Persoonia 45, 2020: 251 – 409
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3767/persoonia.2020.45.10

Fungal Planet description sheets: 1112 – 1181

P.W. Crous[1,2], D.A. Cowan[3], G. Maggs-Kölling[4], N. Yilmaz[2], E. Larsson[5], C. Angelini[6], T.E. Brandrud[7], J.D.W. Dearnaley[8], B. Dima[9], F. Dovana[10], N. Fechner[11], D. García[12], J. Gené[12], R.E. Halling[13], J. Houbraken[1], P. Leonard[14], J.J. Luangsa-ard[15], W. Noisripoom[15], A.E. Rea-Ireland[16], H. Ševčíková[17], C.W. Smyth[18], A. Vizzini[10], J.D. Adam[19], G.C. Adams[20], A.V. Alexandrova[21,22], A. Alizadeh[23], E. Álvarez Duarte[24], V. Andjic[25], V. Antonín[17], F. Arenas[26], R. Assabgui[27], J. Ballarà[28], A. Banwell[29], A. Berraf-Tebbal[30], V.K. Bhatt[31], G. Bonito[32], W. Botha[33], T.I. Burgess[34], M. Caboň[35], J. Calvert[36], L.C. Carvalhais[36], R. Courtecuisse[37], P. Cullington[38], N. Davoodian[39], C.A. Decock[40], R. Dimitrov[41], S. Di Piazza[42], A. Drenth[36], S. Dumez[37], A. Eichmeier[30], J. Etayo[43], I. Fernández[44], J.-P. Fiard[45], J. Fournier[46], S. Fuentes-Aponte[47], M.A.T. Ghanbary[48], G. Ghorbani[49], A. Giraldo[50], A.M. Glushakova[21,51], D.E. Gouliamova[41], J. Guarro[12], F. Halleen[52], F. Hampe[53], M. Hernández-Restrepo[1], I. Iturrieta-González[12], M. Jeppson[5], A.V. Kachalkin[21,54], O. Karimi[48], A.N. Khalid[55], A. Khonsanit[15,56], J.I. Kim[57], K. Kim[47], M. Kiran[55], I. Krisai-Greilhuber[58], V. Kučera[35], I. Kušan[59], S.D. Langenhoven[60], T. Lebel[61], R. Lebeuf[62], K. Liimatainen[63], C. Linde[64], D.L. Lindner[65], L. Lombard[1], A.E. Mahamedi[66], N. Matočec[59], A. Maxwell[25], T.W. May[67], A.R. McTaggart[36], M. Meijer[1], A. Mešić[59], A.J. Mileto[19], A.N. Miller[68], A. Molia[69], S. Mongkolsamrit[15], C. Muñoz Cortés[24], J. Muñoz-Mohedano[26], A. Morte[26], O.V. Morozova[70], L. Mostert[60], R. Mostowfizadeh-Ghalamfarsa[71], L.G. Nagy[72], A. Navarro-Ródenas[26], L. Örstadius[73], B.E. Overton[19], V. Papp[74], R. Para[75], U. Peintner[76], T.H.G. Pham[22], A. Pordel[77], A. Pošta[59], A. Rodríguez[26], M. Romberg[47], M. Sandoval-Denis[1], K.A. Seifert[27,78], K.C. Semwal[79], B.J. Sewall[80], R.G. Shivas[36], M. Slovák[35,81], K. Smith[25], M. Spetik[30], C.F.J. Spies[82], K. Syme[83], K. Tasanathai[15,56], R.G. Thorn[29], Z. Tkalčec[59], M.A. Tomashevskaya[54], D. Torres-Garcia[12], Z. Ullah[55], C.M. Visagie[2], A. Voitk[84], L.M. Winton[85], 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**, *Austroboletus asper* on soil, *Cylindromonium alloxyli* on leaves of *Alloxylon pinnatum, Davidhawksworthia quintiniae* on leaves of *Quintinia sieberi, Exophiala prostantherae* on leaves of *Prostanthera* sp., *Lactifluus lactiglaucus* on soil, *Linteromyces quintiniae* (incl. *Linteromyces* gen. nov.) on leaves of *Quintinia sieberi*, *Lophotrichus medusoides* from stem tissue of *Citrus garrawayi*, *Mycena pulchra* on soil, *Neocalonectria tristaniopsidis* (incl. *Neocalonectria* gen. nov.) and *Xyladictyochaeta tristaniopsidis* on leaves of *Tristaniopsis collina, Parasarocladium tasmanniae* on leaves of *Tasmannia insipida*, *Phytophthora aquae-cooljarloo* from pond water, *Serendipita whamiae as* endophyte from roots of *Eriochilus cucullatus*, *Veloboletus limbatus* (incl. *Veloboletus* gen. nov.) on soil. **Austria**, *Cortinarius glaucoelotus* on soil. **Bulgaria**, *Suhomyces rilaensis* from the gut of *Bolitophagus interruptus* found on a *Polyporus* sp. **Canada**, *Cantharellus betularum* among leaf litter of *Betula*, *Penicillium saanichii* from house dust. **Chile**, *Circinella lampensis* on soil, *Exophiala embothrii* from rhizosphere of *Embothrium coccineum.* **China**, *Colletotrichum cycadis* on leaves of *Cycas revoluta.* **Croatia**, *Phialocephala melitaea* on fallen branch of *Pinus halepensis.* **Czech Republic**, *Geoglossum jirinae* on soil, *Pyrenochaetopsis rajhradensis* from dead wood of *Buxus sempervirens.* **Dominican Republic**, *Amanita domingensis* on litter of deciduous wood, *Melanoleuca dominicana* on forest litter. **France**, *Crinipellis nigrolamellata* (Martinique) on leaves of *Pisonia fragrans*, *Talaromyces pulveris* from bore dust of *Xestobium rufovillosum* infesting floorboards. **French Guiana**, *Hypoxylon hepaticolor* on dead corticated branch. **Great Britain**, *Inocybe ionolepis* on soil. **India**, *Cortinarius indopurpurascens* among leaf litter of *Quercus leucotrichophora.* **Iran**, *Pseudopyricularia javanii* on infected leaves of *Cyperus* sp., *Xenomonodictys iranica* (incl. *Xenomonodictys* gen. nov.) on wood of *Fagus orientalis.* **Italy**, *Penicillium valleboromidaense* from compost. **Namibia**, *Alternaria mirabibensis* on plant litter, *Curvularia moringae* and *Moringomyces phantasmae* (incl. *Moringomyces* gen. nov.) on leaves and flowers of *Moringa ovalifolia, Gobabebomyces vachelliae* (incl. *Gobabebomyces* gen. nov.) on leaves of *Vachellia erioloba, Preussia procaviae* on dung of *Procavia capensis.* **Pakistan**, *Russula shawarensis* from soil on forest floor. **Russia**, *Cyberlindnera dauci* from *Daucus carota*. **South Africa**, *Acremonium behniae* on leaves of *Behnia reticulata, Dothiora aloidendri* and *Hantamomyces aloidendri* (incl. *Hantamomyces* gen. nov.) on leaves of *Aloidendron dichotomum*, *Endoconidioma euphorbiae* on leaves of *Euphorbia mauritanica*, *Eucasphaeria proteae* on leaves of *Protea neriifolia*, *Exophiala mali* from inner fruit tissue of *Malus* sp., *Graminopassalora geissorhizae* on leaves of *Geissorhiza splendidissima*, *Neocamarosporium leipoldtiae* on leaves of *Leipoldtia schultzii*,

Abstract (cont.)

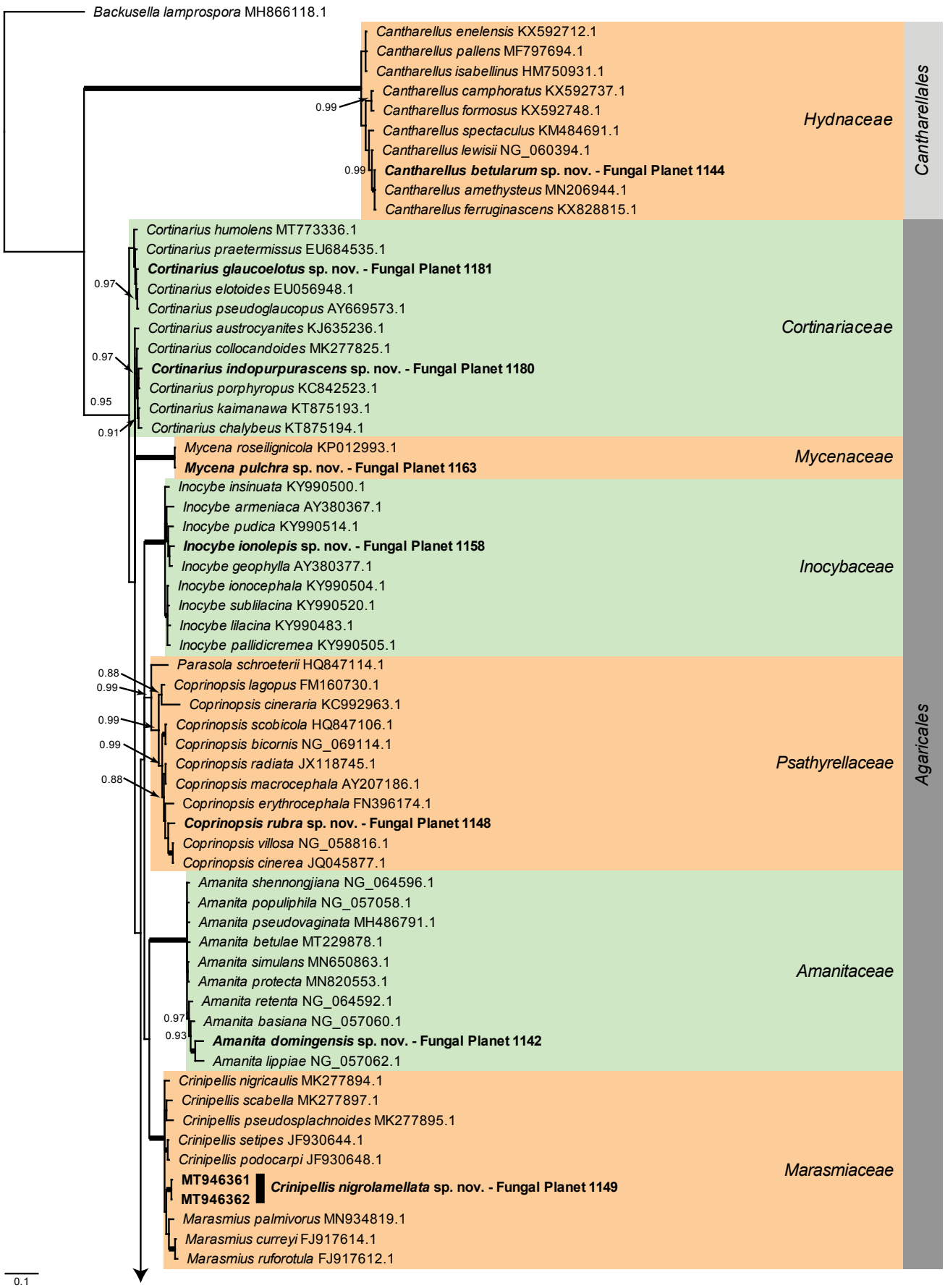
Neocladosporium osteospermi on leaf spots of *Osteospermum moniliferum*, *Neometulocladosporiella seifertii* on leaves of *Combretum caffrum*, *Paramyrothecium pituitipietianum* on stems of *Grielum humifusum*, *Phytopythium paucipapillatum* from roots of *Vitis* sp., *Stemphylium carpobroti* and *Verrucocladosporium carpobroti* on leaves of *Carpobrotus quadrifolius*, *Suttonomyces cephalophylli* on leaves of *Cephalophyllum pilansii*. **Sweden**, *Coprinopsis rubra* on cow dung, *Elaphomyces nemoreus* from deciduous woodlands. **Spain**, *Polyscytalum pini-canariensis* on needles of *Pinus canariensis*, *Pseudosubramaniomyces septatus* from stream sediment, *Tuber lusitanicum* on soil under *Quercus suber*. **Thailand**, *Tolypocladium flavonigrum* on *Elaphomyces* sp. **USA**, *Chaetothyrina spondiadis* on fruits of *Spondias mombin, Gymnascella minnisii* from bat guano, *Juncomyces patwiniorum* on culms of *Juncus effusus*, *Moelleriella puertoricoensis* on scale insect, *Neodothiora populina* (incl. *Neodothiora* gen. nov.) on stem cankers of *Populus tremuloides*, *Pseudogymnoascus palmeri* from cave sediment. **Vietnam**, *Cyphellophora vietnamensis* on leaf litter, *Tylopilus subotsuensis* on soil in montane evergreen broadleaf forest. Morphological and culture characteristics are supported by DNA barcodes.

Article info Received: 15 September 2020; Accepted: 1 October 2020; Published: 19 December 2020.

[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] Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa.
[4] Gobabeb-Namib Research Institute, P.O. Box 953, Walvis Bay, Namibia.
[5] Biological and Environmental Sciences, and Gothenburg Global Biodiversity Centre, University of Gothenburg, P.O. Box 461, SE-40530 Göteborg, Sweden.
[6] Herbario Jardín Botánico Nacional Dr. Rafael Ma. Moscoso, Santo Domingo, Dominican Republic and Via Cappuccini, 78/8 – 33170 Pordenone, Italy.
[7] Norwegian Institute for Nature Research, Gaustadalléen 21, NO-0349 Oslo, Norway.
[8] Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia.
[9] Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary.
[10] Department of Life Sciences and Systems Biology, University of Torino, Viale P.A. Mattioli 25, I-10125 Torino, Italy.
[11] Queensland Herbarium, Mt Coot-tha Road, Toowong, Brisbane, Queensland 4066, Australia.
[12] Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain.
[13] Inst. Systematic Botany, New York Botanical Garden, 2900 Southern Blvd, Bronx, NY, 10458-5126 USA.
[14] P.O. Box 1193, Buderim 4556 Queensland, Australia.
[15] National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand.
[16] University of Tennessee, Knoxville. Knoxville, TN, 37996 USA.
[17] Department of Botany, Moravian Museum, Zelný trh 6, 659 37 Brno, Czech Republic.
[18] Binghamton University, Binghamton, NY, 13902 USA.
[19] 205 East Campus Science Center, Lock Haven University, Lock Haven, PA 17745 USA.
[20] Department of Plant Pathology, 406D Plant Science Hall, 1875 N. 38th street, University of Nebraska, Lincoln, NE, USA.
[21] Lomonosov Moscow State University (MSU), 119234, Leninskie Gory Str. 1/12, Moscow, Russia.
[22] Joint Russian-Vietnamese Tropical Research and Technological Center, Hanoi, Vietnam.
[23] Department of Plant Protection, Faculty of Agriculture, Azarbaijan Shahid madani University, Tabriz, Iran.
[24] Mycology Unit, Microbiology and Mycology Program, Institute of Biomedical Sciences, University of Chile, Santiago, Chile.
[25] Department of Agriculture, Water and Environment, 24 Fricker Rd., Perth, 6105 Western Australia, Australia.
[26] Departamento de Biología Vegetal (Botánica), Facultad de Biología, Universidad de Murcia, 30100 Murcia, Spain.
[27] Biodiversity (Mycology), Agriculture and Agri-Food Canada, Ottawa, ON K1A0C6, Canada.
[28] C/ Tossalet de les Forques, 44, E-08600, Berga, Catalonia, Spain.
[29] Department of Biology, University of Western Ontario, London, Ontario, N6A 5B7, Canada.
[30] MENDELEUM – Institute of Genetics, Mendel University in Brno, Valticka 334, Lednice, 69144, Czech Republic.
[31] Navdanya, 105, Rajpur Road, Dehradun, Uttarakhand, India.
[32] Department of Plant Soil and Microbial Sciences, 1066 Bogue Street, Michigan State University, East Lansing MI, 48824 USA.
[33] ARC Plant Health and Protection, Private Bag X134, Queenswood, Pretoria, 0121, South Africa.
[34] Phytophthora Science and Management, Centre for Climate Impacted Terrestrial Ecosystems, Harry Butler Institute, Murdoch University, Murdoch, WA 6150, Australia.
[35] Institute of Botany, Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Dúbravská cesta 9, SK-84523, Bratislava, Slovakia.
[36] Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Ecosciences Precinct, Level 2C East, GPO Box 267, Brisbane 4001, Queensland, Australia.
[37] ULR 4515 - LGCgE (Laboratoire de Génie Civil et géo-Environnement), ER4 (Fonctionnement des écosystèmes terrestres anthropisés) - LSVF (Laboratoire des sciences végétales et fongiques), Faculté des sciences pharmaceutiques, Université de Lille, 3, rue du Professeur Laguesse, F-59006 Lille Cedex.
[38] The Beeches, Pleck Lane, Kingston Blount, Oxfordshire, OX39 4RU, UK.
[39] National Herbarium of Victoria, Royal Botanic Gardens Victoria, South Yarra, Victoria 3141, Australia.
[40] Mycothèque de l'Université catholique de Louvain (MUCL, BCCMTM), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium.
[41] The Stephan Angeloff Institute of Microbiology, Bulgarian Academy of Sciences, 26 Acad. Georgi Bonchev, Sofia 1113, Bulgaria.
[42] University of Genoa, Department of Earth, Environmental and Life Science, Laboratory of Mycology, Corso Europa 26, 16132 Genoa, Italy.
[43] Department of Biology, IES Zizur, Ronda S. Cristóbal 196,31180 Zizur Mayor, Navarra, Spain.
[44] Myotis-Chile, Duble Almeyda 2010, Ñuñoa, Santiago, Chile.
[45] 3/524, résidence les Cyclades, Rue R. Garcin, F-97200 Fort-de-France.
[46] Las Muros, 09420 Rimont, France.
[47] USDA APHIS PPQ NIS, 10300, Baltimore Avenue, Beltsville, MD 20705, USA.
[48] Department of Plant Protection, Faculty of Agronomy, Sari Agricultural Sciences and Natural Resources University, Sari, Iran.
[49] Department of Plant Protection, College of Agriculture and Natural Resources, University of Tehran, Karaj 31587-77871, Iran.
[50] Radboud University Medical Centre, Geert Grooteplein Zuid 10, 6525 GA Nijmegen, The Netherlands.
[51] Mechnikov Research Institute for Vaccines and Sera, 105064, Moscow, Maly Kazenny by-street, 5A, Russia.
[52] Plant Protection Division, ARC Infruitec-Nietvoorbij, Private Bag X5026, Stellenbosch, 7599, South Africa.
[53] Wetzlarer Strasse 1, 35510 Butzbach, Germany.
[54] All-Russian Collection of Microorganisms, G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, Pushchino, pr. Nauki 5, Russia.
[55] Department of Botany, University of the Punjab, Quaid-e-Azam campus, Lahore 5090, Pakistan.
[56] Plant Microbe Interaction Research Team, Bioscience and Biotechnology for Agriculture, BIOTEC, 113 Thailand Science Park, Pathum Thani 12120, Thailand.
[57] Faculty of Computer Science, Dalhousie University, Halifax, Nova Scotia, B3H 4R2, Canada.
[58] Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Wien, Austria.
[59] Ruđer Bošković Institute, Bijenička cesta 54, HR-10000 Zagreb, Croatia.
[60] Department of Pant Pathology, University of Stellenbosch, Private Bag X1, Matieland, 7602, South Africa.
[61] Botanic Gardens & State Herbarium, Adelaide, South Australia, Australia.
[62] 775, Rang du Rapide Nord, Saint-Casimir, Québec, G0A 3L0, Canada.

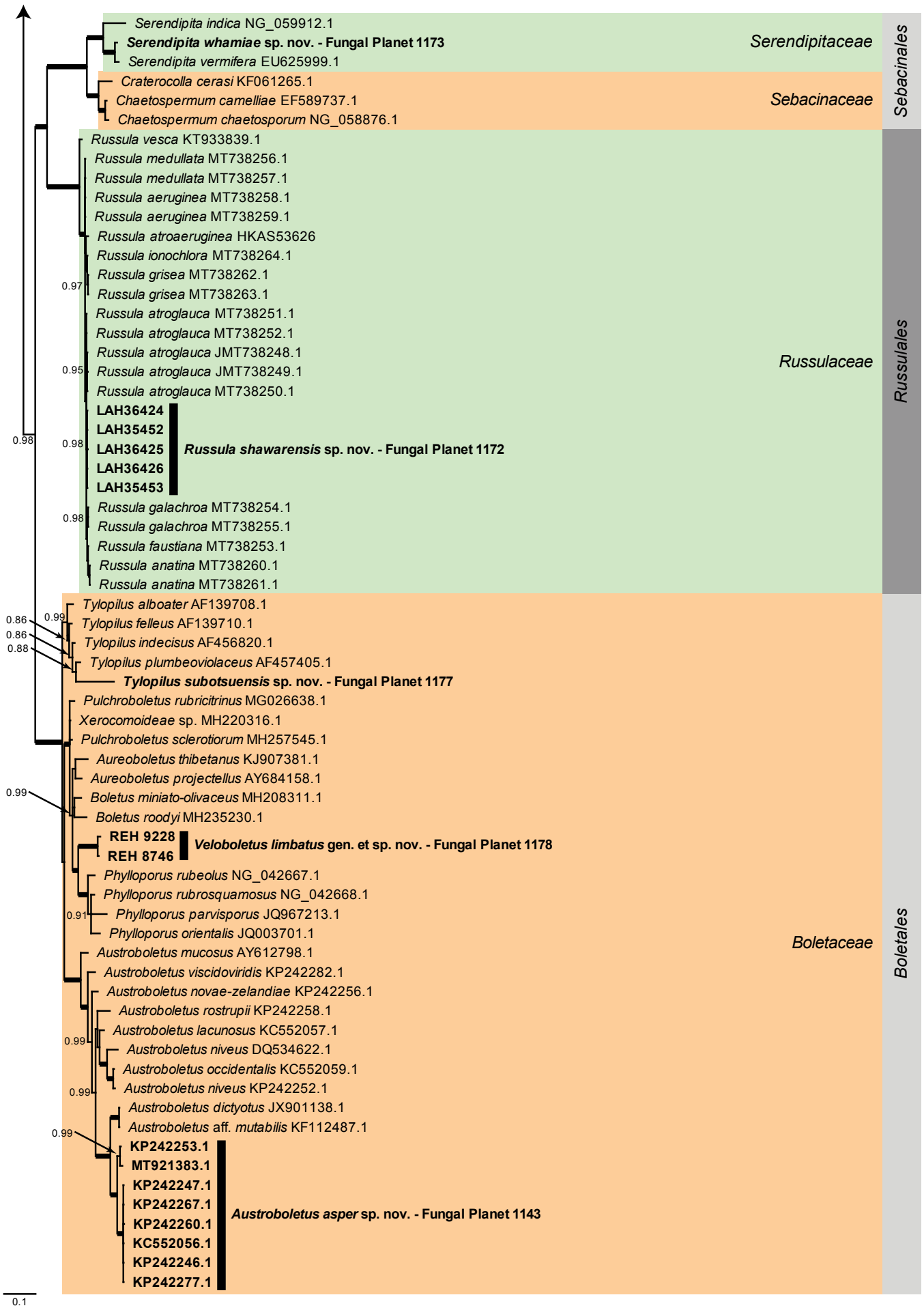
[63] Jodrell Laboratory, Royal Botanic Gardens, Kew, Surrey TW9 3AB, UK.
[64] Ecology and Evolution, Research School of Biology, College of Science, The Australian National University, Canberra, ACT, 2601, Australia.
[65] One Gifford Pinchot Drive Madison, WI, 53726 USA.
[66] Laboratoire de Biologie des Systèmes Microbiens (LBSM), Département des Sciences Naturelles, Ecole Normale Supérieure de Kouba, Alger BP 92, Vieux-Kouba, Alger, Algeria.
[67] Royal Botanic Gardens Victoria, Birdwood Ave, Melbourne, VIC 3004, Australia.
[68] University of Illinois Urbana-Champaign, Illinois Natural History Survey, 1816 South Oak Street, Champaign, Illinois, 61820, USA.
[69] Alette Iversens gate 5, N-3970 Langesund, Norway.
[70] Komarov Botanical Institute of the Russian Academy of Sciences, 197376, 2 Prof. Popov Str., Saint Petersburg, Russia.
[71] Department of Plant Protection, Shiraz University, Shiraz, Iran
[72] Institute of Biochemistry, Biological Research Center, Temesvari krt 62, H-6726 Szeged, Hungary.
[73] Lyckans väg 39A, S-29143 Kristianstad, Sweden.
[74] Institute of Horticultural Plant Biology, Szent István University, H-1518, Budapest, Hungary.
[75] Via Martiri di Via Fani 22, I-61024, Mombaroccio (PU), Italy
[76] Institute of Microbiology, University of Innsbruck, Technikerstrasse 25, 6020 Innsbruck, Austria.
[77] Plant Protection Research Department, Baluchestan Agricultural and Natural Resources Research and Education Centre, AREEO, Iranshahr, Iran.
[78] Department of Biology, Carleton University, 1125 Colonel By Drive, Ottawa, ON K1S 5B6, Canada.
[79] Department of Biology, College of Sciences, Eritrea Institute of Technology, Mai Nafhi, Asmara, Eritrea.
[80] Department of Biology, Temple University, 1900 N. 12th Street, Philadelphia, PA, 19122 USA.
[81] Department of Botany, Charles University, Benátská 2, 128 01 Praha, Czech Republic.
[82] ARC Plant Health and Protection, Private Bag X5017, Stellenbosch, 7599, South Africa.
[83] National Herbarium of Victoria, Royal Botanic Gardens Victoria, South Yarra, Victoria 3141, Australia.
[84] 13 Maple St, Humber Village, Newfoundland and Labrador, A2H 2N2, Canada.
[85] U.S.D.A. Forest Service, Forest Health Protection, 3700 Airport Way, Fairbanks, AK 99709, USA.

Acknowledgements Pedro Crous acknowledges Brett A. Summerell (Royal Botanic Gardens, Sydney, Australia) and Michael J. Wingfield (FABI, University of Pretoria, South Africa), for making several site photographs and field collections available for study. Jan Dijksterhuis is thanked for SEM photomicrographs of *Neocalonectria tristaniopsis*. Katrina Syme and co-authors thank the curation staff at BRI, MEL, PERTH for their help with loans and processing of collections. Funding for fieldwork and sequencing was provided by the Helen McLellan Fund (RBG Victoria). A. Vizzini thanks R. Berndt (Curator of Fungus Collections, Herbaria Z+ZT) for the loan of specimens. The 2015 collecting trips to Martinique directed by R. Courtecuisse were made possible through financial help from Communauté Territoriale de Martinique, Parc Naturel Régional de Martinique (PNRM) and French national Forestry Office (ONF). The study of Aleksey V. Kachalkin and colleagues was supported by the Russian Science Foundation (grant No. 19-74-10002). Isabel Iturrieta-González and colleagues were partially supported by the Spanish Ministerio de Economía, Industria y Competitividad (grant CGL2017-88094-P). Financial support was provided by the VEGA grant agency (project 2/0061/19) to Viktor Kučera and Marek Slovák. The studies of V. Antonín and H. Ševčíková were enabled by support provided to the Moravian Museum by the Ministry of Culture of the Czech Republic as part of its long-term conceptual development programme for research institutions (MK000094862). Abigail E. Rea-Ireland and colleagues acknowledge the National Fish & Wildlife Foundation, the Pennsylvania Game Commission, Greg Turner for material support on project, Lock Haven University, Temple University, Joseph Calabrese, Jacob Adam, Collin Wesley, Alden Mileto, and Alina Pislar, as well as Karen Hughes for allowing Abigail Rea-Ireland to finish this undergraduate research while starting graduate studies at the University of Tennessee, Knoxville. Jacques Fournier gratefully acknowledges the Parc Naturel Amazonien de Guyane for having initiated, funded and organized the field work in Saül in 2018 and 2019, in the context of the ABC inventory project during which the new species *Hypoxylon hepaticolor* was collected. Jed Calvert acknowledges support from the Maxim Foundation for travel, collection and help in the discovery of this taxon. The research of Cobus M. Visagie, Rafik Assabgui & Keith A. Seifert was supported by a grant from the Alfred P. Sloan Foundation Program (grant 2014-06-03) on the Microbiology of the Built Environment. Neven Matočec, Ivana Kušan, Ana Pošta, Zdenko Tkalčec, and Armin Mešić are grateful to the Croatian Science Foundation for their financial support under the project grant HRZZ-IP-2018-01-1736 (ForFungiDNA) and to Miro Pucar for his assistance during the fieldwork. Ana Pošta thanks Croatian Science Foundation for their support under the grant HRZZ-2018-09-7081. Shaun D. Langenhoven and colleagues are grateful to the South African Table Grape Industry, Winetech, the National Research Foundation (grant number: 99916) and Technology and Human Resources for Industry Programme (THRIP) for funding. The grant holders acknowledge that opinions, findings and conclusions or recommendations expressed in any publication generated by the NRF-supported research are that of the authors, and that the NRF accepts no liability whatsoever in this regard. The authors would like to thank Meagan van Dyk for help in formatting the article. This study of Daniel Torres-Garcia, Josepa Gené and Dania García was partially supported by the Spanish Ministerio de Economía, Industria y Competitividad (grant CGL2017-88094-P). Kanoksri Tasanathai and colleagues would like to thank Morakot Tanticharoen and Somvong Tragoonrung, Platform Technology Management Section, National Center for Genetic Engineering and Biotechnology (BIOTEC), Grant No. P19-50231 and CPMO Grant No. P11-00331 for their support of the program Biodiversity studies of entomopathogenic fungi in Thailand. Jean Lodge for her suggestions about the specimens collected in Puerto Rico. The study of Olga V. Morozova was carried out within the framework of a research project of the Komarov Botanical Institute RAS (AAAA-A19-119020890079-6) using equipment of its Core Facility Centre 'Cell and Molecular Technologies in Plant Science' with the financial support of Russian Foundation for Basic Research (project no. 20-04-00349). The study of Alina V. Alexandrova was supported by Moscow State University Grant for Leading Scientific Schools 'Depository of the Living Systems' in the framework of the MSU Development Program. Roy E. Halling acknowledges grants from the National Science Foundation (USA) DEB–0414665, DEB–1020421 and the National Geographic Society Committee for Research and Exploration in grant #8457–08. Logistical support from the Queensland Herbarium (BRI) aided field studies in Queensland. The Queensland Parks and Wildlife Service offered accommodation and orientation on Fraser Island. The staff and resources of the L.B. & D. Cullman Laboratory at the New York Botanical Garden aided in DNA extraction and amplifications. André De Kesel is thanked for providing insights regarding the morphological and developmental terminology of Clémençon (2012). Sandra Abell, Timothy Baroni, Teresa Lebel, Gregory Mueller, Todd Osmundson, and Klaus Querengasser are thanked for field assistance. Sushma Mandava kindly assisted early on in generating *tef1* and LSU sequences and Pooja Singh and Olga Khmelnitsky are thanked for assistance in this project with preliminary molecular phylogenetic and morphological assessments. Dilnora Gouliamova and colleagues were supported by a grant from the Bulgarian Science Fund (KP-06-H31/19). The authors express their gratitude for Borislav Guéorguiev from National Museum of Natural History (Sofia, Bulgaria) for the identification of beetles. Asunción Morte is grateful to AEI/FEDER, UE (CGL2016-78946-R) and Fundación Séneca- Agencia de Ciencia y Tecnología de la Región de Murcia (20866/PI/18) for financial support. Patrick Leonard and John Dearnaley are grateful for the help and advice given by T. Lebel and F. Guard. Milan Spetik and colleagues acknowledge funding by an Internal Grant of Mendel University (IGA-ZF/2020-DP003). The study of Bálint Dima was partly supported by the ELTE Institutional Excellence Program supported by the National Research, Development and Innovation Office (NKFIH-1157-8/2019-DT) in Hungary. Kesiban Özdemir is thanked for sequencing help. *Cortinarius glaucoelotus* was sequenced within ABOL, subproject HRSFM University of Vienna, supported by the Austrian Federal Ministry of Education, Science and Research. Kamal C. Semwal and Vinod K. Bhatt are grateful to the Uttarakhand State Council for Science and Technology (UCoST), Dehradun, Uttarakhand, India for the financial support provided under project no. UCS&T/R&D/LS-1/12-13/4912. The research of Ellen Larsson and Mikael Jeppson was supported by the Swedish Taxonomy Initiative, SLU Artdatabanken (grant 2019.4.3-13).

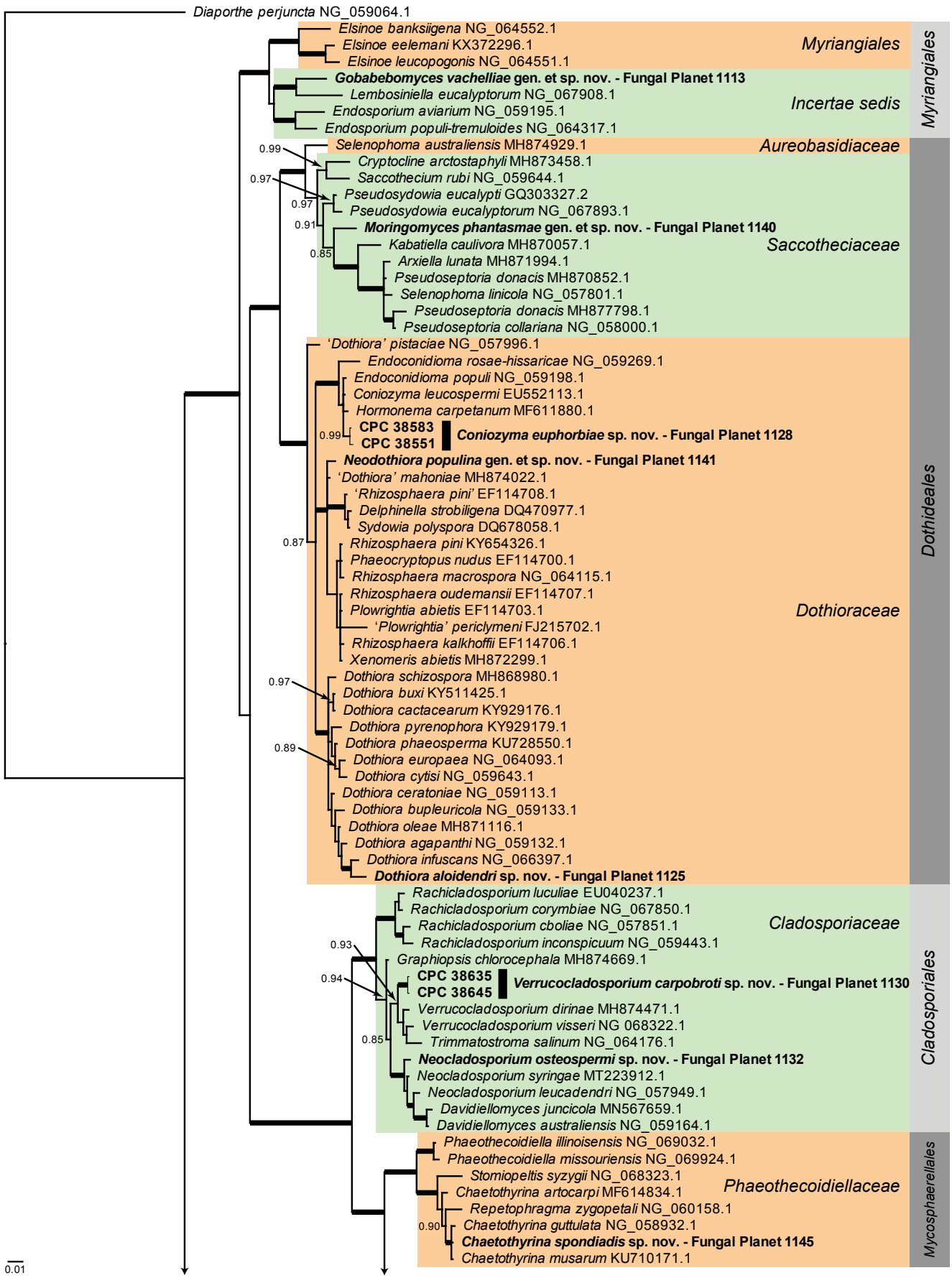


Overview *Agaricomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 435752 trees resulting from a Bayesian analysis of the LSU sequence alignment (130 sequences including outgroup; 979 aligned positions; 571 unique site patterns) 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. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Backusella lamprospora* (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).



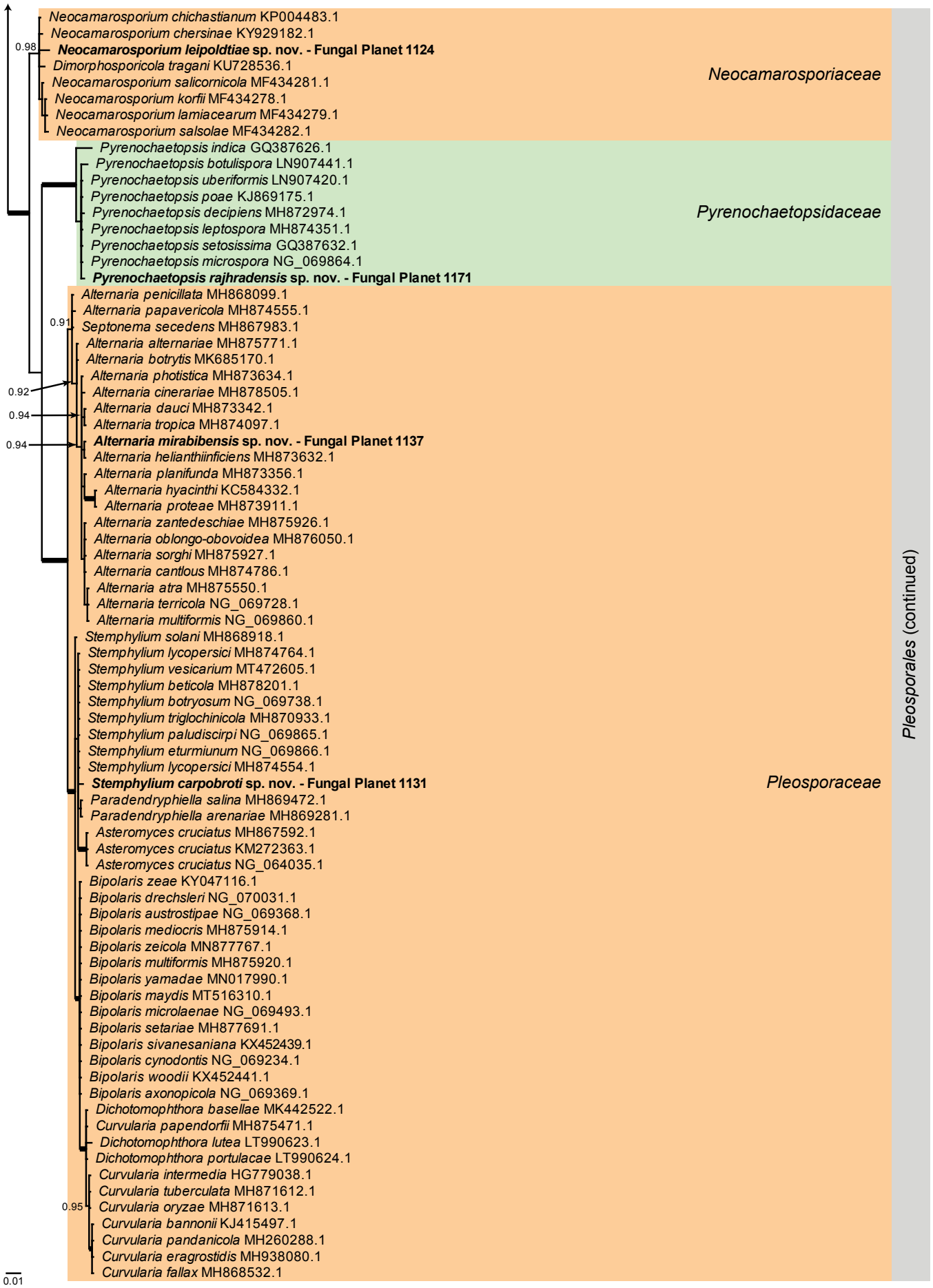
Overview *Agaricomycetes* phylogeny (cont.) – part 2



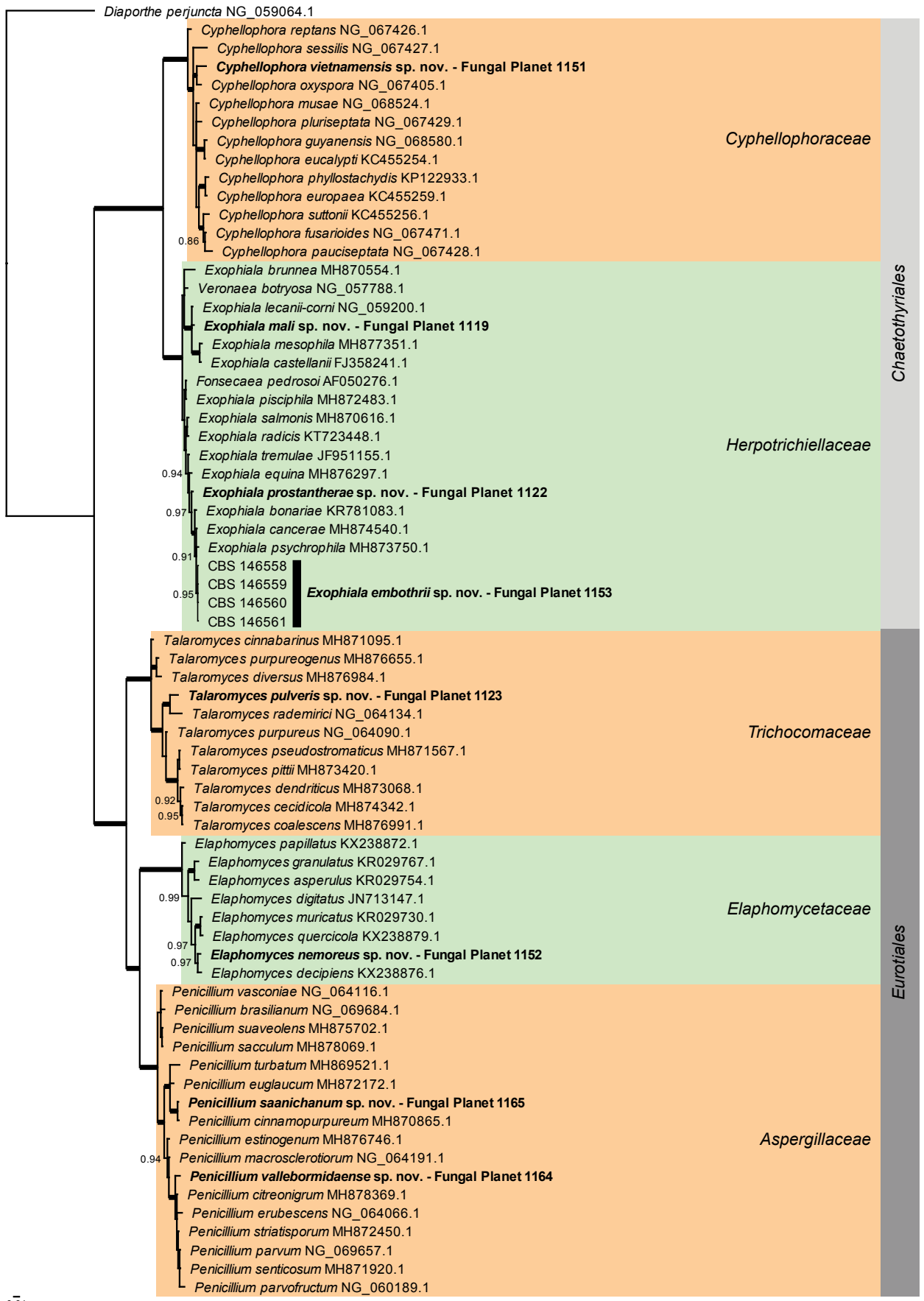
Overview *Dothideomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 146328 trees resulting from a Bayesian analysis of the LSU sequence alignment (233 sequences including outgroup; 824 aligned positions; 341 unique site patterns) 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. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Diaporthe perjuncta* (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

Overview *Dothideomycetes* phylogeny (cont.) – part 2



Overview *Dothideomycetes* phylogeny (cont.) – part 3



Overview *Eurotiomycetes* phylogeny

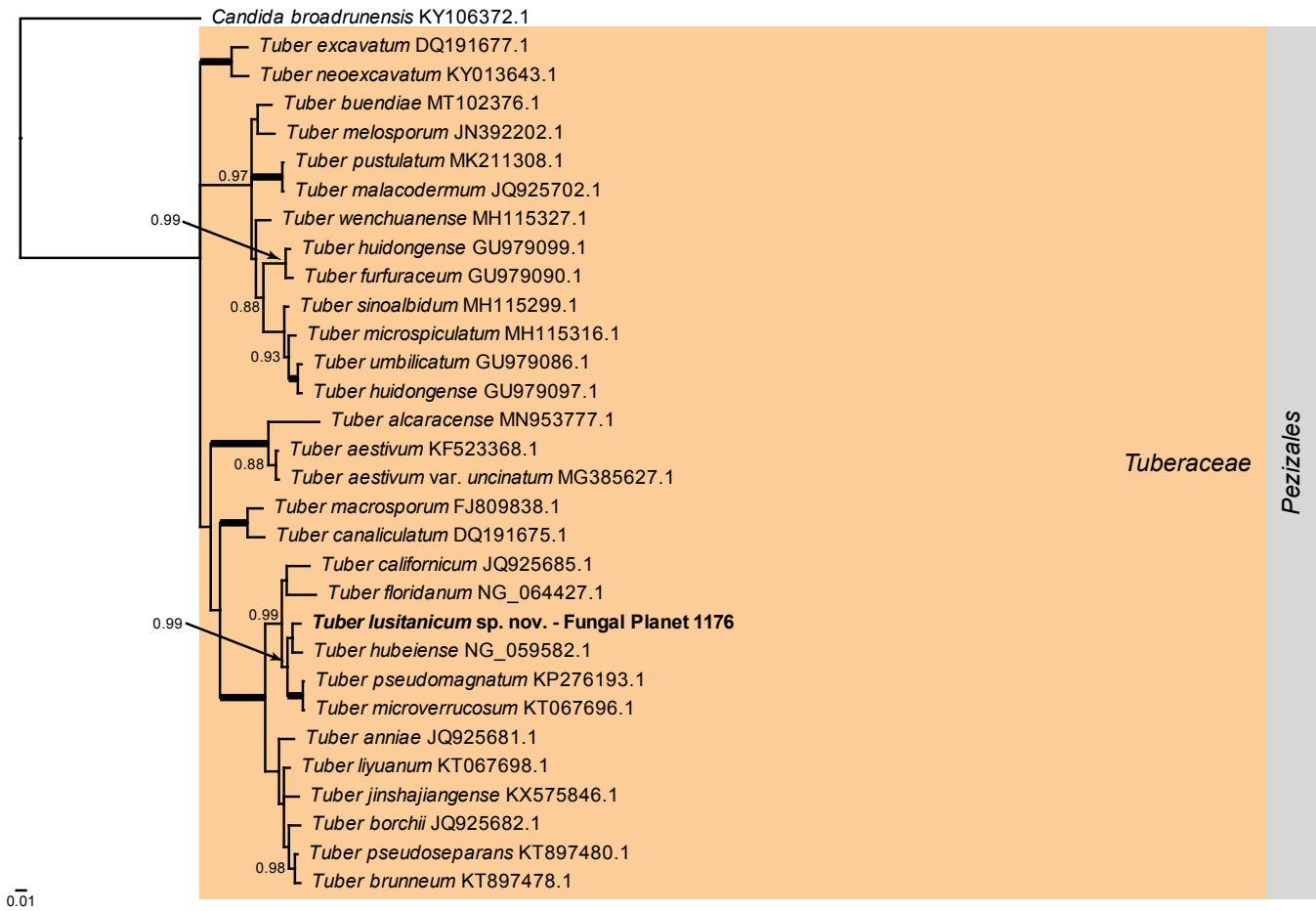
Consensus phylogram (50 % majority rule) of 146 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (70 sequences including outgroup; 838 aligned positions; 267 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Diaporthe perjuncta* (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

Overview *Geoglossomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 46 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (18 sequences including outgroup; 930 aligned positions; 223 unique site patterns) 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. The scale bar represents the expected changes per site. The family and order are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Aspergillus niger* (GenBank KC119204.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

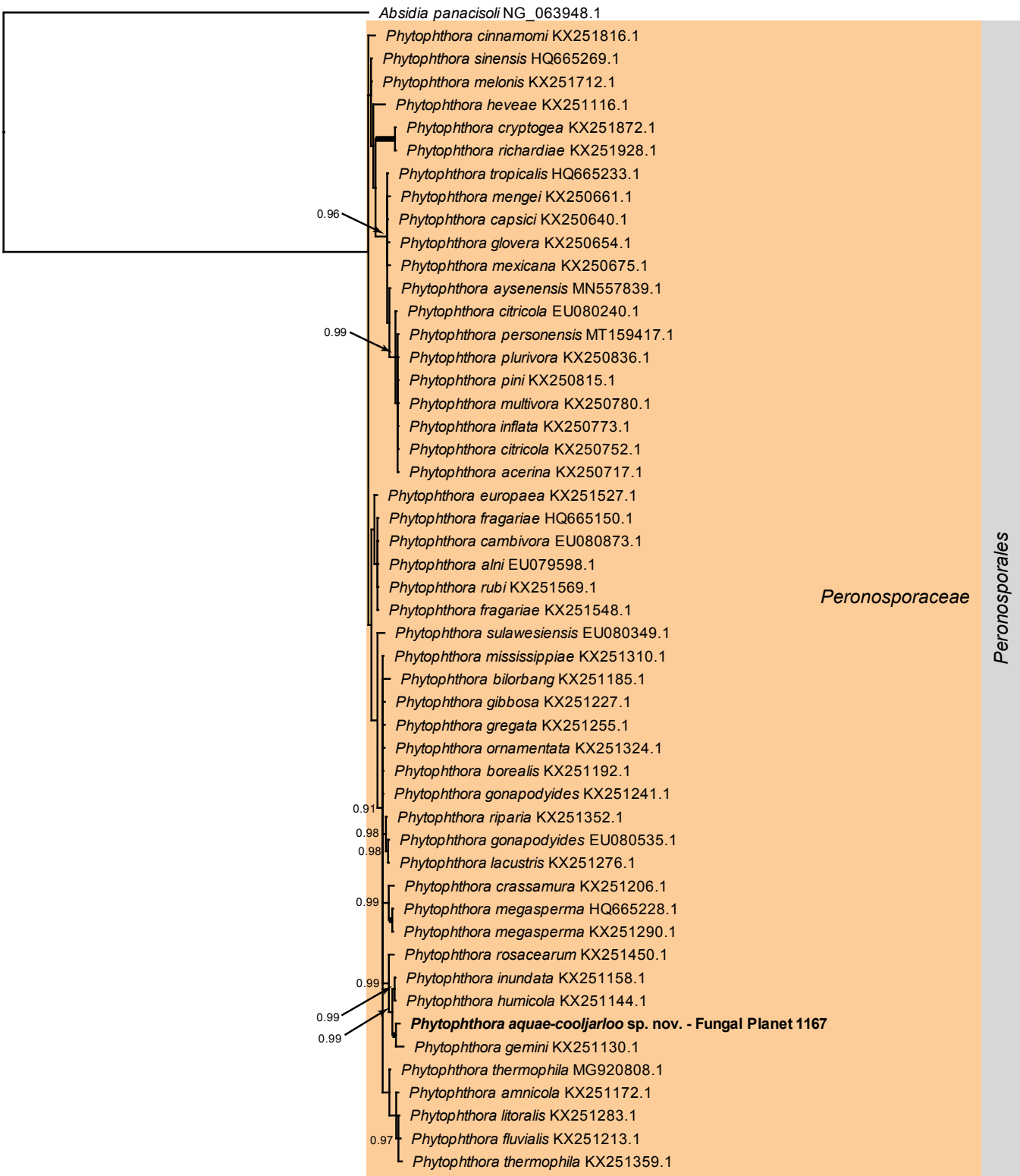
Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 222 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (78 sequences including outgroup; 839 aligned positions; 258 unique site patterns) 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. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Family assignment for *Helotiales* follows Johnston et al. (2019). GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Xylaria hypoxylon* (GenBank AY544648.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).



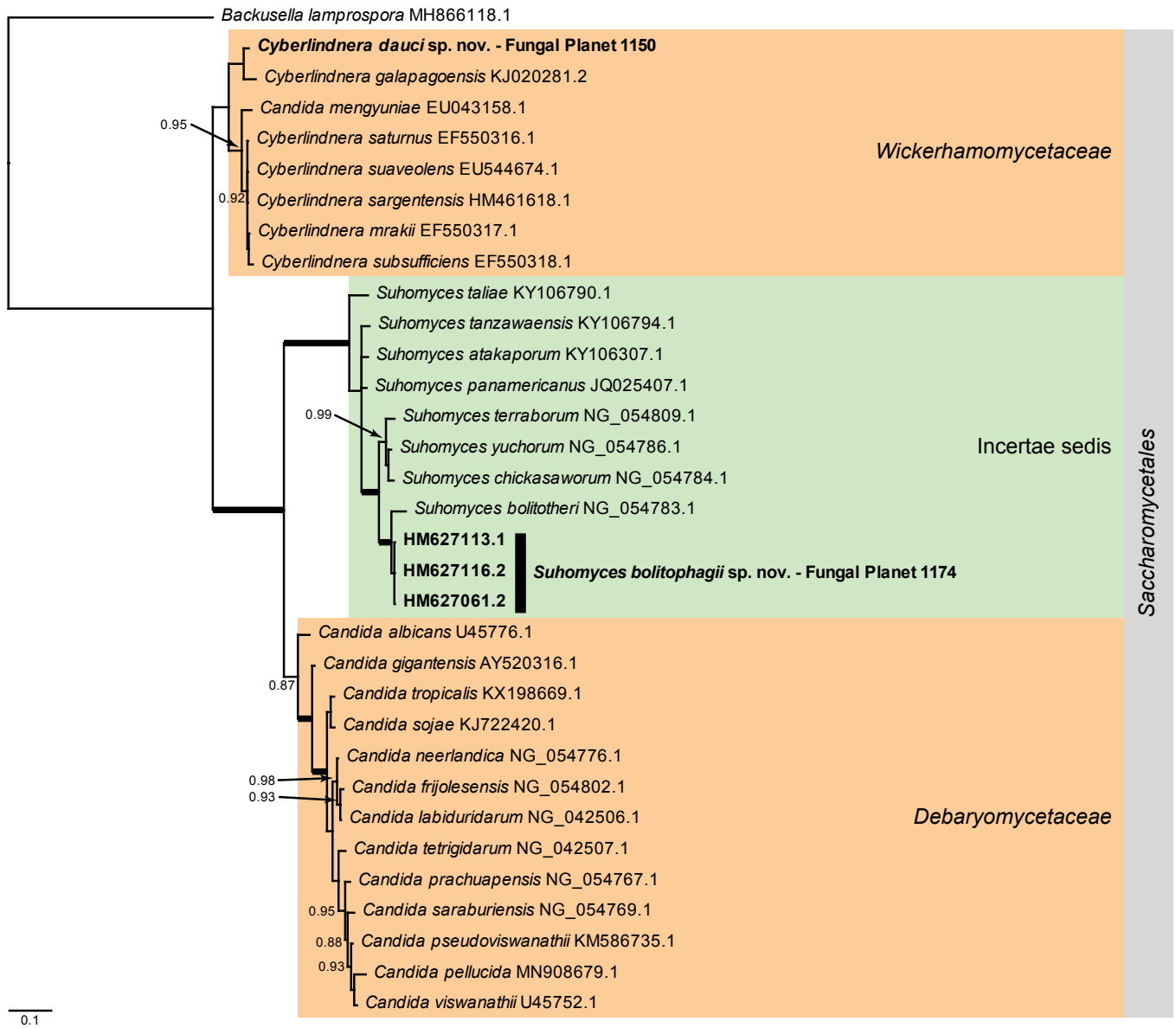
Overview *Pezizomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 52 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (31 sequences including outgroup; 821 aligned positions; 204 unique site patterns) 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. The scale bar represents the expected changes per site. The family and order are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Candida broadrunensis* (GenBank KY106372.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).



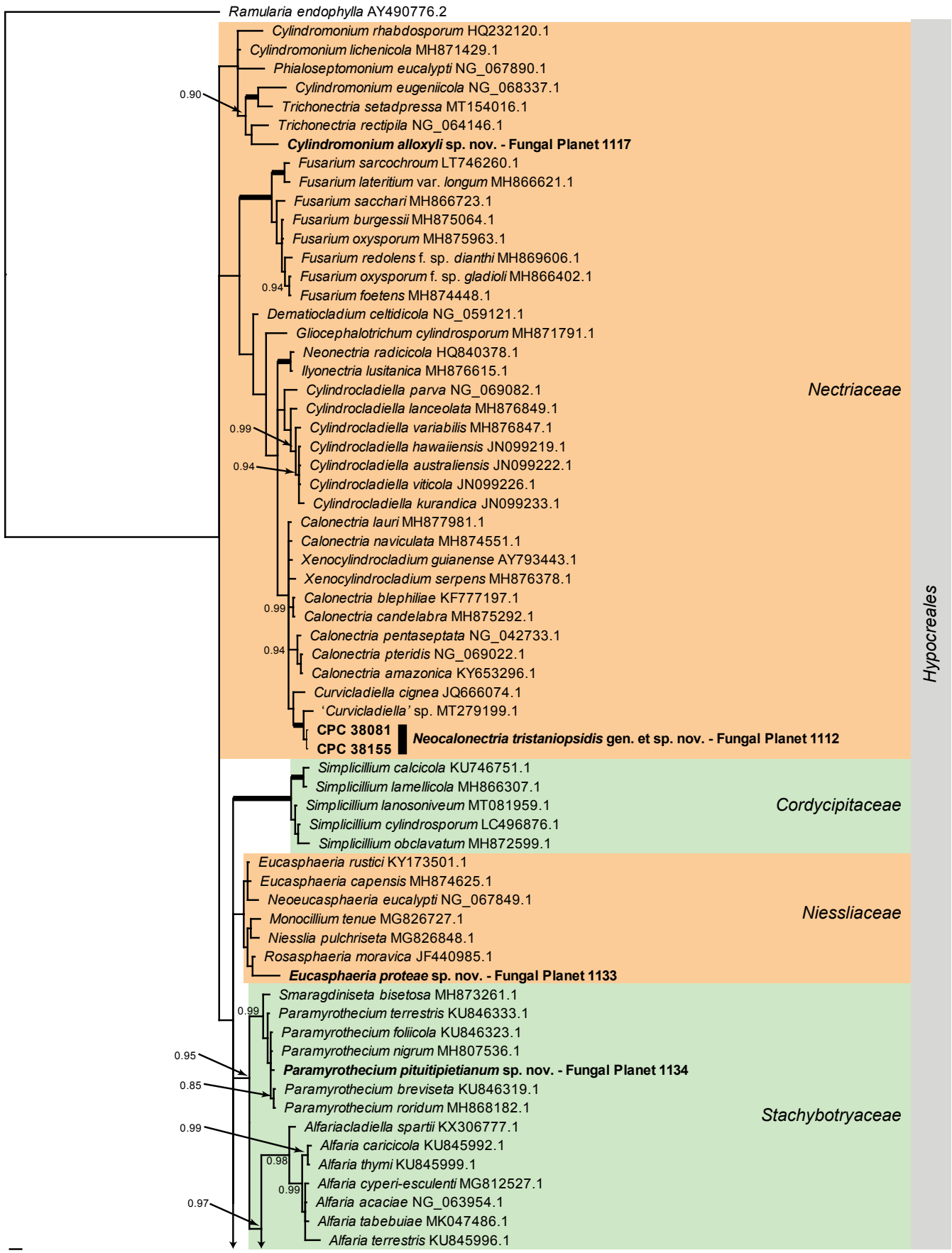
Overview *Phytophthora* phylogeny

Consensus phylogram (50 % majority rule) of 1 260 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (51 sequences including outgroup; 1 305 aligned positions; 130 unique site patterns) 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. The scale bar represents the expected changes per site. The family and order are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Absidia panacisoli* (GenBank NG_063948.1) and the taxonomic novelty described in this study for which LSU sequence data were available is indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).



