inamyloid, acyanophilous to cyanophilous, (2.4–)2.6–2.9(–3.2) × (1.8–)2.1–2.6(–2.9) µm, L = 2.8 µm, W = 2.4 µm, Q = 1.17 (Q ranges from 1–1.4) (n = 50/2).

Typus: **India**, Tamil Nadu, Thiruvannamalai, Javadhu hills, Thenmalai, N12°61'96.88", E78°92'59.86", on living vine of *Lonicera* sp., 3 Feb. 2018, *G. Sugantha*, SMK-TM21 (**holotype** MUBL1102; ITS and LSU sequences GenBank PP375183 and PP375288).

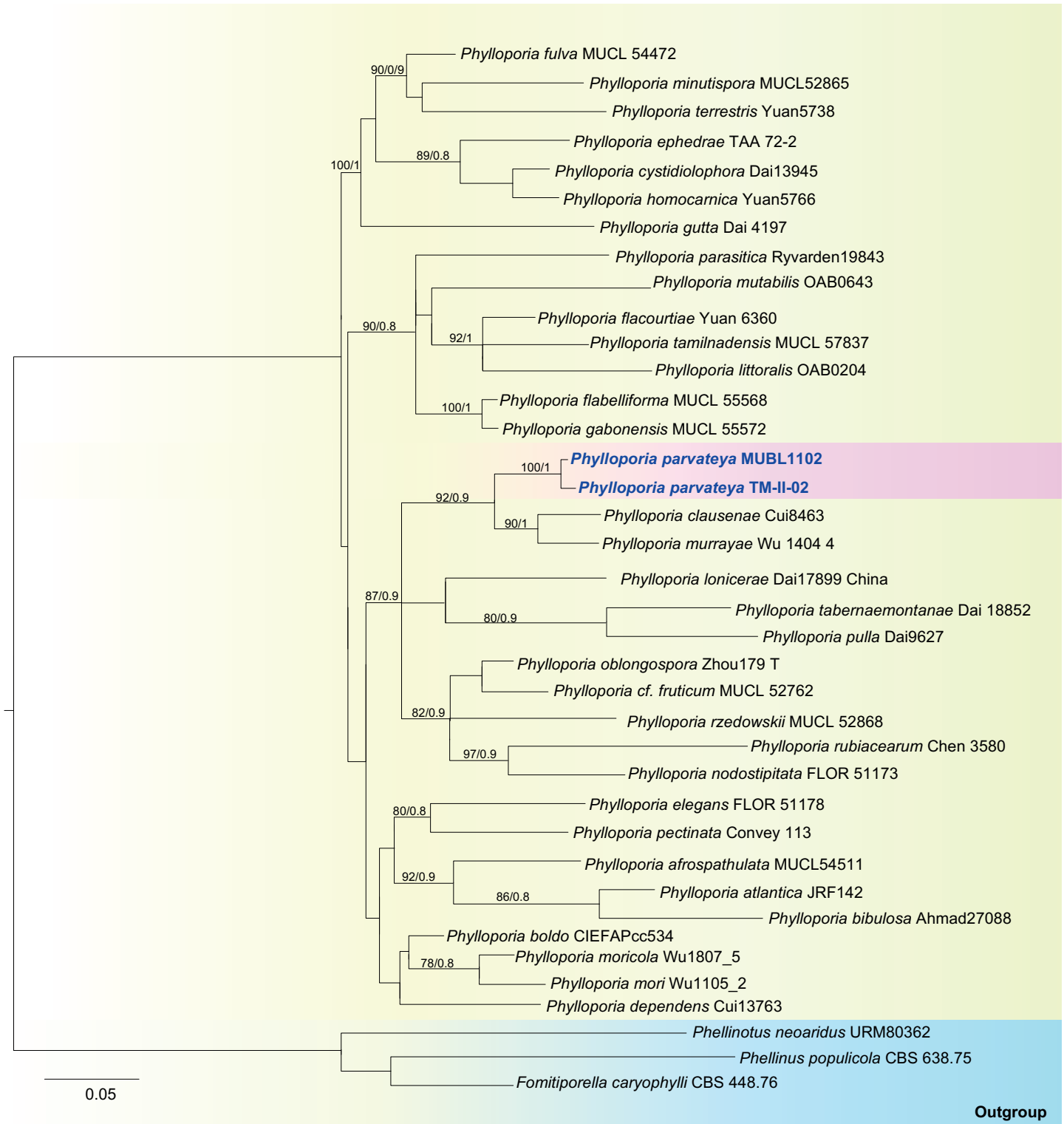
Additional material examined: **India**, Tamil Nadu, Thiruvannamalai, Javadhu hills, Thenmalai, N12°61'92.90", E78°92'25.55", on living vine of *Lonicera* sp., 11 Jan. 2019, *K. Malarvizhi* (**paratype** TM-II-02; ITS and LSU sequences GenBank PP375182 and PP375287).

Notes: *Phylloporia parvateya* clusters as a distinct lineage sister to the *P. clausenae* and *P. murrayae* clade (ML 92 %, 0.9 BP). *Phylloporia parvateya* resembles *P. clausenae* and *P. murrayae*, only in the presence of a duplex context with black line, but our Indian species significantly differs with other morpho-microtaxonomic characters in lacking a sulcate pileus, acute margin, mono-dimitic hyphal system, presence of cystidioles and smaller basidiospores (*Phylloporia parvateya* 2.4–3.2 × 1.8–2.9 µm *vs P. clausenae* 3–4 × 2–3 µm *vs P. murrayae* 3–3.7 × 2.5–3.2 µm) (Zhou *et al*. 2015, Wu *et al*. 2020).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phylloporia* sp. [strain Wu1404-4, GenBank LC528149; Identities = 775/831 (93 %), 10 gaps (1 %)], *Phylloporia* sp. [strain Wu1404-5, GenBank D: LC528150; Identities = 732/799 (92 %), 11 gaps (1 %)], and *Phylloporia clausenae* [strain Cui8463, GenBank MH151186; Identities = 725/799 (91 %), 13 gaps (1 %)]. Closest hits using the **LSU** sequence are *Phylloporia clausenae* [strain Cui8463, GenBank MH165868; Identities = 894/918 (97 %), two gaps (0 %)], *Phylloporia pulla* [strain O6433, GenBank MG738809; Identities = 879/916 (96 %), no gaps], and *Phylloporia murrayae* [strain Wu 1404-6, GenBank LC514411; Identities = 873/907 (96 %), five gaps (0 %)].

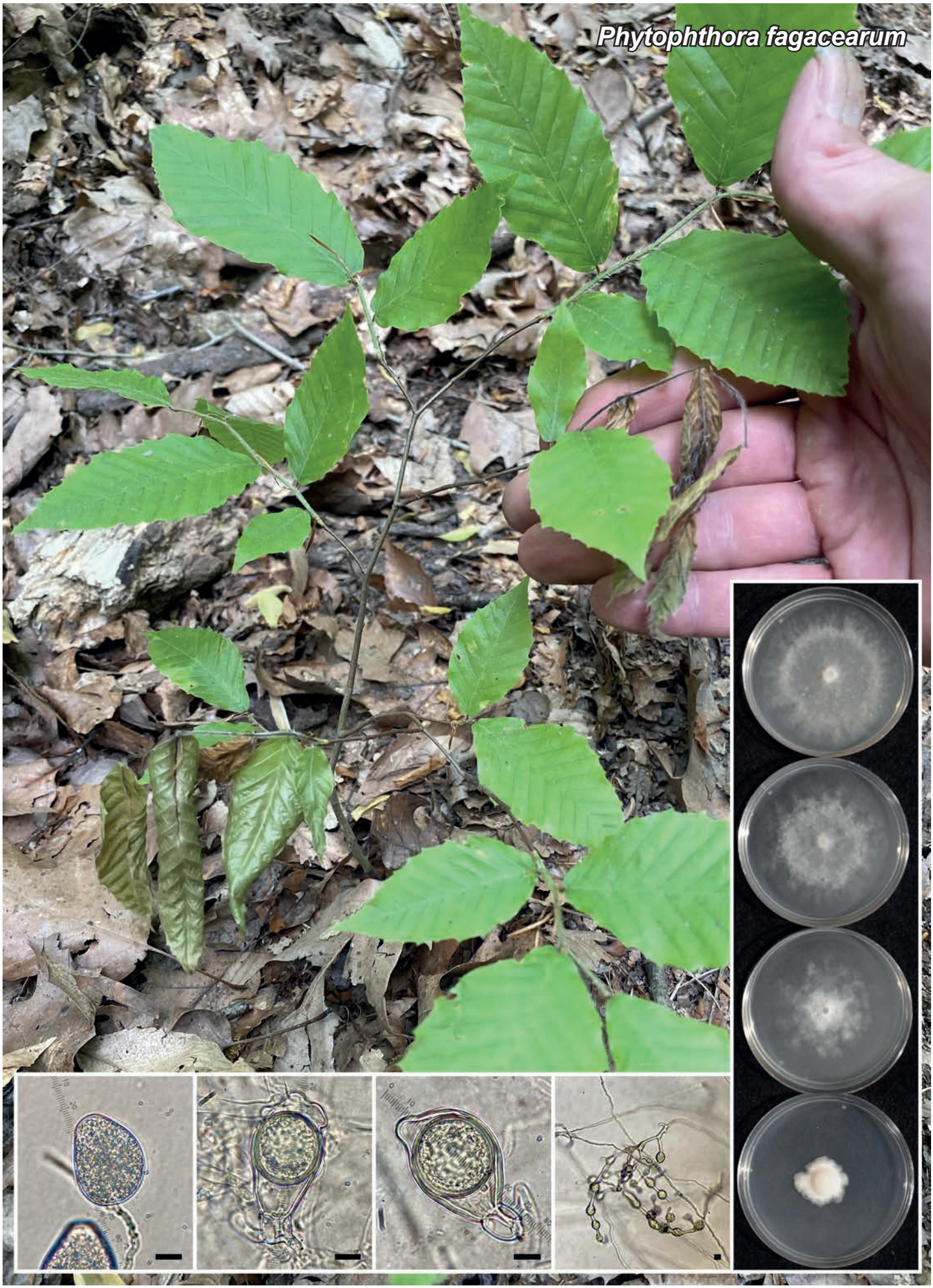
Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Holotype collection area, India. Habitat; pilear surface; transverse section of basidiomata (arrows indicating duplex context with black line); microscope illustrations and *camera lucida* drawing of holotype: tramal hyphae, contextual hyphae; cystidioles; basidioles; basidia and basidiospores. Scale bars: sporocarps = 1 cm; all other structures = 5 µm.



Phylogenetic tree inferred from ITS+LSU sequences of *Phylloporia parvateya* (MUBL1102, holotype and TM-II-02) and related species rooted with *Fomitiporella caryophylli* (CBS 448.76) and *Phellinotus neoaridus* (URM80362). The maximum likelihood (ML) analysis was performed using MEGA v. X (Kumar *et al.* 2018) and the same data were used for a Bayesian analysis using MrBayes v. 3.2.7 (Ronquist *et al*. 2012). Branches are labelled with ML bootstrap support and Bayesian posterior probabilities values (BPP). Novel species is in **bold**. The alignment and tree are available from TreeBASE (study ID: 31230).

S. Gunaseelan, M. Kaliyaperumal & K. Kezo, Centre for Advanced Studies in Botany, University of Madras, Chennai, Tamil Nadu, India-600 025;
e-mail: suganthagunseelan@gmail.com, malar.kaliyaperumal@gmail.com & z.kezh.kezo@gmail.com



Fungal Planet 1656

MycoBank MB 849919

Phytophthora fagacearum D.S. Bily, X. Yang, C.E. Giles & S.N. Jeffers, *sp. nov.*

Etymology: Named after the host from which it was isolated, *Fagus grandifolia*, in the family *Fagaceae*, in the genitive (possessive case), feminine, plural form, meaning that the members of the beech family "possess" or "own" this species.

Classification: *Peronosporaceae*, *Peronosporidae*, *Oomycota*.

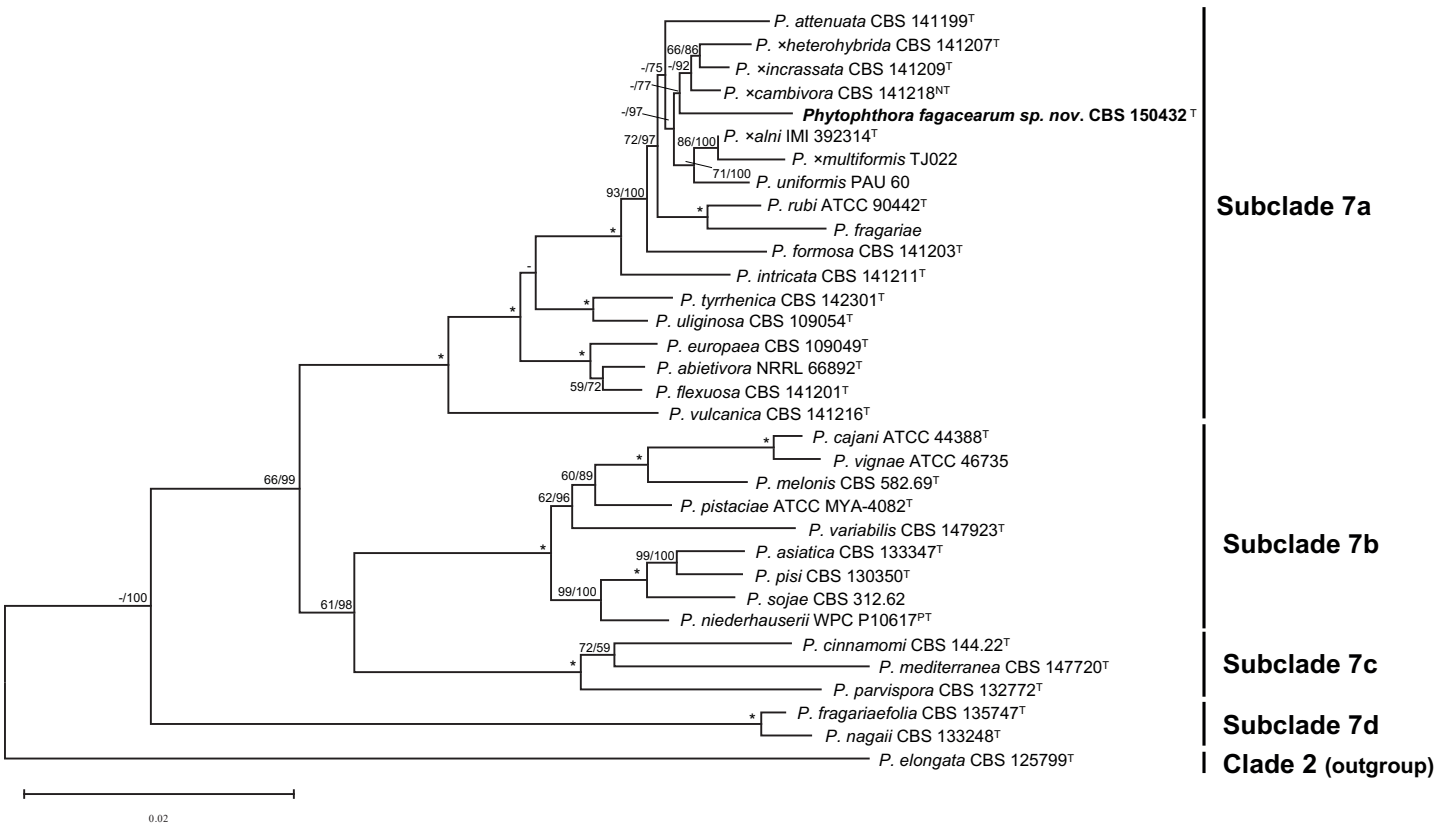
Sporangia produced sparingly on 10 % clarified V8 agar (cV8A) and 10 % V8A flooded with both distilled water and 1.5 % non-sterile soil extract; terminal, persistent, usually produced on unbranched sporangiophores, non-papillate, predominately ovoid (76 %) and occasionally globose (24 %); 30.2 ± 3.5 × 25.2 ± 2.4 µm (overall range 25.5–39.6 × 21.9–30.7 µm), length/width ratio of 1.20 ± 0.08. Simple sporangiophores with internal sporangium proliferation including both extended and nested types. *Hyphal swellings* abundant, in various shapes (catenulate and globose), 9.2 ± 3.5 µm (overall range 4.9–15.8 µm on most media (cV8A, 10 % super cV8A, PAR-V8, PARPH-V8). *Chlamydospores* absent. *Gametangia* abundantly produced in single-isolate cultures (homothallic). *Oogonia* smooth-walled and bullate, occasionally turning golden in colour, and often distorted in shape (globose to ellipsoid to pyriform), 33.3 ± 4.8 µm (overall range 24.7–41.6 µm); oogonium base often distinctly tapered and funnel-shaped. *Oospores* were aplerotic (56 %) to plerotic (44 %), av. 22.7 ± 4.2 µm (overall range 16.1–29.1 µm), with a cell wall diameter averaging 2.03 ± 0.42 µm. *Antheridia* were both amphigynous (56 %) and paragynous (44 %), monoclinous, spherical to ellipsoidal, 11.9 ± 2.2 µm (overall range 7.8–17.4 µm). *Hyphae* hyaline, non-septate, smooth, and fine in diameter, 3.63 ± 1.13 µm (overall range 1.98–6.9 µm). Minimum, optimum, and maximum temperatures for growth were 10 °C, 25 °C, and 38 °C, respectively; radial growth on cV8A in the dark after 7 d for these temperatures was 2.1 ± 0.2 mm, 25.8 ± 0.5 mm, and 4.8 ± 0.0 mm, respectively.

Culture characteristics: Colonies mostly uniform without a distinct pattern and with slightly undulated to entire margins produced on all media [V8A, cV8A, super cV8A, potato dextrose agar (PDA)]. Colonies produced both appressed and aerial mycelium on most media. Colonies on PDA restricted and densely aerial. Sexual structures were produced abundantly in any V8 juice-based medium but not in PDA. Mycelium growth was inhibited (33 %) by hymexazol in PARPH-V8 selective medium and was sensitive to the fungicide mefenoxam at 100 ppm in 5 % cV8A.

Typus: **USA**, Lancaster County, Pennsylvania, 39°46'46.6"N, 76°14'55.8"W, from necrotic leaves and shoots of *Fagus grandifolia* (*Fagaceae*) in a mesophytic old-growth forest remanent along the Susquehanna River, 19 Jun. 2020, *D.S. Bily* (**holotype** PDA2233, culture ex-type CBS 150432; ITS, LSU, *cox1*, *tub2*, *hsp90*, *nadh1*, *nad9*, and *tigA* sequences GenBank MW882105, OQ919737, MW927566, MW927585, OQ923271, MW927556, MW927594, and OQ923272).

Notes: *Phytophthora fagacearum* was recovered from a single *F. grandifolia* sapling; therefore, only one isolate was available for characterisation. In a six-locus phylogeny, *P. fagacearum* (CBS 150432^{T}) is placed in *Phytophthora* subclade 7a (Yang *et al.* 2017). Based on individual pairwise sequence alignments, it differs from its closest relatives *P. attenuata* (CBS 141199^{T}), *P.* ×*cambivora* (CBS 141218^{T}), *P.* ×*heterohybrida* (CBS 141207^{T}), and *P.* ×*incrassata* (CBS 141209^{T}) by 85 bp (98.5 % identity), 95 bp (98.3 % identity), 81 bp (98.5 % identity), and 95 bp (98.3 % identity), respectively. Morphologically, *P. fagacearum* shares its ovoid, non-papillate sporangia, tapering oospores, and hyphal swellings with most clade 7a members. It differs from its closest relatives by its smaller sporangia and l/b ratio, smaller diameter oospores, and higher maximum temperature for growth (Jung *et al*. 2017).

Colour illustrations. Necrotic shoots of *Fagus grandifolia* infected with *P. fagacearum*. Ovoid, non-papillate sporangium; distorted oogonium with plerotic oospore and amphigynous antheridium; oogonium with a tapered base and amphigynous antheridium; globose, catenulate hyphal swellings in dH_2O after 48 h; colonies on cV8A, PAR-V8, PARPH-V8 (growth restricted by hymexazol), and PDA. Scale bars = 10 µm.



A maximum likelihood (ML) tree of *Phytophthora* clade 7 based on concatenated sequences (5 593 bp) of the ITS (843 bp), *tub2* (904 bp), *tigA* (1 591 nt.), *hsp90* (833 bp), *cox1* (643 bp), and *nadh1* (779 bp) genes. Both maximum likelihood (ML) and Bayesian inference analyses generated trees with similar topology using MrBayes v. 3.2.7 and raxmlGUI v. 2.0, respectively. Topology and branch lengths of the ML tree are shown. The ML bootstrap (BS) values and BI posterior probabilities > 50 % are separated by forward slash marks and given near nodes. The BS values and BI probabilities ≤ 50 % and ambiguous topologies are indicated by dash marks. The alignment and tree are available from TreeBASE (study ID: S30704).

D.S. Bily, Office of Plant Industry, Virginia Department of Agriculture and Consumer Services, 102 Governors St. 23219, Richmond, Virginia, USA;
e-mail: devin.bily@vdacs.virginia.gov
X. Yang, Department of Plant Industry, Clemson University, 511 Westinghouse Road 29670 Pendleton, South Carolina, USA;
e-mail: xyang7@clemson.edu
C.E. Giles & S.N. Jeffers, Department of Plant and Environmental Sciences, 214 Biosystems Research Complex 29631, Clemson, South Carolina, USA;
e-mail: cegiles@clemson.edu & sjffrs@clemson.edu

Fungal Planet 1657 MycoBank MB 853193

Pisolithus madagascariensis Rivas-Ferreiro, Dentinger, Suz & A.M. Ainsw., *sp. nov.*

Etymology: The epithet refers to the type locality of this species, which is in Madagascar.

Classification: *Sclerodermataceae*, *Boletales*, *Agaricomycetes*.

Basidiomes subglobose, 25–35 mm wide, close to sessile, with a very short pseudostipe. *Peridium* thin, with a mostly dry, velvety surface, saffron to buff (colour terminology follows Royal Botanic Garden Edinburgh, 1969), cracking when mature, with patches of a dark substance similar in consistency to parts of the glebal matrix. *Pseudostipe* very short, concolourous with the peridium. *Gleba* with a dark brown to black, gelatinous matrix, very thin when dry (< 0.5 mm). *Peridioles* discrete, 1.3–2.2 mm, angular and irregular, easily detachable from the context of the gleba when dry, covered in a thick, velvety, saffron coloured outer layer of thin interwoven hyphae; within it lies a purplish chestnut brown layer of immature spores, enveloping a clay pink core, where the mature spores reside. *Constituent hyphae* either intertwined and ramified, thin walled, hyaline, 1.9–2.5 µm wide, sparsely encrusted with yellow-brown material; or fulvous luteous, thick walled, irregularly septate, 3.75–6.5 µm wide, not encrusted. *Basidiospores* globose, milky coffee to vinaceous buff in mass, yellowish in water, (7.5–)8.75–10 µm diam, including ornamentation of conical, clumped spines, 0.8–1.2 µm in length. *Basidia* very rarely seen, club-shaped, hyaline, 4-spored, (6.2–)7.8–9.8 µm wide and around 21–27 µm long. *Cystidia and cystidioid cells* not observed. *Clamp-connections* present and abundant in the constituent hyphae.

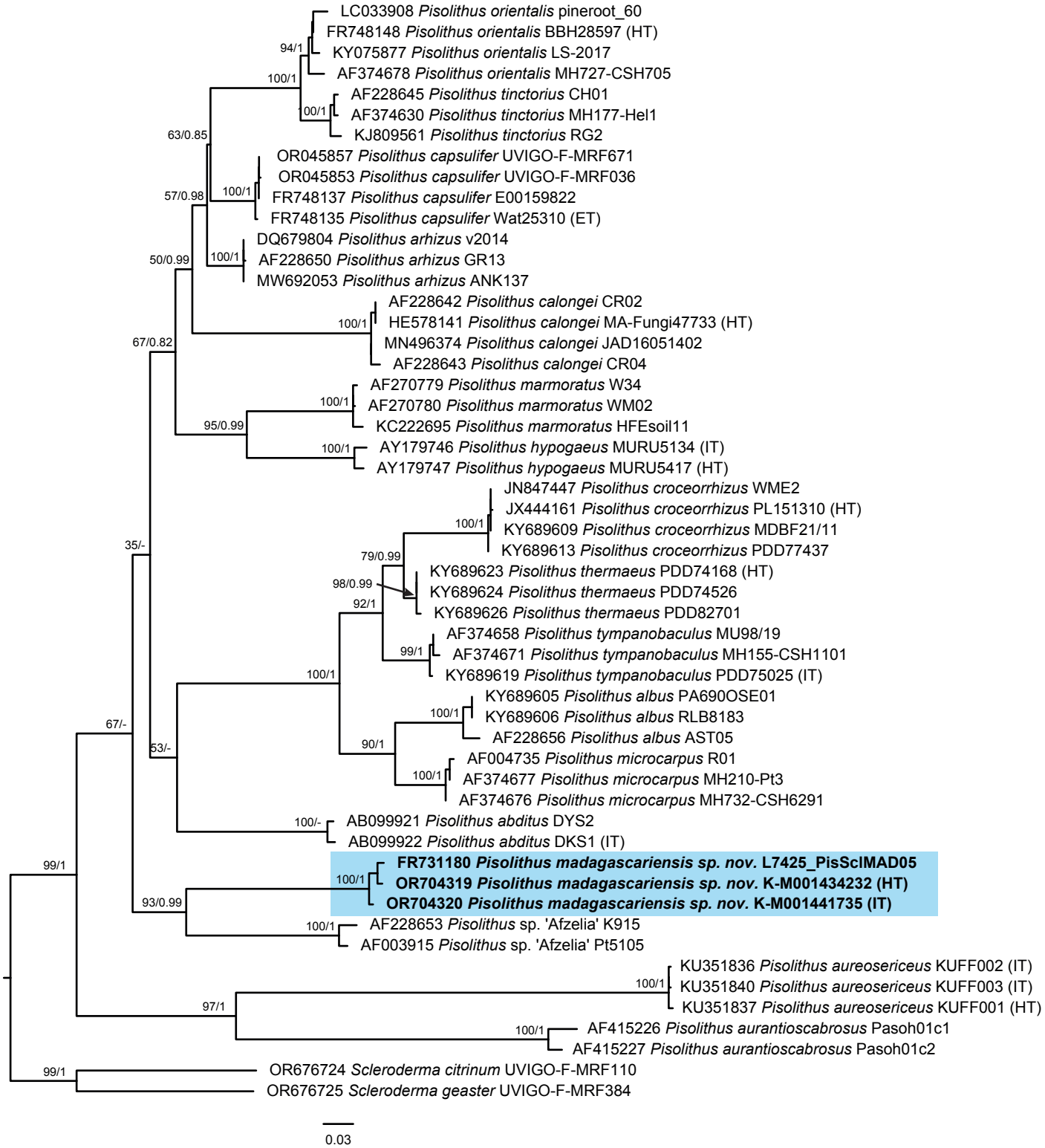
Habit, habitat and distribution: Epigeous, the holotype and isotype specimens growing under *Intsia bijuga*, with *Diospyros* spp., *Sarcolaenaceae* and *Asteropeiaceae* nearby; known to also occur in Isalo National Park and the Anosy region, from environmental DNA sequences obtained from soil and root samples taken under *Intsia bijuga*, *Sarcolaena* sp., *Uapaca* spp. and *Asteropeia* sp. So far, only found in southern Madagascar.

Typus: **Madagascar**, Anosy Region, Taolagnaro, Mandena, 24°57'S, 47°00'E, 16 m a.s.l., on soil under *Intsia bijuga* (*Fabaceae*) with species of *Diospyros*, *Asteropeiaceae* and *Sarcolaenaceae* nearby, 28 Nov. 2012, *B.T.M. Dentinger* (**holotype** K-M001434232; ITS and LSU sequences GenBank OR704319 and OR676700).

Additional material examined: **Madagascar**, Anosy Region, Taolagnaro, Mandena, 24°57'S, 47°00'E, 16 m a.s.l., on soil under *I. bijuga* with species of *Diospyros*, *Asteropeiaceae* and *Sarcolaenaceae* nearby, 28 Nov. 2012, *B.T.M. Dentinger* (**isotype** K-M001441735; ITS sequence GenBank OR704320).

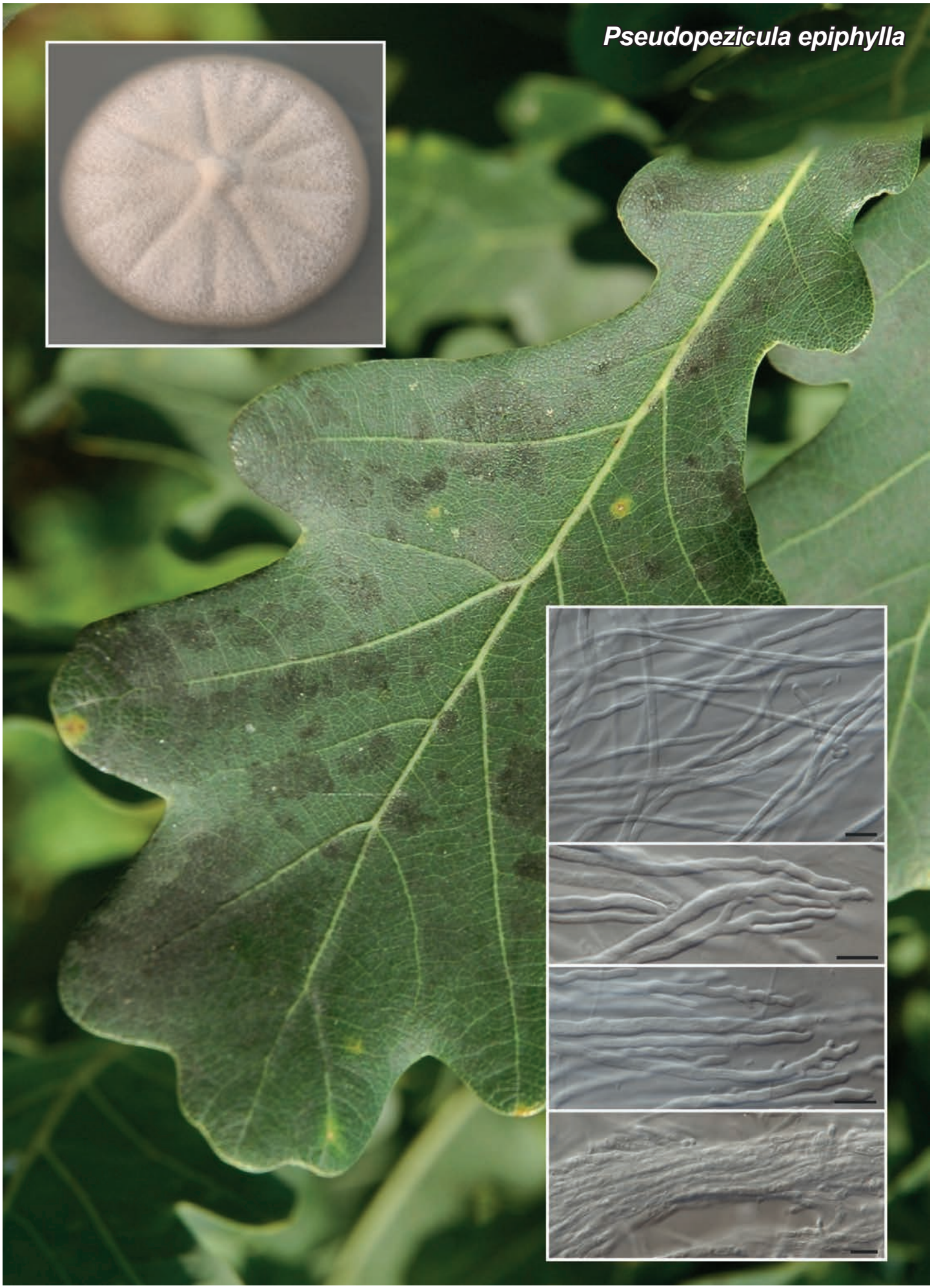
Notes: *Pisolithus madagascariensis* is well differentiated from other *Pisolithus* species by its small size, its velvety saffron-buff peridium and the presence of easily detachable peridioles covered in a thick layer of saffron-coloured hairs. Three other species of *Pisolithus* are known to occur in Madagascar: *P. albus*, *P. marmoratus* and *P. microcarpus*. Several DNA sequences obtained through soil metabarcoding from Madagascar (Tedersoo *et al.* 2021; collected under *Intsia bijuga*, *Sarcolaena*, *Uapaca* and *Asteropeia,* in Isalo National Park and the Anosy region), and one ectomycorrhizal root sample (Tedersoo *et al.* 2011; *Uapaca bojeri* as plant host, in Isalo National Park) were found to belong to this species in our phylogenetic analyses. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit to the ITS sequence of the holotype of *P. madagascariensis* was GenBank FR731180 (% pairwise identity = 99.13 %, query cover = 96 %) corresponding to a mycorrhizal root tip of *Uapaca bojeri* collected in Isalo National Park in Madagascar. Very little is known about the genus *Pisolithus* in continental Africa and Madagascar. Martin *et al.* (1998) and Díez *et al.* (2001) cite a *Pisolithus* species distinct from all others, occurring in Kenya under *Afzelia* trees; our species seems to be related to this Kenyan *Pisolithus* sp., but it is molecularly and ecologically distinct. To our knowledge, *Pisolithus madagascariensis* is the first species of the genus to be formally described and published for East Africa.

Colour illustrations: Path along Mandena Conservation Zone, Madagascar, where the holotype of *Pisolithus madagascariensis* was located (photo credit B.T.M. Dentinger). Right picture shows the holotype after collection; top left shows a longitudinal section of the holotype with the discrete peridioles in the centre; bottom left shows scanning electron micrograph of a spore from the type specimen. Scale bars: basidiome and section = 0.5 cm; spore = 5 µm.



Phylogenetic tree obtained by Maximum Likelihood and Bayesian analyses of the ITS region from *Pisolithus madagascariensis* (highlighted in blue) and related *Pisolithus* species. The alignment was obtained using MAFFT v. 7 (Katoh *et al.* 2019), the phylogenetic analysis was conducted in IQ-TREE v. 1.6.2 (Trifinopoulos *et al.* 2016) and the Bayesian analysis was conducted in MrBayes v. 3.2.7 (Ronquist *et al.* 2012). Two *Scleroderma* species were used as outgroups. Species types are designated with (HT) for holotypes, (IT) for isotypes and (ET) for epitypes. Scale bar = 0.03 expected changes per site. This tree can be found in https://doi.org/10.6084/m9.figshare.24318826. The alignment file can be found in https://doi.org/10.6084/m9.figshare.25517434.

M. Rivas-Ferreiro, Royal Botanic Gardens, Kew, TW9 3AE, Richmond, UK, and Centro de Investigación Mariña (CIM), Universidade de Vigo, 36310, Vigo, Spain; e-mail: m.ferreiro@kew.org
L.M. Suz & A.M. Ainsworth, Royal Botanic Gardens, Kew, TW9 3AE, Richmond, UK; e-mail: l.martinez-suz@kew.org & m.ainsworth@kew.org
B.T.M. Dentinger, Natural History Museum of Utah & School of Biological Sciences, University of Utah, UT 84108, Salt Lake City, Utah, USA; e-mail: bdentinger@nhmu.utah.edu
P. Morán, Centro de Investigación Mariña (CIM), Universidade de Vigo, 36310, Vigo, Spain; e-mail: paloma@uvigo.gal



Fungal Planet 1658 MycoBank MB 853238

Pseudopezicula epiphylla Piątek, Czachura & Stryjak-Bogacka, *sp. nov.*

Etymology: Name refers to the occurrence on the surface of the leaves.

Classification: *Discinellaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium composed of sparsely branched, septate, hyaline, straight to flexuous, thin-walled hyphae, 1.8–4.5 µm wide, often dendroidal at the tips, aerial hyphae often form fascicles. *Conidiophores* and *conidia* not observed [description on malt extract agar (MEA)].

Culture characteristics: Colonies on MEA low convex, whitish to pale cream, reaching 47 mm diam after 4 wk at 15 °C, no growth at 25 °C, with radial furrows from the colony centre toward margin, surface with dense aerial mycelium, margin entire. Reverse yellowish cream. Colonies on potato dextrose agar (PDA) umbonate, pale yellowish cream, 44 mm diam after 4 wk at 15 °C, no growth at 25 °C, with radial furrows from the colony centre toward margin, margin slightly crenate. Reverse yellowish cream.

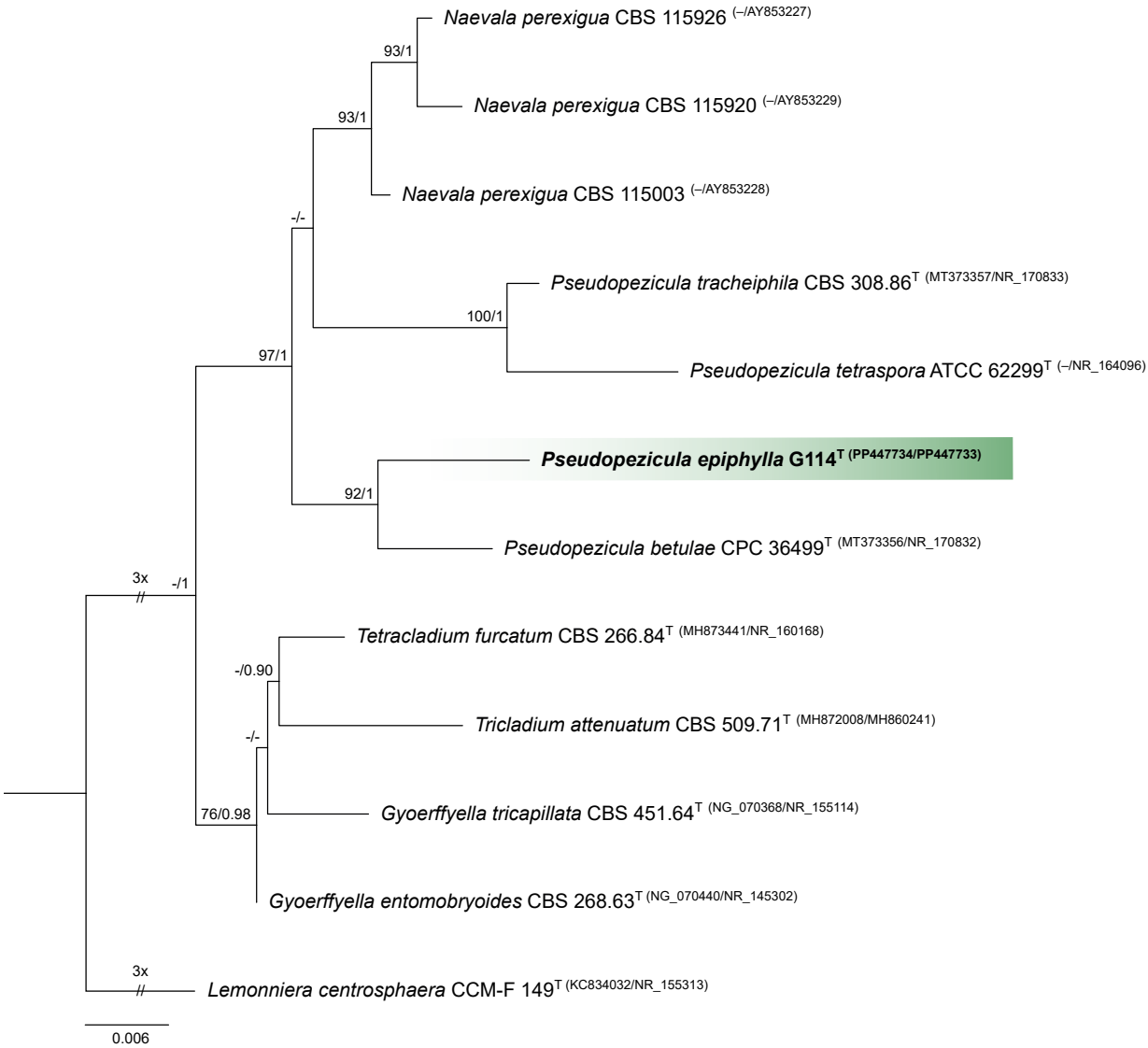
Typus: **Poland**, Podkarpackie Province, Rzeszów County, Rzeszów-Kmity, municipal greenery, isolated from sooty mould community on *Quercus robur* (*Fagaceae*) leaves, 17 Sep. 2018, *M. Piątek, W. Bartoszek & P. Czachura* (**holotype** KRAM F-59990, culture ex-type G114 = CBS 151612; ITS, LSU, and *rpb2* sequences GenBank PP447733, PP447734, and PP449094).

Notes: The genus *Pseudopezicula*, typified by *P. tetraspora*, contains three species that produce a sexual morph with minute apothecia, inoperculate asci and large, ellipsoid ascospores and/or phialophora-like asexual morph (Korf *et al*. 1986, Crous *et al.* 2020). *Pseudopezicula tetraspora* and *P. tracheiphila* are causal agents of angular leaf scorch on *Vitis* and *Parthenocissus* species (*Vitaceae*) in Europe and North America (Korf *et al.* 1986). *Pseudopezicula betulae* has been isolated from leaf spots of *Populus tremuloides* (*Salicaceae*) in the USA (Crous *et al.* 2020). *Pseudopezicula epiphylla* is phylogenetically closely related to *P. betulae*. The latter species forms phialophora-like asexual morph while *P. epiphylla* is sterile in cultures. Sequence divergence between them (19 bp in ITS, 2 bp in LSU, 140 bp in *rpb2*) supports *P. epiphylla* as distinct species. *Pseudopezicula epiphylla* was isolated from a sooty mould community on the leaves of *Quercus robur.* It is the first *Pseudopezicula* species on a host plant in *Fagaceae*.

Naevala perexigua (syn. *N. minutissima*) (cultures CBS 115003, 115920, 115926), which is the type of the genus *Naevala* (Hein 1976, Holm & Holm 1978) clusters within the *Pseudopezicula* clade in our two-locus sequence (LSU, ITS) analyses. This phylogenetic relationship is revealed here for the first time. *Naevala* (1976) is an older generic name than *Pseudopezicula* (1986) and therefore all *Pseudopezicula* species should be reallocated to *Naevala* if one generic name is to be applied to this clade. Multi-locus phylogenetic analyses and epitypification of *Naevala perexigua* are however necessary to propose any nomenclatural changes in this clade.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits (named species) using the **ITS** sequence are *Naevala perexigua* (syn. *N. minutissima*) [culture CBS 115926, GenBank AY853227; Identities = 427/442 (97 %), three gaps (0 %)], *Pseudopezicula betulae* [culture CPC 36499, GenBank NR_170832; Identities = 477/496 (96 %), no gaps] and *Gyoerffyella entomobryoides* [culture CBS 268.63, GenBank NR_145302; Identities = 486/506 (96 %), three gaps (0 %)]. The closest hits using the **LSU** sequence are *Pseudopezicula betulae* [culture CPC 36499, GenBank MT373356; Identities = 833/835 (99 %), no gaps], *Lemonniera aquatica* [culture DSM 104336, GenBank OR243763; Identities = 844/850 (99 %), no gaps] and *Lemonniera terrestris* [culture DSM 104343, GenBank OR243769; Identities = 844/850 (99 %), no gaps]. The closest hits using the ***rpb2*** sequence are *Varicosporium elodeae* [culture CCM F-04276, GenBank MK241435; Identities = 685/852 (80 %), two gaps (0 %)], *Phacidium subcorticalis* [voucher MFLU 19-2902, GenBank MT432243; Identities = 751/945 (79 %), 17 gaps (1 %)] and *Xenosphaeropsis corni* [culture CPC 42402, GenBank OQ627941; Identities = 631/797 (79 %), 15 gaps (1 %)].

Colour illustrations: Leaves of *Quercus robur* with sooty mould communities, Poland. Colony on MEA; hyphae, dendroidal hyphal tips and fascicle of aerial hyphae. Scale bars = 10 µm.



Phylogenetic tree of *Pseudopezicula* species and selected members of *Discinellaceae* obtained from a maximum likelihood analysis of the combined two-locus alignment (1 279 characters, including gaps: LSU/ITS). The maximum likelihood analysis and the Bayesian inference were performed using RAxML-NG v. 1.1.0 and MrBayes v. 3.2.6, respectively (Ronquist *et al.* 2012, Kozlov *et al*. 2019). The position of *Pseudopezicula epiphylla* is indicated in **bold** and marked by coloured block. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values > 70 % and Bayesian posterior probabilities (BPP) > 0.9, respectively (MLB/BPP). *Lemonniera centrosphaera* was used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (https://doi.org/10.6084/m9.figshare.25351285.v1).

M. Piątek, P. Czachura & M. Stryjak-Bogacka, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland; e-mail: m.piatek@botany.pl, p.czachura@botany.pl & m.bogacka@botany.pl

Fungal Planet 1659

MycoBank MB 852645

Purimyces D.O. Ramos & O.L. Pereira, ***gen. nov.***

Etymology: Name refers to the indigenous people called *Puri*, that live in the same regions of the orchid, where the fungus was isolated.

Classification: *Hyphodiscaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium colonises healthy roots of the orchid *Cattleya locatellii*. No reproductive morphs were observed. *Mycelium* septate, branched, smooth-walled, hyaline, forming mycelial strains. Colonies producing sticky exudates, with slimy aerial mycelium.

Type species: *Purimyces orchidacearum* D.O. Ramos & O.L. Pereira

MycoBank MB 852646

Purimyces orchidacearum D.O. Ramos & O.L. Pereira, ***sp. nov.***

Etymology: Name refers to *Orchidaceae*, the botanical family of the host from which this fungus was isolated.

Mycelium septate, branched, smooth-walled, hyaline, forming mycelial strains, 2.09–3.71 µm diam hyphae. *Sexual and asexual morphs* were not observed.

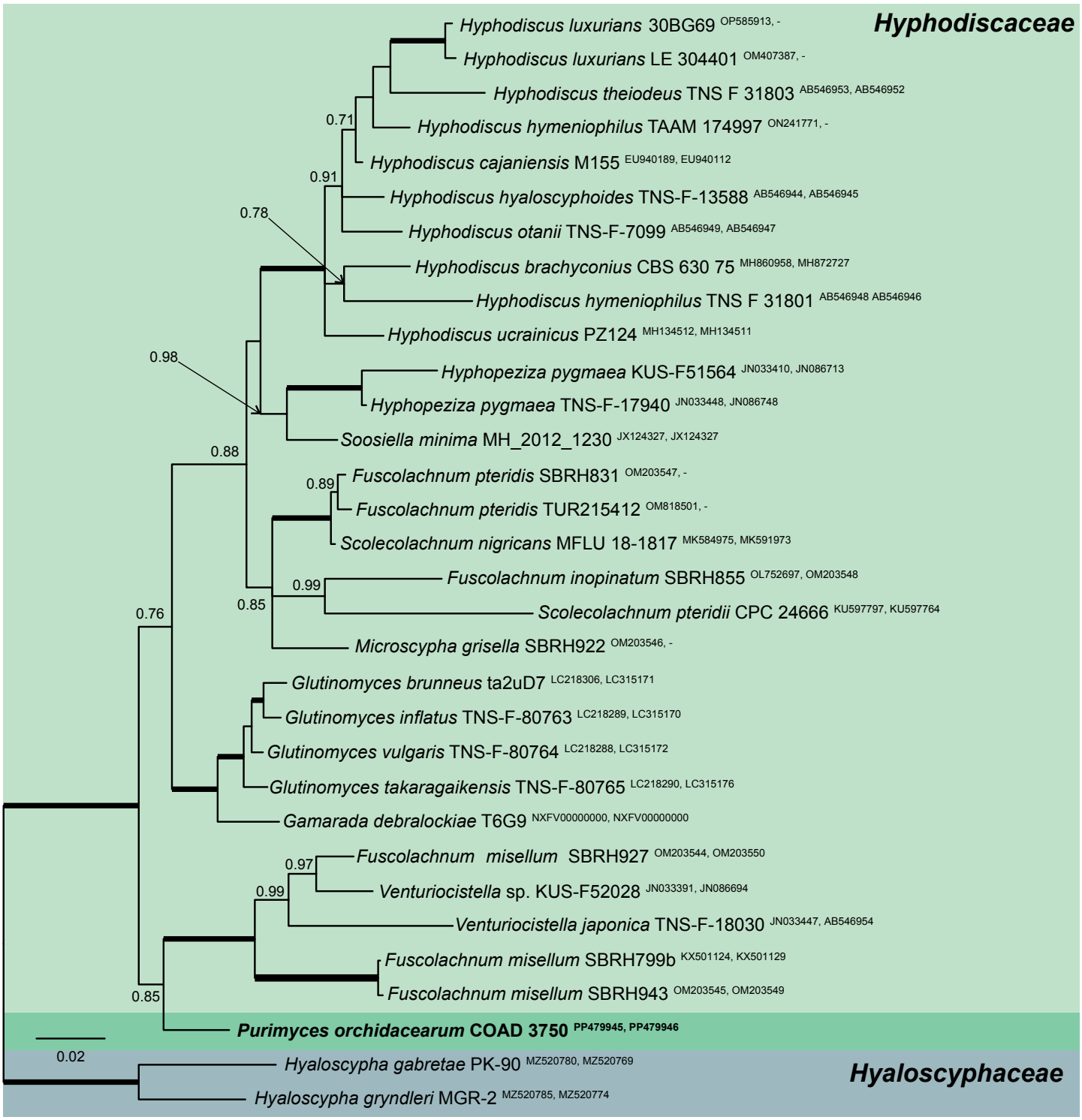
Culture characteristics: Colonies on potato dextrose agar (PDA) circular, with entire margin, white aerial mycelium moderate with hyphal tufts cover in a slime exudate, low convex, rancid odour, white surface and buff colour on reverse (Rayner 1970), reaching 41 mm after 4 wk at 25ºC in the dark. Colonies on malt extract agar (MEA) circular, with entire edge, flat, white aerial mycelium sparse to absent, rancid odour, white surface, reverse buff, reaching 34 mm diam after 4 wk at 25ºC in the dark. Colonies on Czapek yeast agar (CYA) circular to irregular, with entire margin, aerial mycelium moderate with hyphal tufts cover in a slime exudate, low convex, buff colour in the centre to white on the periphery surface, reverse buff, reaching 45 mm diam after 4 wk at 25ºC in the dark.