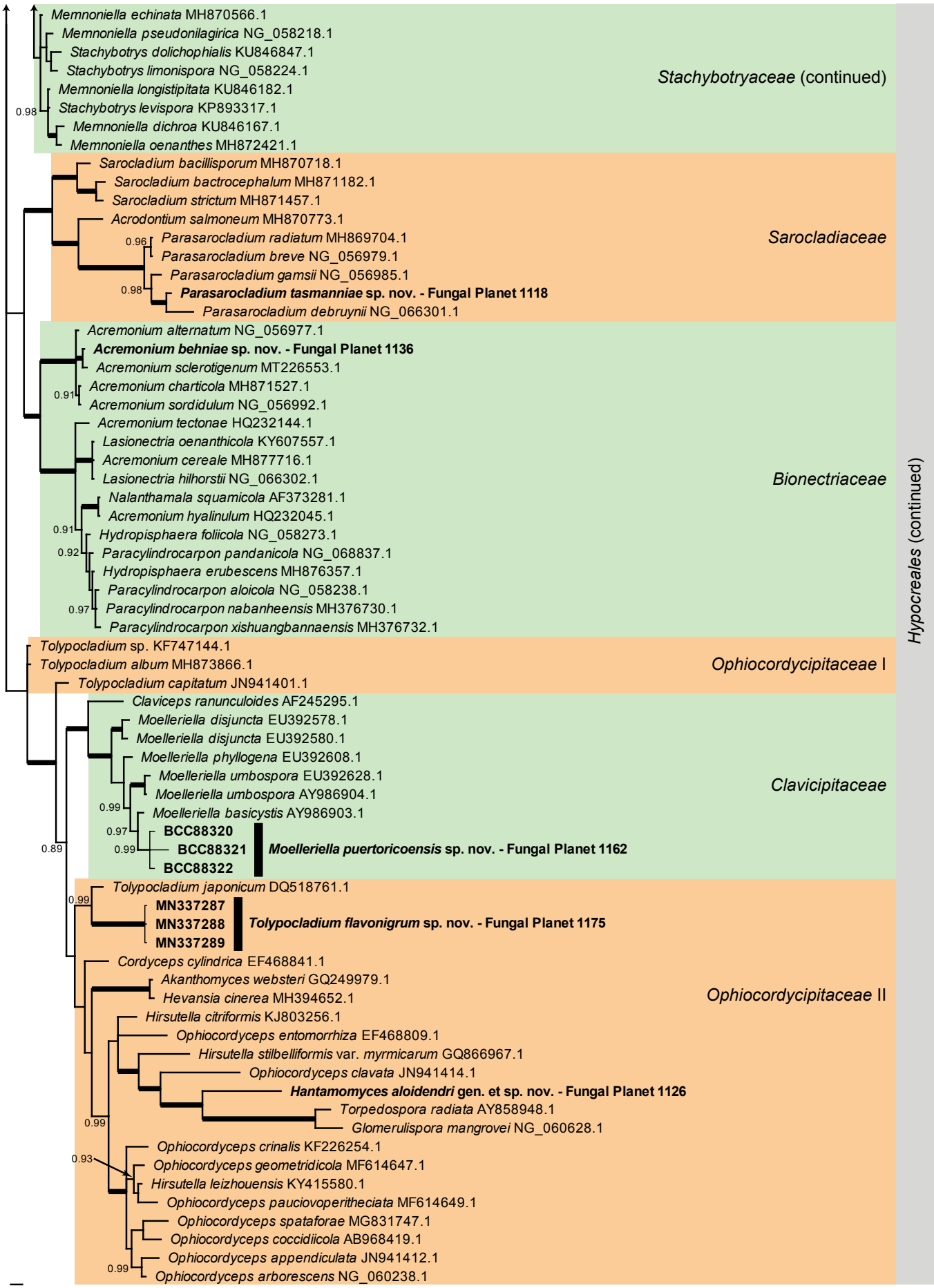
Overview *Saccharomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 69 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (33 sequences including outgroup; 553 aligned positions; 198 unique site patterns) 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. The scale bar represents the expected changes per site. The families and order are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Backusella lamprospora* (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

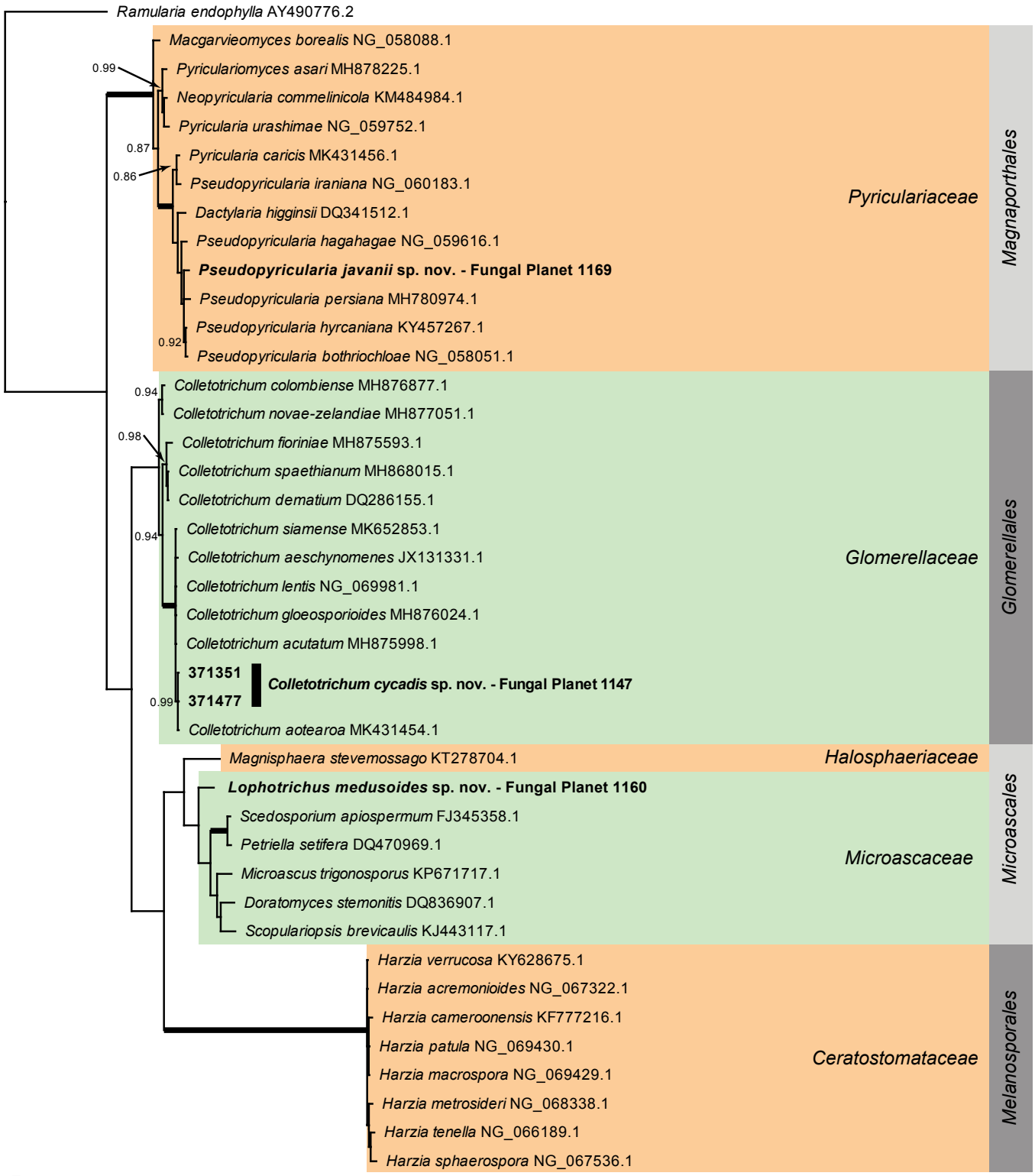


Overview *Sordariomycetes* (*Hypocreales*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 1695002 trees resulting from a Bayesian analysis of the LSU sequence alignment (135 sequences including outgroup; 812 aligned positions; 341 unique site patterns) 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. The scale bar represents the expected changes per site. Families and the order are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Ramularia endophylla* (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

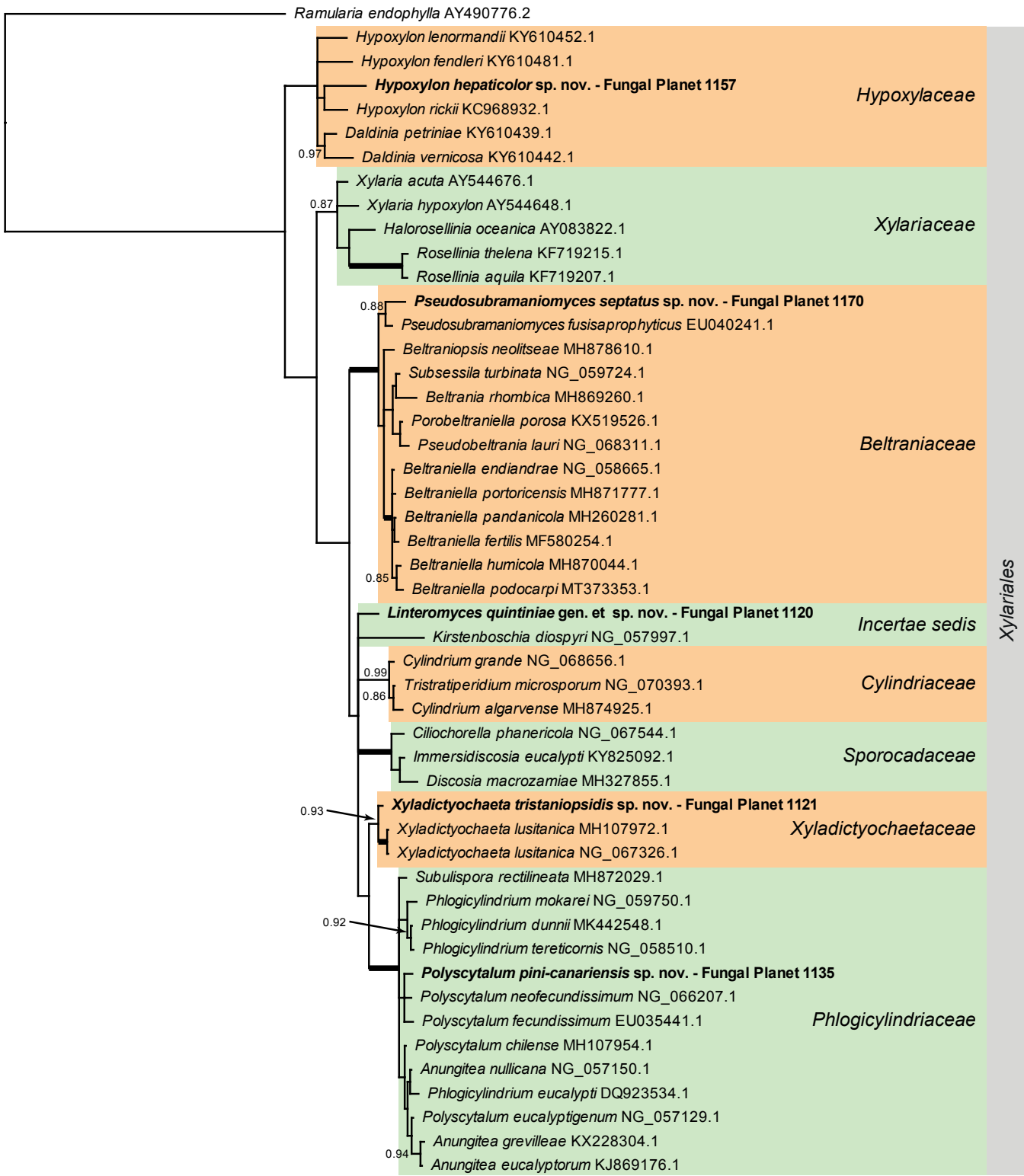


Overview *Sordariomycetes* (*Hypocreales*) phylogeny (cont.) – part 2



Overview *Sordariomycetes* (Other orders) phylogeny

Consensus phylogram (50 % majority rule) of 60 752 trees resulting from a Bayesian analysis of the LSU sequence alignment (41 sequences including outgroup; 807 aligned positions; 247 unique site patterns) 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. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Ramularia endophylla* (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).



Overview *Sordariomycetes* (*Xylariales*) phylogeny

Consensus phylogram (50 % majority rule) of 528002 trees resulting from a Bayesian analysis of the LSU sequence alignment (49 sequences including outgroup; 815 aligned positions; 218 unique site patterns) 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. The scale bar represents the expected changes per site. Families and the order are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Ramularia endophylla* (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 27179).


Neocalonectria tristaniopsidis

Fungal Planet 1112 – 19 December 2020

Neocalonectria Crous, *gen. nov*.

Etymology. Name refers to its superficial resemblance of the genus *Calonectria*.

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiophores consisting of a stipe, a penicillate arrangement of fertile branches, one to several avesiculate stipe extensions, lacking a terminal vesicle; stipe septate, hyaline, smooth; stipe extensions septate, straight to flexuous, terminating in an acicular apical cell. *Conidiogenous apparatus*: primary branches aseptate or 1-septate, secondary and tertiary branches aseptate, each terminal branch producing 2–6 phialides; *phialides* elongate doliiform to reniform, hyaline, aseptate, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight to gently curved, 1-septate, lacking a visible abscission scar, held in parallel cylindrical mucoid clusters. *Mega-* and *microconidia* not seen.

Type species. Neocalonectria tristaniopsidis Crous.
MycoBank MB837819.

Neocalonectria tristaniopsidis Crous, *sp. nov.*

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

Conidiophores consisting of a stipe, a penicillate arrangement of fertile branches, one to several avesiculate stipe extensions, lacking a terminal vesicle; stipe septate, hyaline, smooth, 30–70 × 5–6 µm; stipe extensions septate, straight to flexuous, 70–150(–200) µm long, 3–4 µm wide at the apical septum, terminating in an acicular apical cell. *Conidiogenous apparatus* 50–80 µm long, 30–50 µm wide; primary branches aseptate or 1-septate, 12–20 × 4–5 µm; secondary branches aseptate, 10–12 × 3–4 µm, and tertiary branches aseptate, 8–10 × 3–4 µm, each terminal branch producing 2–6 phialides; *phialides* elongate doliiform to reniform, hyaline, aseptate, 8–12 × 2.5–4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight to gently curved, (39–)40–43(–46) × 3(–3.5) µm (mean 42 × 3 µm), 1-septate, lacking a visible abscission scar, held in parallel cylindrical mucoid clusters. *Mega-* and *microconidia* not seen.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface ochreous, with chains of brown, thick-walled chlamydospores.

Typus. Australia, New South Wales, Limpinwood Nature Reserve, on leaves of *Tristaniopsis collina* (*Myrtaceae*), 26 May 2015, *B.A. Summerell*, HPC 2948 (holotype CBS H-24396, culture ex-type CPC 38081 = CBS 146800, ITS, LSU, *actA*, *cmdA*, *his3, rpb2*, *tef1* and *tub2* sequences GenBank MW175333.1, MW175373.1, MW173091.1, MW173097.1, MW173106.1, MW173109.1, MW173118.1 and MW173130.1, MycoBank MB837820).

Additional material examined. Australia, New South Wales, Limpinwood Nature Reserve, on leaves of *T. collina*, 26 May 2015, *B.A. Summerell*, HPC 2948, CBS H-24400, culture CPC 38155 = CBS 146805, ITS, LSU, *actA*, *cmdA*, *his3*, *rpb2*, *tef1* and *tub2* sequences GenBank MW175334.1, MW175374.1, MW173092.1, MW173098.1, MW173107.1, MW173110.1, MW173119.1 and MW173131.1.

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Penicillate conidiophores giving rise to cylindrical 1-septate conidia on synthetic nutrient-poor agar (scale bars = 10 µm); SEM micrographs captured on host tissue showing conidiophores and conidia (small, aseptate, ellipsoid conidia belong to an acremonium-like fungus). SEM scale bars = 20 µm (left) and 10 µm (right).

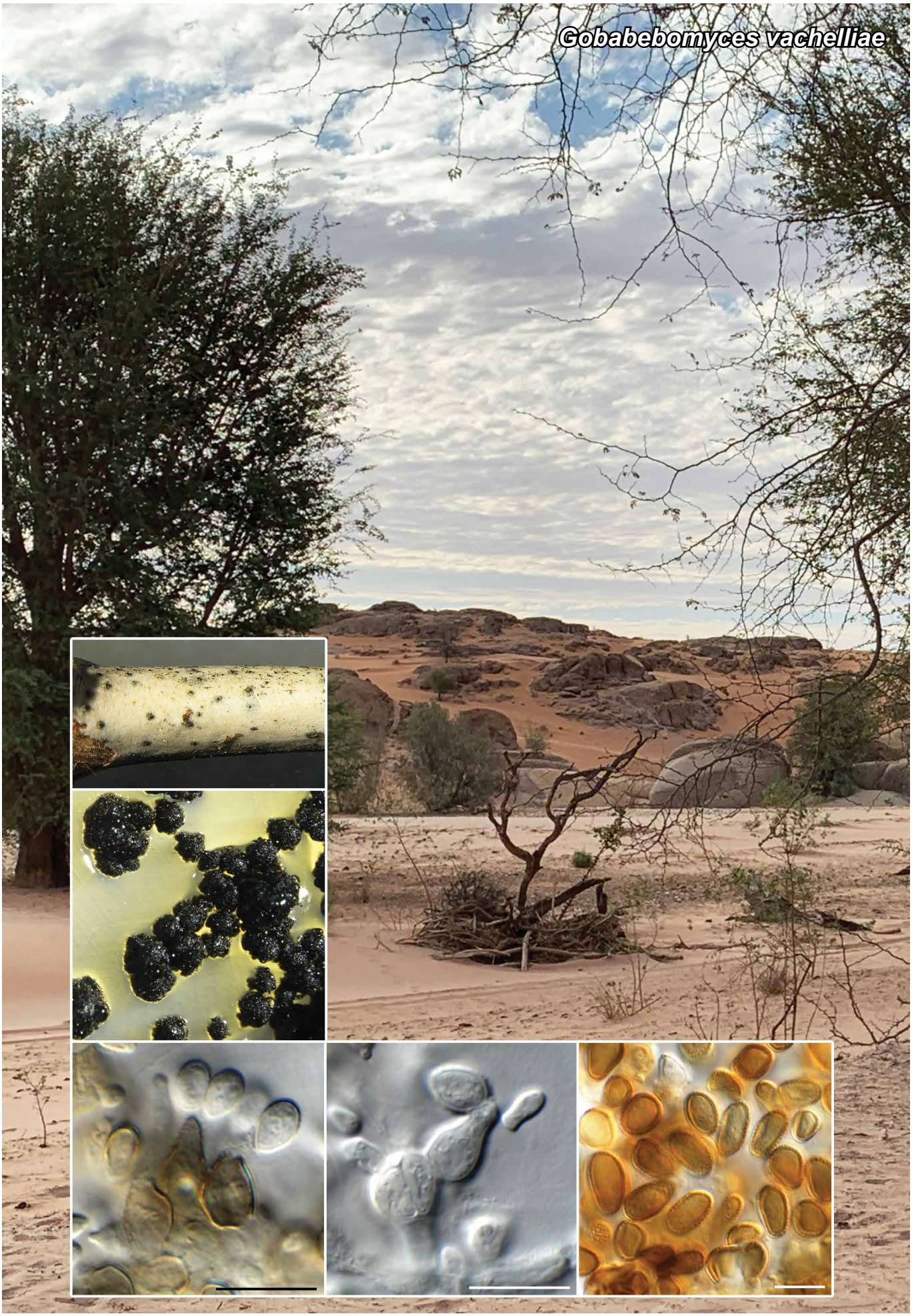
Notes — *Neocalonectria* resembles *Calonectria* and *Xenocylindrocladium* in having penicillate conidiophores with hyaline, cylindrical, septate conidia (Crous 2002). Morphologically it is closer to *Xenocylindrocladium*, as it has multiple stipe extensions per conidiophore that lack terminal vesicles (Decock et al. 1997, Crous et al. 2001). *Neocalonectria* forms a well-supported clade closely related to the genera *Calonectria, Curvicladiella* and *Xenocylindrocladium* (Lombard et al. 2015). Although several stipe extensions were observed arising from conidiophores on host material, cultures of *Neocalonectria* sporulate profusely, but rarely form stipe extensions on synthetic nutrient-poor agar. Morphologically it is hard to argue why the present collection does not belong to the genus *Xenocylindrocladium*, but phylogenetically, it clusters apart, being more closely related to *Curvicladiella*, which has hooked, 1-septate, thick-walled, pigmented, verruculose stipe extensions. A Scanning Electron Microscope (SEM) micrograph of *Neocalonectria tristaniopsidis* can also be seen on the covers of the various issues of Fungal Biology Reviews volume 34, published in 2020.

Blast results are supplied as part of the supplementary material.

Supplementary material

FP1112 Consensus phylogram (50 % majority rule) of 93 002 trees resulting from a Bayesian analysis of the combined 8-gene (ITS, LSU, *actA*, *cmdA*, *his3, rpb2*, *tef1* and *tub2*) sequence alignment (69 sequences including outgroup; 6 214 aligned positions; 418, 203, 347, 600, 395, 668, 504 and 484 unique site patterns, respectively) 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. The scale bar represents the expected changes per site. The taxonomic novelty described in this study is highlighted with **bold** text and the genera are represented by coloured blocks. The culture collection accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Stachybotrys chartarum* (culture CBS 129.13). The alignment is a reduced version of the alignment used by Lombard et al. (2015) and corresponding GenBank accession numbers of the sequences used can be found in that reference. The alignment and tree were deposited in TreeBASE (Submission ID 27179).

Pedro W. Crous & Johannes 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


Gobabebomyces vachelliae

Fungal Planet 1113 – 19 December 2020

Gobabebomyces Crous, *gen. nov*.

Etymology. Name refers to the Gobabeb-Namib Research Institute, where this fungus was collected.

Classification — *Incertae sedis*, *Myriangiales*, *Dothideomycetes.*

Conidiomata erumpent, pycnidial, opening via irregular rupture of epidermis, brown, subglobose, somewhat flattened, exuding a brown conidial mass; wall of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic. *Conidia* solitary, medium brown, verruculose, aseptate, ellipsoid, thick-walled with obtuse ends. Hyphae hyaline to brown, encased in mucoid sheath, constricted at septa, forming hyaline, smooth, aseptate ellipsoid conidia with obtuse ends, becoming brown and verruculose, and undergoing microcyclic conidiation.

Type species. Gobabebomyces vachelliae Crous.
MycoBank MB837821.

Gobabebomyces vachelliae Crous, *sp. nov.*

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

Conidiomata restricted to thorns, erumpent, pycnidial, opening via irregular rupture of epidermis, brown, subglobose, somewhat flattened, 80–150 µm diam, exuding a brown conidial mass; wall of 3–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic, 3–5 × 3–4 µm. *Conidia* solitary, medium brown, verruculose, aseptate, ellipsoid, thick-walled with obtuse ends, (8–)10–11(–12) × (5–)6(–7) µm. In culture hyphae hyaline to brown, 4–6 µm diam, encased in mucoid sheath, constricted at septa, forming hyaline, smooth, aseptate ellipsoid conidia with obtuse ends, 5–7 × 3–4 µm, becoming brown and verruculose, swelling and larger in size, and undergoing microcyclic conidiation.

Culture characteristics — Colonies erumpent, spreading, surface irregular to folded, with sparse aerial mycelium and uneven margin, reaching 10 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. Namibia, Gobabeb-Namib Research Institute, on leaves of *Vachellia* (= *Acacia*) *erioloba* (*Fabaceae*), 19 Nov. 2019, *P.W. Crous*, HPC 3132 (holotype CBS H-24450, culture ex-type CPC 38885 = CBS 146779, ITS and LSU sequences GenBank MW175335.1 and MW175375.1, MycoBank MB837822).

Notes — *Gobabebomyces* is an asexual, coniothyrium-like coelomycetous morph related to *Lembosiniella*, a genus of ascomycetes forming dark brown to black, superficial, irregular leaf spots with linear to Y-shaped hysterothecia on *Eucalyptus* spp. in Australia (Crous et al. 2019b). Species of *Lembosiniella* are sterile in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Elsinoe phaseoli* (strain CBS 165.31, GenBank MH855166.1; Identities = 388/452 (86 %), 30 gaps (6 %)), *Lembosiniella eucalyptorum* (strain CBS 144603, GenBank NR_165601.1; Identities = 379/443 (86 %), 24 gaps (5 %)), and *Elsinoe australis* (strain KNa-5, GenBank FJ010328.2; Identities = 384/451 (85 %), 24 gaps (5 %)). Closest hits using the **LSU** sequence are *Endosporium populi-tremuloides* (strain UAMH 10529, GenBank NG_064317.1; Identities = 778/816 (95 %), nine gaps (1 %)), *Lembosiniella eucalyptorum* (strain CBS 144603, GenBank NG_067908.1; Identities = 774/814 (95 %), six gaps (0 %)), and *Elsinoe banksiigena* (strain CPC 32402, GenBank NG_064552.1; Identities = 772/814 (95 %), five gaps (0 %)).

Colour illustrations. *Vachellia erioloba* trees growing at the Gobabeb-Namib Research Institute. Thorn with conidiomata; colonies on malt extract agar; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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
Neriman Yilmaz, 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: neriman.yilmazvisagie@fabi.up.ac.za
Don A. Cowan, Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: don.cowan@up.ac.za
Gillian Maggs-Kölling, Gobabeb-Namib Research Institute, P.O. Box 953, Walvis Bay, Namibia; e-mail: gillian@gobabeb.org


Graminopassalora geissorhizae

Fungal Planet 1114 – 19 December 2020

Graminopassalora geissorhizae Crous, *sp. nov.*

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

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Sporulating on SNA. *Conidiophores* medium brown, smooth, fasciculate, arising from a brown stroma of pseudoparenchymatal cells, subcylindrical, branched, 3–7-septate, up to 160 µm tall, 4–6 µm diam. *Conidiogenous cells* medium brown, smooth, integrated, subcylindrical, terminal and intercalary, 20–80 × 4–6 µm, with one to several loci, thickened, darkened, refractive, 2–3(–4) µm diam. *Conidia* solitary, medium brown, smooth to finely verruculose, subcylindrical, straight, apex subobtuse, base truncate, guttulate, 1–3-septate, (35–)40–55(–70) × (5–)6–7 µm; hila thickened, darkened and refractive, (2–)3–4 µm diam.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and lobed, feathery margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

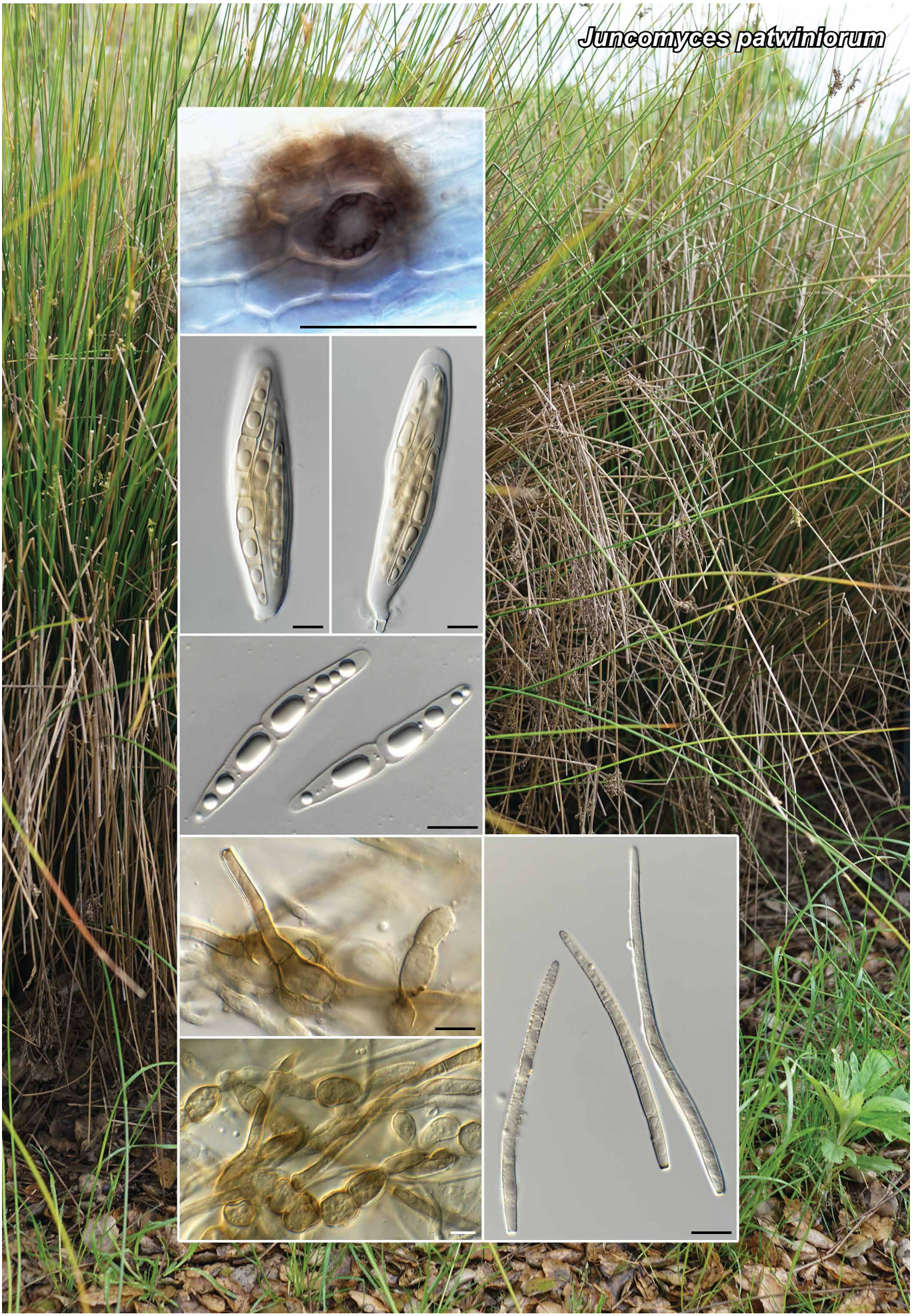
Typus. South Africa, Western Cape Province, Nieuwoudtville, Matjiesfontein, on leaves of *Geissorhiza splendidissima* (*Iridaceae*), 2018, *P.W. Crous*, HPC 3065 (holotype CBS H-24426, culture ex-type CPC 38623 = CBS 146788, ITS, LSU and *rpb2* sequences GenBank MW175336.1, MW175376.1 and MW173111.1, MycoBank MB837823).

Notes — *Graminopassalora*, based on *G. graminis*, is a monotypic genus occurring on members of *Poaceae,* with conidia 15–60 × 5–14 µm, (0–)1(–3)-septate (Braun et al. 2015, Videira et al. 2017). *Graminopassalora graminis* is widespread on a wide range of grasses, and Deighton (1967) considered *G. graminis* an aggregate species, possibly composed of several taxa. *Graminopassalora geissorhizae* is the first member of the genus known from *Iridaceae.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Graminopassalora graminis* (strain MAFF 510604, GenBank MF951321.1; Identities = 383/411 (93 %), three gaps (0 %)), *Pseudocercospora ocimi-basilici* (strain ICMP 21324, GenBank MK210535.1; Identities = 377/407 (93 %), two gaps (0 %)), and *Pseudocercospora ocimicola* (strain CPC 10283, GenBank GU214678.1; Identities = 377/407 (93 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 840/848 (99 %), no gaps), *Ramulariopsis pseudoglycines* (strain CPC 18242, GenBank NG_059693.1; Identities = 829/848 (98 %), no gaps), and *Cercosporella virgaureae* (strain CPC 11461, GenBank KX286977.1; Identities = 829/848 (98 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Zasmidium scaevolicola* (strain CBS 127009, GenBank MF951726.1; Identities = 700/875 (80 %), 25 gaps (2 %)), *Zasmidium citri-griseum* (strain CBS 122455, GenBank MF951695.1; Identities = 705/903 (78 %), 26 gaps (2 %)), and *Zasmidium hakeicola* (strain CBS 144590, GenBank MK442687.1; Identities = 665/860 (77 %), 13 gaps (1 %)).

Colour illustrations. *Geissorhiza splendidissima* with infected leaves. Conidiophores on SNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Juncomyces patwiniorum

Fungal Planet 1115 – 19 December 2020

Juncomyces patwiniorum Crous, *sp. nov.*

Etymology. Name refers to the Patwin indigenous people, who are the stewards of the land on which U.C. Davis campus is located.

Classification — *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Ascomata immersed on culms, globose, brown, 70–100 µm diam, with central, substomatal ostiole, 15–20 µm diam. *Pseudoparaphyses* absent. *Asci* 8-spored, fasciculate, stipitate, fusoid, apex subobtuse, bitunicate, apical chamber absent to 5 µm diam, with basal foot cell present, 75–100 × 19–22 µm. *Ascospores* multiseriate, fusoid, slightly curved, pale brown, finely verruculose, with large central guttules, constricted at median septum, later becoming 3-septate with obtuse ends, (43–)50–52(–55) × (5–)6 µm; germinating from both ends, with germ tubes parallel to the long axis of the spore, not distorting. Asexual morph developing on OA in culture. *Mycelium* forming chains of subglobose, brown chlamydospores, 8–12 µm diam, giving rise to erect, unbranched, subcylindrical, straight to slightly curved *conidiophores*, multiseptate, brown, verruculose, fasciculate, 30–80 × (3–)5–6 µm. *Conidiogenous cells* terminal, integrated, 15–30 × 4–6 µm; scars thickened, darkened and refractive, 2–3 µm diam, mostly solitary. *Conidia* solitary, subcylindrical to narrowly obclavate, slightly flexuous, base truncate, apex subobtuse, medium brown, verruculose, guttulate, (1–)3–6-septate, (70–)80–120(–130) × (3–)4 µm; hilum thickened, darkened and refractive, 2.5–3 µm diam.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface smoke grey, reverse iron-grey; on PDA surface iron-grey, reverse olivaceous grey; on OA surface olivaceous grey.

Typus. USA, California, U.C. Davis campus, on culms of *Juncus effusus* (*Juncaceae*), 2 Apr. 2019, *P.W. Crous*, HPC 2894 (holotype CBS H-24394, culture ex-type CPC 37991 = CBS 146798, ITS, LSU and *rpb2* sequences GenBank MW175337.1, MW175377.1 and MW173112.1, MycoBank MB837825).

Notes — *Juncomyces* represents a monotypic genus in the *Mycosphaerellaceae* (Videira et al. 2017, Crous et al. 2020b). *Juncomyces patwiniorum* is characterised by having immersed ascomata with fusoid, slightly curved, pale brown, finely verruculose ascospores that can become 3-septate with age, and a passalora-like asexual morph with pigmented conidia, and darkened, thickened, refractive hila. *Juncomyces californiensis* is distinct in that it has smaller conidia (45–)55–70(–75) × (6–)7(–8) µm (Crous et al. 2020b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Juncomyces californiensis* (strain CPC 37989, GenBank MT373368.1; Identities = 482/512 (94 %), 12 gaps (2 %)), *Graminopassalora graminis* (strain CBS 113303, GenBank GU214666.1; Identities = 455/515 (88 %), 20 gaps (3 %)), and *Neokirramyces syzygii* (strain CPC 36122, GenBank NR_166317; Identities = 441/496 (89 %), 16 gaps (3 %)). Closest hits using the **LSU** sequence are *Juncomyces californiensis* (strain CPC 37989, GenBank MT373351.1; Identities = 808/808 (100 %), no gaps), *Xenosonderhenia eucalypti* (strain CBS 138858, GenBank MH878634.1; Identities = 865/892 (97 %), three gaps (0 %)), and *Ramularia tovarae* (strain CBS 113305, GenBank NG_069194.1; Identities = 846/874 (97 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Ramularia tovarae* (strain CBS 113305, GenBank KJ504678.1; Identities = 328/400 (82 %), two gaps (0 %)), *Ramularia armoraciae* (strain CBS 253.28, GenBank KX288493.1; Identities = 327/401 (82 %), four gaps (0 %)), and *Ramularia plurivora* (strain CPC 16123, GenBank KJ504653.1; Identities = 325/399 (81 %), no gaps).

Colour illustrations. *Juncus effusus* growing on U.C. Davis campus. Immersed ascoma with substomatal ostiole; asci; fusoid, 1-septate ascospores; conidiogenous cells in culture; conidia conidiogenous cells giving rise to conidia. Scale bars: ascoma = 80 µm, all others = 10 µm.

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


Davidhawksworthia quintiniae

Fungal Planet 1116 – 19 December 2020

Davidhawksworthia quintiniae Crous, *sp. nov.*

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

Classification — *Dermateaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, smooth, septate, 2–3 µm diam hyphae. *Conidiophores* reduced to phialidic conidiogenous cells, ampulliform to doliiform, hyaline, smooth, erect, becoming aggregated in clusters, forming sporodochia on agar surface, 4–15 × 3–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, ends obtuse, (10–)11–12(–15) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and lobate, smooth margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse buff; on PDA surface and reverse dirty white; on OA surface buff.

Typus. Australia, New South Wales, Limpinwood Nature Reserve, Corina lookout, on leaves of *Quintinia sieberi* (*Paracryphiaceae*), 26 May 2015, *B.A. Summerell*, HPC 2945 (holotype CBS H-24399, culture ex-type CPC 38153 = CBS 146963, ITS, LSU, *rpb2* and *tub2* sequences GenBank MW175338.1, MW175378.1, MW173113.1 and MW173132.1, MycoBank MB837828).

Notes — The erect, ampulliform to doliiform phialides, and hyaline, aseptate conidia are reminiscent of the monotypic genus *Davidhawksworthia* (Crous & Groenewald 2016). *Davidhawksworthia quintiniae* is easily distinguished from *D. ilicicola* (on *Ilex aquifolium*, Netherlands; conidia 17–22 × 3–3.5 µm) by its smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dermea libocedri* (strain CBS 138.46, GenBank MH856142.1; Identities = 526/560 (94 %), five gaps (0 %)), *Dermea acerina* (strain CBS 161.38, GenBank MH855942.1; Identities = 524/560 (94 %), eight gaps (1 %)), *Pseudotryblidium neesii* (strain HE300, GenBank MK894293.1; Identities = 524/563 (93 %), six gaps (1 %)) and *Davidhawksworthia ilicicola* (strain CBS 261.95, GenBank KU728516.1; Identities = 517/556 (93 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Davidhawksworthia ilicicola* (strain CBS 734.94, GenBank NG_067307.1; Identities = 892/898 (99 %), no gaps), *Coleophoma cylindrospora* (strain BP-6252, GenBank MH762908.1; Identities = 892/900 (99 %), no gaps), and *Coleophoma camelliae* (strain CBS 101376, GenBank KU728521.1; Identities = 886/894 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Rhizodermea veluwensis* (strain CBS 110615, GenBank KR859354.1; Identities = 747/882 (85 %), no gaps), *Pezicula cornina* (strain CBS 285.39, GenBank KR859333.1; Identities = 731/871 (84 %), four gaps (0 %)), and *Pezicula neoheterochroma* (strain CBS 127388, GenBank KR859338.1; Identities = 744/889 (84 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Davidhawksworthia ilicicola* (strain CBS 261.95, GenBank KU728630.1; Identities = 300/371 (81 %), 14 gaps (3 %)), *Monilia yunnanensis* (strain GND3, GenBank KT736016.1; Identities = 304/378 (80 %), 17 gaps (4 %)), and *Monilinia fructigena* (strain CBS 101499, GenBank KT736015.1; Identities = 303/378 (80 %), 17 gaps (4 %)).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Cylindromonium alloxyli

Fungal Planet 1117 – 19 December 2020

Cylindromonium alloxyli Crous, *sp. nov.*

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

Classification — *Nectriaceae*, *Hypocreales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* solitary, subcylindrical, unbranched, hyaline, smooth, flexuous, erect, 1–2-septate, 30–60 × 2 µm. *Conidiogenous cells* integrated, terminal, hyaline, smooth, subcylindrical, 10–20 × 1.5–2 µm, phialidic, apex with periclinal thickening, lacking collarette. *Conidia* hyaline, smooth, medianly 1-septate, aggregating in cylindrical spore packets, subcylindrical with obtuse ends, (14–)15–17(–18) × 2–3 µm.

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

Typus. Australia, New South Wales, Limpinwood Nature Reserve, Mt Merino, mycophilic on *Meliola* on leaves of *Alloxylon pinnatum* (*Proteaceae*), 26 May 2015, *B.A. Summerell*, HPC 2951 (holotype CBS H-24401, culture ex-type CPC 38159 = CBS 146806, ITS, LSU, *actA*, *his3*, *rpb2*, *tef1* (first and second part) and *tub2* sequences GenBank MW175339.1, MW175379.1, MW173093.1, MW173108.1, MW173114.1, MW173120.1, MW173128.1 and MW173133.1, MycoBank MB837829).

Notes — *Cylindromonium* was recently established as genus to accommodate acremonium-like taxa with unbranched, hyaline conidiophores, and cylindrical, 1-septate conidia (Crous et al. 2019a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cylindromonium lichenicola* (strain CBS 188.70, GenBank MH859549.1; Identities = 540/591 (91 %), 18 gaps (3 %)), *Cylindromonium rhabdosporum* (strain CBS 438.66, GenBank MH858850.1; Identities = 538/590 (91 %), 18 gaps (3 %)), and *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank NR_165572.1; Identities = 534/587 (91 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Cylindromonium lichenicola* (strain CBS 415.70A, GenBank MH871536.1; Identities = 588/608 (97 %), two gaps (0 %)), *Trichonectria rectipila* (strain CBS 132.87, GenBank NG_064146.1; Identities = 583/606 (96 %), two gaps (0 %)), and *Phialoseptomonium eucalypti* (strain CBS 145542, GenBank NG_067890.1; Identities = 571/596 (96 %), two gaps (0 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Simplicillium aogashimaense* (strain JCM 18167, GenBank LC496904.1; Identities = 391/432 (91 %), two gaps (0 %)), *Simplicillium cylindrosporum* (strain JCM 18169, GenBank LC496906.1; Identities = 390/433 (90 %), two gaps (0 %)), and *Nectria marina* (strain MFLUCC 16-0544, GenBank MN433214.1; Identities = 389/432 (90 %), no gaps (0 %)).No significant hits were obtained when the ***actA***, ***his3***, ***rpb2***, ***tef1*** (first part) and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiophores sporulating on a sterile pine needle; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Parasarocladium tasmanniae

Fungal Planet 1118 – 19 December 2020

Parasarocladium tasmanniae Crous, *sp. nov.*

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

Classification — *Sarocladiaceae*, *Hypocreales*, *Sordariomycetes.*

Ascomata perithecial, hyaline, smooth-walled, globose to obpyriform, 50–100 × 50–80 µm; wall of 3–6 layers of hyaline *textura angularis. Asci* obovoid to subcylindrical, hyaline, 8-spored, unitunicate with apical mechanism, not straining in Melzer's reagent, apex slightly flattened, 23–30 × 5–8 µm, stipitate, intermingled among cellular, hyaline paraphyses that dissolve at maturity. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, straight to slightly curved, constricted at median septum, (9–)10–11(–12) × (2.5–)3(–3.5) µm. *Mycelium* consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* hyaline, smooth, subcylindrical, branched below, 1–2-septate, 20–35 × 2–3 µm. *Conidiogenous cells* at times solitary, arising directly from superficial hyphae, or on conidiophores, terminal or intercalary, phialidic, subcylindrical with slight apical taper, 12–30 × 2–3 µm; collarette minute, 1 µm tall, not flared. *Conidia* hyaline, smooth, granular, subcylindrical to fusoid, straight to slightly curved, aseptate, apex subobtuse, base slightly tapered to truncate hilum, 0.5 µm diam, (5–)7–8(–9) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and lobate, even margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA and PDA surface and reverse dirty white; on OA surface buff.

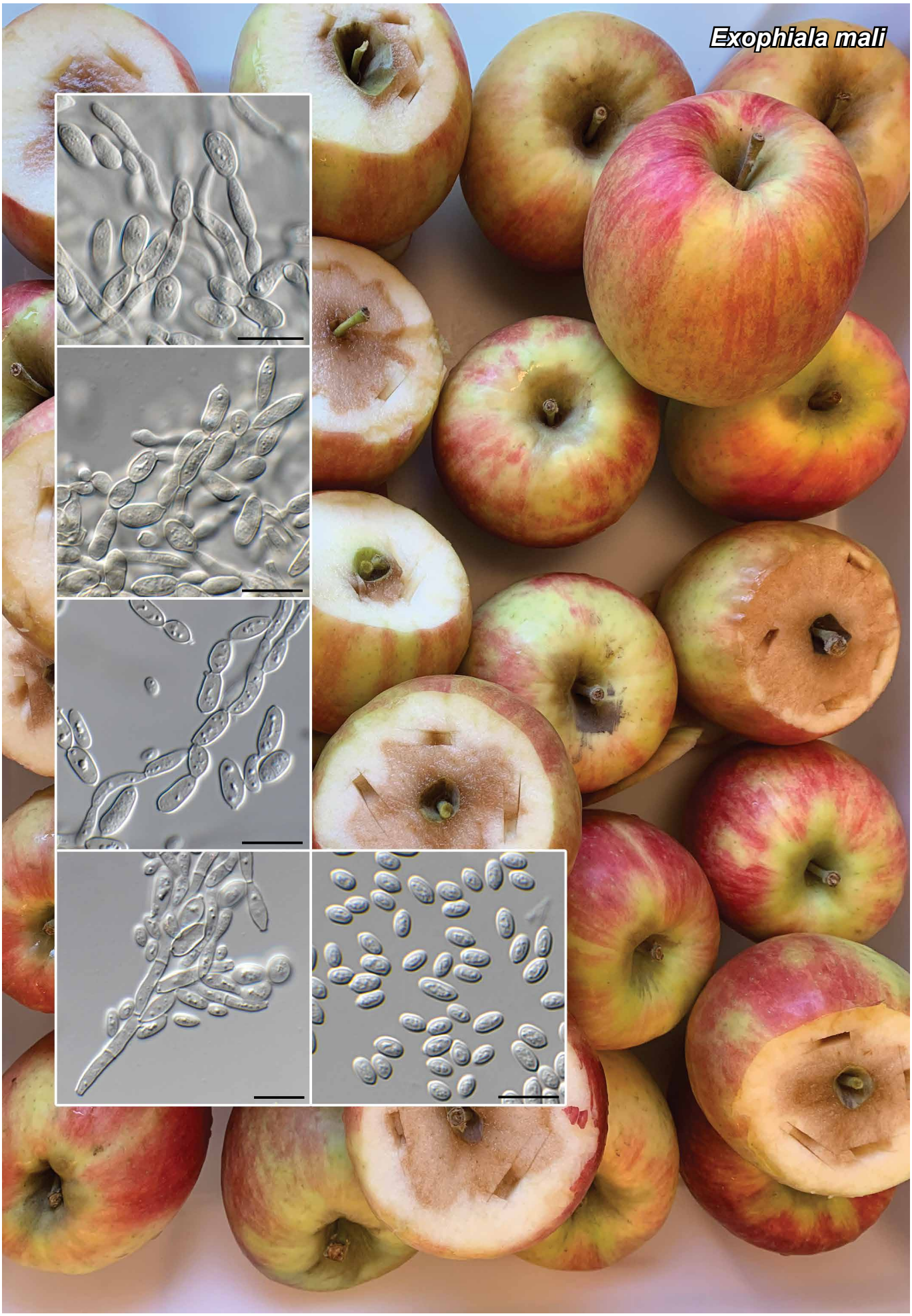
Typus. Australia, New South Wales, Limpinwood Nature Reserve, Mt Merino, on leaves of *Tasmannia insipida* (*Winteraceae*), 26 May 2015, *B.A. Summerell*, HPC 2953 (holotype CBS H-24402, culture ex-type CPC 38162 = CBS 146807, ITS, LSU, *actA*, *tef1* and *tub2* sequences GenBank MW175340.1, MW175380.1, MW173094.1, MW173121.1 and MW173134.1, MycoBank MB837830).

Notes — *Parasarocladium* was recently introduced by Summerbell et al. (2018) to accommodate a distinct clade of acremonium-like fungi, which are commonly isolated from soil (Crous et al. 2018a). As shown here, however, species can also be foliicolous, and have a sexual morph, which has thus far not been observed for any member of *Parasarocladium.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Parasarocladium radiatum* (strain CBS 142.62, GenBank NR_161112.1; Identities = 546/581 (94 %), 11 gaps (1 %)), *Parasarocladium debruynii* (strain CBS 144942, GenBank NR_163316.1; Identities = 540/581 (93 %), 17 gaps (2 %)), and *Parasarocladium gamsii* (as *Acremonium gamsii*; strain CBS 726.71, GenBank NR_159615.1; Identities = 538/584 (92 %), 17 gaps (2 %)). Closest hits using the **LSU** sequence are *Parasarocladium breve* (as *Acremonium breve*; strain CBS 150.62, GenBank FJ176882.1; Identities = 886/901 (98 %), two gaps (0 %)), *Parasarocladium gamsii* (strain CBS 726.71, GenBank MH872068.1; Identities = 885/900 (98 %), two gaps (0 %)), and *Sarocladium strictum* (strain CBS 147.49, GenBank HQ232139.1; Identities = 833/849 (98 %), four gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069413.1; Identities = 594/648 (92 %), 19 gaps (2 %)), *Cordyceps militaris* (strain ATCC 34164, GenBank CP023327.1; Identities = 400/422 (95 %), no gaps), and *Fusarium striatum* (strain CBS 101573, GenBank KM231195.1; Identities = 462/515 (90 %), six gaps (1 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069410.1; Identities = 241/289 (83 %), 19 gaps (6 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Parasarocladium debruynii* (strain CBS 144942, GenBank MK069407.1; Identities = 586/668 (88 %), 27 gaps (4 %)), *Sarocladium spirale* (strain 3-22, GenBank LC464483.1; Identities = 396/482 (82 %), 29 gaps (6 %)), and *Chaetopsina acutispora* (strain CBS 667.92, GenBank KM232029.1; Identities = 317/370 (86 %), 16 gaps (4 %)).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Ascomata and ascospores; ascus; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Exophiala mali

Fungal Planet 1119 – 19 December 2020

Exophiala mali Crous, *sp. nov.*

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

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of smooth, olivaceous, branched, septate, 2.5–3 µm diam hyphae. *Hyphae* becoming constricted at septa in terminal region, forming chains of disarticulating *conidia*, 0–1-septate, 12–15 × 3–5 µm, subcylindrical to ellipsoid, 0–1-septate, 8–10 × 3–4 µm, olivaceous, smooth, guttulate. *Conidiogenous loci* occurring as hyphal pegs on hyphal cells or on conidia, 1–2 × 1–1.5 µm, not thickened nor darkened, giving rise to smaller, ellipsoid *conidia*, olivaceous, smooth, aseptate, 4–7 × 2.5–3 µm.

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

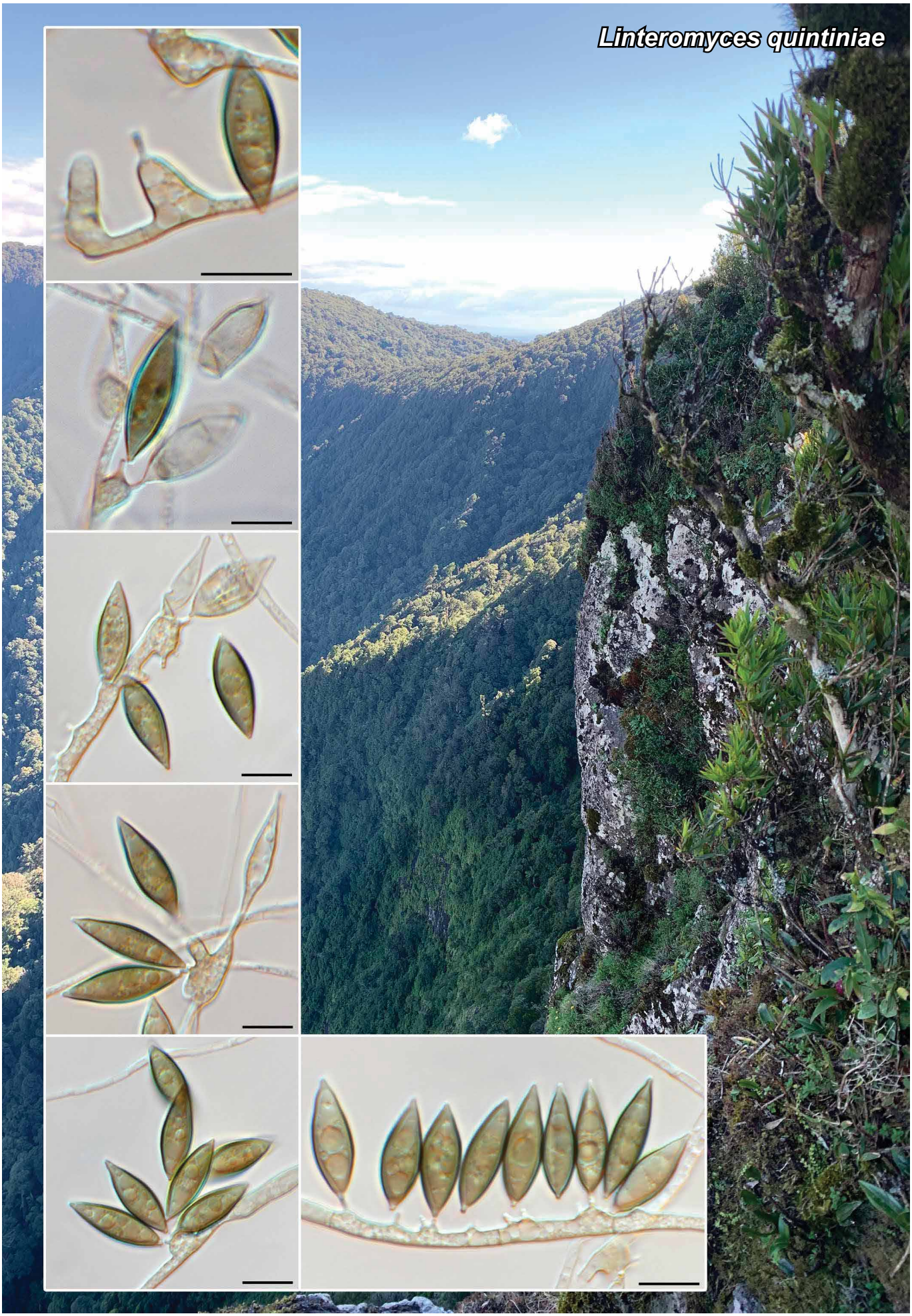
Typus. South Africa, Western Cape Province, Ceres, from inner fruit tissue of *Malus* sp. with cold store damage (*Rosaceae*), June 2018, *P.W. Crous* (holotype CBS H-24408, culture ex-type CPC 38208 = CBS 146791, ITS and LSU sequences GenBank MW175341.1 and MW175381.1, MycoBank MB837831).

Notes — Species of *Exophiala* are commonly isolated from soil, water, and plant debris (Crous et al. 2018b). *Exophiala mali* is a new species of *Exophiala* that was isolated from apples that underwent cold storage damage due to severe low temperatures.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to '*Exophiala lecanii-corni*' (strain CMRP3747, GenBank MT452654.1; Identities = 398/401 (99 %), no gaps), *Exophiala lecanii-corni* (strain CBS 123.33, GenBank NR_145351.1; Identities = 560/579 (97 %), five gaps (0 %)), and *Exophiala pisciphila* (strain G1-2, GenBank KT876529.1; Identities = 592/610 (97 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Exophiala lecanii-corni* (strain CBS 123.33, GenBank NG_059200.1; Identities = 881/884 (99 %), no gaps), *Exophiala pisciphila* (strain CBS 464.81, GenBank AF050273.1; Identities = 859/862 (99 %), no gaps), and *Exophiala castellanii* (strain CBS 158.58, GenBank NG_070513.1; Identities = 873/885 (99 %), one gap (0 %)).

Colour illustrations. Apples with cold store damage. Hyphae and conidiogenous cells; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Linteromyces quintiniae

Fungal Planet 1120 – 19 December 2020

Linteromyces Crous, *gen. nov*.

Etymology. Name refers to the canoe-shaped (L = *Linter-*) conidia.

Classification — *Incertae sedis*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* reduced to conidiogenous cells or subcylindrical, brown, smooth, erect, unbranched, becoming dark brown and thick-walled with age, septate, with integrated terminal conidiogenous cells. *Conidiogenous cells* solitary, erect, integrated on hyphae, pale to medium brown, smooth, doliiform to subcylindrical, with several cylindrical denticles near apex. *Conidia* solitary, aseptate, medium brown, slightly roughened, fusoid, apex and base with apiculus, with paler germ slit along length of conidium body.

Type species. Linteromyces quintiniae Crous.
MycoBank MB837832.

Linteromyces quintiniae Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells or subcylindrical, brown, smooth, erect, unbranched, becoming dark brown and thick-walled with age, up to 8-septate and 100 µm tall, 3–4 µm diam, with integrated terminal conidiogenous cells. *Conidiogenous cells* solitary, erect, integrated on hyphae, pale to medium brown, smooth, doliiform to subcylindrical, 5–20 × 4–6 µm, with several cylindrical denticles near apex, 2–4 × 1–1.5 µm. *Conidia* solitary, aseptate, medium brown, slightly roughened, fusoid, apex and base with apiculus, 1–2 × 1 µm, guttulate, with paler germ slit along length of conidium body, (16–)20–22(–24) × (6–)7 µm.

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

Typus. Australia, New South Wales, Limpinwood Nature Reserve, Corina Lookout, on leaves of *Quintinia sieberi* (*Paracryphiaceae*), 25 May 2015, *B.A. Summerell*, HPC 2945 (holotype CBS H-24409, culture ex-type CPC 38231 = CBS 146792, ITS and LSU sequences GenBank MW175342.1 and MW175382.1, MycoBank MB837834).

Notes — *Linteromyces* resembles the genus *Subramaniomyces*, which has aseptate, polyblastic conidia occurring in branched, acropetal chains on mononematous, branched conidiophores occurring along the length of brown setae. It is morphologically distinct, however, in having solitary conidia, and being phylogenetically unrelated to *Subramaniomyces* (*S. podocarpi,* CBS 143176; Crous et al. 2017a), and close to *Tristratiperidium*, which again has conidia with terminal setulae (Daranagama et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Tristratiperidium microsporum* (strain MFLUCC 15-0413, GenBank NR_164238.1; Identities = 531/581 (91 %), 13 gaps (2 %)), *Kiliophora ubiensis* (strain IPBCC 131080, GenBank KF056850.1; Identities = 527/579 (91 %), 14 gaps (2 %)), and *Kirstenboschia diospyri* (strain CBS 134911, GenBank NR_145171.1; Identities = 505/559 (90 %), 17 gaps (3 %)). Closest hits using the **LSU** sequence are *Xyladictyochaeta lusitanica* (strain CPC 32526, GenBank MH107973.1; Identities = 818/844 (97 %), no gaps), *Castanediella tereticornis* (strain CBS 145068, GenBank NG_068600.1; Identities = 818/846 (97 %), one gap (0 %)), and *Castanediella cagnizarii* (strain CBS 101043, GenBank KP858988.1; Identities = 820/849 (97 %), four gaps (0 %)).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Xyladictyochaeta tristaniopsidis

Fungal Planet 1121 – 19 December 2020

Xyladictyochaeta tristaniopsidis Crous, *sp. nov.*

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

Classification — *Xyladictyochaetaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* erect, brown, smooth, subcylindrical, flexuous, multiseptate, 30–100 × 5–6 µm. *Conidiogenous cells* terminal and intercalary, polyphialidic, 5–17 × 4–5 µm, phialidic opening 1 µm diam, lacking flared collarettes. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, fusoid-ellipsoid, slightly curved, apex subobtuse, base truncate, 1 µm diam, medianly 1-septate, (16–)17–18(–20) × 2.5(–3) µm; each end with flexuous, unbranched appendage, apex central, base eccentric, 3–5 µm diam.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface vinaceous buff, reverse isabelline; on PDA surface and reverse dark mouse grey; on OA surface dark mouse grey.

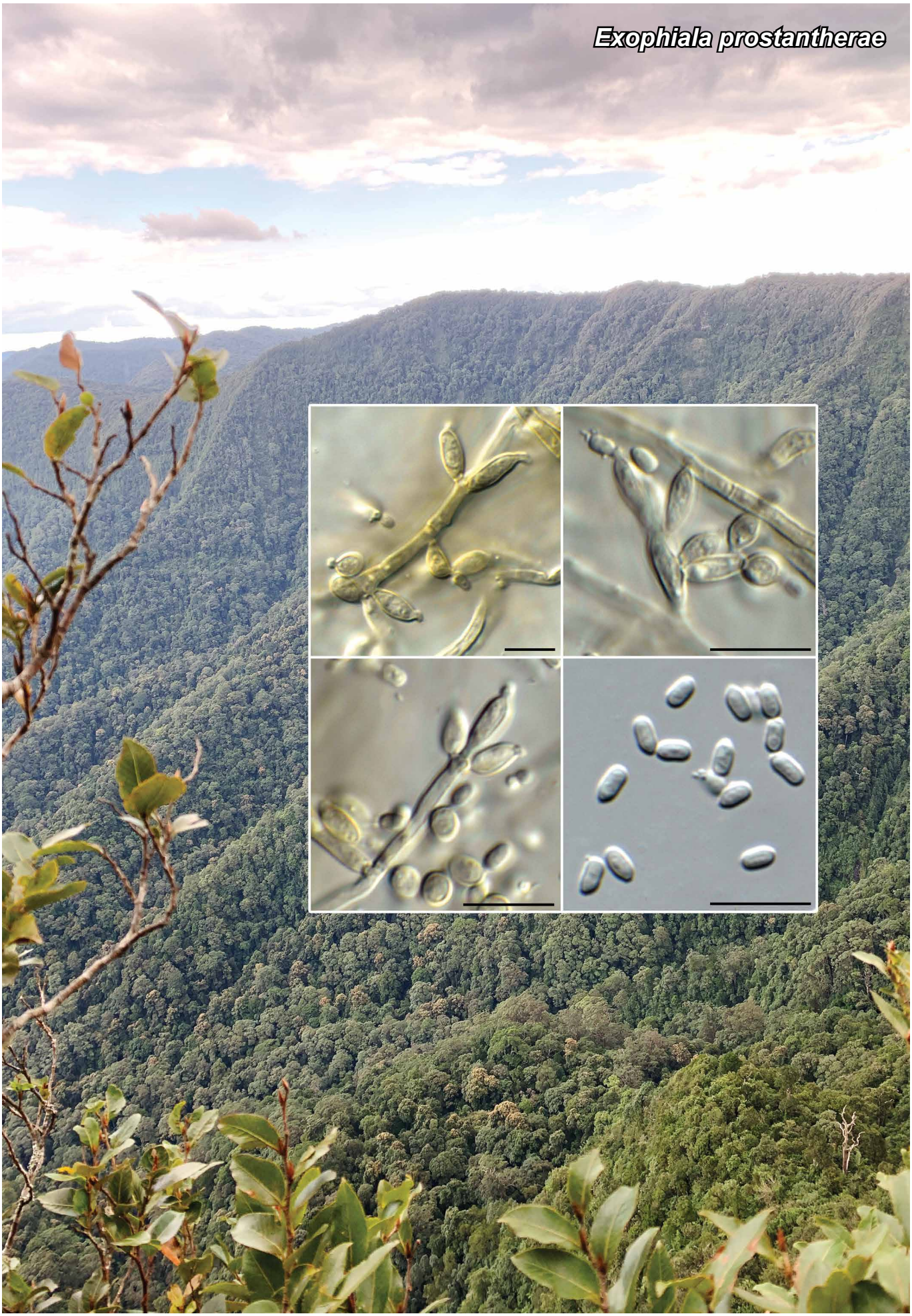
Typus. Australia, New South Wales, Limpinwood Nature Reserve, on leaves of *Tristaniopsis collina* (*Myrtaceae*), 25 May 2015, *B.A. Summerell*, HPC 2948 (holotype CBS H-24410, culture ex-type CPC 38240 = CBS 146793, ITS, LSU, *tef1* and *tub2* sequences GenBank MW175343.1, MW175383.1, MW173122.1 and MW173135.1, MycoBank MB837835).

Notes — The monotypic genus *Xyladictyochaeta* was established by Hernández-Restrepo et al. (2017) to accommodate dictyochaeta-like taxa with terminal and intercalary, polyphialidic conidiogenous cells. *Xyladictyochaeta tristaniopsidis* has slightly larger conidia than *X. lusitanica* (11–16 × 2–2.5 µm in Hernández-Restrepo et al. (2017); (10–)11–12(–13) × (2.5–)3 µm in Crous et al. (2018b)).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Xyladictyochaeta lusitanica* (strain CBS 142290, GenBank NR_154542.1; Identities = 561/575 (98 %), no gaps), *Castanediella eucalyptigena* (strain CBS 143178, GenBank NR_156384.1; Identities = 536/578 (93 %), 12 gaps (2 %)), and *Tristratiperidium microsporum* (strain MFLUCC 15-0413, GenBank NR_164238.1; Identities = 527/585 (90 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Xyladictyochaeta lusitanica* (strain CPC 32526, GenBank MH107973.1; Identities = 784/791 (99 %), no gaps), *Castanediella eucalyptigena* (strain CBS 143178, GenBank NG_067332.1; Identities = 763/784 (97 %), one gap (0 %)), and *Phlogicylindrium eucalypti* (strain CBS 120080, GenBank DQ923534.1; Identities = 768/791 (97 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Xyladictyochaeta lusitanica* (strain CBS 143502, GenBank MH108033.1; Identities = 467/563 (83 %), 20 gaps (3 %)).Closest hits using the ***tub2*** sequence had highest similarity to *Xyladictyochaeta lusitanica* (strain CPC 32526, GenBank MH108054.1; Identities = 416/477 (87 %), 15 gaps (3 %)), and *Cylindrium aeruginosum* (strain CBS 693.83, GenBank KM232124.1; Identities = 295/345 (86 %), 20 gaps (5 %)).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Exophiala prostantherae

Fungal Planet 1122 – 19 December 2020

Exophiala prostantherae Crous, *sp. nov.*

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

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes*.

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* aggregated in clusters, erect, subcylindrical, septate, 5–35 × 2 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical to cymbiform, phialidic, pale brown, smooth, 4–12 × 2.5–3 µm, apex with minute collarette. *Conidia* aseptate, guttulate, pale brown, smooth, subcylindrical, apex obtuse, tapering at base to truncate scar, 0.5 µm diam, (3–)4(–5) × (1.5–)2 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA and PDA surface olivaceous grey, reverse iron-grey; on OA surface iron-grey.

Typus. Australia, New South Wales, Limpinwood Nature Reserve, on leaves of *Prostanthera* sp. (*Lamiaceae*), 26 May 2015, *B.A. Summerell*, HPC 2952 (holotype CBS H-24411, culture ex-type CPC 38251 = CBS 146794, ITS and LSU sequences GenBank MW175344.1 and MW175384.1, MycoBank MB837836).

Notes — *Exophiala prostantherae* is phylogenetically closely related to *E. aquamarina* (from skin of leafy sea dragon, *Phycodures eques*, Boston, USA; conidia ellipsoidal to cylindrical, 6.7–19.2 × 4–4.8 µm; De Hoog et al. 2011) but distinct in having well-defined conidiophores, and smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala aquamarina* (strain IMP-BG-H0001, GenBank MH813288.1; Identities = 550/569 (97 %), four gaps (0 %)), *Cadophora fastigiata* (strain DN12, GenBank KY781375.1; Identities = 601/633 (95 %), four gaps (0 %)), and *Exophiala tremulae* (strain CBS 129355, GenBank NR_159874.1; Identities = 600/632 (95 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Exophiala pisciphila* (strain CBS 100.68, GenBank MH870790.1; Identities = 852/856 (99 %), no gaps), *Exophiala tremulae* (strain UAMH 10998, GenBank JF951155.1; Identities = 852/856 (99 %), no gaps), and *Exophiala equina* (strain CBS 128222, GenBank MH876297.1; Identities = 851/856 (99 %), no gaps).

Colour illustrations. Rainforest at Limpinwood Nature Reserve (photo B. Summerell). Conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Talaromyces pulveris

Fungal Planet 1123 – 19 December 2020

Talaromyces pulveris Crous, *sp. nov.*

Etymology. Name refers to the bore dust (L = *pulvis*) of a beetle, from which it was isolated.

Classification — *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic. *Microconidiophores* monoverticillate or as solitary phialides, short, 1–2-septate, arising from superficial hyphae, 15–25 × 2 µm. *Macroconidiophores* biverticillate, erect, subcylindrical, flexuous, penicillate, 70–300 × 2.5–3 µm, stipe smooth to slightly roughened, multiseptate. *Metulae* two to seven, subcylindrical, hyaline, smooth to slightly roughened, subcylindrical, aseptate, 8–12 × 2–3 µm; additional branches rarely observed. *Conidiogenous cells* phialidic, arranged in whorls of 2–6 per metula, acerose to subcylindrical with apical taper in upper third, 8–13 × 2–3 µm. *Conidia* arranged in long, unbranched chains, aseptate, green in masse, in basipetal chains, subglobose, thick-walled, smooth, 2–2.5 µm diam.

Culture characteristics — Colony diam, 7 d, in mm: CYA, 25 °C: Colonies restricted, non-sulcate, flat, thin; margin entire; mycelium white; sporulation absent or very sparsely produced; soluble pigments absent; exudates absent; reverse white. YES, 25 °C: Similar to CYA, though sporulation lacking. MEA, 25 °C: Colonies non-sulcate, moderately high; margin entire; mycelium white; sporulation sparse to strong; texture floccose to slightly funiculose; soluble pigments absent after 7 d, present after 2 wk, red; exudates absent; conidial colour *en masse* grey-green; reverse brown or dark brown. DG18, 25 °C: See CYA. OA, 25 °C: Similar to CYA, though sporulation poor to moderate; red soluble pigments produced after 2 wk. Colony diam, 7 d, in mm – CYA microcolonies to 5; CYA30°C microcolonies–5; CYA37°C no growth; CYAS no growth; DG18 3–6; MEA 7–10; OA 5–8; YES no growth or microcolonies; CREA no growth.

Typus. France, from bore dust of deathwatch beetle (*Xestobium rufovillosum*) infesting floorboards (*Quercus* wood), 2019, *C.A. Decock* (holotype CBS H-24417, culture ex-type CPC 38523 = MUCL pd8781 = DTO 432-H1 = CBS 146831, ITS, LSU, *cmdA*, *rpb2* and *tub2* sequences GenBank MW175345.1, MW175385.1, MW173099.1, MW173115.1 and MW173136.1, MycoBank MB837837).

Colour illustrations. Sampling site in France. Colony on MEA; conidiophores and conidiogenous cells giving rise to conidial chains. Scale bars = 10 µm.

Notes — *Talaromyces pulveris* represents a new species in section *Purpurei*, phylogenetically most closely related to *T. iowaense* (Samson et al. 2011, Yilmaz et al. 2014, Crous et al. 2018a, Guevara-Suarez et al. 2020). *Talaromyces rademirici* is a sister species of *T. pulveris* and *T. iowaense* (Samson et al. 2011, Yilmaz et al. 2014, Crous et al. 2018a, Guevara-Suarez et al. 2020, Houbraken et al. 2020). *Talaromyces iowaense*, *T. pulveris* and *T. rademirici* grow restrictedly on CYA and are unable to grow on CYA supplemented with 5 % NaCl. *Talaromyces pulveris* grows more restricted on MEA (7–10 mm) than *T. iowaense* (17–18 mm) and *T. rademirici* (14–15 mm). The production of subglobose conidia and inability of *T. pulveris* to grow on CYA incubated at 37 °C is shared with *T. iowaense*. In contrast, the conidia of *T. rademirici* are ellipsoidal and this species is able to grow on CYA incubated at 37 °C. *Talaromyces iowaense* is grows on CREA, while *T. pulveris* and *T. rademirici* are unable to grow on this medium (Yilmaz et al. 2014, Crous et al. 2018a).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Talaromyces pseudostromaticus* (strain AS3.16005, GenBank MT182956.1; Identities = 472/540 (87 %), 33 gaps (6 %)), *Talaromyces pittii* (strain CBS 139.84, GenBank MH861710.1; Identities = 472/540 (87 %), 33 gaps (6 %)), and *Talaromyces aculeatus* (strain BCC<THA> 88118, GenBank MH997879.1; Identities = 465/532 (87 %), 30 gaps (5 %)). Closest hits using the **LSU** sequence are *Talaromyces purpureus* (strain CBS 475.71, GenBank NG_064090.1; Identities = 787/807 (98 %), one gap (0 %)), *Talaromyces rademirici* (strain CBS 140.84, GenBank NG_064134.1; Identities = 815/837 (97 %), one gap (0 %)), and *Talaromyces dendriticus* (strain CBS 660.80, GenBank MH873068.1; Identities = 781/806 (97 %), one gap (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Talaromyces purpureus* (strain CBS 475.71, GenBank KJ885292.1; Identities = 354/410 (86 %), 16 gaps (3 %)), *Talaromyces ptychoconidium* (strain CV2807, GenBank JX140699.1; Identities = 443/550 (81 %), 50 gaps (9 %)), and *Talaromyces cecidicola* (strain CBS 101419, GenBank KJ885287.1; Identities = 285/336 (85 %), seven gaps (2 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Talaromyces rademirici* (strain CBS 140.84, GenBank KM023302.1; Identities = 697/760 (92 %), no gaps), *Talaromyces purpureus* (strain CBS 475.71, GenBank JN121522.1; Identities = 748/825 (91 %), no gaps), and *Talaromyces ptychoconidium* (strain DTO180F1, GenBank MK450880.1; Identities = 772/864 (89 %), no gaps. Closest hits using the ***tub2*** sequence had highest similarity to *Talaromyces rademirici* (strain CBS 140.84, GenBank KJ865734.1; Identities = 395/444 (89 %), nine gaps (2 %)), *Talaromyces iowaense* (as *Talaromyces* sp. GP-2018a; strain EMSL 2233, GenBank MH282578.1; Identities = 390/452 (86 %), 12 gaps (2 %)), and *Talaromyces ptychoconidium* (as *Penicillium* sp. CMV-2008c; strain CV323, GenBank GU385735.1; Identities = 297/346 (86 %), 14 gaps (4 %)).

Pedro W. Crous, Jos Houbraken, M. Meijer & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl, j.houbraken@wi.knaw.nl, m.meijer@wi.knaw.nl & e.groenewald@wi.knaw.nl
Cony A. Decock, Mycothèque de l'Université catholique de Louvain (MUCL, BCCMTM), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium; e-mail: cony.decock@uclouvain.be


Neocamarosporium leipoldtiae

Fungal Planet 1124 – 19 December 2020

Neocamarosporium leipoldtiae Crous, *sp. nov.*

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

Classification — *Neocamarosporiaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, erumpent, globose, 200–300 µm diam, with central ostiole; wall covered by brown, verruculose hyphae, 3–4 µm diam; wall consisting of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells or with a supporting cell, lining the inner cavity, hyaline, smooth, ampulliform with long cylindrical apical part, proliferating percurrently near apex, 12–35 × 5–7 µm. *Conidia* solitary, medium brown, ellipsoid to subcylindrical, apex obtuse, base truncate, muriformly septate, with 3–6 transverse septa, 2–6 oblique or vertical septa, thick-walled, surface roughened, 18–20(–21) × 7(–8) µm.

Culture characteristics — Colonies with abundant aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. South Africa, Western Cape Province, Nieuwoudtville, on leaves of *Leipoldtia schultzei* (*Aizoaceae*), 2018, *P.W. Crous*, HPC 3024 (holotype CBS H-24418, culture ex-type CPC 38531 = CBS 146774, ITS, LSU and *tub2* sequences GenBank MW175346.1, MW175386.1 and MW173137.1, MycoBank MB837838).

Notes — *Neocamarosporium* was established for a genus of camarosporium-like fungi occurring on dying leaves of a *Mesembryanthemum* sp. (*Aizoaceae*) (Crous et al. 2014). *Neocamarosporium leipoldtiae* was collected in the same area, again occurring on a member of the *Aizoaceae.* Phylogenetically, however, it is closely related to *Neocamarosporium salicorniicola*, described from *Salicornia* sp. (*Amaranthaceae*) collected in Thailand (Wanasinghe et al. 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocamarosporium* sp. (strain CF-288928, GenBank MG065823.1; Identities = 544/554 (98 %), one gap (0 %)), *Pleosporales* sp. 6 PV-2016 (strain DW, GenBank KU933734.1; Identities = 534/544 (98 %), two gaps (0 %)), and *Neocamarosporium salicornicola* (strain ZMCS3, GenBank MK809918.1; Identities = 509/520 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Neocamarosporium chichastianum* (strain CBS 137502, GenBank KP004483.1; Identities = 848/853 (99 %), no gaps), *Neocamarosporium salicornicola* (strain MFLUCC 15-0957, GenBank MF434281.1; Identities = 842/848 (99 %), no gaps), and *Chaetosphaeronema hispidulum* (strain CBS 826.88, GenBank EU754145.1; Identities = 862/870 (99 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Neocamarosporium calvescens* (strain T77I1, GenBank MK140511.1; Identities = 265/289 (92 %), one gap (0 %)), *Phoma betae* (strain CBS 109410, GenBank MK255063.1; Identities = 284/311 (91 %), seven gaps (2 %)) and *Dimorphosporicola tragani* (strain CBS 570.85, GenBank KU728616.1; Identities = 412/478 (86 %), 22 gaps (4 %)).

Colour illustrations. Flowers of *Leipoldtia schultzei*. Conidiomata on MEA with central ostiole; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Dothiora aloidendri & Hantamomyces aloidendri

Fungal Planet 1125 & 1126 – 19 December 2020

Dothiora aloidendri Crous, *sp. nov.*

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

Classification — *Dothioraceae*, *Dothideales*, *Dothideomycetes.*

Conidiomata pycnidial, globose, black, glabrous, erumpent, 200–350 µm diam, aggregated in dense clusters, forming a superficial layer on agar, exuding a creamy conidial mass. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform to doliiform, phialidic, 6–9 × 5–7 µm. *Conidia* solitary, straight, subcylindrical, aseptate, guttulate, hyaline, smooth, thin-walled, apex obtuse, tapering at base to truncate hilum, 1–1.5 µm diam, (10–)12–13(–14) × (3–)4 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam after 2 wk at 25 °C. On MEA surface sepia, reverse isabelline; on PDA surface iron-grey, reverse olivaceous-grey; on OA surface olivaceous-grey.

Typus. South Africa, Western Cape Province, Namaqualand, on leaves of *Aloidendron dichotomum* (*Asphodeloideae*), 2018, *P.W. Crous*, HPC 3039 (holotype CBS H-24419, culture ex-type CPC 38535 = CBS 146775, ITS, LSU, *tef1* and *tub2* sequences GenBank MW175347.1, MW175387.1, MW173123.1 and MW173138.1, MycoBank MB837839).

Notes — Species of *Dothiora* commonly form *Dothichiza* and hormonema-like morphs in culture (Crous & Groenewald 2016, 2017), as observed in *D. aloidendri*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dothiora europaea* (strain EXF-12400, GenBank MK460357.1; Identities = 448/469 (96 %), two gaps (0 %)), *Dothiora sorbi* (strain CBS 742.71, GenBank KU728514.1; Identities = 554/591 (94 %), four gaps (0 %)), and *Dothiora elliptica* (strain CBS 736.71, GenBank KU728502.1; Identities = 489/522 (94 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Dothiora infuscans* (strain FMR 16326, GenBank NG_066397.1; Identities = 782/792 (99 %), no gaps), *Dothiora oleae* (strain CBS 472.69, GenBank MH871116.1; Identities = 844/856 (99 %), no gaps), and *Neophaeocryptopus cytisi* (strain MFLUCC 14-0970, GenBank NG_059643.1; Identities = 826/838 (99 %), one gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Dothiora oleae* (strain CBS 235.57, GenBank KU728587.1; Identities = 195/200 (98 %), one gap (0 %)), *Dothiora viburnicola* (strain CBS 274.72, GenBank KU728591.1; Identities = 195/203 (96 %), no gaps), and *Dothiora bupleuricola* (strain CBS 112.75, GenBank KU728579.1; Identities = 194/201 (97 %), three gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Dothiora phillyreae* (strain CBS 473.69, GenBank KU728629.1; Identities = 503/618 (81 %), 21 gaps (3 %)), *Dothiora maculans* (strain CBS 299.76, GenBank KU728621.1; Identities = 470/569 (83 %), 27 gaps (4 %)), and *Dothiora oleae* (strain CBS 152.71, GenBank KU728625.1; Identities = 495/609 (81 %), 32 gaps (5 %)).

Hantamomyces Crous, *gen. nov*.

Etymology. Name refers to the Hantam district where it was collected, Nieuwoudtville, Northern Cape Province, South Africa.

Classification — *Ophiocordycipitaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiophores arising from superficial hyphae, erect, solitary, cylindrical, pale brown, smooth, branched, septate. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical; conidiophores with terminal conidiogenous region with denticulate loci and with separating cell leaving minute collarette; conidiogenous cells giving rise to next cell in zigzag fashion (sympodial), appearing like a drawn out rachis. *Conidia* hyaline, smooth, fusoid, tapering towards both ends to truncate hilum with minute marginal frill and conidia occurring in long, unbranched chains, forming a mucoid droplet with age.

Type species. Hantamomyces aloidendri Crous.
MycoBank MB837840.

Hantamomyces aloidendri Crous, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 2.5–3.5 µm diam hyphae. *Conidiophores* arising from superficial hyphae, erect, solitary, cylindrical, pale brown, smooth, branched, septate, up to 200 µm tall, 2.5–3 µm diam. *Conidiogenous cells* integrated, pale brown, smooth, subcylindrical; conidiophores with terminal conidiogenous region with 1–2 denticulate loci, 1 × 1 µm, with separating cell leaving minute collarette; one locus in basal region above septum, and second locus if present below apical septum, 10–30 × 2.5–3 µm, but conidiogenous cells giving rise to next cell in zigzag fashion (sympodial), appearing like a drawn out rachis. *Conidia* hyaline, smooth, guttulate to granular, fusoid, not to slightly constricted at median septum, tapering towards both ends to truncate hilum with minute marginal frill, scar 1 µm diam, at times somewhat darkened, with conidia occurring in long, unbranched chains, forming a mucoid droplet with age; conidial chains with conidia attached to one another by minute separating cell, with collarette developing at each end, 1–3-septate, (15–)17–18(–20) × (3.5–)4(–5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff.

Typus. South Africa, Western Cape Province, Nieuwoudtville, on leaves of *Aloidendron dichotomum* (*Asphodelaceae*), 2018, *P.W. Crous*, HPC 3020 (holotype CBS H-24432, culture ex-type CPC 38655 = CBS 146814, ITS and LSU sequences GenBank MW175348.1 and MW175388.1, MycoBank MB837841).

Colour illustrations. *Aloidendron dichotomum* growing along the mountain ridge. Left column *D. aloidendri*. Conidiomata on SNA; conidiogenous cells giving rise to conidia; conidia. Right column *Hantamomyces aloidendri*. Conidiophores giving rise to chains of conidia; conidia. Scale bars = 10 µm.

(for Notes see Supplementary material page FP1125 & 1126;
and for tree on Supplemetary material page FP1141)

Pedro W. Crous & Johannes 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


Suttonomyces cephalophylli

Fungal Planet 1127 – 19 December 2020

Suttonomyces cephalophylli Crous, *sp. nov.*

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

Classification — *Massarinaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, immersed in host tissue, pycnidial, globose, brown, 150–200 µm diam; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells, hyaline, smooth, phialidic, 4–6 × 3–5 µm. *Conidia* solitary, aseptate, medium brown, thick-walled, verruculose to spikey, ellipsoid with bluntly rounded ends, (12–)14–16(–18) × (7–)8–10(–12) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and lobate, smooth margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface dirty white in centre, cinnamon in outer region and in reverse; on PDA surface and reverse isabelline to cinnamon; on OA surface cinnamon.

Typus. South Africa, Western Cape Province, Clanwilliam, Rocklands camping, on leaves of *Cephalophyllum pilansii* (*Aizoaceae*), 2018, *P.W. Crous*, HPC 3055 (holotype CBS H-24420, culture ex-type CPC 38541 = CBS 146787, ITS and LSU sequences GenBank MW175349.1 and MW175389.1, MycoBank MB837842).

Notes — The present collection clusters with species of *Suttonomyces* (Wijayawardene et al. 2015), but is distinct from known species in the genus in that it lacks muriformly-septate conidia and paraphyses.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Suttonomyces rosae* (strain MFLU 18-0112, GenBank NR_157548.1; Identities = 447/469 (95 %), three gaps (0 %)), *Stagonospora bicolor* (strain LF2, GenBank KX510131.1; Identities = 347/367 (95 %), three gaps (0 %)), and *Stagonospora pseudopaludosa* (strain CBS 136424, GenBank NR_137840.1; Identities = 348/370 (94 %), four gaps (1 %)). Closest hits using the **LSU** sequence are *Suttonomyces rosae* (strain MFLU 18-0112, GenBank NG_059882.1; Identities = 807/811 (99 %), no gaps), *Helminthosporium velutinum* (strain L136, GenBank KY984355.1; Identities = 838/850 (99 %), no gaps), and *Helminthosporium tiliae* (strain L89, GenBank KY984346.1; Identities = 837/850 (98 %), no gaps).

Colour illustrations. Flower and leaves of *Cephalophyllum pilansii*. Conidiomata on host tissue and on OA (scale bars = 200 µm); conidia (scale bar = 10 µm).

Pedro W. Crous & Johannes 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


Endoconidioma euphorbiae

Fungal Planet 1128 – 19 December 2020

Endoconidioma euphorbiae Crous, *sp. nov.*

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

Classification — *Dothioraceae*, *Dothideales*, *Dothideomycetes.*

Conidiomata erumpent, globose, black, pycnidial, 200–250 µm diam, with central ostiole exuding a black mucoid conidial mass. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to ampulliform, 7–10 × 5–7 µm, proliferating percurrently at apex. *Conidia* solitary, aseptate, golden-brown, thick-walled, verruculose, ellipsoid, apex obtuse, base bluntly rounded, (11–)12–13(–14) × (7–)8(–9) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, feathery margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface and reverse iron-grey; on OA surface olivaceous grey.

Typus. South Africa, Western Cape Province, Nieuwoudtville, on leaves with tip dieback of *Euphorbia mauritanica* (*Euphorbiaceae*), 2018, *P.W. Crous*, HPC 3069 (holotype CBS H-24422, culture ex-type CPC 38551 = CBS 146776, ITS and LSU sequences GenBank MW175350.1 and MW175390.1, MycoBank MB837843).

Additional material examined. South Africa, Western Cape Province, Nieuwoudtville, on leaves with dieback of *Brunsvigia bosmaniae* (*Amaryllidaceae*), 2018, *P.W. Crous*, HPC 3041 (CBS H-24423, culture CPC 38583 = CBS 146777, ITS and LSU sequences GenBank MW175351.1 and MW175391.1).

Endoconidioma Tsuneda et al., Mycologia 96: 1129. 2004.

Synonym. *Coniozyma* Crous, In: Marincowitz et al., CBS Diversity Ser. (Utrecht) 7: 97. 2008.

Endoconidioma carpetanum (Bills et al.) Crous, *comb. nov*. MycoBank MB837886

Basionym. *Hormonema carpetanum* Bills et al., Stud. Mycol. 50: 152. 2004.

Endoconidioma leucospermi (Crous & Denman) Crous, *comb. nov*. MycoBank MB837887

Basionym. *Coniothyrium leucospermi* Crous & Denman, S. Afr. J. Bot. 64: 139. 1998.

Synonym. *Coniozyma leucospermi* (Crous & Denman) Crous, In: Marincowitz et al., CBS Diversity Ser. (Utrecht) 7: 97. 2008.

Notes — *Endoconidioma* (based on *E. populi*) is a genus originally described from twigs of *Populus tremuloides* collected in Canada. It is characterised by having a yeast-like morph in culture, as well as endoconidia, and a coelomycetous, coniothyrium-like morph (Tsuneda et al. 2004). *Endoconidioma* appears to be the oldest name for a clade in the *Dothioraceae* containing species with highly adaptable morphology. *Coniozyma* (based on *C. leucospermi*), is a morphologically highly variable fungus associated leaf spots of *Proteaceae* (Taylor & Crous 2001, Marincowitz et al. 2008), which appears to be better accommodated in *Endoconidioma*. *Endoconidioma euphorbiae* is phylogenetically related to *E. leucospermi* (conidia 6–12 × 3–8 µm *in vivo*, 6.5–15 × 3.5–8 µm *in vitro*; Taylor & Crous 2001), but distinguished based on its slightly larger conidia. Isolates from *Brunsvigia bosmaniae* (CPC 38583, conidia (13–)15–16(–17) × 7(–8) µm) are similar in size, though slightly more subcylindrical, and olivaceous brown in colour, but are accepted as falling within the variation for *E. euphorbiae*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 38551 had highest similarity to *Coniozyma leucospermi* (strain CBS 111289, GenBank EU552113.1; Identities = 579/592 (98 %), four gaps (0 %)), *Hormonema carpetanum* (strain 235J14, GenBank KU516485.1; Identities = 561/574 (98 %), four gaps (0 %)), and *Endoconidioma populi* (strain NWHC 46379-1433_1SD, GenBank MK782233.1; Identities = 516/528 (98 %), three gaps (0 %)). The ITS sequences of CPC 38551 and 38583 differ at two nucleotide positions (590/592 similar nucleotides). Closest hits using the **LSU** sequence of CPC 38551 are *Coniozyma leucospermi* (strain CBS 111289, GenBank EU552113.1; Identities = 844/849 (99 %), no gaps), *Hormonema carpetanum* (strain ATCC 74360, GenBank MF611880.1; Identities = 843/849 (99 %), no gaps), and *Endoconidioma populi* (strain UAMH 10297, GenBank NG_059198.1; Identities = 812/819 (99 %), no gaps). The LSU sequences of CPC 38551 and 38583 differ at one nucleotide position (811/812 similar nucleotides).

Colour illustrations. *Euphorbia mauritanica*. Conidia on SNA, and conidiomata oozing dark brown conidia on PNA (scale bars = 200 µm); conidiogenous cells giving rise to conidia; conidia (scale bars = 10 µm).

(for tree see Supplemetary material page FP1141)

Pedro W. Crous & Johannes 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


Neometuloclados poriella seifertii

Fungal Planet 1129 – 19 December 2020

Neometulocladosporiella seifertii Crous, *sp. nov.*

Etymology. Named after Keith A. Seifert, a Canadian mycologist who is always impressed by hyphomycetes with such magnificent, pigmented, solitary conidiophores.

Classification — *Rutstroemiaceae*, *Helotiales*, *Leotiomycetes.*

Conidiophores dimorphic. *Microconidiophores* erect, medium brown, smooth, solitary, subcylindrical, straight to flexuous, 1–3-septate, 35–70 × 3–5 µm, giving rise to a single, terminal conidiogenous cell. *Conidiogenous cells* 10–30 × 3–4 µm, medium brown, smooth, clavate, with a flat-tipped apical locus, 1–2 µm diam, unthickened, not darkened, giving rise to ramoconidia. *Macroconidiophores* solitary, erect, straight to flexuous, unbranched, subcylindrical, dark brown, smooth, arising from superficial mycelium, 250–600 × 10–16 µm, 5–12-septate, dark brown, smooth, clavate, giving rise to a series of branches, 10–15 × 5–7 µm, which are medium brown, smooth, subcylindrical to clavate, aseptate, base abruptly tapered to flat-tipped locus, 2 µm diam, apex with 2–4 denticles, 1 × 1 µm, unthickened, not darkened, giving rise to secondary ramoconidia. *Primary ramoconidia* fusoid-ellipsoid to subcylindrical or clavate, medium brown, smooth, 0–1-septate, 10–22 × 5–6 µm, with 1–3 apical flat-tipped loci, 1 µm diam, unthickened, not darkened. *Secondary ramoconidia* straight, pale brown, smooth to finely verruculose, 0–1-septate, subcylindrical with obtuse ends, 10–14 × 5–6 µm, base with abrupt taper to truncate hilum, 1–1.5 µm diam, apex with 1–3 denticles, 1 µm diam, not thickened nor darkened, giving rise to branched, dry chains of acropetal *conidia*, pale brown, smooth to finely verruculose, subcylindrical to ellipsoid with obtuse ends, constricted at median septum, (8–)9–10(–12) × (4–)4.5(–5) µm, with a flat-tipped basal hilum and 1–3 apical denticles, 0.5–1 µm diam, not thickened nor darkened.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface isabelline, reverse hazel; on PDA surface isabelline, reverse umber; on OA surface isabelline.

Typus. South Africa, Western Cape Province, Clanwilliam, on leaves of *Combretum caffrum* (*Combretaceae*), 2018, *P.W. Crous*, HPC 3048 (holotype CBS H-24424, culture ex-type CPC 38599 = CBS 146795, ITS and LSU sequences GenBank MW175352.1 and MW175392.1, MycoBank MB837844).

Colour illustrations. Leaves and branches of *Combretum caffrum*. Erect mononematous macroconidiophores on SNA; Clavate conidiophores giving rise to a series of branches and conidiogenous cells; microconidiophores and chains of conidia. Scale bars = 10 µm.

Notes — The hitherto monotypic genus *Neometulocladosporiella* was established for a genus of hyphomycetes occurring on *Eucalyptus* leaves collected in Colombia (Crous et al. 2018c). Morphologically the two species are very similar regarding their conidiophores, branches and conidial dimensions, and they are best distinguished based on the DNA sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neometulocladosporiella eucalypti* (strain CPC 31787, GenBank NR_160350.1; Identities = 535/555 (96 %), one gap (0 %)), *Lanzia allantospora* (strain CBS 124334, GenBank AB926099.1; Identities = 527/559 (94 %), nine gaps (1 %)), and *Rutstroemia firma* (voucher TU 104487, GenBank LT158448.1; Identities = 516/555 (93 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Neometulocladosporiella eucalypti* (strain CPC 31787, GenBank NG_064541.1; Identities = 831/836 (99 %), no gaps), *Lanzia allantospora* (strain CBS 124334, GenBank AB926154.1; Identities = 838/847 (99 %), no gaps), and *Ciboria americana* (voucher KUS-F52240, GenBank JN086702.1; Identities = 744/760 (98 %), no gaps).

Pedro W. Crous & Johannes 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


Verrucocladosporium carpobroti

Fungal Planet 1130 – 19 December 2020

Verrucocladosporium carpobroti Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes.*

Conidiophores solitary, erect, straight to flexuous, branched, subcylindrical, medium brown, verruculose, arising from superficial mycelium, 50–200 × 5–6 µm, 2–10-septate, giving rise to a series of branches, 20–50 × 5–6 µm, which are medium brown, verruculose, subcylindrical, 1–3-septate. *Conidiogenous cells* integrated, subcylindrical, medium brown, verruculose, terminal and intercalary, 20–40 × 3–5 µm; loci thickened, darkened and refractive, 2–3 µm diam. *Primary ramoconidia* fusoid-ellipsoid to subcylindrical, thick-walled, medium brown, verruculose to warty, 0–2-septate, 25–55 × 4–5 µm, with 1–3 apical, flat-tipped loci, 2 µm diam, thickened, darkened. *Secondary ramoconidia* straight, medium brown, verruculose to warty, thick-walled, 0–1-septate, subcylindrical to fusoid-ellipsoid, 15–20 × 4–5 µm; hila thickened and darkened, 1.5–2 µm diam, giving rise to branched, dry chains of acropetal *conidia*, medium brown, verruculose to warty, subcylindrical to fusoid-ellipsoid, 0(–1)-septate, (10–)12–14(–16) × (4–)5–6 µm; hila 1.5–2 µm diam, thickened and darkened.

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

Typus. South Africa, Western Cape Province, Clanwilliam, on leaves of *Carpobrotus quadrifidus* (*Aizoaceae*), 2018, *P.W. Crous*, HPC 3027 (holotype CBS H-24427, culture ex-type CPC 38635 = CBS 146784, ITS and LSU sequences GenBank MW175353.1 and MW175393.1, MycoBank MB837845).

Additional material examined. South Africa, Western Cape Province, Namaqualand, on leaves of *Dimorphotheca* sp. (*Asteraceae*), 2018, *P.W. Crous*, HPC 3040 (CBS H-24430, culture CPC 38645 = CBS 146796, ITS and LSU sequences GenBank MW175354.1 and MW175394.1).

Notes — *Verrucocladosporium* was introduced to accommodate cladosporium-like species having ± planate, non-coronate conidiogenous loci and hila, and warty, verrucose conidia. *Verrucocladosporium carpobroti* is related to *V. dirinae* (conidiophores up to 85 µm long, conidia 4–18 (–23) × (2–)2.5–3.5 µm, 0–1-septate; Crous et al. 2007a), but is morphologically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Verrucocladosporium dirinae* (strain CBS 112794, GenBank NR_152317.1; Identities = 496/509 (97 %), no gaps), *Verrucocladosporium visseri* (strain CPC 36317, GenBank NR_166320.1; Identities = 475/487 (98 %), one gap (0 %)), and *Graphiopsis chlorocephala* (strain CPC 11969, GenBank EU009458.2; Identities = 475/498 (95 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Verrucocladosporium dirinae* (strain MUT<ITA> 4857, GenBank KP671739.1; Identities = 865/873 (99 %), no gaps), *Graphiopsis chlorocephala* (strain CPC 11969, GenBank EU009458.2; Identities = 865/873 (99 %), no gaps), and *Verrucocladosporium visseri* (strain CPC 36317, GenBank NG_068322.1; Identities = 861/869 (99 %), no gaps)

Colour illustrations. Flower of *Carpobrotus quadrifidus*. Conidiophores on SNA; conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Stemphylium carpobroti

Fungal Planet 1131 – 19 December 2020

Stemphylium carpobroti Crous, *sp. nov.*

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

Classification — *Pleosporaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of brown, septate, branched, finely verruculose, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, mostly unbranched, brown, finely verruculose, 40–120 × 4–7 µm, 3–5-septate, becoming swollen towards conidiogenous cell. *Conidiogenous cells* terminal, clavate, brown, finely verruculose, thick-walled, 10–20 × 8–9 µm, with terminal locus, 3–4 µm diam. *Conidia* solitary, dark brown, verruculose, ellipsoid to obovoid, constricted at medium septum, tapering to subobtuse apex, (30–)35–45(–70) × (17–)20–25 µm, with (3–)4(–6) transverse septa, and 1–4 vertical or oblique septa per transverse section.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. South Africa, Western Cape Province, Clanwilliam, on leaves of *Carpobrotus quadrifolius* (*Aizoaceae*), 2018, *P.W. Crous*, HPC 3027 (holotype CBS H-24428, culture ex-type CPC 38637 = CBS 146789, ITS, LSU and *gapdh* sequences GenBank MW175355.1, MW175395.1 and MW173103.1, MycoBank MB837846).

Notes — *Stemphylium carpobroti* is closely related to *S. novae-zelandiae* (conidia (31–)34–40.5(–45.5) × (9–)11–13(–14.5) µm, with 3–5(–7) *transverse septa* and 1–2 *longitudinal* or *oblique septa* per transverse sector; Woudenberg et al. 2017), but is distinct in having larger conidia. *Stemphylium vesicarium* is also closely related, but generally has shorter conidia (see Woudenberg et al. 2017).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Asteromyces cruciatus* (strain CBS 171.63, GenBank NR_159604.1; Identities = 548/564 (97 %), six gaps (1 %)), *Stemphylium vesicarium* (strain NIHHS404, GenBank KY555005.1; Identities = 553/571 (97 %), four gaps (0 %)), and *Stemphylium lucomagnoense* (strain CIRM-BRFM2667, GenBank MK691703.1; Identities = 560/579 (97 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Stemphylium botryosum* (strain CBS 714.68, GenBank NG_069738.1; Identities = 849/851 (99 %), no gaps), *Stemphylium vesicarium* (strain 18ALIM004, GenBank MT472605.1; Identities = 849/851 (99 %), no gaps), and *Stemphylium eturmiunum* (strain CBS 109845, GenBank NG_069866.1; Identities = 842/844 (99 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Stemphylium lycopersici* (strain G9RS, GenBank MN393479.1; Identities = 369/377 (98 %), no gaps), *Stemphylium vesicarium* (strain On16-499, GenBank MK675745.1; Identities = 369/377 (98 %), no gaps), and *Stemphylium globuliferum* (strain SWp202, GenBank KF479194.1; Identities = 369/377 (98 %), no gaps).

Colour illustrations. Leaves of *Carpobrotus quadrifolius*. Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Neocladosporium osteospermi

Fungal Planet 1132 – 19 December 2020

Neocladosporium osteospermi Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetes*.

Mycelium of branched, septate, 2.5–3 µm diam hyphae, mot constricted at septa, medium brown, verruculose. *Conidiophores* reduced to conidiogenous cells on hyphae, or erect, straight, sometimes slightly flexuous, narrowly cylindrical, non-geniculate, or nodulose, unbranched, 0–2-septate, up to 65 µm long, 2–3 µm wide, medium brown, verruculose. *Conidiogenous cells* integrated, mostly terminal, sometimes intercalary, cylindrical, 15–35 µm long, proliferating sympodially with 1–3 conidiogenous loci, 2–3 µm diam, thickened, darkened and refractive. *Ramoconidia* cylindrical, 15–35 × 4–5 µm, 1–3-septate, concolorous with conidiophores, thick-walled, irregularly rough-walled, smooth to verruculose to warty, apically with up to two hila, 2–3 µm diam, thickened, darkened and refractive. *Conidia* catenate, in branched, chains, ellipsoid, fusoid to subcylindrical, (11–)13–16(–20) × (3–)3.5(–4) µm, 0–1-septate, medium brown, thick-walled, smooth to verruculose to warty, somewhat attenuated towards both ends, hila truncate, 2–3 µm diam, darkened, thickened and refractive.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. South Africa, Western Cape Province, Clanwilliam, on leaf spots of *Osteospermum moniliferum* (*Asteraceae*), 2018, *P.W. Crous*, HPC 3035 (holotype CBS H-24429, culture ex-type CPC 38641 = CBS 146813, ITS and LSU sequences GenBank MW175356.1 and MW175396.1, MycoBank MB837847).

Notes — *Neocladosporium* presently contains two species, namely *N. leucadendri* and *N. syringae*, characterised by having conidia with a warty, mucoid outer layer (Bezerra et al. 2017, Crous et al. 2020b). *Neocladosporium osteospermi* adds a third species to the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocladosporium syringae* (strain CPC 35750, GenBank NR_170057.1; Identities = 648/681 (95 %), 13 gaps (1 %)), *Davidiellomyces australiensis* (strain CBS 142165, GenBank NR_154036.1; Identities = 612/687 (89 %), 22 gaps (3 %)), and *Davidiellomyces juncicola* (strain CPC 38038, GenBank NR_166347.1; Identities = 618/699 (88 %), 28 gaps (4 %)). Closest hits using the **LSU** sequence are *Neocladosporium syringae* (strain CPC 35750, GenBank MT223912.1; Identities = 774/778 (99 %), one gap (0 %)), *Neocladosporium leucadendri* (strain CBS 131317, GenBank NG_057949.1; Identities = 833/841 (99 %), no gaps), and *Neocladosporium leucadendri* (as *Toxicocladosporium leucadendri*; strain CPC 29092, GenBank LT799745.1; Identities = 738/746 (99 %), no gaps).

Colour illustrations. Flower of *Osteospermum moniliferum*. Conidiophores and conidiogenous cells giving rise to conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Eucasphaeria proteae

Fungal Planet 1133 – 19 December 2020

Eucasphaeria proteae Crous, *sp. nov.*

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

Classification — *Niessliaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2.5 µm diam hyphae. *Conidiomata* sporodochial, 100–300 µm diam, becoming aggregated, forming large orange, mucoid colonies on agar; basal stroma of hyaline *textura angularis*, giving rise to hyaline, smooth, branched, 3–10-septate conidiophores, subcylindrical, 20–70 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, flexuous, phialidic, hyaline, smooth, 8–20 × 2.5–3 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to slightly curved, apex obtuse, base truncate, 1.5–2 µm diam, 0(–3)-septate, (8–)15–17(–20) × (2–)2.5(–3) µm; 3-septate conidia can become up to 65 µm in length, and frequently undergo microcyclic conidiation.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 25 mm diam after 2 wk at 25 °C. On MEA, PDA and OA, surface and reverse orange.

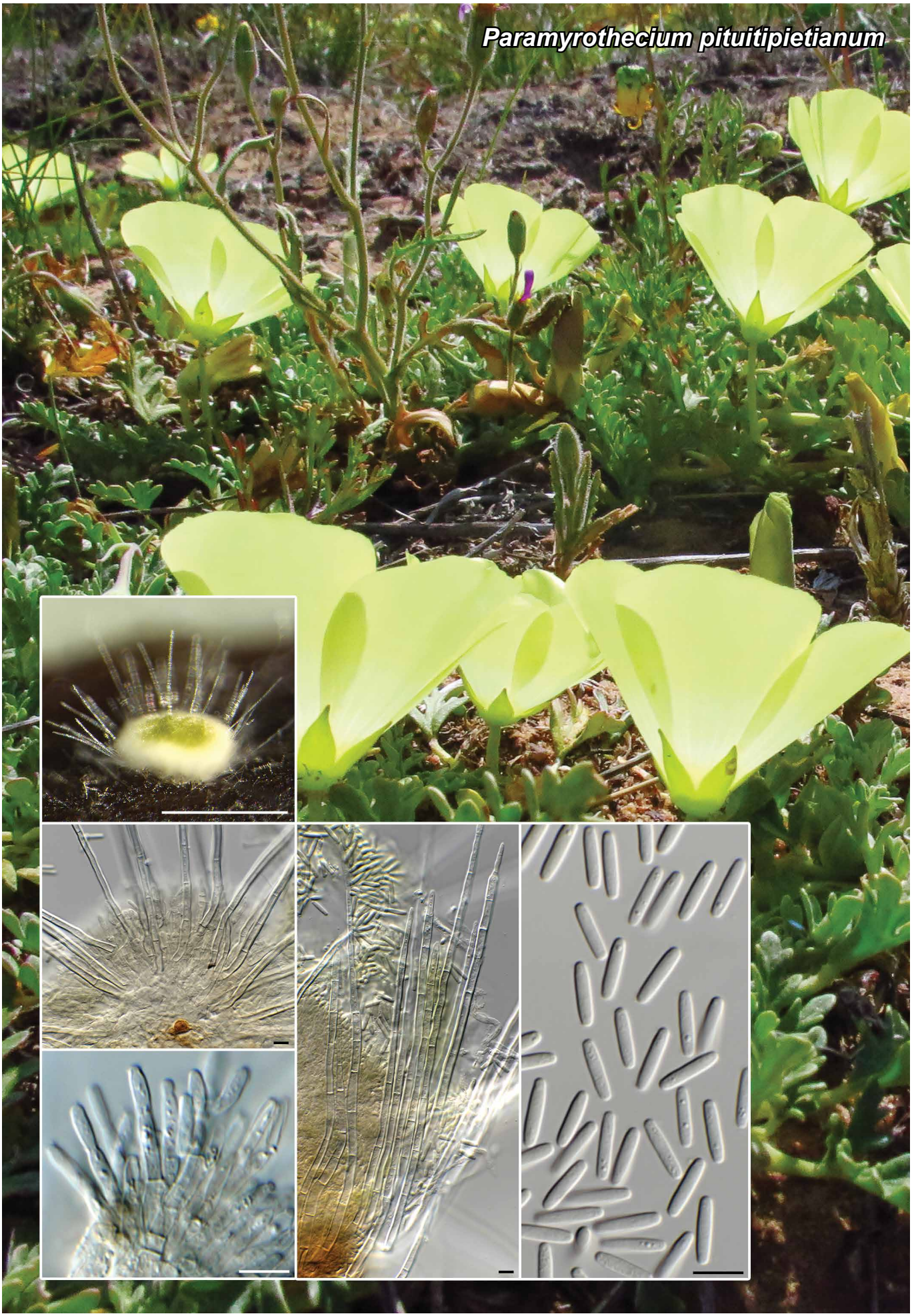
Typus. South Africa, Western Cape Province, Clanwilliam, on leaves of *Protea neriifolia* (*Proteaceae*), 2018, *P.W. Crous*, HPC 3030 (holotype CBS H-24433, culture ex-type CPC 38661 = CBS 146815, ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank MW175357.1, MW175397.1, MW173116.1 and MW173129.1, MycoBank MB837848).

Notes — Culture CPC 38661 was originally derived from hyaline, aseptate microconidia found on the surface of leaves of *Protea neriifolia*. In culture, sporodochia with an *Eucasphaeria* asexual morph developed (Crous et al. 2007b). Based on LSU the present fungus proved to be closely related to *Rosasphaeria moravica*, which was described as forming densely aggregated orange pycnidial conidiomata in culture (Jaklitsch & Voglmayr 2012). Based on the sporodochia, and conidial morphology, the present collection is best accommodated in *Eucasphaeria*, although the relationship with *Rosasphaeria* deserves further study.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Rosasphaeria moravica* (strain CBS 124270, GenBank NR_138377.1; Identities = 489/572 (85 %), 26 gaps (4 %)), *Neoeucasphaeria eucalypti* (strain CBS 145075, GenBank NR_161136.1; Identities = 489/573 (85 %), 35 gaps (6 %)), and *Eucasphaeria rustici* (strain CPC 28946, GenBank NR_154028.1; Identities = 488/573 (85 %), 31 gaps (5 %)). Closest hits using the **LSU** sequence are *Rosasphaeria moravica* (strain LMM, GenBank JF440985.1; Identities = 836/851 (98 %), two gaps (0 %)), *Eucasphaeria capensis* (strain CBS 120027, GenBank EF110619.1; Identities = 855/874 (98 %), two gaps (0 %)), and *Niesslia pulchriseta* (strain CBS 839.96, GenBank MG826846.1; Identities = 854/877 (97 %), five gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Rosasphaeria moravica* (strain LMM, GenBank JF440986.1; Identities = 586/683 (86 %), two gaps (0 %)), *Ophiocordyceps mosingtoensis* (strain BCC 30904, GenBank MK214100.1; Identities = 545/679 (80 %), six gaps (0 %)), and *Ophiocordyceps coccidiicola* (strain NBRC 100682, GenBank AB968545.1; Identities = 542/678 (80 %), two gaps (0 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Tolypocladium tropicale* (strain MX338, GenBank KF747113.1; Identities = 793/864 (92 %), two gaps (0 %)), *Isaria takamizusanensis* (strain F896, GenBank GU979994.1; Identities = 831/911 (91 %), two gaps (0 %)), and *Nectria haematococca* (strain GJS89-70, GenBank AY489624.1; Identities = 831/912 (91 %), four gaps (0 %)).

Colour illustrations. Flowers and leaves of *Protea neriifolia*. Sporodochia on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Paramyrothecium pituitipietianum

Fungal Planet 1134 – 19 December 2020

Paramyrothecium pituitipietianum Crous, *sp. nov.*

Etymology. Composed of pituita (= mucus, snot) and the name Piet (referring to 'Pietsnot' = Snotty Pete, the common South African name of *Grielum humifusum*).

Classification — *Stachybotryaceae*, *Hypocreales*, *Sordariomycetes.*

Conidiomata sporodochial, stromatic, superficial, cupulate, separate to gregarious, oval, 200–350 µm diam with a white, setose fringe surrounding the dark green mucoid conidial mass. *Stroma* well-developed of hyaline *textura angularis. Setae* thick-walled, 7–10-septate, straight to flexuous, hyaline, 100–300 × 4–5 µm, tapering to obtuse apex. *Conidiophores* penicillately branched, hyaline, smooth, 2–4-septate, 20–35 × 3–4 µm. *Conidiogenous cells* phialidic, hyaline, smooth, subcylindrical, tapering at tip, 10–15 × 2–2.5 µm. *Conidia* aseptate, subcylindrical, straight, pale green, smooth, guttulate, ends obtuse, (7–)9–10(–12) × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface folded, buff, reverse luteous; on PDA surface and reverse buff; on OA surface cinnamon.

Typus. South Africa, Western Cape Province, Nieuwoudtville, on stems of *Grielum humifusum* (*Neuradaceae*), 2018, *P.W. Crous*, HPC 3057 (holotype CBS H-24435, culture ex-type CPC 38688 = CBS 146817, ITS, LSU, *cmdA*, *tef1* and *tub2* sequences GenBank MW175358.1, MW175398.1, MW173100.1, MW173124.1 and MW173139.1, MycoBank MB837849).

Notes — Lombard et al. (2016) distinguished *Paramyrothecium* from *Myrothecium* s.str. and the other myrothecium-like genera by their septate, thin-walled setae surrounding the sporodochia. *Paramyrothecium pituitipietianum* is closely related to *P. parvum* (conidia 4–5 × 1–2 µm) and *P. telicola* (conidia (7–)7.5–8.5(–9) × 1–3 µm; Lombard et al. 2016).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramyrothecium parvum* (strain CBS 257.35, GenBank NR_145076.1; Identities = 577/589 (98 %), one gap (0 %)), *Paramyrothecium roridum* (as *Myrothecium roridum*; strain BBA 62764, GenBank AJ301993.1; Identities = 589/602 (98 %), one gap (0 %)), and *Paramyrothecium acadiense* (strain CBS 123.96, GenBank KU846288.1; Identities = 576/589 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Paramyrothecium nigrum* (strain CBS 116537, GenBank NG_069341.1; Identities = 826/827 (99 %), no gaps), *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846323.1; Identities = 826/827 (99 %), no gaps), and *Paramyrothecium roridum* (strain CBS 372.50, GenBank MH868182.1; Identities = 845/847 (99 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Paramyrothecium tellicola* (strain CBS 478.91, GenBank KU846272.1; Identities = 488/600 (81 %), 17 gaps (2 %)), *Paramyrothecium sinense* (strain ZSY8, GenBank MH885437.1; Identities = 470/578 (81 %), 19 gaps (3 %)), and *Xepicula crassiseta* (strain CBS 392.71, GenBank KU847222.1; Identities = 494/608 (81 %), 30 gaps (4 %)). Distant hits using the ***tef1*** sequence had highest similarity to *Neomyrothecium humicola* (strain CBS 310.96, GenBank KU846527.1; Identities = 207/229 (90 %), six gaps (2 %)), *Gregatothecium humicola* (strain CBS 205.96, GenBank KU846402.1; Identities = 212/237 (89 %), ten gaps (4 %)), and *Brevistachys ossiformis* (strain CPC 16031, GenBank KU846092.1; Identities = 209/234 (89 %), nine gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Paramyrothecium* sp. 2 MP-2020 (strain 18ALOM016, GenBank MT671910.1; Identities = 324/330 (98 %), no gaps), *Paramyrothecium terrestris* (strain CBS 564.86, GenBank KU846420.1; Identities = 310/343 (90 %), seven gaps (2 %)), and *Paramyrothecium acadiense* (strain CBS 123.96, GenBank KU846405.1; Identities = 308/342 (90 %), six gaps (1 %)).

Colour illustrations. Characteristic yellow flowers of *Grielum humifusum*. Conidioma on PNA (scale bar = 350 µm); setae; conidiogenous cells; conidia (scale bars = 10 µm).

Pedro W. Crous & Johannes 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


Polyscytalum pini-canariensis

Fungal Planet 1135 – 19 December 2020

Polyscytalum pini-canariensis Crous, *sp. nov.*

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

Classification — *Phlogicylindriaceae*, *Xylariales*, *Sordariomycetes.*

Mycelium consisting of brown, smooth, septate, 2–3 µm diam hyphae. *Conidiophores* erect, solitary, subcylindrical, branched or not, brown, smooth, flexuous, 1–5-septate, 20–40 × 2–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, 10–20 × 2–3 µm, proliferating sympodially, denticulate, flat-tipped, 2.5–3 µm diam, not thickened nor darkened. *Conidia* occurring in unbranched chains, cylindrical with truncate ends, smooth, guttulate, medianly 1-septate, (18–)22–26(–48) × 3(–3.5) µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, even margin, reaching 16 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse isabelline.