Typus: **Brazil**, Minas Gerais, Araponga city, Pedra Redonda, isolated as root endophyte on *Cattleya locatellii* (*Orchidaceae*), 21 Nov. 2021, *O.L. Pereira* (**holotype** VIC 49505, culture ex-type COAD 3750; ITS and LSU sequences GenBank PP479945 and PP479946).

Notes: *Purimyces orchidacearum* differs phylogenetically from every known species of *Hyphodiscaceae*. The genus is placed near to the *Venturiocistella* and *Fuscolachnum s. lat.* clade and differs from these genera by the endophytic association and the absence of reproductive morphs. Colonies morphology of *P. orchidacearum* resembles those of *Gamara* and *Glutionomyces*, two other genera of *Hyphodiscaceae* that lack of sporulation structures and are known to form endophytic and mycorrhizal associations with plants. The individual phylogeny (ITS) showed *P. orchidacearum* to be related to *Gamarada* and *Glutinomyces*, and the concatenated phylogeny (ITS and LSU) placed it near to *Venturiocistella* and *Fuscolachnum*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to the sequence of an "Uncultured *Helotiales*" [clone P5.A1.4, GenBank: JX898955.1, Identities = 524/525 (99 %), no gaps], "Uncultured *Helotiales*" [clone HCB1.56, GenBank: JX317139.1, Identities = 520/526 (99 %), two gaps (0 %)], and "Uncultured *Helotiales*" [clone HCB1.35, GenBank: JX317118.1, Identities = 520/526 (99 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are "Fungal sp." [strain: mh1548.5.3, GenBank: GU552525.1; Identities = 811/816 (99 %), no gaps], *Fuscolachnum misellum* [strain: SBRH943, GenBank: OM203549.1; Identities = 833/841 (99 %), no gaps], and *Fuscolachnum* sp. [strain: SBRH927, GenBank: OM203550.1, Identities = 808/816 (99 %), no gaps].

Colour illustrations: Cattleya locatellii growing above rocks, near to Araponga municipiallity, state of Minas Gerais, Brazil. From top to bottom, colony on PDA after 4 wk at 25 °C; colony on MEA after 4 wk at 25 °C; colony on CYA after 4 wk at 25 °C; From bottom left to right, hyphae growing on PDA; mycelium strains on PDA. Scale bars = 20 µm and 100 µm from left to right.



Bayesian inference tree obtained by phylogenetic analyses based on concatenated dataset of ITS and LSU sequences conducted in MrBayes v. 3.2.7a on XSEDE in the CIPRES science gateway. Only Bayesian posterior probability (pp) values above 0.70 are indicated at the nodes. The branches that presented full statistical support (pp = 1) are thickened. The new species is indicated in bold face. *Hyaloscypha gabretae* PK-90 and *Hyaloscypha gryndleri* MGR-2 were used as outgroup. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25417564).

D.O. Ramos & O.L. Pereira, Departamento de Fitopatologia, Universidade Federal de Viçosa, 36570-900, Viçosa, Minas Gerais, Brazil;
e-mail: danilo.ramos@ufv.br & oliparini@ufv.br

Fungal Planet 1660 MycoBank MB 853239

Quixadomyces sanctacrucensis Czachura & Piątek, *sp. nov.*

Etymology: Named after Góry Świętokrzyskie Mts (Holy Cross Mts) where the fungus was discovered.

Classification: *Parapyrenochaetaceae*, *Pleosporales*, *Dothideomycetes*.

Mycelium composed of branched, septate, hyaline or rarely pale brown, smooth, thin-walled hyphae, 1–3.5 µm wide, forming chlamydospores. *Chlamydospores* globose, subglobose or broadly ellipsoid, pale brown or brown, smooth, aseptate or rarely one-septate, 6–9 × 5–6 µm, produced terminally, single. *Conidiomata* immersed or erumpent, pycnidial, globose or subglobose, up to 600 µm diam, with a central ostiole, exuding a brown conidial mass, enclosed by a wall of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, ampulliform, hyaline, smooth, phialidic, 5.5–6.5 × 3–6 µm. *Conidia* allantoid, rarely ellipsoid, hyaline, sometimes pale brown in mass, smooth, aseptate, 2.5–6.5 × 1.5–2.5 µm [description on oatmeal agar (OA)].

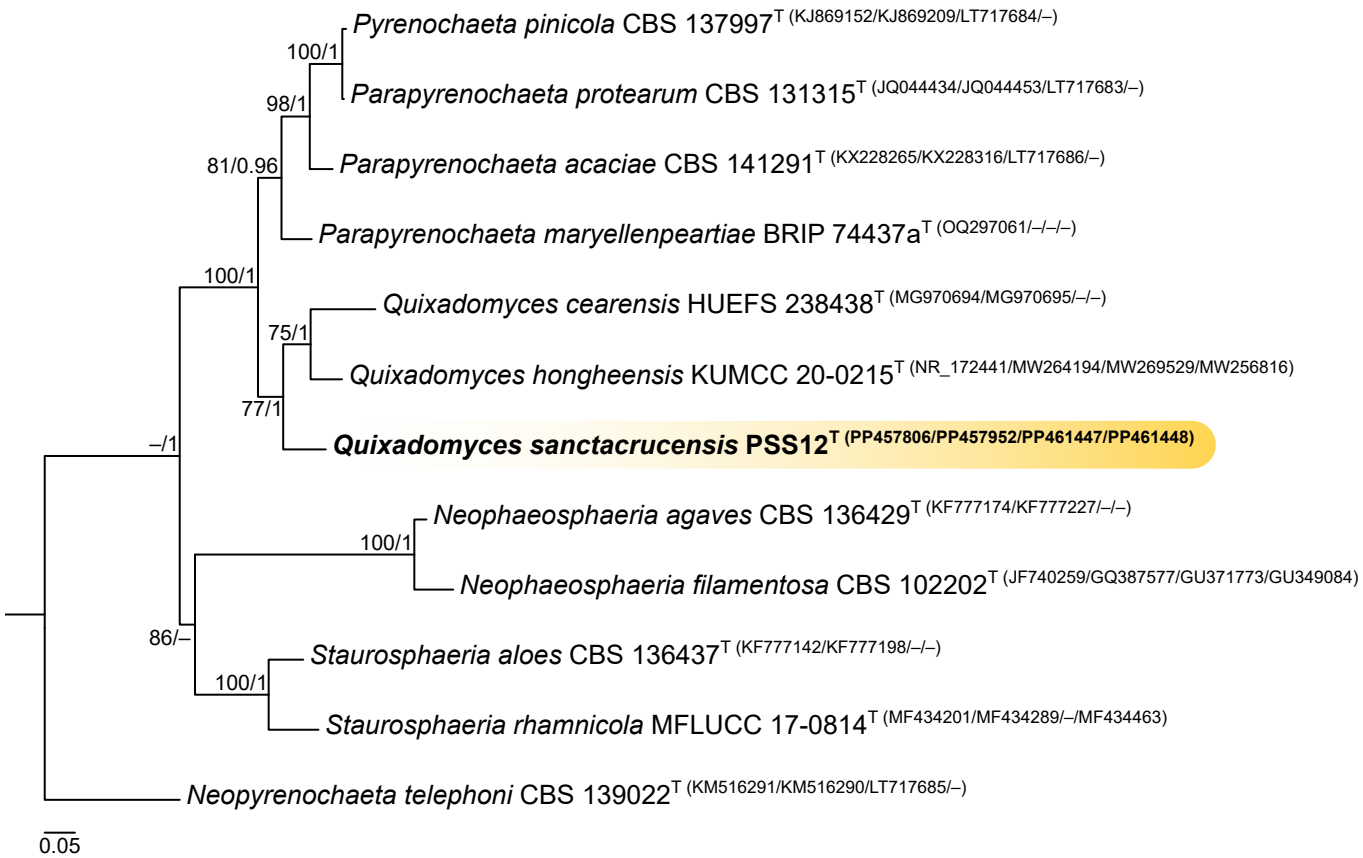
Culture characteristics: Colonies on malt extract agar (MEA) low convex, whitish to pale cream, reaching 21 mm diam after 2 wk at 15 °C and 35 mm diam after 2 wk at 25 °C, surface with dense fluffy aerial mycelium, margin entire or slightly undulate. Reverse yellowish buff. Colonies on potato dextrose agar (PDA) low convex, pale yellowish buff with single greenish dots, reaching 17 mm diam after 2 wk at 15 °C and 30 mm diam after 2 wk at 25 °C, surface with sparse aerial mycelium, margin slightly undulate. Reverse pale yellowish buff. Colonies on oatmeal agar (OA) flat, whitish with pale yellowish margin, reaching 18 mm diam after 2 wk at 15 °C and 30 mm diam after 2 wk at 25 °C, surface with dense aerial mycelium, margin slightly undulate. Reverse cream-coloured.

Typus: **Poland**, Świętokrzyskie Province, Kielce County, Świętokrzyski National Park, Dolina Czarnej Wody, isolated from the resin of *Pinus sylvestris* (*Pinaceae*), 15 Oct. 2020, *P. Czachura* (**holotype** KRAM F-59989, culture ex-type PSS12 = CBS 151613; ITS, LSU, *rpb2*, and *tef1* (second part) sequences GenBank PP457806, PP457952, PP461447, and PP461448).

Notes: The genus *Quixadomyces* was described for *Q. cearensis* that was found on decaying bark in Brazil. The type species lacked conidiophores and conidia and produced only pyrenochaeta-like pycnidia on natural substrate and in cultures (Crous *et al*. 2018). The second member of this genus, *Q. hongheensis*, was isolated from dead twigs of *Dodonaea viscosa* (*Sapindaceae*) in China. The pycnidia of this species were fertile and produced phialidic conidiogenous cells with hyaline, aseptate, allantoid conidia (Wanasinghe *et al.* 2021). *Quixadomyces sanctacrucensis* is also fertile and morphologically similar to *Q. hongheensis*, though it produces chlamydospores. *Quixadomyces sanctacrucensis* is also phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits (named species) using the **ITS** sequence are *Parapyrenochaeta maryellenpeartiae* [culture BRIP 74437a, GenBank OQ297061; Identities = 547/574 (95 %), 10 gaps (1 %)], *Pyrenochaetopsis microspora* [culture NRRL 39060, GenBank HM751085; Identities = 542/569 (95 %), 10 gaps (1 %)] and *Parapyrenochaeta acaciae* [culture CBS 141291, GenBank NR_155674; Identities = 532/561 (95 %), 14 gaps (2 %)]. The closest hits using the **LSU** sequence are *Parapyrenochaeta protearum* [culture CBS 131315, GenBank JQ044453; Identities = 928/928 (100 %), no gaps], *Pyrenochaeta pinicola* [culture CBS 137997, GenBank KJ869209; Identities = 853/854 (99 %), no gaps] and *Quixadomyces hongheensis* [culture KUMCC 20-0215, GenBank MW264194; Identities = 862/864 (99 %), no gaps]. The closest hits using the ***rpb2*** sequence are *Quixadomyces hongheensis* [culture KUMCC 20-0215, GenBank MW269529; Identities = 931/1005 (93 %), no gaps], *Neocucurbitaria pistaciicola* [culture CGMCC 3.24431, GenBank OR262125; Identities = 539/641 (84 %), no gaps] and *Fenestella gardiennetii* [culture CBS 144859, GenBank MK357513; Identities = 837/1002 (84 %), two gaps (0 %)]. The closest hits using the ***tef1*** sequence are *Quixadomyces hongheensis* [culture KUMCC 20-0215, GenBank MW256816; Identities = 753/781 (96 %), no gaps], *Parafenestella ulmicola* [voucher HMJAU 60181, GenBank OL944599; Identities = 751/781 (96 %), no gaps] and *Ophiosphaerella herpotricha* [culture CBS 240.31, GenBank DQ767639; Identities = 751/781 (96 %), two gaps (0 %)].

Colour illustrations: Resin on the bark of *Pinus sylvestris*, Poland. Conidiomata on OA; hypha with chlamydospore; wall of *textura angularis*; conidiogenous cells; conidia. Scale bars = 10 µm.



Phylogenetic tree of *Parapyrenochaeta*, *Quixadomyces* and selected members of the related genera obtained from a maximum likelihood analysis of the combined multi-locus alignment (3 270 characters, including gaps: ITS/LSU/*rpb2*/*tef1*). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and the Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al.* 2012). The position of *Quixadomyces sanctacrucensis* is indicated in **bold** and marked by coloured block. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.9, respectively (MLB/BPP). *Neopyrenochaeta telephoni* was used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (https://doi.org/10.6084/m9.figshare.25400428.v1).

P. Czachura & M. Piątek, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland;
e-mail: p.czachura@botany.pl & m.piatek@botany.pl

Fungal Planet 1661 MycoBank MB 852537

Rhodophana rubrodisca F. Maula, Saba & Asif, *sp. nov.*

Etymology: The epithet "*rubrodisca*" (Latin) refers to its reddish disc on pileus.

Classification: *Entolomataceae*, *Agaricales*, *Agaricomycetes.*

Basidiomata large in size. *Pileus* 2.3–4.6 cm diam, campanulate, flattened umbonate, light reddish brown (2.5YR 8/3; Munsell 1975), covered with dark brown (7.5YR2/3) squamules, central reddish disc (5YR4/6), translucent striate, broadly convex, surface plane, uplifted appressed, deflexed, granular, decurved. *Lamellae* reddish yellow (5YR 7/6), adnexed, even, ventricose, triangular, serrate, adnexed emarginate crowded, adnate and horizontal, regular, edge entire, lamellulae present in 3–4 series of different lengths and alternating with lamellae. *Stipe* 3.7–7.4 × 0.4–0.8 cm, reddish yellow (5YR 7/6), central, equal, hallow, cylindrical to subcylindrical, smooth, thick context, solid, fibrillose, inserted base. *Annulus* absent. *Volva* absent. *Smell* and *taste* are not recorded. *Basidiospores* (9.3–)9.6–13.2(–14) × (8.2–)8.5–9.3(–9.4) µm, Me = 11.1 × 8.9 µm; Qav = 1.3, lacrymoid or subglobose, with 5–6 angular facets in polar view, thick-walled, one central circular guttules, hyaline in 5 % KOH, non-dextrinoid, congophilous. *Basidia* (13.2–)14.4–16.2(–16.6) × (5.7–)5.0–6.3(–7.9) µm, avl × avw = 12.9 × 5.1 µm, clavate, tetrasporic, rarely bisporic, with long sterigmata up to 5.4 µm, smooth, thick-walled, congophilous. *Cheilocystidia* and *pleurocystidia* absent. *Pileipellis* a trichoderm, made up of cylindrical and long and irregular hyphae with 1.8–2.9 µm diam, avw = 1.9 µm, thick-walled, septate, constricted at septa, smooth, branched. *Pileocystidia* absent. *Stipitipellis* made up of narrow cylindrical hyphae with 1.6–2.9 µm diam, avw = 2.1 µm, thin-walled, septate, regularly arranged. *Caulocystidia* missing. *Clamp connections* exist in all tissues.

Habitat: Saprotrophic, solitary, rarely caespitose (in clusters), on nutrient-rich loamy soil under mixed angiospermic vegetation dominated by *Morus alba*.

Typus: **Pakistan**, Khyber Pakhtunkhwa, District Swabi 34.1241°N, 72.4613°E, 340 m a.s.l., in nutrient-rich loamy soil mixed angiospermic vegetation dominated by *Morus alba* (*Moraceae*), 2 Aug. 2022, *F. Maula*, FM152 (**holotype** LAH38133; ITS and LSU sequences GenBank PP357038 and PP390066).

Additional material examined: **Pakistan**, Khyber Pakhtukhwa, District Swabi 34.1241°N, 72.4613°E, 340 m a.s.l., in nutrient-rich loamy soil mixed angiospermic vegetation dominated by *M. alba*, 2 Aug. 2022, *F. Maula*, FM152 (**isotype** LAH38134; ITS and LSU sequences GenBank PP357039 and PP390067).

Notes: Previously, 16 species of the genus *Rhodophana* have been reported globally (Index Fungorum, accessed on 20 Feb. 2024) and this is the first species which is reported from Pakistan. Here, we describe a new species named *R. rubrodisca*, growing in nutrient-rich loamy soil, and is characterised by its large basidiomata (up to 8 cm diam), central reddish disc, surface covered with dark brown squamules, lacrymoid to subglobose basidiospores with 5–6 angular facets in polar view and pileipellis made of cylindrical and long hyphae. According to phylogenetic analyses, based on ITS and combined ITS-LSU datasets, *R. rubrodisca* belongs to a well-supported clade of *Rhodophana* and is closely related to *R. squamulosa* (GenBank KT180329, NR155719), *R. griseobrunnea* (GenBank NR_173192, MT580804), and *R. nitellina* (GenBank OM906885, MH058041), with a fully supported bootstrap value (100 %). Apart from ITS and LSU sequences, *R. squamulosa* differs from *R. rubrodisca* by its small basidiomata, collybioid; in polar view, basidiospores are initially convex with a central depression and 9–12 angular facets (Anil Raj *et al.* 2016). Another phylogenetically closely related species, *R. nitellina*, may be separated from *R. rubrodisca* by ellipsoidal basidiospores, pale brownish cream lamellae, orange brown to red brown glabrous pileus, and a pileipellis cutis (Noordeloos 1988). In the phylogenetic tree, *R. griseobrunnea* another close relative *R. rubrodisca*, may be distinguished from by its tiny basidiospores [7–11(–13) µm in length] and brownish-coloured basidiocarps with a potent farinaceous odour (Musumeci 2020).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Rhodophana squamulosa* [voucher CAL:1262, GenBank KT180329; Identities = (90 %), nine gaps (1 %)], *R. griseobrunnea* [voucher LUG 19799, GenBank MT580804; Identities = (90 %), 10 gaps (1 %)], and *R. nitellina* [voucher MF80542/NS1930, GenBank OM906885; Identities = (90 %), nine gaps (1 %)]. The closest hits using the **LSU** sequence are *Rhodophana squamulosa* [voucher CAL:1262, GenBank KT180330; Identities = (96 %), three gaps (0 %)], and *R. nitellina* [voucher MF80542/NS1930, GenBankKC816961; Identities = (98 %), four gaps (0 %)].

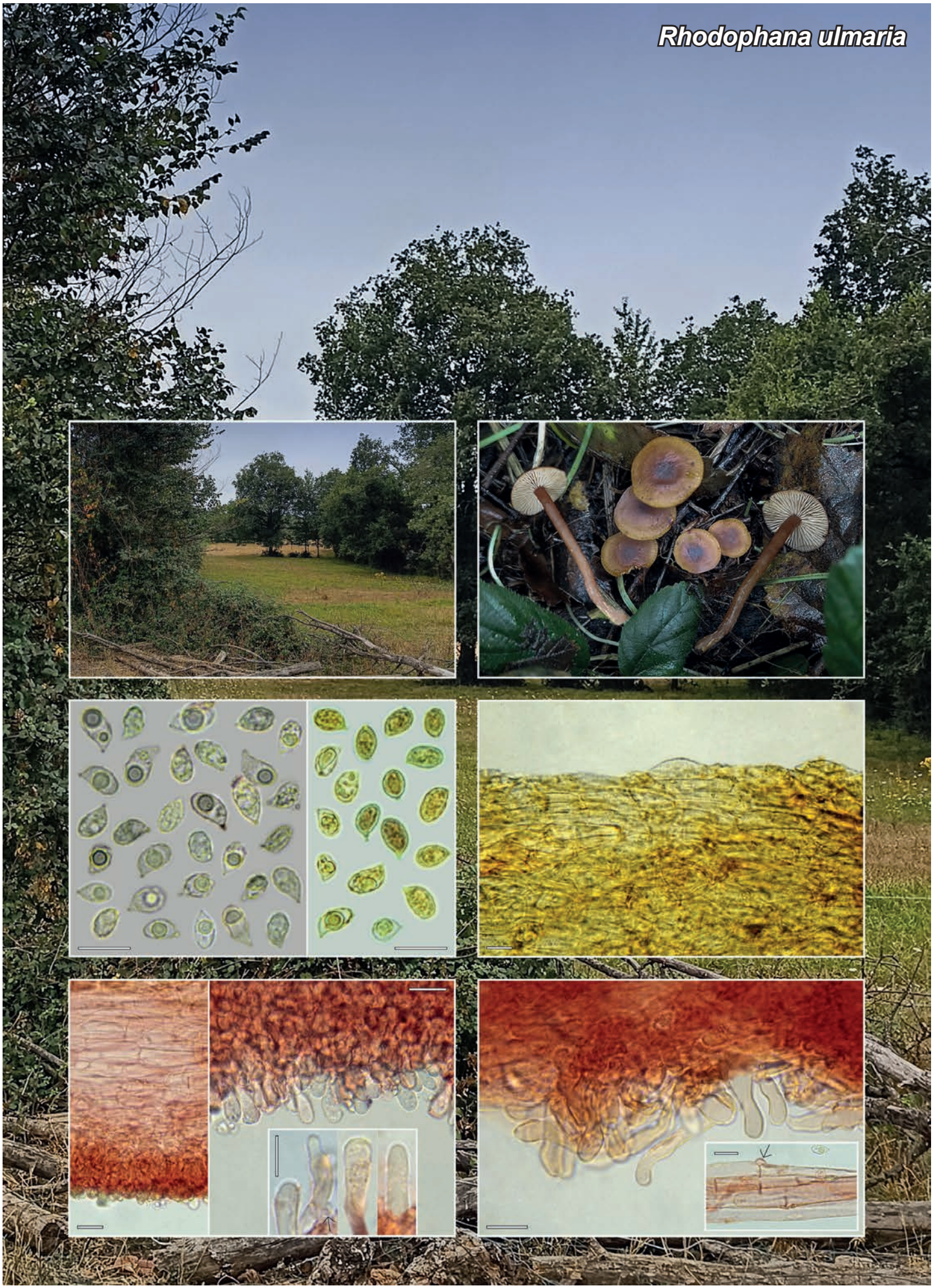
Supplementary material: doi: 10.6084/m9.figshare.25507390 (Table).

Colour illustrations: Pakistan, Khyber Pakhtunkhwa, District Swabi, in nutrient-rich loamy soil mixed angiospermic vegetation dominated by *Morus alba* (photo credit Fazli Maula). Basidiomata of *Rhodophana rubrodisca* in natural habitat; basidiospores, basidia with sterigmata; hyphal septum showing clamp connection; stipitipellis; pileipellis. Basidiospores in 5 % KOH, Melzer's reagent, and Congo red. Scale bars: basidiomata = 1 cm; micromorphology = 10 µm.

Molecular phylogenetic tree inferred from the ITS sequence alignment. The evolutionary analysis was conducted using RAxML-HPC2 v. 8.1.11 on CIPRES, using Maximum Likelihood (ML) and Bayesian Inference (BI) methods (Stamatakis 2014). The tree was rooted to *Lyophyllum leucophaeatum* (GenBank AF357032). The new species is shown in **bold**. The alignment and tree are provided in TreeBASE (study ID: TB2:S31216).

Molecular phylogenetic tree inferred from the combined ITS-LSU sequence alignment. The evolutionary analysis was conducted using RAxML-HPC2 v. 8.1.11 on CIPRES, using Maximum Likelihood (ML) and Bayesian Inference (BI) methods (Stamatakis 2014). The tree was rooted to *Lyophyllum leucophaeatum* (Hae251.97). The new species is shown in bold. The alignment and tree are provided in TreeBASE (study ID: TB2:S31217).

F. Maula, M. Saba & M. Asif, Department of Plant Sciences, Faculty of Biological Sciences, Quaid-i-Azam University, 45320, Islamabad, Pakistan; e-mail: fazlimaula@bs.qau.edu.pk, msaba@qau.edu.pk & m.asif@bs.qau.edu.pk



Fungal Planet 1662 MycoBank MB 852597

Rhodophana ulmaria De la Peña-Lastra & A. Mateos, *sp. nov.*

Etymology: The specific epithet refers to the ecosystem where it was found, *Ulmus minor* forest.

Classification: *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata collybioid. *Pileus* 7–16 mm diam, convex, shortly flattened, sometimes somewhat depressed, with incurved margin and regular margin, strongly striate to 1/2 of radius, cuticle smooth or somewhat rough, somewhat hygrophanous, dry, golden-yellow, tawny, greenish-olivaceous (Ség. 245, 257, 261; Séguy 1936) at margin, pinkish-violet or purplish in the centre, darkening at disc (Ség. 342, 343, 248, 254) and blackening with rubbing or age. *Lamellae* abundant, L = 31–34, moderately appressed and more widely spaced with age, and interspersed with lamellae (l = 1–3), intervening at the bottom, scotate, thick, cream or whitish greyish darkening with age, ridge brownish ferruginous on rubbing, with watery droplets. *Stipe* 31–44 × 1.5–2.5 mm, slender, straight, somewhat curved towards base, central, cylindrical, subequal, smooth, dry, somewhat fistulous, longitudinally fibrillose, somewhat pruinose at apex, whitish strigose at base, reddish-brown, mahogany, subcoloured to pyriform (Ség. 247, 248, 342). *Context* somewhat consistent, pale in the centre and subconcolorous in the cortex. *Odour* with faint rancid, farinaceous-raphanoid and indistinct mild *taste*. *Basidiospores* (4.5–)6.1–*6.7*–7.5(–8.4) × (3–)3.3–*3.8*–4.3(–4.9) µm; Q = (1.3–)1.6–*1.8*–2(–2.1); n = 50; Ve = 51 µm^3, ellipsoidal, amygdaliform or larmiform in side-view and ovoid in frontal projection, sometimes with supra-hilar depression and long prominent apiculum, medium verrucose-asperulate, sometimes nodulate-angulate, not amyloid or dextrinoid, hyaline, with oleaginous contents and with a large guttule. *Basidia* 21–*25.2*–30.5 × 4.8–*6*–7.5 µm, predominantly 4-spored, claviform, with sterigmata 2.5–3.5 µm high, with basal fibulae. *Lamellar trama* regular, with subcylindrical hyphae, 20–35 × 4–7(–12) µm, with fibulae. *Lamellar edge* with basidioloid elements, claviform, sometimes cylindrical or fusiform elements, 25–30 × 5–6.5 µm. *Cheilocystidia* and *pleurocystidia* absent. *Pileipellis* in cutis, with interlaced cylindrical hyphae (5–8 µm wide), somewhat pigmented; subcutis poorly differentiated, with subcylindrical-subphysaloid hyphae (10–22 µm wide). *Stipitipellis* with superficial, cylindrical, parallel hyphae 3.5–9.5 µm thick, with minutely incrusting and parietal pigment, with terminal elements 16–30 – 4–6 µm, cylindrical-claviform or fusiform, thick-walled, at apex. *Clamp connections* present in all tissues.

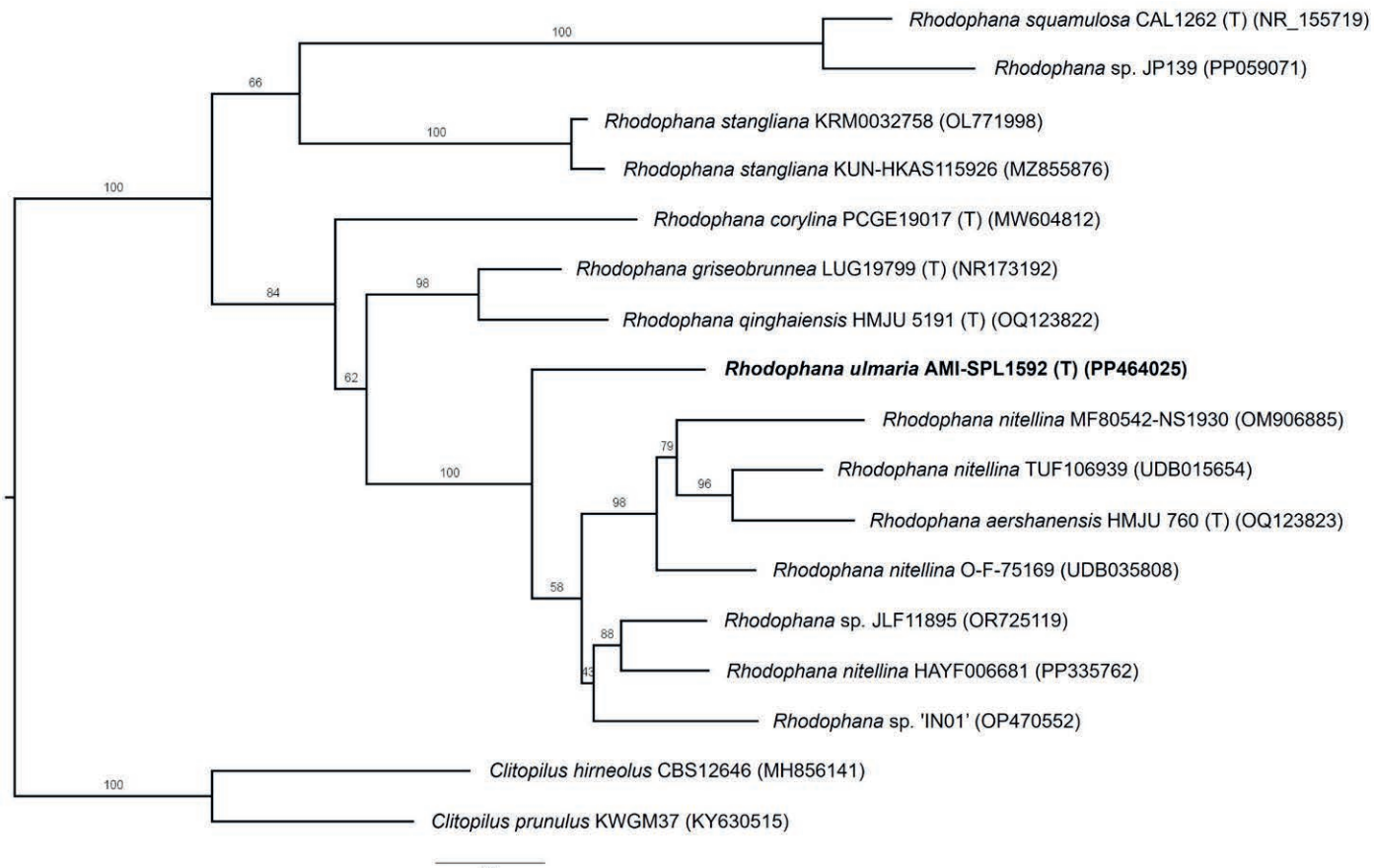
Habitat and distribution: In *Ulmus minor* forest. Currently known only from the type location in northwest Spain.

Typus: **Spain**, Galicia, Lugo, Pantón, Mañente, Campelo, N42°29'55.8", W7°34'29.9", 300 m a.s.l., gregarious in *Ulmus minor* forest, 9 Dec. 2022, *S. De la Peña-Lastra & A. Rego* (**holotype** AMI-SPL1592; ITS and LSU sequences GenBank PP464025 and PP464026).

Additional material examined: **Spain**, Galicia, Lugo, Pantón, Mañente, Campelo, N42°29'55.8", W7°34'29.9", 300 m a.s.l., gregarious in *U. minor* forest, 2 Dec. 2023, *S. De la Peña-Lastra & A. Rego* (AMI-SPL1912).

Notes: *Rhodophana* was originally invalidly described (Kühner 1946), lacking a Latin diagnosis, and only validated several years later (Kühner & Lamoure 1971). However, it fell into disuse and was used as a subgenus of *Rhodocybe* or *Clitopilus* or as a section of *Rhodocybe*, until it was revived based on molecular data (Kluting 2013, Kluting *et al.* 2014). *Rhodocybe* currently includes 15 species (Index Fungorum) with a worldwide distribution. It is characterised by its collybioid shape, hygrophanous pileus, tenacious stipe, coloured spore-print, hyaline, inamyloid and cyanophilic spores, non-carminophilic basidia, absence of hymenial cystidia and with fibulate hyphae; this last character, which was thought not to be present in *Rhodocybe*, has been shown not to occur in some of the species of this genus (Musumeci 2020). Morphologically, *Rhodophana ulmaria* has some similarity with several species of the genus with ochre, orange or reddish fawn colourations, especially with *Rhodophana nitellina* var. *minor*, a taxon well profiled in Papetti (2014), with orange rather than purplish and yellowish greenish tawny yellow, less striate, spores of similar size [(6–)6.5–7.5(–8) × (3.6–)4–5(–5.6) µm, Q = 1.3–*1.5*–1.75] but with some variability and predominance of ovoid spores. In *R. ulmaria* the spore shape is more amygdaliform and narrower [Q = (1.3–)1.6–*1.8*–2(–2.1)]; *R. nitellina* has a much larger size, uniform bright orange colour, no striae on the pileus and larger spores (7.0–10.0 × 5.0–5.5 µm) (Baroni 1981, Noordeloos 1988, Noordeloos & Kosonen 1994) (ITS 89.53 % match); *Rhodophana melleopallens* differs from *R. ulmaria* in having slightly larger basidiomata, a honey-brown colour and smaller spores [(4.0–)4.5–7.0 × 3.0–4.0(–4.5) µm] (Contu 1999, Noordeloos 1983, 1988); *R. canariensis* with not or not very translucently striate pileus, fungicus rather than farinaceous odour, smaller spores [(5.5–)6–7.5 × (3.7–)4–4.5(–4.7) µm] and presence of cheilocystidia (Vizzini *et al*. 2011a); *R. rubroparvula* also has a fungicus odour and smaller spores [(4–)5–6.5 × (2.5–)3–4.5 µm] and caulocystidia (Vizzini *et al*. 2011b); *R. aershanensis* has a pileus and stipe of different colour, dark brown or reddish brown, with distinctly smaller ellipsoid spores [(1.3–)2.7–5.8(–6.6) × (1.2–)2.2–5.1(–6.2) µm, Q = 1.04–1.39] (Xu *et al*. 2023) (ITS 90.77 % match).

Colour illustrations: Spain, Galicia, Lugo, Pantón, Mañente, Campelo, place where the holotype of *Rhodophana ulmaria* was collected. Right column: basidiomata in upper photo correspond with the holotype; middle photo is pileipellis (RC); and the bottom photo is stipitipellis, terminal elements and surface hyphae (two pictures RC). Left column: in middle photo correspond basidiospores (H_2O, RC, IKI-2); and the bottom photo is lamellar trama (left RC), lamellar edge and edge elements (right RC). Scale bars: stipitipellis (left) = 100 µm; all others = 10 µm.



The most probable maximum likelihood (ML) tree obtained with the UltraFast method from the ITS sequence alignment (GenBank or Unite accession numbers in brackets in the tree) shows on the branches the bootstrap ML support values (ML-bs; 1 000 replicates and ≥ 95 % were considered significant) calculated with IQ-TREE v. 2.1.3 (Nguyen et al. 2015). Sequences from type material are indicated with a T.

S. De la Peña-Lastra, University of Santiago de Compostela, Spain; e-mail: saul.delapena@gmail.com
A. Mateos, Sociedad Micológica Extremeña, C/ Sagitario 14, 10001 Cáceres, Spain; e-mail: amateosiz1@gmail.com
A. Rigueiro-Rodríguez, University of Santiago de Compostela, Spain; e-mail: antonio.rigueiro@usc.es

Fungal Planet 1663 MycoBank MB 847927

Russula mukdahanensis Somrith., Sommai, Lueangjaroenkit & Pinruan, *sp. nov.*

Etymology: Refers to the location where the fungus was collected, Mukdahan Province, Thailand.

Classification: *Russulaceae*, *Russulales*, *Agaricomycetes.*

Pileus small to large-sized, 1.2–7 cm diam, parabolic to pulvinate when young, becoming depressed to infundibuliform when mature, surface smooth, dry, dull, cracked with age, pale yellow green (4D colour chart of RHS 2015) to light yellow green (145D; colour chart of RHS 2015) when young, light yellow green (145B) when mature, unchanging when bruised, turning light yellow to yellow (8D) with 3 % KOH, turning to light yellowish pink (26D) with 10 % $FeSO_4$, unchanging with 3 % NaOH. *Lamellae* adnexed, broad, crowded, even, equal, white (NN155D) unchanging when bruised, turning light yellow to yellow (8D) with 3 % KOH, turning to light yellowish pink (26D) with 10 % $FeSO_4$, unchanging with 3 % NaOH. *Stipe* 2–8.5 × 0.7–2.2 cm, central, tapering, longitudinally, smooth, dry, striate, chalky, solid, white (NN155D), unchanging when bruised, turning light yellow to yellow (8D) with 3 % KOH, turning to light yellowish pink (26D) with 10 % $FeSO_4$, unchanging with 3 % NaOH. *Context* 0.2–0.5 cm thick, white (NN155D), spongy to firm unchanging when cut, turning light yellow to yellow (8D) with 3 % KOH, turning to moderate bluish green (126A) with 10 % $FeSO_4$, unchanging with 3 % NaOH. *Odour* indistinct. *Taste* unrecorded. *Spore print* white to cream. *Basidiospores* (50/2/1) 6–9.5 × 5–7.5 µm (Q = 1.09–1.46, Qm = 1.25 ± 0.09), subglobose to broadly ellipsoid; ornamentation amyloid; minute warts, not exceeding 0.2–0.5 µm in height; suprahilar plage indistinct; hilar appendix distinct, 1 µm in height, not amyloid; hyaline in 5 % KOH. *Basidia* 30–46 × 8–12 µm, 4-spored with some 2-spored basidia present, clavate to fusiform; sterigmata 3–5 µm long. *Lamellar trama* mainly composed of nested sphaerocysts, 8–37 µm in diam, and filamentous hyphae 1.5–8 µm thick, hyaline. *Hymenial cystidia* numerous, *ca*. 1 600/mm^2. *Pleurocystidia* 66–74 × 6.3–11 µm, subclavate to clavate, rarely fusiform, with oil-content, thin-walled, usually apex obtuse, mucronate-appendiculate also observed, refractive contents, not changing in SV; abundant near the lamellae edges. *Cheilocystidia* 52–82 × 7–10 µm, similar to those on the sides. Lamellae edges fertile; *marginal cells* 20–29 × 4–9 µm, subclavate to clavate and shorter than basidia. *Pileipellis* orthochromatic in Cresyl Blue, not sharply delimited from the underlying sphaerocysts of the context, distinctly two layered; suprapellis *ca*. 50–110 µm deep, composed of erect or repent hyphae, subpellis *ca*. 350–400 µm, composed of hyphae 1.5–8 µm width, thin-walled, septate. *Acid-resistant incrustations* absent. Hyphal terminations near the pileus margin occasionally branched, flexuous, thin-walled, septate, terminal cells 10–15 × 6–9.5 µm, mainly lageniform, pyriform or clavate, apical obtuse and often with glutinous coating not colouring in any reagent. Terminal cells of hyphae near the pileus centre, often cylindrical and smaller 10–17.5 × 3.5–4.5 µm. *Pileus trama* interwoven with sphaerocysts. *Pileocystidia* absent. *Stipitipellis* a cutis with some repent and oblique hyphae, 2–8 µm width, thin-walled, septate, with sphaerocytes 27.5–62.5 µm diam, some filamentous hyphae pale yellow. *Caulocystidia* absent. *Clamp connections* absent from all tissues.

Habitat and distribution: Currently known only from the type locality, in association with a species of *Dipterocarpus* (*Dipterocarpaceae*).

Typus: **Thailand**, Mukdahan, Mueang Mukdahan district, on soil, 22 Jul. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (**holotype** BBH 48240; ITS, LSU, mtSSU, and *rpb2* sequences GenBank OQ589283, OQ584327, OQ589476, and OQ590014).

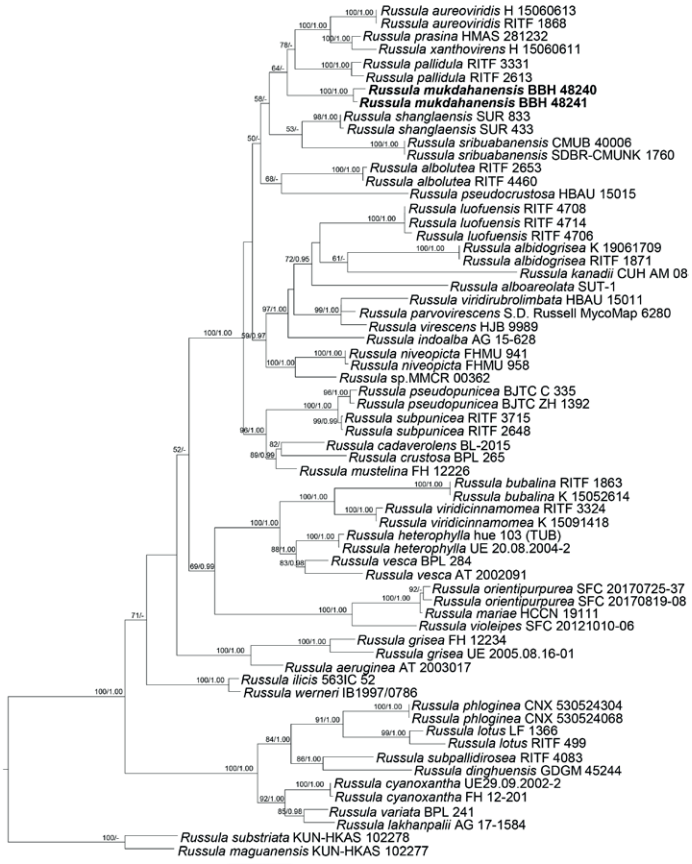
Additional material examined: **Thailand**, Mukdahan, Mueang Mukdahan district, on soil, 22 Jul. 2020, *U. Pinruan, S. Sommai & P. Khamsuntorn* (BBH 48241, ITS, LSU, mtSSU and *rpb2* sequences GenBank, OQ589285, OQ584330, OQ589477, OQ590015).

Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence of the type collection has the closest GenBank BLAST match (100 %) with a sequence identified as unidentified *Russula* from Thailand (GenBank LC680940) and similar sequences identified to species of *R. delica* (99.85 %) from Thailand (GenBank LC068791). The **LSU** sequence of the type collection has the closest GenBank BLAST match (98.17 %) with a sequence identified as *R. mustelina* from Germany (GenBank KT933866), *R. vesca* (97.79 %) from USA (GenBank KT933839) The **mtSSU** sequence identified as *R.* aff. *crustose* (92.80 %) and for ***rpb2*** sequence identified as *R. virescens* (93.67 %) from Sweden.

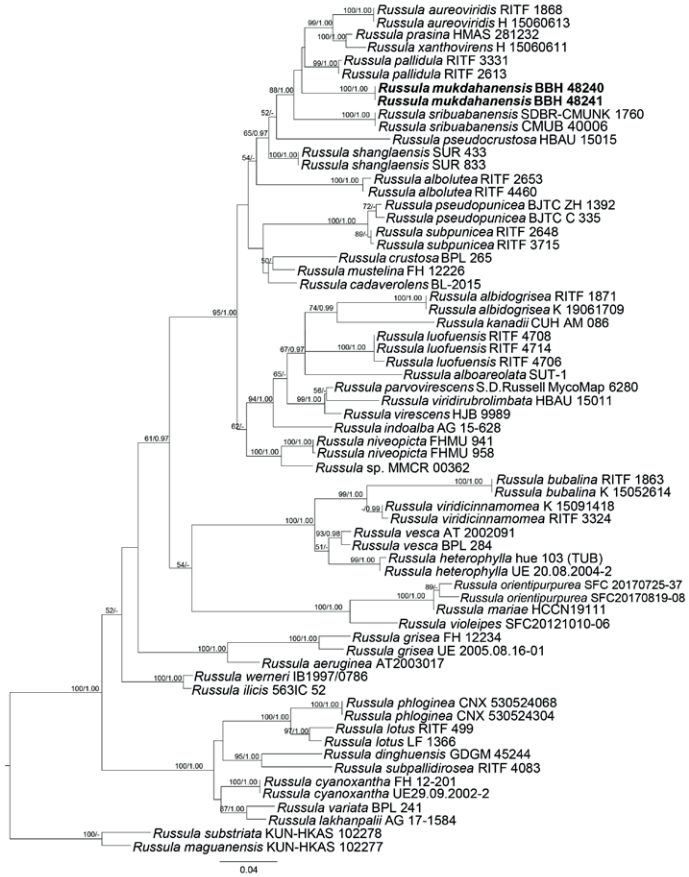
Phylogenetically, *R. mukdahanensis* formed a strongly supported sister group to the other species of subg. *Heterophyllidia* subsect. *Virescentinae*. The morphology of this new *Russula* resembles other species in *Virescentinae* in the size of pileus, shapes and sizes of basidia and basidiospores. Macromorphologically, it differs from other species in cap colour. *Russula mukdahanensis* is similar to *R. prasina* (Hyde *et al*. 2019) in the absence of caulocystidia and pileocystidia. The pleurocystidia of the new *Russula* (66–74 × 6.3–11 µm) are longer than those of *R. aureoviridis* (Das *et al.* 2017) (38–50 × 7–11 µm). Moreover, *Russula mukdahanensis* has longer cheilocystidia than *R. aureoviridis*, *R. pallidula*, *R. prasina* and *R. xanthovirens*.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: The deciduous dipterocarp forest, Mueang Mukdahan district, Mukdahan Province, Thailand, where the holotype was collected. Left top: Basidiomata of BBH 48240; Left centre: The hymenium layer with a basidiospore in Melzer's reagent; Centre: Scanning electron photograph of spores from BBH 48240; Left bottom: Basidia and basidiole, cheilocystidia (centre); Right bottom: Pleurocystidia. Scale bars: basidiomata = 10 mm; all other microscopic structures = 10 µm; spores = 5 µm.



Phylogenetic relationship of *Russula* subsect. *Virescentinae* inferred from ITS sequences. Numbers at the significant nodes represent ML bootstrap values/ Bayesian posterior probabilities, multiplied by 100. Sequences of fungal species obtained in this study are in black bold.



Phylogenetic relationship of *Russula* subsect. *Virescentinae* is based on combined ITS, nrLSU, mtSSU and *rpb2* sequence data inferred from RAxML v. 8.2.12 (Miller et al. 2010). The numbers at the significant nodes represent ML bootstraps greater than or equal to 50 % and Bayesian interference (BI) using MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001) posterior probabilities greater than or equal to 0.95, respectively. Sequences of fungal species obtained in this study are in black bold.

S. Somrithipol, S. Sommai & U. Pinruan, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: sayanh@biotec.or.th, sujinda.som@biotec.or.th & umpawa.pin@biotec.or.th
P. Lueangjaroenkit, Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand, and Biodiversity Center, Kasetsart University (BDCKU), Bangkok, Thailand; e-mail: Piyangkun.lu@ku.th

Fungal Planet 1664

MycoBank MB 853247

Szafranskia Czachura & Piątek, *gen. nov.*

Etymology: Named in honour of Jan Szafrański (1949–2011) for his significant contribution to nature conservation in the Beskid Niski Mts (Low Beskid Mts), the mountain range where the new fungus was found.

Classification: *Neomassarinaceae*, *Pleosporales*, *Dothideomycetes*.

Mycelium composed of branched, septate, hyaline, smooth hyphae. *Conidiomata* erumpent, pycnidial, globose or subglobose, with a central ostiole, enclosed by a wall of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, ampulliform or rarely subcylindrical, aseptate or rarely one-septate, hyaline, smooth, phialidic. *Conidia* ellipsoid, hyaline, subhyaline or pale brown, smooth, aseptate.

Type species: *Szafranskia beskidensis* Czachura & Piątek

MycoBank MB 853248

Szafranskia beskidensis Czachura & Piątek, *sp. nov.*

Etymology: Named after the Beskidy Mts, the mountains within the Carpathians, where the new species was discovered.

Mycelium composed of branched, septate, hyaline, smooth, thin-walled hyphae, 1–4.5 µm wide. *Conidiomata* erumpent, pycnidial, globose or subglobose, up to 500 µm diam, with a central ostiole, exuding a black conidial mass, enclosed by 2–3 layered wall of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, ampulliform or rarely subcylindrical, aseptate or rarely one-septate, hyaline, smooth, phialidic, 4–7.5 × 3–5.5 µm. *Conidia* ellipsoid, hyaline, subhyaline or pale brown, smooth, aseptate, 3–4.5 × 2–2.5 µm [description on oatmeal agar (OA)].

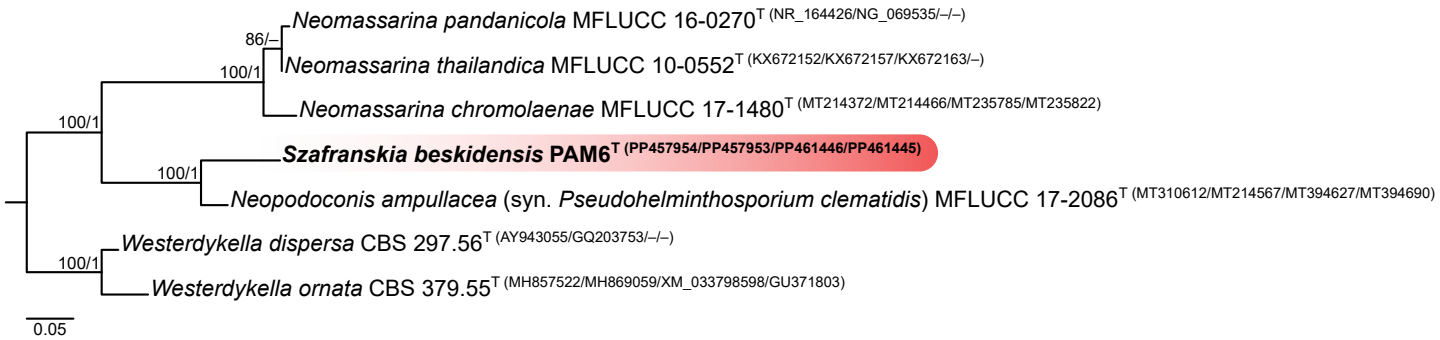
Culture characteristics: Colonies on malt extract agar (MEA) and potato dextrose agar (PDA) low convex, whitish to pale cream, reaching 38/37 mm diam at 15 °C and 35/46 mm diam at 25 °C after 4 wk on MEA and PDA, respectively, surface with dense fluffy aerial mycelium, margin undulate. Reverse buff. Colonies on oatmeal agar (OA) submerged, whitish to pale cream with black conidiomata, reaching 52 mm diam after 4 wk at 15 °C and 60 mm diam after 4 wk at 25 °C, surface with sparse aerial mycelium, margin entire. Reverse beige.

Typus: **Poland**, Podkarpackie Province, Krosno County, Modrzyna Reserve, *ca*. 13 km south of Dukla city, isolated from the resin of *Abies alba* (*Pinaceae*), 22 Oct. 2020, *P. Czachura* [**holotype** KRAM F-59988, culture ex-type PAM6 = CBS 151614; ITS, LSU, *rpb2*, and *tef1* (second part) sequences GenBank PP457954, PP457953, PP461445, and PP461446].

Notes: *Szafranskia* represents a new genus in the pleosporalean family *Neomassarinaceae*, which is closely related to the genus *Neopodoconis* (syn. *Pseudohelminthosporium*), typified by *N. ampullacea* (syn. *P. clematidis*) (Phukhamsakda *et al.* 2020, Koukol & Delgado 2021). *Szafranskia* differs from *Neopodoconis* in having pycnidial conidiomata with conidiophores reduced to conidiogenous cells and hyaline, subhyaline or pale brown, aseptate, ellipsoid conidia. *Neopodoconis* is a hyphomycetous genus known to form macronematous conidiophores, polytretic conidiogenous cells and phragmosporous, euseptate conidia (Phukhamsakda *et al.* 2020, Koukol & Delgado 2021). Both genera are also ecologically different. *Szafranskia* has been isolated from the resin of *Abies alba* in the temperate region (Poland) while *Neopodoconis* is known as saprobe on dead twigs and branches in tropics (Ellis 1961, Phukhamsakda *et al*. 2020, Koukol & Delgado 2021).

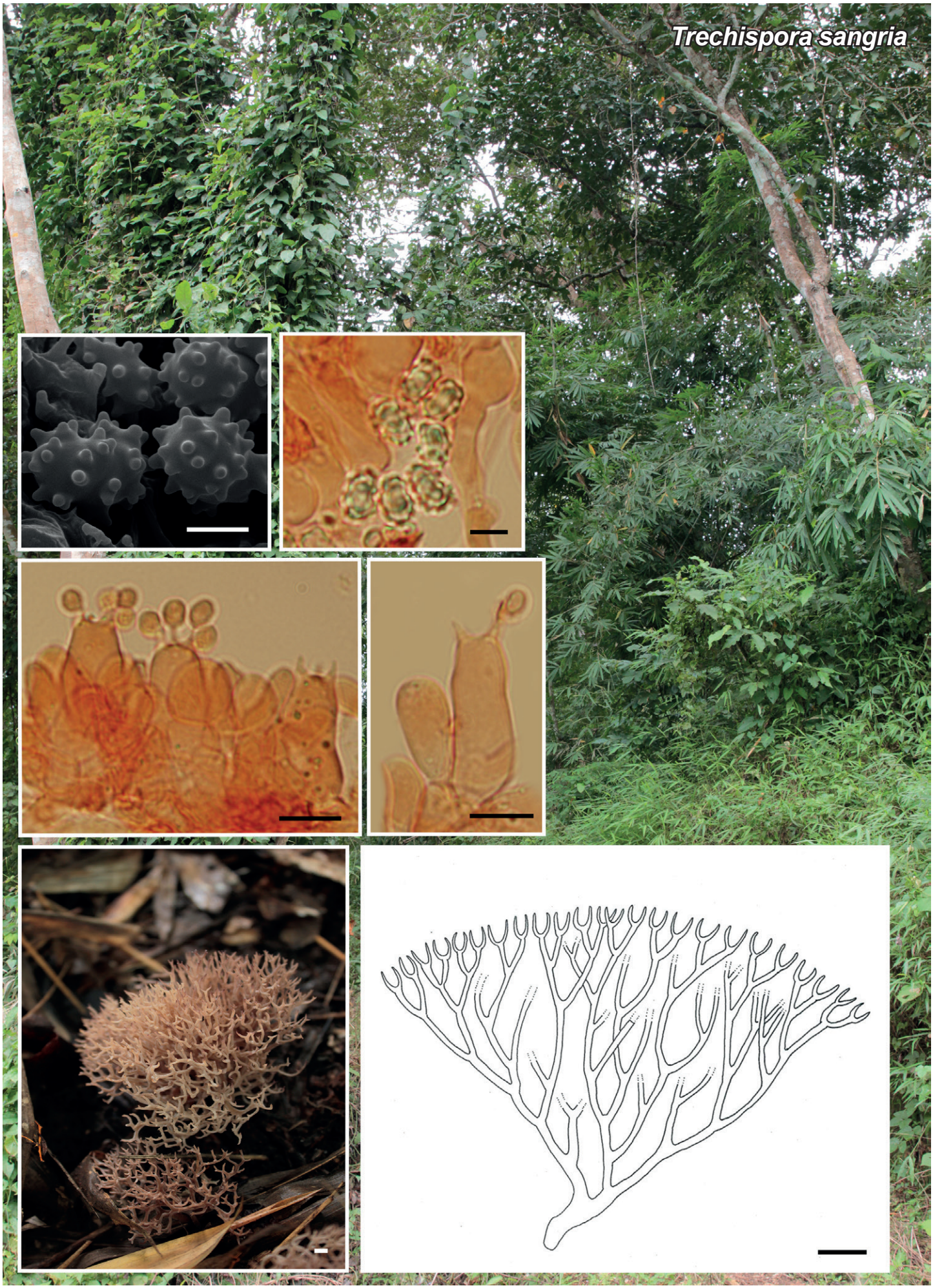
Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits (named species) using the **ITS** sequence are *Pseudohelminthosporium clematidis* [voucher MFLU 17-1494, GenBank NR_170808; Identities = 472/520 (91 %), 12 gaps (2 %)], *Alfoldia vorosii* [culture CBS 145501, GenBank NR_171211; Identities = 360/423 (85 %), 21 gaps (4 %)] and *Lophiostoma pseudomacrostomum* [culture CBS 147524, GenBank MW759249; Identities = 367/436 (84 %), 20 gaps (4 %)]. The closest hits using the **LSU** sequence are *Pseudohelminthosporium clematidis* [culture MFLUCC 17-2086, GenBank NG_073848; Identities = 858/864 (99 %), no gaps], *Preussia intermedia* [voucher UPS: Kruys 304, GenBank GQ203738; Identities = 890/912 (98 %), no gaps] and *Preussia lignicola* [culture 18ALIC002, GenBank MT472604; Identities = 875/898 (97 %), no gaps]. The closest hits using the ***rpb2*** sequence are *Pseudohelminthosporium clematidis* [culture MFLUCC 17-2086, GenBank MT394690; Identities = 520/620 (84 %), no gaps], *Flabelloascoma pistaciae* [culture UESTCC 23.0049, GenBank OR262123; Identities = 470/577 (81 %), two gaps (0 %)] and *Lophiotrema nucula* [culture CBS 627.86, GenBank FJ795463; Identities = 453/558 (81 %), one gap (0 %)]. The closest hits using the ***tef1*** sequence are *Pseudohelminthosporium clematidis* [culture MFLUCC 17-2086, GenBank MT394627; Identities = 829/865 (96 %), no gaps], *Neostagonosporella bambusicola* [culture KUMCC 20-0031, GenBank OP428755; Identities = 845/887 (95 %), two gaps (0 %)] and *Pseudoshiraia conidialis* [culture CNUCC 1353PR, GenBank MZ516168; Identities = 824/866 (95 %), no gaps].

Colour illustrations: Resin on the bark of *Abies alba*, Poland. Conidiomata on OA; conidioma; wall of *textura angularis*; conidiogenous cells; conidia. Scale bars = 10 µm.



Phylogenetic tree of *Neomassarinaceae* species obtained from a maximum likelihood analysis of the combined multi-locus alignment (3 210 characters, including gaps: ITS/LSU/*tef1*/*rpb2*). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and the Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al.* 2012). The position of *Szafranskia beskidensis* is indicated in **bold** and marked by coloured block. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values ≥ 70 % and Bayesian posterior probabilities (BPP) ≥ 0.9, respectively (MLB/BPP). *Westerdykella dispersa* and *W. ornata* were used as an outgroup. The scale bar represents the expected number of changes per site. The alignment was deposited at figshare.com (https://doi.org/10.6084/m9.figshare.25393243.v1).

P. Czachura & M. Piątek, W. Szafer Institute of Botany, Polish Academy of Sciences, Lubicz 46, PL-31-512 Kraków, Poland;
e-mail: p.czachura@botany.pl & m.piatek@botany.pl



Fungal Planet 1665 MycoBank MB 847925

Trechispora sangria Sommai, Pinruan, Yingkulchao & Somrith., *sp. nov.*

Etymology: Refers to the dark purplish red colour of the apex.

Classification: *Hydnodontaceae*, *Trechisporales*, *Agaricomycetes.*

Basidiomata coralloid, 51–62 mm high × 44–81 mm broad, caespitose, densely branched, greyish reddish orange to light reddish brown (177B–C; colour chart of RHS 2015) when fresh, light brownish grey (N200C) when dried. Branches flattened, dichotomous, primary lower branches 4–5 mm wide, terminal branches 2–3 mm wide, dark purplish red (N79A), axils V-shaped, apex cylindrical, fresh tough and elastic. Stipe 16–23 × 2–4 mm, oblated, moderate orange yellow (164B). Context slightly coriaceous, dry, tough at the base of the stipe. All tissue unchanging where cut or bruised. *Odour* not distinctive. *Basidiospores* (4.5–)5–6(–6.2) µm long, (2.8–)3–3.5(–4) µm wide, excluding ornamentation, L = 5.42, W = 3.18, Q = 1.71, n = 75/3; oblong, thick-walled, coarsely echinate, hyaline to greenish in 5 % KOH. Ornamentation acute warts or spines 0.3–1 µm long. *Basidia* primarily 2- to 4-spored, clavate to barrel-shaped, approximately 15–27 × 5.5–9 µm, hyaline, thick-walled, clamped at the base. *Sterigmata* 2.5–5 µm long. *Cystidia* absent. *Hyphal system* monomitic; generative hyphae with clamp connections. *Context hyphae* hyaline, thin-walled, 1.5–7 µm diam. *Hymenium* ≤ 30 µm thick. *Subhymenium ca*. 10 µm thick, composed of hyphae, 2–3 µm diam, thin-walled. Context with subparallel arranged hyphae 1.5–5.5 µm diam, thin-walled, branched, septate with clamped.

Typus: **Thailand**, Tak Province, Mae Sot district, on soil, 20 Jul. 2022, *U. Pinruan, S. Chaimongkol, W. Yingkulchao & S. Somrithipol* (**holotype** BBH 49635; ITS and LSU sequences GenBank OQ589282 and OQ584326).

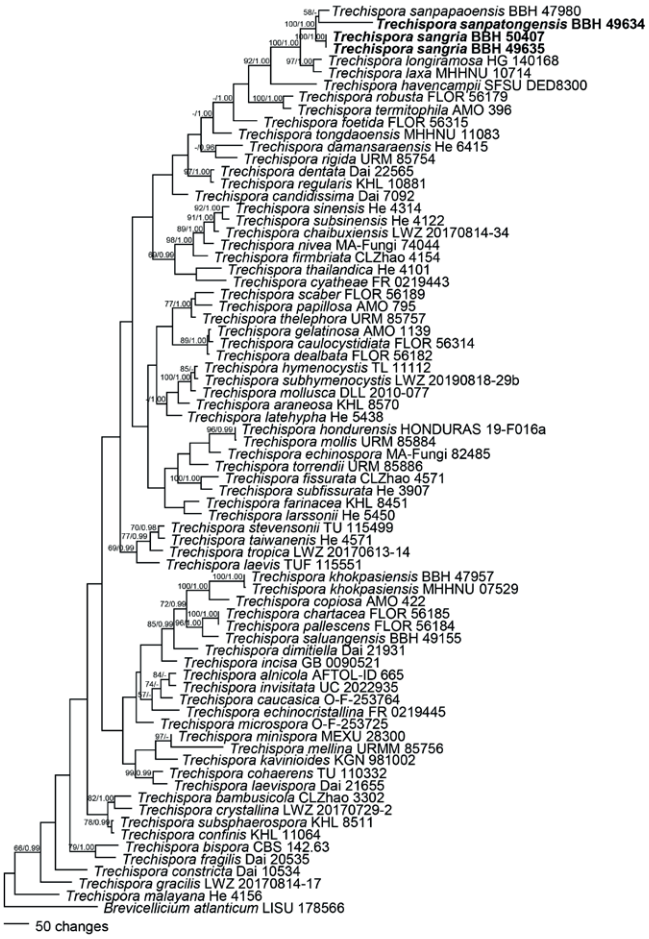
Additional material examined: **Thailand**, Tak Province, Mae Sot district, on soil, 20 Jul. 2022, *U. Pinruan, S. Chaimongkol & W. Yingkulchao*, (BBH 50407; ITS and LSU sequences GenBank OQ589281 and OQ584325).

Colour illustrations: The mixed deciduous forest, Mae Sot district, Tak Province, Thailand, where the holotype was collected (background photo). Left bottom: Basidiomata growing on the soil of BBH 49635 and line drawing of basidiomata; Left centre: Basidia with basidiospores; Basidiospores, scanning electron photograph of spores from BBH 49635. Scale bars: basidiomata = 10 mm; basidia = 10 µm; basidiospore = 5 µm.

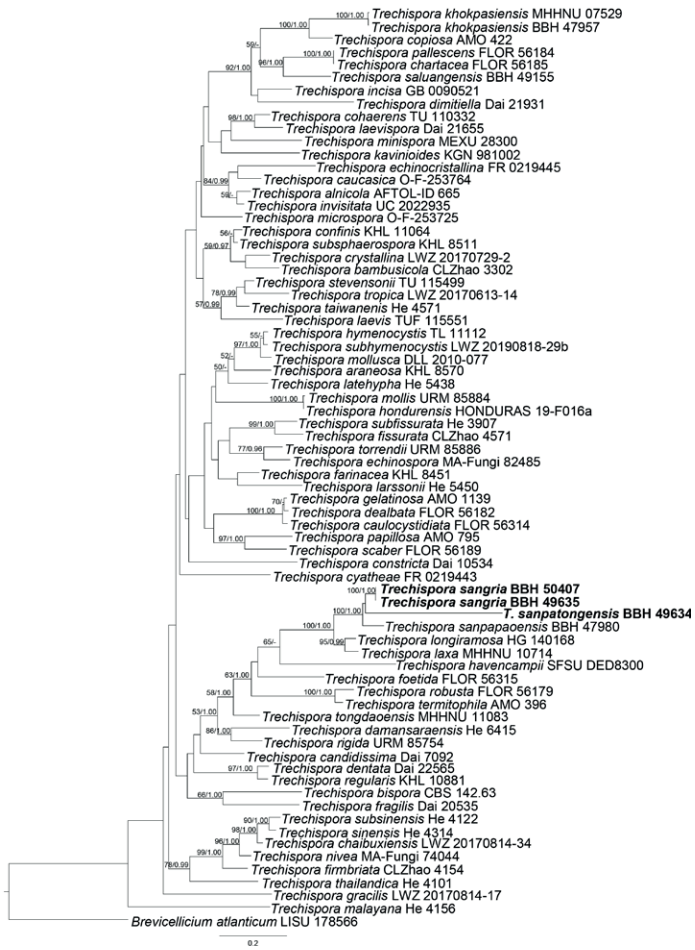
Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence of the type collection has the closest GenBank BLAST match (82.36 %) with a sequence identified as unidentified *Scytinopogon* sp. 2 MEL:2382992 from Australia (GenBank KP012847). For **LSU** sequence of the type collection has the closest GenBank BLAST match (97.86 %) with a sequence identified as *Scytinopogon angulisporus* TFB13611 from USA (GenBank JQ684661) and similar sequences identified as *Trechispora stevensonii* KHL14654 (96.74 %) from Norway (GenBank MH290762).

Phylogenetically, *Trechispora sangria* clusters with *T. longiramosa* and *T. sanpatongensis*, but their fresh and dried basidiocarp colour is different. *Trechispora sangria* has greyish reddish orange to light reddish brown basidiocarps when fresh and light brownish grey basidiocarps when dried whereas basidiocarps of *T. sanpatongensis* are yellowish white from the base to the middle and moderate brown towards the ends when fresh and yellowish white when dried, and those of *T. longiramosa* are cream to buff turning yellowish brown towards the apex when fresh and olivaceous buff turning to dark brown towards the apex when dried. The branch tips of *T. sangria* are dark purple red while the tips of *T. sanpatongensis* are white, and those of *T. longiramosa* are honey-yellow. *Trechispora sanpatongensis* has moderated orange yellow stipes whereas stipes of *T. sangria* are yellowish, and those of *T. longiramosa* are white to cream. Additionally, the stipes of *T. sangria* are oblate and shorter than the cylindrical stipes of *T. sanpatongensis*. *Trechispora sangria* has a larger size of basidiocarps and a relatively smaller size of basidia compared with *T. sanpatongensis*. *Trechispora sangria* has V-shaped branches that differ from the U-shaped branches of *T. longiramosa* (Liu SL *et al.* 2022).

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table).

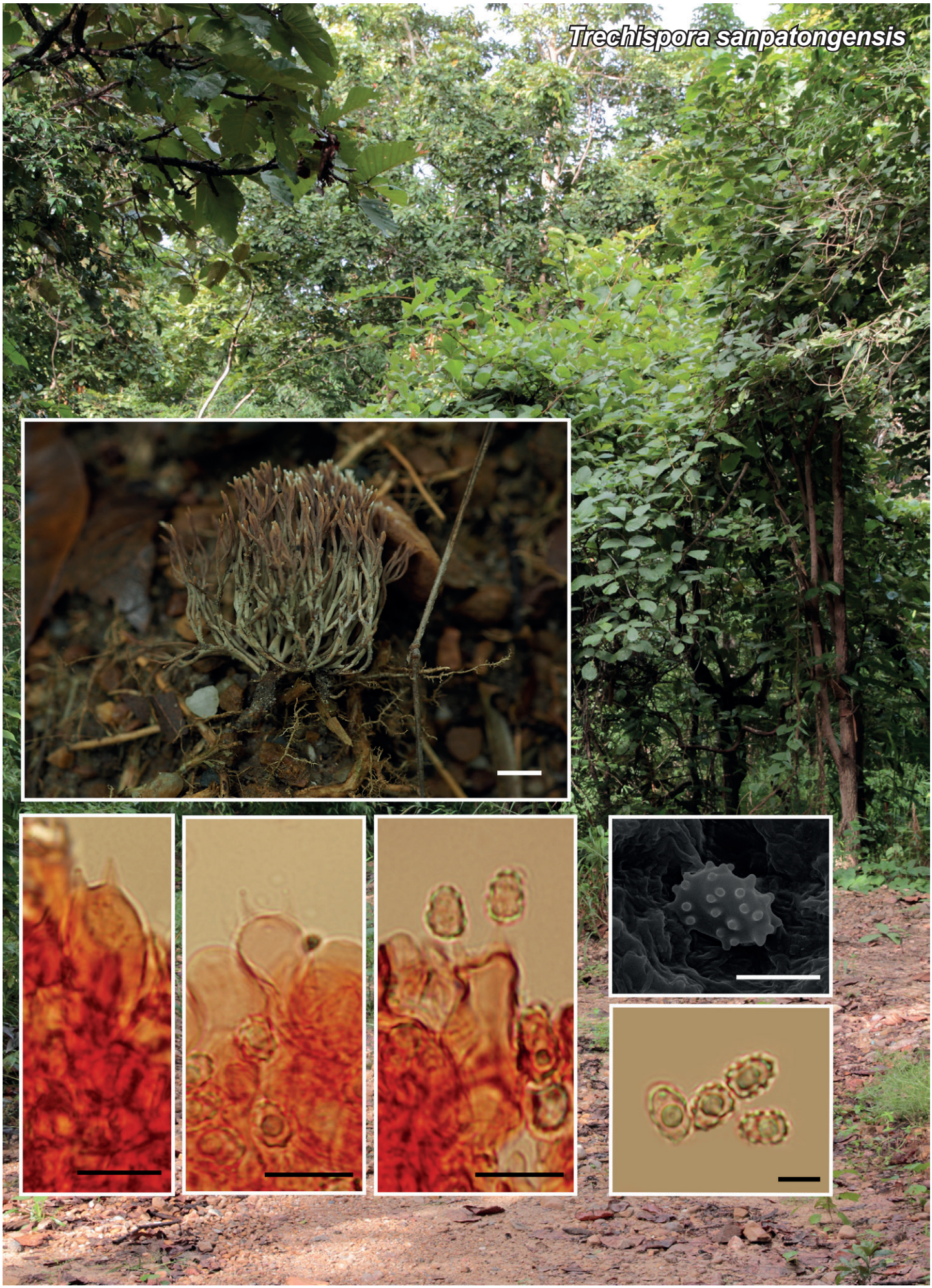


Maximum Parsimony tree based on combined ITS and LSU sequences data. The numbers at the significant nodes represent MP bootstraps greater than or equal to 50 % and BI posterior probabilities greater than or equal to 0.95, respectively. The dataset taxa in *Trechispora* were obtained from previously published studies (Deng *et al.* 2023, Sommai *et al*. 2023). Sequences of fungal species obtained in this study are in black bold.



Phylogenetic tree constructed using RAxML-HPC2 on XSEDE v. 8.2.8 (Stamatakis *et al.* 2008, Stamatakis 2014) on the CIPRES science gateway platform (http://www.phylo.org) (Miller *et al*. 2010) inferred from ITS sequences. Numbers at the significant nodes represent ML bootstrap values/ Bayesian posterior probabilities, multiplied by 100. Sequences of fungal species obtained in this study are in black bold.

S. Sommai, U. Pinruan & S. Somrithipol, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: sujinda.som@biotec.or.th, umpawa.pin@biotec.or.th & sayanh@biotec.or.th
W. Yingkunchao, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand, and Department of Biology, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Ladkrabang, Bangkok, Thailand; e-mail: wittayothin.yin@ncr.nstda.or.th



Fungal Planet 1666 MycoBank MB 847926

Trechispora sanpatongensis Pinruan, Luangsa-ard, Lueangjaroenkit & Chaimongkol, *sp. nov.*

Etymology: Refers to the location where the fungus was collected, San Pa Tong district, Chiang Mai Province, Thailand.

Classification: *Hydnodontaceae*, *Trechisporales*, *Agaricomycetes.*

Basidiomata coralloid, 22–25 mm high × 32–45 mm broad, caespitose, densely branched, yellowish white (156D; colour chart of RHS 2015) from base to middle, moderate brown (165A) towards the ends when fresh, yellowish white (156D) when dried. *Branches* rounded, dichotomous, primary lower branches 1–2 mm wide, white (NN155B), axils V-shaped, apex cylindrical, fresh tough and elastic. *Stipes* 6–8 × 1–3 mm, cylindrical, yellowish white (156D). *Context* moderate, yellowish pink (173D), slightly coriaceous, dry, tough at the base of the stipe. All tissue unchanging where cut or bruised. *Odour* not distinctive. *Basidiospores* (4.7–)5–6 µm long, 3–4 µm wide, excluding ornamentation, L = 5.34, W = 3.44, Q = 1.55, n = 50/2; narrowly ellipsoid, thick-walled, coarsely echinate, hyaline to greenish in 5 % KOH. *Ornamentation* acute warts or spines 0.2–1 µm long. *Basidia* primarily 2- to 4-spored, clavate to barrel-shaped, approximately 14–31 × 6.5–12.5 µm, hyaline, thick-walled, clamped at the base. *Sterigmata* 3–4 µm long. *Cystidia* absent. *Hyphal system* monomitic; generative hyphae with clamp connections. *Context hyphae* hyaline, thin-walled, 2–8 µm diam. *Hymenium* ≤ 33 µm thick. *Subhymenium ca*. 12 µm thick, composed of hyphae, 2.5–4 µm diam, thin-walled. *Context* with subparallel arranged hyphae 2–8 µm diam, thin-walled, branched, septate with clamps.

Typus: **Thailand**, Chiang Mai Province, San Pa Tong district, on soil, 12 Oct. 2021, *U. Pinruan, S. Sommai & P. Khamsuntorn* (**holotype** BBH 49634; ITS and LSU sequences GenBank OQ589474 and OQ584328).

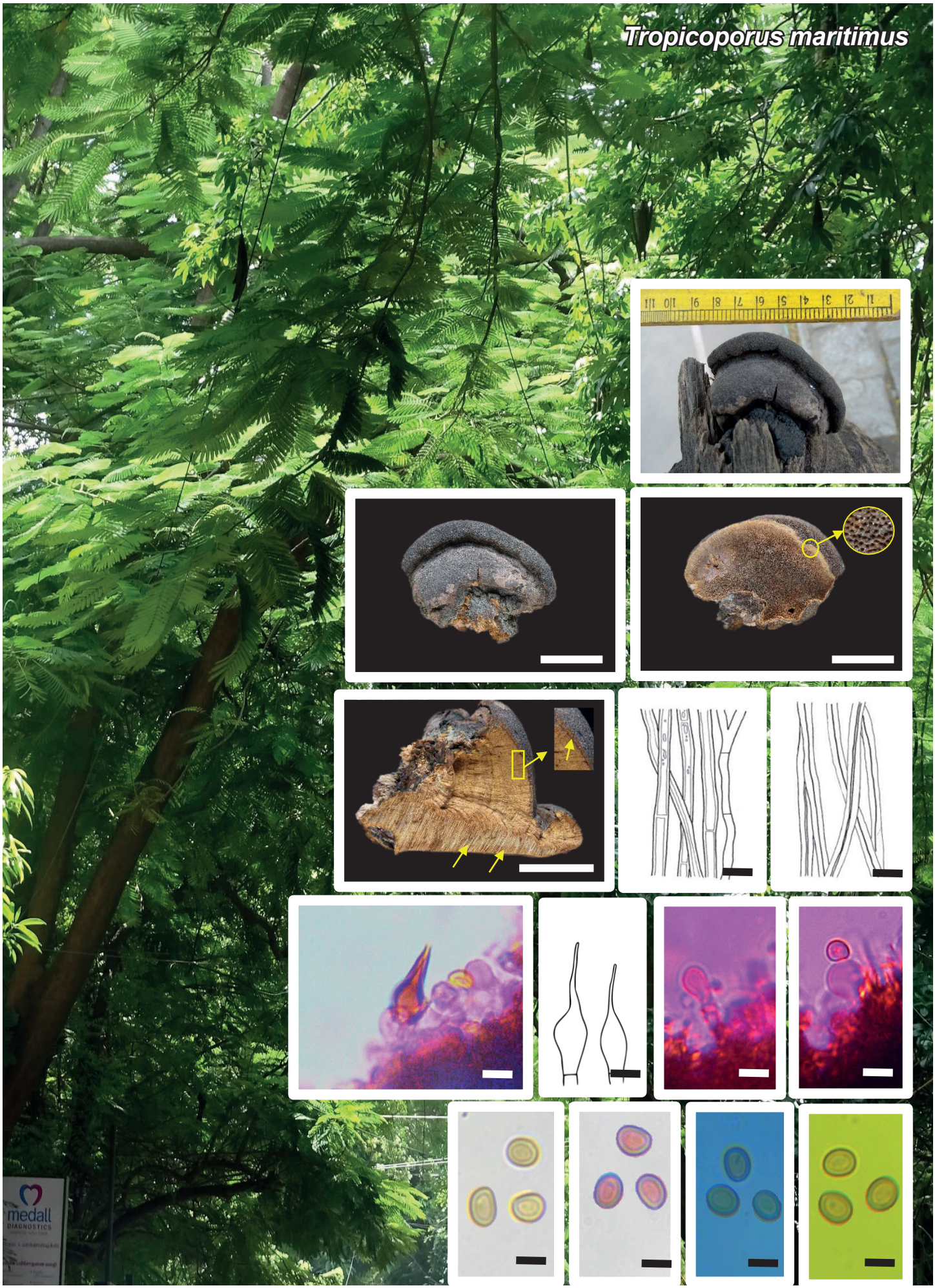
Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the **ITS** sequence of the type collection has the closest GenBank BLAST match (93.81 %) with a sequence listed as unidentified *Scytinopogon* sp. 2 MEL:2382987 from Australia (GenBank KP012842). For **LSU** sequence of the type collection has the closest GenBank BLAST match (99.88 %) with a sequence identified as *Scytinopogon* sp. from Thailand (GenBank MG214695) and similar sequences identified as *Trechispora* sp. HG140168 (99.27 %) from China (GenBank OM339264).

Trechispora sanpatongensis phylogenetically clusters with *T. sangria* and *T. sanpapaoensis*, but it differs in the colour of both fresh and dried basidiocarps, namely, yellowish white from the base to the middle and moderate brown towards the ends when fresh and yellowish white when dried in *T. sanpatongensis*, greyish reddish orange to light reddish brown when fresh and light brownish grey when dried in *T. sangria*, and very pale purple colour when fresh and brownish grey when dried in *T. sanpapaoensis*. The branch tips of *T. sanpatongensis* and *T. sanpapaoensis* are white while the tips of *T. sangria* are dark purple red. *Trechispora sanpatongensis* has yellowish stipes whereas stipes of *T. sangria* are moderated orange yellow, and those of *T. sanpapaoensis* are greyish brown. Additionally, the stipes of *T. sanpatongensis* are cylindrical while those of *T. sangria* are oblate and shorter. *Trechispora sanpatongensis* has a smaller size of basidiocarps and a relatively larger size of basidia compared with *T. sangria* and *T. sanpapaoensis*.

For phylogenetic trees and Table, see *T. sangria* (FP 1665).

Colour illustrations: The deciduous dipterocarp forest, San Pa Tong district, Chiang Mai province, where the holotype was collected (background photo); Left top: Basidiomata growing on the soil of BBH 49634. Left bottom: Basidia. Centre: Basidia with basidiospores. Right bottom: Basidiospores, scanning electron photograph of spores from BBH 49635. Scale bars: basidiomata = 10 mm; basidia = 10 µm; basidiospores = 5 µm.

U. Pinruan & J.J. Luangsa-ard,
Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand; e-mail: umpawa.pin@biotec.or.th & jajen@biotec.or.th
S. Chaimongkol, Plant Microbe Interaction Research Team (APMT), National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) 111 Thailand Science Park, Phahonyothin Road, Khlong Nueng, Khlong Luang, Pathum Thani, 12120, Thailand, and Department of Biology, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Ladkrabang, Bangkok, Thailand; e-mail: soravit.cha@ncr.nstda.or.th
P. Lueangjaroenkit, Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand, and Biodiversity Center, Kasetsart University (BDCKU), Bangkok, Thailand; e-mail: Piyangkun.lu@ku.th



MycoBank MB 852794

Fungal Planet 1667

Tropicoporus maritimus N. Chellapan, V. Vasan & M. Kaliyaperumal *sp. nov.*

Etymology: The species epithet "*maritimus*" derived from Latin word representing the coastal area.

Classification: *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes.*

Basidiomata perennial, pileate, broadly zonate, firmly attached to the surface. *Pileus* projecting up to 4.5 cm, 6.5 cm wide, 2.5 cm at the base. *Pileal surface* greyish brown (9F3; Kornerup & Wanscher 1978) to brownish grey (9F2). *Margin* acute, incurved towards pilear surface, light brown (6D4), 1 mm. *Pore surface* dark brown to brown (6F4, 6D6). *Pores* circular, 3–5/mm. *Context* brown (6D7), duplex with thin black line, up to 1 cm thick. *Tube layer* brown (6D6), 1.9 cm, stratified, each stratum up to 1 mm. *Hyphal system* mono-dimitic, tissue darkening in KOH without hyphal swelling. *Context* generative hyphae thin- to thick-walled, pale yellow to brown, simple septate, rarely branched, 3–4.5 µm diam. *Trama generative hyphae* thin- to thick-walled, hyaline to dark brown, simple septate, rarely branched, 2.5–4.3 µm diam. *Skeletal hyphae* thick-walled with a narrow to wide lumen, yellow to yellowish brown, aseptate, unbranched, 3.3–4 µm diam. *Cystidioles* thin-walled, hyaline, ventricose to fusoid with abruptly narrow apices, 12–20 × 2.1–2.6 µm. *Hymenial setae* ventricose, 18.3–29.4 × 6.3–8.9 µm. *Basidia* clavate to subclavate, 10–12 × 5.8–7.9 µm, with four sterigmata. *Basidiole* clavate, 8.4–12.6 × 4.2–8.1 µm. *Basidiospores* smooth, subglobose to broadly ellipsoid, thin- to thick-walled pale yellow to golden yellow in water, turning golden yellow to brown in KOH, (5.3–)5.5–5.8 × (4.8–)5–5.3 µm (n = 30/2), Q = 1.10 (Q range 1.05–1.15), CB⁻, IKΓ.

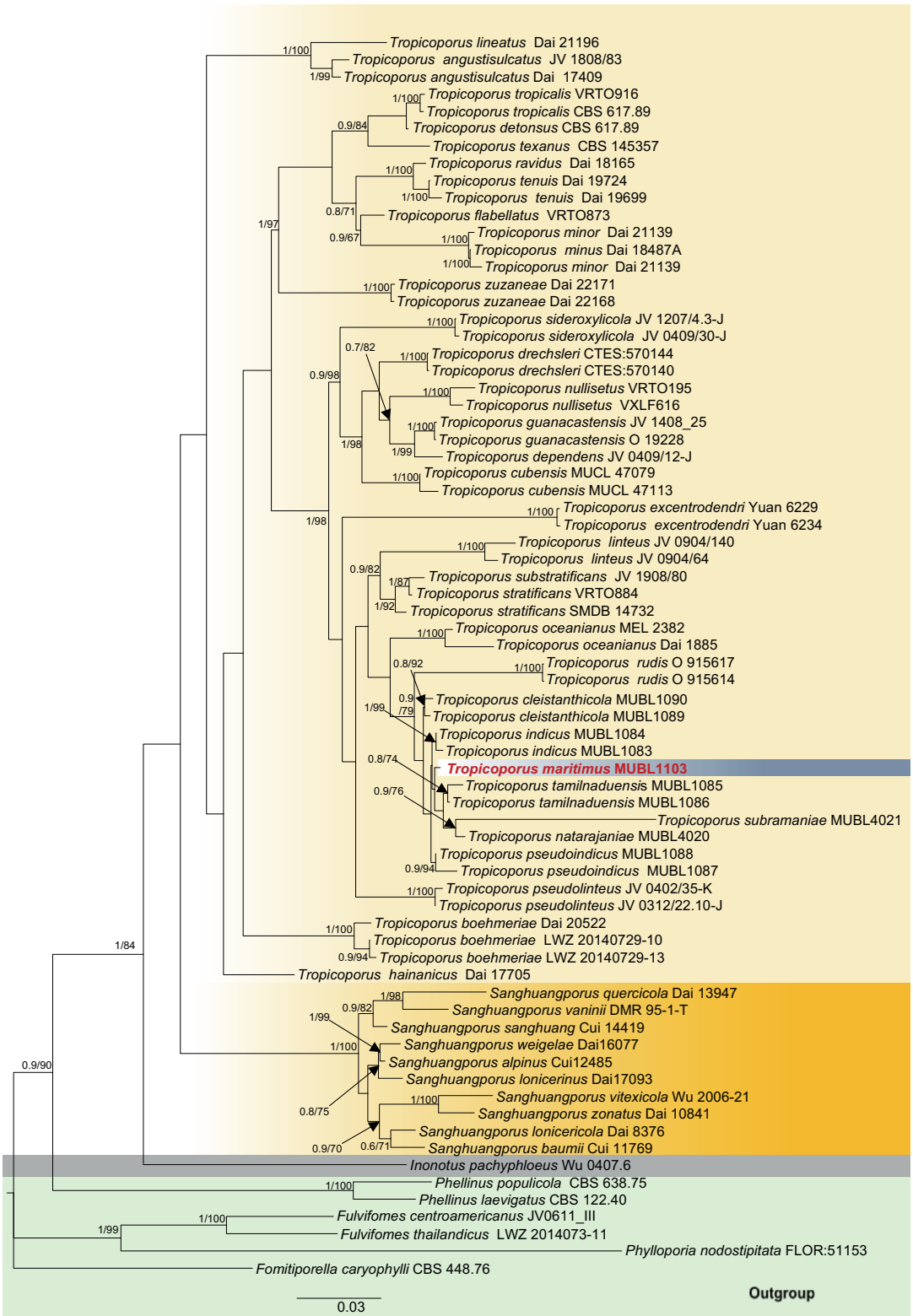
Typus: **India**, Chennai, Besant Nagar, 13.0003°N, 80.2667°E, on living angiosperm tree *Peltophorum pterocarpum* (*Fabaceae*), 8 Sep. 2022, *N. Chellapan*, (**holotype** MUBL1103; ITS and LSU sequences GenBank PP378327 and PP373828).

Notes: The phylogenetic study indicates that *Tropicoporus maritimus* and other related Indian taxa are a sister clade to *T. rudis* (79 % ML/0.9 BPP). *Tropicoporus maritimus* and *T. rudis* are similar in their mono-dimitic hyphal system but the former differs in duplex context, acyanophilic spores and the presence of cystidioles (Wu *et al.* 2022). *Tropicoporus maritimus* and *T. pseudoindicus* are similar in having a broadly zonate pileus, mono-dimitic hyphal system and presences of cystidioles but differ with the latter having a smooth pilei, obtuse margin, pores and larger basidiospores (Gunaseelan *et al*. 2024). *Tropicoporus maritimus, T. subramaniae* and *T. indicus* are similar by having a mono-dimitic hyphal system. The former species differs by having a broadly zonate and uncracked basidiome, obtuse margin and duplex context with thin blackline (Gunaseelan *et al.* 2024, Liu *et al*. 2024). *Tropicoporus maritimus* and *T. natarajaniae* resemble each other in a broadly zonate uncracked pileus and obtuse margin, but *T. maritimus* differs in having larger pores, larger hymenial setae, smaller cystidioles and basidiospore size (Liu *et al*. 2024). Likewise, *T. maritimus* is similar to *T. tamilnaduensis* by having a broadly zonate basidiome, hyphal system and obtuse margin, but significantly differs in other characters (Gunaseelan *et al*. 2024). Two Indian species *viz*., *T. cleistanthicola* and *T. pseudolinteus* significantly differ from *T. maritimus* in morphological and microscopical characters (Vlasàk *et al.* 2013, Gunaseelan *et al.* 2024).

Based on a BLAST search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity with *Tropicoporus rudis* (O 915614) [GenBank KP030796.1; Identities = 611/652 (94 %), 23 gaps (3 %)], *Tropicoporus rudis* (O 9156170) [GenBank KP030797.1; Identities = 595/632 (94 %), no gaps] and *Inonotus* sp. (MEL 2382654) [GenBank KP013017.1; Identities = 608/657 (93 %), 18 gaps (2 %)]. The closest hits using the **LSU** sequence had highest similarity with *Tropicoporus substratificans* (PRM JV 1908_80) [GenBank NG_241945.1; Identities = 867/872 (99 %), no gaps], *Tropicoporus tropicalis* (URM89677) [GenBank MN812248.1; Identities = 862/876 (98 %), four gaps] and *Phellinus undulatus* (MUCL 44139) [GenBank DQ131561.1; Identities = 860/873 (99 %), one gap].

Supplementary material: 10.6084/m9.figshare.25406335 (Table).

Colour illustrations: Holotype collection area, India. Habitat; pilear surface; pore surface; transverse section of basidiomata; microscope illustrations and *camera lucida* drawing of holotype: contextual hyphae; tramal hyphae; hymenial setae; cystidioles; basidioles; basidia bearing spore and basidiospores; basidiospores in water, in KOH, in cotton blue, and in Melzer's reagent. Scale bars: macrophotographs = 5 cm; microphotographs = 5 µm.



Phylogenetic tree inferred from ITS and LSU sequences of *Tropicoporus maritimus* (MUBL1103) and related species rooted with *Fomitiporella caryophylli* (CBS 448.76) and *Phylloporia nodostipitata* (FLOR: 51153). The maximum likelihood (ML) analysis was performed using MEGA X (Kumar *et al*. 2018) and the same data were used for a Bayesian analysis using MrBayes v. 3.2.7 (Ronquist *et al.* 2012). Branches are labelled with ML bootstrap (1 000 replicates) and Bayesian posterior probabilities values. The novel species are **bold** and highlighted. The alignment and tree are submitted in TreeBASE (study ID: 31208).

N. Chellappan, V. Vasan, M. Nagarajan, R. Murugadoss & M. Kaliyaperumal, Centre for Advanced Studies in Botany, University of Madras, Chennai, Tamil Nadu, India; e-mail: naveen.c2900@gmail.com, vigneshwarivasan018@gmail.com, mohanapriya490@gmail.com, rameshmurugadoss@gmail.com & malar.kaliyaperumal@gmail.com

Fungal Planet 1668 MycoBank MB 852635

Tuber aereum Polemis, Daskalopoulos & Zervakis, *sp. nov.*

Etymology: The epithet *aureum* derives from the Latin "*aereus*" (*i.e.*, of copper or bronze colour).

Classification: *Tuberaceae*, *Pezizales*, *Pezizomycetes.*

Ascomata hypogeous, 13–25 mm, irregularly folded and lobed, resembling a crumpled copper foil, less often almost subglobose, smooth or with barely visible appressed small warts, minutely pruinose, always moderately dark copper-brown coloured, rusty tawny (14; code numbers from Colour Identification Chart; Royal Botanic Garden, Edinburg – RBGE 1969), dark brick (20), purplish date (22), and chestnut (36) in fresh and dried state. *Peridium* 250–350 µm thick in total, composed of hyaline, agglutinated, interwoven hyphae (intricate texture), external layer 30–75 µm thick, distinctly pigmented dark brown, of the same texture or indistinctly pseudoparenchymatous, with or without scattered dermatocystidia, few up to 30 × 6 µm. *Gleba* firm, solid, whitish at first, becoming buff (52), clay buff (32) to olivaceous buff (63) at maturity, marbled with numerous branching white and darker veins, seldomly in contact with the peridium. *Odour* pleasant, of smoked bacon mixed with garlic. *Asci* inamyloid, 50–70 × 40–60 µm excluding stalk, pyriform or irregularly subglobose, with a relatively short stalk arising from a crozier, 10–15 µm long, walls 2–4 µm thick, (1–)2–7 ascospores per asci, 3–7-spored asci equally varied. *Ascospores* 15–35(–39) × 11–23(–25) µm, Q = 1.2–1.9(–2.1), excluding ornamentation, at first hyaline, yellowish brown at maturity, broadly ellipsoid to ovoid, often with somewhat pointed apex, ornamented with densely arranged, separate, medium sized spines, 2–4.5(–5.5) µm long. Ascospores from 1-spored asci 30–35(–39) × 19–23 µm, 2-spored asci 21–30(–32) × 14–20 µm, 3-spored asci 20–31 × 12–18 µm, 4-spored asci 19–25 × 13–17 µm, 5-spored asci 16–23 × 12–15 µm, 6-spored asci 16–24 × 11–16 µm, 7-spored asci 15–20 × 11–15 µm.

Habit, habitat and distribution: *Tuber aereum* grows in Mediterranean forests or stands dominated by *Quercus coccifera* often mixed with *Acer sempervirens*, on limestone, in central mountainous regions of Naxos Island in Cyclades, South Aegean, Greece, at altitude range of 450–650 m a.s.l. The ascomata were found from late October until January. Another almost identical sequence was detected in GenBank, labelled as 'uncultured *Tuber* clone HL21.1', originating from Sardinia, Italy (Genbank FJ688113; Liebel *et al.* 2010).