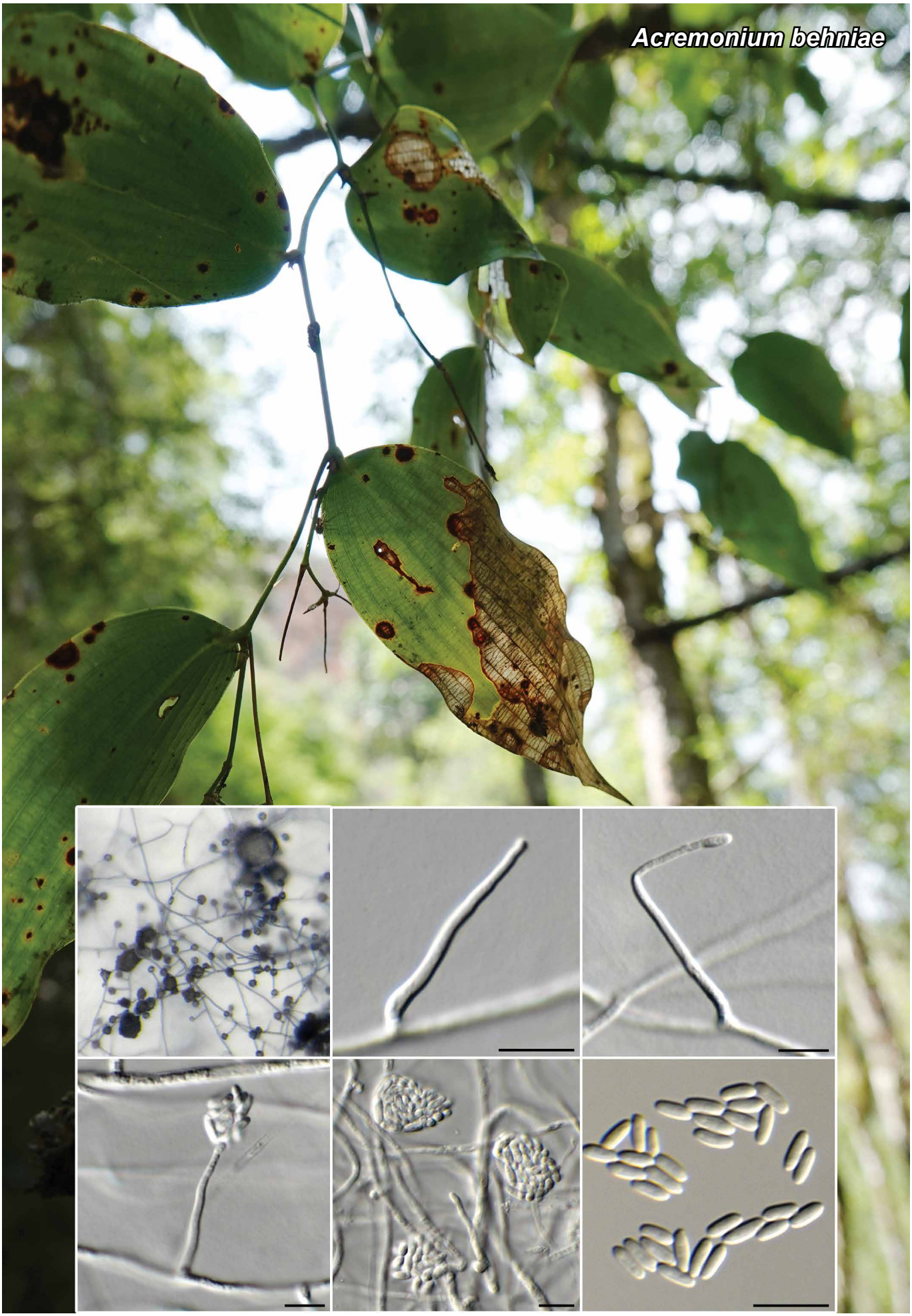
Typus. Spain, Canary Islands, Gran Canaria, N28°3'18" O15°41'43", 520 m, on needles of *Pinus canariensis* (*Pinaceae*), 4 July 2019, *J. Etayo*, HPC 3084 (holotype CBS H-24437, culture ex-type CPC 38727 = CBS 146819, ITS, LSU and *actA* sequences GenBank MW175359.1, MW175399.1 and MW173095.1, MycoBank MB837850).

Notes — *Polyscytalum pini-canariensis* should be compared to *P. pini* (on *Pinus sylvestris*, UK; conidia (0–)1(–2)-septate, 7–12(–14) × 1.5–2(–2.5) µm, conidiophores 50–110(–140) µm; Kirk 1983 and *P. pinicola* (on *Pinus tecunumanii*, Malaysia; conidia (0–)1-septate, (13–)14–15(–16) × 2 µm, conidiophores 40–80 × 2–3 µm; Crous et al. 2020b). The new species can be distinguished based on its shorter conidiophores, and longer conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Polyscytalum neofecundissimum* (strain CBS 143390, GenBank NR_158959.1; Identities = 548/590 (93 %), 12 gaps (2 %)), *Subulispora britannica* (strain ICMP 14767, GenBank EF029198.1; Identities = 533/585 (91 %), 16 gaps (2 %)), and *Polyscytalum pinicola* (strain CPC 36759, GenBank MT223833.1; Identities = 539/606 (89 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence are *Polyscytalum fecundissimum* (strain CBS 100506, GenBank EU035441.1; Identities = 792/801 (99 %), one gap (0 %)), *Polyscytalum chilense* (strain CBS 143387, GenBank MH107954.1; Identities = 824/834 (99 %), one gap (0 %)), and *Polyscytalum eucalyptigenum* (strain CBS 143388, GenBank MH107955.1; Identities = 822/833 (99 %), one gap (0 %)). No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches.

Colour illustrations. *Pinus canariensis* covered in lichens growing on the Canary Islands. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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
Javier Etayo, Department of Biology, IES Zizur, Ronda S. Cristóbol 196,31180 Zizur Mayor, Navarra, Spain; e-mail: jetayosa@educacion.navarra.es


Acremonium behniae

Fungal Planet 1136 – 19 December 2020

Acremonium behniae Crous, *sp. nov.*

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

Classification — *Bionectriaceae*, *Hypocreales*, *Sordariomycetes*.

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells, erect, straight to flexuous, hyaline, smooth, phialidic, arising from superficial hyphae or from hyphal strands, giving rise to mucoid balls of conidia, but conidiogenous cells aggregated on hyphal strands, forming a sporodochial mass on agar surface conidiogenous cells subcylindrical with apical taper, 10–30 × 1.5–2 µm; apex 1–1.5 µm diam, with minute non-flares collarette, 1 µm tall. *Conidia* hyaline, smooth, aseptate, subcylindrical to fusoid-ellipsoid, apex subobtuse, base bluntly rounded, (3.5–)4–5(–6.5) × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff to dirty white.

Typus. South Africa, Northern Province, Tzaneen, Buffelskloof Nature Reserve, on leaves of *Behnia reticulata* (*Asparagaceae*), 2018, *P.W. Crous*, HPC 3156 (holotype CBS H- 24443, culture ex-type CPC 38798 = CBS 146824, ITS and LSU sequences GenBank MW175360.1 and MW175400.1, MycoBank MB837851).

Notes — *Acremonium behniae* is closely related to *A. charticola* (conidiogenous cells 15–45(–60) × 1.5–2(–2.5) µm, conidia 3.2–4.5 × 1.4–2 µm; Gams 1971), but can be distinguished based on dimensions of its conidiogenous cells and conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acremonium charticola* (strain UOA/HCPF 14413, GenBank KC253940.1; Identities = 525/570 (92 %), nine gaps (1 %)) and *Acremonium sclerotigenum* (strain CBS 286.70H, GenBank MH859618.1; Identities = 535/581 (92 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Acremonium sclerotigenum* (strain UBOCC-A-118074, GenBank MT226553.1; Identities = 786/789 (99 %), one gap (0 %)), *Acremonium sordidulum* (strain CBS 385.73, GenBank MH872418.1; Identities = 837/841 (99 %), no gaps), and *Acremonium alternatum* (strain CBS 407.66, GenBank FJ176883.1; Identities = 837/841 (99 %), no gaps).

Colour illustrations. Leaves of *Behnia reticulata*. Sporulating colony on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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


Alternaria mirabibensis

Fungal Planet 1137 – 19 December 2020

Alternaria mirabibensis Crous, *sp. nov.*

Etymology. Name refers to the collection site, namely the Mirabib Rock in the Namib Desert, Namibia, where Stanley Kubrick filmed 'the dawn of mankind' in the movie '2001- A Space Odyssey'.

Classification — *Pleosporaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of pale brown, smooth, branched, septate, 3–4 µm diam hyphae. *Conidiophores* erect, solitary, arising from superficial mycelium, 50–150 × 3–5 µm, 3–6-septate, branched or not, brown, smooth, subcylindrical, straight to flexuous. *Conidiogenous cells* terminal and intercalary, straight to geniculous-sinuous, flexuous, 10–30 × 5–7 µm, with thickened, darkened, 1–2 terminal pores, 2–3 µm diam. *Conidia* occurring in branched chains, conidia brown, verruculose, guttulate, ovoid to ellipsoid, (23–)33–45(–50) × (13–)15–16(–17) µm (body excluding beak), with 3–6(–7) transverse septa, and (1–)2–3(–6) longitudinal or oblique septa, commonly forming a long terminal beak, 20–120 µm long, that becomes a secondary conidiophore, giving rise to terminal and lateral chains of conidia.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 40 mm diam on MEA, but covering dish on PDA and OA after 2 wk at 25 °C. On MEA surface folded, grey olivaceous, reverse isabelline; on PDA surface and reverse grey olivaceous; on OA surface grey olivaceous.

Typus. Namibia, Gobabeb-Namib Research Institute, Mirabib, on plant litter, 19 Nov. 2019, *P.W. Crous*, HPC 3108 (holotype CBS H-24445, culture ex-type CPC 38838 = CBS 146826, ITS, LSU, *actA*, *chs-1*, *cmdA*, *gapdh*, *tef1* and *tub2* sequences GenBank MW175361.1, MW175401.1, MW173096.1, MW173101.1, MW173102.1, MW173104.1, MW173125.1 and MW173140.1, MycoBank MB837852).

Colour illustrations. View from top of Mirabib Rock, looking outwards across the Namib Desert. Conidiophores and conidiogenous cells giving rise to conidial chains. Scale bars = 10 µm.

Notes — *Alternaria mirabibensis* is closely related to *Alternaria burnsii* (CBS 130264) (Woudenberg et al. 2015, Nishikawa & Nakashima 2020), but is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Alternaria alternata* (strain KU20017.1, GenBank MT487794.1; Identities = 552/566 (98 %), two gaps (0 %)), *Alternaria arborescens* (strain ALT-14, GenBank MH879771.1; Identities = 552/566 (98 %), two gaps (0 %)), and *Alternaria burnsii* (strain CBS 130264, GenBank MH865506.1; Identities = 552/566 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Alternaria multiformis* (strain CBS 102060, GenBank NG_069860.1; Identities = 870/871 (99 %), no gaps), *Alternaria terricola* (strain CBS 202.67, GenBank NG_069728.1; Identities = 870/871 (99 %), no gaps), and *Alternaria atra* (strain CBS 125894, GenBank MH875550.1; Identities = 870/871 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Alternaria iridicola* (strain AC139, GenBank LC481866.1; Identities = 179/185 (97 %), no gaps), *Alternaria alternata* (strain LSA2, GenBank KY131956.1; Identities = 186/193 (96 %), no gaps), and *Alternaria tenuissima* (strain U-2, GenBank MN752246.1; Identities = 208/216 (96 %), no gaps). Closest hits using the ***chs-1*** sequence had highest similarity to *Alternaria novae-guineensis* (strain SCSJ08, GenBank MH793684.1; Identities = 233/242 (96 %), no gaps), *Alternaria solani* (strain NL03003, GenBank CP022032.1; Identities = 257/269 (96 %), no gaps), and *Alternaria radicina* (strain BMP0079, GenBank EU141977.1; Identities = 252/264 (95 %), no gaps). Closest hits using the ***cmdA*** sequence had highest similarity to *Alternaria alstroemeriae* (strain CBS 118809, GenBank MH175185.1; Identities = 579/639 (91 %), 15 gaps (2 %)), *Alternaria iridiaustralis* (strain CBS 118486, GenBank MH175191.1; Identities = 578/638 (91 %), 15 gaps (2 %)), and *Alternaria alternata* (strain 17MC, GenBank MG925134.1; Identities = 580/647 (90 %), 25 gaps (3 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Alternaria tenuissima* (strain GP4, GenBank MK451969.1; Identities = 553/577 (96 %), no gaps), *Alternaria longipes* (strain AXLKY2019010, GenBank MN044655.1; Identities = 552/577 (96 %), no gaps), and *Alternaria alternata* (strain D11, GenBank MK732570.1; Identities = 552/577 (96 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Alternaria alternata* (strain EGS 34-016, GenBank AH013339.2; Identities = 284/304 (93 %), no gaps), *Alternaria jacinthicola* (strain Mlb684, GenBank HQ413697.1; Identities = 293/317 (92 %), no gaps), and *Alternaria longipes* (strain KY_2019_012, GenBank MT548042.1; Identities = 247/273 (90 %), five gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Alternaria arborescens* (strain BAS_G1, GenBank MF070272.1; Identities = 282/289 (98 %), no gaps), *Alternaria tenuissima* (strain CBS 124278, GenBank MF070256.1; Identities = 282/289 (98 %), no gaps), and *Alternaria gaisen* (strain CBS 118488, GenBank MF070254.1; Identities = 282/289 (98 %), no gaps).

Pedro W. Crous & Johannes 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
Neriman Yilmaz, 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: neriman.yilmazvisagie@fabi.up.ac.za
Don A. Cowan, Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: don.cowan@up.ac.za
Gillian Maggs-Kölling, Gobabeb-Namib Research Institute, P.O. Box 953, Walvis Bay, Namibia; e-mail: gillian@gobabeb.org


Preussia procaviae

Fungal Planet 1138 – 19 December 2020

Preussia procaviae Crous, *sp. nov.*

Etymology. Name refers to *Procavia capensis* (rock rabbit), from who's dung this fungus was isolated.

Classification — *Sporormiaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata pycnidial, solitary, immersed to erumpent, brown, globose, 60–150 µm diam, with central ostiole, 10 µm diam; wall of 3–6 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, phialidic, 4–5 × 2.5–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, ellipsoid with obtuse ends, 3–4 × 2 µm.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. Namibia, Gobabeb-Namib Research Institute, Mirabib Rock, on dung of *Procavia capensis* (*Procaviidae*), 19 Nov. 2019, *P.W. Crous*, HPC 3110 (holotype CBS H-24446, culture ex-type CPC 38861 = CBS 146827, ITS, LSU, *tef1* and *tub2* sequences GenBank MW175362.1, MW175402.1, MW173126.1 and MW173141.1, MycoBank MB837853).

Notes — The sexual morph of *Preussia procaviae* was not observed on the dung, nor did it develop in culture. However, species of *Preussia* are known to form phoma-like asexual morphs in culture. *Preussia procaviae* is phylogenetically distinct from its closest relatives.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Preussia* sp. (strain CF209171, GenBank KX710223.1; Identities = 510/511 (99 %), one gap (0 %)), *Sporormiella intermedia* (as *Preussia intermedia*; strain OK2L1-26P, GenBank KF871451.1; Identities = 476/494 (96 %), four gaps (0 %)), and *Preussia antarctica* (strain CBS 222.89, GenBank KX710224.1; Identities = 492/514 (96 %), eight gaps (1 %)). Closest hits using the **LSU** sequence are *Preussia minimoides* (strain MEXU 26355, GenBank KF557659.1; Identities = 886/888 (99 %), no gaps), *Sporormiella isomera* (strain CBS 166.73, GenBank MH872355.1; Identities = 886/890 (99 %), two gaps (0 %)), and *Sporormiella intermedia* (as *Preussia intermedia*; strain CBS 364.69, GenBank MH878451.1; Identities = 879/889 (99 %), one gap (0 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Closest hits using the ***tub2*** sequence had highest similarity to *Preussia* sp. 10 MP-2020 (strain 18EPLE010, GenBank MT881917.1; Identities = 371/388 (96 %), two gaps (0 %)), *Preussia lignicola* (strain 18ALIC002, GenBank MT671880.1; Identities = 349/394 (89 %), 14 gaps (3 %)), and *Sporormiella intermedia* (strain 18THES003, GenBank MT881987.1; Identities = 346/393 (88 %), 12 gaps (3 %)).

Colour illustrations. Mirabib Rock in the Namib Desert, where the sample was collected. Conidiomata on SNA (scale bars = 100 µm); superficial view of conidiomatal wall (scale bar = 50 µm); conidiogenous cells (scale bars = 10 µm); conidia (scale bar = 10 µm).

Pedro W. Crous & Johannes 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
Neriman Yilmaz, 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: neriman.yilmazvisagie@fabi.up.ac.za
Don A. Cowan, Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: don.cowan@up.ac.za
Gillian Maggs-Kölling, Gobabeb-Namib Research Institute, P.O. Box 953, Walvis Bay, Namibia; e-mail: gillian@gobabeb.org


Curvularia moringae &
Moringomyces phantasmae

Fungal Planet 1139 & 1140 – 19 December 2020

Curvularia moringae Crous, *sp. nov.*

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

Classification — *Pleosporaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of pale to medium brown, smooth, branched, septate, 4–6 µm diam hyphae. *Conidiophores* solitary, subcylindrical, erect, geniculate-sinuous, mostly unbranched, 1–10-septate, 20–110 × 5–7 µm, medium brown, smooth. *Conidiogenous cells* integrated, terminal or intercalary, subcylindrical, geniculate-sinuous to curved or straight, medium brown, smooth, 12–20 × 5–7 µm; hila thickened, darkened, 2–4 µm diam. *Conidia* solitary, arranged in rosettes, ellipsoid, straight to slightly curved, medium brown, finely roughened, 3–5-distoseptate, guttulate, apex obtuse, base bluntly rounded with darkened, thickened hilum, 1.5–3 µm diam, (30–)40–48(–51) × (16–)17–21(–23) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. Namibia, Gobabeb-Namib Research Institute, on leaves of *Moringa ovalifolia* (*Moringaceae*), 19 Nov. 2019, *P.W. Crous*, HPC 3117 (holotype CBS H-24447, culture ex-type CPC 38873 = CBS 146828, ITS, LSU, *gapdh* and *rpb2* sequences GenBank MW175363.1, MW175403.1, MW173105.1 and MW173117.1, MycoBank MB837854).

Notes — *Curvularia moringae* is phylogenetically distinct from species presently known in the genus (Marin-Felix et al. 2017a, b, 2020).

(notes *Curvularia moringae* continues on Supplementary material page FP1139 & 1140)

Moringomyces Crous, *gen. nov*.

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

Classification — *Saccotheciaceae*, *Dothideales*, *Dothideomycetes.*

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Hyphal cells* becoming swollen, brown, roughened, forming intercalary chains of chlamydospores enclosed in mucoid sheath, initially transversely septate, becoming muriformly septate, becoming swollen, eventually forming *microsclerotia*.

Type species. Moringomyces phantasmae Crous.
MycoBank MB837855.

Moringomyces phantasmae Crous, *sp. nov.*

Etymology. Name refers to the host *Moringa ovalifolia* (Namibian phantom tree), L. *phantasma* = phantom).

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–3 µm diam hyphae. *Hyphal cells* becoming swollen, brown, roughened, forming intercalary chains of chlamydospores enclosed in mucoid sheath, initially transversely septate, becoming muriformly septate, initially 3–4 µm diam, becoming swollen, 8–10 µm diam, eventually forming *microsclerotia*, more prominent and larger on OA than on SNA, up to 100 µm diam.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and feathery, lobate margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. Namibia, Gobabeb-Namib Research Institute, on flower of *Moringa ovalifolia* (*Moringaceae*), 19 Nov. 2019, *P.W. Crous*, HPC 3130 (holotype CBS H-24449, culture ex-type CPC 38883 = CBS 146830, ITS and LSU sequences GenBank MW175364.1 and MW175404.1, MycoBank MB837856).

Notes — *Moringomyces* is related to the genera *Arxiella, Aureobasidium* and *Pseudosydowia*. Other than the microsclerotia, *Moringomyces* did not form any conidiomata or conidia in culture, making morphological comparisons difficult. Genera in this complex have similar culture characteristics, namely pigmented hyphae that are strongly constricted at septa, encased in mucilage, and aggregations of hyphal cells that tend to form microsclerotia.

(notes *Moringomyces phantasmae* continues on Supplementary material page FP1139 & 1140)

Colour illustrations. *Moringa ovalifolia* tree growing in the Namib Desert. Left column *Curvularia moringae*. Conidiophores and conidiogenous cells giving rise to conidia. Right column *Moringomyces phantasmae*. Colonies on SNA; hyphae encased in mucilage; microsclerotium. Scale bars = 10 µm.

Pedro W. Crous & Johannes 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
Neriman Yilmaz, 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: neriman.yilmazvisagie@fabi.up.ac.za
Don A. Cowan, Centre for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Private Bag X20, Hatfield 0028, Pretoria, South Africa; e-mail: don.cowan@up.ac.za
Gillian Maggs-Kölling, Gobabeb-Namib Research Institute, P.O. Box 953, Walvis Bay, Namibia; e-mail: gillian@gobabeb.org


Neodothiora populina

Fungal Planet 1141 – 19 December 2020

Neodothiora Crous, G.C. Adams & Winton, *gen. nov*.

Etymology. Name refers to its superficial resemblance of the genus *Dothiora*.

Classification — *Dothioraceae*, *Dothideales*, *Dothideomycetes.*

Conidiomata solitary, erumpent, brown, subglobose, pycnidial, with central ostiole, exuding a crystalline mucoid conidial cirrhus; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, proliferating percurrently. *Conidiogenous cells* also occurring solitary on superficial hyphae, subcylindrical, hyaline, smooth, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, ellipsoid, apex subobtuse, tapering to truncate apex.

Type species. Neodothiora populina Crous, G.C. Adams & Winton. MycoBank MB837857.

Neodothiora populina Crous, G.C. Adams & Winton, *sp. nov.*

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

On PNA: *Conidiomata* solitary, erumpent, brown, subglobose, pycnidial, with central ostiole, 130–180 µm diam, exuding a crystalline mucoid conidial cirrhus; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, proliferating percurrently, 5–7 × 4–6 µm. *Conidiogenous cells* also occurring solitary on superficial hyphae, ampulliform to subcylindrical, hyaline, smooth, 5–10 × 2–5 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, ellipsoid, apex subobtuse, tapering to truncate apex, 5–6(–7) × 2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, uneven margin, covering dish after 2 wk at 25 °C. On MEA surface mucoid, saffron, reverse saffron with patches of umber; on PDA surface and reverse umber, margin black; on OA surface umber.

Typus. USA, Alaska, -148.7762872 64.63940972, on stem cankers of *Populus tremuloides* (*Salicaceae*), 24 June 2018, *G. Adams & L.M. Winton* (holotype CBS H-24556, culture ex-type CPC 39399 = CBS 147087, ITS, LSU, *tef1* and *tub2* sequences GenBank MW175365.1, MW175405.1, MW173127.1 and MW173142.1, MycoBank MB837858).

Additional materials examined. USA, Alaska, -148.7672229 64.64259316, on stems of *P. tremuloides*, 25 June 2018, *G. Adams & L.M. Winton*, CPC 39397 = CBS 147085, ITS sequence GenBank MW175366.1; USA, Alaska, -148.3288146 64.73376442, on stems of *P. tremuloides*, 19 June 2018, *G. Adams & L.M. Winton*, CPC 39398 = CBS 147086, ITS sequence GenBank MW175367.1; Alaska, Bonanza Creek Experimental Forest, -148.33106. 64.73243, on stems of *P. tremuloides*, 15. Sept. 2020, *L.M. Winton*, Univ. of Alaska Herbarium (ALA) H1280665, H1280672; ibid., on stems of *P. tremuloides*, Jan. 2020, *L.M. Winton*, H1280666–H1280671.

Notes — *Neodothiora* is reminiscent of the genus *Dothiora*, having *Dothichiza* and hormonema-like morphs in culture (Crous & Groenewald 2016, 2017). However, it clusters apart from the type species, *D. pyrenophora*, and thus a new genus is herewith introduced to accommodate this pathogen, which is associated with severe cankers of *Populus tremuloides* in Alaska. In field inoculations, conidiomata developed on the tree bark around points of inoculation, which resembled those that developed in culture (on agar and on PNA).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to 'Uncultured fungus' (strain UPSC_A12_12, GenBank GU564975.1; Identities = 525/527 (99 %), one gap (0 %)), *Scleroconidioma sphagnicola* (strain JJ-18-24, GenBank MK880096.1; Identities = 563/591 (95 %), 13 gaps (2 %)), *Rhizosphaera macrospora* (strain ARSL_071114.1, GenBank

(text continues on Supplementary material page FP1141)

Colour illustrations. Stem canker on *Populus tremuloides*. Conidioma on PNA; conidiomata on SNA; conidiogenous cells; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 150 µm, all others = 10 µm.

Supplementary material

FP1141-1 The first of 1000 equally most parsimonious trees obtained from the LSU alignment (57 sequences including the outgroup; 809 characters including alignment gaps analysed: 566 constant, 122 variable and parsimony-uninformative and 121 parsimony-informative) using PAUP* v. 4.0b10 (Swofford 2003). Tree statistics: TL = 496, CI = 0.653, RI = 0.813, RC = 0.531. Parsimony bootstrap support values > 74 % and Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and thickened lines represent branches present in the parsimony strict consensus tree. The Bayesian analysis using MrBayes v. 3.2.7a (Ronquist et al. 2012) resulted in a Bayesian consensus phylogram based on 633002 sampled trees and 180 unique site patterns (data not shown). The scale bar represents the number of changes. The taxonomic novelties described in this study are highlighted with **bold** text and coloured blocks. GenBank accession and culture/specimen numbers are indicated behind the species names. The two orders are indicated to the left of the tree at the basal branches. The tree was rooted to *Diaporthe perjuncta* (GenBank NG_059064.1). The alignment and tree were deposited in TreeBASE (Submission ID 27179).

FP1141-2 The first of 414 equally most parsimonious trees obtained from the ITS alignment (50 sequences including the outgroup; 518 characters including alignment gaps analysed: 332 constant, 74 variable and parsimony-uninformative and 112 parsimony-informative) using PAUP* v. 4.0b10 (Swofford 2003). Tree statistics: TL = 377, CI = 0.647 RI = 0.882, RC = 0.571. Parsimony bootstrap support values > 74 % and Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and thickened lines represent branches present in the parsimony strict consensus tree. The Bayesian analysis using MrBayes v. 3.2.7a (Ronquist et al. 2012) resulted in a Bayesian consensus phylogram based on 161252 sampled trees and 176 unique site patterns (data not shown). The scale bar represents the number of changes. The taxonomic novelties described in this study is highlighted with **bold** text and coloured blocks. GenBank accession and culture/specimen numbers are indicated behind the species names. The tree was rooted to *Dothidea sambuci* (GenBank NR_111220.1). The alignment and tree were deposited in TreeBASE (Submission ID 27179).

Pedro W. Crous & Johannes 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
Gerard C. Adams, Department of Plant Pathology, 406D Plant Science Hall, 1875 N. 38th Street, University of Nebraska, Lincoln, NE, USA; e-mail: gadams3@unl.edu
Loretta M. Winton, U.S.D.A. Forest Service, Forest Health Protection, 3700 Airport Way, Fairbanks, AK 99709, USA; e-mail: loretta.winton@usda.gov


Amanita domingensis
1
CM
1
CM

Fungal Planet 1142 – 19 December 2020

Amanita domingensis Angelini & Vizzini, *sp. nov.*

Etymology. Referring to the place of the first collection, Santo Domingo, the capital of the Dominican Republic.

Classification — *Amanitaceae*, *Agaricales*, *Agaricomycetes*.

Pileus (4.5–)5.5–6(–8.5) cm diam, campanulate, then convex, plane convex, sometimes depressed at the centre at maturity and then with a poor developed obtuse umbo, margin striated up to 1/3 of the radius; surface glabrous, opaque, oily, viscid when moist, ash grey, covered with general veil remnants in the form of whitish grey floccose patches or warts, more abundant on the centre. *Lamellae* free, sometimes distant, straight, interspersed with lamellulae of varying length, 0.5 cm wide, white then white-yellow and with a finely eroded grey edge. *Stipe* 8–10 × 0.7–0.9 cm, cylindrical, straight or slightly sinuous, narrowing and flared upwards, internally fistulous; surface covered with small, grey fibrillose squamules, sometimes becoming progressively more snakeskin-patterned and greyer towards the base, on a white background. *Volva* ± membranous, slightly adherent, low, internally white, externally whitish in the hypogeous part, grey in the emerging part, tending to fracture horizontally forming one or more rings of dark volval material at the stipe base. *Annulus* absent. *Context* thin, 0.2–0.3 cm thick (in the pileus), white. *Odour* and *taste* not distinctive. *Spores* (10–)11–12(–13.5) × 8–9 µm (av. 11.4 × 8.5 µm, Q_m = 1.35), broadly ellipsoid to oblong, thin-walled, mostly containing one large drop, hyaline, inamyloid, with slightly prominent and eccentric apiculus. *Basidia* 30–50 × 13–15 µm, clavate, mostly tetrasporic, sometimes bisporic, with sterigmata up to 5 µm long. *Marginal cells* present but not abundant, not emerging over the basidia, mostly consisting of single thin-walled elements, sometimes bi-catenulate, rarely tri-catenulate, whose basal element, when present, has a mostly ovoid shape, while the terminal one has a pyriform or ovoid-claviform shape, 16–22 × 10–11 µm wide. *Partial veil* consisting of sphaeropedunculate elements on the lamellar edge, 25–30 × 22–25 µm wide. *Universal veil* (volva) mixed in structure (membranous + spherocytic) consisting of intertwining hyphae 5–6 µm wide, with also subglobose to sphaeropedunculate elements, 30–45 × 20–35 µm wide. *Subhymenium* a puzzle layer of cubic-multifaceted cells, about 50 µm wide. *Lamellar trama* divergent. *Pileipellis* an ixocutis of stretched and variously intertwined hyphae, with rounded terminals up to 7 µm wide, completely immersed in a hyaline gelatinous layer. *Context* of non-inflated hyphae, 3–9 µm wide. *Stipitipellis* a cutis, similar to pileipellis, but non-gelatinized, consisting of parallel non-inflated hyphae, 5–7 µm wide, covered by a layer of hyphae of the universal veil with elongated, pyriform, large terminal elements, 70–180 µm wide; occasionally, with pedunculate spherocytes, residues of the partial veil, similar in shape and size to those of the lamellar edge, 25–35 × 20–25 µm wide. *Stipititrama* acrophysalidic. *Clamp-connections* absent.

Colour illustrations. Dominican Republic, Puerto Plata, Sosua, deciduous natural forest. Fresh basidiomes in field (holotype JBSD130784); volva detail; fresh basidiomes in field (JBSD130785); spores. Scale bars = 1 cm (basidiomes), 10 µm (spores).

Habitat & Distribution — Exclusive in deciduous woods (probably associated with *Coccoloba diversifolia*), from the plains (but far from the beaches) to the hills, gregarious or as single specimens, in autumn and winter. Common.

Typus. Dominican Republic, National Garden of Santo Domingo, Distrito Nacional, six specimens collected on litter of deciduous wood, 24 Nov. 2014, *C. Angelini* (holotype JBSD130784, ITS and LSU sequences GenBank MT991052 and MT991057, MycoBank MB837379).

Additional materials examined. Dominican Republic, National Garden of Santo Domingo, Distrito Nacional, on litter of deciduous wood, 18 Nov. 2013, *C. Angelini* JBSD130785 (ITS and LSU sequences GenBank MT991053 and MT991058); Puerto Plata, Sosua, 25 Dec. 2016, *C. Angelini* JBSD130786 (ITS and LSU sequences GenBank MT991054 and MT991059).

Notes — *Amanita domingensis* is one of the few Dominican *Amanita* species not in association with conifers and represents the most common and abundant *Amanita* in the deciduous forests. It belongs in sect. *Vaginatae* (subg. *Amanita*) where, in the molecular analysis, it occupies an isolated position. *Amanita arenicola* from Puerto Rico and the British Virgin Islands, which is common on the beaches in association with *Coccoloba uvifera*, is distinguished from the new species by its exclusively sabulicolous habitat, the veil, the stipe, the lamellae and the lamellar edge that are completely white at all developmental stages (Miller et al. 2000) and the different ITS sequence, 448/527 bp (85 %) similar. *Amanita antillana* described from Trinidad and Tobago as an ectomycorrhizal associate of *Coccoloba pubescens* and *Haematoxylum campechianum*, differs by the olive brown pileus, usually devoid of velar remnants and with a shortly striated margin, the fragile ochraceous brown volva that often disappears from the stipe at maturity, and broader spores, 10–13.5(–15) × 7.5–11.5(–13) µm (Dennis 1952, Pegler 1983).

Supplementary material

FP1142 Maximum-likelihood analysis of the nrITS region of *Amanita* sect. *Vaginatae* species was performed with RAxML v. 8 (Stamatakis 2014) using the GTR+G model (1000 bootstrap replicates, bootstrap support values ≥ 70 % are shown). The scale bar represents the number of nucleotide changes per site.

Alfredo Vizzini & Francesco Dovana, Department of Life Sciences and Systems Biology, University of Torino, Viale P.A. Mattioli 25, I-10125 Torino, Italy; e-mail: alfredo.vizzini@unito.it & francescodovana@gmail.com
Claudio Angelini, Herbario Jardín Botánico Nacional Dr. Rafael Ma. Moscoso, Santo Domingo, Dominican Republic and Via Cappuccini, 78/8 – 33170 Pordenone, Italy; e-mail: claudio_angelini@libero.it


Austroboletus asper

Fungal Planet 1143 – 19 December 2020

Austroboletus asper K. Syme, Bonito, T. Lebel, Fechner & Halling, *sp. nov.*

Etymology. Asper (rough), in reference to the ornamentation of the basidiospores.

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes*.

Pileus 3.5–9.5(–22) cm broad when expanded, conico-convex to convex to plano-convex, rarely glutinous to viscid when young and fresh, becoming minutely areolate tomentose to matted tomentose and dry as gluten dissipates, often with a suede-like texture, with white, sterile appendiculate veil remnants, cinnamon brown to brown to cocoa brown (8A3,2; 7E8,7,6; 7D7,6; 6B3; 6C–D–E8,7,6,5; 5C6; Kornerup & Wanscher, 1983). *Flesh* white, unchanging, up to 2 cm deep, with mild *odour* and *taste*. *Tubes* depressed to deeply depressed around stipe, white when young, soon pinkish brown (8D4; 7C4), usually staining brown (6E8,7). *Stipe* 3.5–8(–12) cm long, 0.6–1.7(–3.4) cm broad, equal to subclavate, strict or curved, sometimes slightly tapered at base, alveolate to lacunose-reticulate, sometimes coarsely so, white above, occasionally pale yellowish, sometimes pale brownish below on reticulum when fresh, often yellow to brownish orange (5B7, 6C7) at base, especially with age, rarely viscid below when young and moist, otherwise dry, with interior white, unchanging, pithy to hollow with age, white or sometimes pale yellow in the base, with white rhizomorphs.

Spores (12.1–)14.3–18.7(–20) × 4.4–5.5 µm (av. = 16.23 × 4.92 µm, Q = 3.33, spores *n* = 159, specimens *n* = 8), faintly wrinkled to very finely and uniformly rugulose to irregularly granular (light microscope) or irregularly foveate with low, short meandering ridges and low, isolated tubercles (SEM), weakly dextrinoid in Melzer's. *Basidia* 29–36 × 6–11 µm, four-sterigmata, clavate, hyaline. *Tube trama* boletoid and divergent, inamyloid, with occasional laticiferous elements, with hyphae, 3.5–10 µm broad. *Hymenial cystidia* 50–60 × 12–20 µm, scattered, embedded in the hymenium with rostrate portion protruding, fusoid rostrate to ventricose rostrate with septum separating a broad rostrum from ventricose portion, hyaline, thin-walled, inamyloid. *Pileus trama* inamyloid, hyaline in KOH, with hyphae 5–8 µm broad. *Pileipellis* a tangled, erect, dense trichodermium, soon collapsing; hyphae with rare hyaline encrustations, hyaline or otherwise a pale ochraceous in KOH, 5–8 µm broad. *Stipitipellis* a tangled trichodermium of thin-walled, hyaline, soon collapsing hyphae, rarely with obvious end cells.

Habit, Habitat & Distribution — Solitary to gregarious on soil or sand with *Agonis flexuosa*, *Allocasuarina fraseriana*, *A. littoralis*, *Corymbia calophylla*, *Eucalyptus diversicolor*, *E. guilfoylei*, *E. marginata*, *E. pilularis*, *E. racemosa*, *Leptospermum* sp., *Lophostemon* sp., and *Syncarpia glomulifera*. At present, known in Queensland, Tasmania, Victoria, Western Australia.

Typus. Australia, Western Australia, Denmark, 1874 South Coast Highway, SE section, S34.9861° E117.2876°, 5 May 2013, *K. Syme 2828* (holotype MEL2371703, isotype NY02072470, ITS and *rpb1* sequences GenBank KP242152 and KP242055, MycoBank MB836723).

Additional material examined. Australia, Queensland, Tablelands, Davies Creek National Park, Davies Creek Road, 12.6 km from Kennedy Hwy, S17.0264° E145.6°, 680 m, 19 Feb. 1992, *Halling 6827* (PERTH, NY, LSU sequence GenBank KP242247); Wide Bay District, Great Sandy National Park, Fraser Island, near Lake Birrabeen, S25.4918° E153.054°, 108 m, 4 June 2009, *Halling 9159* (BRI, NY); Fraser Island, S25.4095° E153.086°, 112 m, 6 June 2009, *Halling 9172* (BRI, NY, LSU, *rpb*1 and *rpb*2 GenBank sequences MT921383, MT932084 and MT928122); Fraser Island, Cornwells Road near Kingfisher Bay, S25.4019° E153.031°, 94 m, 24 May 2010, *Halling 9362* (BRI, NY, ITS, *rpb*1 and *rpb*2 sequences GenBank KP242158, KP242047 and KP242087); Fraser Island, Northern Road, ± 1 km N of Cornwells Road, S25.4253° E153.059°, 100 m, 26 May 2010, *Halling 9393* (BRI, NY, *rpb*1 sequence GenBank KP242057); Victoria, Colac Otway, Carlisle Sate Park, Cricket Pitch Track, 7.5 km W of Gellibrand, S38.5428° E143.477°, 170 m, 9 May 2005, *Halling 8685* (MEL, NY, ITS sequence GenBank KP242166); Western Australia, Denmark, off Sunny Glen Rd, state forest N of Plantagenet loc 6722, 6 June 1996, *Syme 877* (PERTH, ITS and *rpb*2 sequences GenBank KP242218 and KP242111); adjoining Plantagenet loc 6721, S34.9315° E117.4435°, 6 May 1998, *Syme 955* (PERTH); Walpole-Nornalup National Park, The Knoll lower walk, S34.9938° E116.727°, 18 May 2001, *Syme 1139* (PERTH, MEL, LSU and ITS sequences GenBank KP242267 and KP242165).

Additional GenBank sequences. *rpb1*: KP242085; *rpb2*: KP242126, KP242127; ITS: KP242164, KP242173, KP242174, KP242186, KP242187, KP242204, KP242216

Notes — In Australia, there are other *Austroboletus* spp. with similar macromorphology, i.e., pileus colour, texture, and viscidity when fresh and moist. Degrees of separation are based on geographic distribution along with spore size and ornamentation. *Austroboletus occidentalis* appears to be restricted to Western Australia and has shorter, more citriform spores with similar, but coarser ornamentation and possesses a smooth plage (e.g., *Syme 2082*: PERTH8105421, NY02449690), a feature not noted in the protologue (Watling & Gregory 1986). Two other currently undescribed species (*Austroboletus* sp. 5, sp. 6) are only known from Queensland and tropical Northern Territory. A key feature of these latter is the asperulate spore ornamentation that can be difficult to see with a compound light microscope. However, with patience, high resolution optics equipped with Nomarski DIC lenses, a discrete ornamentation can be observed especially if the plage can be seen in adaxial and profile views.

Colour illustrations. Sclerophyll forest of *Eucalyptus diversicolor*, *Corymbia calophylla* and *Agonis flexuosa* near Denmark, Western Australia (photo K. Syme). Habit (*Syme 2828*, type); spores with DIC light microscope and with SEM; pileipellis; hymenial cystidium. Scale bars = 5 cm (habit), 5 µm (SEM), 10 µm (light micrographs).

Katrina Syme, National Herbarium of Victoria, Royal Botanic Gardens Victoria, South Yarra, Victoria 3141, Australia; e-mail: katrinasyme@gmail.com
Gregory Bonito, Department of Plant Soil and Microbial Sciences, 1066 Bogue Street, Michigan State University, East Lansing MI, 48824 USA; e-mail: bonito@mail.msu.edu
Teresa Lebel, Botanic Gardens & State Herbarium, Adelaide, South Australia, Australia; e-mail: teresa.lebel@sa.gov.au
Nigel Fechner, Queensland Herbarium, Mt Coot-tha Road, Toowong, Brisbane, Queensland 4066, Australia; e-mail: nigel.fechner@des.qld.gov.au
Roy E. Halling, Inst. Systematic Botany, New York Botanical Garden, 2900 Southern Blvd, Bronx, NY, USA 10458-5126; e-mail: rhalling@nybg.org


Cantharellus betularum

Fungal Planet 1144 – 19 December 2020

Cantharellus betularum Voitk & Thorn, *sp. nov.*

Etymology. *Betularum* (Latin: of birches) refers to the tree associates of the species.

Classification — *Hydnaceae, Cantharellales, Agaricomycetes*.

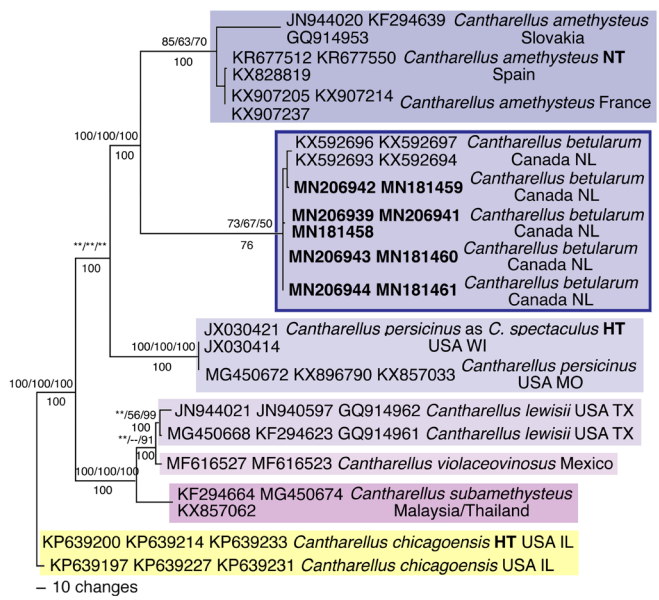
Pileus 20–70 mm diam, margins inrolled, becoming plane, then funnel-shaped and irregularly wavy, opaque, yellow-gold, with thin amethyst coating that breaks up into small scales, becoming violet brown, then brown; scales often absent and amethyst colour not common. *Hymenium* folds moderately spaced, wide, blunt, sinuous, forked, cross-veined and anastomosing, deeply decurrent to almost absent; pale yellow to almost white. *Stipe* 5–25 × 30–65 mm, enlarging upwards, solid, yellow. *Context* whitish yellow; *odour* sweet and fruity. All tissues stain reddish brown with injury or prolonged exposure. Aberrant forms in exposed habitats vary from solitary pegs to fused multicephalic basidiomes. *Basidiospores* (two observers, five collections, seven sporocarps, 131 spores) (7.7–)8.7–14.3 × (3.9–)4.6–7.1(–7.7) µm (av. 10.4 × 5.6 µm), av. Q = 1.9; elliptical-oblong, usually narrower at the apex, slightly bent, with an asymmetric constriction; content homogeneous. *Basidia* 65–90 × 7.7–11.6 µm; 4–6-spored; clavate. No *cystidia*. *Clamp connections* in all tissues. Wide range in micromorphology between individual basidiomes and collections.

Habitat & Distribution — Solitary or gregarious in leaf litter of *Betula*, hitherto known from three sites in the Bay of Islands region of western Newfoundland.

Typus. Canada, Newfoundland and Labrador, Humber Village, trail to Barry's Lookout, 48.988, -057.792, 159 m a.s.l., in leaf litter under *Betula papyrifera*, *B. cordifolia* and *B. alleghaniensis* (*Betulaceae*), 14 Sept. 2013, *Andrus Voitk 13.09.14.av01* (holotype DAOM 721702, isotype DAOM 734027, nrLSU sequences GenBank KX592700–KX592701, MycoBank MB836965).

Collection and sequence data of 14 paratypes: All same site as holotype (Canada, Newfoundland and Labrador, Humber Village, trail to Barry's Lookout, 48.988, -057.792, 159 m a.s.l.) and collector (A. Voitk) except where noted below, 24 Aug. 2008, *09.08.24.av04* (DAOM 72173), Tef1: MN181459, ITS-LSU: MN206942; 25 Aug. 2010, *10.08.25.av02* (DAOM 734021), Tef1: MN181461, ITS-LSU: MN206944, MN206945; 12 Aug. 2011, *11.08.12.av01* (DAOM 734022), Tef1: MN181460, ITS-LSU: MN206943; 10 Aug. 2012, *12.08.10.av01* (DAOM 734016); 2 Sept. 2012, *12.09.02.av11* (DAOM 734024), Tef1: KX592690, LSU: KX592691, KX592692; 3 Oct. 2012, 12.10.03.av01 (DAOM 734025), Tef1: KX592693, ITS: KX592696, KX592697, LSU: KX592694, KX592695; 11 Aug. 2013, *13.08.11.av01* (DAOM 734017); 30 Sept. 2013, *13.09.30.av04* (DAOM 734018), 1 Oct. 2013, *13.10.01.av02* (DAOM 734019), 30 Sept. 2017, *M. Voitk, 17.09.30.av01* (DAOM 984767), Tef1: MN181458, ITS: MN206939, LSU: MN206940, MN206941; 2 Sept. 2018, *18.09.02.av01* (DAOM 984768); Humber Village, trail to Weldon's, 48.99, -057.76, 30 Aug. 2011, *A. Voitk, 11.08.30.av02* (DAOM 734023), LSU: KX592688, KX592689; same locale, 21 Aug. 2013, *M. Voitk, 13.08.21.av01* (DAOM 734026), LSU: KX592698, KX592699; near Frenchman's Cove, 49.046, -058.185, *E. Humber, 14.09.01.av01* (DAOM 734020).

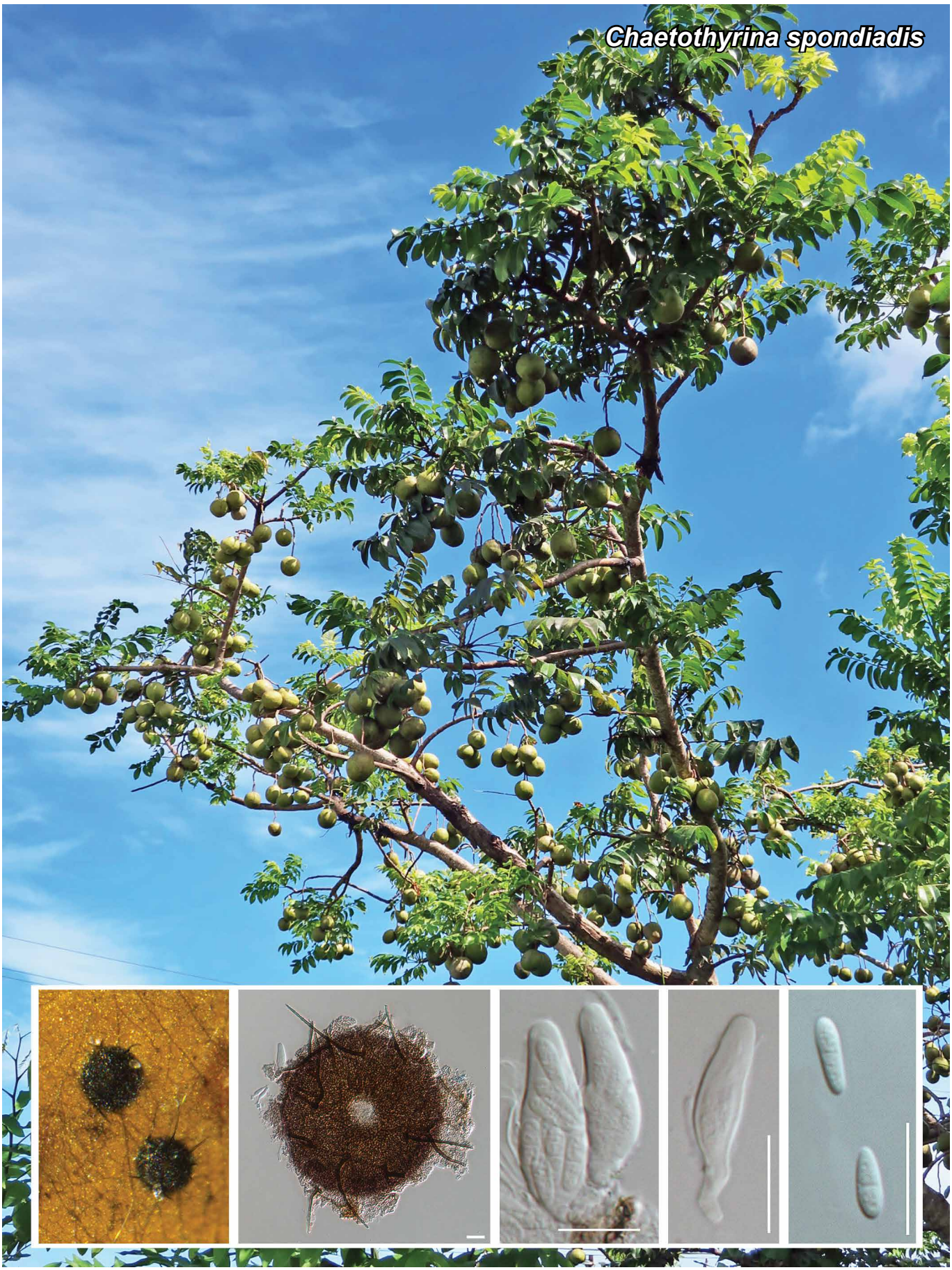
Notes — Using LSU sequence data, we previously reported this species as *Cantharellus amethysteus* (Thorn et al. 2017), but ITS, LSU and *tef*1 are all required to differentiate these two taxa phylogenetically. *Cantharellus betularum* differs from *C. amethysteus* by growing on a different continent (impediment to continued genetic mixing), in a region about 10 °C colder, on average, and with birch, not the oak (*Quercus*) or beech (*Fagus*; both *Fagaceae* and not native to Newfoundland) most commonly recorded with *C. amethysteus*. We have not seen *C. amethysteus*, but the description by Buyck (2000) suggests that its amethyst scales are more consistent and prominent than those of *C. betularum*, which are often absent, and its spores are broader (av. 6.5 vs 5.6 µm). Other North American vinaceous-violaceous species are not found in Newfoundland (Buyck & Hofstetter 2011, Herrera et al. 2018), and *C. betularum* has not been reported outside the Island. Amethyst scales, longer spores, association with birch, and sequence data separate it from *C. camphoratus* and *C. enelensis*, the two other golden chanterelles in Newfoundland (Thorn et al. 2017).



One of 119 equally most parsimonious trees based on sequences of nrITS, nrLSU, and *tef1*, with node support above branches from Bayesian inference (BI: MrBayes v. 3.2.6, Ronquist et al. 2012), 1 000 bootstrap replicates in maximum likelihood (ML; MEGA X, Kumar et al. 2018, Stecher et al. 2020), and 100 bootstrap replicates in maximum parsimony (MP; PAUP v. 4.0b10, Swofford 2003), and percent consensus among the 119 equally most parsimonious MP trees below. Branches with less than 50 % support are marked with dashes (--) and those that collapsed in a particular analysis are marked with asterisks (**). New sequences are indicated in **bold**, and sequences from types are indicated as HT (holotype) or NT (neotype).

Colour illustrations. Canada, Newfoundland, Humber Village, near trail to Barry's Lookout, a mixed forest dominated by *Betula papyrifera*, *B. cordifolia* and *B. alleghaniensis*, where the holotype was collected. Left: typical appearance of *C. betularum*, with stipitate basidiomata, one fused multicephalic specimen and two peg-like specimens. Note the lighter, blunted hymenial folds, almost absent on the peg form, and brownish orange staining. Centre: close-up of pileus, showing lavender scales, when present. Right: basidiospores, original magnification × 1 000 (modified from Thorn et al. 2017: f. 2B, with permission). Scale bars = 1 cm (basidiomes) and 10 µm (basidiospores).

R. Greg Thorn & Alicia Banwell, Department of Biology, University of Western Ontario, London, Ontario, N6A 5B7, Canada; e-mail: rgthorn@uwo.ca & abanwel2@uwo.ca
Jee In Kim, Faculty of Computer Science, Dalhousie University, Halifax, Nova Scotia, B3H 4R2, Canada; e-mail: jeein.j.kim@gmail.com
Renée Lebeuf, 775, Rang du Rapide Nord, Saint-Casimir, Québec, G0A 3L0, Canada; e-mail: renee.lebeuf@gmail.com
Andrus Voitk, 13 Maple St, Humber Village, Newfoundland and Labrador, A2H 2N2, Canada; e-mail: seened@gmail.com


Chaetothyrina spondiadis

Fungal Planet 1145 – 19 December 2020

Chaetothyrina spondiadis Fuentes-Aponte, K. Kim & Romberg, *sp. nov*.

Etymology. Named for *Spondias*, the host genus from which this fungus was collected.

Classification — *Phaeothecoidiellaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Causes flyspeck on fruits of *Spondias*. *Ascomata* thyrothecial, circular, medium to dark brown, gregarious to solitary, superficial, 164.5–254 µm diam, ostiolate, margin entire to slightly irregular. *Setae* 49–112.5 µm long, wider at the base, scattered on the surface of the thyrothecia, straight, unbranched, septate, brown, smooth, easily removed. Upper wall consisting of 2–3 layers of cells, dark brown, *textura epidermoidea*. *Hamathecium* consisting of septate, hyaline pseudoparaphyses, 1.5–2 µm wide, sometimes branched at the tip. *Asci* bitunicate, oblong to pyriform, 24.7–50.8 × 8.8–16.4 µm, with eight biseriate ascospores. *Ascospores* hyaline, ovoid to elongated ovoid, 11.3–15.75 × 2.5–5.6 µm, 1-septate, often slightly constricted at septum, ends rounded, walls smooth.

Culture characteristics — Colonies slow-growing, reaching 15–30 mm diam after 35 d at 25 °C on MEA. Colony pulvinate, circular, entire, with a light grey surface, and reverse dark iron-grey.

Typus. USA, Puerto Rico, Hatillo, on fruits of *Spondias mombin* (*Anacardiaceae*), Nov. 2018, *S. Fuentes-Aponte* (holotype BPI 911218, culture ex-type CBS 145915, ITS and LSU, sequences GenBank MT339448 and MT339447, MycoBank MB835259).

Additional material examined. USA, Puerto Rico, San Juan, *S. mombin,* 1961, *M. Farr*, BPI 644792; San Juan, *Spondias* sp., 1966, *F. Pollack*, BPI 644782; San Juan, *Spondias* sp., 1969, *F. Pollack*, BPI 646405; San Juan, *S. dulcis*, 1970, *F. Pollack*, BPI 646519. – Intercepted specimens: USA, intercepted in Miami, Florida, entering from Jamaica, *S. cytherea*, 1963, *F. Pollack*, BPI 646407; intercepted in New York, New York, entering from Brazil, *S. mombin*, 1964, *F. Pollack*, BPI 646446; entering from Trinidad, *S. dulcis*, 1966, *A. Watson*, BPI 646243.

Notes — *Chaetothyrina* was described in 1913 by Theissen, with type species *Chaetothyrina musarum*. Several species have been described in the genus, mainly on tropical hosts including *Artocarpus* (*Chaetothyrina artocarpi*), *Mangifera* (*Chaetothyrina guttulata*), *Anacardium* (*Chaetothyrina megalospora*) and *Musa* (*Chaetothyrina musarum*) (Singtripop et al. 2016). The measurements of salient characters for most of these species overlap. Stevenson (1975) identified the fungus causing flyspeck on *Spondias cytherea* and *Spondias mombin* in Puerto Rico as *Chaetopeltopsis tenuissima* which was later transferred to *Chaetothyrina as C. tenuissima* (Müller & Von Arx 1962). *Chaetothyrina tenuissima* (*Asterina tenuissima*) was described from *Hevea brasilensis* in Sri Lanka by Petch (1906) with the following characters: 'perithecia 130–160 µm diam, asci 30–40 × 9–12, spores 13 × 4, one-septate, constricted, fusoid, hyaline'. Other superficial, thyrothecial fungi with similar ascospores reported from *Spondias* include *Stomiopeltis* sp. reported from Venezuela on *Spondias mombin* and *Schizothyrium* sp. reported from *Spondias purpurea* in the West Indies. *Chaetothyrina spondiadis* is genetically distinct from both *Stomiopeltis* and *Schizothyrium* and clearly belongs to *Chaetothyrina*. It is morphologically distinct from *C. tenuissima*, having larger thyrothecia, asci and ascospores.

Few described *Chaetothyrina* species have sequences available in public databases. In a megablast search of the NCBI GenBank, ITS sequences of *C. spondiadis* showed highest identity to *Chaetothyrina guttulata* (GenBank NR_153923.1, 98.17 %) and *Chaetothyrina musarum* (GenBank KX372275.1, 96.88 %). Alignment of the ITS regions of these and other fungi in the *Capnodiales* revealed several indels and SNPs between the sequences of the two other species of *Chaetothyrina* available publicly and *Chaetothyrina spondiadis*.

Colour illustrations. Puerto Rico, type locality, tree of *Spondias mombin*. Thyrothecia on host; thyrothecium; asci; ascospores. Scale bars = 10 µm.

Megan Romberg, Katherine Kim & Stephanie Fuentes-Aponte, USDA APHIS PPQ NIS, 10300, Baltimore Avenue, Beltsville, MD 20705, USA; e-mail: Megan.k.romberg@usda.gov, Katherine.s.kim@usda.gov & Stephanie.e.fuentes@usda.gov


Circinella lampensis

Fungal Planet 1146 – 19 December 2020

Circinella lampensis E. Alvarez, C. Muñoz & I. Fernandez, *sp. nov.*

Etymology. Referring to Lampa, where this fungus was collected, Lampa Caves, Santiago, Chile.

Classification — *Lichtheimiaceae*, *Mucorales*, *Mucoromycetes*.

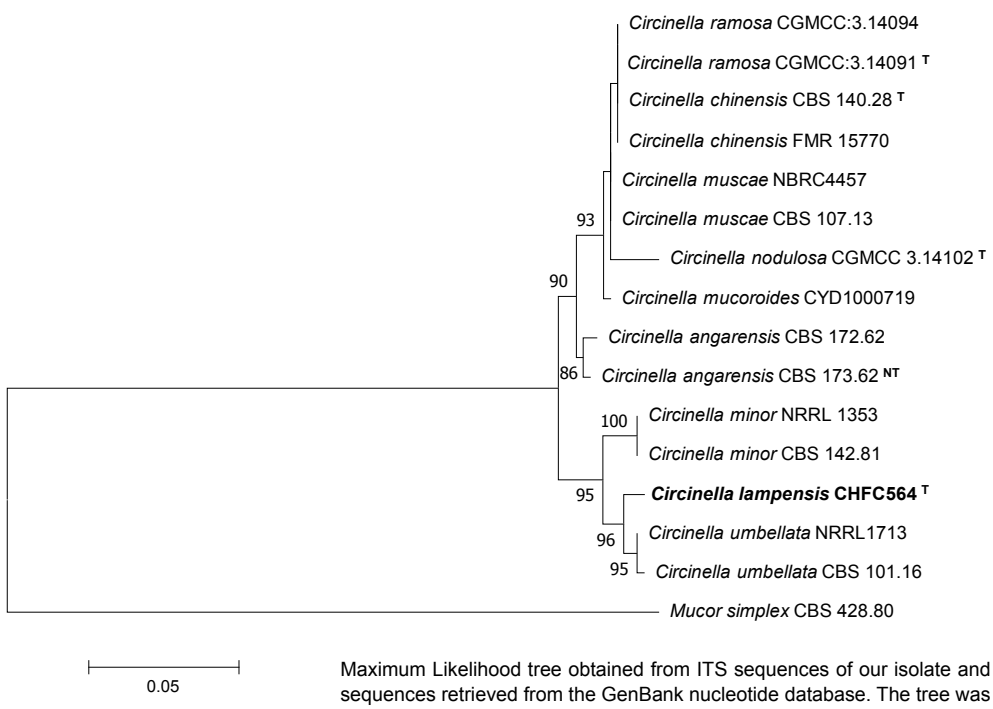
Hyphae hyaline, 5–10 µm wide, thin- to thick-walled, smooth, aseptate. *Sporangiophores* erect, 2–20 mm high, branched, hyaline to brownish when older, producing sporangia mainly in umbels of 4–6, circinate branches, often uniseptate stalks; *sporangia* spherical or subglobose, brown to black in transmitted light, 40–75 µm diam, but mostly about 55 µm; *columellae* ranging from 15–30 µm, but usually 20 µm, globose to subglobose or pyriform in shape; *sporangiospores* (4.5–)5–7.5 µm diam, mostly 6 µm, globose to subglobose, biconcave in the frontal view, singly hyaline to slightly coloured. *Zygospores* and *chlamydospores* not observed.