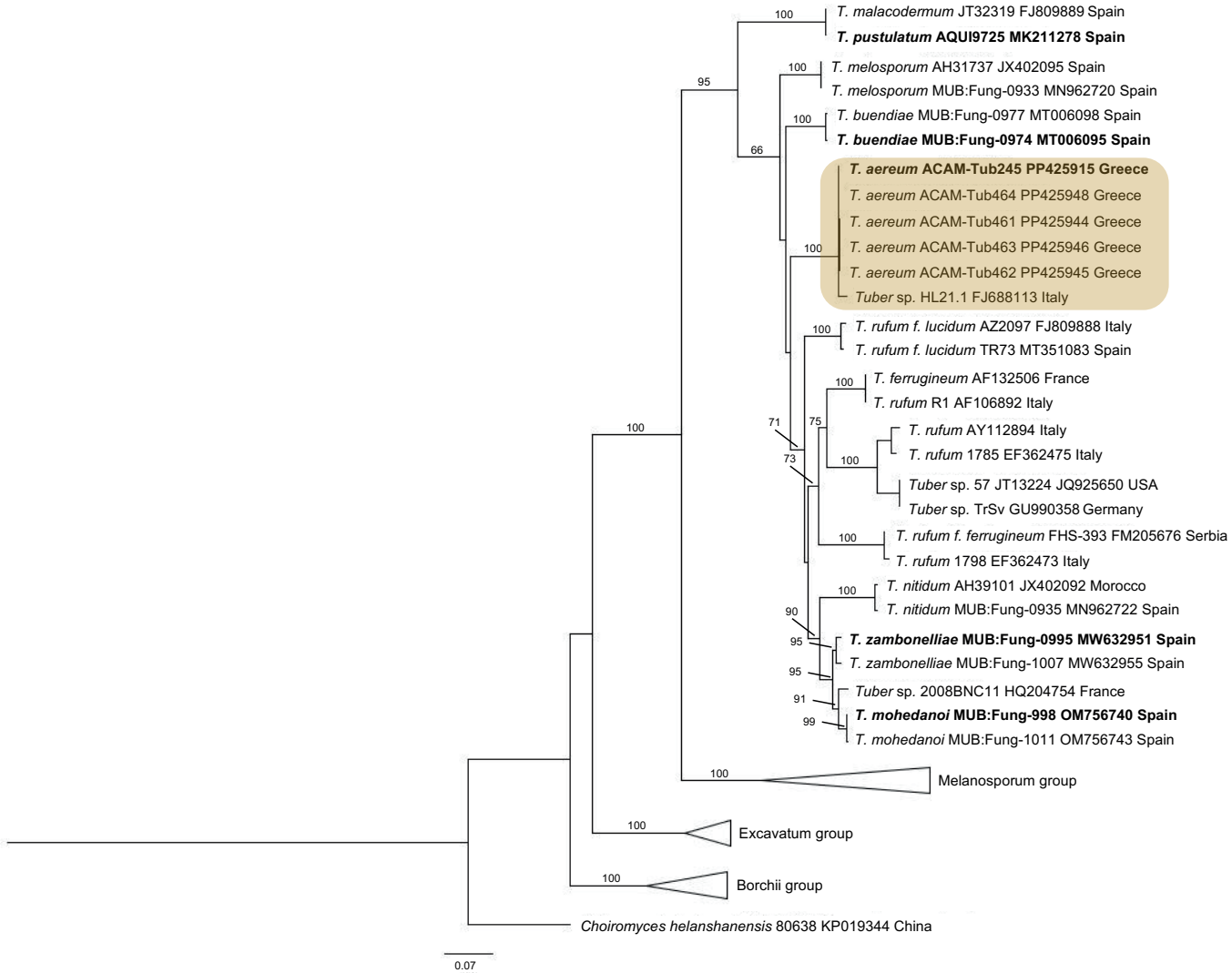
Typus: **Greece**, Naxos Island, Filoti, on limestone, under *Q. coccifera* (*Fagaceae*) and *A. sempervirens* (*Sapindaceae*), 30 Oct. 2020, *leg*. *E. Papadopoulos* (**holotype** ACAM-Tub245; ITS and LSU sequences GenBank PP425915 and PP425961).

Additional materials examined. **Greece**, Naxos Island, Stavros Keramotis, on limestone, under *Q. coccifera* and *A. sempervirens*, 10 Jan. 2024, coll. *E. Papadopoulos* (**paratype** ACAM-Tub461; ITS and LSU sequences GenBank PP425944 and PP425963); *ibid*., 28 Nov. 2023, (ACAM-Tub462; ITS and LSU sequences GenBank PP425945 and PP425966); 12 Dec. 2023, (ACAM-Tub463; ITS and LSU sequences GenBank PP425946 and PP425967); 20 Dec. 2023, (ACAM-Tub464; ITS and LSU sequences GenBank PP425948 and PP425969).

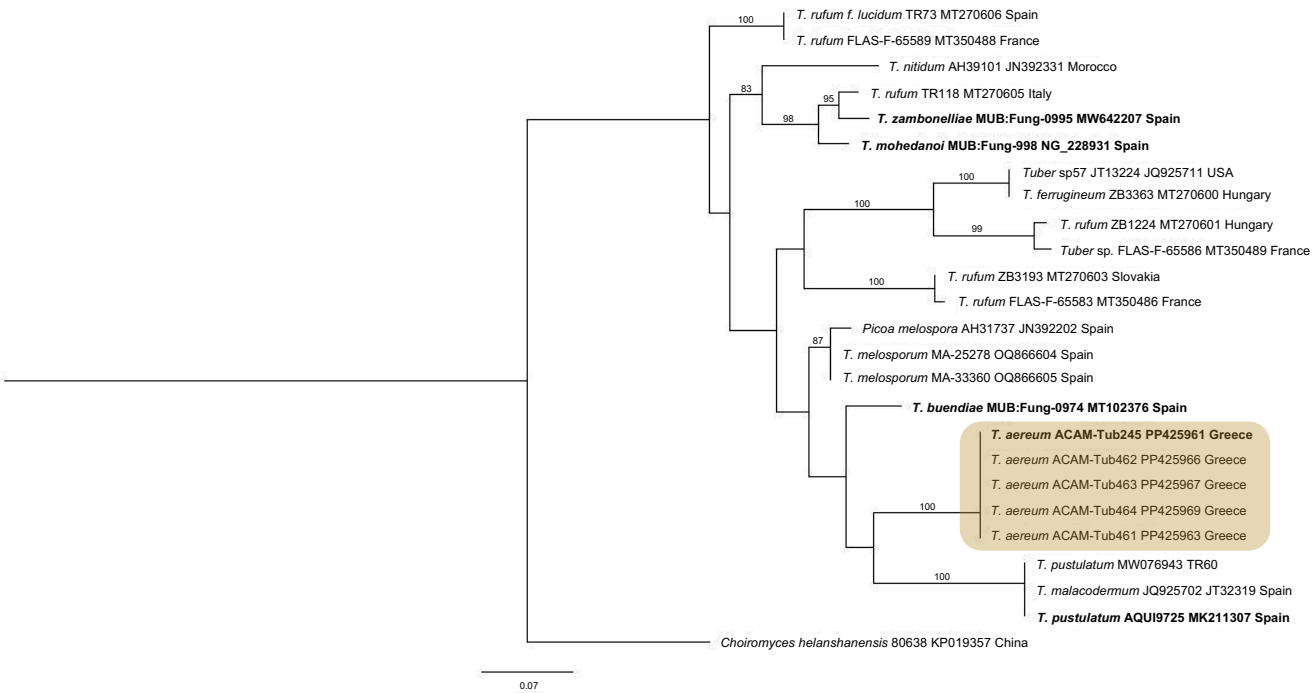
Notes: *Tuber aereum* is a small irregularly folded and copper-brown coloured truffle within the Rufum group, and is characterised by minutely warty to almost smooth peridium of plectenchymatic structure, mainly with 3–7-spored asci, and ascospores with dense and relatively large spines that do not form any kind of reticulum. Its closest phylogenetic relative *T. melosporum – i.e*., another Mediterranean species from evergreen *Quercus* forests – is clearly differentiated morphologically due to its unique smooth ascospores (Alvarado *et al.* 2012). *Tuber buendiae*, with similar ecogeographic characteristics, forms ascomata with darker brown colours, distinctly warty peridium and ascospores with reticulate ornamentation (Crous *et al.* 2020).

Based on a megablast search of INSDC (GenBank) nucleotide database, the closest hit using the **ITS** sequence of the type material is a sequence from *Tuber* clone HL21.1 [(FJ688113; query cover= 70 %, identity = 438/441 (99 %), three gaps], which groups with *T. aereum* according to our phylogenetic analysis. With regard to other taxa, *T. aereum* exhibited the highest similarity to *T. melosporum* (six GenBank accessions; identities = 88–89 %, gaps = 1 %), *T. buendiae* (eight GenBank accessions; identities = 86–87 %, gaps = 3 %), while some other similar sequences were identified as *T. rufum s.l.* The closest hits using the LSU sequence were with sequences of *T. melosporum* (three GenBank accessions, identities = 97 %), *T. buendiae* (two GenBank accessions, identities = 96–97 %), and with a few other sequences of the Rufum group.

Colour illustrations: Habitat of *Tuber aereum sp. nov.*, in Naxos Island (Greece), in a *Quercus coccifera* forest. Ascomata; mature ascospores; peridium. Scale bars: mature ascospores = 10 µm; peridium = 20 µm.



Maximum likelihood (ML) phylogenetic tree depicting *Tuber aereum sp. nov.* as part of the *T. rufum* group, inferred from ITS sequences using the IQ-TREE web server (Nguyen *et al.* 2015, Trifinopoulos *et al*. 2016). Branch support values were obtained using the ultrafast bootstrap (1 000 replicates) implemented in the IQ-TREE software (Hoang *et al.* 2018). Alignment of sequences was performed using the ClustalW algorithm of MEGA11 software (Tamura *et al.* 2021), while the online tool of TrimAL software (Capella-Gutiérrez *et al.* 2009) was used to trim the aligned sequences. Visualisation of phylogenetic tree was done by FigTree v. 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The sequences obtained in the present study (*T. aureum sp. nov.*) appear in a coloured box. Sequences originating from type material are indicated in **bold**. Bootstrap support values (≥ 60 %) appear at the nodes. *Choiromyces helanshanensis* (GenBank KP019344) was used as outgroup. The scale bar indicates the expected number of changes per site. Final alignments and phylograms are deposited in TreeBASE (study ID: 31215).



Maximum likelihood (ML) phylogenetic tree depicting *Tuber aereum sp. nov.* as part of the *T. rufum* group, inferred from LSU sequences using the IQ-TREE web server (Nguyen *et al.* 2015, Trifinopoulos *et al*. 2016). Branch support values were obtained using the ultrafast bootstrap (1 000 replicates) implemented in the IQ-TREE software (Hoang *et al.* 2018). Alignment of sequences was performed using the ClustalW algorithm of MEGA11 software (Tamura *et al.* 2021), while the online tool of TrimAL software (Capella-Gutiérrez *et al.* 2009) was used to trim the aligned sequences. Visualisation of phylogenetic tree was done by FigTree v. 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The sequences obtained in the present study (*T. aureum sp. nov.*) appear in a coloured box. Sequences originating from type material are indicated in **bold**. Bootstrap support values (≥ 60 %) appear at the nodes. *Choiromyces helanshanensis* (GenBank KP019357) was used as outgroup. The scale bar indicates the expected number of changes per site. Final alignments and phylograms are deposited in TreeBASE (study ID: 31215).

E. Polemis, V. Daskalopoulos & G.I. Zervakis, Department of Crop Science, Agricultural University of Athens, Iera Odos 75, 11855 Athens, Greece; e-mail: eliasp@ath.forthnet.gr, vassilismks@gmail.com & zervakis@aua.gr

Fungal Planet 1669 MycoBank MB 850899

Tuber arriacaense G. Moreno, J.R. Carlavilla & J.L. Manjón, *sp. nov.*

Etymology: Named for being collected in the vicinity of the Roman archaeological site Arriaca-El Tesoro (Guadalajara), Spain.

Classification: *Tuberaceae*, *Pezizales*, *Pezizomycetes.*

Ascomata hypogeous, 0.5–4 cm in size, pale brown, globose or subglobose, sometimes lobed, reddish brown to dark brown. *Peridium* covered with little roughly polygonal warts; about 80–200 µm thick, composed of pseudoparenchymatic cells, 8–15 µm diam and cracking with yellowish tones. *Gleba* firm, solid, whitish at first, becoming light reddish brown at maturity, marbled with branching white veins, with plectenchymatous structure, 4–5 µm wide. *Odour* something bituminous but pleasant. *Asci* inamyloid, 63–84 × 40–57 µm including stalk, globose or subglobose, with a short stalk arising from a crozier, stalk 10–20 × 7–13 um, 1–5(–6)-spored. *Ascospores* 12.9–43.7(–45) × 11.6–29.4(–30) µm, av. 28.3 × 20.5 µm, Qav = 1.8 (n = 25), including ornamentation, at first hyaline, yellowish brown at maturity, ellipsoid, ornamented with short, separate spines, 2–3 µm long. Ascospores from 1-spored asci 32–45 × 25–30 µm, 2-spored asci 29–35 × 20–25 µm, 3-spored asci 21–28 × 17–19 µm, 4-spored asci 20–26 × 16–20 µm, 5-spored asci 17–23 × 13–17 µm, and 6-spored asci 16–20 × 15–17 µm.

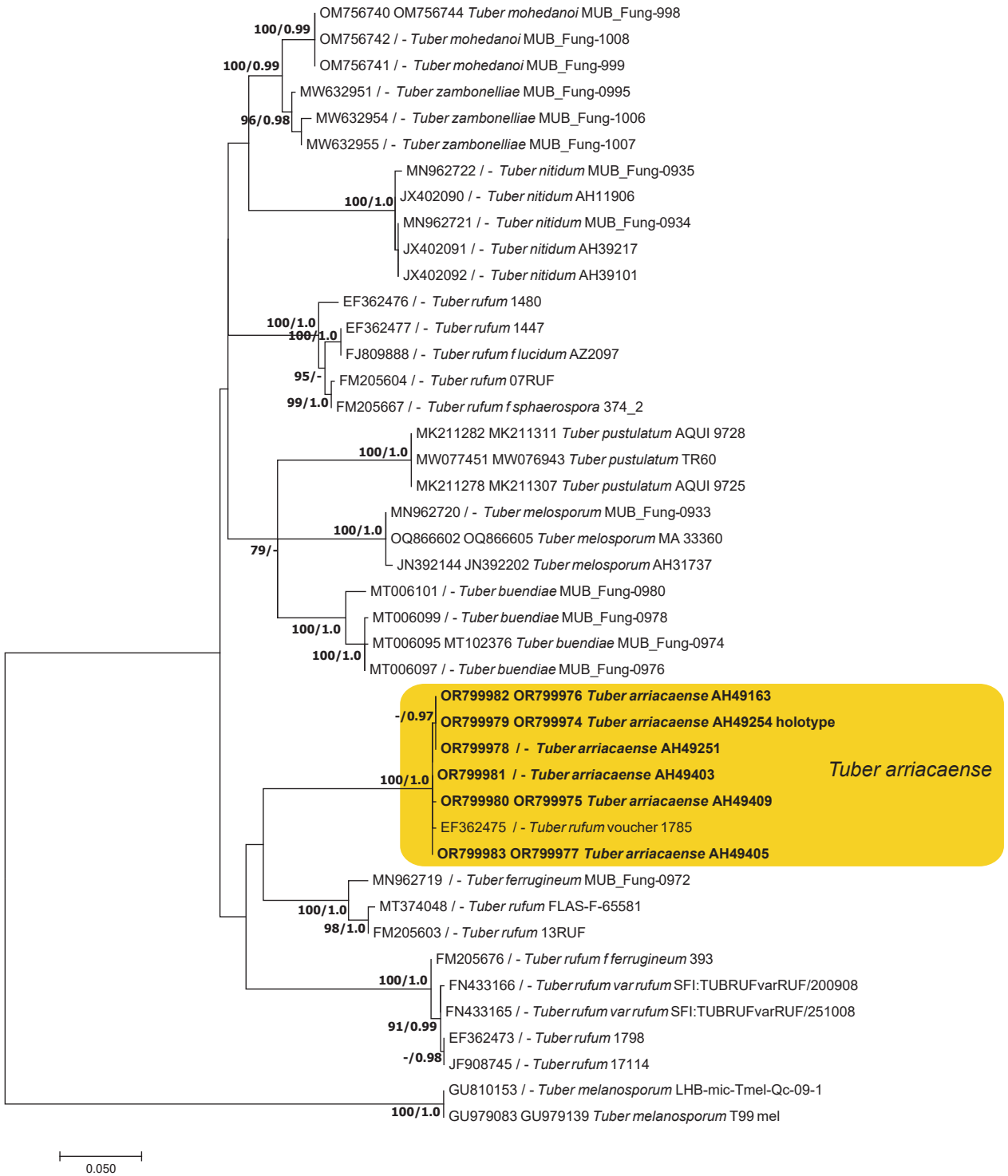
Ecology and distribution: *Tuber arriacaense* forms mycorrhizae with *Populus pyramidalis* and *Populus nigra* (*Salicaceae*) in Central Spain. The species occurs from May to September with high soil humidity and warm temperature.

Typus: **Spain**, Guadalajara (La Chopera Urbanization), in soil under *Populus pyramidalis*, 15 May 2021, *J.L. Manjón & Luky (dog)* (**holotype** AH 49254; ITS and LSU sequences GenBank OR799979 and OR799974).

Additional materials examined: **Spain**, Guadalajara (La Chopera Urbanization), in soil under *Populus pyramidalis*, Jun. 2020, *J.L. Manjón & Luky (dog)*, AH 49162; *idem*., 13–21 Aug. 2020, AH 49163 (ITS and LSU sequences GenBank OR799982 and OR799976); *idem*., 12 Jun. 2021, AH 49405 (ITS and LSU sequences GenBank OR799983 and OR799977); *idem*., Jun. 2021, AH 49251 (ITS sequence GenBank OR799978); *idem*., from Jun. to Sep. 2021, AH 49404; *idem*., 28 Jun. 2023, AH 49406; *idem*., 28 Jun. 2023, AH 49407; *idem*., 20 Jul. 2023, AH 49408; *idem*., 9 Aug 2023, AH 49412; *idem*., 29 Aug. 2023, AH 49413; *idem*., 29 Aug. 2023, AH 49414; *idem*., 8 Sep. 2023, AH 49403 (ITS sequence GenBank OR799981); Guadalajara (La Chopera Urbanization), in *Populus nigra*, 24 Jul. 2023, *J.L. Manjón & Luky (dog)*, AH 49409 (ITS and LSU sequences GenBank OR799980 and OR799975); *idem*., 25 Jul. 2023, AH 49410; *idem*., 31 Jul. 2023, AH 49411.

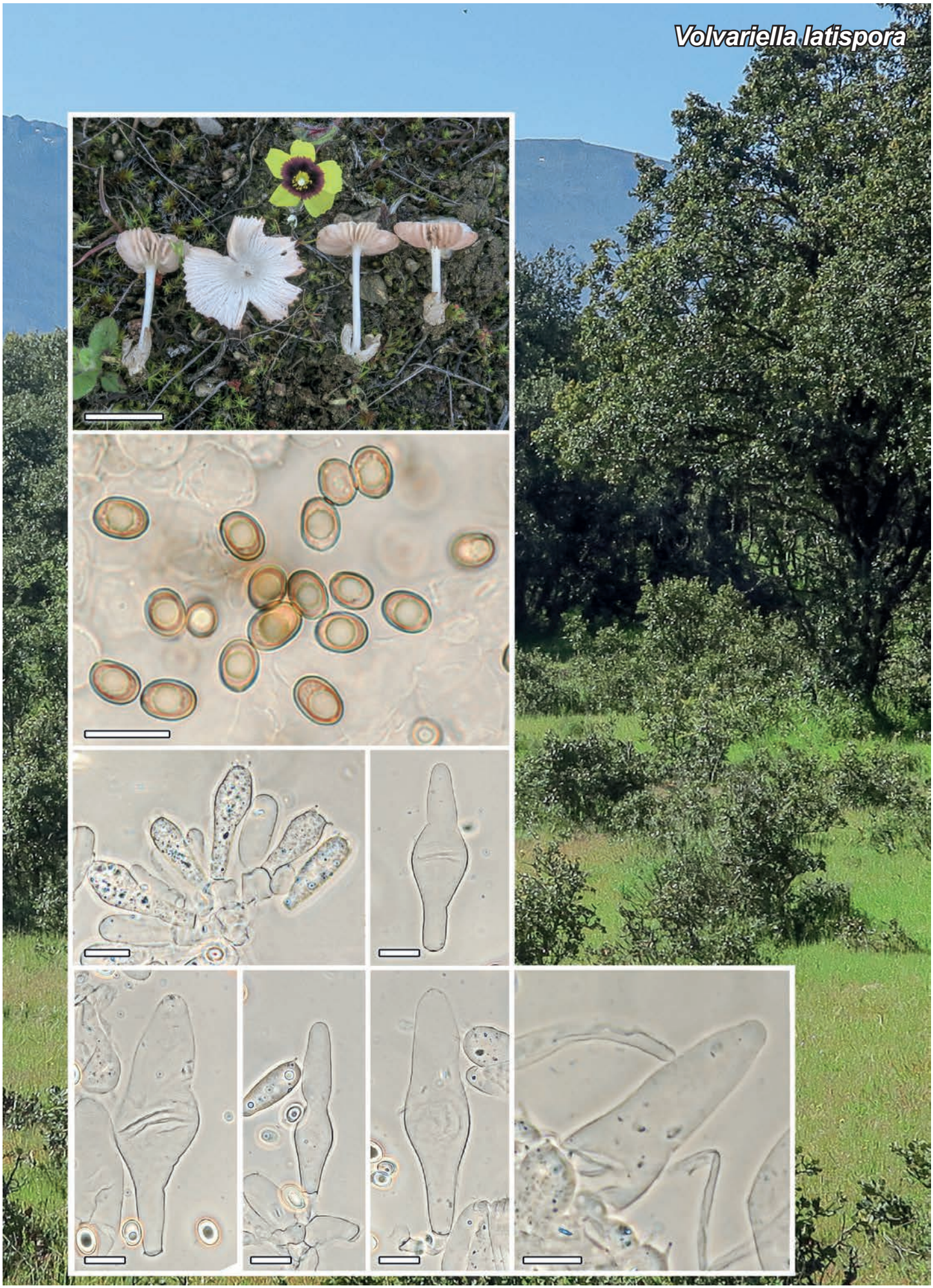
Notes: *Tuber arriacaense* is a pale brown truffle that clusters in the *rufum* clade, and is characterised by roughly polygonal warts, reddish brown at maturity, marbled with branching white veins and growing in *Populus* spp. (*Salicaceae*) mainly in summer. *Tuber arriacaense* resembles *T. nitidum* (88 % of similarity of ITS sequence), but in addition to genetic differences, *T. nitidum* differs by having a basal cavity and smooth peridium (Ceruti *et al*. 2003). The smooth peridium of *T. nitidum* has also been recorded by Montecchi & Sarasini (2000). *Tuber zambonelliae*, another similar species (87 % of similarity of its sequence), with smooth peridium, minutely pruinose and sporulation in calcareous soil, in *Quercus ilex* subsp. *ballota* forest (*Fagaceae*) (Crous *et al.* 2021a). *Tuber buendiae* is close to *T. arriacaense* with reddish brown ascomata that clusters in the rufum clade, and characterised by its minutely warted peridium, brown gleba marbled with white and dark veins and spiny-reticulate spores, growing in calcareous soil, in *Quercus ilex* subsp. *ballota* forest (*Fagaceae*) (Crous *et al.* 2020). *Tuber requienii* is a species described by Tulasne (1851), near Tarascon (France), in *Quercus coccifera,* which numerous authors have considered a synonym of *Tuber rufum* or *T. ferrugineum*. However, Riousset *et al.* (2001), consider it an independent species. There are no molecular studies of this species to compare it with the one proposed here, but it is clearly differentiated by its habitat. *Tuber ferrugineum* and *Tuber rufum* are considered a complex species that still need to be studied (Crous *et al.* 2021a). The proposed new species was also found in Italy (Sala Bolognese, Bologna) as *Tuber rufum* (GenBank EF362475), without habitat specification (Iotti *et al.* 2007).

Colour illustrations: Guadalajara (La Chopera Urbanization) and Luky (Lagotto Romagnolo truffle dog) marking in *Populus nigra* garden where different samples were collected. Ascomata AH 49254 holotype and AH 49405 paratype in *Populus pyramidalis*; peridium warts, peridium, section, detail of peridium and gleba cells, ascus and mature ascospores from AH 49254 holotype. Scale bars: ascomata = 1 cm; peridium warts = 1 mm; peridium section = 100 µm; detail of peridium and gleba cells, ascus and ascospores = 10 µm.



Maximum likelihood (ML) tree inferred from the combined ITS and LSU rDNA sequences of the *Tuber rufum* clade with *Tuber melanosporum* as outgroup. The sequences obtained in the present study are highlighted in **bold**. The first value on the branches represents the ML bootstrap proportions (≥ 70 %) and the value after the slash shows the posterior probability calculated by a Bayesian analysis (≥ 0.95).

G. Moreno, J.R. Díaz-Carlavilla & J.L. Manjón, Departamento de Ciencias de la Vida (Área de Botánica), Facultad de Biología, Universidad de Alcalá, 28805 Alcalá de Henares, Spain; e-mail: gabriel.moreno@uah.es, juan.carlavilla@gmail.com & josel.manjon@uah.es



Fungal Planet 1670 MycoBank MB 850524

Volvariella latispora G. Moreno, A. Sánchez & P. Alvarado, *sp. nov.*

Etymology: Name reflects its broad spores.

Classification: *Pluteaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps annual, with a central stipe. *Cap* 0.8–1.6 cm, convex, plano-convex, sometimes subapplanate, striate up to the umbo (mature basidiomes), whitish in colour, slightly floccose up to the umbo, because of remnants of the universal veil. *Gills* (lamellae = 25–32; lamellulae escasas), free, ventricose, up to 1.2–1.8 mm broad, first concolourous with the cap, pale pink when mature, with a concolourous edge. *Stem* 1–1.4 × 0.10–0.12 mm, cylindrical, somewhat thickened at the base, solid, white, glabrous. Volva saccate, 0.43–0.67 × 0.34–0.54 mm, membranous, fragmenting in 2–4 lobes, whitish-grey, darker when mature. *Odour* not distinctive. *Taste* none. *Basidia* 4-spored, 25–35 × 8–11 µm, sterigmata up to 3 µm long. *Spores* 6.5–8.7(–9) × 4–6.6 µm, av. 7.6 × 5.3 µm, Qav = 1.45 (n = 25 holotype), pinkish, ellipsoid to broadly ellipsoid, thick-walled, without germ pore, non-amyloid, cyanophilous, smooth, with lipid vacuoles. *Cheilocystidia* and *Pleurocystidia* scarce but present, fusiform to lageniform, 40–80 × 12–25 µm. *Caulocystidia* absent. *Pileipellis* in cutis, composed of cylindrical hyphae 5–10(–15) µm thick). *Velipellis* formed by hyaline smooth hyphae, exceeding 150 µm in length and about 12–20 µm thick. *Clamps* absent.

Habitat and distribution: Growing solitary to gregarious on sandy acid soil with *Tuberaria guttata*, *Rumex bucephalophorus* and bryophytes. Rare in the studied area.

Typus: **Spain**, Segovia, Revenga, on grassy soils in a *Quercus ilex* ssp. *rotundifolia* stand with *Tuberaria guttata*, *Rumex bucephalophorus* and bryophytes, 20 May 2016, *A. Sánchez* (**holotype** AH 49362; ITS, LSU, *TEF1*, and *RPB2* sequences GenBank OR671197, OR663991, OR666980, and OR666978).

Additional materials examined: **Spain**, Segovia, Revenga, on grassy soils in a *Quercus ilex* ssp. *rotundifolia* stand with *Tuberaria guttata*, *Rumex bucephalophorus* and bryophytes, 10 May 2016, *A. Sánchez* (**paratype** AH 49361; ITS, LSU, *TEF1*, and *RPB2* sequences GenBank OR671198, OR663992, OR666979, and OR666977); *idem*., 19 May 2016 (**paratype** AH 49249; ITS and LSU sequences GenBank OR671195 and OR663989); *idem*., 7 May 2021 (**paratype** AH 49250; ITS and LSU sequences GenBank OR671196 and OR663990).

Notes: The genus *Volvariella* was included in the family *Pluteaceae*, along with *Pluteus* (Boekhout 1990, Justo 2011a) and *Volvopluteus* (Justo *et al.* 2011b) until it was recently split into its own family *Volvariellaceae* (Vizzini *et al*. 2024). *Volvariella latispora* is characterised by its small size, whitish-grey volva, smooth, ellipsoid to broadly ellipsoid spores measuring 5–8.7(–9) × 4–6.6 µm, fusiform to lageniform cystidia and presence of a velipellis at the apex of the pileus formed by hyaline filaments. Its basidiomes were found growing directly on cleared grassy areas of a *Quercus ilex* stand on acidic soil. *Volvariella pusilla* is similar in size and grows in the same habitat, but has narrower spores measuring 5.5–7 × 4–5.5 µm (Boekhout 1990).

The Bayesian and ML phylogenetic analyses based on ITS and LSU rDNA suggest that the samples studied belong in the main clade of *Volvariella s. str*., differing from the most basal groups of this genus: 1) the one including *V. volvacea* and *V. bombycina* and 2) the clade including *V. pulla*, *V. niveosulcata*, *V. guttulosa*, *V. perciliata* and *V. bilobata*. The currently known nuclear ribosomal RNA gene data of the genus *Volvariella* did not allow to infer any other phylogenetic relationship of *V. latispora*.

Supplementary material: doi: 10.6084/m9.figshare.25406335 (Table)

Colour illustrations: Spain, Segovia, Revenga, acidic soil where the holotype was collected. Basidiomata; spores; velipellis; basidia and basidioles, pleurocystidia, cheilocystidium at the edge of lamella (holotype). Scale bars: basidiomata = 1 cm; spores, velipellis, basidia, cheilocystidium under LM = 10 µm.

A 50 % majority rule ITS-28S rDNA consensus phylogram of the genus *Volvariella* (*Volvariellaceae, Pluteineae*) (with selected sequences of *Volvopluteus* as outgroup) obtained using MrBayes from 31 125 sampled trees. Nodes were annotated if they were supported by ≥ 0.95 Bayesian posterior probability (left) or ≥ 70 % maximum likelihood bootstrap proportions (right). Non-significant support values are exceptionally represented inside parentheses. Sequences newly generated in this study are in **bold**.

G. Moreno, Departamento de Ciencias de la Vida (Unidad Docente de Botánica), Facultad de Ciencias, Universidad de Alcalá, E–28805 Alcalá de Henares, Madrid, Spain; e-mail: gabriel.moreno@uah.es
A. Sánchez, Departamento de Ciencias de la Vida (Unidad Docente de Botánica), Facultad de Ciencias, Universidad de Alcalá, E–28805 Alcalá de Henares, Madrid, Spain; e-mail: a.sanchez.garci@gmail.com
P. Alvarado, ALVALAB, Dr. Fernando Bongera st. Severo Ochoa bldg. S1.04, 33006 Oviedo, Spain; e-mail: pablo.alvarado@gmail.com

Fungal Planet 1671 MycoBank MB 853785

Elsinoe atypica Crous & M.J. Wingf., *sp. nov.*

Etymology: Name refers to the atypical foliar symptoms.

Classification: *Elsinoaceae*, *Myriangiales*, *Dothideomycetidae*, *Dothideomycetes*.

Leaf spots resembling *Pachysacca*, but no sexual morph observed. *Asexual morph* immersed in host tissue, *conidiomata* 200–300 µm diam, hyaline, with tightly aggregated hyaline, smooth, subcylindrical *conidiophores*, multiseptate, branched, up to 120 µm tall, 2–4 µm diam. *Conidiogenous cells* integrated, terminal and lateral, polyphialidic, 15–20 × 2.5–3 µm. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, subcylindrical, apex obtuse, base with minute truncate hilum, 6–7 × 2.5(–3) µm.

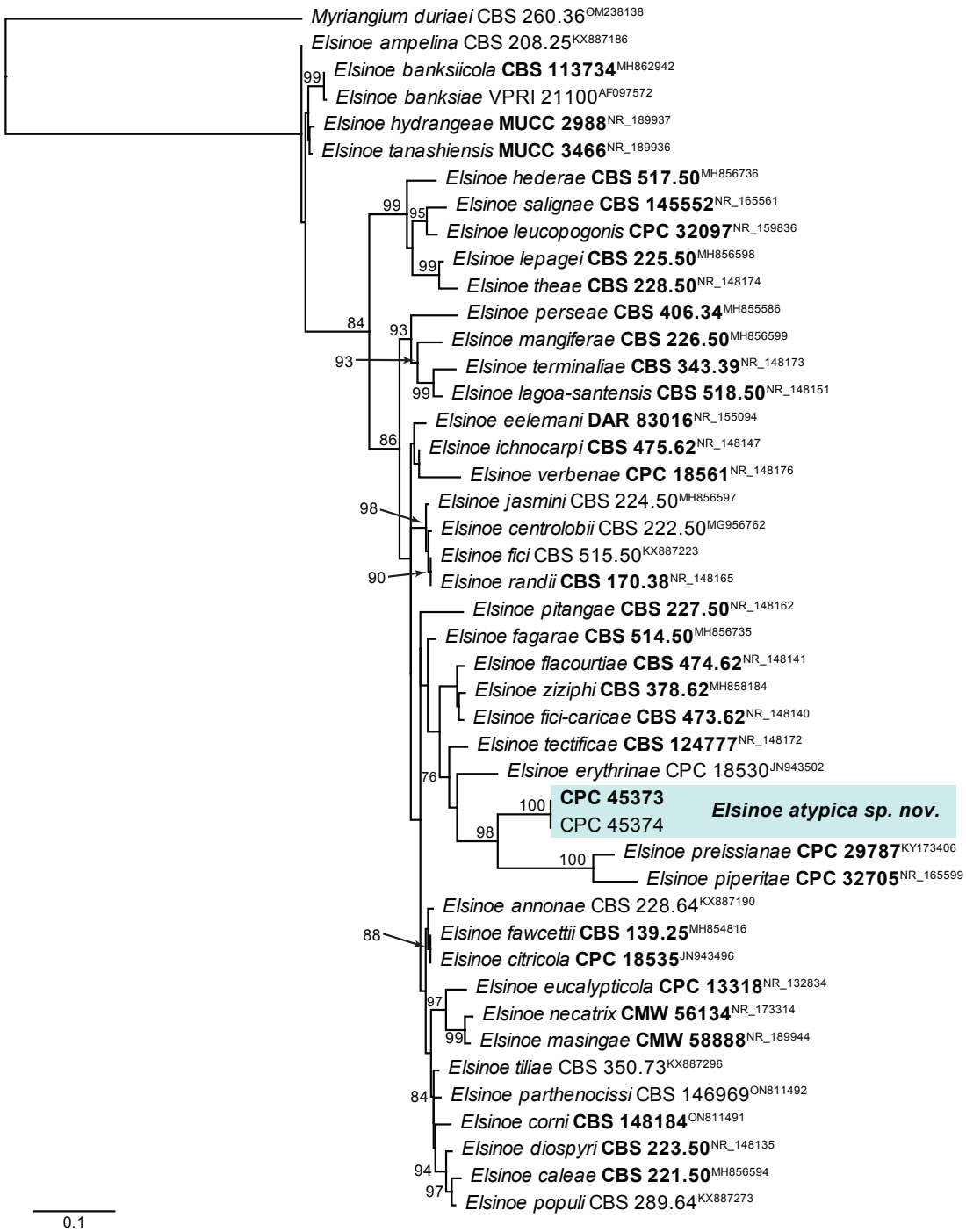
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, 2–3 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse scarlet; on OA surface scarlet with diffuse scarlet pigment.

Typus: **Indonesia**, Kalimantan, Balikpapan, on leaf of *Eucalyptus pellita* (*Myrtaceae*), 1 Nov. 2010, *M.J. Wingfield*, HPC 4071 (**holotype** CBS H-25359; culture ex-type CPC 45373 = CBS 150780; ITS, LSU and *rpb2* sequences GenBank PP791410.1, PP791439.1 and PP780608.1); *ibid.*, CPC 45374 = CBS 150781; ITS, LSU and *rpb2* sequences GenBank PP791411.1, PP791440.1 and PP780609.1.

Notes: The Indonesian collection described here resembles *Pachysacca* in symptomatology, but based on DNA sequence data is best accommodated in *Elsinoe*. *Pachysacca* is genus of foliar pathogens occurring on *Eucalyptus* but is presently not known from culture and thus DNA sequence data. It is characterised by amphigenous dark leaf spots, dendritic growth, a subepidermal stroma containing globose locules that give rise to bitunicate asci with septate, hyaline ascospores, and a pycnidial spermatial morph (Swart 1982, Crous *et al.* 2019b). The resemblance to *Pachysacca* lies in its having submerged conidiomata and dendritic growth, but lacked ascomata, and the lesions remained brown, and did not turn black as in *Pachysacca*. Swart (1982) reported spermatia to be 3 ´ 0.5–1 µm, thus smaller than the Indonesian collection. In the original description of *Pachysacca*, Sydow (1930) referred to a conidial morph in the stroma of *Pachysacca eucalypti*, which he described as *Phomachora eucalypti* (conidia 7.5–13 ´ 2.5–3.5 µm, conidiogenous cells 12–23 ´ 2–3 µm), thus larger than the present collection. Although the foliar symptoms of the present collection differ from a scab disease of *Eucalyptus* typical of *Elsinoe* (Fan *et al.* 2017, Pham *et al*. 2021, Roux *et al*. 2023) we have placed it in that genus for the present even though the symptoms and immersed conidiomata are atypical of *Elsinoe*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 45373 had highest similarity to *Elsinoe parthenocissi* [strain CBS 146969, GenBank ON811492.1; Identities = 547/607 (90 %), 28 gaps (4 %)], *Elsinoe ichnocarpi* (strain CBS 475.62, GenBank MH858216.1; Identities = 546/611 (89 %), 28 gaps (4 %)), and *Elsinoe fawcettii* [strain CBS 139.25, GenBank MH854816.1; Identities = 546/611 (89 %), 32 gaps (5 %)]. The ITS sequences of CPC 45373 and CPC 45374 are identical (590/590 nt). Closest hits using the **LSU** sequence of CPC 45373 are *Sphaceloma lagoa-santensis* [strain CBS 518.50, GenBank MH868258.1; Identities = 851/859 (99 %), no gaps], *Elsinoe perseae* [strain CBS 406.34, GenBank NG_063977.1; Identities = 851/859 (99 %), no gaps], and *Sphaceloma asclepiadis* [strain CPC 18544, GenBank JN940383.1; Identities = 850/858 (99 %), no gaps]. The LSU sequences of CPC 45373 and CPC 45374 are identical (850/850 nt). Closest hits using the ***rpb2*** sequence of CPC 45373 had highest similarity to *Elsinoe phaseoli* [strain 165.31, GenBank KT216560.1; Identities = 735/890 (83 %), six gaps (0 %)], *Elsinoe ricini* [strain CBS 403.63, GenBank KX887161.1; Identities = 613/743 (83 %), two gaps (0 %)], and *Elsinoe akebiae* [strain MUCC 2982, GenBank OQ472906.1; Identities = 612/742 (82 %), no gaps]. The *rpb2* sequences of CPC 45373 and CPC 45374 are identical (888/888 nt).

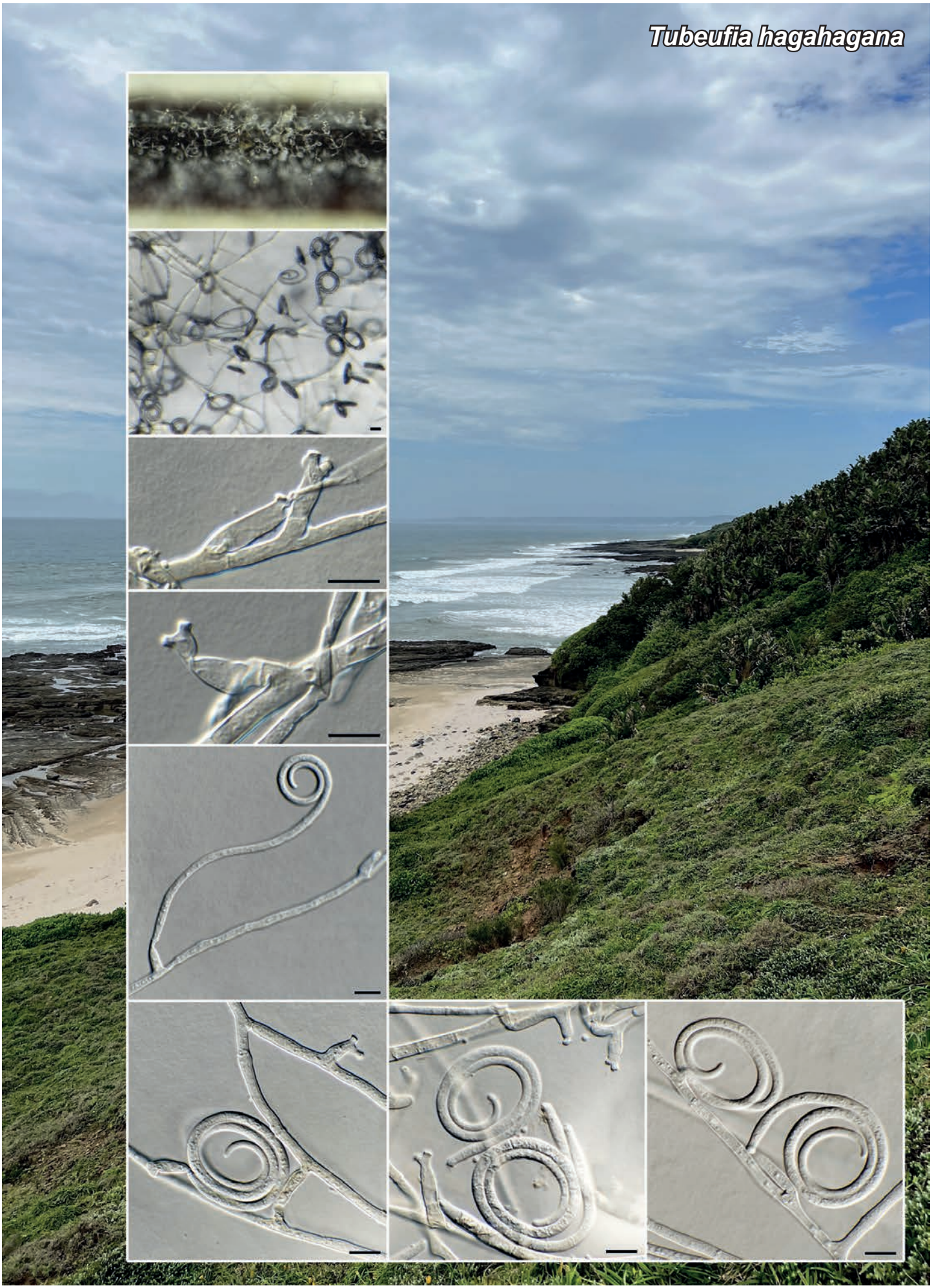
Colour illustrations: Eucalyptus leaf litter, Indonesia. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -3043.328) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Elsinoe* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Myriangium duriaei* (CBS 260.36; GenBank OM238138) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 45 strains including the outgroup; 542 characters including alignment gaps analysed: 193 distinct patterns, 109 parsimony-informative, 59 singleton sites, 374 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

M.J. Wingfield, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: mike.wingfield@fabi.up.ac.za



Fungal Planet 1672

MycoBank MB 853787

Tubeufia hagahagana Crous, *sp. nov.*

Etymology: Name refers Haga Haga, Eastern Cape Province, South Africa where it was collected.

Classification: *Tubeufiaceae*, *Tubeufiales*, *Pleosporomycetidae*, *Dothideomycetes.*

Mycelium consisting of pale brown, hyaline, smooth, septate, branched, 3.5–4 µm diam hyphae. *Conidiophores* pale brown, smooth, unbranched, subcylindrical, 15–30 × 3–5 µm, 0–1-septate. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical, polyblastic, 10–25 × 3–4 µm; loci unthickened, truncate, 2 µm diam. *Conidia* solitary, helicoid, hyaline, smooth, multiseptate, with 2–3 filaments, apex obtuse, base truncate, 3–4 µm diam; conidia (25–)30–40(–45) µm diam.

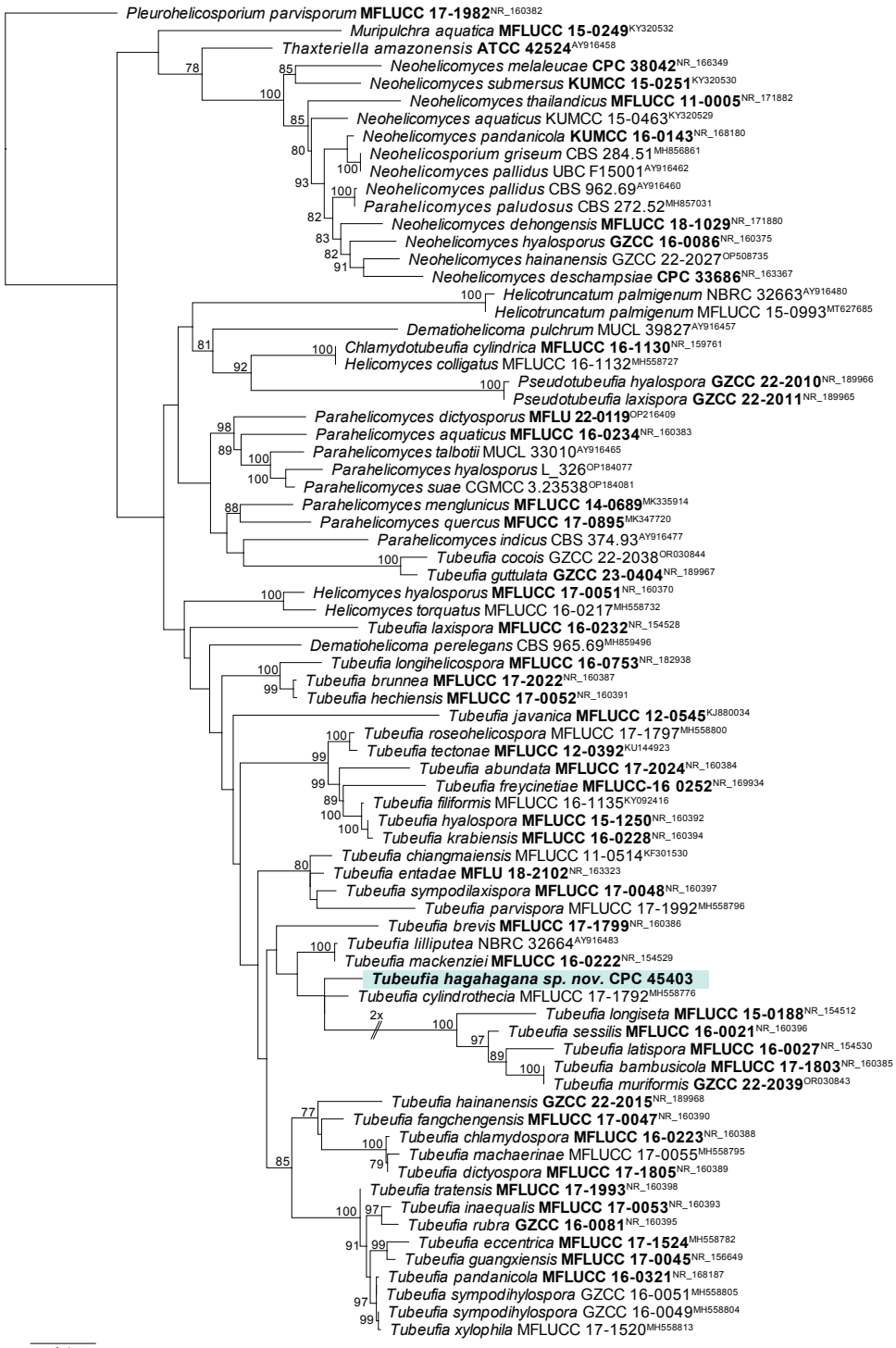
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

Typus: **South Africa**, Eastern Cape Province, Haga Haga, Amathole, on leaves of *Hypoxis angustifolia* (*Hypoxidaceae*), 1 Dec. 2022, *M.J. Wingfield*, HPC 4073 [**holotype** CBS H-25306; culture ex-type CPC 45403 = CBS 150787; ITS, LSU and *tef1* (second part) sequences GenBank PP791412.1, PP791441.1 and PP780622.1].