Culture characteristics — Colonies on potato dextrose agar (PDA) attaining 90 mm diam after 9–10 d at 25 °C, cottony, whitish to light greyish, reverse hyaline. Growth observed at 15 and 25 °C, but no growth at 5 and 37 °C.

Typus. Chile, Santiago, Lampa caves, from soil, Jan. 2020, *E. Alvarez, C. Muñoz & I. Fernandez* (holotype ChFC-564 in Chilean Fungal Collection preserved in a metabolically inactive state, ex-type culture ChFC-2020564; ITS and LSU sequences GenBank MT764259 and MW082021, MycoBank MB836221).

Notes — Based on BLAST search results, the closest hits with the ITS sequence were *Circinella umbellata* (GenBank JN205858; Identities = 596/611 (97.55 %), six gaps (0 %)) and *C. minor* (GenBank MH854640; Identities = 588/611 (96 %), eight gaps (1 %)).

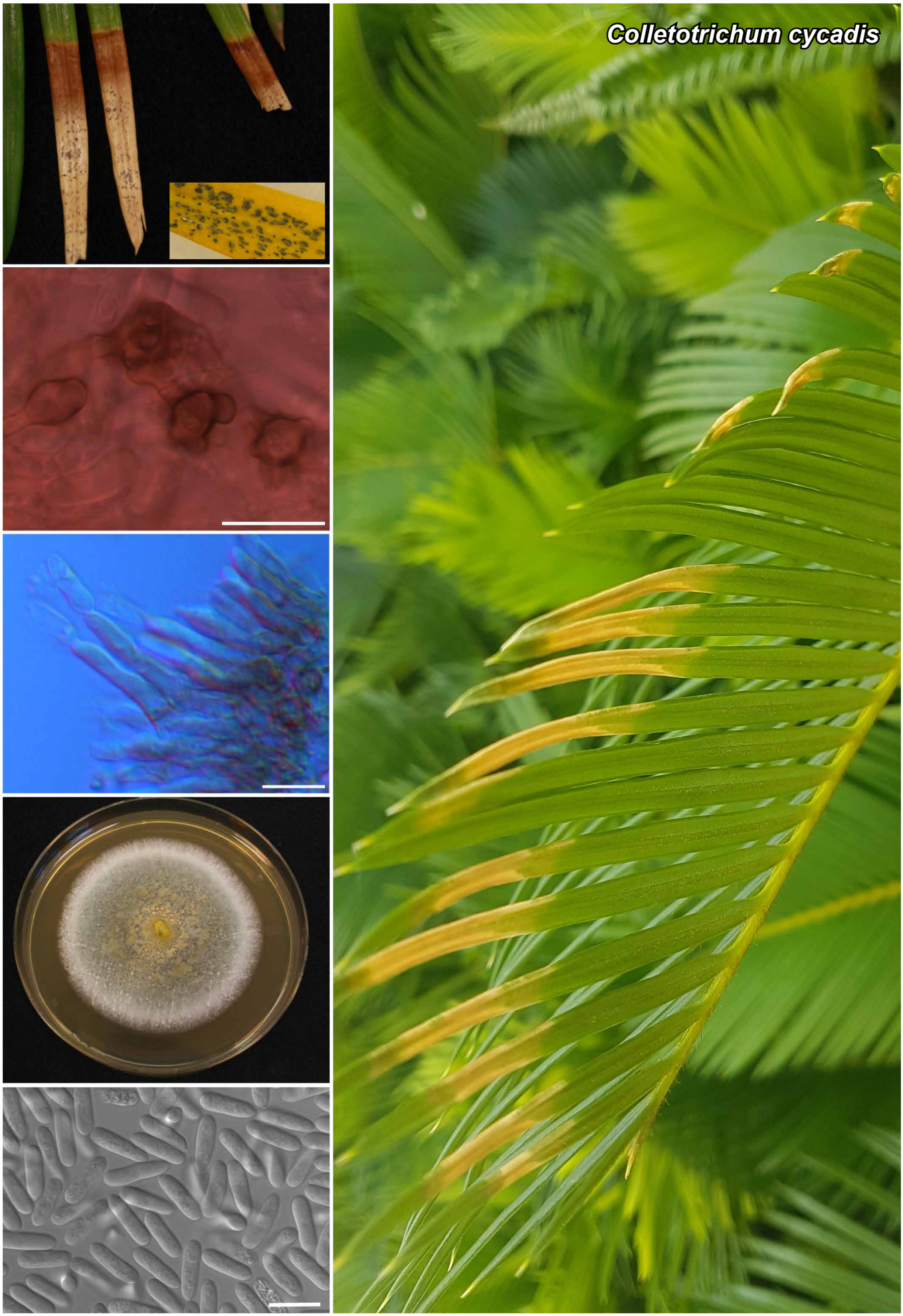
Phylogenetic inference, performed using the ITS sequences of different *Circinella* spp., including the type species *C. umbellata*, demonstrated that our fungus represents a new species of the genus *Circinella*, being closely related to the species *C. umbellata*. Macroscopically, *C. lampensis* resembles *C. umbellata* (Hesseltine & Fennell 1955). Both species showed whitish greyish colonies on all media tested. However, microscopically, *C. lampensis* presents umbels of up to six sporangia, contrasting to *C. umbellata* which produce umbels of up to 12 sporangia. Also, *C. lampensis* differs from *C. umbellata* in having smaller sporangia (up to 75 µm diam vs up to 120 µm diam in *C. umbellata*), usually smaller sporangiospores (5–7.5 µm vs 4.5–10.5 µm in *C. umbellata*), and smaller columellae (15–30 µm vs 84–90 µm in *C. umbellata*). In addition, *C. minor* can be distinguished from *C. lampensis* due the larger size of its sporangia and columellae (40–90 µm, and 12–75 µm vs 40–75 µm, and 15–30 µm, respectively).



Maximum Likelihood tree obtained from ITS sequences of our isolate and sequences retrieved from the GenBank nucleotide database. The tree was built by using PhyML v. 3.0 (Guindon et al. 2010a, b). Bootstrap support values (≥ 70 %) are given above the branches. *Mucor simplex* CBS 428.80 was used as outgroup. The new species proposed in the present study is indicated in **bold**. ^{T} = ex-type.

Colour illustrations. Lampa caves, Santiago de Chile; colony after 7 d at 25 °C on PDA; umbel with sporangia; sporangia and columella; sporangiospores. Scale bars = 50 µm (sporangia borne in umbel), 10 µm (all others).

Eduardo Álvarez Duarte & Constanza Muñoz Cortés, Mycology Unit, Biomedical Sciences Department, University of Chile, Santiago, Chile; e-mail: ealvarezd@med.uchile.cl, camunoz19@outlook.es
Ignacio Fernández, Myotis-Chile, Duble Almeyda 2010, Ñuñoa, Santiago, Chile; e-mail: i.fernandezlatapiat@gmail.com


Colletotrichum cycadis

Fungal Planet 1147 – 19 December 2020

Colletotrichum cycadis Andjic, Maxwell & Smith, *sp. nov.*

Etymology. Named after the host genus, *Cycas*, from which it was isolated.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

Sexual morph not observed. *Asexual morph on malt extract agar* (MEA) (microscopic preparations in lacto-glycerol, with at least 30 measurements per structure). *Hyphae* hyaline to pale brown, smooth-walled, septate, branched. *Mycelium* white, becoming olive grey with age. *Conidiomata* acervular, brown to black. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline to pale brown, smooth-walled, aseptate, occasionally septate, mostly cylindrical, gradually thinner towards the apex, (7.5–)11–12(–17.5) × (2–)2.5–3(–4.5) µm (av. ± SD = 11.5 ± 2.3 × 2.6 ± 0.6 µm, L/W ratio = 4.4). *Conidia* aseptate, hyaline, smooth-walled, cylindrical to fusoid with obtuse ends, sometimes tapering towards the apex, contents granular or guttulate, 9.5–13.5 × 3–4 µm (av. ± SD = 11.5 ± 0.65 × 3.5 ± 0.2 µm, L/W ratio = 3.3). *Appressoria* single or in small groups, pale to dark brown, smooth-walled, variable in shape, ovate to irregularly lobed, often tapering towards apex, 4.5–8 × 2–5.5 µm (av. ± SD = 6.1 ± 1.1 × 4.5 ± 0.9 µm, L/W ratio = 1.3).

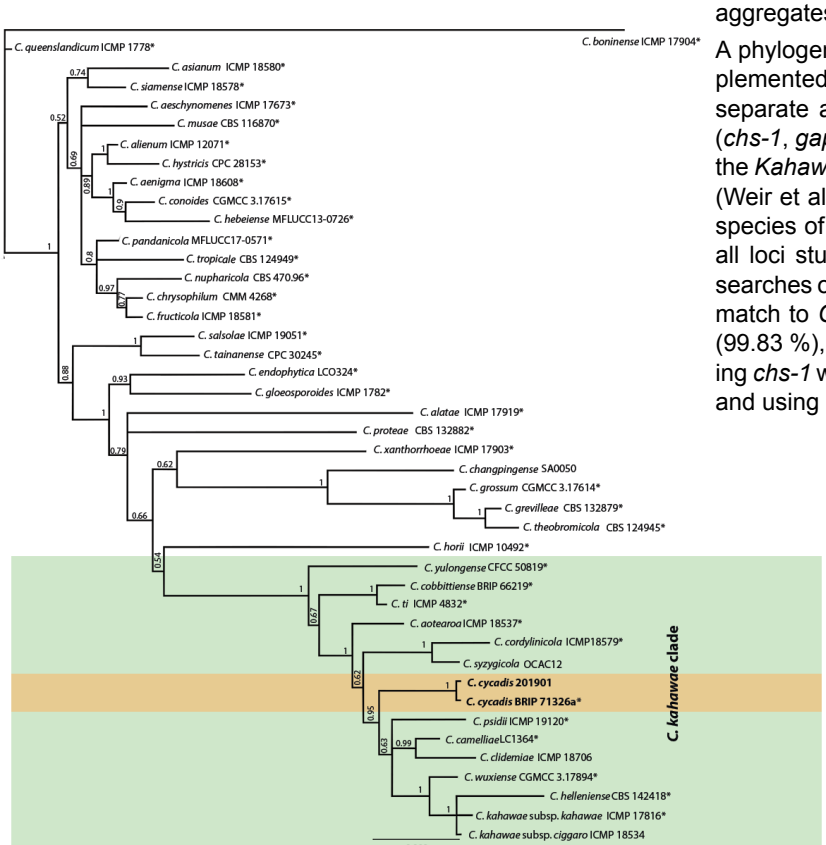
Culture characteristics — Colonies grown from single conidium on MEA reaching 70–80 mm diam after 10 d at 25 °C in the dark, light grey (5Y 7/1) to light olive grey (5Y 6/2) (Munsell & Munsell 2000); with orange conidial ooze on the surface of colony, aerial mycelium white, tufted near centre. Reverse dark olive grey (5Y 3/2), surrounded with white cottony mycelium.

Typus. China, Fujian, Zhangzhou, on leaves of *Cycas revoluta*, intercepted at Australian border, July 2019, *V. Andjic & A. Maxwell* (holotype BRIP 71326a, includes holotype culture, LSU, ITS, *chs-1*, *gapdh* and *tub2* sequences GenBank MW136942, MT439915, MT439917, MT439919, and MT439921, MycoBank MB836054).

Additional material examined. China, Fujian, Zhangzhou, on leaves of *Cycas revoluta*, intercepted at Australian border, July 2019, *V. Andjic & A. Maxwell*, AQISWA201901 (culture dead), LSU, ITS, *chs-1*, *gapdh* and *tub2* sequences GenBank MW136943, MT439916, MT439918, MT439920, and MT439922.

Notes — Leaf spots were observed on the young leaves of *Cycas revoluta* in a post entry quarantine greenhouse in Carabooda, Western Australia, Australia. Infected plants were destroyed and the pathogen remains absent from Australia (Australian Plant Pest Database 2020). The leaf symptoms were characterised by chlorosis starting from the tip of the leaf going towards the base where it becomes cream and then dark brown. Conidiomata occur in small, black, irregular shaped aggregates, sometimes clustered in concentric circles.

A phylogenetic tree obtained using Bayesian analysis as implemented in Geneious R10 (https://www.geneious.com) of separate and combined sequence data from four gene loci (*chs-1*, *gapdh*, ITS and *tub2*) placed the pathogenic fungus in the *Kahawae* clade in the *C. gloeosporioides* species complex (Weir et al. 2012). It is phylogenetically distinct from all other species of the *Kahawae* clade and can be distinguished with all loci studied, except LSU and *tub2*. Based on megablast searches on NCBIs GenBank nucleotide database, the closest match to *C. cycadis* using the LSU sequences was *C. lentis* (99.83 %), using ITS was *C. cobbttiense* (98.92 % identity), using *chs-1* was *C. wuxiense* and *C. aotearoa* (98.62 % identity), and using *gapdh* was *C. aotearoa* (98.91 % identity).



Phylogenetic tree from Bayesian analysis based on combined gene sequences (*chs-1*, *gapdh*, ITS and *tub2*) showing the phylogenetic relationships amongst the newly described taxon *C. cycadis* (in **bold**) and known species in the *C. gloeosporoides* complex. Bayesian posterior probabilities (PP > 0.95) are shown at the nodes. The tree is rooted with *C. boninense* (ICMP 17904). Ex-type cultures are marked with an asterisk (*). The alignment and tree were deposited in TreeBASE (Submission ID S26714).

Colour illustrations. *Cycas revoluta* plant. Symptomatic leaves; appressoria; conidiogenous cells; colony on MEA at 10 d; conidia. Scale bars = 10 µm.

Vera Andjic, Aaron Maxwell & Keelin Smith, Department of Agriculture, Water and Environment, 24 Fricker Rd., Perth, 6105 Western Australia, Australia; e-mail: vera.andjic@agriculture.gov.au, aaron.maxwell@agriculture.gov.au & keelin.smith@agriculture.gov.au


Coprinopsis rubra

Fungal Planet 1148 – 19 December 2020

Coprinopsis rubra Örstadius, E. Larss. & L. Nagy, *sp. nov*.

Etymology. The epithet refers to the red cap and veil colour.

Classification — *Psathyrellaceae*, *Agaricales*, *Agaricomycetes*.

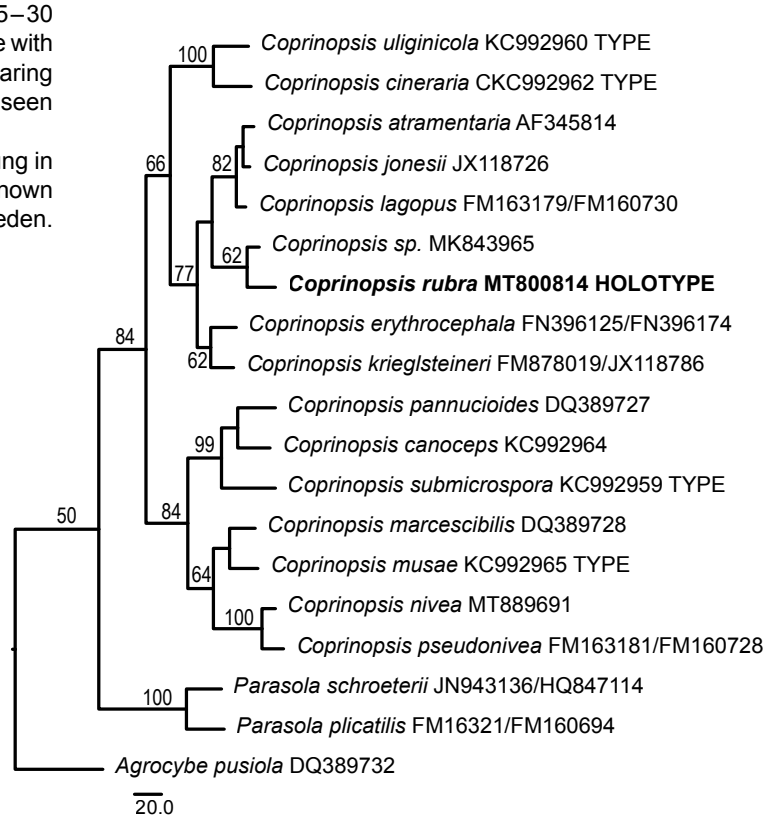
Basidiomata small, coprinoid. *Pileus* at first ellipsoid, campanulate, then expanded convex to plane, umbonate, 6–12 mm wide, radially grooved, red to pale red below the veil, when mature or old pallescent becoming grey tinged; veil vividly red to dark red, covering greater part of surface, splitting into flocci especially at centre. *Lamellae* free, medium spaced, L = c. 25, when young whitish, becoming brown to blackish, with pale red edge, partly deliquescent. *Stipe* 12–20 × 1–2 mm, thickened towards base, not root-like extended, concolorous with cap at base, with pale red to whitish upper part, fibrillose, with flocculose veil remnants particularly towards base. *Smell* not distinctive; *taste* not recorded. *Basidiospores* 8–10 × 4.8–5.4 µm (av. 8.8–9.2 × 5.1 µm, Qav = 1.7–1.8), oblong, ellipsoid, ovoid, sometimes slightly irregular, in profile flattened on one side, neither amygdaliform nor phaseoliform, rarely broken, in water red (Mu. 2.5YR 4/8, Munsell 1975), with small, central, rather distinct germ pore. *Basidia* 4-spored, 15–30 × 7–8 µm, surrounded by (3–)4(–5) pseudoparaphyses. *Pleurocystidia* 35–65 × 20–32 µm, subutriform, ventricose, clavate, sphaeropedunculate, numerous, pale. *Cheilocystidia* 15–50 × 12–30 µm, similar to pleurocystidia in shape, ellipsoid, numerous. *Pileipellis* a cutis made up of hyphae with short, 7–14 µm wide cells. *Veil cells* 20–80 × 5–30 µm, pale to moderately red intracellular pigmented; surface with dark red spots, irregularly and loosely attached, disappearing when gently tapping on the coverslip. *Clamp connections* seen at stem base mycelium and veil hyphae.

Habitat & Distribution — Growing scattered on cow dung in pastures, only manured from the grazing animals. So far known from three localities in Halland, a southern province of Sweden.

Typus. Sweden, Halland, Steninge, Lövängen, about 15 km N of Halmstad, on cow dung, 28 Aug. 2019, *B. Larsson* (EL387-19, holotype GB-0207585, ITS-LSU sequence GenBank MT800814, MycoBank MB836567).

Additional materials examined. Sweden, Halland, Varberg, Vadkärr, on cow dung, 17 Aug. 2018, *K. Persson* (LÖ73-18, GB); Halland, Steninge, Lövängen, about 15 km N of Halmstad, on cow dung, 30 Aug. 2019, *B. Larsson & K. Persson* (LÖ47-19, GB-0207595); Halland, Mannarp, on cow dung, 18 Sept. 2009, *L. Nagy, M. Jeppson & T. Knutsson* (NL-2758).

Notes — *Coprinopsis rubra* can be recognised by the striking dark red colour of its cap and veil, coprophilous habitat, and rather small spores. The species belongs to subsection *Lanatuli* (Uljé 2005) characterised by a hairy-floccose veil made up of elongate elements. Subsection *Alachuani* differs in having diverticulate often thick-walled elements (Uljé 2005). *Coprinopsis erythrocephala* is morphologically closely related but can be separated by larger basidiomata, a soon disappearing veil, larger pleurocystidia, larger spores, and a non-coprophilous habitat. In the phylogenetic analysis *C. rubra* comes out closest to an ITS sequence of an unknown species of *Coprinopsis* from Brazil, and in the sister clade to *C. erythrocephala*.



Phylogram obtained using PAUP* v. 4.0a (Swofford 2003) based on ITS and LSU sequence data showing the position of *C. rubra* in the Atramentarii and Lanatuli clades (Nagy et al. 2013). Bootstrap values are indicated on branches and the holotype is marked in **bold**.

Colour illustrations. Sweden, Halland, Steninge, Lövängen, a pasture from the type locality. Basidioma (Varberg, Vadkärr, LÖ73-18); basidiomata (Steninge, holotype); spores; pleurocystidia (above) and cheilocystidia (below); veil cells. Scale bars = 1 cm (basidiomata), 10 µm (spores, cystidia and veil).

Leif Örstadius, Lyckans väg 39A, S-29143 Kristianstad, Sweden; e-mail: leif.orstadius@gmail.com
Ellen Larsson, Biological and Environmental Sciences, University of Gothenburg, Box 461, 40530 Göteborg, Sweden, and Gothenburg Global Biodiversity Centre, Box 461, SE40530 Göteborg, Sweden; e-mail: ellen.larsson@bioenv.gu.se
László G. Nagy, Institute of Biochemistry, Biological Research Center, Temesvari krt 62, H-6726 Szeged, Hungary; e-mail: lnagy@fungenomelab.com


Crinipellis nigrolamellata

Fungal Planet 1149 – 19 December 2020

Crinipellis nigrolamellata Antonín, Fiard, Ševčíková, Dumez & Courtec., *sp. nov.*

Etymology. The epithet refers to the lamellae that become black with age.

Classification — *Marasmiaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 5–10 mm broad, convex-conical to broadly conical with a shallow central umbilicus and involute to inflated margin, then broadly conical with central umbo with distinct umbilicus, distinctly radially fibrillose, fibrils projecting up to 1 mm beyond pileus margin, margin shallowly sulcate, dark brown to black-brown (8F3–5; Kornerup & Wanscher 1978) at centre, other parts brown-argillaceous or brown (6E5), outermost part paler (± 8D5) or even dirty whitish in old basidiomata. *Lamellae* moderately close, L = 24–28, l = 3, emarginate and with small tooth, slightly ventricose, (greenish) grey (± 5D3), with finely pubescent, at first whitish edge; edge and adjacent parts becoming stainy to entirely black. *Stipe* 15–45 × 0.5–1(–1.5) mm, cylindrical, very slightly broadened at base, insititious, entirely tomentose to adpressedly hairy, strigose at base, sometimes longitudinally striate, entirely dark brown to black-brown (concolorous with pileus centre). *Rhizomorphs* absent. *Basidiospores* (7.5–)8–9.5(–10) × (2.7–)3–4 µm, av. 8.7 × 3.5 µm, E = (2–)2.3–2.8(–2.9), Q = 2.4–2.5, fusoid, lacrimoid, thin-walled, colourless or greyish brownish in KOH, sometimes with one septum, non-dextrinoid. *Basidia* 17–20 × 6–8 µm, 4-spored, clavate; rare sclerobasidia present, black in KOH. *Basidioles* 13–25 × 3–9 µm, clavate, subcylindrical, subfusoid. *Cheilocystidia* 11–27 × 6–8.5(–10) µm, clavate, fusoid, rarely subutriform, mostly with apical projections or (rarely) subcoralloid, less frequently simple, thin- to slightly thick-walled, colourless to often with dark (greyish) blackish contents in KOH. *Pleurocystidia* (17–)20–35 × 6–9 µm, fusoid, sometimes subrostrate, thin-walled, mostly colourless or pale greyish in KOH. *Pileipellis* (hypotrichium) a cutis composed of cylindrical, thin- to slightly thick-walled, non-dextrinoid, 3–8 µm wide hyphae; pileus hairs up to c. 1300 × 2–6(–9) µm, cylindrical, obtuse to subacute, thick-walled (walls up to 1.5(–4) µm), often curved especially at base, often septate or with obliterated lumen, dextrinoid, walls reddish brown in H_2O, brown-olivaceous to pale olivaceous in KOH, covered with granular or irregular brown incrustation, more frequently towards base. *Stipitipellis* a cutis composed of cylindrical, slightly thick-walled, 2–5 µm wide, walls ± colourless or pale brownish in H_2O; stipe hairs similar to pileus ones, 15–600 × 4–17 µm. *Clamp connections* present.

Habit, Habitat & Distribution — Solitary or in groups on fallen leaves in forests. So far known only from Martinique, France.

Typus. France, Martinique, Trinité com., Tartane, Point Rouge Reserve, Pointe à Bibi, on leaves of *Pisonia fragrans* (*Nyctaginaceae*), 3 Nov. 2015, *R. Courtecuisse* (holotype LIP 0201684, LSU and ITS sequences GenBank MT946361 and MT946363, MycoBank MB836917).

Colour illustrations. Locality (France, Martinique, Caravelle NR). From top to bottom: basidiomata; stipe hair. *Drawing*: basidia, basidiospores, cheilocystidia, pileus hairs, stipe hair, pleurocystidia. Scale bars = 1 cm (basidiomata), 10 µm (all microcharacters).

Additional materials examined. France, Martinique, Trinité com., Tartane, Caravelle Nature Reserve, Anse Four à Chaux, on fallen leaves, 4 Nov. 2015, *V. Antonín* & *R. Courtecuisse* (LIP 0201685, LSU and ITS sequences GenBank MT946362 and MT946364); ibid., on fallen leaves, 17 Dec. 2001, *J.P. Fiard F2480* (LIP 0701686).

Notes — *Crinipellis nigrolamellata* is characterised by a dark brown to black-brown pileus and stipe, lamellae becoming black, non-dextrinoid, narrow basidiospores, small cheilocystidia mostly with apical projections, well-developed pleurocystidia, and hairs walls reddish brown in H_2O, brown-olivaceous to pale olivaceous in KOH, and covered with brown incrustation. Black coloured lamellae are described in *C. bisulcata* known from Ecuador and Venezuela. It differs by shorter and differently shaped basidiospores, 6.3–8.5 × 3.1–3.8 µm (mostly 7–8.5 × 3–3.8 µm) and longer, 37–56 × 4–7.5 µm, cheilocystidia (Singer 1942). However, Singer mentioned that the black lamellae colour of the type specimen may be caused by a bad preservation – specimens were preserved in alcohol at first and then dried. *Crinipellis brunnescens* also has lamellae brown to black with age or when where bruised. It differs by a smaller stipe, 8–12 × 0.4–0.8 mm, larger basidiospores, 6–10 × 4–5 µm and the absence of pleurocystidia (Kerekes & Desjardin 2009).

Other phylogenetically relatively close species never have dark coloured lamellae. Moreover, *C. malesiana* has a brown to brownish orange pileus at the margin with age, larger basidiospores, longer pleurocystidia, larger, mostly simple cheilocystidia (Kerekes & Desjardin 2009); *C. actinophora* also differs by a shorter stipe, the presence of rhizomorphs and the absence of pleurocystidia (Singer 1955, Kerekes & Desjardin 2009); *C. pallidipilus* has golden brown, then pallescent pileus hairs, a shorter stipe, abundant rhizomorphs, larger basidiospores, cheilocystidia with numerous digitate projections and lacks pleurocystidia (Antonín et al. 2014); *C. wandoensis* differs by well-developed rhizomorphs, broader basidiospores and absent pleurocystidia (Antonín et al. 2014).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Crinipellis* sp. (strain GL-2017, GenBank LT716050.1; Identities = 615/648 (95 %), eight gaps (1 %)) and the type of *Crinipellis pallidipilus* (strain BRNM 751595, GenBank KF380833.1; Identities = 572/603 (95 %), 11 gaps (1 %)). Closest hits using the **LSU** sequence are *Crinipellis setipes* (strain Bandala 4085, GenBank MN567618.1; Identities = 998/1021(98 %), 4 gaps (0 %)) and *Crinipellis nigricaulis* (strain G1325, GenBank MK277894.1; Identities = 997/1021(98 %), 4 gaps (0 %)).

Supplementary material

FP1149 Phylogram: Best tree from the ML analysis of the nrITS dataset for *Crinipellis nigrolamellata* and related species with *Marasmius crinis-equi* as outgroup. Phylogenetic analyses were carried out online at http://phylogeny.lirmm.fr/ (Dereeper et al. 2008) with PhyML v. 3.0 (Guindon et al. 2010a). Multiple sequence alignments were carried out with MUSCLE v. 3.7 (Edgar 2004). Trees were constructed using TreeDyn v. 198.3 (Chevenet et al. 2006) and edited with the newly generated sequences in **bold**.

Vladimír Antonín & Hana Ševčíková, Dept. of Botany, Moravian Museum, Zelný trh 6, 659 37 Brno, Czech Republic; e-mail: vantonin@mzm.cz & hsevcikova@mzm.cz
Régis Courtecuisse & Sylvain Dumez, ULR 4515 - LGCgE (Laboratoire de Génie Civil et géo-Environnement), ER4 (Fonctionnement des écosystèmes terrestres anthropisés) - LSVF (Laboratoire des sciences végétales et fongiques), Faculté des sciences pharmaceutiques, Université de Lille, 3, rue du Professeur Laguesse, F-59006 Lille Cedex; e-mail: regis.courtecuisse@univ-lille.fr & sylvain.dumez@univ-lille.fr
Jean-Pierre Fiard, 3/524, résidence les Cyclades, Rue R. Garcin, F-97200 Fort-de-France; e-mail: jpfiard@gmail.com


Cyberlindnera dauci

Fungal Planet 1150 – 19 December 2020

Cyberlindnera dauci A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

Etymology. Name refers to *Daucus carota* from which the species was isolated.

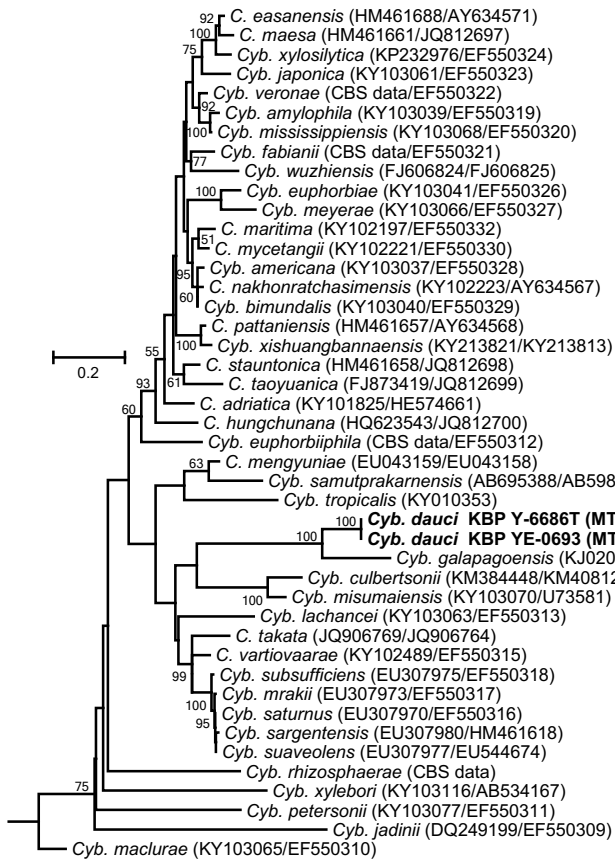
Classification — *Wickerhamomycetaceae*, *Saccharomycetales*, *Saccharomycetes*.

On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, butyrous, with a smooth surface and entire margin. Cells are subglobose, ovoid to elongate (2–5.5 × 2.5–6.5 µm) and occur singly or in pairs, dividing by multilateral budding. After growth on potato dextrose agar (PDA) cells have visible lipid-like body. *Ascospores*, *pseudohyphae* and *true hyphae* have not been observed during 4 wk at 10 and 25 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, PDA, cornmeal agar (CMA), McClary acetate agar and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, sucrose and raffinose are positive. Glucose, inulin, sucrose, raffinose, trehalose (delayed weak), cellobiose, salicin, L-rhamnose, D-xylose, ethanol, glycerol, D-mannitol (weak), D-glucitol, DL-lactic acid (weak), succinic acid, citric acid and arbutin are assimilated; no growth occurs on melibiose, galactose, lactose, maltose, melezitose, methyl alpha-D-glucoside, soluble starch, L-sorbose, L-arabinose, D-arabinose, D-ribose, methanol, erythritol, ribitol, galactitol, *myo*-inositol, D-glucosamine, N-acetyl-D-glucosamine, hexadecane, 2-keto-D-gluconate, 5-keto-D-gluconate and D-glucuronate. Assimilation of nitrogen compounds: positive for ammonium sulfate, cadaverine, creatinine, creatine, L-lysine, D-glucosamine, and negative for potassium nitrate. Growth on vitamin-free medium and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth on MEA with 10 % NaCl is delayed weak. Growth with 0.01 % and 0.1 % cycloheximide is negative. Starch-like compounds are not produced. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 27.5 °C.

Typus. Russia, Moscow region, from carrot sample bought on local market, Feb. 2020, *A.M. Glushakova*, fvmr-2 (holotype KBP Y-6686, preserved in a metabolically inactive state, ex-type cultures VKM Y-3058 = DSM 111207 = CBS 16524, SSU, ITS-D1/D2 domains of LSU nrDNA, *tef1* and *rpb1* sequences GenBank MT636884, MT636878, LR814018 and LR814019, MycoBank MB836776).

Additional material examined. Russia, Moscow region, from carrot sample bought on local market, Feb. 2020, *A.M. Glushakova*, KBP YE-0693, ITS-D1/D2 domains of LSU nrDNA sequences GenBank MT936327 and MT939260.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed asexual yeasts suggested that they were conspecific and represented a hitherto undescribed species of *Cyberlindnera*. Based on the NCBI GenBank nucleotide database, the best hit using the **ITS** sequence is *Cyberlindnera galapagoensis* CBS 13997T (GenBank NR_159816; 86.56 % similar, 48 subst. and 29 gaps), using **LSU** it is *Cyb. galapagoensis* CBS 13997T (GenBank KJ020281; 96.98 % similar, 17 subst.), using **SSU** it is *Candida mengyuniae* CBS 10845T (GenBank EU043157; 96.28 % similar, 48 subst. and 14 gaps), using ***tef1*** it is *Cyb. mrakii* CBS 1707T (GenBank EU307984; 92.92 % similar, 26 subst. and 4 gaps) and using ***rpb1*** it is *Cyb. fabianii* YJS4271 (GenBank LK052886; 82.51 % similar, 109 subst. and 1 gap). In compliance with a recent phylogenetic analysis of the *Cyberlindnera* clade (Zheng et al. 2017), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Cyberlindnera dauci* can be physiologically differentiated from the phylogenetically most close species *Cyb. galapagoensis* based on its ability to assimilate trehalose, cellobiose, L-rhamnose and DL-lactic acid.



Maximum likelihood (ML) tree for the *Cyberlindnera* clade obtained from the combined analysis of ITS and LSU sequence data. The alignment included 1 194 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model (GTR) with Gamma distribution and invariant sites (G+I) was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). *Pichia membranifaciens* NRRL Y-2026 (DQ104710/U75725) was used as outgroup (hidden).

Colour illustrations. Russia, Moscow region, carrots on local market (photo provided by Yu.A. Kachalkina). *Cyberlindnera dauci* KBP Y-6686: growth of yeast colonies on MEA, yeast cells on PDA and MEA (after 7 d at 25 °C). Scale bar = 5 µm.

Anna M. Glushakova, Lomonosov Moscow State University, 119234, Moscow, Leninskie Gory Str. 1/12, Russia, and Mechnikov Research Institute for Vaccines and Sera, 105064, Moscow, Maly Kazenny by-street, 5A, Russia; e-mail: glushakova.anya@yandex.ru
Maria A. Tomashevskaya, All-Russian Collection of Microorganisms, G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, Pushchino, pr. Nauki 5, Russia; e-mail: tomkotik@rambler.ru
Aleksey V. Kachalkin, Lomonosov Moscow State University, 119234, Moscow, Leninskie Gory Str. 1/12, Russia, and All-Russian Collection of Microorganisms, G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms RAS, 142290, Pushchino, pr. Nauki 5, Russia; e-mail: kachalkin_a@mail.ru


Cyphellophora vietnamensis

Fungal Planet 1151 – 19 December 2020

Cyphellophora vietnamensis Iturrieta-González, Dania García, Guarro & Gené, *sp. nov.*

Etymology. Name refers to the geographical region where the fungus was collected.

Classification — *Cyphellophoraceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of branched, septate, subhyaline to pale olivaceous, smooth-walled hyphae, 1–1.5 µm diam. *Conidiophores* commonly macronematous, mononematous or in groups of 2–4, growing laterally or terminally on hyphae, erect, more or less penicillately branched, up to 250 µm long, with stipe pale brown to brown, smooth- and thick-walled; branches bearing terminally groups of 2–3 phialides, pale brown, asperulate to verruculose; micronematous conidiophores also present, consisting in phialides growing directly or on short supporting cells from vegetative hyphae. *Phialides* lageniform, 12–20 × 2–3.5 µm at the broad part, tapering to a long cylindrical neck with a conspicuous collaret slightly darker than the rest of the phialide, pale olivaceous, smooth-walled. *Conidia* in long unbranched chains (up to 90 conidia), 0(–1)-septate, ellipsoidal to somewhat fusoid, with truncate ends, obovoid when terminal, pale olivaceous, smooth-walled, 4–7 × 1–2 µm. *Chlamydospores* absent. *Sexual morph* not observed.

Culture characteristics — Colonies on potato dextrose agar (PDA) reaching 18–19 mm diam after 2 wk at 25 °C, brownish grey to grey (4D2/4B1) (Kornerup & Wanscher 1978), final edge olive (2F8), velvety, radially folded, aerial mycelium scarce, irregular margin; reverse olive (2F8). On potato carrot agar (PCA) reaching 18–20 mm after 2 wk at 25 °C, olive grey to olive (3D2/3F8), velvety, flat, aerial mycelium scarce, regular margin; reverse olive (2F8). On oatmeal agar (OA) reaching 18–19 mm diam after 2 wk, pale grey to olive (1B1/2F8), velvety at the centre, flat, aerial mycelium scarce, irregular margin; producing a metallic brightness on the border of the colony; reverse olive (2F8). Urease positive; laccase production negative.

Cardinal temperatures for growth — Minimum 15 °C, optimum 25 °C, maximum 30 °C.

Typus. Vietnam, Northeast region, on unidentified dead leaf, Aug. 2011, *J. Guarro* (holotype CBS H-24475, cultures ex-type FMR 17714 = CBS 146924; ITS, LSU and *tub2* sequences GenBank LR814107, LR814108 and LR814116, MycoBank MB836045).

Notes — Based on a megablast search of NCBIs GenBank database, the **LSU** sequence of *C. vietnamensis* showed a similarity of 98.22 % (829/844) with the sequence of *C. oxyspora* (CBS 698.73, GenBank NG_067405) and 97.75 % (825/844) with that of *C. suttonii* (CBS 125441, GenBank MH874978); the **ITS** sequence was 96.71 % (558/577) similar with that of *Phialophora capiguarae* (ex-type strain CBS 132767, GenBank KF928464) and a 88.61 % (537/606) with respect to *C. oxyspora* (IFM 51368, GenBank AB190870); and the ***tub2*** sequence was 94.65 % (336/355) similar with that of *P. capiguarae* (strain CBS 131954, GenBank KF928593) and a 77.74 % (255/328) with respect to *C. ludoviensis* (CMRP 1317, GenBank KX583749). Phylogenetic reconstruction with ITS, LSU and *tub2* loci (Attili-Angelis et al. 2014) of the accepted species of *Cyphellophora* and *Phialophora*, including the type species of the respective genera (i.e., *C. laciniata* CBS 190.61 and *P. verrucosa* CBS 140326), showed that the new species is allocated in a strongly supported clade with *C. oxyspora* and *P. capiguarae,* but being closely related to the latter species. Our phylogeny supports that *P. capiguarae* as well as *P. attinorum*, both described by Attili-Angelis et al. (2014), belong to the *Cyphellophora* clade. Although *P. capiguarae* was previously considered a species of *Cyphellophora* (Gomes et al. 2016), the formal taxonomic change was not proposed. Therefore, respective new combinations are proposed below.

Morphologically, *C. vietnamensis* differs from *P. capiguarae* mainly by having unbranched conidial chains, which are smaller (4–7 × 1–2 µm vs 6.5–9 × 1.9–2.5 µm in *P. capiguarae*) and commonly aseptate, absence of chlamydospores, and a moderately faster growth (PDA, 18–19 mm vs 13–14 mm in *P. capiguarae*; OA, 18–19 mm vs 14–15 mm in *P. capiguarae*) after 2 wk at 25 °C. *Cyphellophora vietnamensis* clearly differs from *C. oxyspora* (Gams & Holubová-Jechová 1976, Réblová et al. 2013) by its long penicillate conidiophores.

Cyphellophora attinorum (Attili-Angelis et al.) Iturrieta-González, Gené, Dania García, *comb. nov*. — MycoBank MB836046

Basionym. Phialophora attinorum Attili-Angelis et al., '*attae*' Fungal Diversity 65: 68. 2014.

Typus. Brazil, Fazenda Santana, Botucatu, São Paulo, from the cuticle of *Atta capiguara* gynes, Nov. 2008, *A.P.M. Duarte*, *F.L.A. Guedes* & *D. Attili-Angelis* (holotype and cultures ex-type CBS 131958; ITS, LSU and *tub2* sequences GenBank KF928463, KF928527 and KF928591).

Notes — *Cyphellophora attinorum* is closely related to *C. livistonae* (Crous et al. 2012, Madrid et al. 2016) and *C. sessilis* (De Hoog et al. 1999, Réblová et al. 2013), both species formerly classified in *Phialophora*. Morphologically, *C. attinorum* can be differentiated from *C. livistonae* by the production of shorter (1.6–4.2 vs (4–)7–8(–10) µm) and aseptate conidia, and by the absence of chlamydospores. Chlamydospores in *C. livistonae* are intercalary, 0–1-septate, measuring 8–10 × 3–5 µm (Crous et al. 2012). *Cyphellophora sessilis* differs by its shorter (up 3 µm; up to 4.2 in *C. attinorum*) and obovoidal conidia (broadly ellipsoidal in *C. attinorum*).

Cyphellophora capiguarae (Attili-Angelis et al.) Iturrieta-González, Gené, Dania García, *comb. nov.* — MycoBank MB836047

Basionym. Phialophora capiguarae Attili-Angelis et al., Fungal Diversity 65: 70. 2014.

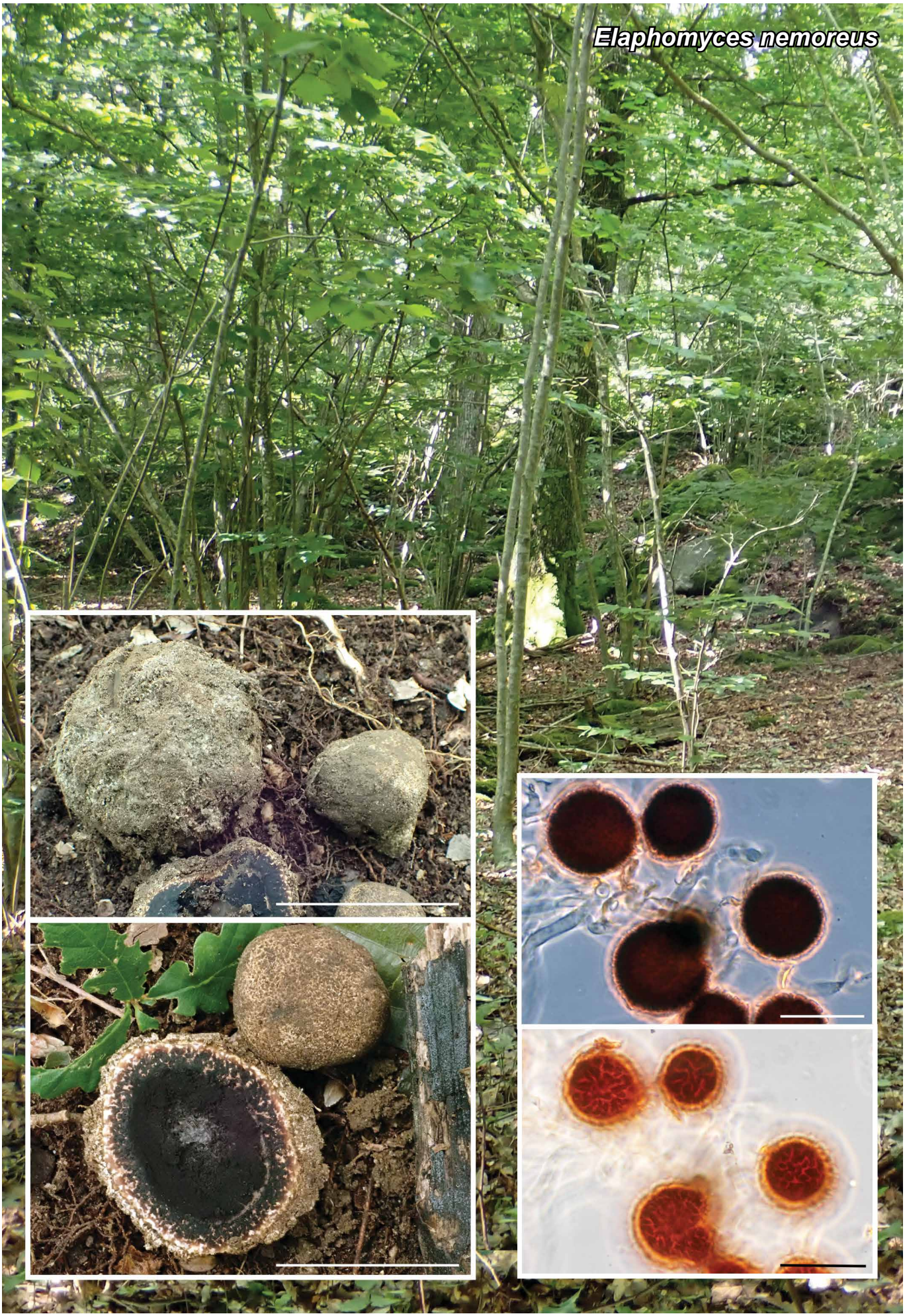
Typus. Brazil, Fazenda Santana, Botucatu, São Paulo, from cuticle of *Atta capiguara* gynes, Dec. 2009, *F.C. Pagnocca, N.S. Nagamoto, A.P.M. Duarte* & *D. Attili-Angelis* (holotype and cultures ex-type CBS 132767; ITS, LSU and *tub2* sequences GenBank KF928464, KF928528 and KF928592).

Colour illustrations. Vietnam, Northeast region. Colony sporulating on OA after 2 wk at 25 ºC; conidiophores, phialides and conidia after 18 d. Scale bars = 10 mm (colony), = 10 µm (microscopic structures).

Supplementary material

FP1151 Maximum likelihood tree obtained from the combined analysis of ITS, LSU and *tub2* sequences of the genus *Cyphellophora* and representative species of the genus *Phialophora*. New species and new combinations proposed are indicated in **bold** face.

Isabel Iturrieta-González, Josepa Gené, Josep Guarro & Dania García, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain;
e-mail: isabeliturrieta@gmail.com, josepa.gene@urv.cat, josep.guarro@urv.cat & dania.garcias@urv.cat


Elaphomyces nemoreus

Fungal Planet 1152 – 19 December 2020

Elaphomyces nemoreus Jeppson, Molia & E. Larss., *sp. nov.*

Etymology. Name refers to the occurrence in deciduous woodlands.

Classification — *Elaphomycetaceae*, *Eurotiales*, *Eurotiomycetes.*

Ascomata subglobose 1–6 cm diam. *Peridial surface* yellowish grey-brown with a covering of low and flat, obtuse, somewhat darker warts or platelets on a lighter background. Ascomata are found solitary or in small groups and are covered by a pale yellow to sulphur yellow mycelial layer encrusting soil. Cortex and mycelial covering constructed of loosely to intricately interwoven thin-walled, hyaline to yellowish hyphae, 2–5 µm diam, sometimes with slightly encrusted walls. Areas between the warts are formed by compacted parallel bundles of hyaline compacted hyphae. *Peridium* in section thick (fresh up to 5 mm), distinctly marbled with large ochraceous to dark brown or purplish brown and irregularly rounded marbles divided by winding, more or less radially arranged whitish veins. Peridium formed by loosely to intricately interwoven hyphae up to 10 µm diam, in darker areas of the marbling with adhering brown grains of extra-cellular pigments. *Gleba* young greyish white, web-like, later pulverulent and black. *Asci* not observed. *Ascospores* dark brown, globose, in KOH 3 % 23–32 µm (av. 26 µm) including ornamentation, 17–25 µm (av. 22 µm) ornamentation excluded, in Hoyer´s solution significantly smaller: 20–25.5 µm (av. 22 µm) including ornamentation, 16.5–22 µm (av. 18.7 µm) ornamentation excluded. Ornamentation in side view with broad spines and warts up to 3 µm high. A surface view reveals groups of spines with confluent apices, with age coalescing to form coarse meshes and crests.

Habitat & Distribution — Found associated with *Fagus sylvatica* and *Quercus robur* on basic and acidic soils. Likely to have a northern distribution range in Europe, but occurs also in Southern Europe.

Typus. Sweden, Bohuslän, Valla, Sundsby, deciduous woodland under *Quercus robur* and *Fagus sylvatica*, 20 m asl., N58.065348° E11.676246°, 17 July 2020, *E. Larsson & M. Jeppson 11077* (holotype GB-0207587, ITS-LSU sequence GenBank MT872017, MycoBank MB837347).

Additional materials examined. ***Elaphomyces decipiens***: Sweden, Gotland, Mästerby, wooded meadow under *Quercus robur*, 24 Oct. 2019, *E. Larsson 268-19* (GB-0207592), ITS-LSU sequence GenBank MT872011. ***Elaphomyces nemoreus***: Norway, Agder, Farsund, 2013, *A. Molia 351-2013* (O-F21484), ITS-LSU sequence GenBank KR029742; Aust-Agder, Arendal, 9 Nov. 2013, *A. Molia et al.* (O-F21513), ITS-LSU sequence GenBank KR027943. – Sweden, Bohuslän, Valla, Sundsby, deciduous woodland under *Fagus sylvatica*, 26 Aug. 2014, *K. Rense & M. Jeppson 10151* (GB-0207593), ITS-LSU sequence GenBank MF614923; ibid., 17 July 2020, *E. Larsson & M. Jeppson 11180* (GB); Bohuslän, Ljung, Tjöstelseröd, under *Quercus robur*, 24 Apr. 2020, *E. Larsson & M. Jeppson 11141* (GB), ITS sequence GenBank MT872012; ibid., 24 Apr. 2020, *E. Larsson & M. Jeppson 11139* (GB-0207589); Bohuslän, Resteröd, under *Fagus sylvatica*, 20 Nov. 2019, *E. Larsson 382-19* (GB-0207590), ITS-LSU sequence GenBank MT872015; ibid., 16 Apr. 2020, *E. Larsson 44-20* (GB-0207591), ITS-LSU sequence GenBank MT872013; Bohuslän, Uddevalla, Rimnersvallen, deciduous woodland under *Quercus robur*, 3 Aug. 2016, *A. Molia & M. Jeppson 10482* (GB-0207594), ITS sequence GenBank MT872016; Västergötland, V. Tunhem, deciduous woodland under *Quercus robur*, 26 Dec. 2019, *A. Bohlin, E. Larsson & M. Jeppson 11076* (GB-0207588), ITS sequence GenBank MT872014.

Notes — *Elaphomyces nemoreus* belongs to *Elaphomyces* section *Elaphomyces* subsection *Muricati*. It is closely related to *E. decipiens* (with a neotype recently designated by Paz et al. 2017), with which it shares the characteristic marbled peridium with whitish, more or less radially arranged veins and the ochraceous to dark purplish brown, irregularly rounded, large marbles. Both species have a cortex surface with low flat, grey-brown warts. In *E. nemoreus* the surface warts typically appear as plates forming a cheetah pattern. In *E. decipiens* the hyphal crust surrounding the ascomata is creamy white whereas in *E. nemoreus* it has distinct sulphur yellow tinges. The spores are similar in size and ornamentation in the two species.

In Molia et al. (2020), a genetic divergence was observed within *E. decipiens*. Further sequenced collections from Scandinavia confirmed this observation and the occurrence of two genetically distinct but morphologically similar species. So, we here recognise *E. nemoreus* as a distinct species in the subsection *Muricati*. In the phylogenetic analyses it comes out with support as a sister species to *E. decipiens* from which it differs by five substitutions and two 1–2 bp insertion/deletion events in the ITS1 region and two substitutions in the ITS2 region. Based on the sequences included here no gene flow between the two genotypes can be observed, which supports their evolutionary autonomy. The sequences originating from North America submitted to GenBank as *E. decipiens* (EU837299, EU846311) did not come out together with the neotype of *E. decipiens* nor with the herein described species, and these two sequences are shown to be more closely related to *E. barrioi* and the recently described *E. bucholtzii* (Crous et al. 2020a).

Elaphomyces nemoreus is recorded from coastal areas of south-western Scandinavia (Norway and Sweden) where it occurs in south-facing, warm forest habitats with *Fagus sylvatica* and *Quercus robur,* often on acid, but more nutrient-rich soils. *Elaphomyces nemoreus* is more frequently encountered in Scandinavia than *E. decipiens*, that must be regarded as rare but with confirmed finds from meadow areas under *Quercus robur* on calcareous ground. *Elaphomyces decipiens* may have a more southern European distribution range, but sequence data published in Paz et al. (2017) indicate that also *E. nemoreus* occurs under *Fagus* in northernmost Spain.

Colour illustrations. *Elaphomyces nemoreus* (holotype), habitat. Ascomata; ascospores in side view and surface view. Scale bars = 10 µm (ascospores), 50 mm (ascomata).

Supplementary material

FP1152 Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *E. nemoreus* in *Elaphomyces* subsection *Muricati*. Bootstrap values are indicated on branches, *E. nemoreus* is marked in **bold** and the holotype is indicated.

Mikael Jeppson & Ellen Larsson, Biological and Environmental Sciences, and Gothenburg Global Biodiversity Centre, University of Gothenburg, P.O. Box 461, SE-40530 Göteborg, Sweden; e-mail: mikael.jeppson@bioenv.gu.se & ellen.larsson@bioenv.gu.se
Anne Molia, Alette Iversens gate 5, N-3970 Langesund, Norway; e-mail: anne.molia@nhm.uio.no


Exophiala embothrii

Fungal Planet 1153 – 19 December 2020

Exophiala embothrii Sand.-Den. & Giraldo López, *sp. nov.*

Etymology. Named after the plant genus on whose rhizosphere the fungus was isolated, *Embothrium*.

Classification — *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

Mycelium consisting of hyaline to pale brown, smooth, branched, septate, 1–3 µm diam hyphae, torulose hyphae seldom present. *Conidiophores* short, erect, cylindrical, septate, poorly differentiated 18–50 µm long, 1–2.5 µm wide at the widest portion, often reduced to conidiogenous cells born laterally on the hyphae. *Conidiogenous cells* terminal or lateral on conidiophores and hyphae, subcylindrical to doliiform, 3.5–12.5 × 1–3 µm, or more commonly as lateral pegs borne terminal or intercalary on undifferentiated hyphae, 0.5–1.5 × 0.5–1 µm. *Conidia* aseptate, (sub)hyaline, ellipsoidal to cylindrical, (2.5–)4.5–6(–7) × 1.5–2.5 µm, often forming palisades alongside the hyphae or small heads on the tip of conidiophores. *Chlamydospores* and *budding cells* not observed.

Culture characteristics — Colonies on malt extract agar (MEA) dull green to olivaceous grey, velvety to cottony, slightly raised to umbonate, margin entire. Reverse olivaceous black without diffusible pigment.

Typus. Chile, Los Lagos Region, Osorno, from rhizosphere of *Embothrium coccineum* (*Proteaceae*), 1 Jan. 2019, *A. Giraldo* & *N. Sandoval-Giraldo* (holotype CBS H-24520, culture ex-type CBS 146558, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045817, MW045821, MW055980 and MW055976, MycoBank MB837535).

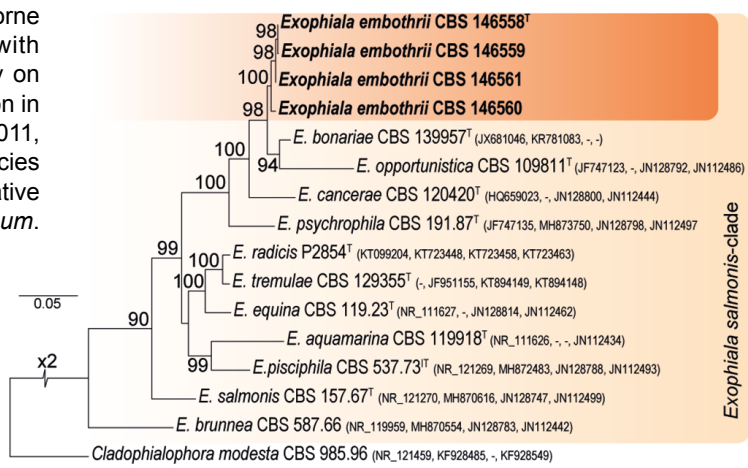
Additional materials examined. Chile, Los Lagos Region, Osorno, from rhizosphere of *Embothrium coccineum*, 1 Jan. 2019, *A. Giraldo* & *N. Sandoval-Giraldo*, CBS 146559 ITS, LSU, *tef1* and *tub2* sequences GenBank MW045818, MW045822, MW055981 and MW055977; ibid., CBS 146560, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045819, MW045823, MW055982 and MW055978; ibid., CBS 146561, ITS, LSU, *tef1* and *tub2* sequences GenBank MW045820, MW045824, MW055983 and MW055979.

Notes — *Exophiala embothrii* clusters within the salmonis-clade of *Exophiala*. This clade includes typically waterborne mesophilic species, some of which are associated with superficial and in some cases invasive infections mostly on cold-blooded animals, but also including agents of infection in humans and other homeothermic animals (De Hoog et al. 2011, Najafzadeh et al. 2018, Garzon et al. 2019). The new species described here was isolated from the rhizosphere of a native South American *Proteaceae* species, *Embothrium coccineum*.

Colour illustrations. *Embothrium coccineum* ('Notro' or 'Chilean firetree') with the Osorno volcano on the background (photo by Samuel Troncoso Sandoval, from Wikimedia Commons, license CC BY-SA 3.0). Conidiophores; conidiogenous cells; conidia. Scale bars = 5 µm.

Similarly, two other genetically related *Exophiala* species of the salmonis-clade, *E. radicis* and *E. tremulae,* are known to inhabit plant roots of *Microthlaspi perfoliatum* (*Brassicaceae*) and *Populus tremula* (*Salicaceae*), respectively (Crous et al. 2011, Maciá-Vicente et al. 2016). A four-gene phylogeny based on ITS, LSU, *tef1* and *tub2* sequences showed that *E. embothrii* is phylogenetically closely related to *E. opportunistica* and *E. bonariae*. However, *E. embothrii* differ by its consistently more elongated conidia and phialides, the absence of budding cells and the scarce presence of moniliform hyphae.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Exophiala opportunistica* (strain CBS 637.69, GenBank JF747121.1; Identities = 549/549 (100 %), 0 gaps), and *Exophiala opportunistica* (strain CBS 122269, GenBank JF747124.1; Identities = 549/549 (100 %), 0 gaps). Closest hits using the LSU sequence are *Exophiala psychrophila* (strain CBS 191.87, GenBank MH873750.1; Identities = 812/815 (99 %), no gaps), *Exophiala bonariae* (strain CCFEE 5899, GenBank KR781082.1; Identities = 812/815 (99 %), no gaps), and *Exophiala cancerae* (strain CBS 115142, GenBank MH874540.1; Identities = 814/816 (99%), 1 gap (0%)). Closest hits using the *tef1* sequence had highest similarity to *Exophiala opportunistica* (strain CGMCC:3.17515, GenBank KP347908.1; Identities = 192/201 (96 %), no gaps), *Exophiala opportunistica* (strain CGMCC:3.17507, GenBank KP347907.1; Identities = 192/201 (96 %), no gaps), and *Exophiala cancerae* (strain CBS 117491, GenBank JN128799.1; Identities = 173/201 (86 %), 3 gaps (1 %)). Closest hits using the *tub2* sequence had highest similarity to *Exophiala opportunistica* (strain CBS 112269, GenBank JN112487.1; Identities = 408/408 (100 %), no gaps), and *Exophiala opportunistica* (CBS 637.69, GenBank JN112490.1; Identities = 405/408 (99 %), no gaps).



Maximum likelihood tree (RAxML, conducted in the CIPRES science gateway) from the analysis of combined ITS, LSU, *tef1* and *tub2* sequences (total 1 957 bp) of members of the *Exophiala salmonis* clade. Bootstrap support values above 70 % are indicated on the nodes. The new species proposed in this study is indicated in **bold**. T and IT denotes ex-type and ex-isotype cultures. GenBank reference sequence accession numbers for ITS, LSU, *tef1* and *tub2* are indicated between parentheses. The tree is rooted to *Cladophialophora modesta* (CBS 985.96).

Marcelo Sandoval-Denis, Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; e-mail: m.sandoval@wi.knaw.nl
Alejandra Giraldo, Radboud University Medical Centre, Geert Grooteplein Zuid 10, 6525 GA Nijmegen, The Netherlands; e-mail: Alejandra.GiraldoLopez@radboudumc.nl


Geoglossum jirinae

Fungal Planet 1154 – 19 December 2020

Geoglossum jirinae V. Kučera, Ševčíková, Slovák, *sp. nov.*

Etymology. The name 'jirinae' honours the collector of the holotype, Jiřina Hrabáková.

Classification — *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

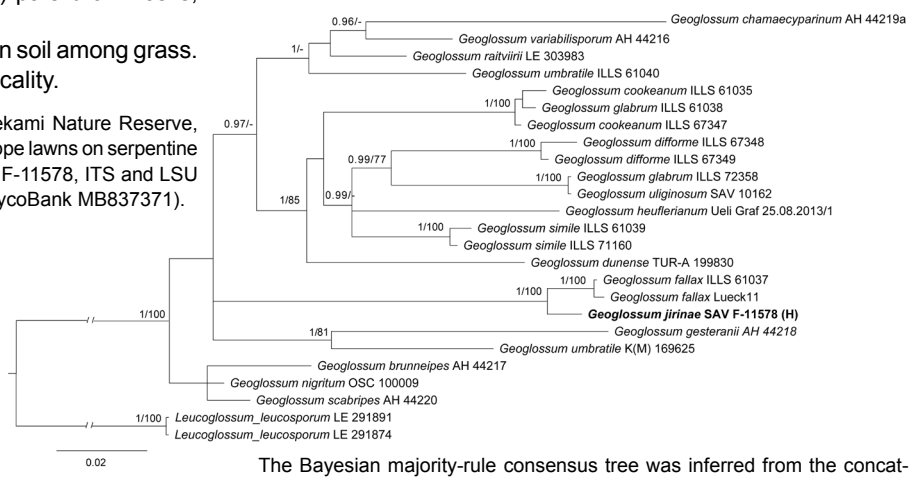
Ascomata solitary, scattered, clavate, stipitate, 18–36 × 2–4 mm, dry, black. *Ascigerous part* lanceolate or broadly clavate, 1/3–2/3 of the total ascomata length, black, compressed in cross section, clearly delimited from the stipe, smooth both in fresh and dry conditions. *Stipe* cylindrical, oval in cross section, 9–15 × 1.5–2.5 mm, robust, with black squamules, slightly thickened upward. *Asci* cylindrical to clavate, (123–)135–145(–166) × 14–17 µm (all measurements of microscopic characters refer to material examined in 3 % KOH), Q = 7.8–9.7, unitunicate, inoperculate, 8-spored, with euamyloid ascoapical apparatus and inamyloid wall in MLZ and IKI. *Ascospores* elongated clavate to ellipsoid baculiform, usually slightly curved, (39–)45–57(–60) × 5–6(–6.5) µm, Q = 7–10(–12), first hyaline, finally becoming brown in water, blackish in 5 % KOH, 1–4(–7)-septate when mature, most often with three septa, smooth. *Ascoconidia* not observed. *Paraphyses* numerous, longer than asci, straight, sparsely or moderately septate, 2–3 µm wide, hyaline, agglutinated by light brown amorphous matter in apical part. *Apical cells of paraphyses* variable, cylindrical, clavate to capitate, curved, contorted, sometimes bifurcate, or proliferating, mostly 22–47 × 2–3 µm, some cells inflated up to 10 µm. *Stipe surface* squamulose. Hyphae of the squamules straight, moderately septate, formed by chains of several (4–7) pale brown cells, apical cells clavate.

Habit, Habitat & Distribution — Solitary, on soil among grass. The species is known only from the type locality.

Typus. Czech Republic, Hrubšice village, Nad řekami Nature Reserve, N49°05'35" E16°17'33", elev. 257 m, on soil in dry steppe lawns on serpentine slopes, 16 Nov. 2019, *J. Hrabáková*, (holotype SAV F-11578, ITS and LSU sequences GenBank MT940893 and MT940893, MycoBank MB837371).

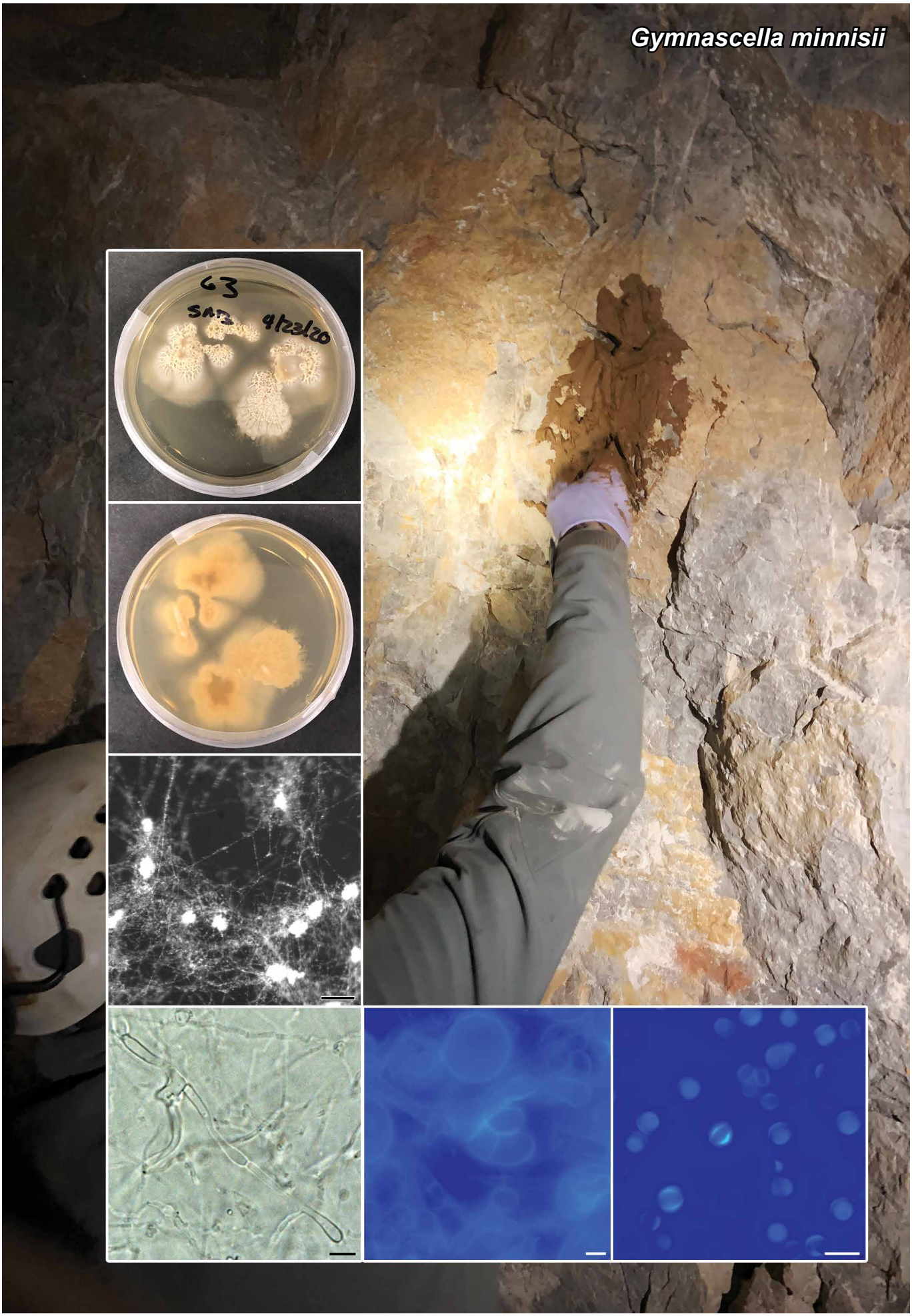
Colour illustrations. Steppe lawns on serpentine slopes near Hrubšice village in the Czech Republic. Macro- and microscopic structures of holotype: ascomata; ascospores (in KOH); amyloid reaction of the ascoapical apparatus (in IKI); paraphyses (in 3 % KOH); stipe surface (in 3 % KOH). Scale bars = 1 cm (ascomata), 10 µm (microscopic structures).

Notes — The combination of characters involving short ascospores (45–55 × 5–6 µm) with predominantly three septa (occasionally 0–7) and stipe with scales, and long (22–45 × 2–3.5 µm) slightly curved last cell of paraphyses is unique for this *Geoglossum* species. Macromorphologically similar *G. fallax* differs in longer (65–105 × 5–7 µm) and more septate (7–12) spores (Durand 1908). The steppe habitat on calcareous soil could host also *G. cookeanum* which is different in chain-forming apical cells of paraphyses, almost smooth stipe and 7-septate ascospores (Minter & Cannon 2015). Very close in having a squamulose stipe, spores (50–60 × 4–6 µm) with 1–3 (5–7 when mature) septa is *G. vleugelianum,* but the difference is in the coloured and stout, upwardly clavulate paraphyses with pyriform or globose apical cells and easily removed tufts of hyphae on the stipe; *G. elongatum* has likewise elongate paraphyses and relatively short spores (50–60 × 5–7 µm) with 0–7 septa (Nannfeldt 1942), but has setose hairs on the stipe and therefore was relocated to *Hemileucoglossum* (Arauzo & Iglesias 2014). It was impossible to verify the type specimen of *G. elongatum* due to undergoing renovation of the fungarium building (S), but the presence of setose hairs on the stipe is the basic character of the genus *Hemileucoglossum*. Possibly similar could also be *G. fumosum* with a densely squamulose stipe, short spores (30–40 × 4.5–5.5 µm) and asci (100–125 × 12–17 µm), but the ascigerous part characteristically looks like it is impregnated by brown smoke (Hakelier 1967).



The Bayesian majority-rule consensus tree was inferred from the concatenated dataset of ITS-LSU sequences. The dataset included *G. jirinae* (H: holotype), relevant *Geoglossum* species, and *Leucoglossum leucosporum* as an outgroup (TreeBASE study S26857). Bayesian inference was run in MrBayes v. 3.2.7a, using four independent chains, 10 M generations, and a sampling frequency of 1 000 (Ronquist et al. 2012). The best-fit partitioning schemes and models were estimated for the concatenated tree, using the greedy search mode as implemented in the PartitionFinder v. 2.1.1 (Lanfear et al. 2016). The maximum likelihood analysis was computed in RAxML v. 8.2.12 (Stamatakis 2014). Analyses were computed in the CIPRES Science Gateway v. 3.3 (Miller et al. 2010). Numbers above branches indicate Bayesian posterior probabilities ≥ 0.95 and the maximum likelihood bootstrap support values ≥ 85 %. The scale bar represents the number of nucleotide changes per site.

Viktor Kučera, Plant Science and Biodiversity Centre, Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 9, 845 23, Bratislava, Slovakia; e-mail: viktor.kucera@savba.sk
Marek Slovák, Plant Science and Biodiversity Centre, Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 9, 845 23, Bratislava, Slovakia, and Department of Botany, Charles University, Benátská 2, 128 01 Praha, Czech Republic; e-mail: marek.slovak@savba.sk
Hana Ševčíková, Department of Botany, Moravian Museum, Zelný trh 6, 659 37, Brno, Czech Republic; e-mail: hanyzka@mail.muni.cz


Gymnascella minnisii
63
SAT3
4/22/20

Fungal Planet 1155 – 19 December 2020

Gymnascella minnisii Adam, Rea-Ireland, Smyth & Overton, *sp. nov.*

Etymology. Named after Andrew Minnis who first mentioned the specimen as 24MN30 (GenBank JX270629) in a survey of Eastern United States bat hibernacula in 2013 after the initial outbreak of White-nose syndrome of bats.

Classification — *Gymnoascaceae*, *Onygenales*, *Eurotiomycetes.*

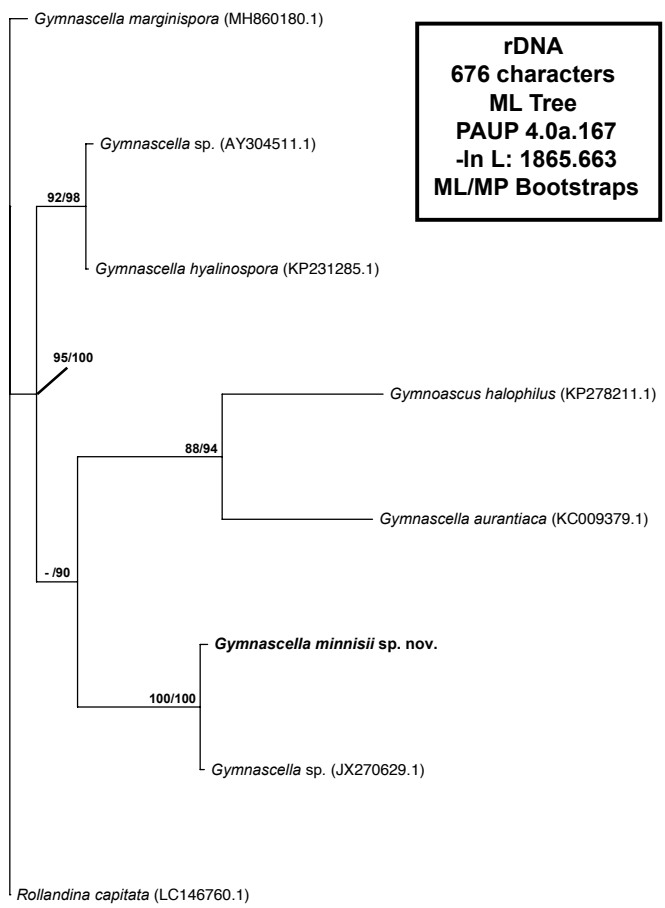
On oatmeal salt sediment agar: *Ascomata* gymnothecial-like, more hyphal than peridial, solitary, globose, measuring 28–118.5 (av. = 56.80, n = 40) µm diam; yellow grey (3B6; Kornerup & Wanscher 1978); developing slowly and ripening within 90 d at 25 °C (12 h white fluorescent light / 12 h dark). *Ascomatal* initials clavate with thin curled hyphae; peridial hyphae light orange to gold yellow (5A4–5B7), smooth and septate with distinct appendages measuring 3.8–31 (av. = 14.86, n = 11) × 1.7–4. (av. = 1.93, n = 11) µm. *Asci* globose to ovoid, 8-spored, 6.8–10 (av. = 8.5, n = 11) µm diam. *Ascospores* globose to hat- or saturn-shaped, measuring 2.6–4 (av. = 3.34, n = 19) × 2.8–3.5 (av. = 3.13, n = 13) µm.

Culture characteristics — On Sabouraud dextrose agar (SAB) acidified with 120 µL 85 % lactic acid for optimal pigment production, (12 h white fluorescent light / 12 h dark at 25 °C): Colony yeast-like, at first yellow-grey (3A3–3B6), in age darkening slightly after 90 d. On synthetic nutrient-poor agar (SNA), colony filamentous, at first white to pale yellow-white on SNA (2A1–2A2).

Typus. USA, Pennsylvania, Blair County, Canoe Creek State Park, Canoe Creek Hartman Mine, from bat guano, 15 Mar. 2012, *B. Overton* LHU G3 (dried, non-metabolically active holotype CUP-70725, in Cornell University Plant Pathology Fungarium, metabolically active culture CBS 147160, ITS sequence GenBank MT988379, MycoBank MB836835).

Colour illustrations. Background photo of Canoe Creek Hartman Mine. Colony front colour on SAB at 90 d; colony back colour on SAB at 90 d; dissecting scope image of ascomata on SNA; DIC racket hyphae; fluorescence image of claw-like initials in calcofluor white; ascospores displaying hat- or saturn-shape in calcofluor white. Scale bar = 100 µm (ascomata), 2 µm (ascomatal initial), 5 µm (all others)

Notes — *Gymnascella minnisii* can be differentiated from other species of *Gymnascella* due to the absence of conidial development. The ascomata of *G. minnisii* are more hyphal and less developed than the peridial ascomata described in *Pseudogymnoascus* species. Additionally, the hat- or saturn-shaped ascospores place this species in the *Onygenales*. Genetic analysis of the ITS gene of *G. minnisii* suggests that the new species described here is identical to the ITS gene sequence of isolate 24MN30 (Lorch et al. 2013) deposited in GenBank (accession number JX270629). Isolate 24MN30 has remained an undescribed species since the publication of their work. This work is the first to unite 24MN30 and LHU G3 under one name through morphological and molecular data. This species forms racket hyphae similar to that observed by Peck (1985).



Phylogenetic placement of *Gymnascella minnisii* compared to close relatives on a maximum likelihood tree with maximum likelihood/maximum parsimony bootstrap support values. *Gymnascella minnisii* is highlighted in **bold**. This analysis was based on a single gene alignment, utilising nrDNA sequences (ITS1, ITS4 primers; White et al. 1990) only. PAUP v. 4.0a build 167 (Swofford 2003) was utilised to conduct the 1 000 bootstrap maximum parsimony analysis and maximum likelihood analysis. The maximum likelihood analysis utilised the General Time Reversible (GTR) nucleotide model with rate matrix set to estimate, and variable sites set to gamma distribution. Bootstrap support values greater than 70 % are shown on nodes in the following order: maximum likelihood/maximum parsimony. The alignment was deposited in TreeBASE (submission S26902).

Jacob D. Adam, Alden J. Mileto & Barrie E. Overton, 205 East Campus Science Center, Lock Haven University, Lock Haven, PA 17745 USA; e-mail: jacob.d.adam.42@gmail.com, ajm1653@lockhaven.edu & boverton@lockhaven.edu
Abigail E. Rea-Ireland, University of Tennessee, Knoxville. Knoxville, TN, 37996 USA; e-mail: abbyliz52@gmail.com
Christopher W. Smyth, Binghamton University, Binghamton, NY, 13902 USA; e-mail: chris.smyth.psu@gmail.com


Pseudogymnoascus palmeri

Fungal Planet 1156 – 19 December 2020

Pseudogymnoascus palmeri Rea-Ireland, Smyth, Lindner & Overton, *sp. nov.*

Etymology. Named after Jonathan M. Palmer, formerly of the United States Forest Service, for his many contributions to the study of *Pseudogymnoascus* and his contributions to establishing mating-type genes for the genus.

Classification — *Pseudeurotiaceae*, *Thelebolales*, *Leotiomycetes*.

On Rose Bengal Agar (RBA): *Ascomata* gymnothecial, solitary, globose, measuring 85.3–172.5 (av. = 125.3, n = 10) × 60–161.8 (av. = 112.9, n = 10) µm in size; grey orange (5B3-6; Kornerup & Wanscher 1978); developing rapidly and ripening within 10 d at 25 °C (12 h white fluorescent light / 12 h dark). *Ascomatal* initials coiled to irregular; peridium is a gymnothecium composed of *textura intricata*, the peridial hyphae darkly pigmented brownish yellow (5C7), smooth to minutely roughened with distinct appendages. *Asci* ovoid, 8-spored, 6.7–9.5 (av. = 7.6, n = 35) × 4.9–7.3 (av. = 5.9, n = 35) µm. *Ascospores* aseptate, fusoid to ellipsoid, smooth, grey orange (5B36-6); 2.9–4.1 (av. = 3.4, n = 80) × 1.8–3 (av. = 2.3, n = 80) µm.

Culture characteristics — (12 h white fluorescent light / 12 h dark at 25 °C): Colony colour analysed on Sabouraud dextrose agar (SAB) acidified with 120 µL 85 % lactic acid for optimal pigment production rather than RBA because the pink colour of the agar compromises interpretation of fungal pigmentation. Colony reverse at first yellow white (4A2), maturing to grey orange (5B3-6) with age after 10 d. On oatmeal salt sediment agar, colony reverse colour is diffuse light orange to orange (6A5-7).

Typus. USA, Pennsylvania, Centre County, Woodward Cave, from sediment, 2019, *B. Overton* LHU 407 (dried, non-metabolically active holotype CUP-70724, in Cornell University Plant Pathology Fungarium, metabolically active culture CBS 147159 in the CBS Collection of the Westerdijk Fungal Biodiversity Institute ITS, *rpb2*, and *tef1* sequences GenBank MT988150, MW054468, MW054467; MycoBank MB837413).

Notes — *Pseudogymnoascus palmeri* produces sexual structures on SNA and RBA in the presence of a bacterium co-isolated from the original sediment sample. A BLAST search of the bacterial co-isolate's 16S rDNA provided a 100 % match with *Pseudomonas moorei.* Culture became sterile after removal of the co-isolated bacterium using SAB acidified with 120 µL 85 % lactic acid. Sterility was maintained, even when the fungal isolate was re-plated onto RBA or SNA. Morphological analyses suggest that *P. palmeri* and *P. roseus* could be sister taxa. They are similar in the morphological characteristics of gymnothecial ascomata production and ascospore size. Samson (1972) described *P. roseus* as being characterised by pinkish to reddish ascomata, roughened appendages with spines or warts, and the presence of aleurioconidia. *Pseudogymnoascus palmeri* can be distinguished from *P. roseus* based on conidiogenesis (*P. palmeri* does not produce conidia) and colour (*P. palmeri* ascomata are grey orange). Samson (1972) did not describe the reverse colour of colony plates, but as a morphological character in *Pseudogymnoascus*, this should not be ignored (Crous et al. 2019c). Minnis & Lindner (2013) were the first to examine many *Pseudogymnoascus* taxa using modern phylogenetic methods. This work builds off their multi-gene approach, utilising three of the five phylogenetically informative loci useful for phylogenetic species resolution within the genus *Pseudogymnoascus* (Minnis & Linder 2013).

Colour illustrations. Background photo of Woodward Cave, Pennsylvania, USA. Confocal laser-scanning image of gymnothecium; DIC image of ascospores on synthetic nutrient-poor agar (SNA); colony back colour on SAB at 10 d; ascomatal initials on SNA at 10 d; asci and peridial hyphae on SNA. Scale bars = 20 µm (gymnothecium), 2 µm (ascomatal initial), 5 µm (all others).

The three-locus phylogenetic analysis conducted in this study indicates strong support for the placement of *P. palmeri* (LHU 407) in a clade with isolate WSF 3629 (Minnis & Linder 2013). Phylogenetically, WSF 3629 is closely related to clade G in the *P. roseus* complex (Palmer et al. 2014). This isolate is also of significant interest due to its phylogenetic proximity to the white-nose syndrome pathogen, *P. destructans*.

The relationship of this complex to *P. destructans* has not been fully resolved, even with a five-gene analysis (Minnis & Linder 2013). WSF 3629 was suggested as a new species by Palmer et al. (2014) but has remained an undescribed species since the publication of their work. This study honours the work of Palmer, and formally describes the new species as *Pseudogymnoascus palmeri* sp. nov. and identifies a new strain of this species (LHU 407) from Pennsylvania.

In addition to morphology, phylogenetic analysis of a three-gene multi-locus alignment (ITS nrDNA, *rpb2* and *tef1*) support the description of isolates LHU 407 and WSF 3629 as the phylogenetic species *P. palmeri*, distinct from clade G in the *P. roseus* complex. This study generated the three-locus dataset for isolate LHU 407. The challenge in resolving the clade G in the *P. roseus* complex, as well as its association with *P. destructans*, highlights the need for greater biodiversity sampling of the genus *Pseudogymnoascus*. The multi-gene data for isolate WSF 3629, and the remainder of the *Pseudogymnoascus* species, were derived from Minnis & Linder (2013), as well as previous species descriptions for *P. lindneri* and *P. turneri* (Crous et al. 2019c). The outgroup taxon was *Gymnascella minnisii*, GenBank *rpb2* and *tef1* sequences MW054470, MW054469, also described in this issue of Fungal Planet.

Supplementary material

FP1156 Phylogenetic placement of *Pseudogymnoascus palmeri* sp. nov. on a strict consensus maximum parsimony tree with maximum likelihood/maximum parsimony bootstrap support values (based on 1 000 bootstrap pseudo-replicates), was determined from analysis of a multi-gene alignment of rDNA (primers ITS1, ITS4; White et al. 1990), *rpb2* (primers RPB2-7cF, RPB2-11aR; Liu et al. 1999), and *tef1* (primers EF1-983F, EF1-2218R; Rehner & Buckley 2005). PAUP v. 4.0a build 167 (Swofford 2003) was used to conduct the maximum parsimony analysis. The parsimony analysis generated a single most parsimonious tree which was also the strict consensus. A maximum likelihood analysis was completed using GARLI v. 2.01 (Zwickl 2006) on the CiPRES Science Gateway (Miller et al. 2010). A consensus tree was generated from a single replicate ML analysis with 1 000 bootstrap pseudo-replications. There were no significant topological differences between the parsimony and likelihood consensus trees. For maximum likelihood, the General Time Reversible (GTR) evolutionary model was utilised, the proportion of invariant sites was set to estimate, and the model of rate heterogeneity was set to gamma distribution. Bootstrap support values located at nodes are: Maximum Likelihood/Maximum Parsimony. Alignment and tree(s) are deposited in TreeBASE (study 27014).

Abigail E. Rea-Ireland, University of Tennessee, Knoxville, TN, 37996 USA; e-mail: abbyliz52@gmail.com
Christopher W. Smyth, Binghamton University, Binghamton, NY, 13902 USA; e-mail: chris.smyth.psu@gmail.com
Daniel L. Lindner, One Gifford Pinchot Drive Madison, WI, 53726 USA; e-mail: daniel.l.lindner@usda.gov
Brent J. Sewall, Department of Biology, Temple University, 1900 N. 12th Street, Philadelphia, PA, 19122 USA; e-mail: bjsewall@temple.edu
Barrie E. Overton, 205 East Campus Science Center, Lock Haven University, Lock Haven, PA, 17745 USA; e-mail: boverton@lockhaven.edu


Hypoxylon hepaticolor

Fungal Planet 1157 – 19 December 2020

Hypoxylon hepaticolor J. Fourn. & A.N. Mill., *sp. nov.*

Etymology. From Latin *hepar, hepatis* = liver and *color* = colour, for the reddish brown stromatal surface colour reminiscent of that of liver.

Classification — *Hypoxylaceae*, *Xylariales*, *Sordariomycetes*.

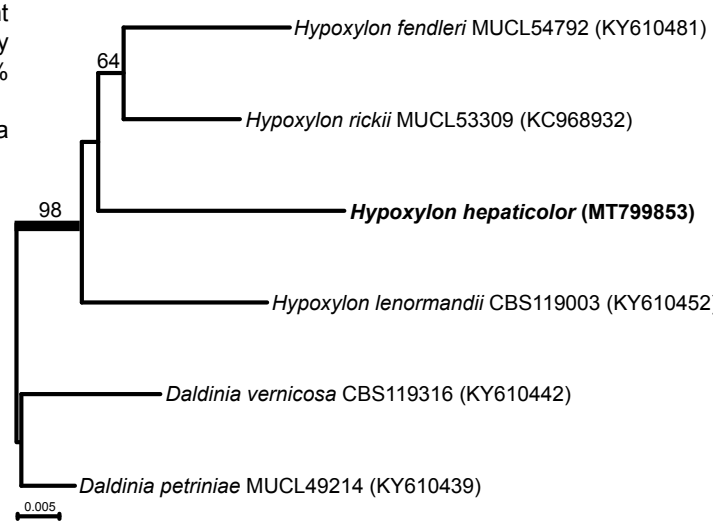
Stromata pulvinate to effused-pulvinate, 2–10 mm long × 2–6 mm wide × 1–1.6 mm thick, coalescent into compound stromata up to 35 mm long × 13 mm wide with irregularly lobate contours, with unexposed to slightly exposed perithecial contours and abrupt margins; outermost coating dark brick (60) (Rayner 1970) with a faint vinaceous (57) tone, pruinose, wearing off on elevations and revealing a shiny blackish crust composed of waxy granules appearing light brown when bruised, honey (64) to cinnamon (62) when observed in water under the microscope, releasing sienna (8) KOH-extractable pigments within 1 min with a fugacious amber (47) halo, fading to light sienna with a marked vinaceous tone at 15 min, eventually pale greyish sepia (106) upon prolonged incubation; subperithecial tissue blackish, 0.3–0.8 mm thick, woody, with shiny black, carbonaceous, obliquely oriented strands. *Perithecia* lanceolate, 0.75–0.95 mm high × 0.2–0.25 mm diam. *Ostioles* umbilicate, most often inconspicuous. *Paraphyses* hyphal, thin-walled, remotely septate, 4–6 µm wide at base, tapering to 1.5–2 µm wide above asci, discretely embedded in mucilaginous material. *Asci* cylindrical, long-stipitate, originating from long ascogenous hyphae in unilateral spicate arrangement, with eight overlapping, uniseriately arranged ascospores, the spore-bearing parts 60–69 × 6–7.5 µm, the stipes fragile, 90–150 µm long, with a discoid apical apparatus, apically convex with a sharp rim, 0.7–0.9 × 2.1–2.5 µm (av. 0.8 × 2.4 µm, n = 20), bluing in Melzer's reagent. *Ascospores* (8.8–)9.4–11.4(–11.8) × (4.5–)4.9–5.9(–6.3) µm, n = 120 (av. 10.4 × 5.4 µm), ellipsoid almost equilateral, with narrowly to less commonly broadly rounded ends, the lowermost ascospore in the ascus elongated with somewhat rhomboid ends, dark brown, with a wide straight germ slit c. 2/3 spore length with blurred contours, longitudinally to slightly obliquely oriented; perispore not dehiscent in 10 % KOH; epispore smooth

Habitat & Distribution — On dead corticated branches in a tropical forest. Known only from Saül, French Guiana.

Typus. French Guiana, Maripasoula, Saül, shortcut toward the airfield, disturbed secondary rainforest, on a dead corticated branch 1.5–2 cm diam, N3.622159 W53.204166, c. 190 m, 20 June 2019, *J. Fournier*, GYJF 19127 (holotype LIP, isotypes HAST, ILLS00121426, ITS and LSU sequences GenBank MT799854 and MT799853, MycoBank MB837614).

Additional materials examined. French Guiana, Maripasoula, Saül, shortcut toward the airfield, disturbed secondary rainforest, on bark, N3.623524, W53.206542, c. 200 m, 17 June 2019, *J. Fournier*, GYJF 19011 (LIP); trail head toward Roche Bateau, disturbed secondary rainforest, on bark, N3.620498, W53.199309, 22 June 2019, *J. Fournier*, GYJF 19209 (LIP) (immature).

Notes — *Hypoxylon hepaticolor* can be distinguished by its carbonaceous, effused-pulvinate stromata up to 1.6 mm thick with reddish brown surface and concolorous KOH-extractable pigments, lanceolate perithecia and ellipsoid-equilateral ascospores 10.4 × 5.4 µm on average, with a germ slit less than spore length and a perispore indehiscent in 10 % KOH. This combination of characters does not match any known *Hypoxylon* species. Carbonaceous stromata with lanceolate perithecia suggest possible affinities with the species recently reinstated in *Pyrenopolyporus*, accommodating taxa formerly placed in *Hypoxylon* characterised by peltate to discoid massive stromata over 2.5 mm thick and frequently irregularly shaped ascospores with a perispore indehiscent in 10 % KOH (Wendt et al. 2018). The stromata of the new species are not discoid or peltate and do not reach the thickness encountered in *Pyrenopolyporus*. Furthermore, affinities with this genus are not supported by our molecular results, which suggest affinities with *Hypoxylon*. Its three closest relatives in the LSU-based phylogenetic tree are notably different in having waxy-woody stromata with orange KOH-extractable pigments and ascospores with a spore-length germ slit and a perispore dehiscent in KOH.



Maximum likelihood tree of LSU sequences generated using RAxML HPC2 (Stamatakis 2014) on the CIPRES v. 3.3 portal (Miller et al. 2010). *Hypoxylon hepaticolor* is in **bold**. RAxML bootstrap support values above 70 % are shown above the nodes and Bayesian posterior probability scores above 0.95 are shown as thickened branches. GenBank accession numbers for LSU sequences are given after taxon names.

Colour illustrations. French Guiana, Maripasoula, Saül, forest trail where the holotype was collected. Habit of coalescent stromata; stroma in vertical section; stromatal waxy granules observed in water; pigments released in 10 % KOH; long-stipitate ascus; ascospores; apical apparatus in Melzer's reagent; germ slits on ascospores. Scale bars = 5 mm (stromata), 0.5 mm (section), 10 µm (granules, ascospores), 50 µm (ascus), 5 µm (apical apparatus, germ slits). Photos: Gilles Corriol (background) and Jacques Fournier.

Andrew N. Miller, University of Illinois Urbana-Champaign, Illinois Natural History Survey, 1816 South Oak Street, Champaign, Illinois, 61820, USA; e-mail: amiller7@illinois.edu
Jacques Fournier, Las Muros, 09420 Rimont, France; e-mail: jfournzeroneuf@gmail.com


Inocybe ionolepis

Fungal Planet 1158 – 19 December 2020

Inocybe ionolepis Cullington & E. Larss., *sp. nov.*

Etymology. Refers to the purple scales on the pileus.

Classification — *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 15–35 mm diam, campanulate to obtusely conical with an obtuse to broad umbo, slightly incurved margin, expanding with age, surface silky fibrillose with large flat depressed scales as young, dark purple and brown around the umbo and purple-lilac towards the margin, contrasting to the pale whitish subpellis trama. Fading with age to become pale greyish lilac at margin. *Cortina* pale greyish white with a violet tinge. *Lamellae* moderately crowded, interspersed with lamellulae, sinuate to emarginate, first pale grey with a lilac tint, later greyish brown. *Stipe* 35–45 × 3–5 mm, equal, equal to slightly bulbous, pale with greyish lilac tint, yellowish tint at the base, pruinose at apex to 1/3 of the stipe, in lower part fibrillose, covered with thin walled hyaline hyphae 5–12 µm wide. *Smell* slightly spermatic. *Basidia* clavate, 4-spored, (21.2–)28.8(–33) × (7–)8.6(–10.3) µm. *Spores* smooth ellipsoid to subamygdaliform with obtuse apex and distinct apiculus (8.6–)9.5(–11.2) × (4.6–)5.1(–6.1) µm, Q = (1.82–)1.84(–1.96) (n = 85). *Pleurocystidia* (48–)54(–71) × (11–)14(–16) µm (n = 50), lageniform to subutriform, with pedicel, usually abundant with crystals at apex, walls 2–3.5 µm thick, mostly pale colourless. *Cheilocystidia* similar to pleurocystidia but shorter, (32–)40(–46) × (13–)16(–18) µm (n = 20), lageniform to broadly utriform, walls 2.5–4.5 µm thick. *Paracystidia* hyaline, pyriform to clavate (14–)17(–22) × (8–)9(–10) µm (n = 10). *Caulocystidia* at apex similar to pleurocystidia, abundant, with crystals, less so further down (40–)50(–70) × (14–)16(–18) µm (n = 10), fusiform to more cylindrical, caulocystidioid hairs thin-walled, sometimes septate, 40–100 × 9–12 µm, cauloparacystidia few. *Pileipellis* a compact interwoven cutis of cylindrical hyphae, thin-walled, smooth, hyaline (5–)6–10(–13) µm wide. *Clamp connections* present in all tissue.

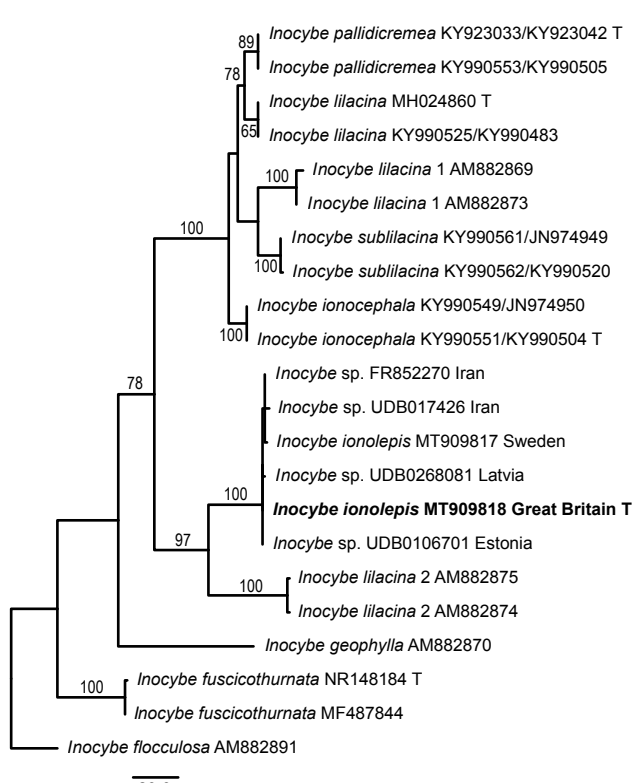
Ecology & Distribution — Associated with deciduous trees, *Fagus sylvatica* and *Quercus robur*. Basidiomata so far only known from England and Sweden, however ITS sequence data generated from soil samples show a wider distribution with occurrence in Iran, Estonia and Latvia.

Typus. Great Britain, England, Gloucestershire, Forest of Dean, near Acorn Patch, 21 Sept. 2017, *P. Cullington*, in deciduous forest on stony soil under *Fagus sylvatica* (holotype K(M)236689, isotype GB, ITS-LSU sequence GenBank MT909818, and MycoBank MB836902).

Additional material examined. Sweden, Gotland, Linde, Linde Prästänge, Forest meadow on calcareous ground, under *Quercus robur*, close to *Corylus avellana* and *Betula pendula*, 25 Oct. 2019, *E. Larsson* 279-19, GB-0207596, ITS-LSU sequence GenBank MT909817.

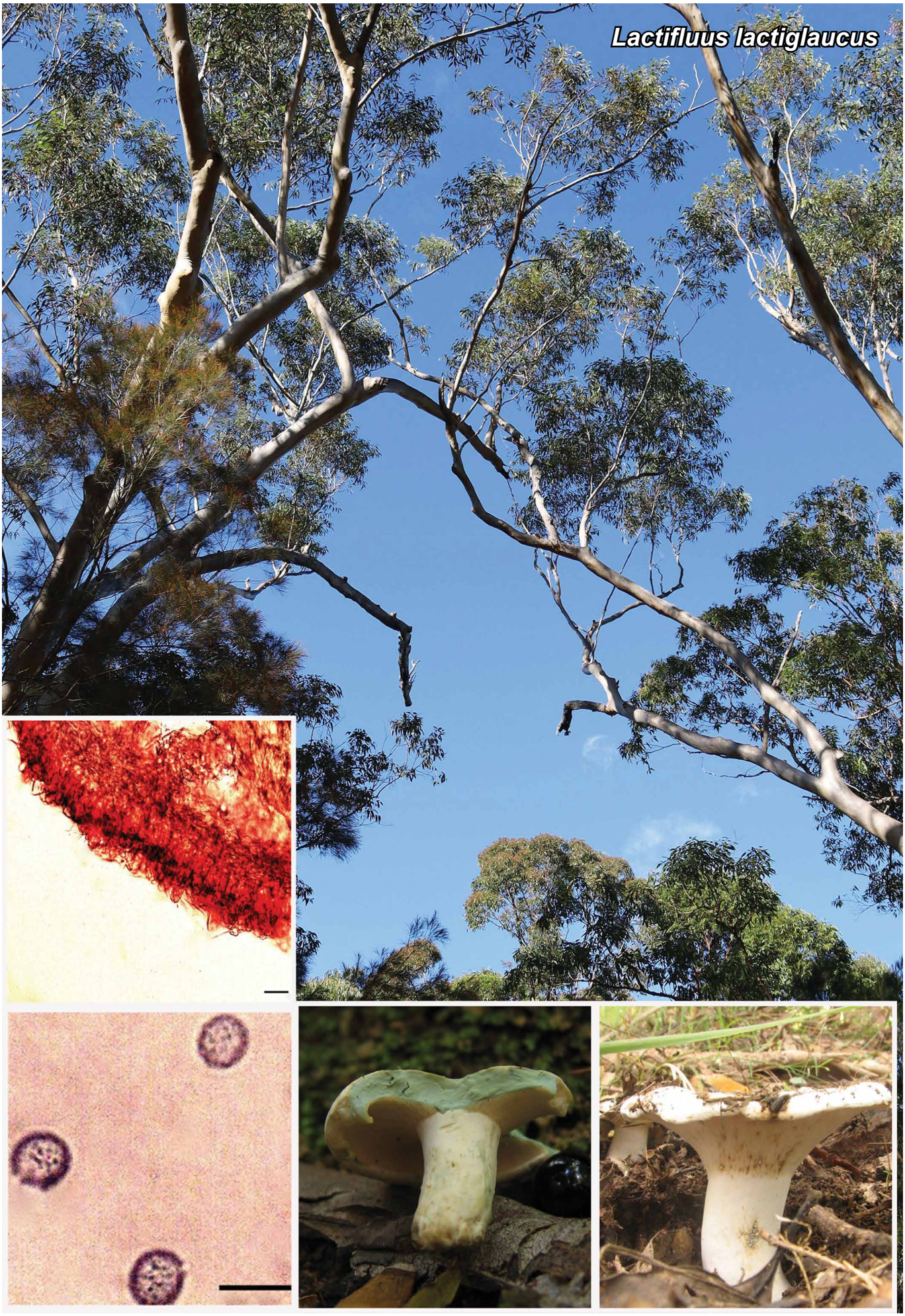
Colour illustrations. *Inocybe ionolepis* habitat, forest meadow Linde prästänge, Gotland, Sweden. In situ basidiomata (GB-0207596); detail of pileus scales, cheilocystidia and basidiospores (holotype K(M)236689). Scale bars = 10 µm for spores, 20 µm cheilocystidia.

Notes — *Inocybe ionolepis* belongs in the *I. geophylla* group and the purple-lilac species surrounding *I. lilacina* (Matheny & Swenie 2018). The group is identified to host a high phylogenetic diversity and the name *I. lilacina* has been applied to many taxa in Europe (Ryberg et al. 2008). The group is still in need of further investigations with solid documentation of macromorphology and ecology. *Inocybe ionolepis* is characterised by having a pileus with a brown umbo and purple-lilac scales, and a pale yellowish tint at the stipe base. In dry condition the scales are distinctive, see the cap detail bottom right photo, but the scales colour fade and is affected after rain, and maybe also by late season fruiting. The young lamellae have a distinct lilac tone, that with age are becoming greyish brown with a pale lilac tint. Blast search of NCBIs GenBank nucleotide database and the UNITE database identified five additional ITS sequences of *I. ionolepis* generated from soil samples, suggesting the species to have a broad distribution range in Europe and Iran. In the phylogenetic analysis it comes out in a sister clade to *I. lilacina* 2 from Europe (Matheny & Swenie 2018). The two sequenced collections in the *I. lilacina* 2 clade originates from deciduous forests like *I. ionolepis*, while the two sequenced collections in *I. lilacina* 1 that comes out in a sister clade to *I. sublilacina* originates from coniferous forests. This suggests that there is an ecological differentiation within the group.



Phylogram based on ITS and LSU sequence data showing the position of *I. iololepis* in the *I. lilacina* group. Bootstrap support values are indicated on branches and the sequence of the holotype is marked in **bold**. Multiple sequence alignments were carried out with MAFFT (https://mafft.cbrc.jp/alignment/server/). The alignment was checked and adjusted manually, heuristic searches and bootstrap parsimony analyses were performed using PAUP v. 4.0b10 (Swofford 2003).

Ellen Larsson, Biological and Environmental Sciences, University of Gothenburg, and Gothenburg Global Biodiversity Centre, Box 461, SE40530 Göteborg, Sweden; e-mail: ellen.larsson@bioenv.gu.se
Penny Cullington, The Beeches, Pleck Lane, Kingston Blount, Oxfordshire, UK, OX39 4RU; e-mail: pennyculli@btinternet.com
Kare Liimatainen, Jodrell Laboratory, Royal Botanic Gardens, Kew, Surrey TW9 3AB, UK; e-mail: K.Liimatainen@kew.org


Lactifluus lactiglaucus

Fungal Planet 1159 – 19 December 2020

Lactifluus lactiglaucus P. Leonard & Dearnaley, *sp. nov.*

Etymology. *lactiglaucus* means green milk and refers to the colour of the latex.

Classification — *Russulaceae*, *Agaricales*, *Agaricomycetes.*

Pileus centrally depressed to infundibuliform, 60–100 mm diam; surface dry, slightly velutinate, sometimes rugulose, usually with dirt adhering, azonate, white with some buff colouration at centre; margins in-rolled at first. *Lamellae* subdecurrent, crowded, anastomosing, off-white, very narrow (< 2 mm), turning slowly greenish on bruising and finally dirty brownish after some hours, lamellulae absent. *Stipe* cylindrical, 40–60 × 12–18 mm, glabrous, stout, very solid, white, green blotched if injured. *Flesh* white, thick, exuding a thick latex. *Latex* white, quickly turning greyish green to pistachio green (29D4-5; Kornerup & Wanscher 1978), turning orange or yellow with KOH. *Smell* of honey or baked bananas. *Spore print* white. *Spores* subglobose, a few broadly ellipsoid, 6.8–8.4 × 5.5–7.4 µm, av. 7.3 ± 0.4 × 6.4 ± 0.5 µm, Q = 1.04–1.3, Qav = 1.15 ± 0.06; ornamentation of low, slowly amyloid warts with fine lines joined to them like flagella, forming a partial reticulum; plage inamyloid, 2 µm (some spores remaining inamyloid at least in dried material). *Basidia* narrowly clavate, 45–50 × 6–8 µm, sterigmata 2–3 µm long, 2- and 4-spored basidia present. *Pleurocystidia* numerous, thin-walled, narrowly clavate, 50–60 × 8–10 µm, extending 10–15 µm beyond basidia. *Cheilocystidia* numerous, similar to pleurocystidia, forming an almost sterile layer along the gill edge. *Pileipellis* an unusual type of ixocutis, resembling the hyphoepithelium illustrated (G on page 21) by Hielmann-Clausen et al. (1998), hyphae in suprapellis only 3–4 µm wide. No lactifers seen in suprapellis.

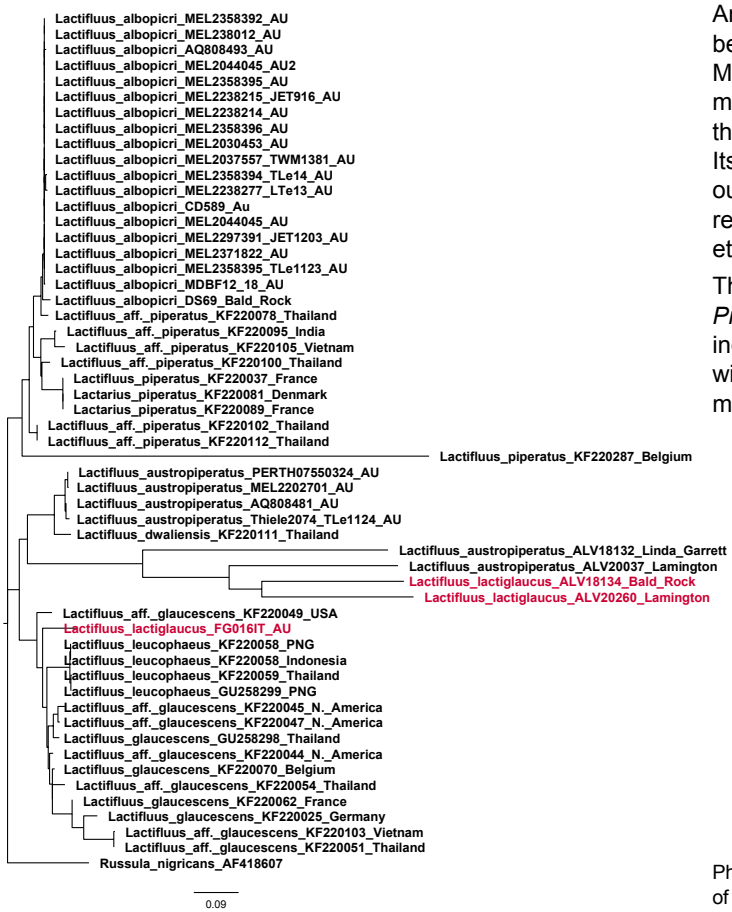
Habitat & Distribution — Gregarious in wet sclerophyll forest amongst leaf litter under *Eucalyptus* spp. So far only known from three sites in south east Queensland.

Typus. Australia, Queensland, Lamington National Park, 30 Mar. 2019, *P. Leonard*, (holotype PL640319 in BRI, ITS sequence GenBank MW007669, MycoBank MB837537).

Additional materials examined. Australia, Queensland, Bellthorpe, 21 Jan. 1985, *T. Young*, AQ646335 (BRI); New South Wales, Bald Rock National Park, 10 Apr. 2015, *P. Leonard*, PL630415 (BRI).

Notes — This robust white fungus with hot peppery milk that turns pistachio green should be readily recognised in the field, yet it is only known from three collections. The earliest collection was identified as *L. pergamenus,* a synonym for the European species *L. glaucescens*. The European species is found in deciduous forests on calcareous soils and is said to be rather rare despite being reported from Northern Europe, North America and Japan. The Queensland collections are distinct, being found with *Eucalyptus* s.lat. in wet sclerophyll forests. Morphologically they are distinguished by more abundant milk that is almost immediately green and microscopically by the spores that are more globose than the European species. Its separation from the European collections is supported by our molecular analysis that places it in the same clade as the recently published *L. austropiperatus* and *L. albopicrus* (Crous et al. 2020a).

There appear to be at least four *Lactifluus* species in section *Piperates* in Australia. They all have predominantly white fruiting bodies, crowded gills, hot to acrid tasting latex, and spores with low (< 0.5 µm) ornamentation. *Lactifluus lactiglaucus* is the most readily recognised on account of its green latex.



Phylogenetic tree: Maximum likelihood tree of the ITS-nrDNA for a selection of *Lactifluus* species, aligned using MUSCLE and constructed using MEGA X.

Colour illustrations. Wet sclerophyll forest in south-east Queensland. Lower right sporocarp (holotype); lower centre right abundant green latex; lower centre left subglobose spores with low ornamentation; lower left pileipellis. Scale bars = 10 µm. All photos © Patrick Leonard.

Patrick Leonard, P.O. Box 1193, Buderim 4556 Queensland, Australia; e-mail: patbrenda.leonard@bigpond.com
John D.W. Dearnaley, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: John.dearnaley@usq.edu.au


Lophotrichus medusoides

Fungal Planet 1160 – 19 December 2020

Lophotrichus medusoides Calvert, McTaggart & R.G. Shivas, *sp. nov.*

Etymology. Named for the resemblance of ascomata to Medusa of Greek mythology, a Gorgon described as a winged woman with living venomous snakes for hair.

Classification — *Microascaceae*, *Microascales*, *Sordariomycetes.*

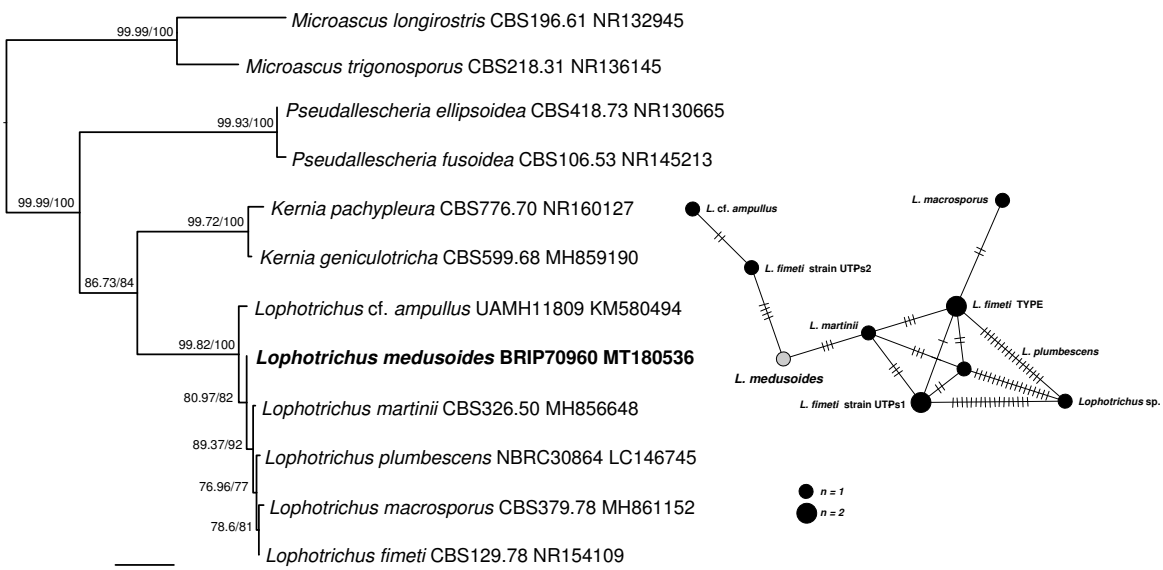
Mycelium on potato-dextrose agar (PDA) smooth, branched, sub-hyaline to pale yellow, hyphae 2–4 µm diam. *Ascomata* perithecial, immersed or partly immersed, globose to subglobose, scattered, 250–400 µm diam, with beaks 120–200 × 30–40 µm, with peridium composed of dark brown *textura angularis*; ascomatal appendages numerous, dark flexuous, up to 1.5 mm long, abundant on the beak, curved and narrowed at the apex. *Asci* evanescent, broadly clavate, 30–36 × 20–24 µm, thin-walled, 8-spored. *Ascospores* ellipsoidal, 7.5–9.5 × 5.5–6.5 µm, apices rounded, yellowish brown, with a germ pore at each end; wall even, 1–1.5 µm wide, smooth, extruded in a mass loosely held by ostiolar appendages.

Culture characteristics — On PDA after 2 wk in the dark at 23 °C colonies 3.5 cm diam, flat, with sparse aerial mycelium, cream white, ascomata concentrated toward margin; with irregular darkened patches after 3 wk; reverse cream white.

Typus. Australia, Queensland, Iron Range, Lockhart River Rd, isolated from stem tissue of *Citrus garrawayi* (*Rutaceae*), 19 July 2019, *J. Calvert* (holotype specimen BRIP 70690, includes the ex-type culture BRIP 70690, ITS and LSU sequences GenBank MT180536 and MT186160, MycoBank MB834991).

Notes — *Lophotrichus medusoides* was isolated as an endophyte from stem tissue of *Citrus garrawayi*, which is an understory tree endemic to tropical rainforests in the Cape York region of northern Queensland. Species of *Lophotrichus* have been described from mammal dung and soil and are morphologically similar to *Microascus, Pseudallescheria* and *Kernia* (Sandoval-Denis et al. 2016). Other taxa in the *Microascales* have been reported in association with *Citrus* as either endophytes, e.g., *Scedosporium*, or pathogens, e.g., *Ceratocystis* (De Beer et al. 2014). A phylogenetic analysis of the ITS region showed *Lophotrichus* was monophyletic and that *L. medusoides* shared a most recent common ancestor with coprophilic taxa. It differs in morphology to *L. fimeti*, which lacks beaks on ascomata, to *L. plumbescens*, which has two types of ascomatal hairs, and to *L. martinii*, which has larger ascospores and shorter, wavy ascomatal hairs (Guarro et al. 2012). It differs from *L. indicus*, which has broad ascospores with obtuse ends and ascomata that have abundant terminal hairs (Saxena & Mukerji 1970).

BLASTn results of the ITS sequence of *L. medusoides* indicated similarity to type sequences of *L. fimeti* (NR_154109; Identities = 480/485 (98.97 %), no gaps), and *Enterocarpus grenotii* (NR_159852; Identities = 502/530 (94.72 %), six gaps (1 %)). The LSU sequence shared 1 056/1 096 (96 %) sequence identities with *Cephalotrichum purpureofuscum* (GenBank MF041789). A network analysis of ITS sequences showed a difference of three parsimony-informative characters between *L. medusoides* and *L. martinii* (GenBank MH856648) and four between *L. medusoides* and *L. fimeti* (GenBank MF161105).



Mid-point rooted phylogram from a maximum likelihood search using IQ-TREE v. 1.3.11.1 (Nguyen et al. 2015) with 10 000 ultra-fast bootstraps (Minh et al. 2013), 10 000 replicates of an approximate likelihood ratio test (aLRT), and a best-fit model of evolution (command -m TEST). ITS sequences aligned with MAFFT in UGENE v. 1.30.0 (Okonechnikov et al. 2012). The aLRT and UFBootstrap values are indicated at nodes. Minimum spanning network of all available *Lophotrichus* ITS sequences generated using POPART v. 1.7 (Leigh & Bryant 2015); hashes indicate number of parsimony informative characters between taxa.

Colour illustrations. Monsoon rainforest in the Iron Range, Cape York Peninsula, Far North Queensland, Australia. Ascomata showing long ascomatal hairs; *textura angularis*; ascospores from ruptured ascomata; 8-spored unitunicate ascus; hyphae. Scale bars = 1 mm (top left), 10 µm (all others).

Jed Calvert, Alistair R. McTaggart, Lília Costa Carvalhais, André Drenth & Roger G. Shivas,
Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Ecosciences Precinct,
Level 2C East, GPO Box 267, Brisbane 4001, Queensland, Australia;
e-mail: J.Calvert@uq.net.au, A.Mctaggart@uq.edu.au, L.Carvalhais@uq.edu.au, A.Drenth@uq.edu.au & R.Shivas@uq.edu.au


Melanoleuca dominicana
5 µm
s
p
b
ca
10 µm
ch

Fungal Planet 1161 – 19 December 2020

Melanoleuca dominicana Angelini, Para & Vizzini, *sp. nov.*

Etymology. The name *dominicana* (Spanish) refers to the occurrence of the species in the Dominican Republic.

Classification — *Incertae sedis* in the *Pluteineae*, *Agaricales*, *Agaricomycetes*.