Notes: Species of *Tubeufia* are common in tropical and temperate regions, often occurring on wood and leaf litter. The genus presently includes 56 accepted species (Ma *et al*. 2023). *Tubeufia hagahagana* is phylogenetically closely related to *T. cylindrothecia* (conidia coiled 1.5–3.5 times, filaments 4.5–5.5 µm diam, conidiophores 50–81 ´ 5–7 µm, based on reference strain MFLUCC 16-1283; Luo *et al*. 2017), but is morphologically distinct, having narrower filaments and shorter conidiophores.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tubeufia cylindrothecia* [strain MFLUCC 11-0076, GenBank MT627709.1; Identities = 545/566 (96 %), eight gaps (1 %)], *Tubeufia longihelicospora* [strain NWBB9, GenBank OM331691.1; Identities = 407/436 (93 %), eight gaps (1 %)], and *Tubeufia sympodilaxispora* [voucher HKAS 97430, GenBank NR_160397.1; Identities = 527/566 (93 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Tubeufia mackenziei* [voucher MFLU 16-2661, GenBank NG_059739.1; Identities = 849/849 (100 %), no gaps], *Tubeufia cylindrothecia* [strain GZCC19-0446, GenBank MW133859.1; Identities = 867/868 (99 %), no gaps], and *Tubeufia fangchengensis* [as *Tubeufia* sp. YZL-2018h; strain MFLUCC 17-0047, GenBank MH558908.1; Identities = 839/845 (99 %), one gap (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Tubeufia cylindrothecia* [strain MFLUCC 17-1792, GenBank MH550968.1; Identities = 415/422 (98 %), no gaps], *Tubeufia hainanensis* [strain GZCC 23-0589, GenBank OR058860.1; Identities = 397/413 (96 %), no gaps], and *Tubeufia mackenziei* [strain MFLUCC 16-0222, GenBank KY117031.1; Identities = 405/422 (96 %), no gaps].

Colour illustrations: Haga Haga, Eastern Cape Province, South Africa. Conidiophores on pine needle agar; conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



Most likely phylogram (score -8608.910) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Tubeufia* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Pleurohelicosporium parvisporum* (MFLUCC 17-1982; GenBank NR_160382) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 76 strains including the outgroup; 690 characters including alignment gaps analysed: 410 distinct patterns, 255 parsimony-informative, 70 singleton sites, 365 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TVM+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

M.J. Wingfield, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: mike.wingfield@fabi.up.ac.za

Fungal Planet 1673 MycoBank MB 853788

Hyaloscypha caricicola Crous & Osieck, *sp. nov.*

Etymology: Name refers to the host genus from which it was isolated, *Carex*.

Classification: *Hyaloscyphaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* penicillate, erect, subcylindrical, unbranched, dark brown, smooth, thick-walled, 4–8-septate, 60–150 × 4–5 µm; base swollen, lacking rhizoids, covered in mucoid layer. *Conidiogenous apparatus* penicillate, consisting of primary branches that give rise to 1–4 phialides, 8–10 × 2–2.5 µm, dark brown, smooth, subcylindrical. *Conidiogenous cells* phialidic, medium brown, smooth, 10–18 × 2–2.5 µm; terminal collarette prominently flared, apex 2.5–3 µm diam. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical, (3–)4–5(–6) × 1.5(–2) µm, with obtuse ends.

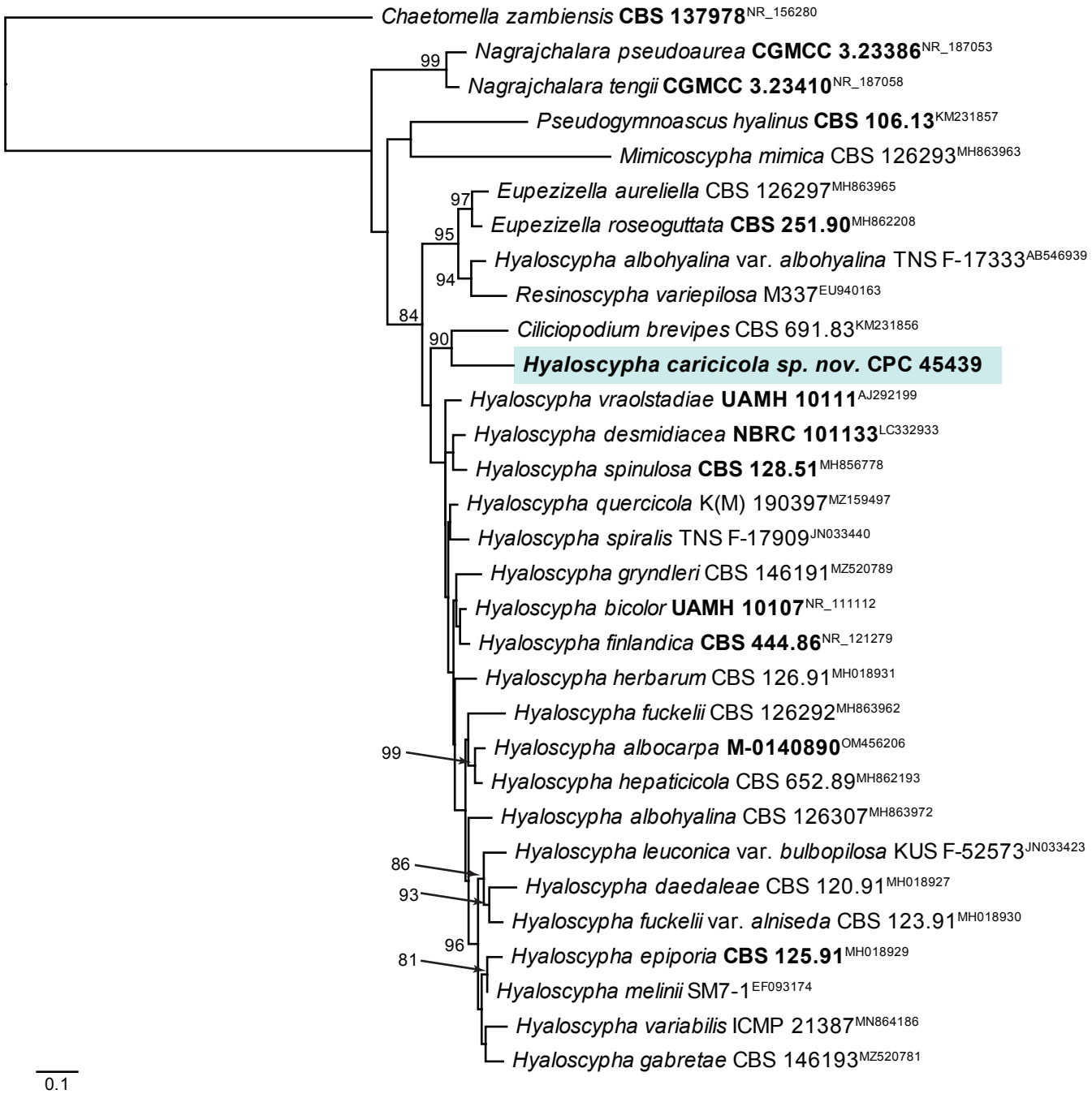
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale olivaceous grey to olivaceous grey, reverse olivaceous grey.

Typus: **Netherlands**, Groningen Province, Vlagtwedde, Liefsthingsbroek, N53°00'13'' E07°07'04'', on leaves of *Carex* sp. (*Cyperaceae*), *E.R. Osieck*, 13 Nov. 2022, HPC 4069 = WI-67, coll. 4579A (**holotype** CBS H-25308; culture ex-type CPC 45439 = CBS 150791; ITS, LSU, *cmdA*, *rpb1* and *rpb2* sequences GenBank PP791413.1, PP791442.1, PP780601.1, PP780605.1 and PP780610.1).

Notes: *Hyaloscypha* includes several widely distributed, asexual species that grow endophytically and form mycorrhizal relationships with plant roots (Vohník *et al.* 2022). The sexual morph concerns mostly lignicolous, small discomycetes, like *H. albohyalina, H. fuckelii, H. quercicola* (Huhtinen 1989). *Hyaloscypha caricicola* was isolated from leaves of *Carex* sp. incubated in moist chambers, and its ecology remains unknown. Phylogenetically it represents a distinct lineage, being most similar to *H. finlandica* [conidiogenous cells (15–)18–20(–29) × (2–)2.5–3 µm, conidia 4.5–6 × 1.5–3 µm; Wang & Wilcox 1985, Fehrer *et al*. 2019].

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hyaloscypha finlandica* [strain NoF 3138, GenBank MT276005.1; Identities = 412/442 (93 %), six gaps (1 %)], *Ciliciopodium brevipes* [strain CBS 691.83, GenBank KM231856.1; Identities = 406/438 (93 %), three gaps (0 %)], and *Hyaloscypha bicolor* [strain 293, GenBank MT908291.1; Identities = 406/438 (93 %), seven gaps (1 %)]. Closest hits using the **LSU** sequence are *Ciliciopodium brevipes* [strain CBS 691.83, GenBank KM231736.1; Identities = 829/845 (98 %), one gap (0 %)], *Hyaloscypha gryndleri* [strain CBS 145337, GenBank NG_081312.1; Identities = 828/847 (98 %), no gaps], and *Hyaloscypha spinulosa* [strain CBS 479.67, GenBank MH870748.1; Identities = 860/880 (98 %), no gaps]. Closest hits using the ***cmdA*** sequence had highest similarity to *Ciliciopodium brevipes* [strain CBS 691.83, GenBank KM231451.1; Identities = 535/686 (78 %), 35 gaps (5 %)], *Sclerotinia sclerotiorum* [GenBank CP017814.1; Identities = 319/403 (79 %), 22 gaps (5 %)], and *Botrytis cinerea* [strain Sl3, GenBank CP080985.1; Identities = 312/399 (78 %), 16 gaps (4 %)]. Closest hits using the ***rpb1*** sequence had highest similarity to *Hyaloscypha aureliella* [strain M234, GenBank JN985241.1; Identities = 636/751 (85 %), six gaps (0 %)], *Hyaloscypha hepaticola* [strain M339, GenBank JN985233.1; Identities = 631/750 (84 %), four gaps (0 %)], and *Hyaloscypha intacta* [voucher TK7111, GenBank MT216624.1; Identities = 625/750 (83 %), four gaps (0 %)]. A blast2 comparison between the *rpb1* sequence of CPC 45439 and *Ciliciopodium brevipes* (strain CBS 691.83, GenBank KM232291.1) revealed a similarity of 79 % (582/741 nt, including 27 gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Mimicoscypha lacrimiformis* [voucher KH.17.02, GenBank MT228687.1; Identities = 778/902 (86 %), no gaps], *Hyaloscypha vitreola* [voucher SH14/10, GenBank MT228681.1; Identities = 766/893 (86 %), no gaps], and *Olla transiens* [voucher TK7125, GenBank MT228689.1; Identities = 769/899 (86 %), no gaps]. A blast2 comparison between the *rpb2* sequence of CPC 45439 and *Ciliciopodium brevipes* (strain CBS 691.83, GenBank KM232432.1) revealed a similarity of 83 % (736/883 nt, including 29 gaps).

Colour illustrations: Carex undergrowth, Liefsthingsbroek, Vlagtwedde, the Netherlands. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -4713.565) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Hyaloscypha* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Chaetomella zambiensis* (CBS 137978; GenBank NR_156280) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 31 strains including the outgroup; 702 characters including alignment gaps analysed: 334 distinct patterns, 182 parsimony-informative, 113 singleton sites, 407 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
E.R. Osieck, Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, Netherlands; e-mail: panurus@ziggo.nl

Fungal Planet 1674 MycoBank MB 853789

Dematipyriforma americana Crous & Jurjević, *sp. nov.*

Etymology: Name refers to the United States of America, the country where it was collected.

Classification: *Pleurotheciaceae*, *Pleurotheciales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of pale brown, verruculose, branched, septate, 2–3 µm diam hyphae. *Microsclerotia* immersed in agar, subglobose, subhyaline, smooth, muriformly septate, 20–30 µm diam. *Conidiophores* dimorphic. *Conidiogenous loci* integrated on hyphae, giving rise to erect *primary conidia*, clavate, brown, smooth, muriformly septate, 20–40 × 10–20 µm. *Secondary conidiophores* dactylaria-like, erect, solitary, hyaline, smooth, subcylindrical, 0–2-septate, 5–25 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, 3–7 × 2.5–3 µm, with several cylindrical denticles, 1–2 × 1 µm. *Secondary conidia* hyaline, smooth, 0–1-septate, guttulate, fusoid-ellipsoid, slightly curved, ends subobtuse, (6–)8–9(–10) × 2.5–3 µm.

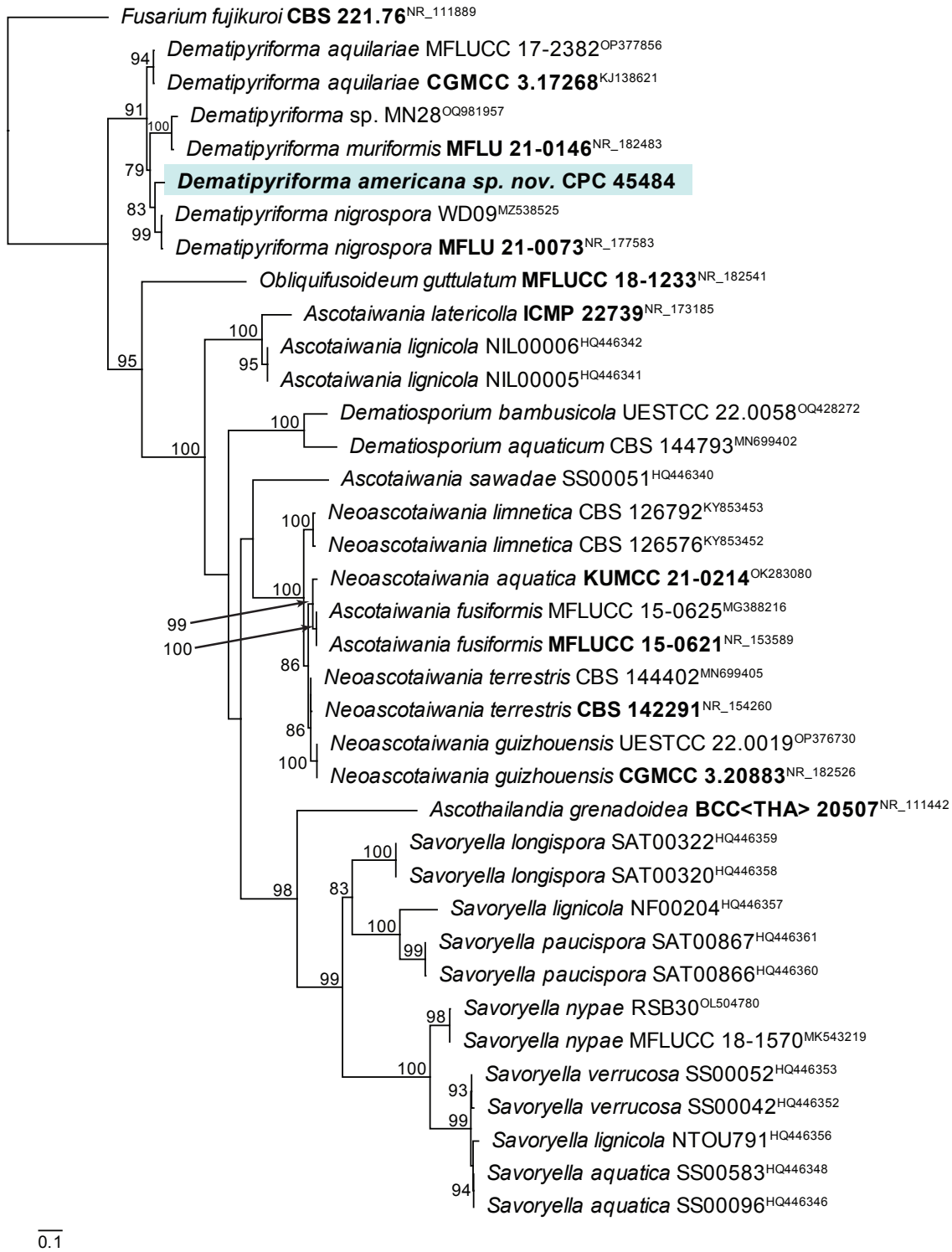
Culture characteristics: Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA, MEA and OA surface and reverse olivaceous grey.

Typus: **USA**, Ohio, Fermont, swab from basement wall, Oct. 2022, *Z. Jurjević*, 5760 [**holotype** CBS H-25310; culture ex-type CPC 45484 = CBS 150793; ITS, LSU and *tef1* (second part) sequences GenBank PP791414.1, PP791443.1 and PP780623.1].

Notes: *Dematipyriforma* (based on *D. aquilariae***)** was established for a genus of dematiaceous hyphomycetes with monoblastic conidiogenous cells and solitary dictyoconidia (Sun *et al.* 2017), and presently includes six species. ***Dematipyriforma americana*** is related to *D. nigrospora*, which has smaller conidia, 15–31 × 16–33 µm (Bonmee *et al*. 2021).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dematipyriforma nigrospora* [voucher MFLU 21-0073, GenBank NR_177583.1; Identities = 568/595 (95 %), six gaps (1 %)], *Dematipyriforma aquilariae* [strain RAY-11, GenBank OP377856.1; Identities = 534/574 (93 %), seven gaps (1 %)], and *Dematipyriforma muriformis* [voucher MFLU 21-0146, GenBank NR_182483.1; Identities = 523/576 (91 %), 14 gaps (2 %)]. Closest hits using the **LSU** sequence are *Dematipyriforma* sp. JY-2023b [clone N25_9, GenBank OR129690.1; Identities = 819/819 (100 %), no gaps], *Dematipyriforma aquatica* [as *Dematipyriforma* sp. MAW-2020a; voucher SUMCC H-12001, GenBank MT522155.1; Identities = 826/827 (99 %, no gaps], and *Dematipyriforma nigrospora* [voucher MFLU 21-0073, GenBank NG_088275.1; Identities = 781/791 (99 %), no gaps]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Dematipyriforma aquilariae* [strain MFLUCC 17-2382, GenBank OP473035.1; Identities = 731/756 (97 %), two gaps (0 %)], *Dematipyriforma nigrospora* [voucher LSP03, GenBank MZ567100.1; Identities = 706/731 (97 %), no gaps], and *Dematipyriforma muriformis* [voucher MFLU 21-0146, GenBank OM672032.1; Identities = 716/756 (95 %), two gaps (0 %)].

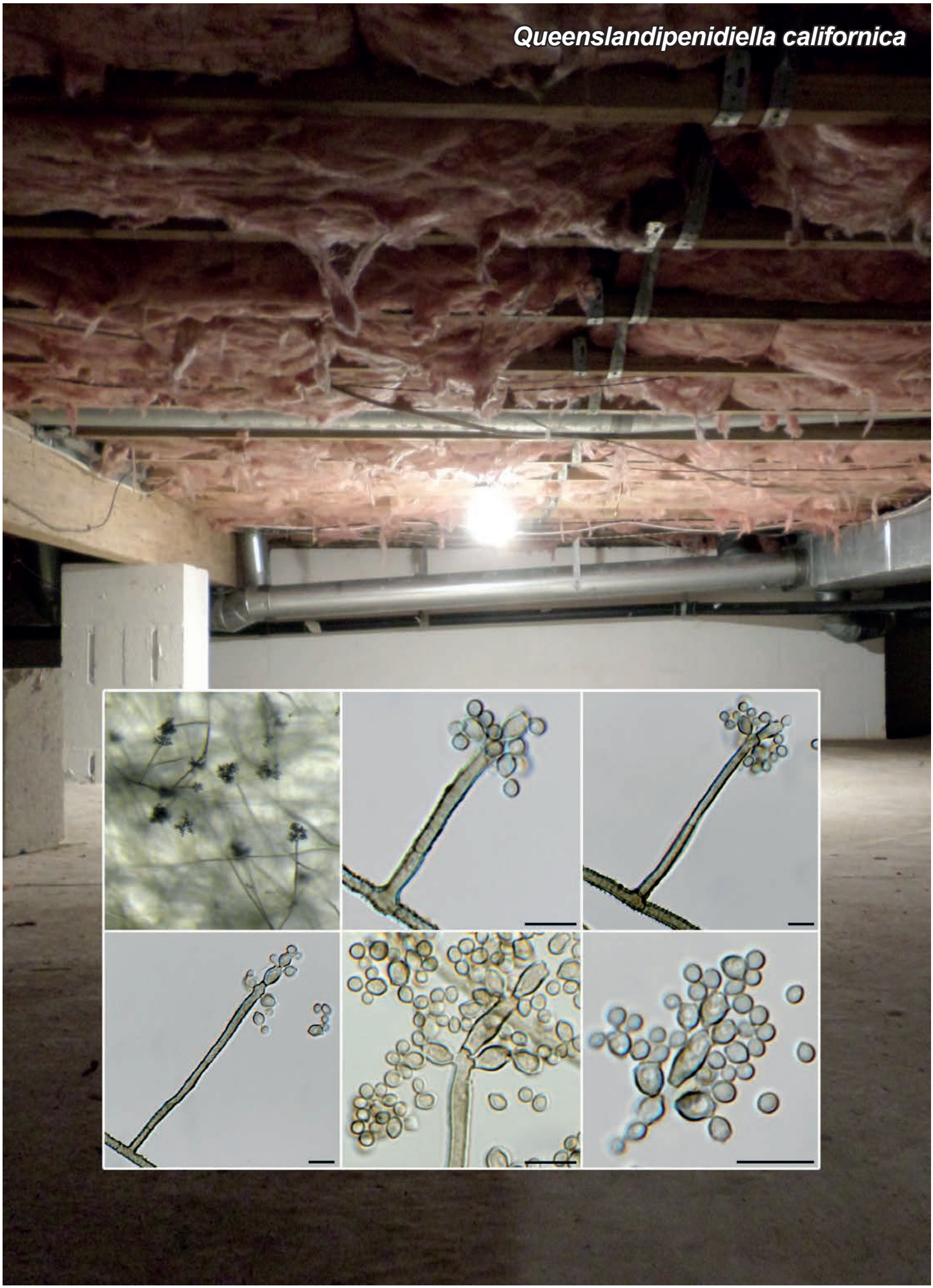
Colour illustrations: basement inside building, Fermont, Ohio, USA. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to muriformly septate conidia, and 0–1-septate conidia. Scale bars = 10 µm.



Most likely phylogram (score -7397.399) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Dematipyriforma* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Fusarium fujikuroi* (CBS 221.76; GenBank NR_111889) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 37 strains including the outgroup; 751 characters including alignment gaps analysed: 509 distinct patterns, 403 parsimony-informative, 76 singleton sites, 272 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Ž. Jurjević & A. Pinto, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & AmPinto@emsl.com



Fungal Planet 1675 MycoBank MB 853790

Queenslandipenidiella californica Crous & Jurjević, *sp. nov.*

Etymology: Name refers to the state of California, USA, where it was collected.

Classification: *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

Mycelium consisting of medium brown, warty, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical with apical conidiogenous apparatus, medium brown, verruculous, 2–6-septate. Apical conidiophore cell giving rise to 1–3 ellipsoid to subovoid, brown, smooth to roughened, thick-walled, lateral primary branches, 5–8 × 3–4 µm; central branch subcylindrical, 8–12 × 3–4 µm, giving rise to apical cluster of 1–3 ellipsoid to subovoid lateral branches or conidiogenous cells. *Conidiogenous cells* brown, smooth, subovoid to ellipsoid, 1–3 per lateral branch, 4–6 × 2.5–3 µm; loci polyblastic, flat, unthickened, 0.5–1 µm diam. *Conidia* in short chains of 1–3, thick-walled, ellipsoid to subovoid, brown, smooth to finely roughened, 3–5 × 2.5–3 µm; hila not thickened nor darkened, 0.5 µm diam.

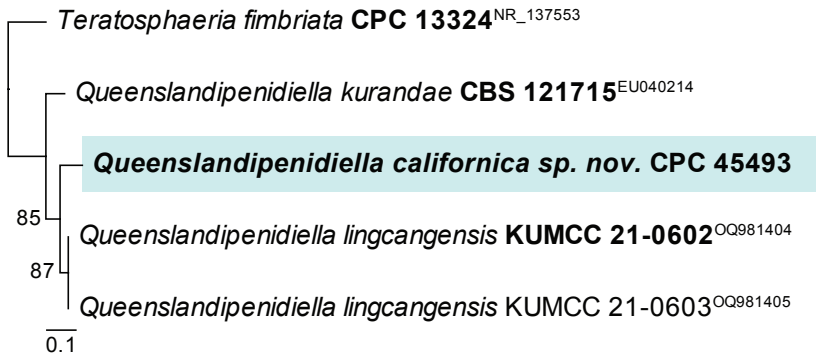
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron grey.

Typus: **USA**, California, Valley Centre, on wood in crawlspace, Dec. 2022, *Z. Jurjević*, 5782 (**holotype** CBS H-25313; culture ex-type CPC 45493 = CBS 150796; ITS, LSU, *actA* and *cmdA* sequences GenBank PP791415.1, PP791444.1, PP780597.1 and PP780602.1).

Notes: *Queenslandipenidiella* is a penidiella-like genus based on *Q. kurandae*, isolated from the exudate of bleeding stem cankers of trees in Queensland, Australia (Quaedvlieg *et al.* 2014). Phylogenetically, *Q. californica* is most similar to *Q. lingcangensis* (conidiogenous cells 5.8–10 ´ 3.9–4.5 µm, conidia 2.8–3.6 ´ 2.1–2.8 µm; Ren *et al.* 2024), but distinct in that it has smaller conidiogenous cells and larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Queenslandipenidiella lingcangensis* (as *Queenslandipenidiella* sp. YE-2023a; strain KUMCC 21-0603, GenBank OQ981405.1; Identities = 474/511 (93 %), 14 gaps (2 %)), *Queenslandipenidiella kurandae* (as *Penidiella kurandae*; strain CPC 13333, GenBank EU040214.2; Identities = 457/519 (88 %), 20 gaps (3 %)), and *Penidiella columbiana* (strain CBS 486.80, GenBank MH861288.1; Identities = 452/525 (86 %), 33 gaps (6 %)). Closest hits using the **LSU** sequence are *Queenslandipenidiella lingcangensis* (as *Queenslandipenidiella* sp. YE-2023a; strain KUMCC 21-0603, GenBank OQ981400.1; Identities = 793/805 (99 %), no gaps), *Queenslandipenidiella kurandae* (strain CBS 121715, GenBank KF901860.1; Identities = 701/731 (96 %), eight gaps (1 %)), and *Racoleus japonicus* (strain TNS L-132529, GenBank LC779822.1; Identities = 760/809 (94 %), four gaps (0 %)). The ***actA*** sequence was 90 % similar to *Queenslandipenidiella kurandae* (strain CBS 121715, GenBank KF903538.1; Identities = 338/374 (90 %), no gaps). The ***cmdA*** sequence was 90 % similar to *Queenslandipenidiella kurandae* (strain CBS 121715, GenBank KF902663.1; Identities = 360/401 (90 %), 11 gaps (2 %)).

Colour illustrations: Crawlspace at Valley Centre, California, USA. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -1335.986) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Queenslandipenidiella* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Teratosphaeria fimbriata* (CPC 13324; GenBank NR_137553) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: five strains including the outgroup; 519 characters including alignment gaps analysed: 76 distinct patterns, 30 parsimony-informative, 87 singleton sites, 402 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Ž. Jurjević & S. Balashov, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & sbalashov@emsl.com

Fungal Planet 1676

MycoBank MB 853791

Beaucarneamyces Crous, ***gen. nov.***

Etymology: Name refers to *Beaucarnea*, the host genus from which it was isolated.

Classification: *Neodactylariaceae*, *Neodactylariales*, *Pleosporomycetidae*, *Dothideomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, hyaline, rarely 1-septate, 4–25 × 2–3 µm, polyblastic with several aggregated truncate apical denticles, 1.5–2 µm diam. *Conidia* solitary, fusoid-ellipsoid, widest in middle, hooked, apex subobtuse, base truncate, 1.5–2 µm, 3-septate, hyaline with central two cells pale brown, smooth, (15–)20–25(–30) × (4–)5(–6) µm.

Type species: *Beaucarneamyces stellenboschensis* Crous

MycoBank MB 853792

Beaucarneamyces stellenboschensis Crous, ***sp. nov.***

Etymology: Name refers to Stellenbosch, South Africa, where it was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, hyaline, rarely 1-septate, 4–25 × 2–3 µm, polyblastic with several aggregated truncate apical denticles, 1.5–2 µm diam. *Conidia* solitary, fusoid-ellipsoid, widest in middle, hooked, apex subobtuse, base truncate, 1.5–2 µm, 3-septate, hyaline with central two cells pale brown, smooth, (15–)20–25(–30) × (4–)5(–6) µm.

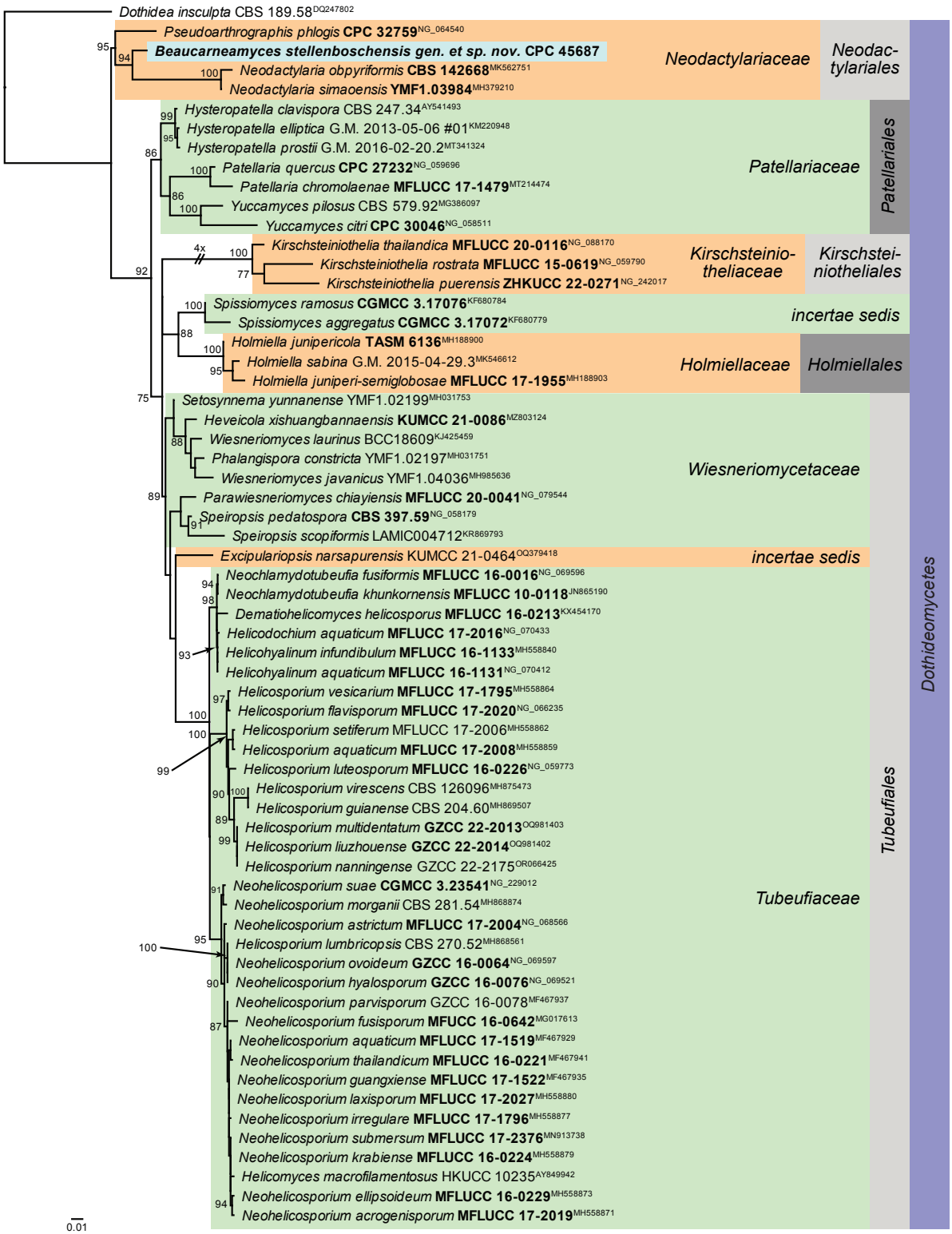
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface pale grey olivaceous and reverse olivaceous grey; on PDA surface and reverse olivaceous grey; on OA surface umber.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Beaucarnea stricta* (*Asparagaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4112 (**holotype** CBS H-25324; culture ex-type CPC 45687 = CBS 150808; ITS and LSU sequences GenBank PP791416.1 and PP791445.1).

Notes: *Beaucarneamyces* is related to *Pseudoarthrographis*, but is distinct from that genus in that it lacks chains of olivaceous arthroconidia (Crous *et al.* 2018). It also resembles *Neodactylaria* (Qiao *et al.* 2020), although the latter has flexuous, septate, pigmented conidiophores with a rachis of polyblastic conidiogenous loci, and obpyriform conidia. Several genera listed in Seifert *et al*. (2011) need to be considered, *i.e*. *Aquaphila* (distinct, having pigmented hyphae with chlamydospores) and *Parvosympodium* (*nom. inval*., linked to *Stomiopeltopsis*; Ramaley 2002). *Beaucarneamyces* is thus introduced as new genus to accommodate the present collection from leaves of *Beaucarnea stricta.*

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NR_160349.1; Identities = 480/569 (84 %), 28 gaps (4 %)], *Neodactylaria simaoensis* [strain YMF1.03984, GenBank MH379209.1; Identities = 476/577 (82 %), 37 gaps (6 %)], and *Neodactylaria obpyriformis* [strain FMR 14604, GenBank NR_154267.1; Identities = 475/576 (82 %), 39 gaps (6 %)]. Closest hits using the **LSU** sequence are *Pseudoarthrographis phlogis* [strain CPC 32759, GenBank NG_064540.1; Identities = 834/871 (96 %), no gaps], *Wiesneriomyces laurinus* [strain LAMIC036112, GenBank KR869804.1; Identities = 792/837 (95 %), six gaps (0 %)], and *Setosynnema yunnanense* [strain YMF1.02680, GenBank MH985635.1; Identities = 799/846 (94 %), six gaps (0 %)].

Colour illustrations: Leaves of *Beaucarnea stricta*, South Africa. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



Most likely phylogram (-score -4791.440) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Beaucarneamyces* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Dothidea insculpta* (CBS 189.58; GenBank DQ247802) and the novelty described here is highlighted with a coloured block and **bold** font. The branch of the *Kirschsteiniotheliales* clade was shortened to facilitate layout. Families, orders and the class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 63 strains including the outgroup; 849 characters including alignment gaps analysed: 267 distinct patterns, 203 parsimony-informative, 58 singleton sites, 588 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;

Fungal Planet 1677

MycoBank MB 853793

Knufia dianellae Crous, *sp. nov.*

Etymology: Name refers to *Dianella,* the host genus from which it was isolated.

Classification: *Trichomeriaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of smooth, pale brown, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, arising from superficial mycelium, subcylindrical, pale brown, smooth, up to 100 µm tall, 3–4 µm diam, multiseptate, giving rise to a complex network of branched ramoconidia and chains of conidia that again can branch to form new conidial chains. *Ramoconidia* subcylindrical, smooth, guttulate, 0–1-septate, 10–25 × 3–4 µm, polyblastic, giving rise to additional ramoconidia or chains of terminal conidia. *Conidial chains* branched or unbranched, pale brown, smooth, guttulate, subcylindrical, 1–20-septate, disarticulating into smaller conidial fragments, 12–13 × 2–3 µm; hila not thickened nor darkened, 1.5–2 µm diam.

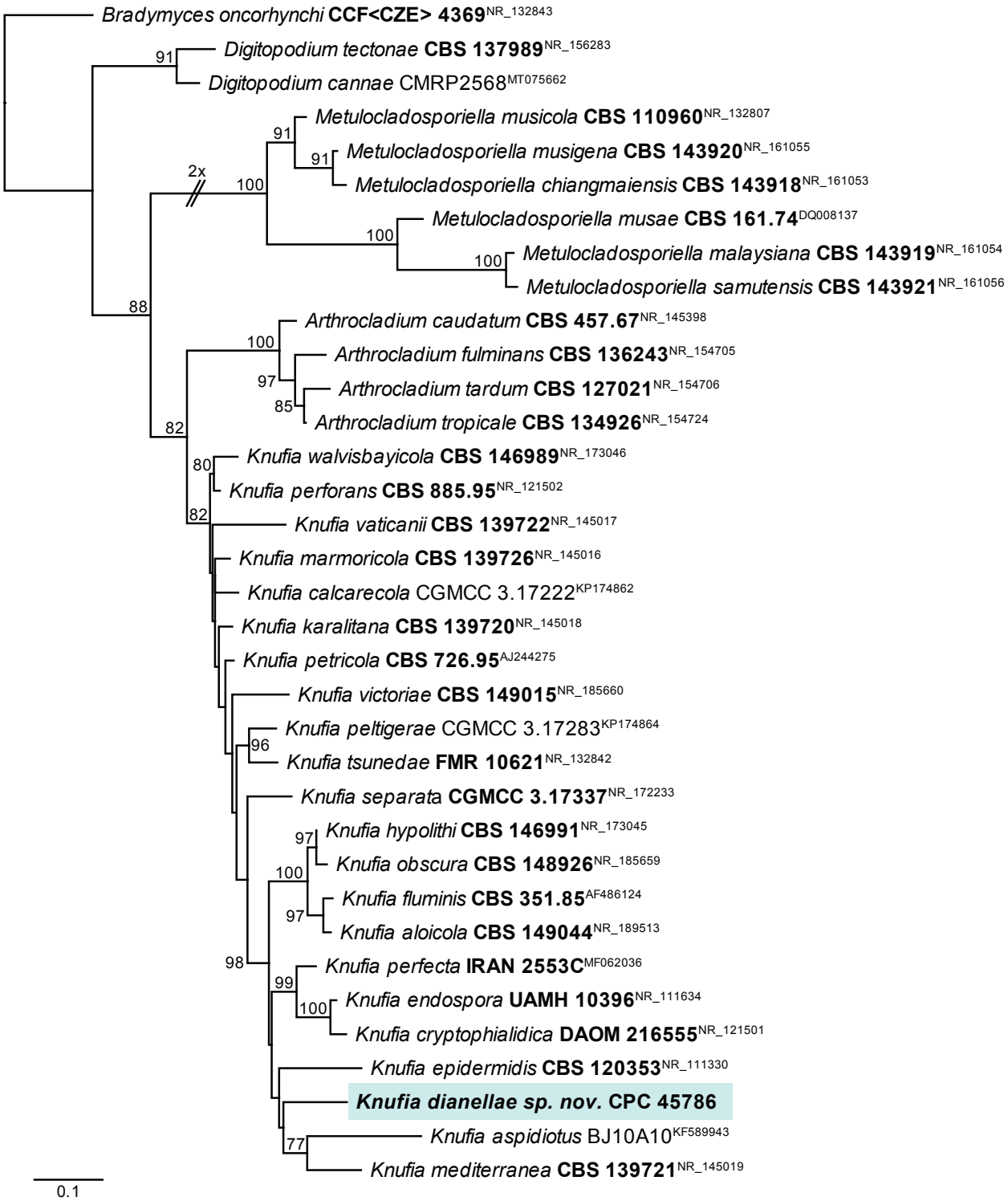
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Dianella caerulea* (*Asphodelaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4121 [**holotype** CBS H-25361; culture ex-type CPC 45786 = CBS 150810; ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank PP791417.1, PP791446.1, PP780606.1, PP780624.1 and PP780628.1].

Notes: *Knufia* is a genus of melanised ascomycetes that is commonly found in extreme environments (rock and soil inhabiting, lichenicolous, opportunistic human pathogens, insect associates and plant pathogens (Isola *et al.* 2022). *Knufia dianellae* represents a filamentous, more penidiella-like morph, which was not isolated from an extreme environment, but rather from dead leaves of *Dianella caerulea,* suggesting that placing this fungus in *Knufia* may well render it paraphyletic. For now, we choose to not introduce a new genus, pending further revision of this complex.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Digitopodium cannae* [strain CMRP2568, GenBank MT075662.1; Identities = 669/754 (89 %), 44 gaps (5 %)], *Bradymyces graniticola* [strain CCF 5193, GenBank LT558704.1; Identities = 657/744 (88 %), 36 gaps (4 %)], and *Knufia cryptophialidica* [strain DAOM 216555, GenBank JN040501.1; Identities = 668/735 (91 %), 31 gaps (4 %)]. Closest hits using the **LSU** sequence are *Knufia mediterranea* [strain CCFEE 6211, GenBank KR781080.1; Identities = 822/833 (99 %), one gap (0 %)], *Knufia perforans* [strain CBS 885.95, GenBank FJ358237.1; Identities = 855/877 (97 %), two gaps (0 %)], and *Knufia marmoricola* [strain CCFEE 5716, GenBank KR781074.1; Identities = 828/851 (97 %), two gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Knufia petricola* [strain A95, GenBank MT859426.1; Identities = 784/858 (91 %), four gaps (0 %)], *Knufia calcarecola* [as *Knufia* sp. LS-2015a; strain CGMCC 3.17225, GenBank KP175007.1; Identities = 779/856 (91 %), no gaps], and *Lithohypha guttulata* [strain FMR 20100, GenBank OX346319.1; Identities = 776/856 (91 %), no gaps]. No significant hits were obtained when the ***rpb1*** and ***tub2*** sequences were used in blastn and megablast searches. When the ***rpb1*** sequence is used in a blast2 search against *Knufia rpb1* sequences, then the closest hits had highest similarity to *Knufia* sp. LS-2015d [strain CGMCC 3.17298, GenBank KP226522.1; Identities = 458/599 (76 %), no gaps], *Knufia epidermidis* [strain CGMCC 3.17228, GenBank KP226510.1; Identities = 326/441 (74 %), 13 gaps (2 %)], and *Knufia petricola* [strain CBS 600.93, GenBank KC978742.1; Identities = 347/485 (72 %), 12 gaps (2 %)].

Colour illustrations: Flowers of *Dianella caerulea* in South Africa. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -5105.859) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Knufia* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Bradymyces oncorhynchi* (CCF<CZE> 4369; GenBank NR_132843) and the novelty described here is highlighted with a coloured block and **bold** font. The branch of the *Metulocladosporiella* clade was shortened to facilitate layout. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 35 strains including the outgroup; 729 characters including alignment gaps analysed: 366 distinct patterns, 229 parsimony-informative, 74 singleton sites, 426 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1678

MycoBank MB 853795

Melanina restionis Crous, *sp. nov.*

Etymology: Name refers to the host genus *Restio*, from which it was isolated.

Classification: *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium smooth, hyaline, becoming pale brown, branched, constricted at septa, with 2–3 µm diam hyphae, swelling in older hyphae, forming chlamydospores-like cells, 3–4 µm diam. *Conidiophores* reduced to conidiogenous cells, intercalary and terminal on hyphae (toruloid hyphae), doliiform, pale brown, mono- to polyphialidic, 4–7 × 3–4 µm; loci 1–1.5 µm diam. *Conidia* solitary, aseptate, smooth, hyaline, becoming pale brown, guttulate, ellipsoid, 4–5 × 2–3 µm; undergoing microcyclic conidiation when mature, becoming up to 7 µm long, 4 µm wide.

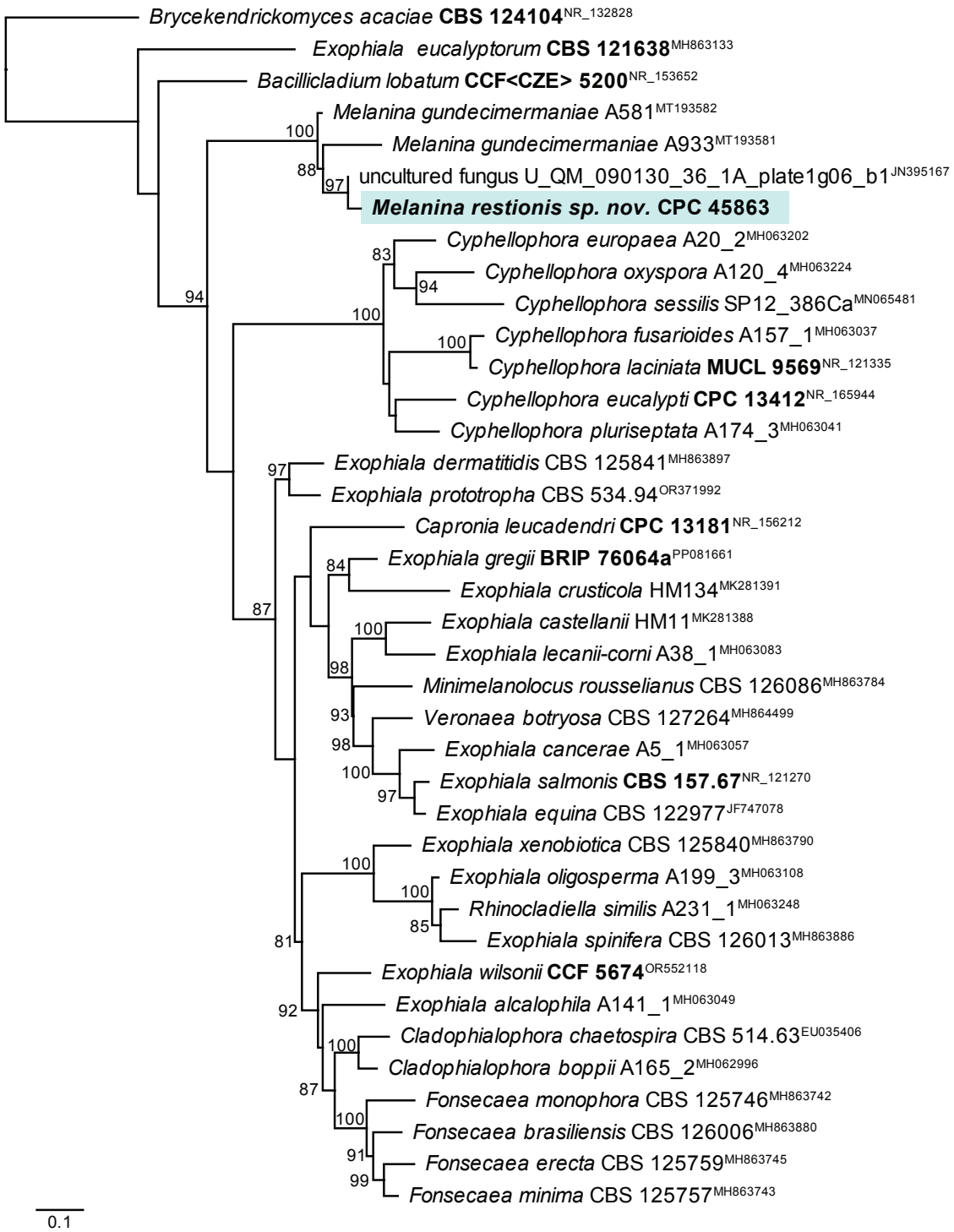
Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, even margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse fuscous black; on OA surface fuscous black.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Restio duthieae* (*Restionaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4111 (**holotype** CBS H-25327; culture ex-type CPC 45863; ITS sequence GenBank PP791418.1).

Notes: *Melanina* was introduced for a hyphomycetous genus isolated from epilithic, crust-forming lichens occurring in subalpine habitats. It is characterised by toruloid hyphae, and an exophiala-like morph (Muggia *et al*. 2021). *Melanina restionis* forms a distinct lineage isolated from dead leaves and shoots of *Restio duthieae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Melanina gundecimermaniae* [strain L2628, GenBank OQ921006.1; Identities = 555/571 (97 %), four gaps (0 %)], *Exophiala equina* [strain A183_1, GenBank MH063076.1; Identities = 548/632 (87 %), 33 gaps (5 %)], *Exophiala dermatitidis* [strain CBS 125841, GenBank MH863897.1; Identities = 559/653 (86 %), 34 gaps (5 %)], *Bacillicladium lobatum* [strain CCF 5200, GenBank NR_153652.1; Identities = 565/665 (85 %), 46 gaps (6 %)], and *Exophiala eucalyptorum* [strain CBS 121638, GenBank MH863133.1; Identities = 601/721 (83 %), 36 gaps (4 %)].

Colour illustrations: Restio duthieae in South Africa. Mycelium on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -8050.284) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Melanina* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Brycekendrickomyces acaciae* (CBS 124104; GenBank NR_132828) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 38 strains including the outgroup; 683 characters including alignment gaps analysed: 416 distinct patterns, 277 parsimony-informative, 89 singleton sites, 317 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1679 MycoBank MB 853796

Lomaantha quercina Crous, *sp. nov.*

Etymology: Name refers to the host genus *Quercus*, from which it was isolated.

Classification: *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetidae, Sordariomycetes*.