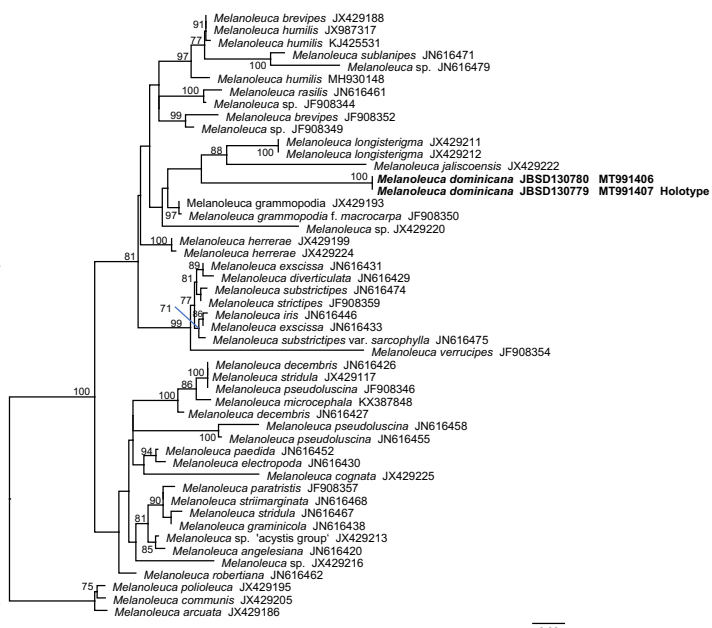
Pileus 4–5 cm diam, applanate, depressed with an umbilicate centre, rarely with a large and low umbo; pileus surface smooth, opaque, always very dark in the centre, brownish, up to blackish brown, otherwise ochre-brown, grey-brownish, also ash-grey. *Lamellae* medium crowded, with numerous lamellulae (l = 1–3) of various lengths emarginated with long decurrent tooth, straight, white. *Stipe* 3.5–4 × 0.5–1 cm, central, cylindrical, enlarged at the apex, clavate at the base, longitudinally fibrillose, from brown to dirty greyish brown, blackening at the base. *Context* white brownish in the pileus, brown in the stipe, brown blackish in the stipe base. *Odour* and *taste* not distinctive. *Spores* 5.8–7.8 × 4.8–6 µm (av. 7 × 5.3 µm, Q = 1.16–1.51, Q_m = 1.32), subglobose, hyaline, warty; warts isolated rarely with thin ridges, with evident suprapicular zone, amyloid. *Basidia* 2–4-spored, 31.5–36 × 7.2–9.6 µm, clavate, with pedunculate fusiform base. *Cheilocystidia* 38.4–48 × 4.8–9.6 µm, very numerous, mainly nettle-hair shaped (urticoid) to fusoid with a transversal septum and crystals at the apex (exscissa-type). *Pleurocystidia* not observed. *Paracystidia* very numerous, cylindroid-clavate to irregularly clavate. *Pileipellis* a cutis with up to 4 µm wide hyphae, confusedly intertwined with few emerging elements. *Pileocystidia* not observed. *Stipitipellis* a cutis with parallel hyphae from which scattered cauloparacystidia emerge; outermost hyphae cylindrical, up to 170 µm long and 3.5 µm wide, in the inner layer cylindrical to allantoid, up to 48 µm long ad 8.5 µm wide. *Caulocystidia* not observed. *Cauloparacystidia* cylindroid to flexuous, cylindroid-clavate, sometimes bifurcate, 21.5–36 × 3.4–7.2 µm. *Lamellar trama* regular, with parallel, slightly intertwined hyphae, 5–7 µm wide. *Clamp connections* absent in all tissues.

Habitat & Distribution — Growing solitary on tropical forest litter with both deciduous and coniferous trees, from sea level to the mountains. Uncommon in the studied area. So far known only from the Dominican Republic.

Typus. Dominican Republic, La Vega, Jarabacoa, two basidiomes on litter from a tropical mountain forest, with both broad-leaved and coniferous trees (*Pinus occidentalis*), 6 Dec. 2014, *C. Angelini* (holotype JBSD130779, ITS sequence GenBank MT991407, MycoBank MB837378).

Additional materials examined. Dominican Republic, Puerto Plata, Sosua, one basidiome collected on litter of a heavily anthropized humid woodland of deciduous trees, a few km from the sea, 29 Nov. 2013, *C. Angelini* JBSD130781; ibid., 30 Nov. 2013, *C. Angelini*, JBSD130780, ITS sequence GenBank MT991406.

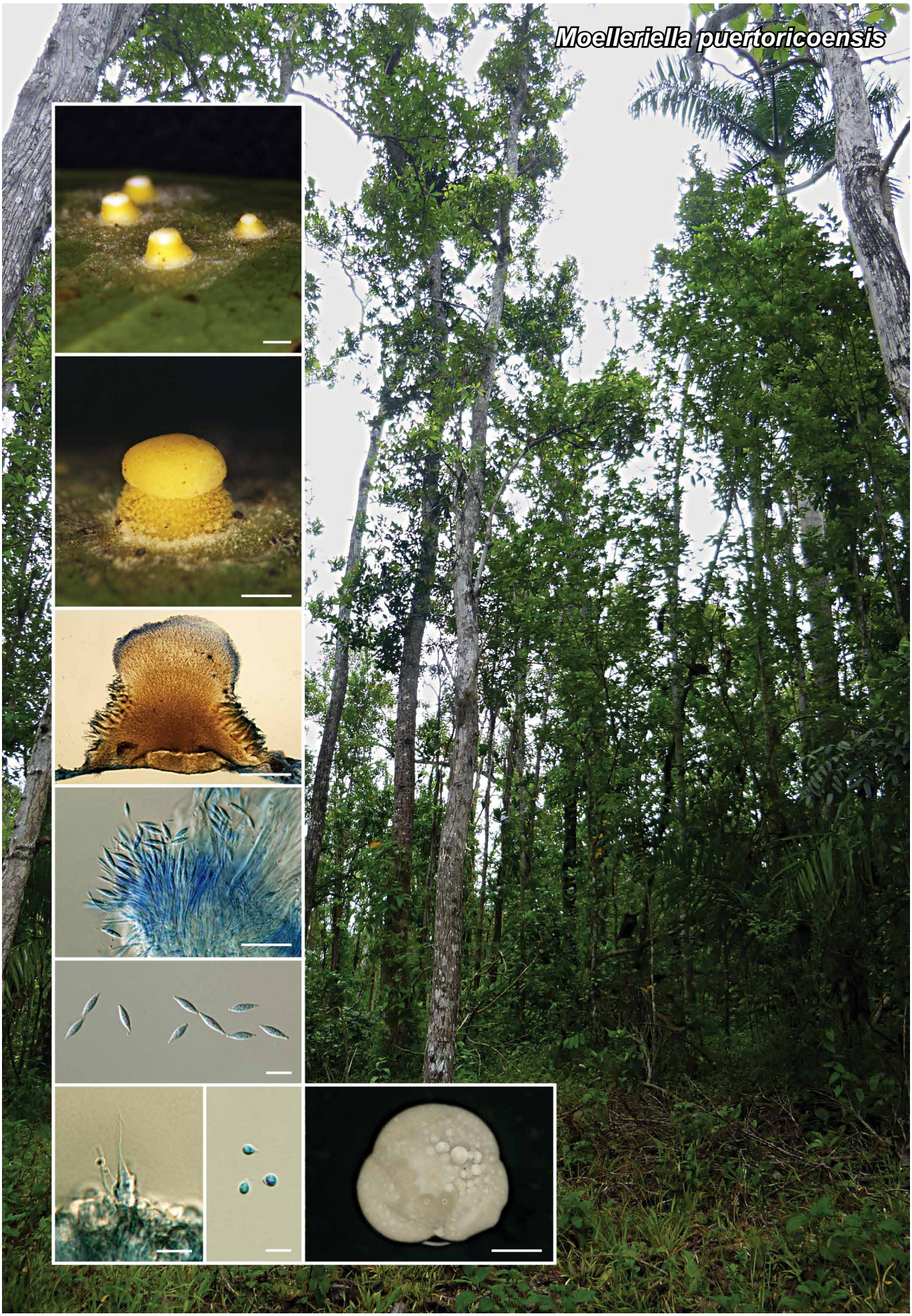
Notes — The new species belongs in subg. *Urticocystis.* The two collections of *Melanoleuca dominicana* clustered in a strongly supported clade (MLB = 100) sister to *M. jaliscoensis* and *M. longisterigma* clade but without support. *Melanoleuca dominicana* is well differentiated from the other *Melanoleuca* species described in literature, based on morphological and/or molecular characteristics. *Melanoleuca tucumanensis*, *M. tucumanensis* var. *colorata* and *M. tucumanensis* var. *striata* from Argentina (Singer & Digilio 1951, Raithelhuber 1974) have larger spores (7.5–10.3 × 6.2–7.5 µm, Singer & Digilio 1951; 7.2–9.6 × 4.8–7.2 µm, pers. obs.). Despite several attempts, it was not possible to sequence neither the type nor other available collections of these three latter taxa. *Melanoleuca jaliscoensis* from Mexico differs from *M. dominicana* by its larger pileus (6.5–10 cm broad) and presence of pleurocystidia (Sánchez-García et al. 2013). *Melanoleuca longisterigma* from Mexico is distinguished by up to 10 µm long spores, a relevant percentage of mono- to bisporic basidia with long sterigmata and cylindrical to fusoid non-septate cheilocystidia without apical crystals (Sánchez-García et al. 2013). *Melanoleuca yucatanensis* from Mexico has pleurocystidia and shows shorter spores, (5.2–)6–7 µm long (Bon 1984).



Maximum-likelihood analysis of the nrITS region of *Melanoleuca* subg. *Urticocystis* species was performed with RAxML v. 8 (Stamatakis 2014) using the GTR+G model (1000 bootstrap replicates). Only maximum-likelihood bootstrap support values ≥ 70 % are shown in the phylogenetic tree. The scale bar represents the number of nucleotide changes per site.

Colour illustrations. Dominican Republic, La Vega, Jarabacoa, *Pinus occidentalis* forest, where the holotype specimen was collected. *Melanoleuca dominicana* basidiomata in field (holotype JBSD130779); fresh basidiomata after being collected (JBSD130780); fresh pileus (JBSD130781); lamellae attachment detail; cheilocystidia and spores; line drawings (spores, basidia, cheilocystidia, paracystidia, stipitipellis). Scale bars = 1 cm (basidiomes), 10 µm (cheilocystidia and spores, pictures).

Alfredo Vizzini & Francesco Dovana, Department of Life Sciences and Systems Biology, University of Torino, Viale P.A. Mattioli 25, I-10125 Torino, Italy; e-mail: alfredo.vizzini@unito.it & francescodovana@gmail.com
Claudio Angelini, Herbario Jardín Botánico Nacional Dr. Rafael Ma. Moscoso, Santo Domingo, Dominican Republic and Via Cappuccini, 78/8 – 33170 Pordenone, Italy; e-mail: claudio_angelini@libero.it
Roberto Para, Via Martiri di Via Fani 22, I-61024, Mombaroccio (PU), Italy; e-mail: r.para@alice.it


Moelleriella puertoricoensis

Fungal Planet 1162 – 19 December 2020

Moelleriella puertoricoensis Mongkolsamrit, Noisripoom & Luangsa-ard, *sp. nov.*

Etymology. Name refers to Puerto Rico, the location where this species was collected.

Classification — *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes.*

Specimens found on the underside of dicotyledonous leaves of forest plants. Hosts are scale insect nymphs (Hemiptera). *Stromata* discoid, distinctly stud-shaped, up to 3 mm diam, and 1–2.5 mm high, pale yellow, base surrounded by a white membranous hypothallus. *Conidiomata* scattered around a narrow neck, with a pale yellow to yellow mass of conidia. *Conidiogenous cells* phialidic, aschersonia-like, cylindrical, straight, up to 55 µm long, 1–2 µm wide, forming a compact layer. *Conidia* hyaline, fusoid, with acute ends, aseptate, (10–)11–12.5(–14) × 2–3 µm. *Paraphyses* absent. Hirsutella-like synasexual morph scattered on the upper surface of stroma, *phialides* with a long thin neck, entire phialides up to 25 µm, 3–5 µm wide, *conidia* globose, 4–5 µm diam. *Sexual morph* not observed.

Culture characteristics — Colonies developed from germinating conidia. The conidia germinated within 24 h on potato dextrose agar (PDA). Colonies reaching a diam of 1 cm after 3 wk at 25 °C. Colonies compact with white mycelium, colonies reverse uncoloured. Conidia produced after 30 d, hyaline thinly spreading on colonies, fusoid, with acute ends, aseptate, 9–12 × 2–3 µm.

Typus. USA, Puerto Rico, Rio Abajo State Forest, on scale insect (Hemiptera) attached to underside of dicotyledonous leaves, 19 Jan. 2018, *S. Mongkolsamrit*, *J.J. Luangsa-ard & S. Wongkanoun* (holotype BBH43763, culture ex-type BCC88320, ITS, LSU and *tef1* sequences GenBank MW115297, MN954683 and MN944389, MycoBank MB834780).

Additional materials examined. USA, Puerto Rico, Rio Abajo State Forest, on scale insect (Hemiptera) attached to underside of dicotyledonous leaves, 19 Jan. 2018, *S. Mongkolsamrit*, *J.J. Luangsa-ard & S. Wongkanoun*, BBH43763 (BBC88321), ITS, LSU and *tef1* sequences GenBank MW115298, MN954684 and MN944390; BBH43764 (BCC88322), ITS, LSU and *tef1* sequences GenBank MW115299, MN954682 and MN944391.

Colour illustrations. Background photo of side of a trail in Rio Abajo State Forest; fungi on hosts, side view of stroma showing stud-shaped and conidiomata, conidiogenous cells, conidia, hirsutella-like on stroma, conidia, culture derived from conidia on PDA (sporulation present). Scale bars = 1 and 2 mm (stromata), 20 µm (phialides), 10 µm (conidia, hirsutella-like phialides and conidia), 3 mm (culture).

Notes — The gross macromorphology of the natural samples of *M. puertoricoensis* closely resembles the asexual morph of *M. basicystis* (Chaverri et al. 2008) and *M. pongdueatensis* (Li et al. 2016) that were found in Costa Rica and Thailand, respectively. These three species have discoid, distinctly stud-shaped stroma and conidiomata scattered around a narrow neck of the stroma, with a pale yellow to yellow mass of conidia. Conidia in *M. puertoricoensis* and *M. pongdueatensis* are fusoid with acute ends and the width of conidia are in the same range (10–14 × 2–3 µm vs 9–12.5 × 1.5–2.5 µm). Conidia of *M. basicystis* are ventricose with acute ends (11–15.5 × 3–5 µm) and wider than those reported in *M. puertoricoensis* and *M. pongdueatensis*. *Moelleriella puertoricoensis* and *M. basicystis* lack paraphyses while they are present in *M. pongdueatensis*, linear, filiform, up to 110 × 1–2 µm. Additionally, *M. puertoricoensis* and *M. pongdueatensis* have a hirsutella-like synasexual morph scattered on the upper surface of the stroma, phialides with a long thin neck (25 × 5 µm vs 20 × 1–2 µm), globose (4–5 µm) and citriform (2–3 × 1–2.5 µm) conidia, respectively. The results of our molecular phylogenetic study strongly support and separate *M. puertoricoensis* from other known species. *Moelleriella puertoricoensis* is therefore proposed as a new species belonging to *Moelleriella* from the Neotropics.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Moelleriella basicystis* (strain ROKI2770, GenBank EF190282.1; Identities = 546/594 (92 %), 21 gaps (3 %)), and *Orbiocrella* sp. (strain BCC33248, GenBank KJ138267.1; Identities = 300/349 (86 %), 22 gaps (6 %)).

Closest hits using the **LSU** sequence had highest similarity to *Moelleriella basicystis* (strain F183147, GenBank EU392577.1; Identities = 276/279 (99 %), 1 gap (0 %)), and *Moelleriella phyllogena* (strain CUP 67340, GenBank AY518372.1; Identities = 276/279 (99 %), 1 gap (0 %)).

Closest hits using the ***tef1*** sequence are *Moelleriella basicystis* (strain F183147, GenBank EU392653.1; Identities = 856/912 (94 %), no gaps (0 %)), and *Moelleriella basicystis* (strain P.C. 374, GenBank AY986928.1; Identities = 854/910 (94 %), no gaps (0 %)).

Supplementary material

FP1162-1 Phylogenetic reconstruction of *M. puertoricoensis* was done using a combined dataset comprising LSU and *tef1* sequences. The data was analysed using Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference. The MP analysis was conducted on the combined data set using PAUP v. 4.0b10 (Swofford 2002), adopting random addition sequences (100 replications), with gaps being treated as missing data. A bootstrap (BP) analysis was performed using the maximum parsimony criterion in 1 000 replications. The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) under a GTR model, with 1 000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.7a (Ronquist et al. 2012), with 5 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values/RAxML bootstrap support values/Bayesian posterior probabilities (BPP) times 100. Thickened lines in the tree represent 99–100 % bootstrap support values and 99–100 BPP.

FP1162-2 List of species and GenBank accession numbers of sequences used in this study.

Suchada Mongkolsamrit, Wasana Noisripoom & Janet Jennifer Luangsa-ard, National Center for Genetic Engineering and Biotechnology (BIOTEC), 113 Thailand Science Park, Phahonyothin Rd., Khlong Nueng, Khlong Luang, Pathum Thani 12120, Thailand; e-mail: suchada@biotec.or.th, wasana.noi@biotec.or.th & jajen@biotec.or.th


Mycena pulchra

Fungal Planet 1163 – 19 December 2020

Mycena pulchra P. Leonard, *sp. nov.*

Etymology. *pulchra* means pretty and refers to the fungus in its setting on a paperbark tree.

Classification — *Mycenaceae*, *Agaricales*, *Agaricomycetes.*

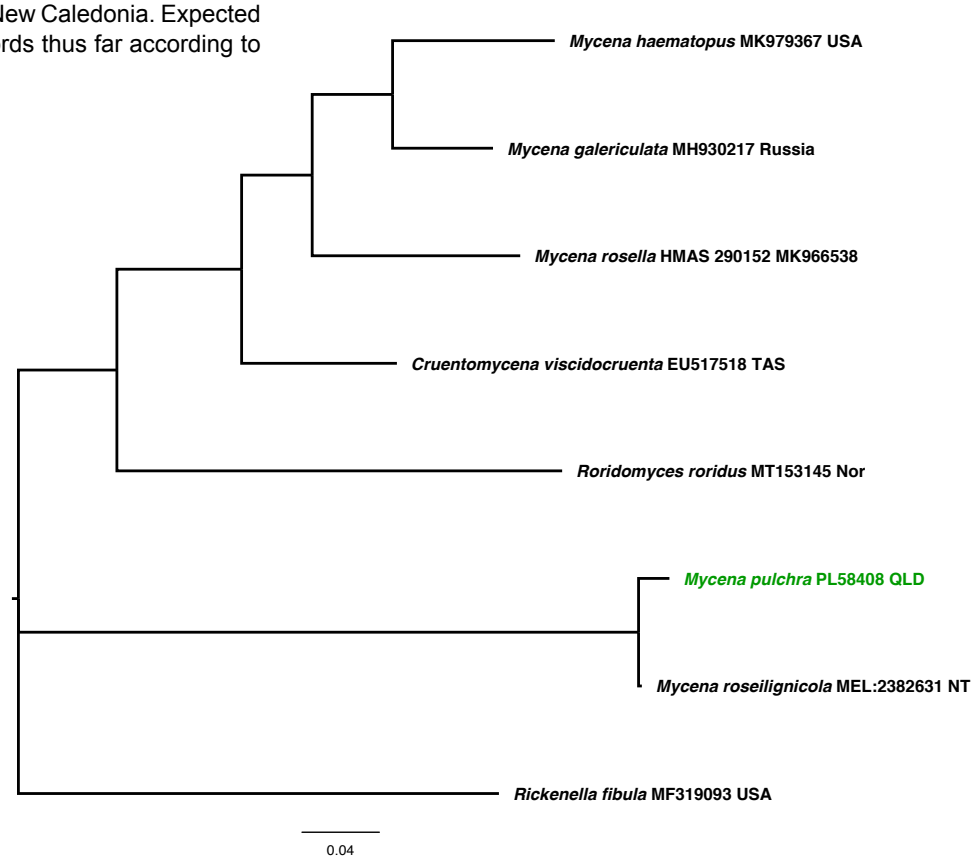
Pileus convex with a central umbilicus, 15–40 mm diam, bright reddish pink (9A6, 11A8; Kornerup & Wanscher 1978), flamingo pink, fading to pale pink with age; margin ± smooth. *Lamellae* adnate or with a subdecurrent tooth, white, lamellulae arranged in two series alternating with lamellae, 16–18 lamellae reach the stipe. *Stipe* cylindrical to somewhat flattened, tough, centrally attached, curved, 15–30 × 1.5–4 mm; bright reddish pink, but paler than cap and white towards base; fruiting singly or in small caespitose groups. *Flesh* white, thin. *Spore print* white. *Spores* ellipsoid, 10.4–14.6 × 5.7–8.8 µm (av. 13 ± 1.23 × 6.7 ± 0.84, Q = 1.5–2.5, Qav = 1.96 ± 0.3), spore contents weakly amyloid with Melzer's reagent. *Basidia* strongly clavate, 45–60 × 10–12 µm, 4-spored. *Pleurocystidia* clavate, 44–50 × 7.5–11 µm, amyloid granular contents. *Cheilocystidia* numerous, forming an almost sterile edge to the gill, 40–100 × 8–20 µm; ventricose or narrowly utriform. *Pileipellis* an irregular cutis, hyphae 7–12 µm, clamps absent.

Habitat & Distribution — Growing in borer holes on the living trunks of the swamp paperbark, *Melaleuca quinquinervia*. Sporocarps found from just above flood level to about 2 m above ground level. Also seen on wounds where the tree has been damaged by storms or pruning. Appears to follow the distribution of *Melaleuca quinquinervia* with confirmed records from Eastern Australia and Western New Caledonia. Expected in New Guinea but there are no records thus far according to Maas Geesteranus & Horak (1995).

Typus. Australia, Queensland, Tewantin, Heritage Park, 13 Apr. 2008, *J. Heavey* (holotype PL58408, Brisbane, ITS sequence GenBank MT988148, MycoBank MB837369).

Notes — This flamingo pink fungus is associated with wounds and borer holes in live paperbark trees. It grows on the tree trunk beneath the layers of bark and requires a wound or an insect hole in order to emerge and fruit.

There are 16 collections under the name *Mycena roseilignicola* on I-Naturalist. Two are recorded on *Melaleuca* and appear to conform with *M. pulchra*. Six others are on dead wood and exhibit the striate cap that Corner (1994) describes. The eight other specimens either lack sufficient information to form a judgement or exhibit attachment via a distinct mycelial pad which is not a feature of *M. pulchra* nor mentioned by Corner (1994) for *M. roseilignicola*.



Maximum likelihood tree of the ITS-nrDNA for a selection of *Mycena* species, aligned using MUSCLE and constructed using MEGA X.

Colour illustrations. Paperbark forest in south-east Queensland. Lower right fruiting body emerging from borer hole (holotype); lower centre fruiting body in tree wound; lower left pileipellis. All photos © Patrick Leonard. Scale bars = 20 µm.

Patrick Leonard, P.O. Box 1193, Buderim 4556 Queensland, Australia; e-mail: patbrenda.leonard@bigpond.com


Penicillium valleboormidaense

Fungal Planet 1164 – 19 December 2020

Penicillium valleboramidaense Houbraken & Di Piazza, *sp. nov.*

Etymology. Latin, name refers to Valle Bormida, the region from which the type specimen was collected.

Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes.*

Conidiophores monoverticillate; stipes non-vesiculate, smooth, short, 13–25(–35) × 1.5–2.5 µm; phialides ampulliform, 3–6 per conidiophore, 7–8.5(–10) × 2–2.5(–3) µm. *Conidia* smooth, globose to subglobose, 2–2.5(–3) µm. *Ascomata* or sclerotia not observed.

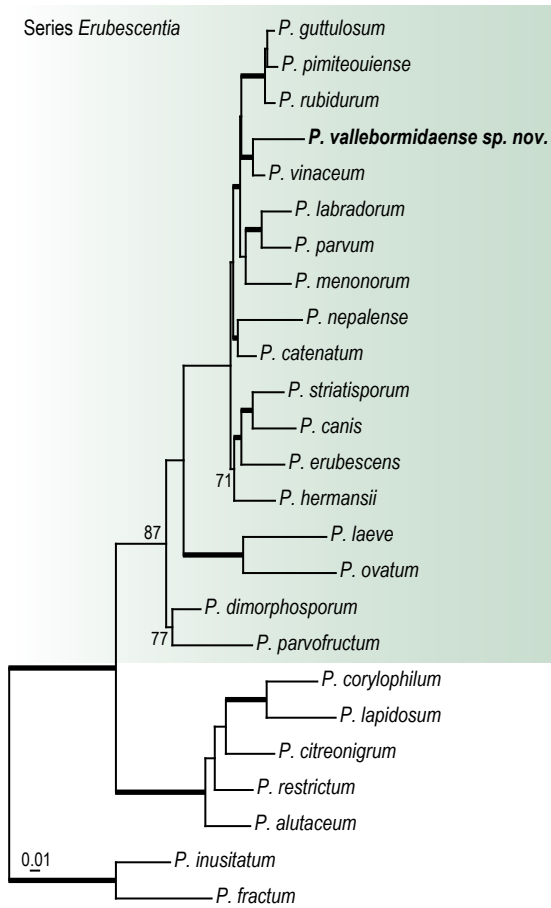
Culture characteristics (25 °C, 7 d) — Czapek yeast extract agar (CYA): Colonies non-sulcate, elevated in centre; margin slightly irregular; mycelium pale yellow; texture velvety; sporulation absent; soluble pigments brown, moderately produced; exudates absent; reverse brown. Malt extract agar (MEA): Colonies non-sulcate, slightly elevated in centre; margin slightly irregular; mycelium pale yellow; texture floccose; sporulation poor in centre, profuse in a ring between centre and edge, absent at edge; soluble pigments absent; exudates absent; conidia *en masse* pale grey green; reverse brown, pale brown at edge. Yeast extract sucrose agar (YES): Colonies randomly sulcate (radial and concentric), slightly elevated; margins slightly irregular; mycelium pale yellow; texture floccose in centre, velvety at edge; sporulation absent; soluble pigment absent; exudates absent; reverse pale brown. Dichloran 18 % glycerol agar (DG18): Colonies non-sulcate, plane, raised at the centre; margins entire; mycelium pale yellow in centre, white at edge; texture velvety; sporulation absent; soluble pigments absent; exudates absent; reverse pale yellow-brown. Oatmeal agar (OA): Colonies non-sulcate, plane, low; margins slightly irregular; mycelium yellow; texture velvety; sporulation absent; soluble pigments present, pale brown, poorly produced; exudates absent. Creatine agar (CREA): poor growth, acid production absent, base production absent. Colony diam, after 7 d, in mm — CYA 18–22; CYA 30 °C 22–26; CYA 37 °C 16–20; MEA 18–22; DG18 20–23; YES 21–25; OA 18–22; CREA 9–11.

Typus. Italy, Savona, Valle Bormida, Ferrania (Cairo Montenotte), from compost 18 d in maturation, 26 June 2018, *S. Di Piazza* (holotype CBS H-24527, culture ex-type CBS 147064 = DTO 402-H5; ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank MT316359, MW092765, MW115862, MW115863 and MW115864; MycoBank MB837659).

Notes — A BLAST search of *BenA*, *CaM* and *RPB2* sequences of *P. valleboramidaense* CBS 147064 against an in-house reference sequence database containing data of all accepted *Penicillium* species (Houbraken et al. 2020), did not retrieved any high similarity hits. A homology search with the ITS sequence retrieved *P. pimiteouiense* (99.2 %), *P. guttulosum* (99.0 %) and *P. vinaceum* (98.9%) as most similar species.

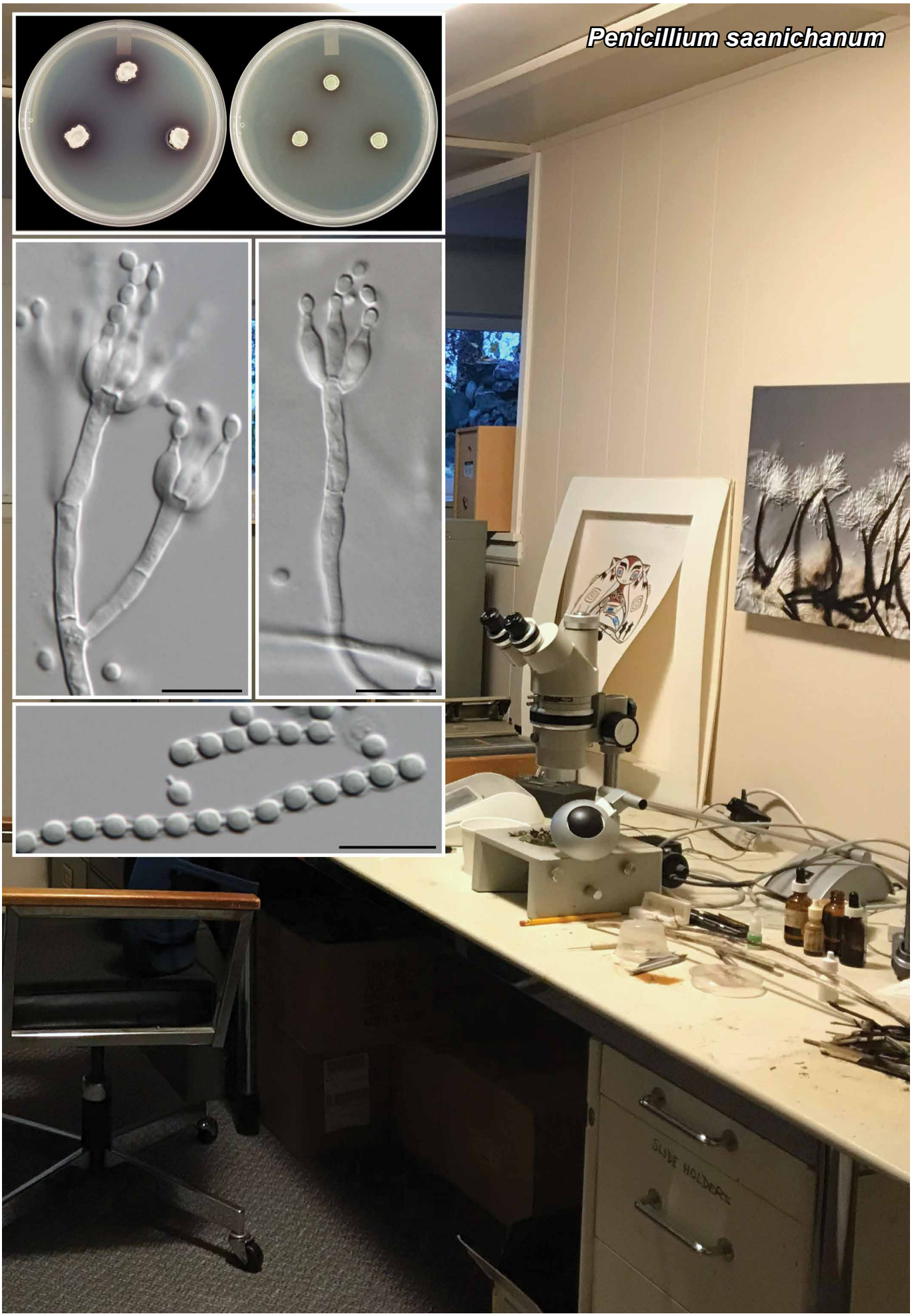
Colour illustrations. Compost pile during ripening process. Colonies (7 d, 25 °C), left to right, first row: CYA, MEA, second row: CYA reverse, YES observe; conidiophores; conidia. Scale bars = 10 µm.

Based on the phylogenetic analysis, *P. valleboramidaense* belongs to series *Erubescentia* of section *Exilicaulis*. *Penicillium valleboramidaense* grows rather slowly on CYA, MEA, DG18 and YES, is able to grow at 37 °C and produces short, monoverticillate conidiophores. These features are shared with many other species in series *Erubescentia* (Houbraken et al. 2020), confirming the results of the phylogenetic analysis. The new species is phylogenetically most closely related to NRRL 739, the ex-type of *P. vinaceum*. The sequence similarity scores with this strain are: *BenA* 95.0 % (identities = 459/478), *CaM* 90.6 % (identities = 444/490) and *RPB2* 93.8 % (identities = 837/892). *Penicillium vinaceum* is characterised by the (copious) production of ruby or vinaceous exudates on CYA and other media. In contrast, no exudate production is observed in *P. valleboramidaense*. Furthermore, the mycelium of *P. valleboramidaense* is pale yellow coloured, while the mycelium in *P. vinaceum* is white (Pitt 1980).



Maximum likelihood tree of *Penicillium* strains belonging to section *Exilicaulis* series *Erubescentia* based on 1871 aligned nucleotides (combined *BenA*, *CaM* and *RPB2* sequences). Strain and GenBank accession numbers used in the analysis can be found in Houbraken et al. (2020). Analysis performed using RAxML v. 8.2.12 (Stamatakis 2014). Bootstrap 1000 re-samplings; only bootstrap support values above 70 % are presented at the nodes and branches of > 95 % are thickened. *Penicillium fractum* and *P. inusitatum* were used as outgroup. The scale bar indicates the number of substitutions per site.

Simone Di Piazza, University of Genoa, Department of Earth, Environmental and Life Science, Laboratory of Mycology, Corso Europa 26, 16132 Genoa, Italy; e-mail: simone.dipiazza@unige.it
Jos Houbraken, Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; e-mail: j.houbraken@wi.knaw.nl


Penicillium saanichanum

Fungal Planet 1165 – 19 December 2020

Penicillium saanichanum Visagie, Assabgui & Seifert, *sp. nov*.

Etymology. Latin, *saanichanum*, named after Saanich, the municipality where the noted Canadian mycologist Bryce Kendrick collected the house dust sample that this species was isolated from.

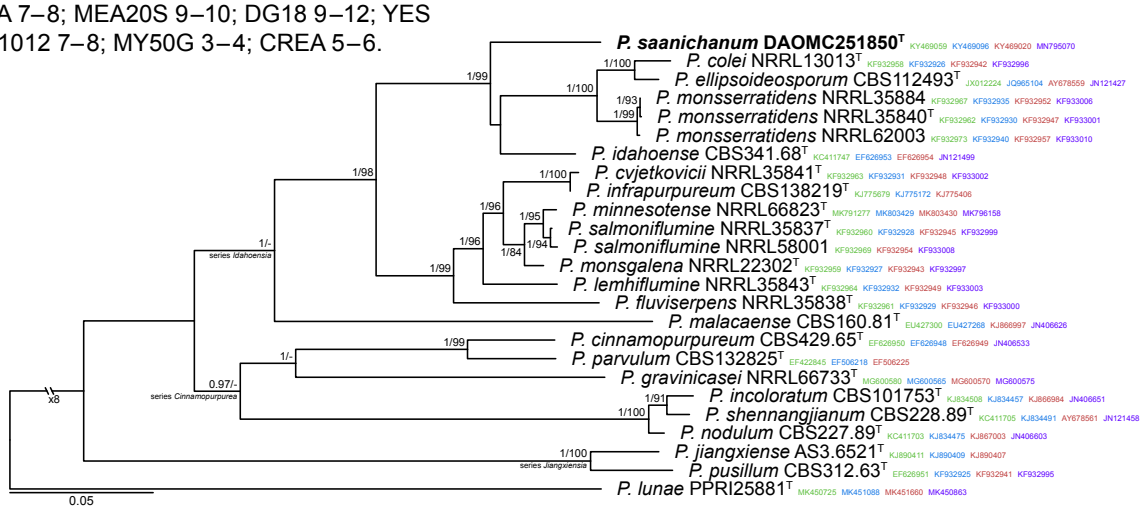
Classification — *Aspergillaceae*, *Eurotiales*, *Eurotiomycetes*.

Conidiophores monoverticillate and loosely divaricate; *stipes* smooth, 19–60 × 2–3 µm; *vesicles* 3–4.5 µm; *branches* 16–23 µm; *phialides* ampulliform, 5–12 per metula, 7.5–11 × 2.5–3.5 µm (8.6 ± 1.1 × 2.6 ± 0.2); *conidia* smooth, subglobose to globose, 2–3 × 2–3 µm (2.7 ± 0.2 × 2.5 ± 0.1), av. width/length = 0.92, n = 72.

Culture characteristics (25 °C, 7 d) — On Czapek yeast autolysate agar (CYA): Colonies moderately deep, sunken in centre, slightly sulcate; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderate, conidia *en masse* greenish grey to dull green (27C2–D3–4; colour codes based on Kornerup & Wanscher (1967)); soluble pigments red, inconspicuous; exudates absent; reverse dark ruby (12F8). On Blakeslee's malt extract agar (MEA): Colonies moderately deep, planar; margins low, narrow, entire; mycelia white; texture velutinous; sporulation moderately dense, conidia *en masse* dull green to greyish green (26D3–4–E5); soluble pigments red, inconspicuous; exudates absent; reverse violet brown to dark ruby (10E6–12F8). On 20 % sucrose CYA (CYA20S): Colonies with conidia *en masse* greyish green (26D5–E5), otherwise similar to CYA. On 20 % sucrose MEA (MEA20S): Colonies less dense than those on MEA, lacking soluble pigment and red reverse colour, otherwise similar to MEA. On dichloran 18 % glycerol agar (DG18): Colonies similar to those on MEA. On yeast extract sucrose agar (YES): Colonies similar to those on MEA. On creatine sucrose agar (CREA): Growth good, no acid produced. Colony diam (in mm): CYA 9–11; CYA37C no growth; CYA20S 10–12; MEA 7–8; MEA20S 9–10; DG18 9–12; YES 12–15; OA 4–5; MY1012 7–8; MY50G 3–4; CREA 5–6.

Typus. Canada, North Saanich, from house dust, May 2017, coll. *B. Kendrick*, isol. *C.M. Visagie* (holotype DAOM 745787, cultures ex-type DAOMC 251850 = KAS 6184; LSU, ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MN807447, KY469059, KY469096, KY469020, MN795070, MycoBank MB835962).

Notes — A BLAST search of our *BenA* sequence against a locally curated reference dataset placed the new species in section *Cinnamopurpurea* series *Idahoensia* (Visagie et al. 2014, Houbraken et al. 2020). *Penicillium saanichanum* is characterised by restricted growth and monoverticillate conidiophores, characters typical of species classified in section *Cinnamopurpurea*. Morphologically and phylogenetically it is most similar to *P. idahoense*. However, the new species is morphologically distinct from *P. idahoense* based on its generally more restricted growth on most agar media, its red soluble pigments produced on CYA, and the absence of sclerotia (Paden 1971, Pitt 1980).



Combined phylogeny of *Penicillium* section *Cinnamopurpurea* based on ITS, *BenA*, *CaM* and *RPB2*. Aligned data sets (MAFFT v. 7.450; Katoh & Standley 2013) were analysed using Maximum Likelihood (IQ-tree v. 1.6.12; Nguyen et al. 2015) and Bayesian Inference (MrBayes v. 3.2.7a; Ronquist et al. 2012). Bootstrap support values (≥ 80 %) and posterior probabilities (≥ 0.95) are given above 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* = purple). The tree is rooted to *P. lunae*.

Colour illustrations. Bryce Kendrick's home laboratory. Colonies on CYA and MEA; conidiophores; conidia. Scale bars = 10 µm.

Cobus M. Visagie, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa; e-mail: cobus.visagie@fabi.up.ac.za
Rafik Assabgui, Biodiversity (Mycology), Agriculture and Agri-Food Canada, Ottawa, ON K1A0C6, Canada; e-mail: rafik.assabgui@canada.ca
Keith A Seifert, Biodiversity (Mycology), Agriculture and Agri-Food Canada, Ottawa, ON K1A0C6, Canada / Department of Biology, Carleton University, 1125 Colonel By Drive, Ottawa, ON K1S 5B6, Canada; e-mail: keith.seifert@carleton.ca


Phialocephala melitaea

Fungal Planet 1166 – 19 December 2020

Phialocephala melitaea Matočec, I. Kušan, Pošta, Tkalčec & Mešić, *sp. nov.*

Etymology. Lat. *melitaeus* - which refers to Mljet (lat. *Melita*, *ex* C. Plinius Secundus), island in the Adriatic Sea.

Classification — *Mollisiaceae*, *Helotiales*, *Leotiomycetes*.

Ascomata apothecial, shallowly cupulate and with basal depression when young, plate shaped to plane when fully mature, superficial, sessile, ± circular to much irregular from the top view, *0.8–1.4(–2) mm diam, gregarious but mutually distanced. Hymenium, when in fresh state, in the central part greyish to pale lead-grey with bluish tones, perimarginal area beige to pale grey, not wrinkled but finely pruinose; margin ± irregular, lobed and wavy in fully mature apothecia, entire, ± sharp, white, subglabrous; excipular surface in upper part whitish, lower part brownish, slightly roughened. Subicular hyphae macroscopically not discernible. *Hymenium* *70–85 µm thick. *Asci* cylindrical with conical-subtruncate to rounded apex, *60–82 × (6.4–)6.7–8.1 µm, *pars sporifera* *19–25.5 µm, 8-spored, in living state protruding above paraphyses up to 18 µm, base cylindrical-truncate, arising from croziers, in Lugol's solution (IKI) apical ring of medium amyloidity (2bb), *Calycina*-type. *Ascospores* piscioid to subscutuliform, with tapered to somewhat rounded poles, sometimes slightly bent, aseptate, *(7.8–)8.2–*9.8*–11.5(–12.6) × (2.4–)2.6–*2.9*–3.2(–3.4) µm, *Q = 2.7–*3.4*–4.1(–4.3), hyaline, smooth, uninucleate, nearly eguttulate or with several dispersed tiny lipid bodies (LBs), *0.4–0.7 µm diam, freshly ejected without sheath remnants, biseriate inside *asci; in IKI unstained, nucleus slightly contrasted. *Paraphyses* cylindrical-obtuse, rarely apically clavate, apical cell *27–63 × 3.4–5 µm, straight, simple, thin-walled, *containing few globose or obloid rarely elongated, moderately refractive and hyaline semi-resistant vacuolar bodies (SVB), with age become yellowish; in †KOH without yellow reaction; in *IKI SVBs golden yellow; in *brilliant cresyl blue (CRB) violet blue and after addition of †KOH light ruby red. *Subhymenium* *15–21 µm thick at the middle flank, hyaline, composed of densely packed epidermoid cells, *3.2–5.6 µm wide. *Medullary excipulum* *18–28 µm thick at the middle flank, reaching *36 µm in the lower flank, subhyaline to hyaline, stretches as a continuous layer towards the margin, composed of *textura prismatica*, cells *12–28 × 3–10.5 µm, thin-walled, slightly gelatinised (purple in CRB), devoid of crystals. *Ectal excipulum* *28–40 µm thick at the middle flank, reaching *58 µm in the basal part, ochre brown to greyish brown, composed of *textura angularis* with elongated elements, cells *9–25.6 × 5.6–14 µm, walls *0.7–0.9 µm thick, upper flank hyaline and indistinguishable from medulla, terminal cells contain single, hyaline and globose SVB, lower flank rich in dark brown intercellular pigment, cell walls brown, thickened, *0.8–1.2 µm. *Marginal tissue* completely hyaline, *21–25 µm thick, composed of *textura porrecta-prismatica*, cells *7.5–14.6 × 2.3–5.7 µm, thin-walled, outermost cells cylindrical-clavate, each containing single globose hyaline SVB. *Subicular hyphae* sparse, confined to an apothecial base and lower flank, flexuous, greyish-brown, smooth, cells *19–23 × 3.3–5 µm, walls *0.6–0.8 µm thick, enveloped in gel up to *1.8 µm thick. Asterisk (*) denotes living and cross (†) dead state. Ascus amyloidity is termed after Baral (1987) and spore shape after Kušan et al. (2014).

Colonies after 14 d in the dark at 24 °C on 3 % malt extract agar (MEA) 32–34 mm diam, centrally pronouncedly papillate, with woolly aerial hyphae; margin radially diffuse, hyaline; surface whitish grey near the margin, pale clay buff towards the centre, clay pink in the centre; reverse dark grey to blackish sepia. Exudates present in the central part, droplets honey brown. *Conidiophores* developed only after 5 mo, mycelium consisting of hyaline to subhyaline hyphae only in colonial margin, others brown-walled, smooth, septate, branched, *2.2–4.2 µm wide, wall *0.3–0.6 µm, often producing loops or covered with large tuberculate exudates, *1.5–3.8 µm high, some hyphae produce large flat subhyaline plaques under which granular brown pigment develops. *Conidiophores* micronematous, crawling or erect, greyish brown, smooth, cylindrical, with slightly thickened walls, conidiophore stem *9–13 × 4–4.8 µm, 0–1-septate, rami richly and tightly branched. *Conidiogenous cells* phialidic, terminal, conoid, ventricose or ampulliform, *7.8–10.5 × 3–4.1 µm, collarettes flaring, *1.5–2.2 × 1.4–2.1 µm, hyaline. *Conidia* hyaline, dimorphic, primary conidia oblong to narrowly ellipsoid, aseptate, *2.9–4.3 × 1.6–1.7 µm, secondary conidia globose to subglobose, aseptate, base often subtruncate, *1.8–2.3 µm.

Distribution & Habitat — Known so far only from the type locality on the island of Mljet, Croatia. Type collection was found on a branch of *Pinus halepensis* lying in thick litter, in the evergreen thermo-Mediterranean forest.

Typus. Croatia, Dubrovnik-Neretva County, Island of Mljet, Prožura, near Prožurska blatina, 5 m asl, N42°43'57" E17°38'41"; on fallen decorticated main branch of *Pinus halepensis*, majority of the apothecia were growing on old fruitbody of *Phellinus* sp., only partially directly on wood, in a forest of *P. halepensis*, *Viburnum tinus*, *Myrtus communis*, *Arbutus* × *andrachnoides*, *Coronilla* sp. and *Laurus nobilis*, 16 Mar. 2020, *I. Kušan & M. Pucar* (holotype CNF 2/11027, ex-type culture CBS 147182, ITS and LSU sequences GenBank MT957536 and MT957586, MycoBank MB836891).

Notes — Tanney & Seifert (2020) assigned species of true *Phialocephala* to a genus separated from *Mollisia* s.str., a view accepted here. The most closely related species *Phialocephala biguttulata* differs by ascospores containing two large polar guttules, paraphysis apical cells largely occupied by elongated refractive VBs, excipular tissue stained deep green by KOH and finally not producing conidiogenous structures in axenic culture. There are two other species, *P. cladophialophoroides* and *P. aylmerensis*, members of the same clade. The apothecial morph is not known for the first species whereas it produces acropetal conidial moniliform cell chains (cf. Crous et al. 2017b), and the latter differs in having more stout and

(text continues on Supplementary material page FP1166)

Colour illustrations. Croatia, Mljet Island, near Prožurska blatina (type locality). Apothecia; 14-d-old colonies on MEA, colony centre with exudates; asci and croziers in *H_2O, ascus in *IKI; ascospores in *H_2O; paraphyses in *H_2O, *IKI and *CRB; phialides with collarettes, conidiophores (two pictures); hyphal loops, colony hyphae bearing exudates, apothecial subicular hyphae with gel envelope, colony hyphae with plaques and pigmented granules, vertical median section of the apothecium. Scale bars = 10 mm (colony), 1 mm (apothecia, colony centre), 50 µm (apothecial anatomy), 10 µm (microscopic elements).

Supplementary material

FP1166 Phylogenetic tree obtained from maximum likelihood analysis based on ITS sequences of *Phialocephala melitaea* and related species.

Neven Matočec, Ivana Kušan, Ana Pošta, Zdenko Tkalčec & Armin Mešić, Ruđer Bošković Institute, Bijenička cesta 54, HR-10000 Zagreb, Croatia; e-mail: nmatocec@irb.hr, ikusan@irb.hr, aposta@irb.hr, ztkalcec@irb.hr & amesic@irb.hr


Phytophthora aquae-cooljarloo

Fungal Planet 1167 – 19 December 2020

Phytophthora aquae-cooljarloo R. Mostowfizadeh-Ghalamfarsa & T.I. Burgess, *sp. nov.*

Etymology. Named for the association of this species with water at the place Cooljarloo.

Classification — *Peronosporaceae*, *Peronosporidae*, *Oomycota.*

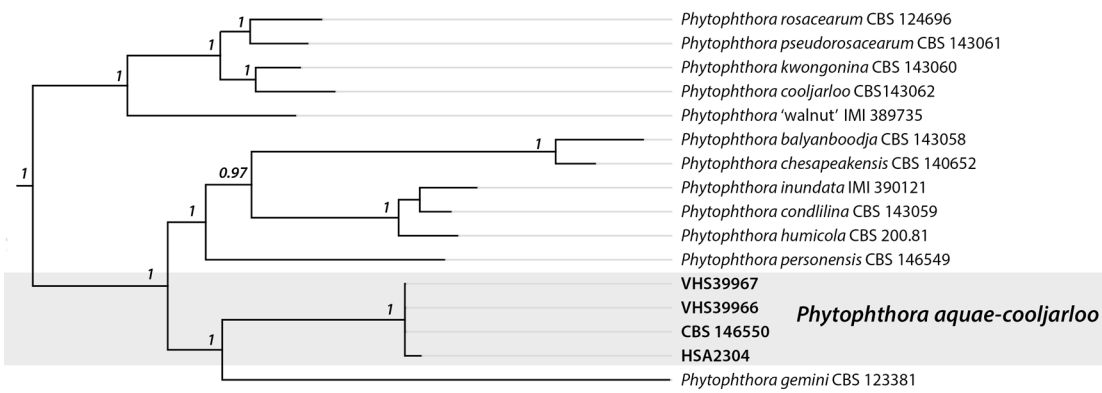
Sporangia produced on V8 agar (V8A) and carrot agar (CA) flooded with both distilled water and non-sterile soil extract; terminal, non-papillate, mostly ellipsoid to ovoid and limoniform, sometime obovoid; 66 ± 11.2 × 37 ± 4.5 µm (overall range 38–101 × 29–54 µm), length/breadth ratio of 1.9 ± 0.2. *Sporangial proliferation* in chains of internally proliferating sporangia, both nested and extended. *Hyphal swellings* absent. *Chlamydospores* common, globose, thin-walled, 9–(20 ± 5)–33 µm. *Gametangia* were produced in single cultures (homothallic). *Oogonia,* smooth-walled, globose, golden to brown 34 ± 4.5 µm (isolates ranged from 23–47 µm). *Oospores* were aplerotic, with an average of 30 ± 4 µm (isolate means 19 to 41 µm). *Oospore walls* were av. 3.2 ± 0.9 µm, oospore wall index 0.5. *Antheridia* were paragynous, monoclinous, spherical to ellipsoidal, ranged from 5 to 17 µm in length (av. 12 ± 1.7 µm) and 5 to 14 µm in breadth (av. 9 ± 1.7 µm). *Hyphae* were hyaline, normally not septate, 4–5 µm wide. Minimum, optimum and maximum temperatures for growth were 4 °C, 30 °C and 35 °C, respectively. Radial growth rate on CA in the dark at 30 °C was 3.9 ± 1.3 mm/d.

Culture characteristics — The colony patterns on all media were uniform with the exception of potato dextrose agar (PDA) which produced rose-shaped pattern in some isolates. Aerial mycelia were observed on some colonies specially on PDA.

Typus. Australia, Western Australia, Cooljarloo, baited from pond water, collected by Department of Biosecurity, Conservation and Attractions, 20 Sept. 2017 (holotype MURU484, culture ex-type CBS 146550 = VHS36940, ITS, *Btub*, *hsp90*, *coxI*, *nadh1* and LSU sequences GenBank MT210484, MT210475, MT210480, MT210466, MT210470 and MT210485, MycoBank MB835165).

Additional materials examined. Australia, Western Australia, Cooljarloo baited from pond water, collected by Department of Biosecurity, Conservation and Attractions, 18 Sept. 2019, cultures VHS39966, VHS39967; 1996, culture HSA2304.

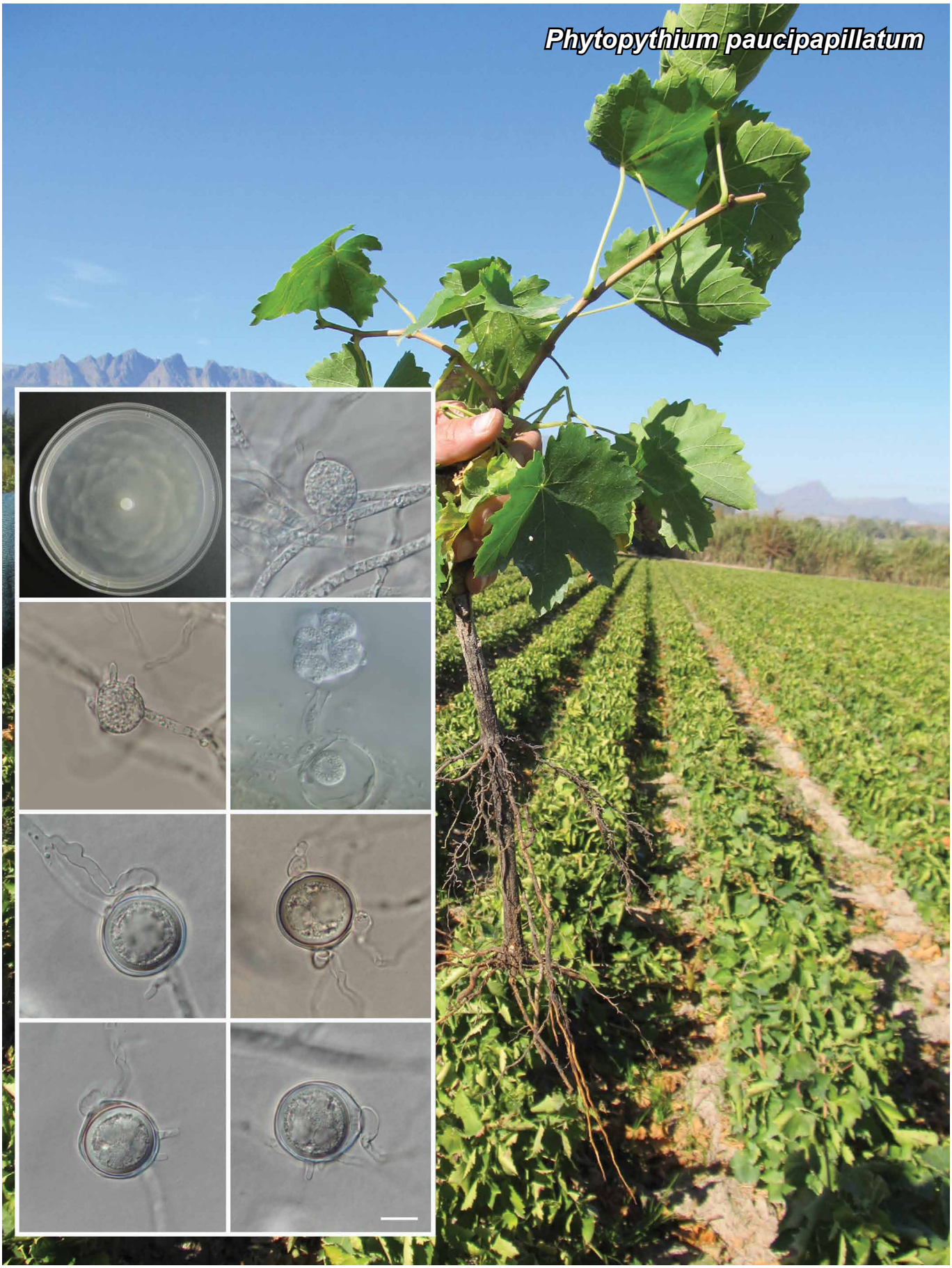
Notes — Isolates of *Phytophthora aquae-cooljarloo* constitute a well-supported monophyletic group sharing a common ancestor with *P. gemini* (Man in 't Veld et al. 2011). These species together with *P. humicola* (Ko & Ann 1985), *P. inundata* (Brasier et al. 2003), *P. condilina* (Burgess et al. 2018), *P. balyanboodja* (Burgess et al. 2018), *P. chesapeakensis* (Man in 't Veld et al. 2019), and *P. personensis* (Crous et al. 2020a) cluster within clade 6a of the *Phytophthora* phylogeny (Burgess et al. 2018). In a multigene phylogeny of the ITS, *Btub, hsp90*, *cox*I and *nadh1* gene regions, *P. aquae-cooljarloo* differs from its sister taxon, *P. gemini,* by 8.8 %. Morphologically, *P. aquae-cooljarloo* is similar to other species in clade 6a, producing terminal, ellipsoid to ovoid, persistent, non-papillate sporangia, and it is also a high-temperature tolerant *Phytophthora* species. Isolates of *P. aquae-cooljarloo* are homothallic and produce abundant oospores in culture similarly to *P. humicola, P. inundata,* and *P. condilina.* Unlike *P. balyanboodja, P. chesapeakensis* and *P. gemini*, *P. aquae-cooljarloo* produces chlamydospores, but does not form any hyphal swellings which differs from all other species in the clade except *P. balyanboodja. Phytophthora aquae-cooljarloo* has been isolated over a 25-yr-period from seasonal ponds in the dry *Banksia* shrublands (the kwongan) in the sandplains north of Perth, Western Australia at a single location, Cooljarloo.



Bayesian inference tree based on a concatenated ITS, *Btub, hsp90*, *cox*I and *nadh1* sequence alignment showing the placement of *Phytophthora aquae-cooljarloo* in *Phytophthora* Clade 6a. The tree was generated in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) as a plugin in Geneious Prime® 2019.2.3 (www.geneious.com) using the GTR substitution model. The posterior probability values are shown at the nodes. The tree was rooted to *P. thermophila* (not shown) and the novel species is shown in **bold** font.

Colour illustrations. Typical kwongan vegetation, north of Perth, Western Australia (Photo: Giles Hardy). Typical ellipsoid and limoniform sporangia; aplerotic oogonia with paragynous antheridia; small chlamydospore; uniform colony on V8 agar. Scale bar = 20 µm.

Reza Mostowfizadeh-Ghalamfarsa, Department of Plant Protection, Shiraz University, Shiraz, Iran; e-mail: rmostowfi@shirazu.ac.ir
Treena I. Burgess, Phytophthora Science and Management, Centre for Climate Impacted Terrestrial Ecosystems, Harry Butler Institute, Murdoch University, Murdoch, WA 6150, Australia; e-mail: tburgess@murdoch.edu.au


Phytopythium paucipapillatum

Fungal Planet 1168 – 19 December 2020

Phytopythium paucipapillatum S.D. Langenhoven, W.J. Botha & L. Mostert, *sp. nov.*

Etymology. The specific epithet refers to the sparsely papillated sporangia and oogonia.

Classification — *Pythiaceae*, *Pythiales*, *Oomycetes.*

Hyphae up to 5 µm thick, lacking hyphal swellings. *Sporangia* apical, unilaterally intercalary or perpendicular on sporangiophore, some sporangia clustered in groups of 3–5 at apex of sporangiophore, connected by short hyphal segments. *Sporangia* globose, subglobose, ovoid, obovoid, limoniform to ellipsoid or distorted shapes, 15–34 µm diam, most 19–25 µm diam. *Sporangia* mostly apapillate germinating directly, some papillate, internally proliferating with extended proliferation. *Papilla* apical or subapical, close to sporangiophore, 4–5 µm. *Zoospores* biflagellate, differentiated extrasporangially in an ephemeral vesicle, released through discharge tubes 3.7–5 µm wide, 7.5–11 µm long. *Zoospore cysts* spherical, 9–11 µm diam. *Oogonia*, small globose terminal, intercalary, some unilaterally intercalary, (18–)20–23(–26) (av. 22) µm diam, some oogonia ornamented with one to three short, blunt papillae. *Antheridia* up to three per oogonium, mostly monoclinous, or occasionally diclinous at a distance. *Antheridia* applied lengthwise to oogonium wall with a central fertilisation tube, antheridial cell 4–5 × 11–20 µm with an undulating contour and one to several constrictions; some antheridia applied broadly apical to oogonium. *Oospores* plerotic or nearly so, (14–)18–20(–23) (av. 20) µm diam, wall thickness 0.9–1.9 µm. Occasionally two oospores per oogonium. Ooplast 7–13 µm diam. Aplerotic index 76.9 %, ooplast index 54.4 %, oospore wall index 45.2 %.