Mycelium consisting of brown, septate, branched, 3–4 µm diam hyphae. *Conidiophores* subcylindrical, brown, smooth, 1–5-septate, 20–50 × 4–6 µm. *Conidiogenous cells* terminal and intercalary, pyriform to ovoid, brown, smooth-walled, with terminal pore, 10–25 × 6–8 µm. *Conidia* solitary, long ellipsoid, distoseptate, red-brown, eguttulate, granular; hilum inconspicuous, internal, 3–7-septate, (27–)30–40(–46) × (9–)10(–11) µm.

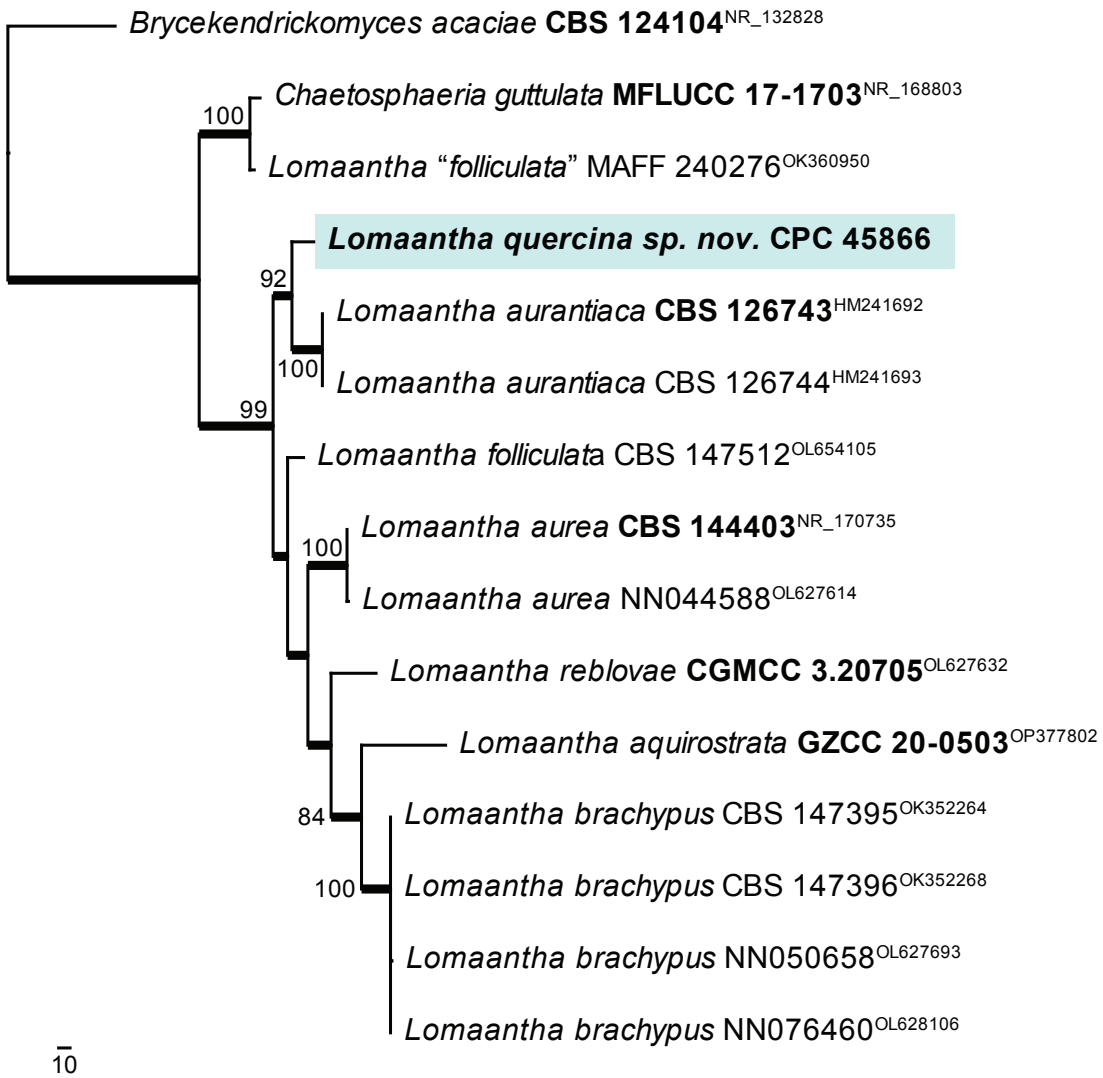
Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and feathery margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA surface and reverse fuscous black; on PDA surface and reverse umber; on OA surface umber, with diffuse umber pigment.

Typus: **South Africa**, Western Cape Province, J.S. Marais Garden, on twigs of *Quercus suber* (*Fagaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4122 (**holotype** CBS H-25328; culture ex-type CPC 45866 = CBS 150811; ITS and LSU sequences GenBank PP791419.1 and PP791447.1).

Notes: Delgado *et al.* (2024) recollected *Ellisembia coronata*, the type species of the polyphyletic *Ellisembia,* and distinguished it from *Lomaantha*, which includes *Pyrigemmula aurantiaca*, the type species of *Pyrigemmula* (Magyar *et al*. 2011, Wu & Diao 2022). *Lomaantha quercina* is morphologically very similar to the type species of *Pyrigemmula*, *P. aurantiaca* [conidia 0–5(–7)-septate, (17.6–)22.4–24.0(–27.2) × 6.5–8.0 µm], having short conidiophores, and a thick-layer of tightly aggregated conidia, pointing upwards in clusters.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lomaantha aurantiaca* [as *Pyrigemmula aurantiaca*; strain CPC 18063, GenBank HM241692.1; Identities = 555/584 (95 %), seven gaps (1 %)], *Lomaantha brachypus* [strain NN076460, GenBank OL628106.1; Identities = 392/430 (91 %), 13 gaps (3 %)], and *Lomaantha aurea* [strain CBS 144403, GenBank NR_170735.1; Identities = 372/414 (90 %), six gaps (1 %)]. Closest hits using the **LSU** sequence are *Lomaantha aurantiaca* [as *Pyrigemmula aurantiaca*; strain CPC 18063, GenBank HM241692.1; Identities = 832/844 (99 %), one gap (0 %)], *Lomaantha folliculata* [strain CBS 147152, GenBank OL654162.1; Identities = 831/843 (99 %), no gaps], and *Lomaantha aurea* [strain CBS 144403, GenBank MH836376.1; Identities = 829/843 (98 %), no gaps].

Colour illustrations: Bark of *Quercus suber* in South Africa. Colony on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



The first of six equally most parsimonious trees obtained from a maximum parsimony phylogenetic analysis (Swofford 2003) of the *Lomaantha* ITS nucleotide alignment. The tree was rooted to Brycekendrickomyces acaciae (CBS 124104; GenBank NR_132828) and the scale bar indicates the number of changes. Parsimony bootstrap support values from 1 000 replicates and > 79 % are shown at the nodes and the novelty described here is highlighted with a coloured block and **bold** font. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. Branches present in the strict consensus tree are thickened. Alignment statistics: seven strains including the outgroup; 559 characters including alignment gaps analysed: 230 constant, 169 variable and parsimony-uninformative and 160 parsimony-informative. Tree statistics: Tree Length = 561, Consistency Index = 0.791, Retention Index = 0.739, Rescaled Consistency Index = 0.585. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1680

MycoBank MB 853797

Periconia floridana Crous & Jurjević, *sp. nov.*

Etymology: Name refers to the state of Florida, USA, where it was collected.

Classification: *Periconiaceae*, *Massarineae*, *Pleosporales, Pleosporomycetidae, Dothideomycetes*.

Mycelium consisting of hyaline, smooth to roughened, branched, septate, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, flexuous, medium brown, roughened, multiseptate, but prominently constricted at septa, with individual cells 10–15 × 3–5 µm, disarticulating off like arthroconidia. *Conidiogenous cells* integrated, terminal and intercalary, 10–14 × 3–5 µm, with inconspicuous loci (1–2 µm diam) giving rise to short conidial chains. *Conidia* globose, thick-walled, dark brown, verruculose, guttulate, aseptate, (6–)7–8(–9) µm diam.

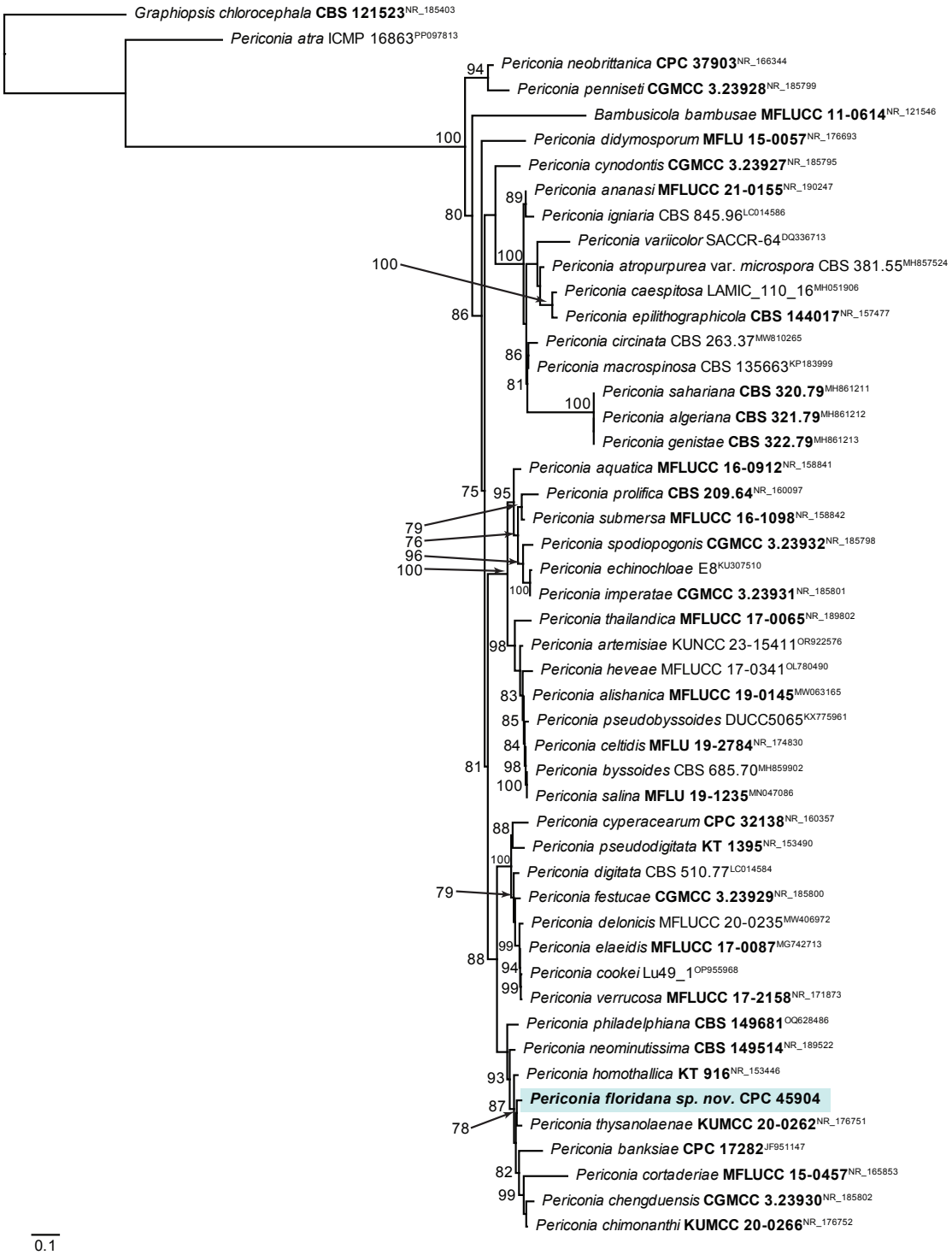
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale grey olivaceous and reverse olivaceous grey.

Typus: **USA**, Florida, Fort Lauderdale, outside air, Jan. 2023, *Z. Jurjević*, 5794 (**holotype** CBS H-25329; culture ex-type CPC 45904 = CBS 150884; ITS and LSU sequences GenBank PP791420.1 and PP791448.1).

Notes: *Periconia floridana* is a typical *Periconia* species having solitary macronematous conidiophores, with spherical conidial heads, polyblastic conidiogenous cells (terminal and intercalary), and catenate, globose, dark brown, aseptate, verruculose conidia. It is phylogenetically related but distinct from *P. homothallica*, a sexual species that did not form a *Periconia* morph in culture (Tanaka *et al.* 2015), and *Periconia thysanolaenae* (conidia 4.5–6 × 4–6 µm; Yang *et al*. 2022), but has larger conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia homothallica* [voucher HHUF 29105, GenBank NR_153446.1; Identities = 505/523 (97 %), seven gaps (1 %)], *Periconia chimonanthi* [strain KUMCC 20-0266, GenBank NR_176752.1; Identities = 510/535 (95 %), eight gaps (1 %)], and *Periconia thysanolaenae* [strain KUMCC 20-0262, GenBank NR_176751.1; Identities = 517/545 (95 %), 18 gaps (3 %)]. Closest hits using the **LSU** sequence are *Periconia neominutissima* [strain CBS 149514, GenBank NG_242103.1; Identities = 835/843 (99 %), no gaps], *Periconia thysanolaenae* [strain KUMCC 20-0262, GenBank NG_081511.1; Identities = 879/890 (99 %), two gaps (0 %)], and *Periconia neobrittanica* [strain CPC 37903, GenBank NG_068342.1; Identities = 871/882 (99 %), no gaps (0 %)].

Colour illustrations: Outer landscape in Fort Lauderdale, Florida, USA. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -5646.021) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Periconia* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Graphiopsis chlorocephala* (CBS 121523; GenBank NR_185403) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 49 strains including the outgroup; 631 characters including alignment gaps analysed: 362 distinct patterns, 233 parsimony-informative, 75 singleton sites, 323 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Ž. Jurjević & A. Erhard, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & aerhard@emsl.com

Fungal Planet 1681 MycoBank MB 853799

Dwiroopa aeria Crous & Jurjević, *sp. nov.*

Etymology: Name refers to the fact that it was sampled from air.

Classification: *Dwiroopaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*.

Conidiomata pycnidial, semi-immersed, globose to subglobose, pale brown with dark brown conidia, 70–150 µm diam; wall of 2–4 layers of pale brown *textura angularis*, opening by irregular rupture. Conidiophores reduced to conidiogenous cells lining inner cavity, ampulliform to subcylindrical, hyaline to pale olivaceous with percurrent proliferation, 3–15 × 3–5 µm. Conidia solitary, obovoid, aseptate, dark green-brown, thick-walled, appearing granuclar in off-plane focus, with 3–6 longitudinal slits, (14–)16–18(–19) × (12–)14–15 µm; hilum slightly protruding, truncate, 2 µm diam.

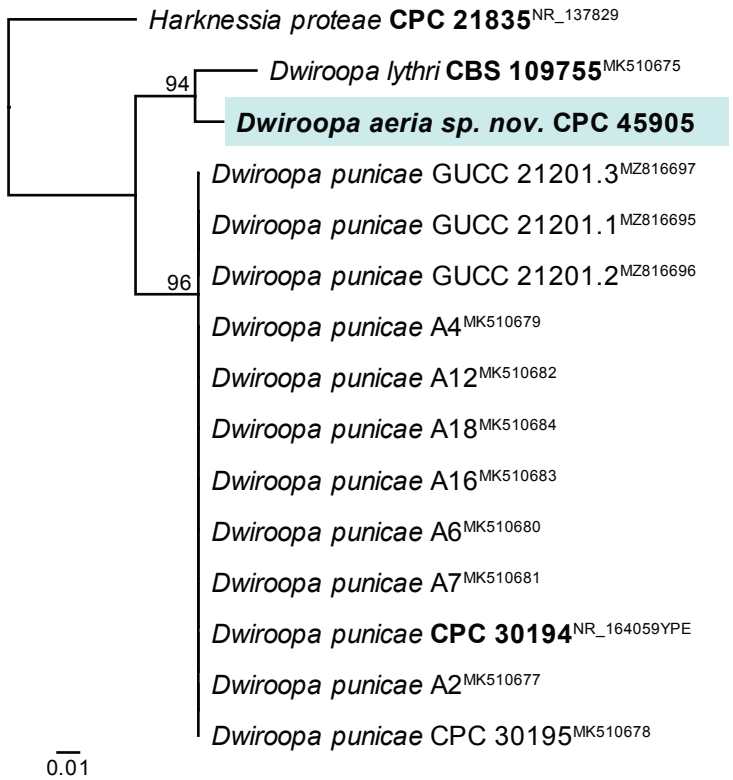
Culture characteristics: Colonies flat, spreading, with sparse aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse olivaceous grey; on OA olivaceous grey.

Typus: **USA**, Florida, Fort Lauderdale, bedroom air, Jan. 2023, *Z. Jurjević*, 5795 (**holotype** CBS H-25330; culture ex-type CPC 45905 = CBS 150812; ITS, LSU, *his3* and *tub2* sequences GenBank PP791421.1, PP791449.1, PP780604.1 and PP780629.1).

Notes: *Dwiroopa* includes three species, namely *D. lythri* (on *Lythrum salicaria*; macroconidia 10.6–18.5 µm × 8.9–15.4 µm), *D. ramya* (on branch of unknown tree; macroconidia 21.2–26.9 × 12.0–17.2 µm; Farr & Rossman 2003), and *D. punicae* [on leaves of *Punica granatum*; macroconidia (12–)13–16(–20) × (10–)12–14(–15) µm; Xavier *et al*. 2019]. *Dwiroopa aeria* has macroconidia that overlap with those of *D. punicae*, though they tend to have a smaller mean range, and *D. aeria* is also phylogenetically distinct.

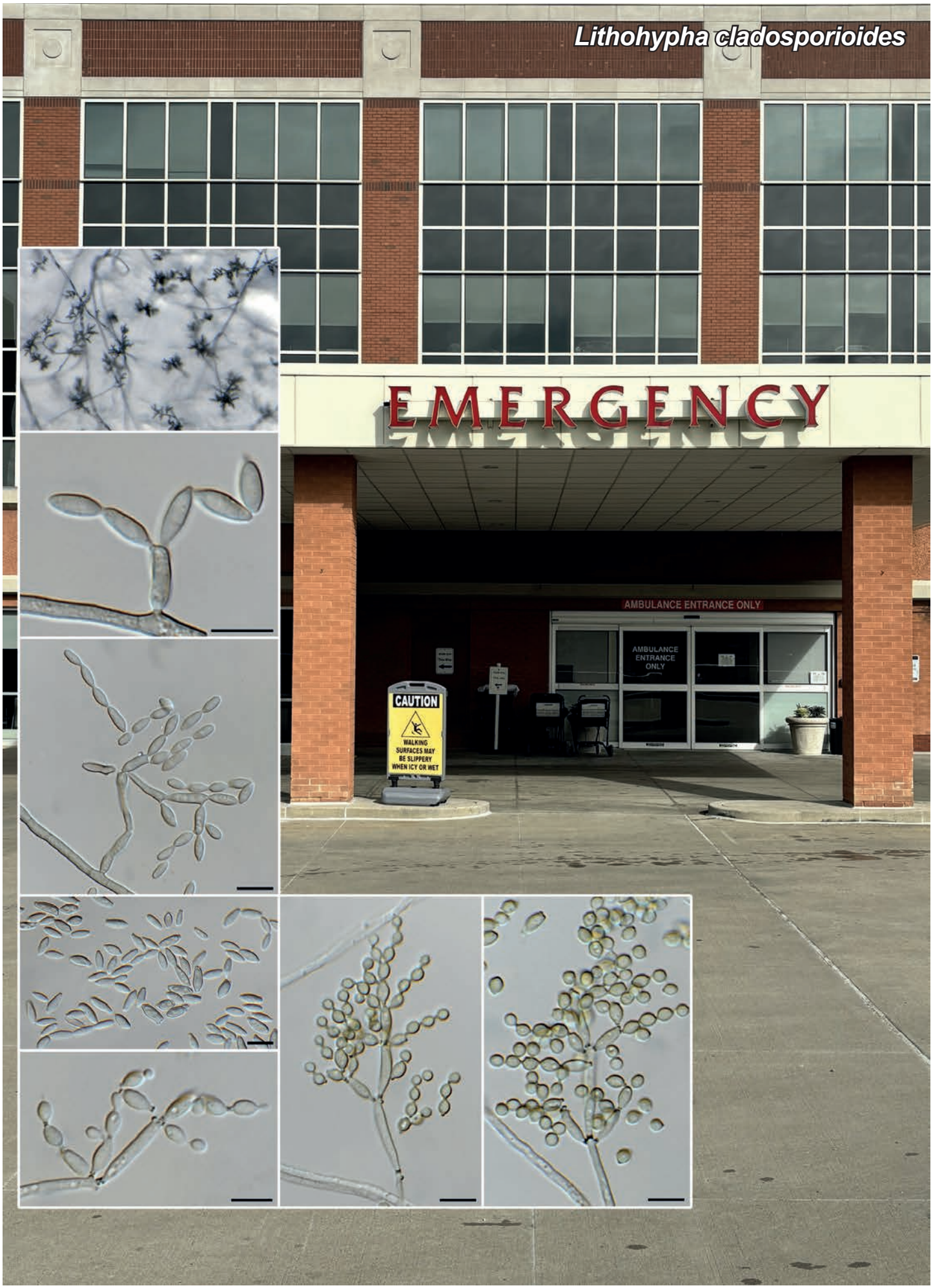
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dwiroopa lythri* [strain CBS 109755, GenBank MN172410.1; Identities = 502/523 (96 %), eight gaps (1 %)], *Dwiroopa punicae* [strain CBS 143163, GenBank NR_164059.1; Identities = 541/577 (94 %), 11 gaps (1 %)], and *Foliocryphia eucalyptorum* [strain CBS 142536, GenBank NR_155102.1; Identities = 532/585 (91 %), 18 gaps (3 %)]. Closest hits using the **LSU** sequence are *Aurantiosacculus acutatus* [strain CPC 13704, GenBank NG_042618.1; Identities = 860/868 (99 %), two gaps (0 %)], *Harknessia hawaiiensis* [strain CPC 15003, GenBank JQ706230.1; Identities = 860/868 (99 %), two gaps (0 %)], *Harknessia pseudohawaiiensis* [strain CPC 13001, GenBank JQ706232.1; Identities = 860/868 (99 %), two gaps (0 %)], *Dwiroopa lythri* [voucher BPI 747560, GenBank NG_059065.1; Identities = 855/863 (99 %), two gaps (0 %)], and *Dwiroopa punicae* [strain A1, GenBank MK510686.1; Identities = 854/862 (99 %), three gaps (0 %)]. No significant hits were obtained when the ***his3*** sequence was used in blastn and megablast searches. Closest hits using the ***tub2*** sequence had distant similarity to *Dwiroopa punicae* [strain A12, GenBank MK510715.1; Identities = 668/826 (81 %), 70 gaps (8 %)], *Harknessia eucalyptorum* [strain CPC 85, GenBank AY720779.1; Identities = 275/343 (80 %), 32 gaps (9 %)], and *Harknessia renispora* [strain CBS 153.71, GenBank AY720769.1; Identities = 271/339 (80 %), 23 gaps (6 %)].

Colour illustrations: Bedroom in Fort Lauderdale, Florida, USA. Conidiomata on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidioma (top) = 150 µm, all others = 10 µm.



Most likely phylogram (score -1293.751) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Dwiroopa* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Harknessia proteae* (CPC 21835; GenBank NR_137829) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 15 strains including the outgroup; 623 characters including alignment gaps analysed: 66 distinct patterns, 24 parsimony-informative, 50 singleton sites, 549 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: K2P+I. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Ž. Jurjević & S. Balashov, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & sbalashov@emsl.com



Fungal Planet 1682 MycoBank MB 853800.

Lithohypha cladosporioides Crous & Jurjević, *sp. nov.*

Etymology: Name refers to its cladosporium-like morphology.

Classification: *Trichomeriaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 2–2.5 µm diam hyphae. *Conidiophores* solitary, erect, cladosporium-like, 60–120 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, 10–30 × 2–3 µm; scars thick-walled, darkened, 1–1.5 µm diam. *Primary ramoconidia* aseptate, subcylindrical, pale brown, smooth, 15–20 × 2–3 µm, with 1–3 apical loci; *secondary ramoconidia* subcylindrical to fusoid, 15–25 × 2–3 µm; *intermediary conidia* fusoid-ellipsoid, 5–8 × 2.5–3 µm; *terminal conidia* in short chains, linked by a short isthmus, ellipsoid to obovoid, pale brown, verruculous, 3.5–5 × 3–3.5 µm.

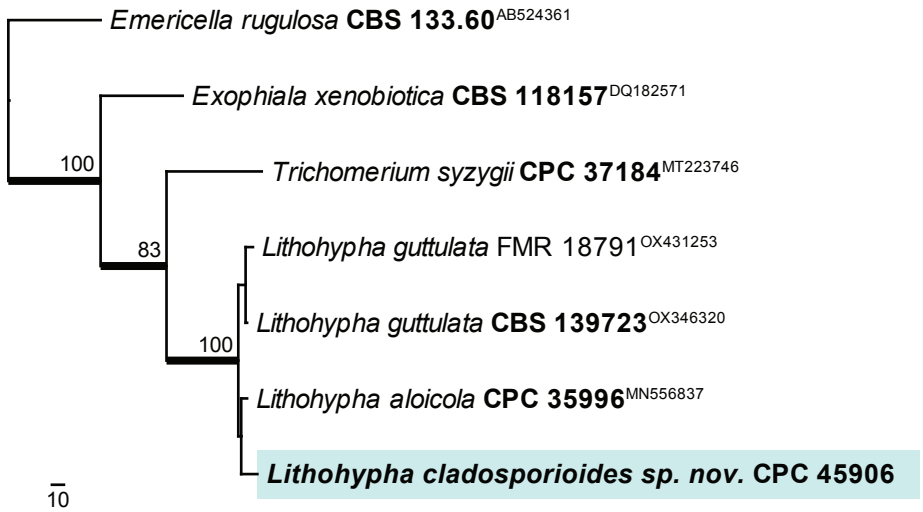
Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and smooth, even margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus: **USA**, Florida, Fort Lauderdale, hospital swab, Jan. 2023, *Z. Jurjević*, 5798 [**holotype** CBS H-25331; culture ex-type CPC 45906 = CBS 150813; ITS, LSU, *tef1* (second part) and *tub2* sequences GenBank PP791422.1, PP791450.1, PP780625.1 and PP780630.1].

Notes: *Lithohypha* (based on *L. guttulata*) was introduced for a sterile hyphomycete isolated from rock in the Vatican City State (Isola *et al.* 2016). Isolates are slow-growing, and rarely form chlamydospores. The present collection is closely related to *L. guttulata*, but is morphologically distinct in that it sporulated abundantly, forming cladosporium-like conidiophores, and chains of ellipsoid to obovoid, verruculous conidia. Morphologically it resembles *L. aloicola* (leaves of *Aloe* sp., South Africa, ramoconidia 10–13 × 2.5–3 µm, terminalconidia occurring in branched chains, (6–)7–9(–10) × 2.5–3 µm; Crous *et al*. 2019c), but has a different conidial morphology.

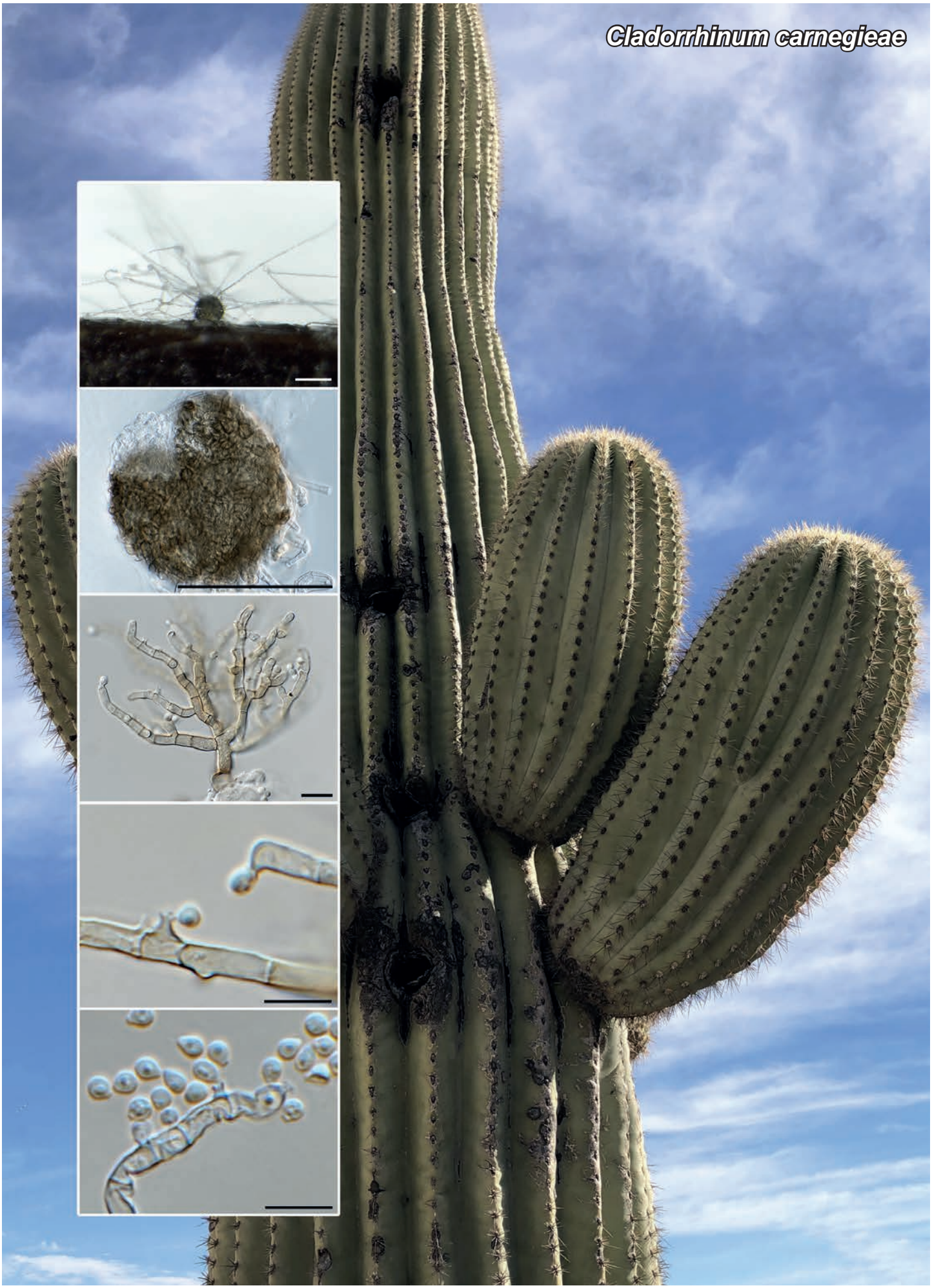
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lithohypha guttulata* [strain CCFEE 5908, GenBank KP791770.1; Identities = 566/569 (99 %), one gap (0 %)], *Lithohypha aloicola* [strain CPC 35996, GenBank NR_166313.1; Identities = 571/578 (99 %), one gap (0 %)], and *Knufia fluminis* [strain FJII_L6_SW_P1, GenBank MT704889.1; Identities = 569/581 (98 %), three gaps (0 %)]. Closest hits using the **LSU** sequence are *Lithohypha guttulata* [strain FMR 20100, GenBank OX346377.1; Identities = 864/864 (100 %), no gaps], *Lithohypha aloicola* [strain CPC 35996, GenBank NG_068316.1; Identities = 852/852 (100 %), no gaps], and *Neophaeococcomyces catenatus* [strain CBS 650.76, GenBank NG_070445.1; Identities = 836/879 (95 %), six gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Lithohypha guttulata* [strain FMR 20100, GenBank OX346319.1; Identities = 820/833 (98 %), no gaps], *Anthracina saxicola* [strain CGMCC 3.17349, GenBank KP174997.1; Identities = 762/831 (92 %), no gaps], and *Knufia calcarecola* [as *Knufia* sp. LS-2015a; strain CGMCC 3.17225, GenBank KP175007.1; Identities = 761/830 (92 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Lithohypha guttulata* [strain FMR 18791, GenBank OX431253.1; Identities = 334/344 (97 %), one gap (0 %)], and *Lithohypha aloicola* [strain CBS 146070, GenBank MN556837.1; Identities = 544/563 (97 %), two gaps (0 %)].

Colour illustrations: Hospital at Fort Lauderdale, Florida, USA. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



The first of three equally most parsimonious trees obtained from a maximum parsimony phylogenetic analysis (Swofford 2003) of the *Lithohypha tub2* nucleotide alignment. The tree was rooted to *Emericella rugulosa* (CBS 133.60; GenBank AB524361) and the scale bar indicates the number of changes. Parsimony bootstrap support values from 1 000 replicates and > 79 % are shown at the nodes and the novelty described here is highlighted with a coloured block and **bold** font. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. Branches present in the strict consensus tree are thickened. Alignment statistics: seven strains including the outgroup; 428 characters including alignment gaps analysed: 194 constant, 140 variable and parsimony-uninformative and 94 parsimony-informative. Tree statistics: Tree Length = 369, Consistency Index = 0.905, Retention Index = 0.690, Rescaled Consistency Index = 0.625. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Ž. Jurjević & S. Balashov, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & sbalashov@emsl.com



Fungal Planet 1683 MycoBank MB 853801

Cladorrhinum carnegieae Crous & Jurjević, *sp. nov.*

Etymology: Name refers to *Carnegiea*, the host genus from which it was isolated.

Classification: *Podosporaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*.

Mycelium consisting of dark brown, thick-walled, smooth, branched, septate, 4–5 µm diam hyphae, forming chains of ellipsoid *chlamydospores* in older hyphae, 8–10 µm diam, constricted at septa; becoming pale brown to subhyaline towards apex of hyphae, forming intricate bush-like, branched sporulation structures. *Conidiophores* multiseptate, branched or not, 20–80 × 3–5 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, 5–15 × 3–4 µm, monophialidic with flared collarette, 2–3 µm diam. *Conidia* solitary, aseptate, hyaline, guttulate, obovoid, hilum truncate, 1 µm diam, 2.5–3.5 × 2.5–3 µm. *Ascomata* perithecial, solitary, globose, brown, 50–100 µm diam, with immature asci, but remaining sterile; also forming brown mycelial plaques attached to bottom surface of Petri dish.

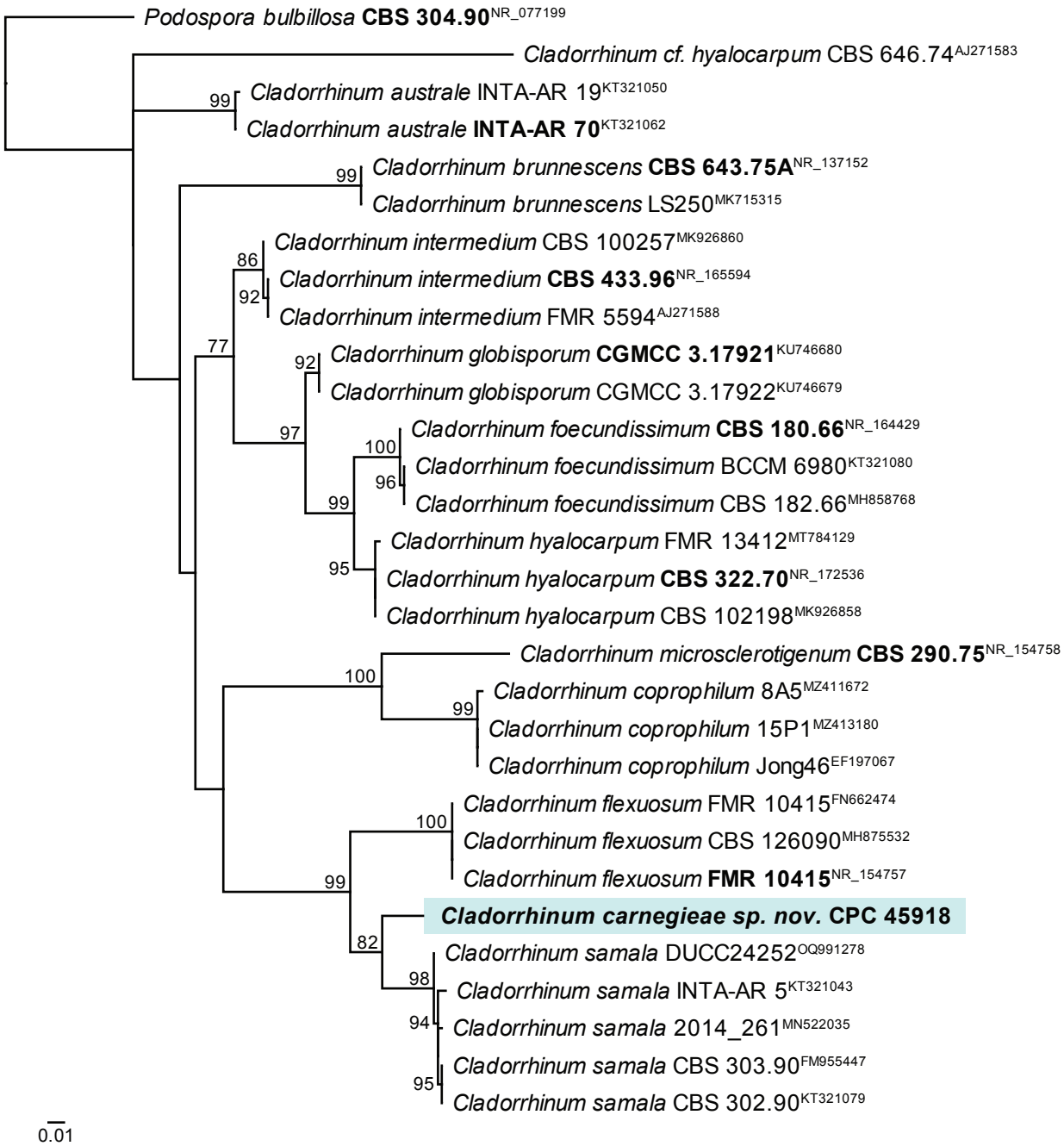
Culture characteristics: Colonies flat, spreading, with moderate to abundant aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus: **USA**, Arizona, Tortilla Flat (Apache trail), *Carnegiea gigantea* (*Cactaceae*), Mar. 2023, *Z. Jurjević*, 5817 (**holotype** CBS H-25332; culture ex-type CPC 45918 = CBS 150814; ITS, LSU and *tub2* sequences GenBank PP791423.1, PP791451.1 and PP780631.1).

Notes: *Cladorrhinum* forms mucoid masses of aseptate conidia from intercalary conidiogenous cells with lateral phialidic openings (Madrid *et al*. 2011). *Cladorrhinum carnegieae* is related to *C. samala* [conidia (2–)3–3.5(–4) ´ (1.5–)2–2.5(–3) µm; Mouchacca & Gams 1993), but is morphologically and phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cladorrhinum samala* [strain INTA-AR 112, GenBank KT321075.1; Identities = 509/539 (94 %), 19 gaps (3 %)], *Cladorrhinum flexuosum* [strain FMR 10415, GenBank NR_154757.1; Identities = 496/537 (92 %), 16 gaps (2 %)], and *Cladorrhinum australe* [strain INTA-AR 63, GenBank KT321060.1; Identities = 483/539 (90 %), 22 gaps (4 %)]. Closest hits using the **LSU** sequence are *Cladorrhinum samala* [strain DUCC24252, GenBank OQ991295.1; Identities = 863/865 (99 %), one gap (0 %)], *Podospora inflatula* [strain CBS 413.82, GenBank MH873254.1; Identities = 829/832 (99 %), no gaps], and *Podospora costaricensis* [as *Cercophora costaricensis*; voucher SMH4021, GenBank AY780059.1; Identities = 869/873 (99 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Cladorrhinum foecundissimum* [strain CBS 391.42, GenBank HQ877462.1; Identities = 247/260 (95 %), four gaps (1 %)], *Papulaspora equi* [strain CBS 128687, GenBank KT006928.1; Identities = 397/474 (84 %), 27 gaps (5 %)], and *Podospora bulbillosa* [strain CBS 304.90, GenBank MK926961.1; Identities = 391/474 (82 %), 27 gaps (5 %)].

Colour illustrations: *Carnegiea gigantea* in Arizona, USA. Conidioma on synthetic nutrient-poor agar; conidioma; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 200 µm, all others = 10 µm.



Most likely phylogram (score -2565.114) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Cladorrhinum* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Podospora bulbillosa* (CBS 304.90; GenBank NR_077199) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 30 strains including the outgroup; 558 characters including alignment gaps analysed: 231 distinct patterns, 137 parsimony-informative, 43 singleton sites, 378 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Ž. Jurjević & S. Balashov, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & sbalashov@emsl.com

Fungal Planet 1684 MycoBank MB 853802

Dothiora americana Crous & Jurjević, *sp. nov.*

Etymology: Name refers to United States of America, where it was isolated.

Classification: *Dothioraceae*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*.

Mycelium consisting of branched, septate, brown, smooth, thick-walled, 4–5 µm diam hyphae, covered in mucilage. *Conidiophores* reduced to conidiogenous cells, integrated, intercalary, subcylindrical, 3–7 × 4–5 µm, with lateral loci, denticle like, phialidic, 1–2 × 1.5–2 µm, giving rise to solitary conidia. *Conidia* hyaline, smooth, guttulate, subcylindrical, aseptate, ends obtuse, 4–9 × 2–3 µm, undergoing microcyclic conidiation with age, becoming brown, thick-walled, muriformly septate, 10–20 × 4–6 µm, covered in mucilaginous layer.

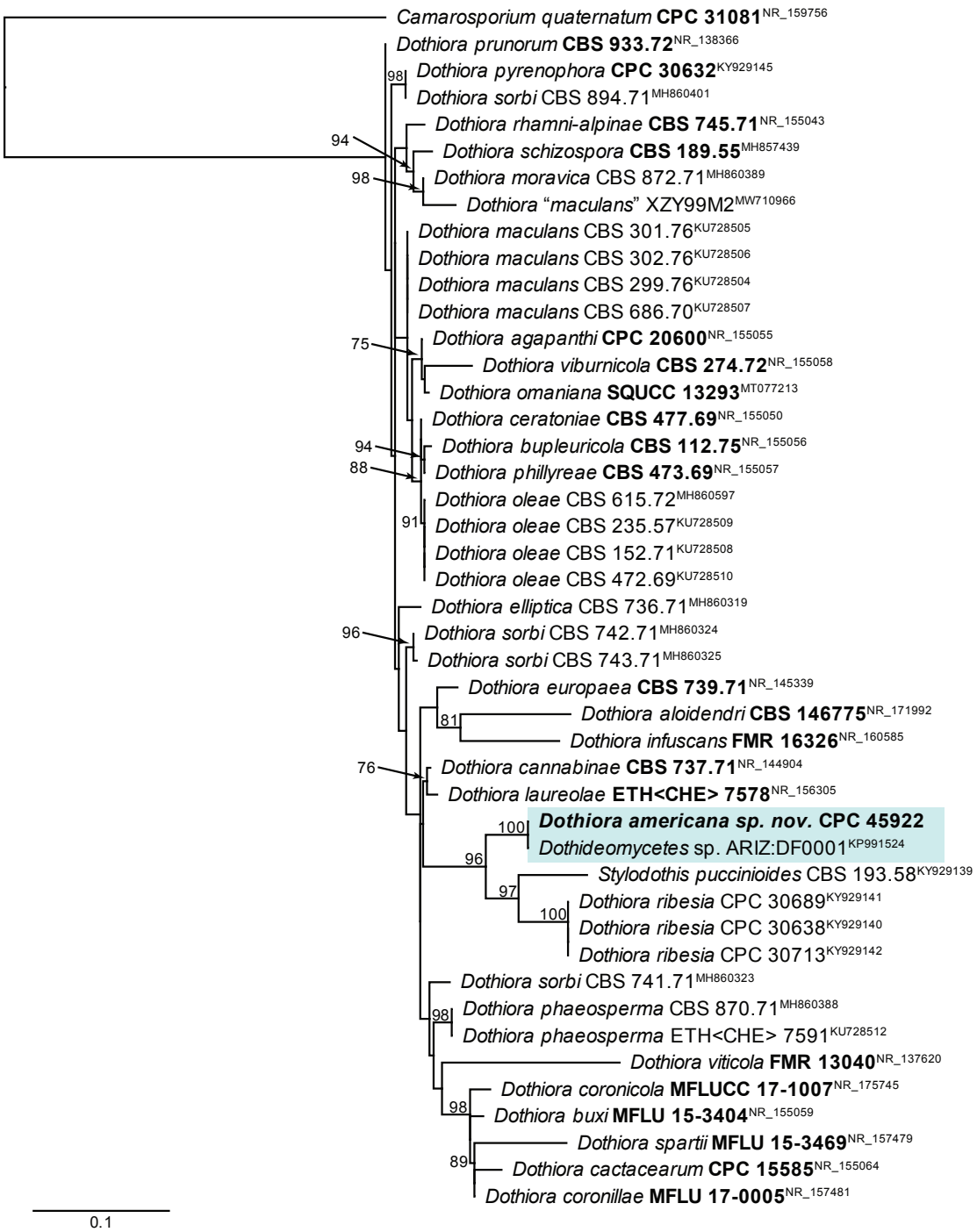
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 3–5 mm diam after 1 wk at 25 °C. On MEA, PDA and OA surface and reverse fuscous black.

Typus: **USA**, Nebraska, Hyannis, outside air, Mar. 2023, *Z. Jurjević*, 5824 [**holotype** CBS H-25334; culture ex-type CPC 45922 = CBS 150817; ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank PP791424.1, PP791452.1, PP780617.1 and PP780632.1].

Notes: Although *Dothiora* (based on *D. pyrenophora*) produces a *Dothichiza* coelomycetous asexual morphs in culture (Crous & Groenewald 2017), the present collection sporulated like a hyphomycete, and did not form conidiomata. Phylogenetically however, it clusters with other species of *Dothiora*, and if related to, but distinct from *D. ribesia*. Further collections need to be added to clarify is the present taxon represents yet another genus in this complex.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dothideomycetes* sp. [voucher ARIZ DF0001, GenBank KP991524.1; Identities = 508/508 (100 %), no gaps], *Dothiora ribesia* [strain CPC 30713, GenBank KY929142.1; Identities = 495/508 (97 %), two gaps (0 %)], and *Stylodothis puccinioides* [strain CBS 193.58, GenBank KY929139.1; Identities = 495/509 (97 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Dothidea muelleri* [strain CBS 191.58, GenBank EU167593.1; Identities = 843/845 (99 %), no gaps], *Dothiora ribesia* [as *Dothidea ribesia*; strain CPC 30638, GenBank KY929173.1; Identities = 860/863 (99 %), no gaps], and *Stylodothis puccinioides* [voucher HMAS 285382, GenBank OQ534514.1; Identities = 859/862 (99 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Dothiora ribesia* [strain CPC 30638, GenBank KY929192.1; Identities = 261/320 (82 %), 21 gaps (6 %)], *Ramulariopsis gossypii* [strain RGNP1, GenBank OQ925681.1; Identities = 121/125 (97 %), no gaps], and *Dothiora oleae* [strain CBS 615.72, GenBank KU728589.1; Identities = 123/129 (95 %), no gaps]. Closest hits using the ***tub2*** sequence had highest similarity to *Dothiora maculans* [strain CBS 299.76, GenBank KU728621.1; Identities = 502/631 (80 %), 44 gaps (6 %)], *Dothiora aloidendri* [strain CPC 38535, GenBank MW173138.1; Identities = 497/632 (79 %), 52 gaps (8 %)], and *Dothiora phillyreae* [strain CBS 473.69, GenBank KU728629.1; Identities = 492/627 (78 %), 43 gaps (6 %)].

Colour illustrations: Hyannis, Nebraska, USA. Colony on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia; primary and secondary conidia. Scale bars = 10 µm.



Most likely phylogram (score -3038.095) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Dothiora* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Camarosporium quaternatum* (CPC 31081; GenBank NR_159756) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 45 strains including the outgroup; 618 characters including alignment gaps analysed: 232 distinct patterns, 85 parsimony-informative, 177 singleton sites, 356 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Ž. Jurjević & A. Erhard, EMSL Analytical, Inc., 200 Route 130 North, Cinnaminson, NJ 08077 USA; e-mail: zjurjevic@emsl.com & aerhard@emsl.com

Fungal Planet 1685

MycoBank MB 853803

Alfaria elegiae Crous, *sp. nov.*

Etymology: Name refers to *Elegia*, the host genus from which it was isolated.

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Conidiomata immersed in agar to superficial, acervular to sporodochial, 100–200 µm diam; wall of 3–4 layers of pale brown *textura angularis*. *Conidiophores* hyaline, smooth, subcylindrical, branched at apex, 0–2-septate, 15–60 × 4–5 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, subhyaline, smooth, 10–18 × 3–4 µm; proliferating inconspicuously percurrently at apex. *Conidia* subcylindrical, guttulate, straight to flexuous, smooth, hyaline, apex subobtuse, base truncate, aseptate, (42–)45–48(–52) × (3–)3.5(–4) µm.

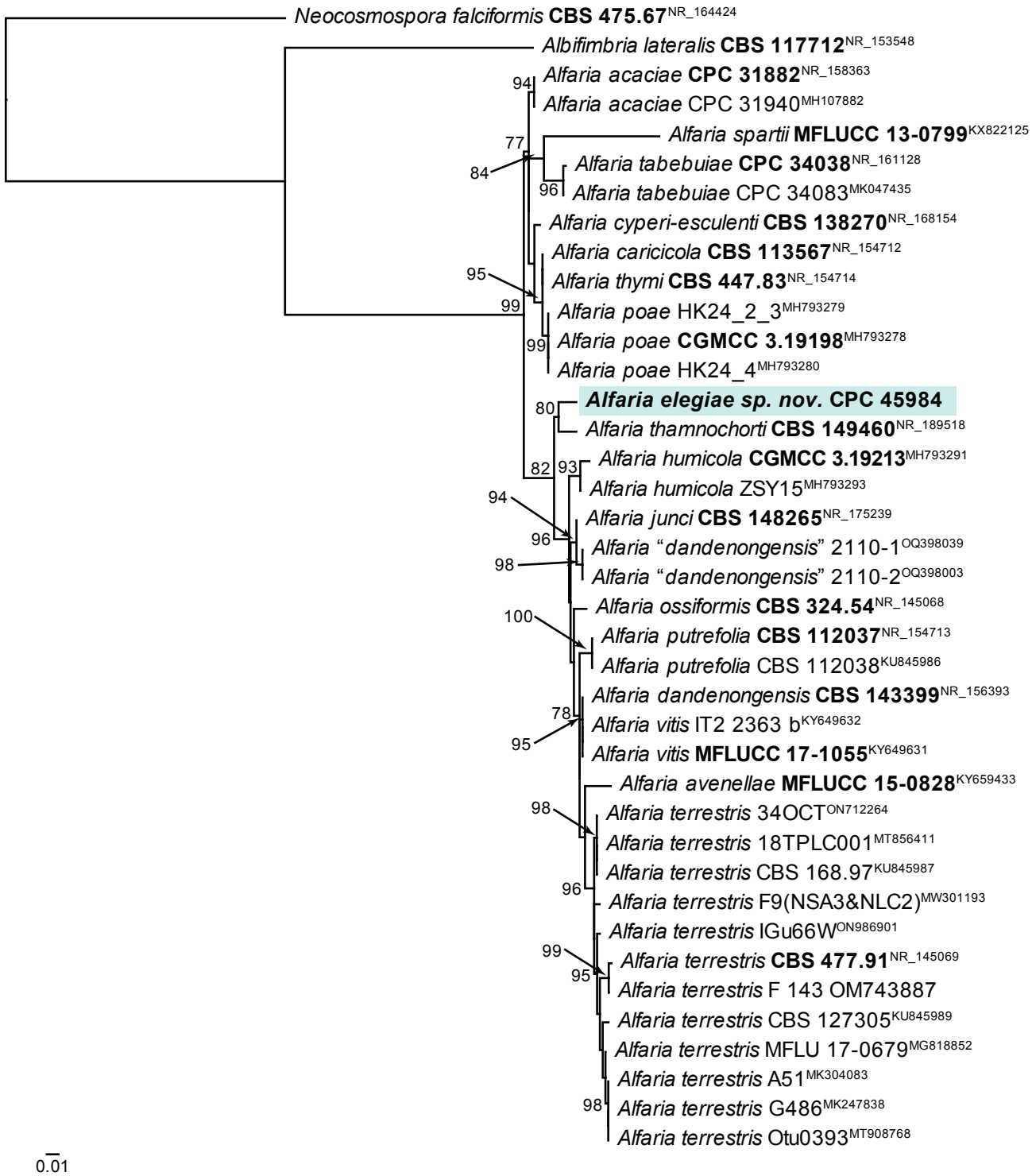
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and lobate, feathery margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA surface dirty white and reverse sienna; on PDA surface and reverse saffron; on OA surface saffron.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on culms of *Elegia ebracteata* (*Restionaceae*), 13 Apr. 2023, *P.W. Crous*, HPC 4157 [**holotype** CBS H-25335; culture ex-type CPC 45984 = CBS 150818; ITS, LSU, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PP791425.1, PP791453.1, PP780603.1, PP780611.1, PP780618.1 and PP780633.1].

Notes: *Alfaria* (based on *A. cyperi-esculenti*) was established for a fungus causing a disease on *Cyperus esculentus* in Spain (Crous *et al.* 2014). *Alfaria elegiae* is closely related to *A. dandenongensis* [conidia (8–)9–11(–12) × (2–)2.5–3 µm; Crous *et al.* 2017], which is morphologically quite distinct, and *A. thamnochorti* [conidia (25–)30–45(–50) × 2(–3) µm; Crous *et al.* 2023b], which is morphologically similar, but has slightly smaller conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alfaria dandenongensis* [strain CBS 143399, GenBank NR_156393.1; Identities = 551/565 (98 %), four gaps (0 %)], *Alfaria thamnochorti* [strain CBS 149460, GenBank NR_189518.1; Identities = 502/516 (97 %), two gaps (0 %)], and *Alfaria vitis*]strain MFLUCC 17-1055, GenBank KY649631.1; Identities = 524/539 (97 %), five gaps (0 %)]. Closest hits using the **LSU** sequence are *Alfaria thamnochorti* [strain CBS 149460, GenBank NG_242099.1; Identities = 813/813 (100 %), no gaps], *Alfaria terrestris* [strain CBS 168.97, GenBank KU845996.1; Identities = 825/827 (99 %), no gaps], and *Alfaria dandenongensis* [strain CBS 143399, GenBank NG_069537.1; Identities = 825/828 (99 %), no gaps]. Closest hits using the ***cmdA*** sequence had highest similarity to *Alfaria ossiformis* [strain CBS 324.54, GenBank KU845977.1; Identities = 456/506 (90 %), four gaps (0 %)], *Alfaria humicola* [strain ZSY15, GenBank MH885434.1; Identities = 407/456 (89 %), five gaps (1 %)], and *Alfaria dandenongensis* [strain CBS 143399, GenBank MG386135.1; Identities = 444/498 (89 %), five gaps (1 %)]. Closest hits using the ***rpb2*** sequence had highest similarity to *Alfaria thamnochorti* [strain CPC 43155, GenBank OQ627939.1; Identities = 712/718 (99 %), no gaps], *Alfaria dandenongensis* [strain CBS 143399, GenBank MG386146.1; Identities = 674/718 (94 %), no gaps], and *Alfaria ossiformis* [strain CBS 324.54, GenBank KU846002.1; Identities = 659/703 (94 %), no gaps]. Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Alfaria thamnochorti* (strain CPC 43155, GenBank OQ627948.1; Identities = 373/390 (96 %), one gap (0 %)], *Alfaria ossiformis* [strain CBS 324.54, GenBank KU846009.1; Identities = 347/408 (85 %), 23 gaps (5 %)], and *Alfaria terrestris* [strain CBS 127305, GenBank KU846012.1; Identities = 346/410 (84 %), 18 gaps (4 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Alfaria terrestris* [strain CBS 477.91, GenBank KU846019.1; Identities = 303/319 (95 %), two gaps (0 %)], *Alfaria ossiformis* [strain CBS 324.54, GenBank KU846015.1; Identities = 300/318 (94 %), no gaps], and *Alfaria acaciae* [strain CBS 143504, GenBank MH108035.1; Identities = 300/318 (94 %), one gap (0 %)].

Colour illustrations: Elegia ebracteata in Kirstenbosch, South Africa. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -2058.826) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Alfaria* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Neocosmospora falciformis* (CBS 475.67; GenBank NR_164424) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 39 strains including the outgroup; 570 characters including alignment gaps analysed: 180 distinct patterns, 70 parsimony-informative, 79 singleton sites, 421 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3e+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1686

MycoBank MB 853804

Gardeniomyces Crous, *gen. nov.*

Etymology: Name refers to *Gardenia*, the host genus from which it was isolated.

Classification: *Sebacinaceae*, *Sebacinales*, *Agaricomycetidae*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae. *Conidiophores* reduced to conidiogenous cells on aerial hyphae or forming hyphal tufts, with conidiogenous cells terminal and intercalary. *Conidiogenous cells* hyaline, smooth, subcylindrical with slight apical taper, monophialidic, flexuous, without prominent collarette. *Conidia* solitary, aggregating in mucoid mass, aseptate, obovoid, straight to slightly curved to gibbous, hyaline, smooth, hilum truncate, basal or laterally displaced.

Type species: *Gardeniomyces kirstenboschensis* Crous

MycoBank MB 853805

Gardeniomyces kirstenboschensis Crous, *sp. nov.*

Etymology: Name refers to Kirstenbosch, South Africa, where it was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells on aerial hyphae or forming hyphal tufts up to 180 µm tall, 1.5–2 µm diam with conidiogenous cells terminal and intercalary. *Conidiogenous cells* hyaline, smooth, subcylindrical with slight apical taper, monophialidic, flexuous, without prominent collarette, 13–35 × 1.5–2 µm. *Conidia* solitary, aggregating in mucoid mass, aseptate, obovoid, straight to slightly curved to gibbous, hyaline, smooth, hilum truncate, basal or laterally displaced, 1 µm diam, 4–5 × 2.5–3 µm.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and feathery margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse sienna; on PDA and OA surface and reverse dirty white.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, from rotting fruit of *Gardenia thunbergia* (*Rubiaceae*), 13 Apr. 2023, *P.W. Crous*, HPC 4166 (**holotype** CBS H-25336; culture ex-type CPC 45988 = CBS 150819; ITS and LSU sequences GenBank PP791426.1 and PP791454.1).

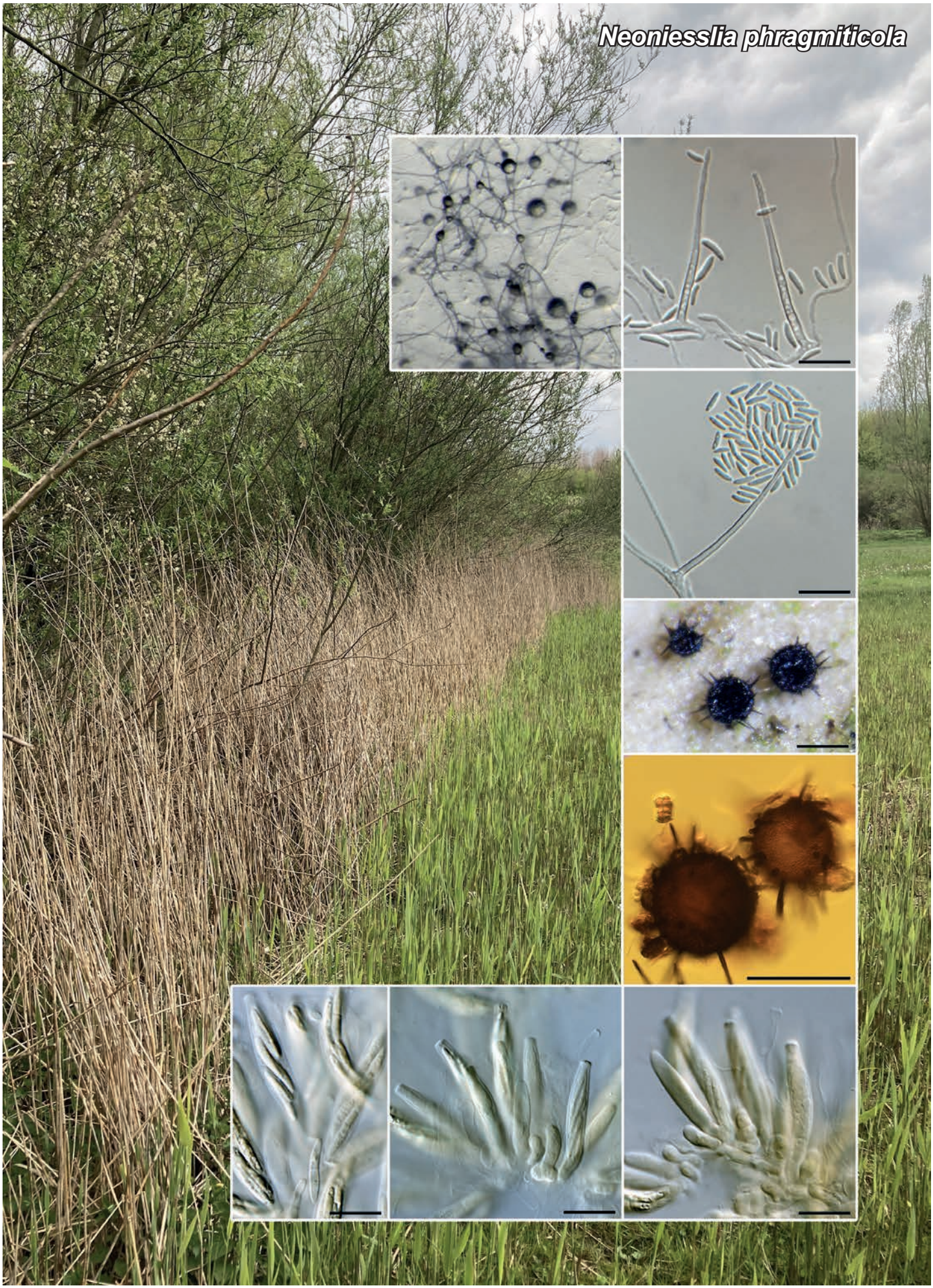
Notes: *Gardeniomyces* is acremonium-like in general morphology (see Hou *et al.* 2023), but is phylogenetically unrelated, clustering with *Paulisebacina*, a monotypic member of *Sebacinaceae*, characterised by thin basidiocarps lacking dikaryophyses, and lacking clamp connections (Oberwinkler *et al.* 2014). Although no basidia were observed, the fact that conidia were at times gibbose in shape, with displaced hila, suggest that they could be basidiospores. However, spores aggregated in mucoid masses on solitary conidiogenous cells, again suggesting that it is an asexual morph. Further collections are therefore needed to resolve the various morphs of its lifecycle.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paulisebacina allantoidea* [strain RoKi 179, GenBank KF061266.1; Identities = 430/568 (76 %), 66 gaps (11 %)], *Chaetospermum chaetosporum* [strain CBS 154.59, GenBank NR_126146.1; Identities = 472/639 (74 %), 74 gaps (11 %)], and *Efibulobasidium albescens* [strain RJB 12952, GenBank AF384860.1; Identities = 331/417 (79 %), 37 gaps (8 %)]. Closest hits using the **LSU** sequence are *Pterula gracilis* [strain CBS 554.85, GenBank MH873593.1; Identities = 797/884 (90 %), 19 gaps (2 %)], *Cortinarius carbonellus* [voucher PDD 103685, GenBank KJ635222.1; Identities = 794/883 (90 %), 16 gaps (1 %)], and *Phlegmacium carbonellum* [voucher PDD 70502, GenBank NG_058790.1; Identities = 794/883 (90 %), 16 gaps (1 %)]. The LSU sequences currently available for *Sebacinales* on GenBank are all significantly shorter than the sequence used in the blast search, as well as the representative sequences from other orders and therefore the *Sebacinales* sequences did not appear in the list of best hits.

Colour illustrations: Rotting fruit of *Gardenia thunbergia*, Kirstenbosch, South Africa. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Most likely phylogram (score -7865.729) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Agaricomycetes* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Cystobasidiopsis lactophilus* (CBS 7527; GenBank KY107423) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Families, orders and the class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 74 strains including the outgroup; 911 characters including alignment gaps analysed: 468 distinct patterns, 287 parsimony-informative, 99 singleton sites, 525 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM3+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl



Fungal Planet 1687

MycoBank MB 853806

Neoniesslia Crous & Osieck, *gen. nov.*

Etymology: Name refers to its morphological similarity to *Niesslia*.

Classification: *Incertae sedis*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate hyphae, frequently forming hyphal coils. *Conidiophores* erect, flexuous, subcylindrical, swollen at base, reduced to *conidiogenous cells* that are thick-walled in basal region, tapering towards apex, monophialidic, with minute, non-flared collarette. *Conidia* aggregating in mucoid mass, hyaline, smooth, aseptate, guttulate, fusoid, curved. *Ascomata in vivo* superficial, perithecial, dark brown, globose, ostiolata, collapsing at maturity, covered in dark brown spines, thick-walled, acutely tapered. *Asci* unitunicate, 8-spored, narrowly ellipsoid, slightly curved, stipitate, apex truncate, with apical mechanism, not blueing in Melzer's reagent. *Ascospores* multiseriate, hyaline, smooth, guttulate, fusoid-ellipsoid, subobtuse ends, medianly 1-septate.

Type species: *Neoniesslia phragmiticola* Crous & Osieck

MycoBank MB 853807

Neoniesslia phragmiticola Crous & Osieck, *sp. nov.*

Etymology: Name refers to *Phragmites*, the host genus from which it was isolated.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5 µm diam hyphae, frequently forming hyphal coils. *Conidiophores* erect, flexuous, subcylindrical, swollen at base, 2.5–3.5 µm diam, reduced to *conidiogenous cells* that are thick-walled in basal region, tapering towards apex, monophialidic, with minute, 0.5 µm long non-flared collarette, 40–60 × 2–2.5 µm. *Conidia* aggregating in mucoid mass, hyaline, smooth, aseptate, guttulate, fusoid, curved, (5–)6–7(–9) × 1.5–2 µm. *Ascomata in vivo* superficial, perithecial, dark brown, globose, ostiolata, collapsing at maturity, 70–100 µm diam, covered in dark brown spines, thick-walled, acutely tapered, 20–40 × 4–5 µm. *Asci* unitunicate, 8-spored, narrowly ellipsoid, slightly curved, stipitate, apex truncate, with apical mechanism, not blueing in Melzer's reagent, 30–40 × 5–6 µm. *Ascospores* multiseriate, hyaline, smooth, guttulate, fusoid-ellipsoid, subobtuse ends, medianly 1-septate, (11–)12–13(–15) × (2–)2.5 µm.

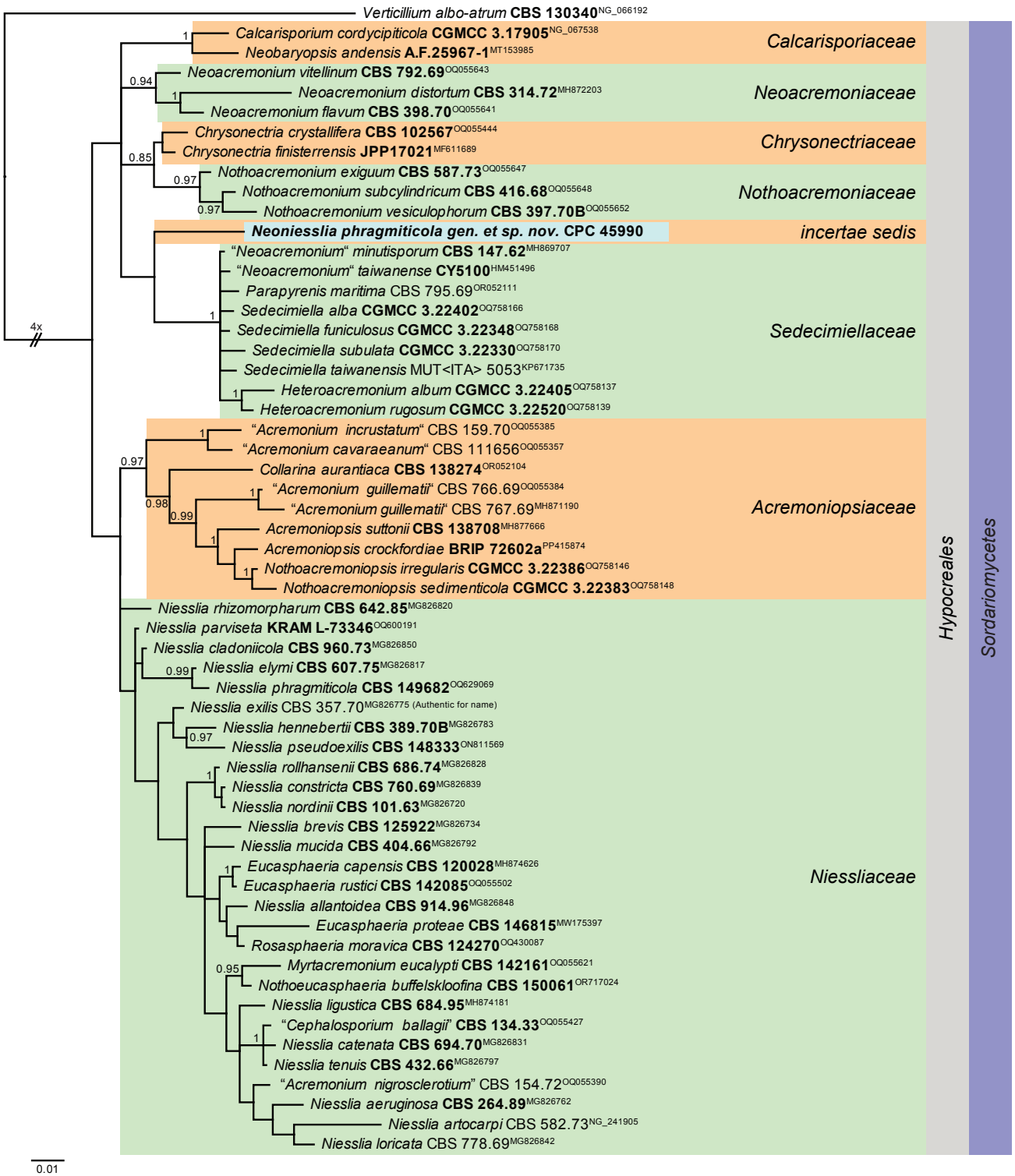
Culture characteristics: Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. pale luteous; on OA surface pale luteous.

Typus: **Netherlands**, Utrecht Province, Nieuw Wulven, near Houten, N52°03'01'', E05°09'43'', on leaf sheaths of standing dead culms of *Phragmites australis* (*Poaceae*), 20 Apr. 2023, *E.R. Osieck*, HPC 4175 = WI-82, coll. 4668 [**holotype** CBS H-25337; culture ex-type CPC 45990 = CBS 150820; ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank PP791427.1, PP791455.1, PP780619.1 and PP780634.1].

Colour illustrations: Phragmites along woodland border, Nieuw Wulven, near Houten, the Netherlands. Conidiophores and conidiogenous cells giving rise to conidia; ascomata with setae; asci with ascospores. Scale bars: ascomata = 100 µm, all others = 10 µm.

Notes: *Niesslia* was recently treated by Gams *et al*. (2019), and circumscribed to have small, superficial, dark brown to black, shiny, spine-covered *ascomata in vivo*, clavate asci with an inconspicuous ring, and hyaline, 1-septate ascospores. The asexual morph is monocillium-like, and has a thick-walled basal region, with or without a sterile vesicle, and hyaline, aseptate conidia. *Neoniesslia* is morphologically similar, except for the absence of sterile vesicles. Using the key provided by Gams *et al*. (2019) the sexual morph of this species keys out as *Niesslia exosporioides*, but the latter has smaller spores: 6.5–9.5 × 1.5–1.8 µm. Strikingly, Dennis (1983) mentions a spore size of 10–13 × 2–2.5 µm for this species. This represents the third *Niesslia/Neoniesslia* on *Phragmites* from the collection area (see Crous *et al*. 2023b, Fungal Planet 1498).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cosmospora* aff. *viliuscula* [strain GJS732, GenBank JN995630.1; Identities = 497/558 (89 %), 28 gaps (5 %)], *Cosmospora viliuscula* [strain G.J.S. 10-114, GenBank KJ676155.1; Identities = 494/555 (89 %), 28 gaps (5 %)], and *Cosmospora khandalensis* [strain S.D. Russell MycoMap # 3288, GenBank ON561738.1; Identities = 497/560 (89 %), 30 gaps (5 %)]. Closest hits using the **LSU** sequence are *Sedecimiella alba* [strain CGMCC 3.22402, GenBank OQ758166.1; Identities = 781/808 (97 %), two gaps (0 %)], *Niesslia ilicifolia* [strain CBS 459.74, GenBank MG826798.1; Identities = 792/820 (97 %), four gaps (0 %)], and *Neoacremonium minutisporum* [strain CBS 147.62, GenBank NG_228791.1; Identities = 789/818 (96 %), two gaps (0 %)]. No significant hits were obtained when the ***tef1*** (first part) sequence was used in blastn and megablast searches. Closest hits using the ***tub2*** sequence had highest similarity to *Myrtacremonium eucalypti* [strain CBS 142161, GenBank KY979912.1; Identities = 317/387 (82 %), 21 gaps (5 %)], *Ijuhya corynospora* [strain CBS 342.77, GenBank KY684188.1; Identities = 316/386 (82 %), 19 gaps (4 %)], and *Cosmospora obscura* [strain MAFF 241484, GenBank KC291903.1; Identities = 307/377 (81 %), 14 gaps (3 %)].



Consensus phylogram (50 % majority rule) of 47 478 trees resulting from a Bayesian analysis of the *Hypocreales* LSU nucleotide alignment (58 sequences including outgroup; 803 aligned positions; 169 unique site patterns; 3 165 000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist *et al*. 2012). Bayesian posterior probabilities (PP) >0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. Families, the order and the class are indicated with coloured blocks to the right of the tree. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Verticillium albo-atrum* (CBS 130340; GenBank NG_066192) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. The scale bar represents the expected changes per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
E.R. Osieck, Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, Netherlands; e-mail: panurus@ziggo.nl

Fungal Planet 1688

MycoBank MB 853808

Thamnochortomyces Crous, ***gen. nov.***

Etymology: Name refers to *Thamnochortus*, the host genus from which it was isolated.

Classification: *Arachnopezizaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, hyphae, forming sporodochia. *Conidiophores* integrated on hyphae, hyaline, smooth, subcylindrical, straight to geniculate-sinuous, branched or not, septate. *Conidiogenous cells* integrated, terminal and intercalary, proliferating sympodially, with flattened scars. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate, septate; with age becoming elongated and swelling, undergoing microcyclic conidiation.

Type species: *Thamnochortomyces kirstenboschensis* Crous

MycoBank MB 853809

Thamnochortomyces kirstenboschensis Crous, ***sp. nov.***

Etymology: Name refers to Kirstenbosch, South Africa, where it was collected.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2.5 µm diam hyphae, forming sporodochia. *Conidiophores* integrated on hyphae, hyaline, smooth, subcylindrical, straight to geniculate-sinuous, branched or not, 0–3-septate, 5–30 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, 5–15 × 2–3 µm, proliferating sympodially, with flattened scars, 1–1.5 µm diam. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, apex obtuse, base truncate, 0–1(–3)-septate, (10–)12–17(–22) × (2–)2.5–3 µm; with age becoming elongated and swelling, undergoing microcyclic conidiation, up to 40 µm long, and 4 µm wide (also depending on culture medium).

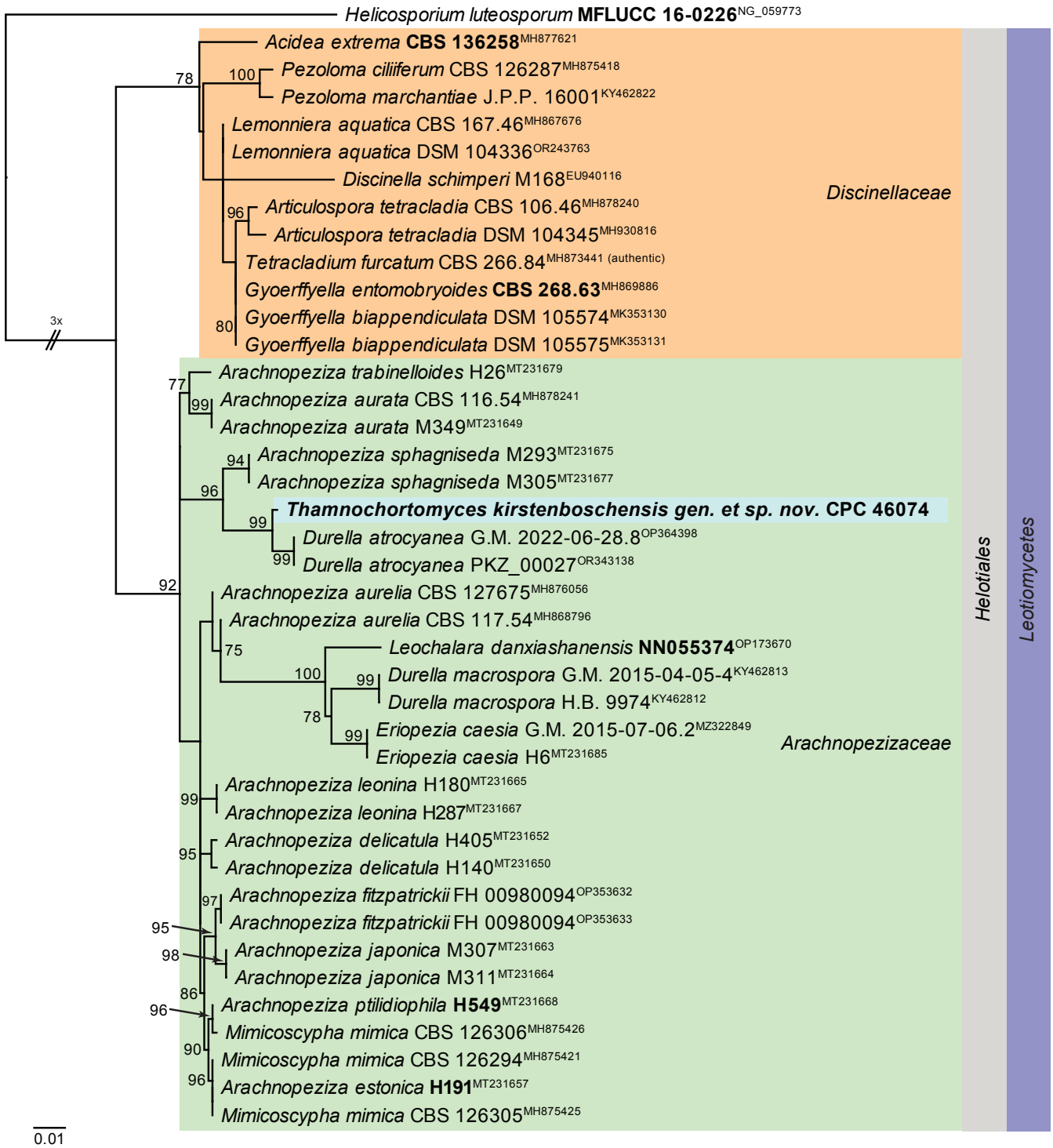
Culture characteristics: Colonies erumpent, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse scarlet to peach.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on culms of *Thamnochortus fraternus* (*Restionaceae*), 13 Apr. 2023, *P.W. Crous*, HPC 4162 (**holotype** CBS H-25338; culture ex-type CPC 46074 = CBS 150885; ITS and LSU sequences GenBank PP791428.1 and PP791456.1).

Notes: *Thamnochortomyces* is a hyphomycetous morph related to the sexual genus *Arachnopeziza* (Kosonen *et al*. 2021), which generally does not sporulate in culture. *Thamnochortomyces* is relatively nondescript, forming sporodochia, and having integrated conidiophores with sympodial blastic conidiogenesis, forming hyaline, subcylindrical, septate conidia. Because this fungus cannot be placed in *Arachnopeziza,* and is introduced here as a new genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Durella atrocyanea* [voucher PKZ_00027, GenBank OR343138.1; Identities = 484/542 (89 %), 16 gaps (2 %)], *Arachnopeziza delicatula* [voucher TNS-F12770, GenBank JN033433.1; Identities = 475/544 (87 %), 17 gaps (3 %)], and *Mimicoscypha mimica* [strain CBS 126306, GenBank MH863971.1; Identities = 474/543 (87 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Arachnopeziza fitzpatrickii* [voucher FH 00980094, GenBank OP353632.1; Identities = 816/838 (97 %), four gaps (0 %)], *Arachnopeziza trabinelloides* [voucher GJO0071771, GenBank MT231679.1; Identities = 781/803 (97 %), two gaps (0 %)], and *Arachnopeziza aurelia* [strain CBS 127675, GenBank MH876056.1; Identities = 814/838 (97 %), four gaps (0 %)].

Colour illustrations: Thamnochortus fraternus in Kirstenbosch, South Africa. Colony on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -2631.407) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Helotiales* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Helicosporium luteosporum* (MFLUCC 16-0226; GenBank NG_059773) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Families, the order and the class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 41 strains including the outgroup; 817 characters including alignment gaps analysed: 182 distinct patterns, 91 parsimony-informative, 61 singleton sites, 665 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1689 MycoBank MB 853810

Acremonium agapanthi Crous, *sp. nov.*

Etymology: Name refers to *Agapanthus,* the host genus from which it was isolated.

Classification: *Bionectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

Mycelium consisting of branched, septate, hyaline, smooth, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells arising from superficial hyphae, flexuous, subcylindrical with slight apical taper, hyaline, smooth, monophialidic, collarettes minute, not flared, 15–35 × 2–2.5 µm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, subcylindrical, straight, apex subobtuse, base truncate, 1 µm diam, (5–)6–7(–13) × 2(–2.5) µm, with age conidia become abnormally long, up to 20 µm, but remain aseptate.

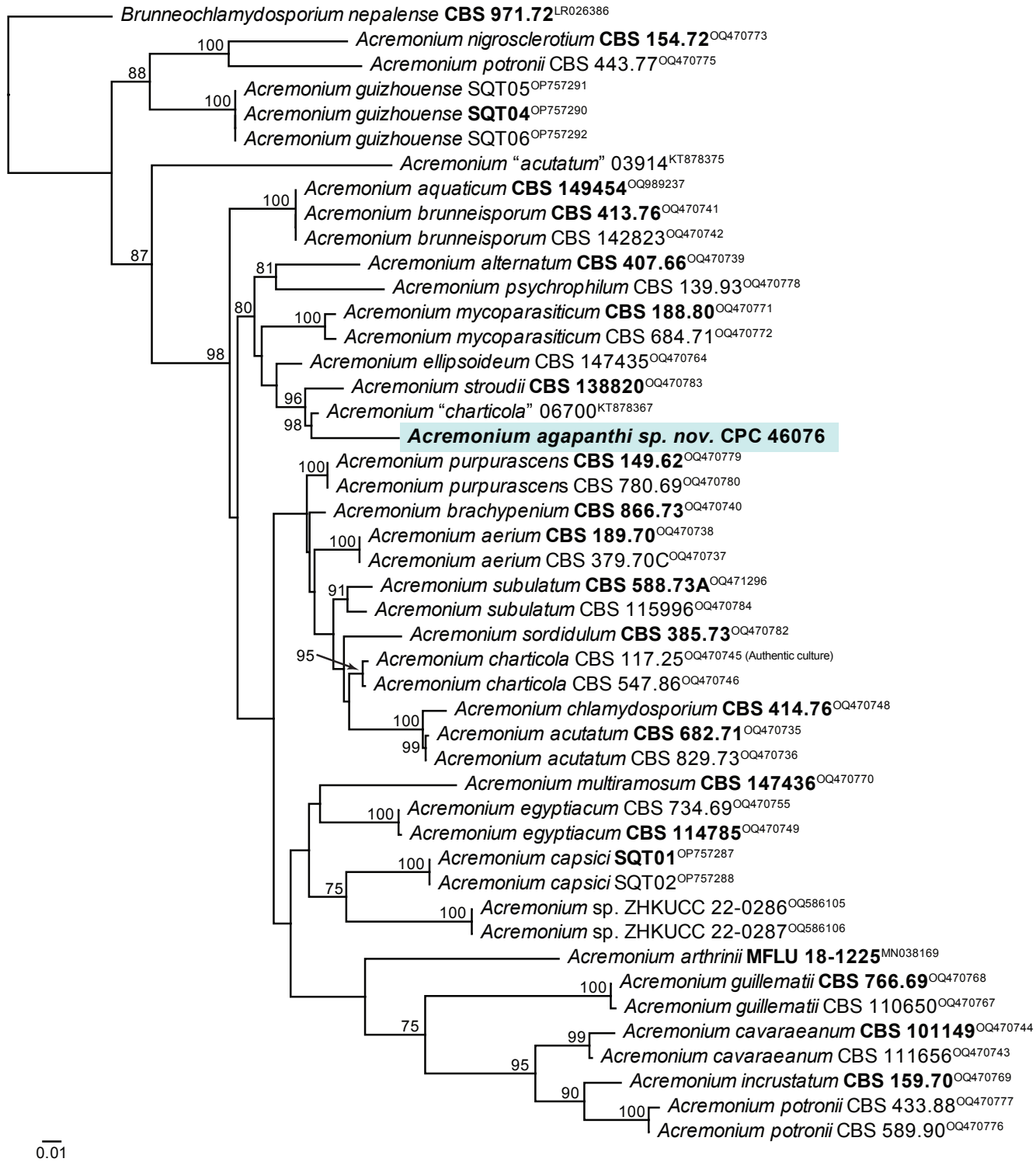
Culture characteristics: Colonies flat, spreading, surface folded with sparse aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface and reverse apricot; on PDA and OA surface and reverse luteous.

Typus: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on culms of *Agapanthus praecox* (*Amaryllidaceae*), 13 Apr. 2023, *P.W. Crous*, HPC 4163 [**holotype** CBS H-25339; culture ex-type CPC 46076 = CBS 150821; ITS, LSU, *actA*, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank PP791429.1, PP791457.1, PP780598.1, PP780612.1, PP780626.1 and PP780635.1]; *ibid*., culture CPC 46098 = CBS 150823; ITS, LSU, *actA*, *rpb2* and *tub2* sequences GenBank PP791430.1, PP791458.1, PP780599.1, PP780613.1 and PP780636.1.

Notes: The polyphyletic nature of *Acremonium* (based on *A. alternatum*) was recently addressed by Hou *et al*. (2023). *Acremonium agapanthi* is a species of *Acremonium s.str*., closely related to *A. alternatum* (conidia 3.1–5.3 × 1.2–2.1 µm; Gams 1971, Summerell *et al.* 2011), from which it is distinct in having larger conidia.

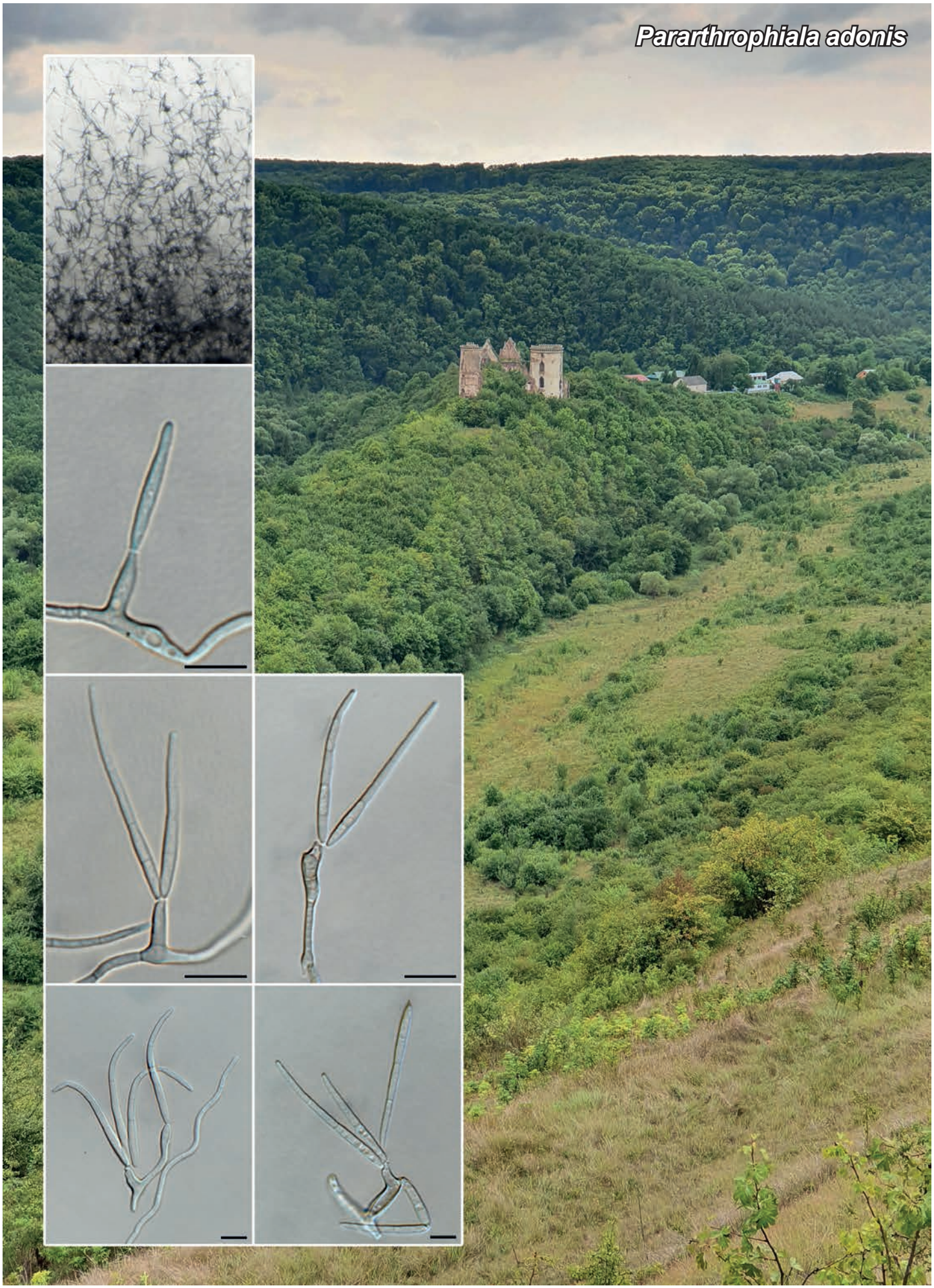
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 46076 had highest similarity to *Acremonium alternatum* [strain CBS 407.66, GenBank OQ429442.1; Identities = 478/499 (96 %), three gaps (0 %)], *Acremonium psychrophilum* [strain CBS 732.92, GenBank MH862386.1; Identities = 533/560 (95 %), eight gaps (1 %)], and *Acremonium alternatum* [strain CBS 407.66, GenBank NR_144913.1; Identities = 496/523 (95 %), five gaps (0 %)]. The ITS sequences of CPC 46076 and CPC 46098 are 100 % identical (539/539). Closest hits using the **LSU** sequence of CPC 46076 are *Acremonium sclerotigenum* [strain CBS 395.70A, GenBank MH871515.1; Identities = 802/808 (99 %), no gaps], *Acremonium alternatum* [strain PAV-M 1.093, GenBank KF993388.1; Identities = 802/808 (99 %), no gaps], and *Acremonium egyptiacum* [strain CBS 114785, GenBank OQ055362.1; Identities = 771/777 (99 %), no gaps]. The LSU sequences of CPC 46076 and CPC 46098 are 100 % identical (788/788). Closest Closest hits using the ***actA*** sequence of CPC 46076 had highest similarity to *Acremonium aquaticum* [strain CBS 149454, GenBank OQ989189.1; Identities = 577/633 (91 %), seven gaps (1 %)], *Tilachlidium brachiatum* [strain CBS 505.67, GenBank KM231249.1; Identities = 562/652 (86 %), 19 gaps (2 %)], and *Hapsidospora chrysogena* [as *Acremonium chrysogenum*; GenBank AF056976.1; Identities = 571/674 (85 %), 36 gaps (5 %)]. The *actA* sequences of CPC 46076 and CPC 46098 are 99 % identical (632/637, no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Acremonium psychrophilum* [strain CBS 139.93, GenBank OQ453875.1; Identities = 673/761 (88 %), four gaps (0 %)], *Acremonium alternatum* [strain CBS 407.66, GenBank OQ560696.1; Identities = 598/674 (89 %), no gaps], and *Acremonium mycoparasiticum* [strain CBS 684.71, GenBank OQ453869.1; Identities = 654/762 (86 %), six gaps (0 %)]. The *rpb2* sequences of CPC 46076 and CPC 46098 are 98 % identical (798/811). Closest hits using the ***tef1*** (second part) sequence of CPC 46076 had highest similarity to *Monocillium* sp. BGE-2018c [strain CBS 240.75, GenBank MG896418.1; Identities = 442/461 (96 %), no gaps], *Acremonium charticola* [strain 06700, GenBank KT878367.1; Identities = 408/426 (96 %), no gaps], and *Acremonium egyptiacum* [as *Monocillium* sp.; strain CBS 391.89, GenBank MG896419.1; Identities = 430/461 (93 %), no gaps]. Closest hits using the ***tub2*** sequence of CPC 46076 had highest similarity to *Acremonium sclerotigenum* [strain W12, GenBank OQ716755.1; Identities = 265/299 (89 %), six gaps (2 %)], *Acremonium* sp.[strain KUC21242, GenBank KT207658.1; Identities = 246/279 (88 %), six gaps (2 %)], and *Acremonium aquaticum* [strain CBS 149454, GenBank OQ989251.1; Identities = 404/479 (84 %), 20 gaps (4 %)]. The *tub2* sequences of CPC 46076 and CPC 46098 are 100 % identical (478/478).

Colour illustrations: Agapanthus praecox in Kirstenbosch, South Africa. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram (score -5699.903) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Acremonium tef1* nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Brunneochlamydosporium nepalense* (CBS 971.72; GenBank LR026386) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 46 strains including the outgroup; 814 characters including alignment gaps analysed: 282 distinct patterns, 230 parsimony-informative, 32 singleton sites, 552 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl



Fungal Planet 1690

MycoBank MB 853811

Pararthrophiala Crous & Akulov, *gen. nov.*

Etymology: Name refers to the related genus *Arthrophiala*.

Classification: *Trichomeriaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of pale olivaceous, smooth, branched, aseptate hyphae. *Conidiophores* erect, arising from superficial hyphae, straight to geniculous-sinuous, unbranched, subcylindrical, medium brown, smooth, septate, proliferating sympodially with several apical, truncate loci. *Conidia* solitary, olivaceous, guttulate, smooth, obclavate, flexuous, apex subobtuse, base obconically truncate, septate; hila unthickened, nor darkened.

Type species: *Pararthrophiala adonis* Crous & Akulov

MycoBank MB 853812

Pararthrophiala adonis Crous & Akulov, *sp. nov.*

Etymology: Name refers to *Adonis*, the host genus from which it was isolated.

Mycelium consisting of pale olivaceous, smooth, branched, aseptate, 1.5–2 µm diam hyphae. *Conidiophores* erect, arising from superficial hyphae, straight to geniculous-sinuous, unbranched, subcylindrical, medium brown, smooth, 0–2-septate, 10–20 × 2–3 µm, proliferating sympodially with several apical, truncate loci, 1–1.5 µm diam. *Conidia* solitary, olivaceous, guttulate, smooth, obclavate, flexuous, apex subobtuse, base obconically truncate, 3(–4)-septate, (25–)30–40(–45) × 2–2.5 µm; hila unthickened, nor darkened, 1.5 µm diam.

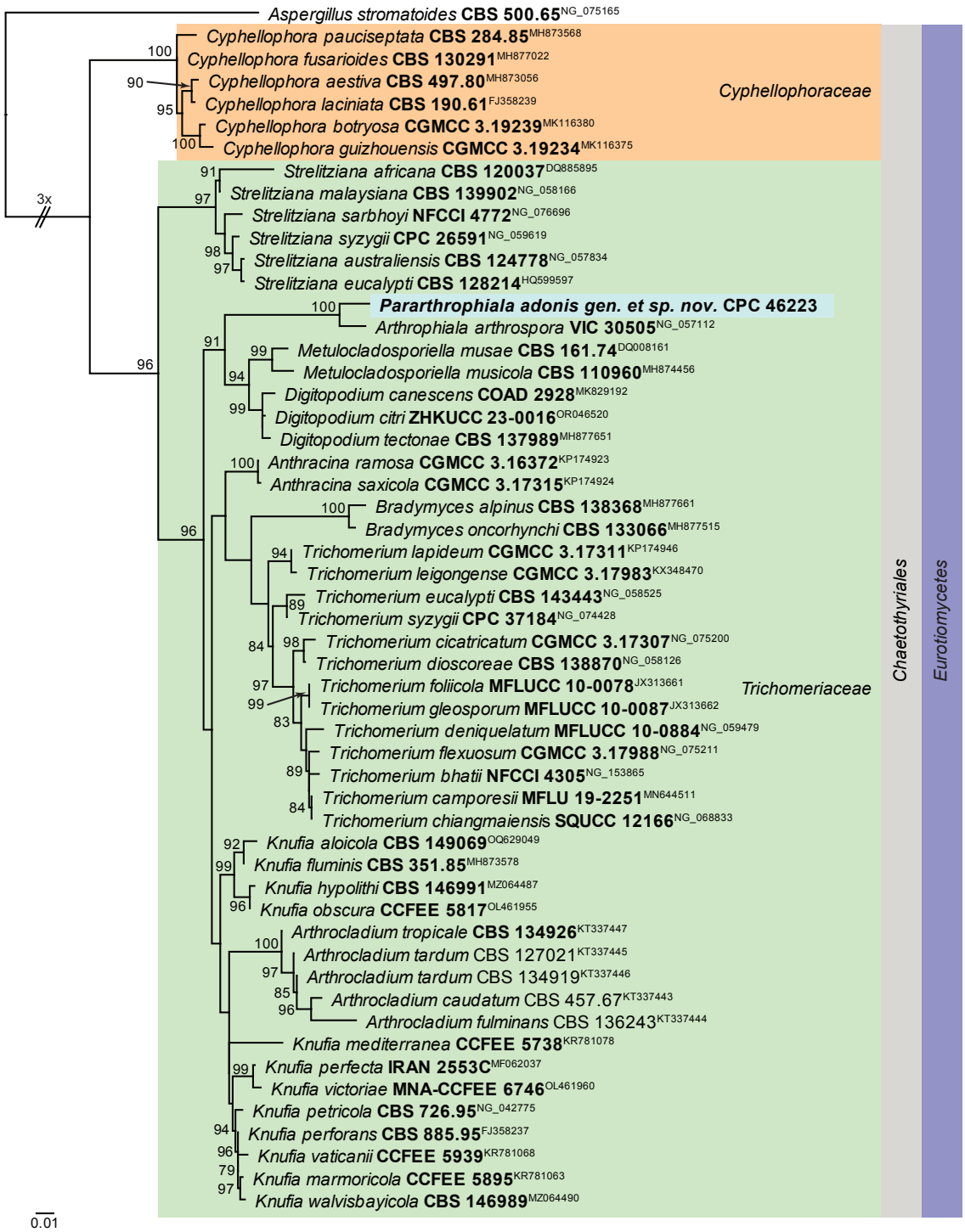
Culture characteristics: Colonies flat, spreading, surface folded, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA and OA surface and reverse ochreous.

Typus: **Ukraine**, Ternopil region, Zalischyky district, National Nature Park, Dniester Canyon, forest near Dzhuryn waterfall, on dead stems of *Adonis vernalis* (*Ranunculaceae*), 16 Apr. 2023, *A. Akulov*, HPC 4188 = CWU (Myc) AS 8636 (**holotype** CBS H-25340; culture ex-type CPC 46223 = CBS 150825; ITS and LSU sequences GenBank PP791431.1 and PP791459.1).

Notes: *Pararthrophiala* somewhat resembles the genus *Arthrophiala* (see Soares *et al.* 2009, Crous *et al.* 2016). *Arthrophiala* is dimorphic, and has a pseudocercospora-like cercosporoid morph, but also has a phialidic morph in culture, producing dimorphic conidia. *Paraarthrophiala* lacks dimorphic conidia and conidial chains.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Strelitziana africana* [strain GX02, GenBank GQ850386.1; Identities = 308/355 (87 %), ten gaps (2 %)], *Neostrelitziana acaciigena* [strain CBS 139903, GenBank NR_137987.1; Identities = 375/439 (85 %), 27 gaps (6 %)], and *Strelitziana eucalypti* [strain AM23, GenBank KM246179.1; Identities = 354/417 (85 %), 21 gaps (5 %)]. Closest hits using the **LSU** sequence are *Arthrophiala arthrospora* [voucher VIC 30505, GenBank NG_057112.1; Identities = 803/822 (98 %), five gaps (0 %)], *Knufia hypolithi* [strain CBS 146991, GenBank NG_076736.1; Identities = 778/823 (95 %), five gaps (0 %)], and *Anthracina saxicola* [strain CGMCC 3.17349, GenBank KP174921.1; Identities = 777/822 (95 %), five gaps (0 %)].

Colour illustrations: Dniester Canyon, forest near Dzhuryn waterfall, Ukraine. Conidiophores on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.



Most likely phylogram (score -4321.993) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Chaetothyriales* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Aspergillus stromatoides* (CBS 500.65; GenBank NG_075165) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Families, the order and the class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 54 strains including the outgroup; 821 characters including alignment gaps analysed: 238 distinct patterns, 156 parsimony-informative, 75 singleton sites, 590 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
A. Akulov, Department of Mycology and Plant Resistance, V. N. Karazin Kharkiv National University, Maidan Svobody 4, 61022 Kharkiv, Ukraine;
e-mail: alex_fungi@yahoo.com

Fungal Planet 1691 and 1692

MycoBank MB 853813

Periconia calamagrostidicola Crous, *sp. nov.*

Etymology: Name refers to *Calamagrostis*, the host genus from which it was isolated.

Classification: *Periconiaceae*, *Massarineae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiophores arising from a weakly developed stroma of brown *textura intricata*, up to 120 µm wide, 20–30 µm deep; conidiophores in clusters of up to 40, in tuft-like clusters, stipe dark brown, thick-walled, roughened, multiseptate, up to 500 µm tall, 7–10 µm diam at base; fertile region after approx. 200 µm (at one or two succeeding cells), consisting of a primary branch, subcylindrical, dark brown, 10–30 × 5–8 µm, giving rise to sub-ellipsoid secondary branches, 10–15 × 8–9 µm, forming ellipsoid conidiogenous cells, dark brown, verruculous, 6–10 × 6–7 µm, mono- to polyblastic, which give rise to short chains of conidia. *Conidia* medium to dark brown, verruculose, globose, thick-walled, (13–)15–16(–17) µm diam; stipe extends above conidiogenous region, forming 1–3 stipe extensions that are mostly curved to curled, tapering to subobtuse apex, dark brown, thick-walled, roughened, multi-septate, approx. 300 µm long, apex 3–4 µm diam; in culture conidia are 12–15 µm diam, but conidiophores rarely develop; forming pale brown. Globose ascomatal initials formed submerged in OA, but remained sterile.

Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface olivaceous grey and reverse umber; on PDA surface and reverse umber; on OA surface smoke grey.

Typus: **Netherlands**, Utrecht Province, Soest, Soester Duinen, on old leaves of *Calamagrostis arenaria* (*Poaceae*), *A. van Iperen*, 23 May 2023, HPC 4201 [**holotype** CBS H-25342; culture ex-type CPC 46238 = CBS 150887; ITS, LSU and *tef1* (first part) sequences GenBank PP791432.1, PP791460.1 and PP780620.1].

Notes: *Periconia calamagrostidicola* resembles species in the *Parapericonia* complex, having punctiform sporodochial conidiomata arising from a stroma, flexuous conidiophores that terminate in sterile setae, being fertile in the mid region, with mono- to polyblastic conidiogenous cells, that give rise to short chains of verruculose, aseptate conidia (Monteiro *et al.* 2017). Phylogenetically, however, the present collection clusters in the genus *Periconia*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periconia neominutissima* (strain ICMP 18731, GenBank PP097814.1; Identities = 502/540 (93 %), nine gaps (1 %)), *Periconia thysanolaenae* (strain KUMCC 20-0262, GenBank NR_176751.1; Identities = 501/540 (93 %), eight gaps (0 %)), and *Periconia macrospinosa* (strain BRPET25, GenBank MT658103.1; Identities = 503/542 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Periconia philadelphiana* (strain CPC 42854, GenBank OQ629068.1; Identities = 814/829 (98 %), one gap (0 %)), *Sporidesmium tengii* (strain HKUCC 10837, GenBank DQ408559.1; Identities = 824/842 (98 %), two gaps (0 %)), and *Periconia banksiae* (strain CBS 129526, GenBank NG_064279.1; Identities = 823/842 (98 %), one gap (0 %)). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Septoriella hollandica* (strain CBS 145374, GenBank MK540160.1; Identities = 441/496 (89 %), nine gaps (1 %)), *Jeremyomyces labinae* (strain CBS 144617, GenBank MK442695.1; Identities = 404/504 (80 %), 23 gaps (4 %)), and *Diederichomyces cladoniicola* (strain CBS 128026, GenBank KP170668.1; Identities = 398/505 (79 %), 31 gaps (6 %)).

MycoBank MB 853814

Cytosporella calamagrostidis Crous, *sp. nov.*

Etymology: Name refers to *Calamagrostis*, the host genus from which it was isolated.

Classification: *Gomphillaceae*, *Ostropales*, *Lecanoromycetes*.

Conidiomata solitary to aggregated, globose, 250–350 µm diam, acervular, hyaline, giving rise to a mucoid conidial mass. *Conidiophores* lining the basal layer, hyaline, smooth, branched or not, at times reduced to conidiogenous cells, subcylindrical, 1–3-septate, 5–15 × 2.5–3.5 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical, terminal and intercalary, phialidic with percurrent proliferation, 5–7 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid with obtuse ends, (5–)6–7 × 2–2.5 µm.

Culture characteristics: Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse saffron; on PDA surface and reverse pale luteous; on OA surface saffron.

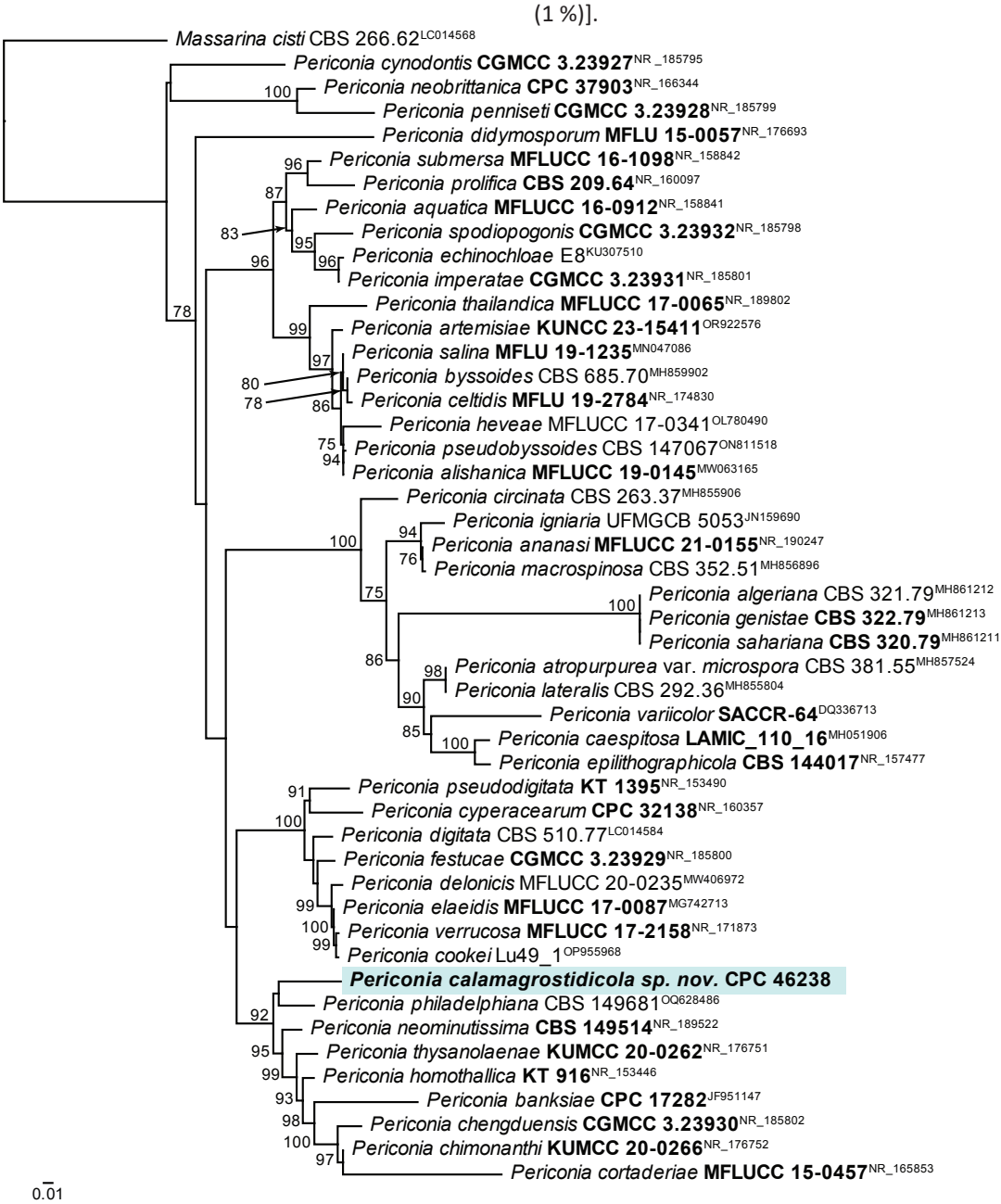
Typus: **Netherlands**, Utrecht Province, Soest, Soester Duinen, on old leaves of *Calamagrostis arenaria* (*Poaceae*), *A. van Iperen*, 23 May 2023, HPC 4201 (**holotype** CBS H-25341; culture ex-type CPC 46236 = CBS 150826; ITS, LSU and *rpb1* sequences GenBank PP791433.1, PP791461.1 and PP780607.1).

Notes: Although the taxonomy of *Cytosporella* is still unresolved (Sutton 1980), the present collection is tentatively

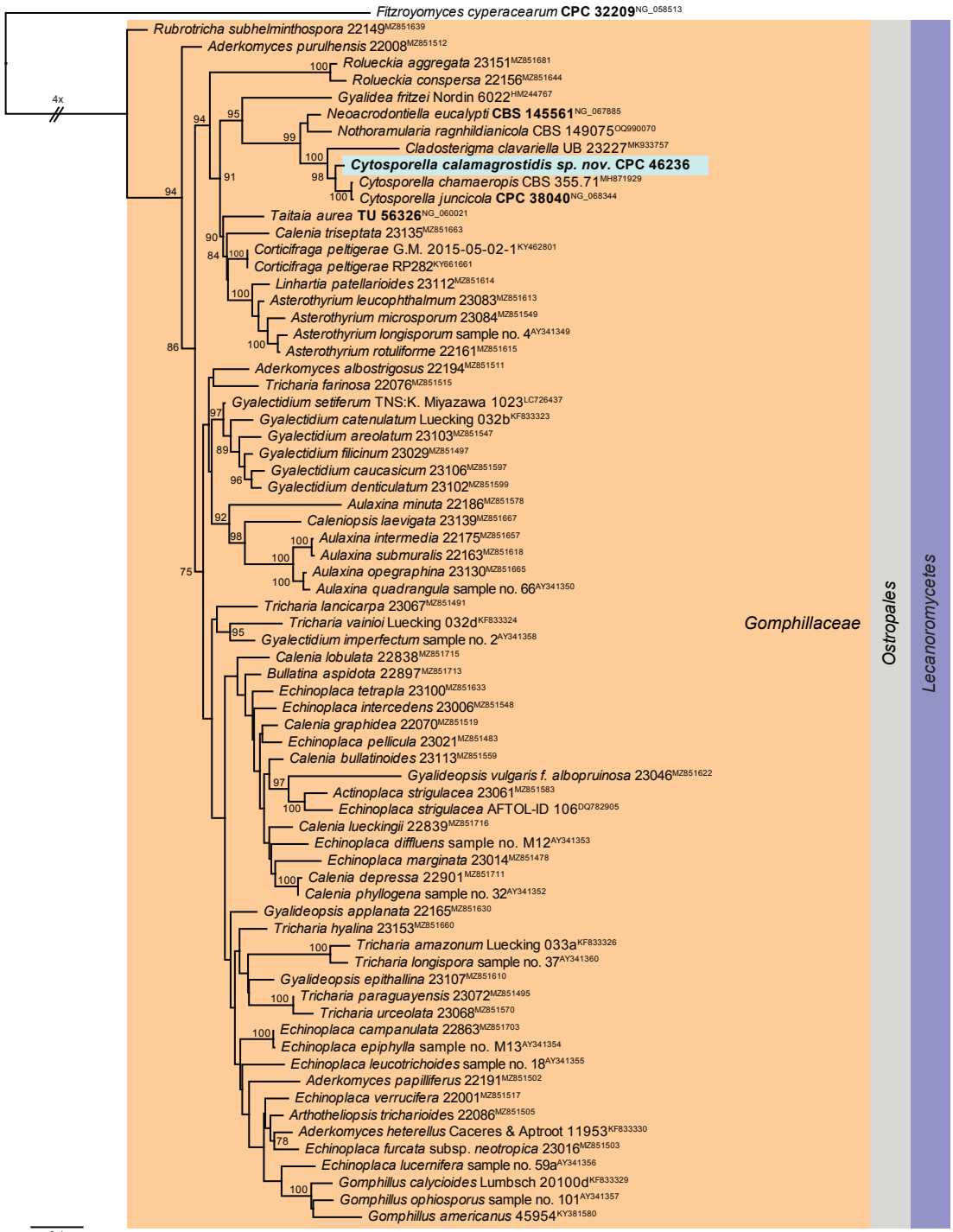
Colour illustrations: Soester Duinen, the Netherlands. Right column (*Periconia calamagrostidicola*). Fasciculate conidiophores with setae in vivo. conidiophores and conidiogenous cells giving rise to conidia; conidia. Left column (*Cytosporella calamagrostidis*). Conidioma on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: conidioma (right column) = 250 µm, all others = 10 µm.

accommodated in this genus, also being related to species such as *C. juncicola* (Crous *et al.* 2019c) and *C. chamaeropis* (Crous *et al.* 2020).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cytosporella juncicola* [strain CPC 38040, GenBank NR_166348.1; Identities = 563/665 (85 %), 52 gaps (7 %)], *Corticifraga ramalinae* [voucher Pinault (holotype MARSSJ), GenBank ON569808.1; Identities = 502/582 (86 %), 46 gaps (7 %)], and *Neoacrodontiella eucalypti* [strain CBS 145561, GenBank NR_165567.1; Identities = 455/538 (85 %), 33 gaps (6 %)]. Closest hits using the **LSU** sequence are *Acarospora thamnina* [voucher DS8352, GenBank KF024746.1; Identities = 519/534 (97 %), one gap (0 %)], *Cytosporella juncicola* [strain CPC 38040, GenBank NG_068344.1; Identities = 824/853 (97 %), four gaps (0 %)], and *Cytosporella chamaeropis* [strain CBS 355.71, GenBank MH871929.1; Identities = 822/851 (97 %), four gaps (0 %)]. Closest hits using the ***rpb1*** sequence had distant similarity to *Aderkomyces heterellus* [voucher Caceres & Aptroot 11953, GenBank KF833353.1; Identities = 528/698 (76 %), 17 gaps (2 %)], *Echinoplaca epiphylla* [voucher ECHEPI1977, GenBank KC020295.1; Identities = 448/587 (76 %), six gaps (1 %)], and *Calenia monospora* [voucher Luecking 032h, GenBank KF833350.1; Identities = 431/567 (76 %), seven gaps (1 %)].



Most likely phylogram (score -4919.290) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Periconia* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Massarina cisti* (CBS 266.62; GenBank LC014568) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 48 strains including the outgroup; 593 characters including alignment gaps analysed: 313 distinct patterns, 197 parsimony-informative, 60 singleton sites, 336 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).



Most likely phylogram (score -9237.169) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Ostropales* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Fitzroyomyces cyperacearum* (CPC 32209; GenBank NG_058513) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. The family, order and class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 72 strains including the outgroup; 613 characters including alignment gaps analysed: 351 distinct patterns, 247 parsimony-informative, 53 singleton sites, 312 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: GTR+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1693

MycoBank MB 853815

Zenophaeosphaeria Crous & Osieck, *gen. nov.*

Etymology: Name refers to its morphological similarity to *Phaeosphaeria*.

Classification: *Sympoventuriaceae*, *Venturiales*, *Pleosporomycetidae*, *Dothideomycetes*.

Ascomata immersed to erumpent, perithecial, globose, papillate, brown; wall of 3–4 layers of brown *textura angularis*, with central ostiole. *Pseudoparaphyses* hyaline, septate, branched, anastomosing, hyphae-like. *Asci* bitunicate, 8-spored, hyaline, straight to slightly curved, narrowly fusoid-ellipsoid, with prominent apical chamber, stipitate. *Ascospores* multiseriate, fusoid-ellipsoid, pale brown, constricted at median septum, 3-septate, thick-walled, finely verruculose, surrounded with mucilaginous sheath, with large guttule per cell.

Type species: *Zenophaeosphaeria calamagrostidis* Crous & Osieck

MycoBank MB 853816

Zenophaeosphaeria calamagrostidis Crous & Osieck, *sp. nov.*

Etymology: Name refers to *Calamagrostis*, the host genus from which it was isolated.

Ascomata (*in vivo*) immersed to erumpent, perithecial, globose, papillate, brown, 60–90 µm diam; wall of 3–4 layers of brown *textura angularis*, with central ostiole, 20–25 µm diam. *Pseudoparaphyses* hyaline, septate, branched, anastomosing, hyphae-like, 2–3 µm diam. *Asci* bitunicate, 8-spored, hyaline, straight to slightly curved, narrowly fusoid-ellipsoid, with prominent apical chamber, short stipitate, 40–50 × 8–11 µm. *Ascospores* multiseriate, fusoid-ellipsoid, pale brown, constricted at median septum, with cell above isodiametric and slightly swollen, 3-septate, thick-walled, finely verruculose, surrounded with mucilaginous sheath, with large guttule per cell, (14–)15(–16) × (4.5–)5(–6) µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse dark mouse grey.

Typus: **Netherlands**, North Holland Province, Texel, De Koog, dunes, N53°04'29'', E04°43'55'', on culms of *Calamagrostis arenaria* (*Poaceae*), 25 Apr. 2023, *E.R. Osieck*, HPC 4179 = WI-86, coll. 4676 [**holotype** CBS H-25360; culture ex-type CPC 46090 = CBS 150822; ITS, LSU, *actA*, *rpb2* and *tef1* (first part) sequences GenBank PP791434.1, PP791462.1, PP780600.1, PP780614.1 and PP780621.1].

Colour illustrations: White dunes with *Calamagrostis arenaria*, Texel, the Netherlands. Ascoma *in vivo*; asci, ascospores and pseudoparaphyses; germinating ascospores. Scale bars: ascoma = 100 µm, all others = 10 µm.

Notes: *Zenophaeosphaeria* resembles the genus *Phaeosphaeria* in having immersed, papillate ascomata, pseudoparaphyses, bitunicate asci, and pigmented ascospores with a sheath, but is phylogenetically distinct. The spores are small compared to most *Phaeosphaeria* species (with spores mostly longer than 18 µm). Only *Phaeosphaeria lutea* (confined to *Luzula*) has similar spores (Leuchtmann 1984). Of the species occurring on *Calamagrostis* (= *Ammophila*), it needs to be compared with *P. marram*, which has larger 3-septate ascospores 25–33 × 7–8 µm (Shoemaker & Babcock 1989). Phylogenetically, however, *Zenophaeosphaeria* is related to several asexual genera in the *Sympoventuriaceae* (Wei *et al.* 2022b).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had distant similarity to *Fuscohilum siciliana* [strain CBS 105.85, GenBank NR_168753.1; Identities = 385/468 (82 %), 44 gaps (9 %)], *Ochroconis musae* [strain NBRC 113466, GenBank LC414360.1; Identities = 357/442 (81 %), 29 gaps (6 %)], and *Ochroconis mirabilis* [strain UM 578, GenBank KP639587.1; Identities = 357/442 (81 %), 29 gaps (6 %)]. Closest hits using the **LSU** sequence are *Pinaceicola cordae* [strain CBS 675.82, GenBank MH873281.1; Identities = 829/855 (97 %), five gaps (0 %)], *Pinaceicola pini* [strain CBS 463.82, GenBank MH873264.1; Identities = 822/854 (96 %), four gaps (0 %)], and *Fusicladium ramoconidii* [strain CBS 462.82, GenBank EU035439.1; Identities = 822/854 (96 %), four gaps (0 %)]. No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches. Closest hits using the ***rpb2*** sequence had highest similarity to *Sterila eucalypti* [strain CPC 14943, GenBank MK887806.1; Identities = 530/638 (83 %), three gaps (0 %)], *Ochroconis anomala* [strain Lx CH40, GenBank HE575205.1; Identities = 578/715 (81 %), two gaps (0 %)], and *Yunnanomyces phoenicis* [strain MFLUCC 19-0254, GenBank MK986484.1; Identities = 575/715 (80 %), two gaps (0 %)]. Closest hits using the ***tef1*** (first part) sequence had distant similarity to the coding regions of *Scolecobasidium variabile* [strain NBRC 32268, GenBank DQ307356.1; Identities = 166/181 (92 %), four gaps (2 %)], *Scolecobasidium cateniphorum* [strain NBRC 30449, GenBank DQ307353.1; Identities = 161/175 (92 %), no gaps], and *Scolecobasidium acanthi* [strain LC19368, GenBank OQ442215.1; Identities = 162/176 (92 %), two gaps (1 %)].

Most likely phylogram (score -8188.399) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Venturiales* LSU nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Diaporthe perjuncta* (BPI 748437; GenBank NG_059064) and the novelty described here is highlighted with a coloured block and **bold** font. Some branches were shortened to facilitate layout. Families, orders and the class are shown to the right of the tree in coloured blocks. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 80 strains including the outgroup; 799 characters including alignment gaps analysed: 370 distinct patterns, 285 parsimony-informative, 70 singleton sites, 444 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
E.R. Osieck, Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, Netherlands; e-mail: panurus@ziggo.nl

Fungal Planet 1694 MycoBank MB 853817

Wingfieldomyces cypericola Crous, *sp. nov.*

Etymology: Name refers to *Cyperus*, the host genus from which it was isolated.

Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Ascomata pseudothecial, globose, 250–300 µm diam, brown, erumpent, aggregated; wall of 3–6 layers of brown *textura angularis. Pseudoparaphyses* intermingled among asci, hyaline, septate, hyphae-like, 2.5–4 µm diam. *Asci* 8-spored, subcylindrical to fusoid-ellipsoid, bitunicate, stipitate, in clusters, ocular chamber 1.5–2 µm diam, 55–75 × 10–12 µm. *Ascospores* multiseriate, medium brown, guttulate, granular, smooth, 2-septate, becoming slightly constricted at septa, wider in median cell, with obtuse ends, (8–)20–22(–23) × 4.5–5 µm.

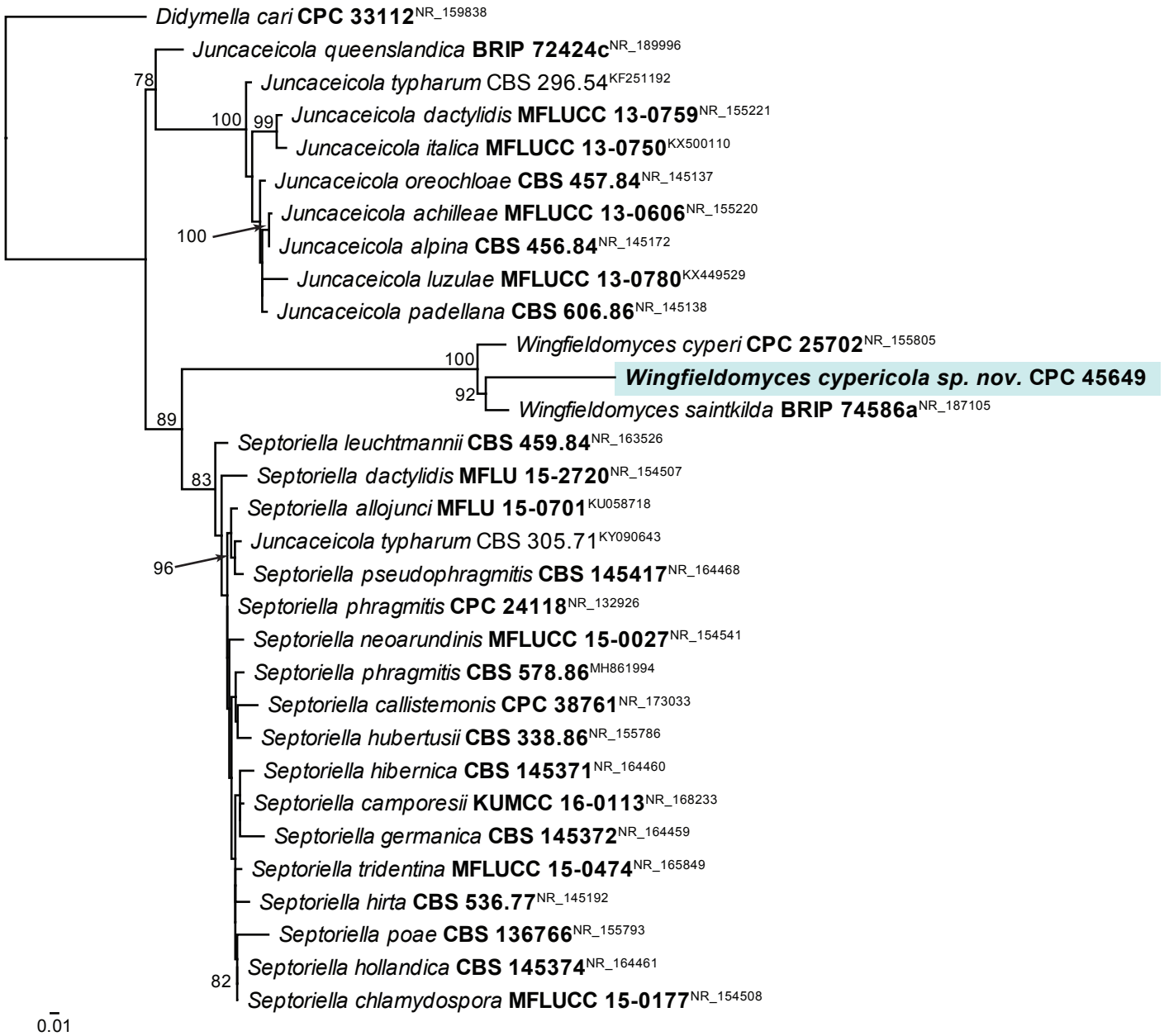
Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface pale luteous and reverse luteous; on PDA surface and reverse pale luteous; on OA surface pale luteous.

Typus: **South Africa**, Western Cape Province, Stellenbosch Botanical Garden, on dead leaves of *Cyperus papyrus* (*Cyperaceae*), 4 Mar. 2023, *P.W. Crous*, HPC 4117 (**holotype** CBS H-25317; culture ex-type CPC 45649 = CBS 150800; ITS, LSU and *tub2* sequences GenBank PP791435.1, PP791463.1 and PP780637.1).

Notes: *Wingfieldomyces* [based on *W. cyperi* on *Cyperus sphaerocephala*, ascospores (26–)27–29(–31) × (3.5–)4(–4.5) µm] is similar to *W. cyperi*, but has smaller ascospores. Both species occur on *Cyperus* in South Africa, whereas *W. saintkilda* occurs on an unidentified plant in Australia, and is only known from DNA data (Thompson *et al.* 2023).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Wingfieldomyces cyperi* [strain CPC 25702, GenBank NR_155805.1; Identities = 426/450 (95 %), three gaps (0 %)], *Wingfieldomyces saintkilda* [strain BRIP 74586a, GenBank NR_187105.1; Identities = 584/643 (91 %), 19 gaps (2 %)], and *Phaeosphaeria caricicola* [strain SG-G9, GenBank OR701700.1; Identities = 413/458 (90 %), 9 gaps (1 %)]. Closest hits using the **LSU** sequence are *Wingfieldomyces cyperi* [strain CPC 25702, GenBank NG_059684.1; Identities = 840/842 (99 %), no gaps], *Wingfieldomyces saintkilda* [strain BRIP 74586a, GenBank OQ892172.1; Identities = 864/867 (99 %), no gaps], and *Parastagonospora avenae f. sp. tritici* [as *Phaeosphaeria avenaria f. sp. triticae*; strain ATCC 26370, GenBank EF590323.2; Identities = 857/876 (98 %), two gaps (0 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Wingfieldomyces cyperi* [strain CBS 141450, GenBank MK540178.1; Identities = 436/467 (93 %), two gaps (0 %)], *Paraphoma melnikii* [voucher MF-9.182.1, GenBank MG779454.1; Identities = 386/456 (85 %), 25 gaps (5 %)], and *Paraloratospora schoenoplecti* [strain CPC 43149, GenBank OQ627960.1; Identities = 386/458 (84 %), 22 gaps (4 %)].

Colour illustrations: Cyperus papyrus in Stellenbosch Botanical Garden, South Africa. Ascomata on oatmeal agar; asci and ascospores. Scale bars: ascomata = 300 µm, all others = 10 µm.



Most likely phylogram (score -2931.630) obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Wingfieldomyces* ITS nucleotide alignment. Bootstrap support values from 5 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 74 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Didymella cari* (CPC 33112; GenBank NR_159838) and the novelty described here is highlighted with a coloured block and **bold** font. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 31 strains including the outgroup; 560 characters including alignment gaps analysed: 242 distinct patterns, 145 parsimony-informative, 63 singleton sites, 352 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TPM2+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl

Fungal Planet 1695 MycoBank MB 853818

Neptunomyces juncicola Crous & Osieck, *sp. nov.*

Etymology: Name refers to *Juncus*, the host genus from which it was isolated.

Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

Conidiomata pycnidial, erumpent, globose, 180–220 µm diam, brown, ostiolate; wall of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining cavity, hyaline, smooth, ampulliform, phialidic, 3–5 × 4–5 µm. *Conidia* solitary, subcylindrical to fusoid-ellipsoid, aseptate, apex subobtuse, hilum truncate, golden brown, smooth, 7–8 × 2–2.5 µm. *Ascomata* (*in vivo*) pseudothecial, immersed to erumpent, brown, subglobose, papillate, 80–150 µm diam, neck up to 100 µm tall; wall of 3–4 layers of brown *textura angularis. Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, branched, anastomosing, 3–4 µm diam, hyphae-like. *Asci* bitunicate, 8-spored, fusoid-ellipsoid, short stipitate, with visible ocular chamber, 2 µm diam, 75–90 × 16–18 µm. *Ascospores* tri- to multiseriate, fusoid-ellipsoid, ends subobtuse, 5–7 transverse septa, 2–4 oblique or vertical septa, constricted at median septum, with cell above slightly swollen, thick-walled, prominently verruculose, enclosed in wide mucoid sheath, straight to lightly curved, golden brown, (28–)30–32(–35) × 7–8 µm.

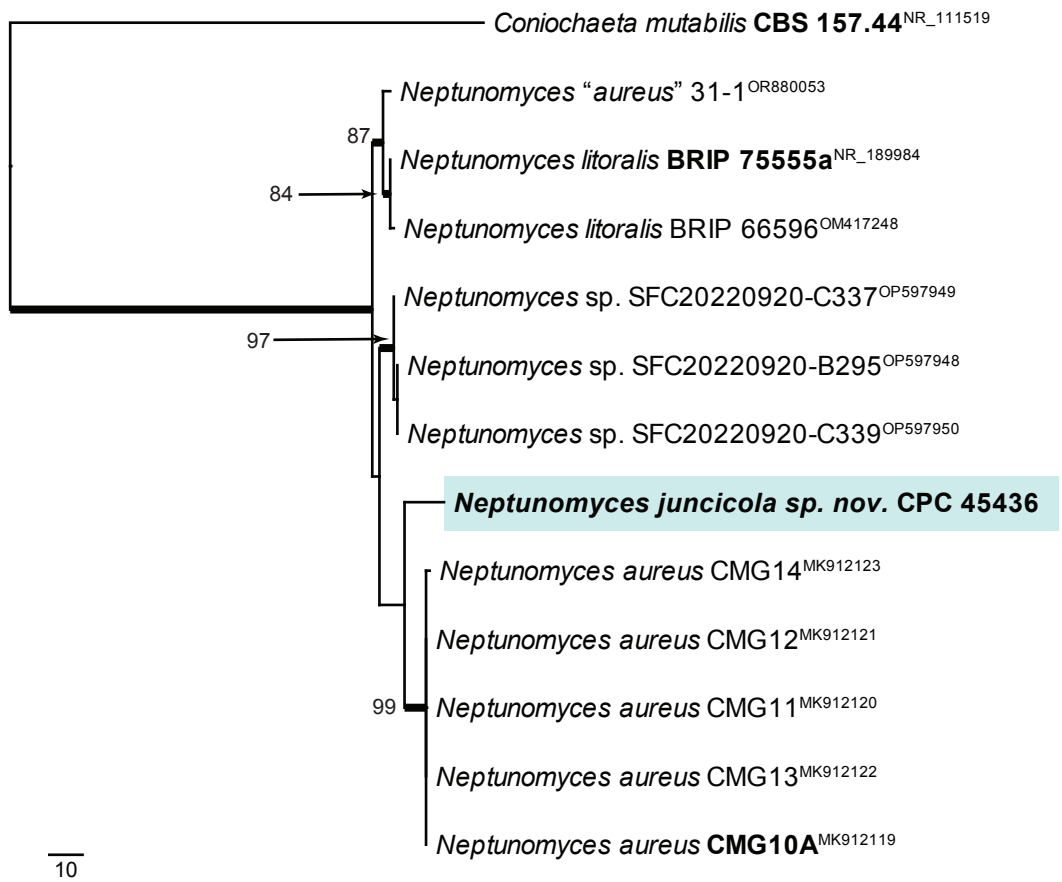
Culture characteristics: Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface pale luteous and reverse luteous; on PDA surface and reverse bay; on OA surface pale luteous.

Typus: **Netherlands**, North Holland Province, Texel, De Cocksdorp, De Slufter, N53°07'48'', E04°48'28'', on culms of *Juncus maritimus* (*Juncaceae*), 6 Dec. 2022, *E.R. Osieck*, HPC 4099 = WI-72, coll. 4596 [**holotype** CBS H-25307; culture ex-type CPC 45436 = CBS 150790; ITS, LSU, *tef1* (second part) and *tub2* sequences GenBank PP791436.1, PP791464.1, PP780627.1 and PP780638.1].

Notes: *Neptunomyces* (based on *N. aureus*) was established for a fungus isolated from macroalgae (*Gracilaria gracilis*) in Portugal, with conidia being subcylindrical, golden-yellow, 7 × 2.7 µm (Gonçalves *et al.* 2019). A second species, *N. litoralis*, was described from beach sand in Australia, but lacks any morphological description (Tan & Shivas 2023). *Neptunomyces juncicola* also has cylindrical, golden brown conidia (7–8 × 2–2.5 µm) as described for *N. aureus,* and reports the first sexual morph for the genus. The three presently known species are phylogenetically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neptunomyces litoralis* [voucher BRIP 75555a, GenBank NR_189984.1; Identities = 630/645 (98 %), nine gaps (1 %)], *Neptunomyces aureus* [strain 31-1, GenBank OR880053.1; Identities = 508/521 (98 %), seven gaps (1 %)], and *Phialemonium inflatum* [strain PCA5P, GenBank KY305083.1; Identities = 627/646 (97 %), seven gaps (1 %)]. Closest hits using the **LSU** sequence are *Neptunomyces* sp. [strain BRIP 66596, GenBank OM333561.1; Identities = 856/864 (99 %), no gaps], *Neptunomyces litoralis* [strain BRIP 75555a, GenBank NG_242141.1; Identities = 874/883 (99 %), one gap (0 %)], and *Kalmusia variispora* [strain HF2S31, GenBank OP179207.1; Identities = 871/884 (99 %), two gaps (0 %)]. Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Neptunomyces aureus* [strain CMG14, GenBank MK948002.1; Identities = 852/879 (97 %), one gap (0 %)], *Paraphaeosphaeria hydei* [strain LC12564, GenBank MK336062.1; Identities = 837/873 (96 %), no gaps (0 %)], and *Austropleospora keteleeriae* [strain MFLUCC 18-1551, GenBank MK360045.1; Identities = 835/879 (95 %), one gap (0 %)]. Closest hits using the ***tub2*** sequence had highest similarity to *Neptunomyces aureus* [strain CMG14, GenBank MK934134.1; Identities = 504/552 (91 %), seven gaps (1 %)], *Microsphaeropsis arundinis* [strain BEOFB3200m, GenBank MH791362.1; Identities = 306/345 (89 %), eight gaps (2 %)], and *Paraconiothyrium cyclothyrioides* [strain UTHSC DI16-268, GenBank LT796942.1; Identities = 243/309 (79 %), 14 gaps (4 %)].

Colour illustrations: Saltmarsh of De Slufter, Texel, the Netherlands. Conidioma on oatmeal agar; conidiogenous cells giving rise to conidia; conidia; immersed ascomata on *Juncus* sheath; section through ascoma; ascomatal neck; asci; ascospores. Scale bars: conidioma = 200 µm; ascomata = 150 µm, all others = 10 µm.



The first of six equally most parsimonious trees obtained from a maximum parsimony phylogenetic analysis (Swofford 2003) of the *Neptunomyces* ITS nucleotide alignment. The tree was rooted to *Coniochaeta mutabilis* (CBS 157.44; GenBank NR_111519) and the scale bar indicates the number of changes. Parsimony bootstrap support values from 1 000 replicates and > 79 % are shown at the nodes and the novelty described here is highlighted with a coloured block and **bold** font. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. Branches present in the strict consensus tree are thickened. Alignment statistics: 13 strains including the outgroup; 542 characters including alignment gaps analysed: 294 constant, 225 variable and parsimony-uninformative and 23 parsimony-informative. Tree statistics: Tree Length = 273, Consistency Index = 0.967, Retention Index = 0.885, Rescaled Consistency Index = 0.855. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
E.R. Osieck, Jkvr. C.M. van Asch van Wijcklaan 19, 3972 ST Driebergen-Rijsenburg, Netherlands; e-mail: panurus@ziggo.nl

Fungal Planet 1696 MycoBank MB 853819

Microdochium buffelskloofinum Crous & M.M. Costa, *sp. nov.*

Etymology: Name refers to the Buffelskloof Nature Reserve, South Africa, where it was collected.

Classification: *Amphisphaeriaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*.

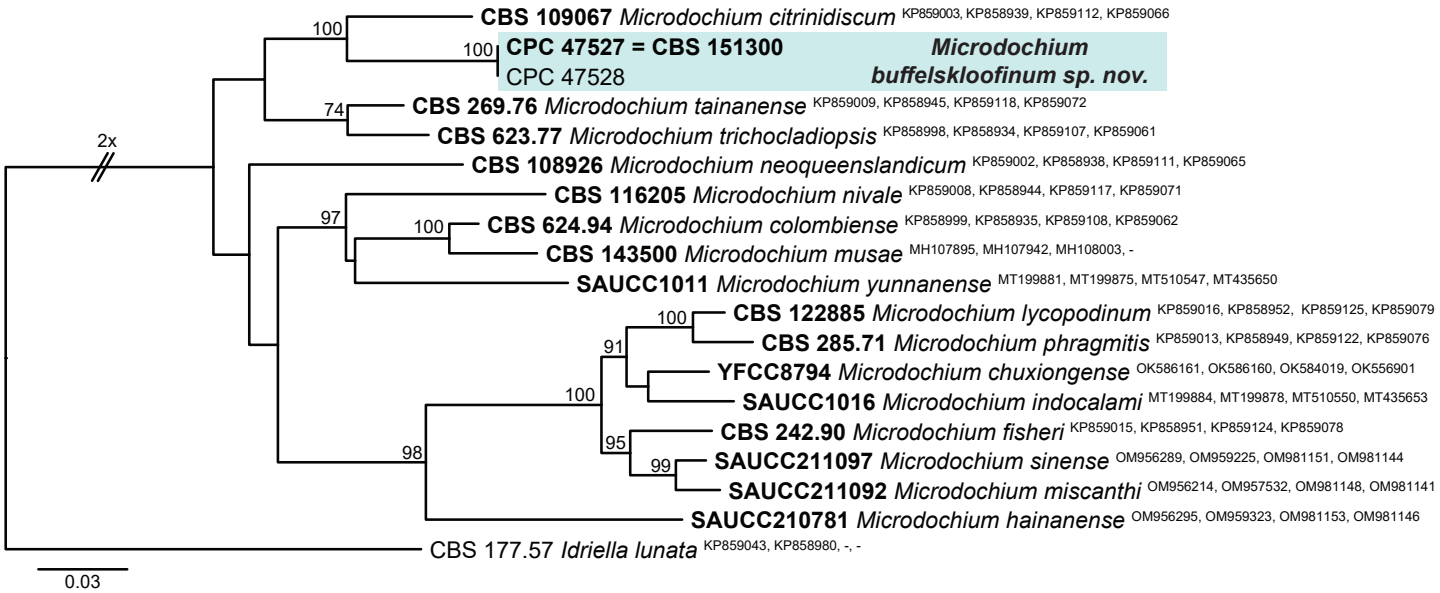
Conidiomata sporodochial, superficial, globose, up to 250 µm diam, giving rise to an orange conidial mass. *Conidiophores* arising from submerged hyphae, hyaline, smooth, branched, septate, up to 50 µm tall, 2–3 µm diam, with apical cells giving rise to 1–3 conidiogenous cells. *Conidiogenous cells* terminal and intercalary, subulate to subcylindrical, straight to curved, sympodial, polyblastic, 10–15 × 1.5–2 µm. *Conidia* solitary, hyaline, smooth, guttulate, flexuous to curved, multiseptate, subcylindrical, apex subobtuse, basal cell tapering to a truncate hilum, 1 µm diam, (95–)110–130(–150) × 2 µm.

Culture characteristics: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse orange; on OA surface orange.

Typus: **South Africa**, Mpumalanga Province, Buffelskloof Nature Reserve, on seeds of *Eragrostis cf. racemosa*, 5 Aug. 2022, *P.W. Crous*, HPC 3993 (**holotype** CBS H-25358; culture ex-type SA1SD = CPC 47527 = CBS 151300; ITS, LSU, *rpb2* and *tub2* sequences GenBank PP791437.1, PP791465.1, PP780615.1 and PP780639.1); *ibid*., culture CPC 47528; ITS, LSU, *rpb2* and *tub2* sequences GenBank PP791438.1, PP791466.1, PP780616.1 and PP780640.1.

Notes: *Microdochium* includes important plant pathogens, particularly on grasses and cereals. Although *Microdochium* species were formerly regarded to be fusarioid fungi, their sporodochia do not give rise to phialidic conidiogenous cells as in *Fusarium*, their conidia have a truncate hilum rather than a basal foot-cell, and sexual morphs reside in *Monographella*, not *Gibberella* (Hernández-Restrepo *et al.* 2016, Crous *et al*. 2021b). Phylogenetically *M. buffelskloofinum* represents a distinct lineage, which is morphologically characterised by its long, flexuous, multiseptate conidia.

Colour illustrations: Poaceae in Buffelskloof Nature Reserve, South Africa. Conidiomata on oatmeal agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 250 µm, all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.1.3 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020) of the *Microdochium* ITS, LSU, *RPB2* and *TUB* nucleotide alignment. Bootstrap support values from 10 000 ultrafast bootstrap replicates (Hoang *et al.* 2018) are shown at the nodes (> 73 % are shown; only values > 94 % are significant). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. The tree was rooted to *Idriella lunata* (CBS 177.57) and the novelties described here are highlighted with coloured blocks and **bold** font. The root branch was shortened to facilitate layout. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 19 strains including the outgroup; 2 965 characters including alignment gaps analysed: 694 distinct patterns, 519 parsimony-informative, 152 singleton sites, 2 295 constant sites. The best-fit model identified in IQ-TREE using the ModelFinder option was for ITS and *RPB2*: K2P+I+G4, LSU: K2P+I, and *TUB*: TN+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.25406335).

P.W. Crous, M.M. Costa & J.Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands;
e-mail: p.crous@wi.knaw.nl, m.costa@wi.knaw.nl & e.groenewald@wi.knaw.nl

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