Cultural characteristics — Colony growth pattern on potato dextrose agar (PDA) and potato carrot agar (PCA) rosaceous, corn meal agar (CMA) slight aerial mycelium with coarsely radiate pattern and numerous micro tufts of aerial mycelium. Grows on PARP and PARPH selective media. Cardinal temperatures: min 10 °C, opt 25 °C, max 30 °C on PCA. Average growth rate at the optimum temperature was 8.55 mm/d for the STE-U isolates and 7.44 mm/d for MAFF 241149 on PCA. Growth study on CMA, min 10 °C, max 30 °C or between 30 °C and 35 °C for STE-U isolates and the MAFF isolate, respectively. The optimum growth temperature was 25 °C for STE-U 7843, 7844, 7847 and MAFF 241149. The optimum temperature for STE-U 7845, 7846 and 7848 was 30 °C. The average growth rate for the STE-U isolates with optimum growth temperatures at 25 °C and 30 °C were 9.77 mm/d and 10.63 mm/d, respectively. The average growth rate for the MAFF isolate was 8.79 mm/d.

Colour illustrations. Grapevine nursery, Wellington, South Africa. Colony growth on corn meal agar; sub-globose papillate sporangium; young, terminal multipapillate sporangium; zoospore discharge into a vesicle with a zoospore remaining in the sporangium; intercalary oogonium with monoclinous antheridium; oogonium with three antheridia attached; oogonia with papillation on its surface. Scale bar = 10 µm.

Typus. South Africa, Western Cape Province, Wellington, *Vitis* sp. asymptomatic roots (*Vitaceae*), May 2013, *S.D. Langenhoven* (holotype and culture ex-type stored in a metabolically inactive state CBS 144082 = STE-U 7843; *COI* and ITS sequences GenBank KX372742 and KX372749, MycoBank MB819417).

Additional materials examined. South Africa, Western Cape Province, Wellington, grapevine roots (STE-U 7844, STE-U 7845, STE-U 7846, STE-U 7847, STE-U 7848). – Japan, Nagano, uncultivated soil, collection date and collector unknown (as *Ovatisporangium* sp. 5, culture MAFF 241149).

Notes — *Phytopythium paucipapillatum* sp. nov. was isolated from a nursery grapevine in South Africa. The inclusion of *Ovatisporangium* sp. 5 isolate MAFF 241149 in the species *P. paucipapillatum* is supported by morphological and phylogenetic data. Phylogenetically, *P. paucipapillatum* isolates formed a well-supported monophyletic clade with ITS (96 % bootstrap support and posterior probability of 1.0) and *COI* (99 % bootstrap support and posterior probability of 0.99). *Phytopythium paucipapillatum* was distinct from, but related to *P. chamaehyphon*, *P. helicoides*, *P. fagopyri* and *Phytopythium* sp. WJB-3 (of which only ITS is available). Morphological characteristics unique to *P. paucipapillatum* isolates were the plerotic and aplerotic oospores, compared to the mentioned closely related species with exclusively aplerotic oospores (Van der Plaats-Niterink 1981, McLeod et al. 2009, Baten et al. 2015). In addition, *P. paucipapillatum* is the only species with oogonial ornamentation as compared to *P. chamaehyphon*, *P. helicoides*, *P. fagopyri* and *Phytopythium* sp. WJB-3. Furthermore, the oogonia of *P. paucipapillatum* sometimes contain two oospores, unlike those of the above mentioned closely related species (including *Phytopythium* sp. WJB-3). Regarding internal proliferation, no nested proliferation was observed in *P. paucipapillatum*, as compared to *P. chamaehyphon*, *P. fagopyri* and *P. helicoides* – all of which display internal, nested proliferation. Furthermore, no internal proliferation has been observed for *Phytopythium* sp. WJB-3.

Supplementary material

FP1168-1 Maximum likelihood phylogeny of the internal transcribed spacer-nuclear ribosomal DNA region displaying species of the genus *Phytopythium*. Maximum likelihood analyses were performed in PhyML v. 3.3 (Guindon et al. 2010) under the best model (GTR+I+G for both ITS and *COI*) as estimated using the Akaike Information Criterion in jModelTest v. 2 (Darriba et al. 2012). Support values were calculated from 100 bootstrap replicates. Maximum likelihood bootstrap percentages and Bayesian posterior probability values are indicated at the nodes. Support values less than 60 % bootstrap or 0.60 posterior probability are omitted or indicated with '–'.

FP1168-2 Maximum likelihood phylogeny of the cytochrome c oxidase subunit 1 (*COI*) gene region displaying species of the genus *Phytopythium*. Both trees have been lodged in TreeBASE (study S22566).

Shaun D. Langenhoven & Lizel Mostert, Department of Pant Pathology, University of Stellenbosch, Private Bag X1, Matieland, 7602, South Africa; e-mail: lmost@sun.ac.za & langenhovensd@gmail.com
Chris F.J. Spies, ARC Plant Health and Protection, Private Bag X5017, Stellenbosch, 7599, South Africa; e-mail: SpiesC@arc.agric.za
Wilhelm Botha, ARC Plant Health and Protection, Private Bag X134, Queenswood, Pretoria, 0121, South Africa; e-mail: BothaW@arc.agric.za
Francois Halleen, Plant Protection Division, ARC Infruitec-Nietvoorbij, Private Bag X5026, Stellenbosch, 7599, South Africa; e-mail: HalleenF@arc.agric.za


Pseudopyricularia javanii

Fungal Planet 1169 – 19 December 2020

Pseudopyricularia javanii A. Pordel & G. Ghorbani, *sp. nov.*

Etymology. The species name is proposed in honour of Professor Mohammad Javan-Nikkhah, Iranian mycologist.

Classification — *Pyriculariaceae*, *Magnaporthales*, *Sordariomycetes*.

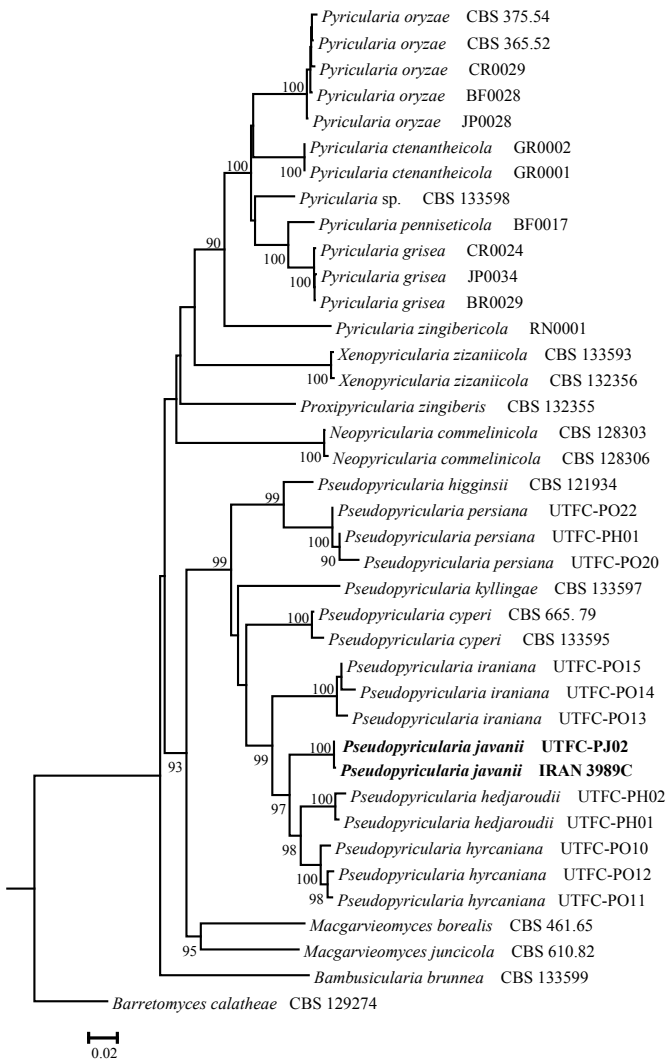
Mycelium on synthetic nutrient-poor agar (SNA), water agar (WA) supplemented with *Cyperus* leaves, and oatmeal agar (OA), consisting of smooth, hyaline, branched, septate hyphae. *Conidiophores* scattered, solitary, erect, pale brown, swollen at the base, macronematous, mononematous, typically unbranched, sometimes branched, straight, typically consisting of 0–5-septate, 35–85(–112) × 3–5 µm. *Conidiogenous cells* integrated, terminal, intercalary, sympodial, cylindrical, geniculate, denticulate; denticles cylindrical, thin-walled, pale brown. *Conidia* solitary, dry, obclavate, hyaline, (20–)25–35(–40) × 6–7 µm, 2-septate, hilum often protuberant. *Sexual morph* unknown.

Culture characteristics — Colonies on OA transparent, greenish olivaceous, reaching 34 mm diam after 1 wk at 23–25 °C; on potato dextrose agar (PDA) transparent, grey, and black reverse, reaching 37 mm diam after 1 wk at 23–25 °C.

Typus. Iran, Gilan Province, Someh Sara region, on infected leaves of *Cyperus* sp. (*Cyperaceae*), 15 Nov. 2018, *A. Pordel* (holotype in Iranian Research Institute of Plant Protection, IRAN 18060F, ex-type culture IRAN 3989C; ITS, LSU, *CAL*, *RPB1* sequences GenBank MT472570, MT472574, MT472593 and MT472595, MycoBank MB837644).

Additional material examined. Iran, Gilan Province, Someh Sara region, on infected leaves of *Cyperus* sp. (*Cyperaceae*), 15 Nov. 2018, *A. Pordel* (UTFC-PJ02; ITS, *CAL*, *RPB1* sequences GenBank MT472569, MT472594 and MT472596).

Notes — *Pseudopyricularia javanii* is similar to *Ps. higginsii*, *Ps. cyperi, Ps. iraniana, Ps. kyllingae*, *Ps. persiana*, and *Ps. hagahagae* in having 2-septate conidia (Klaubauf et al. 2014, Pordel et al. 2017, Crous et al. 2018a). However, the conidia of *Pseudopyricularia javanii* are larger than those of *Ps. higginsii*, *Ps. cyperi, Ps. kyllingae*, and shorter than *Ps. persiana*, and *Ps. hagahagae*. It differs from *Ps. iraniana* in conidial shape, and size. To clarify the phylogeny of *Ps. javanii* within *Pseudopyricularia*, sequence data of *CAL*/ITS/*RPB1* were combined. In the multi-gene analyses (gene boundaries of *CAL*: 1–723, ITS: 724–1263, *RPB1* 1264–2265) of 39 isolates (37 taxa from NCBI and two sequenced specimens of new taxa), 2978 characters including the alignment gaps were used. The phylogenetic tree suggested phylogenetic relatedness of the taxa from Iran to *Pseudopyricularia* with high statistical support (MLBP = 99 %). In the LSU sequences, the highest level of similarity (99.15 %; 819/826) was to *Ps. bothriochloae* (reference sequence accession NG_058051.1), and *Ps. hyrcaniana* (99.27 %; 820/826, GenBank KY457267), although the conidia in the new species is 2-septate. In species with 2-septate conidia, *Ps. hagahagae* has the highest level of similarity (98.87 %; 790/799; reference sequence accession NG_059616), although the conidia of *Ps. javanii* are smaller than *Ps. hagahagae* (conidial size; (38–)41–45(–49) × (7–)8(–9) µm).



Maximum Likelihood tree inferred with MEGA v. 6 software (Tamura et al. 2013) from the combined *CAL*, ITS and *RPB1* gene regions of 39 isolates. The novel species is shown in **bold**. Bootstrap support values from ML ≥ 90 % are provided above internodes.

Colour illustrations. *Cyperus* growing in Iran. Solitary, erect, unbranched conidiophore; obclavate conidia. Scale bars = 10 µm.

Adel Pordel, Plant Protection Research Department, Baluchestan Agricultural and Natural Resources Research and Education Centre, AREEO, Iranshahr, Iran; e-mail: a_pordel@areeo.ac.ir
Golzar Ghorbani, Department of Plant Protection, College of Agriculture and Natural Resources, University of Tehran, Karaj 31587-77871, Iran; e-mail: Golzar.ghorbani@ut.ac.ir


Pseudosubramaniomyces septatus

Fungal Planet 1170 – 19 December 2020

Pseudosubramaniomyces septatus Torres-Garcia, Gené, Dania García, *sp. nov.*

Etymology. Name refers to the presence of septate conidia.

Classification — *Beltraniaceae*, *Xylariales*, *Sordariomycetes*.

On potato carrot agar (PCA) at 25 °C. *Mycelium* partly superficial, partly immersed, composed of branched, septate, pale brown, smooth hyphae, 1.5–2 µm wide. *Conidiophores* solitary, erect, unbranched, septate, pale brown at the base, hyaline at the apex, smooth, subcylindrical, 9–66 × 2–3 µm. *Conidiogenous cells* integrated, terminal, polyblastic, sympodial, denticulate, with up to five denticles, hyaline, smooth, subcylindrical, 14–22 × 2–2.5 µm. *Conidia* dry, at first solitary, latter forming short branched or unbranched chains, dimorphic; apical conidia aseptate, pale brown, smooth, cylindrical to subcylindrical, with obtuse apex and truncate base, 27–34 × 2.5–4 µm; intercalary conidia (including ramoconidia), 0–1(–2)-septate, hyaline to subhyaline, smooth, fusoid or navicular, 12–24.5 × 2–4 µm. *Sexual morph* not observed.

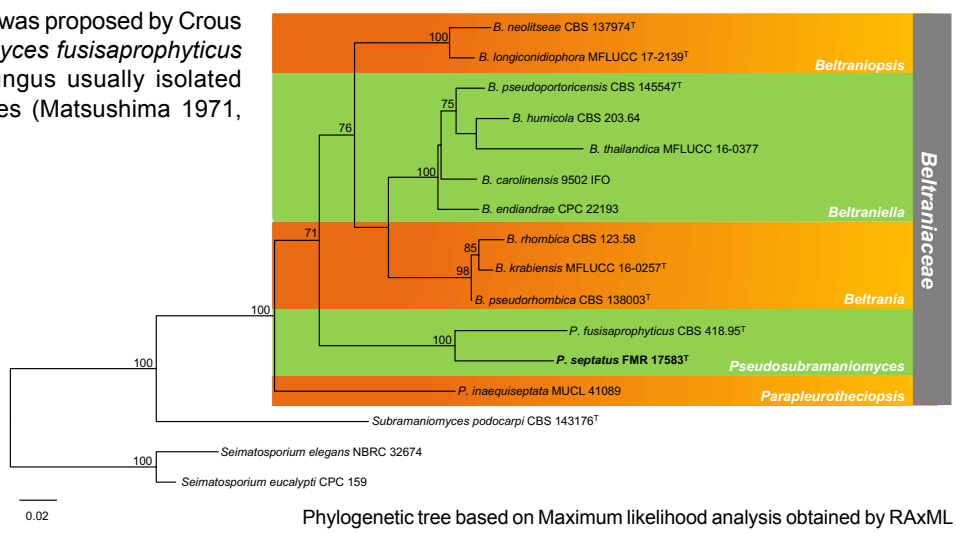
Culture characteristics at 25 °C after 1 wk — Colonies on PCA reaching 12–16 mm diam, slightly elevated, dull green (30E4) to white (1A1) (Kornerup & Wanscher 1978), velvety, regular margin; reverse dull green (30E4) to white (1A1); sporulation sparse. On potato dextrose agar (PDA) reaching 21 mm diam, slightly elevated, greyish brown (5E3) to white (1A1), velvety, regular margin; reverse yellowish white (3A2); sporulation absent. On oatmeal agar (OA) reaching 9–12 mm diam, flat, white (1A1), velvety, regular margin; reverse brownish grey (4F2) to greyish yellow (4C5); sporulation absent.

Cardinal temperature for growth — Opt 25 °C, max 30 °C, min 5 °C.

Typus. Spain, Catalonia, Barcelona province, Montseny Natural Park, El Sot de l'Infern stream, fluvial sediments, Oct. 2018, *D. Torres-Garcia* (holotype FMR H-17583, culture ex-type FMR 17583, also in CBS; LSU and ITS sequences GenBank LR700217 and LR700216, MycoBank MB837574).

Notes — *Pseudosubramaniomyces* was proposed by Crous et al. (2017a) based on *Subramaniomyces fusisaprophyticus* (= *Ramularia fusisaprophytica*), a fungus usually isolated from decaying leaves of different trees (Matsushima 1971, Kirk 1982). The genus is characterised by having solitary, unbranched conidiophores and terminal, polyblastic, denticulate conidiogenous cells, which give rise to catenate conidia. It resembles *Subramaniomyces* but differs by the lack of lateral conidiogenous cells and tends to have pale brown conidiophores, in contrast to the dark brown conidiophores observed in *Subramaniomyces* (Varghese & Rao 1980, Crous et al. 2017a). Of note however is that the presence of dimorphic conidia (i.e., hyaline to pale brown, ellipsoidal to broadly fusoid intercalary conidia vs elongate fusoid to acicular and brown terminal conidia), typical of *S. fusisaprophyticus* (Kirk 1982) and also observed in *P. septatus*, was not mentioned in the protologue of *Pseudosubramaniomyces*. *Pseudosubramaniomyces septatus* differs from *P. fusisaprophyticus* and other accepted species of *Subramaniomyces* (Varghese & Rao 1980, Braun & Hill 2002, Da Cruz et al. 2007, Crous et al. 2017a) mainly by the presence 0–2-septate intercalary conidia. Furthermore, *P. septatus* has longer intercalary (12–24.5 µm) and terminal (27–34 µm) conidia than those of *P. fusisaprophyticus,* which measure (13–)17–18.5(–21) µm and (18–)25–31 µm long, respectively (Kirk 1982).

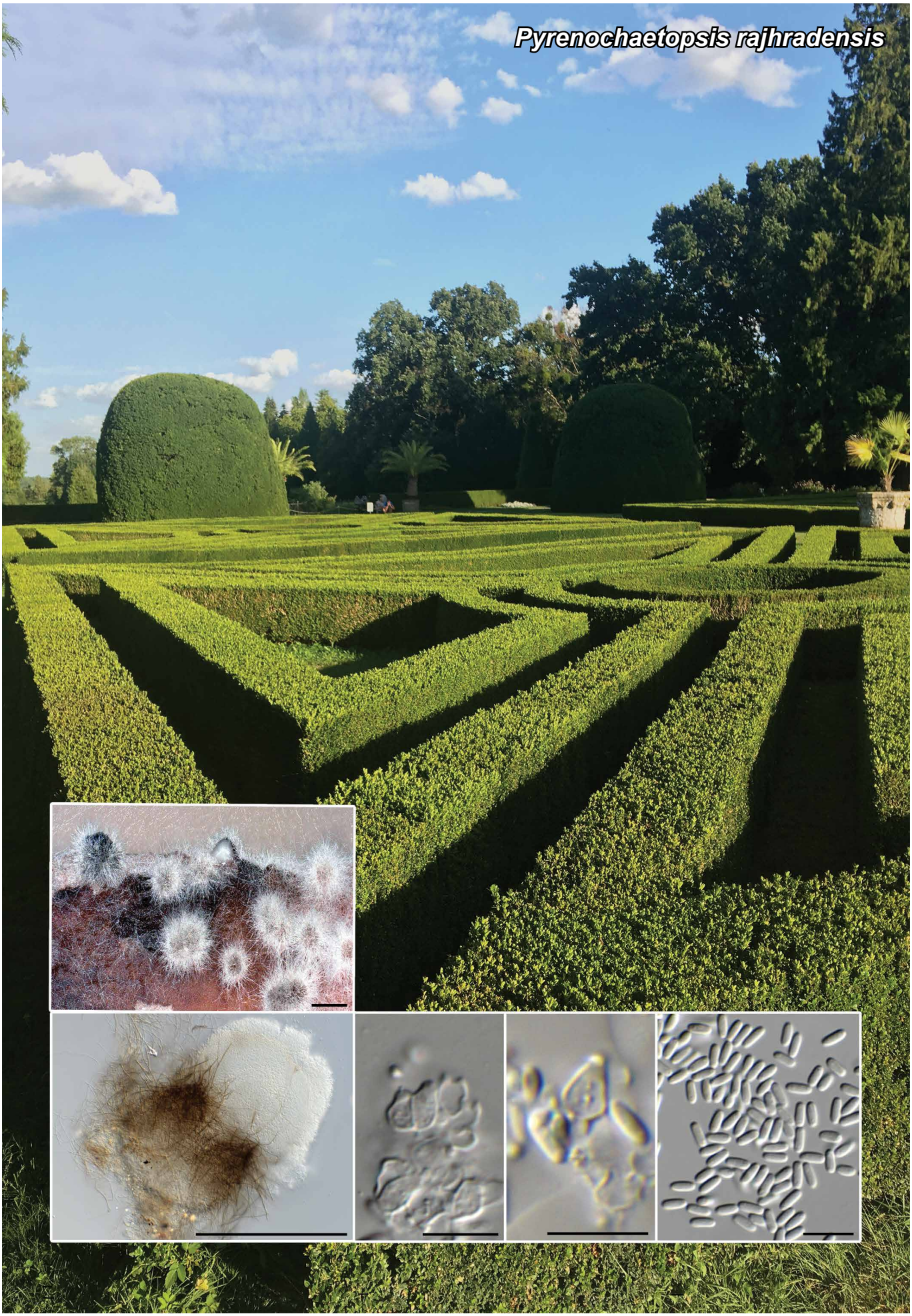
Our phylogenetic analysis using the barcodes LSU and ITS places *P. septatus* close to the species *P. fusisaprophyticus* in the family *Beltraniaceae*. A megablast search using **LSU** sequences shows that *P. septatus* has a similarity of 98.27 % (737/750) with *P. fusisaprophyticus* (CBS 418.95; GenBank EU040241.1) and 97.60 % (732/750) with *Beltraniopsis neolitseae* (CBS 137974; GenBank MH878610.1); meanwhile the similarity using **ITS** barcode was 91.24 % (500/548) with *P. fusisaprophyticus* (CBS 418.95; GenBank EU040241.1) and 90.42 % (500/553) with *B. neolitseae* (CBS 137974; GenBank NR148072.1).



Phylogenetic tree based on Maximum likelihood analysis obtained by RAxML using the combined LSU and ITS sequences of *Pseudosubramaniomyces* and related genera in the family *Beltraniaceae*. Bootstrap support values above 70 % are indicated on the nodes. The alignment included 1 530 bp and was performed using Kimura-2 parameter Gamma distribution with Invariant sites (G+I) as the best nucleotide substitution model. The tree was rooted with *Seimatosporium elegans* NBRC 32674 and *Seimatosporium eucalypti* CPC 159. The alignment was constructed with MEGA v. 6 software (Tamura et al. 2013). The new species proposed in this study is indicated in **bold** face. A superscript ^{T} denotes ex-type cultures.

Colour illustrations. Montseny Natural Park, Catalonia, Spain. Colony on PDA and PCA after 7 d at 25 °C; conidiophores and conidia after 14 d at 25 °C. Scale bars = 25 µm (habitat in PCA), 10 µm (microscopic structures in PCA).

Daniel Torres-Garcia, Josepa Gené & Dania García, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili, Sant Llorenç 21, 43201 Reus, Tarragona, Spain; e-mail: daniel.torres@urv.cat, josepa.gene@urv.cat & dania.garcias@urv.cat


Pyrenochaetopsis rajhradensis

Fungal Planet 1171 – 19 December 2020

Pyrenochaetopsis rajhradensis Spetik, Eichmeier & Berraf-Tebbal, *sp. nov.*

Etymology. Named after Rajhrad (Czech Republic) where the fungus was collected.

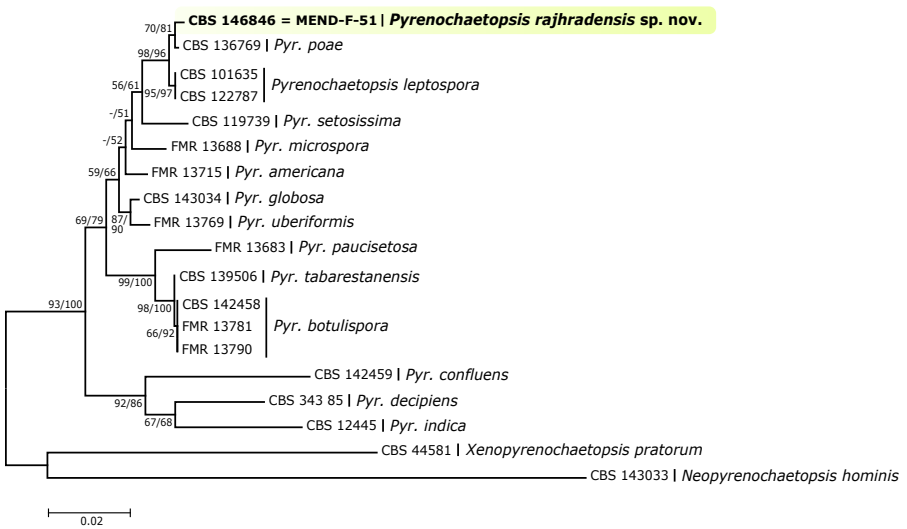
Classification — *Pyrenochaetopsidaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata pycnidial, brown, solitary or aggregated, semi-immersed, globose to ovoid, setose, ostiolate, uniloculate. *Conidiogenous cells* phialidic, hyaline, discrete and integrated. *Conidia* hyaline, aseptate, cylindrical to allantoid, guttulate, (3.6–)4.1–4.9(–5.7) × (1.4–)1.6–2.2(–2.4) µm (av. ± S.D. 4.5 ± 0.4 × 1.8 ± 0.2 µm, L/W ratio = 2.5). *Sexual morph* unknown.

Culture characteristics — Colonies on potato dextrose agar (PDA) reaching 23.8 mm diam at 25 °C after 10 d, margin regular, floccose, dirty white; reverse white. On malt extract agar (MEA) reaching 22 mm diam after 10 d, margin regular, floccose, dirty white; reverse white. On oatmeal agar (OA) reaching 25.8 mm diam after 10 d, margin regular, floccose, white; reverse white.

Typus. Czech Republic, Rajhrad, isolated as saprobe from dead wood of *Buxus sempervirens* (*Buxaceae*), July 2018, *M. Spetik* (holotype CBS H-24478, ex-type culture CBS 146846 = MEND-F-51, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT853115, MT853182, MT857727, MT857725 and MT857726, MycoBank MB836856).

Notes — Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Pyrenochaetopsis leptospora* (GenBank MT453283.1; Identities = 471/471 (100 %), no gaps), *Phoma* sp. (GenBank MN401018.1; Identities = 471/471 (100 %), no gaps) and *Pyrenochaetopsis leptospora* (GenBank LR216648.1; Identities = 471/471 (100 %), no gaps). The closest hits using the **LSU** sequence had the highest similarity to *Pyrenochaetopsis microspora* (GenBank NG_069864.1; Identities = 937/939 (99 %), no gaps), *Pyrenochaetopsis leptospora* (GenBank NG_069858.1; Identities = 937/939 (99 %), no gaps) and *Pyrenochaetopsis* sp. (GenBank KJ395496.1; Identities = 937/939 (99 %), no gaps); closest hits using the ***rpb2*** sequence are *Pyrenochaetopsis leptospora* (GenBank LT623283.1; Identities = 893/906 (99 %), no gaps and GenBank LT623282.1; Identities = 846/858 (99 %), no gaps), *Phaeopoacea festucae* (GenBank MF795835.1; Identities = 840/854 (98 %), 2/854 (0 %)) and *Pyrenochaetopsis poae* (GenBank LT623286.1; Identities = 864/906 (95 %), no gaps). The closest hits using the ***tef1-α*** sequence had the highest similarity to *Pyrenochaetopsis leptospora* (GenBank MF795881.1; Identities = 266/281 (95 %), 3/281 gaps (1 %)), *Parastagonospora novozelandica* (GenBank MK540151.1; Identities = 57/58 (98 %), no gaps) and *Parafenestella rosacearum* (GenBank MK357586.1; Identities = 186/245 (76 %), 27/245 gaps (11 %)). The closest hits using the ***tub2*** sequence had the highest similarity to *Pyrenochaetopsis poae* (GenBank KJ869243.1; Identities = 407/407 (100 %), no gaps), *Pyrenochaetopsis leptospora* (GenBank MF795917.1; Identities = 402/407 (99 %), no gaps and GenBank LT623242.1; Identities = 325/332 (98 %), no gaps).



Maximum likelihood tree obtained from the ITS, *tub2*, LSU and *rpb2* gene sequences of *Pyrenochaetopsis* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 7.0 (Kumar et al. 2016). The combined LSU, ITS, *tub2* and *rpb2* sequence data set consisted of 17 *Pyrenochaetopsis* strains with *Xenopyrenochaetopsis pratorum* and *Neopyrenochaetopsis hominis* as the outgroup taxa and consisted of 2 195 characters. Of these 1 643 were constant, 188 were variable and parsimony-uninformative and 337 were parsimony-informative. A heuristic search of these 337 parsimony-informative characters resulted in 1 000 equally parsimonious trees of 467 steps with CI = 0.72, RI = 0.65 and HI = 0.28. The ML analysis yielded a best scoring tree with the final ML optimization likelihood value of –4554.41 (ln) and a gamma distribution shape parameter value of α = 0.1411. All individual trees obtained from single gene datasets were essentially similar in topology and not substantially different from the tree generated from the concatenated dataset. One of the two ML trees obtained is presented with ML/MP bootstrap support values at the nodes. The alignment and tree are available in TreeBASE (Submission ID: 26835).

Colour illustrations. Buxus sempervirens growing in Lednice castle garden. Pycnidia forming on sterile poplar twig on WA; pycnidium in culture oozing conidia; conidiogenous cells; conidia. Scale bars = 200 µm (pycnidia), 10 µm (all others).

Milan Spetik, Akila Berraf-Tebbal & Ales Eichmeier, MENDELEUM – Institute of Genetics, Mendel University in Brno, Valticka 334, 69144, Czech Republic; e-mail: milan.spetik@mendelu.cz, ales.eichmeier@mendelu.cz & qqberraf@mendelu.cz
Alla Eddine Mahamedi, Laboratoire de Biologie des Systèmes Microbiens (LBSM), Département des Sciences Naturelles, Ecole Normale Supérieure de Kouba, Alger BP 92, Vieux-Kouba, Alger, Algeria; e-mail: aladin1342@yahoo.com


Russula shawarensis

Fungal Planet 1172 – 19 December 2020

Russula shawarensis Kiran & Khalid, *sp. nov.*

Etymology. The specific epithet, *shawarensis*, refers to the Shawar Valley, the locality from where the type was collected.

Classification — *Russulaceae*, *Russulales*, *Agaricomycetes*.

Pileus medium to large-sized, 40–90 mm diam, semi-globose, convex to hemispheric, expanding plane and centrally slightly depressed; cuticle thin, adnate, hardly peeling, areolate; margin incurved and entire when young, later recurved, when mature radially splitting; surface matt, smooth, light pinkish brown (9.3 R 6.4/0.9) to grey buff (4.1 GY 7/0.3), discolouring to light brown (0.6Y 5.8/2.2) (Kornerup & Wanscher 1978). *Lamellae* moderately distant, adnate-emarginate, equal, frequently forking, brittle, cream white, spotted light yellow-brown after handling, lamellulae very rare to absent, edge even, concolorous. *Stipe* 25–60 × 10–12 mm, obclavate, central, velvety, white with yellow-brown to brown spots, especially near the base. *Context* white, changing to yellowish brown upon bruising, compact. *Spores* (5.9–)6.6–7.8(–9.2) × (5.1–)5.7–6.7(–8.6) µm, av. 7.2 × 6.2 µm, subglobose to broadly ellipsoid, Q = (1.0–)1.08–1.26(–1.4), Q_{av} = 1.17; ornamentation of small, distant to moderately distant (4–5(–6) in a 3 µm diam circle) amyloid spines, (0.8–)0.9–1.1(–1.2) µm high, radially oriented from suprahilar spot, occasionally fused in pairs, ((0–)1(–2) fusions in the circle), connected by dispersed fine line connections ((0–)1–2(–3) in the circle); suprahilar spot distinct, not amyloid or with few small amyloid dots. *Basidia* (31.5–)34–39.5(–41) × (7–)9–10.5(–11) µm, av. 37 × 10 µm, 2–4-spored, clavate; basidiola first cylindrical or ellipsoid, then clavate, c. 4–10 µm wide. *Hymenial cystidia* on lamellar sides widely dispersed, 200–300/mm², (66–)72–92.5(–105) × (9.5–)10–13(–14) µm, av. 82.1 × 11.4 µm, fusiform or rarely clavate, often pedicellate, apically acute or sometimes obtuse and mostly with 4–17 µm long appendage; contents heteromorphous, crystalline-banded, turning brown to almost greyish black in sulfovanillin; abundant near the lamellae edges, (55–)61–76(–88) × (6–)8–11.5(–13.5) µm, av. 68.5 × 9.6 µm, more frequently clavate, sometimes also cylindrical, usually obtuse, frequently apically constricted or appendiculate. *Lamellar edges* fertile; marginal cells not well differentiated, smaller, c. 10–20 × 4–5 µm, cylindrical or clavate. *Pileipellis* orthochromatic in Cresyl blue, not sharply delimited from the underlying context, 175–200 µm deep, strongly gelatinised; suprapellis 45–55 µm deep, disconnected, of dense, ascending and near the surface repent hyphal terminations; gradually passing to 45–120 µm deep subpellis of irregularly oriented, intricate, (2.5–)3–4(–4.5) µm wide hyphae. Acid-resistant incrustations absent. *Hyphal terminations in pileipellis* near the pileus margin, composed of 2–3 unbranched cells with the basal cell often shorter and inflated, often slightly flexuous, thin-walled; terminal cells (23–)33–63.5(–81) × (2.5–)3–4.5(–5) µm, av. 48.2 × 3.8 µm, mainly cylindrical, apically often slightly attenuated; subterminal cells usually equally wide and sometimes shorter, usually unbranched. Hyphal terminations near the pileus centre slightly smaller, terminal cells (23–)32–51(–64.5) × (3–)3.5–5(–7) µm, av. 41.5 × 4.2 µm, subterminal and lower cells more frequently inflated. *Pileocystidia* near the pileus margin very abundant, mainly one-celled, cylindrical to narrowly clavate, thin-walled, terminal cells (31.5–)33–90(–155) × (4.5–)6–8(–9) µm, av. 61.6 × 6.7 µm, apically mainly obtuse, contents heteromorphous, slowly turning greyish in sulfovanillin. Pileocystidia near the pileus centre similar, terminal cells (22–)30–86(–166) × (5–)6–8.5(–9.5) µm, av. 58 × 7 µm. Cystidioid hyphae in subpellis and context dispersed, contents heteromorphous-banded.

Typus. Pakistan, Khyber Pakhtunkhwa province, Malakand division, Swat district, Lower Shawar, alt. 1200 m, on the floor of *Quercus floribunda* dominated moist temperate forest mixed with a few pines, 7 Sept. 2015, *Z. Ullah & M. Kiran* MK-KS49 (holotype LAH 35453, ITS and LSU sequences GenBank MT738294 and MT738269, MycoBank MB836118).

Additional materials examined. Pakistan, Khyber Pakhtunkhwa province, Malakand division, Swat district, Lower Shawar, alt. 1200 m, on the floor of *Quercus floribunda* dominated moist temperate forest mixed with a few pines, 7 Sept. 2015, *Z. Ullah* MK-KS26 (LAH 35452, ITS, LSU and *rpb2* sequences GenBank MT738291, MT738266 and MT732175,); ibid., 26 July 2018, *Z. Ullah & J. Khan* AS 48 (LAH36424, ITS, LSU and *rpb2* sequences GenBank MT738290, MT738265 and MT732174); AS 61 (LAH36425, ITS, LSU and *rpb2* sequences GenBank MT738292, MT738267 and MT732176); AS 75 (LAH36426, ITS, LSU and *rpb2* sequences GenBank MT738293, MT738268 and MT732177).

Notes — The ITS sequence of the type collection has the closest GenBank BLAST match (97.8 %) with a sequence identified as *Russula atroglauca* originating from Kyrgyzstan (GenBank MK351735). More than 80 sequences that fall in the UNITE species hypothesis SH1423803.08FU of *R. atroglauca* (www/unite.ut.ee) are within 96 % GenBank BLAST identity. To distinguish the Pakistani collections from *R. atroglauca* and other European species of the section *Griseinae*, we performed phylogenetic multilocus analysis of ITS, LSU and *rpb2* regions (for the phylogenetic tree and analysed sequences see Supplementary material FP1172-1+2). To avoid misidentification

(text continues on Supplementary material page FP1172)

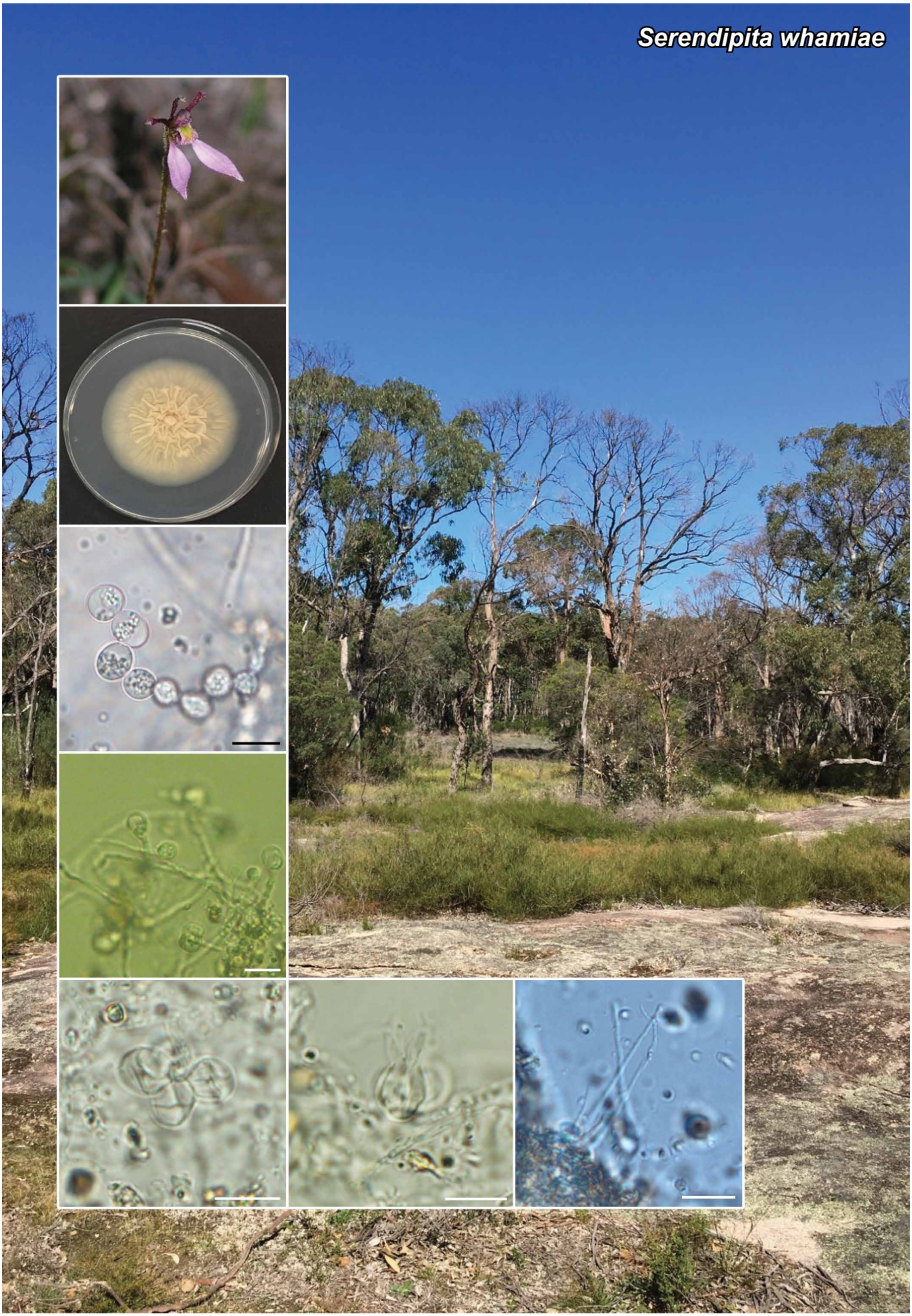
Colour illustrations. *Quercus floribunda* dominated forest in Lower Shawar (Khyber Pakhtunkhwa province, Pakistan) where the holotype was collected. Left top: Pileal surface of collection LAH 35453. Centre bottom: basidiomata of collection LAH 35452. Right top: Scanning electron photograph of spores from LAH 35452. Line drawings all from the holotype LAH 35453. Right bottom: basidia and basidiola (left top), marginal cells (centre) and spores (left bottom), hymenial cystidia near the lamellae edges (right top) and lamellae sides (right bottom). Left bottom: pileocystidia near the pileus centre (left top) and near the pileus margin (left bottom), hyphal terminations near the pileus centre (right top) and near the pileus margin (right bottom) from holotype. Scale bars = 10 mm (basidiomata), 5 µm (spores), 10 µm (all other microscopic structures).

Supplementary material

FP1172-1 Maximum likelihood phylogeny estimated for members of subsection *Griseinae* inferred from ITS, LSU and *rpb2* regions in RAxML-173 HPC2 v. 8.2.10 (Stamatakis 2015), with rapid bootstrapping (1000 iterations), computed on the CIPRES web server (www.phylo.org; Miller et al. 2010) under default settings including a General Time Reversible (GTR) + Gamma (G) model of sequence evolution. Bootstrap support values followed by Bayesian posterior probabilities computed in MrBayes v. 3.2 (Ronquist et al. 2012) are indicated at the nodes. Species names are followed by herbarium codes and country of origin.

FP1172-2 List of samples and sequences used.

Munazza Kiran, Zia Ullah & Abdul Nasir Khalid, Department of Botany, University of the Punjab, Quaid-e-Azam campus, Lahore 5090, Pakistan; e-mail: munazzakiran@gmail.com, ziaullah.phd.mmg@pu.edu.pk & drankhalid@gmail.com
Miroslav Caboň, Institute of Botany, Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Dúbravská cesta 9, SK-84523, Bratislava, Slovakia; e-mail: miroslav.cabon@gmail.com
Felix Hampe, Wetzlarer Strasse 1, 35510 Butzbach, Germany; e-mail: felix.hampe@email.de


Serendipita whamiae

Fungal Planet 1173 – 19 December 2020

Serendipita whamiae Dearnaley, T.W. May & Linde, *sp. nov.*

Etymology. Named in honour of the well-known naturalist of the Stanthorpe region, Dell Wham.

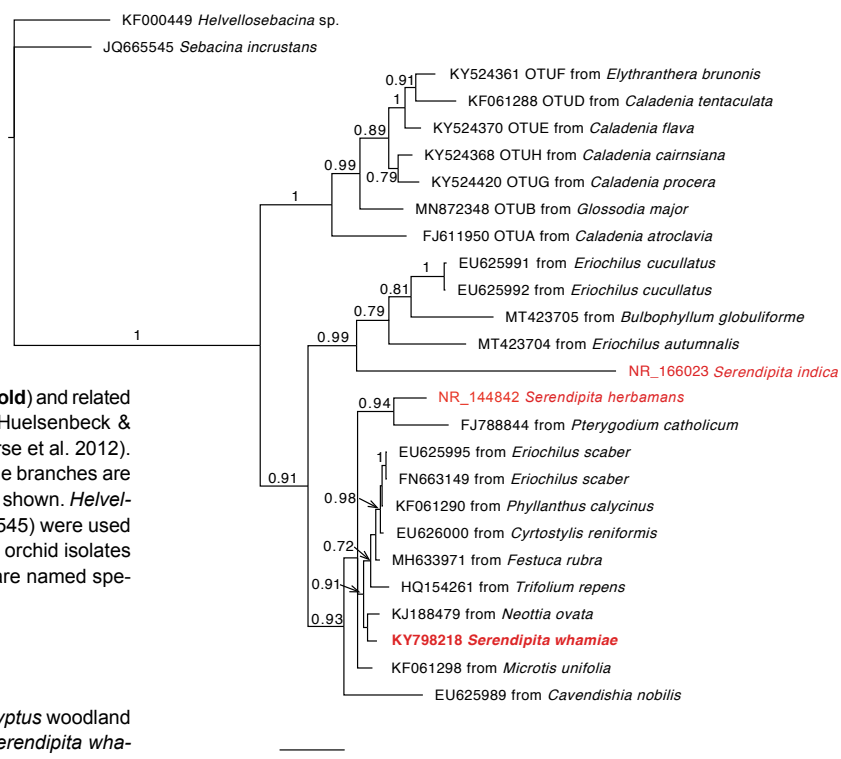
Classification — *Serendipitaceae*, *Sebacinales*, *Agaricomycetes*.

Sporophore produced by the soil on agar method (Warcup & Talbot 1967), grey, resupinate hyphae occurring loosely on the surface of soil clods. *Probasidia* globose 5–9 µm to subglobose 7–9 × 6–8 µm diam, some with sub-basidial cells. *Metabasidia* crucially septate, in groups of 2–3 on short stalks from hyphae, globose, 7 µm diam, to subglobose, 6–8 µm diam. *Basidia* ovate, 7–11 × 6–7 *µm* diam, longitudinally septate, with 2–4 sterigmata. *Sterigmata* 5–21 µm long, narrowing at apex. *Basidiospores* vermiform, some with septa, 11–50 × 1–2 µm diam.

Culture characteristics — Colonies on potato dextrose agar (PDA) up to 6 cm diam after 3 wk growth at 22 °C, pinkish buff, flattened, without aerial mycelium, margins irregular, surface wrinkled in the central part, reverse pinkish buff. *Hyphae* hyaline, thin-walled, lacking clamps, 2 µm in width. *Monilioid cells* globose, 7 µm diam to subglobose, 6–11 × 5–10 µm diam, in chains.

Typus. Australia, Queensland, Stanthorpe, Girraween National Park, open *Eucalyptus* woodland, S27°49'13" E151°58'47", alt. 1008 m, isolated as an endophyte from roots of *Eriochilus cucullatus* (*Orchidaceae*), 7 Apr. 2016, *J.D.W. Dearnaley* EC3A (holotype BRIP 71159 living culture stored in a metabolically inactive state, ITS and LSU sequences GenBank KY798218 and MT422063, MycoBank MB835492).

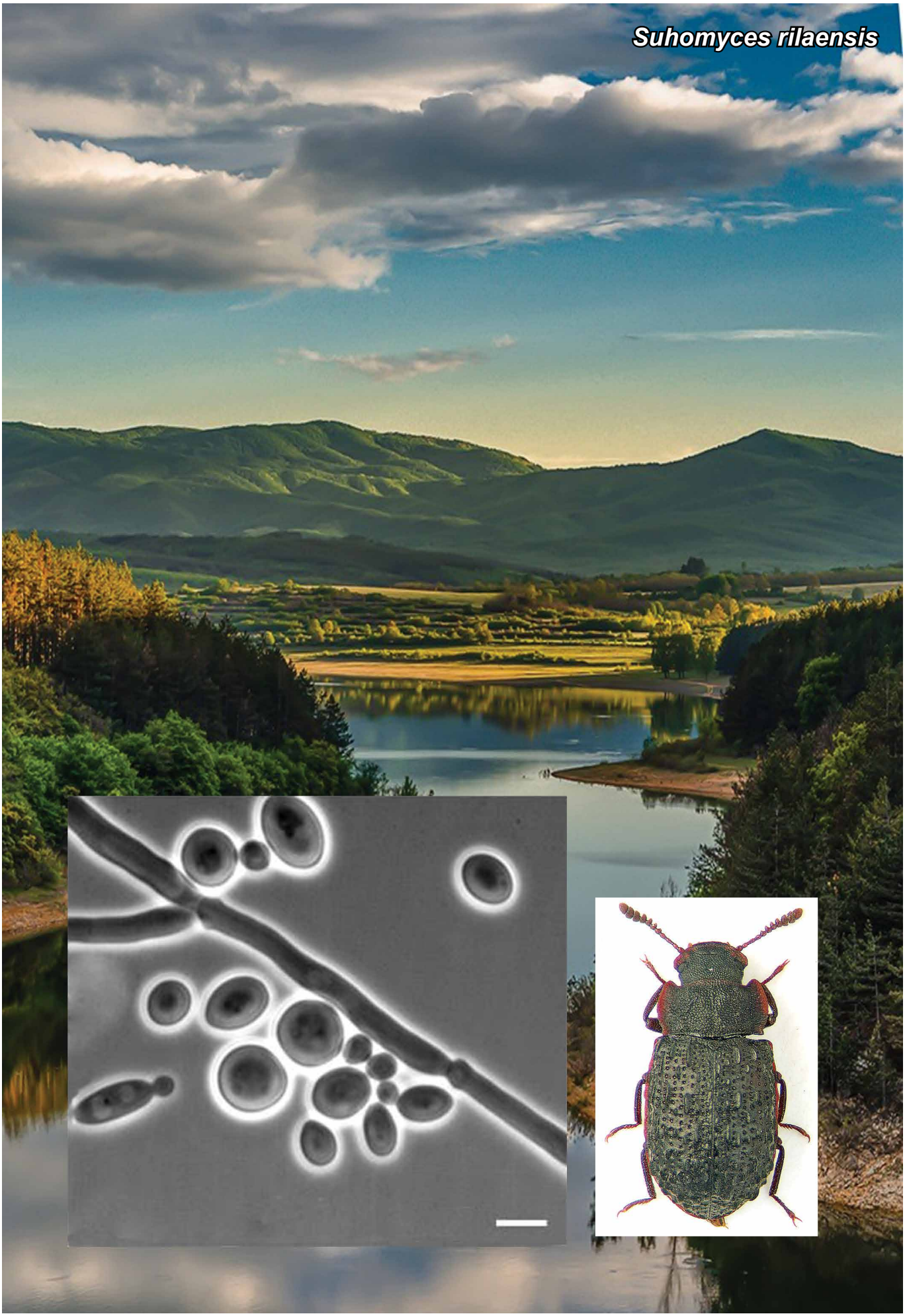
Notes — *Serendipita* is a genus of Agaricomycetous fungi, many of which occur as endophytes in the roots of grasses, ericoids, liverworts and orchids (Weiss et al. 2016). The group is characterised by longitudinally septate basidia, long, worm-like basidiospores and DNA sequence data (Oberwinkler 1964, Roberts 1993, Basiewicz et al. 2012, Riess et al. 2014). *Serendipita whamiae* is a new species of *Serendipitaceae* with morphological similarities to the type species, *S. vermifera*, including probasidia 5–9 µm, longitudinally septate basidia and vermiform basidiospores, although the latter are shorter (11–50 µm) than that described by Oberwinkler (1964), Warcup & Talbot (1967) and Roberts (1993) at 30–60 µm, 45–64 µm, 21–86 µm, respectively. Compared to sequenced, named species within *Serendipita*, *S. whamiae* is distinct on BLAST matches from *S. herbamans* (ITS; 87 % identity over 637 bp; GenBank NR_144842) and *S. indica* (ITS; 68 % identity over 685 bp; GenBank NR_166023) and also from the type of the genus, *S. vermifera* (LSU; 87 % identity over 568 bp; GenBank HM030724). Otherwise, there is a series of unnamed environmental and endophyte sequences (EU625995 to KY798218) that form a well-supported clade including the sequence from the type of *S. whamiae* (all within 96 % similarity) that could prove conspecific, but for which morphological data is not available. Whitehead et al. (2017) found that *Serendipita* defined by multigene species delimitation had maximum within species variation of 4.1 % for ITS.



Bayesian inference tree of ITS sequences from *S. whamiae* (**bold**) and related *Sebacinales* species in GenBank using MrBayes v. 3.2.7 (Huelsenbeck & Ronquist 2001) as implemented in Geneious v. 10.2.6 (Kearse et al. 2012). ClustalW was used for the alignment. The numbers above the branches are Bayesian posterior probabilities with values less than 0.7 not shown. *Helvellosebacina* sp. (KF000449) and *Sebacina incrustans* (JQ66545) were used as outgroups. Sequences labelled OTUA etc. are Australian orchid isolates categorised by Whitehead et al. (2017). Sequences in red are named species of *Serendipita*.

Colour illustrations. *Eriochilus cucullatus* (inset) in *Eucalyptus* woodland at Girraween National Park (Photo credit Ian Milinovich). *Serendipita whamiae* (clockwise from top left) colony on PDA; monilioid cells; probasidia; metabasidia; basidium; basidiospores. Scale bars = 1 cm (colony and inset), 10 µm (all others).

John D.W. Dearnaley, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: john.dearnaley@usq.edu.au
Tom W. May, Royal Botanic Gardens Victoria, Birdwood Ave, Melbourne, VIC 3004, Australia; e-mail: tom.may@rbg.vic.gov.au
Celeste Linde, Ecology and Evolution, Research School of Biology, College of Science, The Australian National University, Canberra, ACT, 2601, Australia; e-mail: celeste.linde@anu.edu.au


Suhomyces rilaensis

Fungal Planet 1174 – 19 December 2020

Suhomyces rilaensis R.A. Dimitrov & Gouliamova, *sp. nov.*

Etymology. *Ri-la-en-sis*, referring to the locality *Rila National Park* from which this species was is olated.

Classification — Incertae sedis, *Saccharomycetales*, *Saccharomycetes.*

After 7 d at 25 °C in 5 % glucose-yeast extract broth, *cells* are spherical, subglobose, ellipsoidal and oblong, 2–7 × 2–9 µm, occurring singly or in clusters. *Asexual reproduction* is by multilateral budding. After 7 d at 25 °C on 5 % malt extract agar (MEA) the *culture* is cream, butyrous, smooth, glistening, convex and with an entire margin fringed with filaments. Dalmau plate culture after 10 d on yeast morphology agar results in the formation of pseudohyphae. *Aerobic growth* is dimorphic, center is erased, and the margin is completely eroded, fringed with filaments. *Ascospore production* was not detected either alone or in pairs on yeast extract, malt extract agar (YMA), 5 % MEA, McClary acetate agar, potato dextrose agar (PDA), malt agar (MA2) and diluted V8 agar.

Fermentation — Glucose is fermented. Galactose, maltose, sucrose, lactose and raffinose are not fermented.

Carbon assimilation — D-glucose, D-galactose, D-glucosamine (+,w), D-ribose, D-xylose, α,α-trehalose, cellobiose (+,w), salicin, arbutin, glycerol, meso-erythritol, ribitol, xylitol (+,w), D-glucitol, D-mannitol, Glucono b-lactone (+,w), 2 keto-D-gluconate, D-gluconate (w,-), succinate, citrate, ethanol and propane 1,2 diol are assimilated. L-Sorbose, L-arabinose, D-arabinose, L-rhamnose, sucrose, maltose, methyl α –glucoside, melibiose, lactose, raffinose, melezitose, inuline, soluble starch, galactitol, myo-inositol, D-glucuronate, D-galactouronate, DL-lactate, methanol, butane 2,3 diol, quinic acid, saccharate and galactonic acid are not assimilated.

Nitrogen assimilation — Nitrite, ethylamine, L-lysine are assimilated. Nitrate, creatine, creatinine, N-acetyl- glucosamine and imidazole are not assimilated.

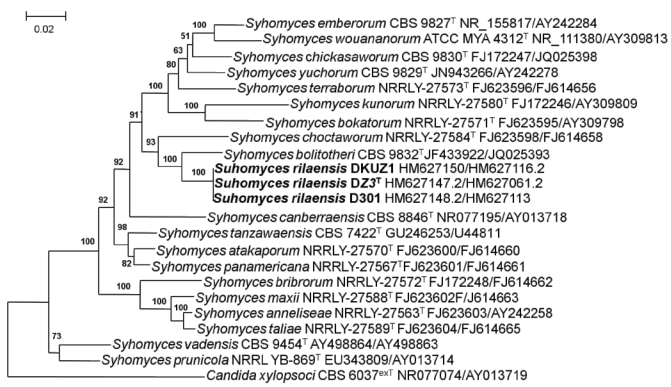
Other tests — Growth in medium containing 0.01 and 0.1 % cyclohexemide is negative. Growth in medium containing 50 % and 60 % glucose is negative. Starch production, urea and DBB tests are negative. Growth in medium containing 10 % NaCl is positive. Growth in 15 % NaCl is negative. Growth at 25 °C, 30 °C, 35 °C and 37 °C is positive. Growth at 42 °C is negative. Growth without all vitamins test is negative.

Typus. Bulgaria, in Podgorie area below Samuilovo village, from the gut of *Bolitophagus interruptus* found on a *Polyporus* sp., *D. Gouliamova* (holotype DZ3 preserved in metabolically inactive state in the yeast collection of the Institute of Microbiology, Sofia, Bulgaria. The ex-type culture is deposited at National bank for microorganisms and cell cultures (NBIMCC), Sofia Bulgaria, and at the CBS-KNAW culture collection of Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands as NBIMCC 8930 = CBS 12453; D1/D2 LSU and ITS sequences GenBank HM627113 and HM627148, MycoBank MB802451).

Additional materials examined. Bulgaria, in vicinity of Rila monastery, strain isolated from the gut of *Bolitophagus reticulatus,* D301 = NBIMCC 8929 = CBS 12443, D1/D2 LSU and ITS sequences GenBank HM627061 and HM627147; DKUZ1 isolated from unidentified grasshopper (*Orthoptera*), NBIMCC 8931 = CBS 12460, D1/D2 LSU and ITS sequences GenBank HM627116 and HM627150.

Colour illustrations. A view of reservoir Koprinka in Rose Valley, Bulgaria. Morphology of cells of *Suhomyces rilaensis* DZ3^{T} in 5 % glucose broth after 1 wk; *Bolitophagus interruptus* (Photo credits to S. Zayakov and K. Makarov, https://www.zin.ru/Animalia/Coleoptera/eng/bolintkm.htm). Scale bar = 5 µm.

Notes — *Suhomyces tanzawaensis* was isolated from mosses in Japan (Nakase et al. 1988) and had no known close relatives for a long time. In 2001 six additional species were isolated from mushrooms, plants and insect frass (Kurtzman 2001). Suh et al. (2004) isolated 16 new yeast species belonging to the clade from the gut of mushroom feeding insects (Suh et al. 2004). Kurtzman et al. (2016) proposed a new genus *Suhomyces* to accommodate members of the clade. During a yeast biodiversity survey conducted in Bulgaria in 2008–2011 three conspecific yeast strains (100 % identity in both LSU nrDNA and ITS nrDNA sequences) belonging to the genus *Suhomyces* were isolated from the gut of beetles. Three strains, DZ3, D301 and DKUZ, have the most similar sequences in the database belonging to *S. bolitotheri* (97 % identity in LSU nrDNA sequence) and *S. tanzawaensis* (88 % identity in ITS1+2 nrDNA sequence), thus indicating that the three Bulgarian strains represent a new yeast species. Phylogenetic analysis of combined LSU rDNA and ITS sequences placed the new species and *S. bolitotheri* in a separate subclade (100 % support). Pairwise analysis of the sequences from multiple alignment data showed that the new strains show 73 % similarity (242 identical nt.: 626 subst., 36 gaps) in ITS-LSU nrDNA with *S. bolitotheri* and 75 % similarity (248 identical nt.: 622 subst., 86 gaps) with *S. choktaworum*. The results of the phylogenetic analyses were confirmed by the comparative analysis of physiological profiles of the yeast strains and closest relatives on the phylogenetic tree. The analysis showed that six physiological characteristics distinguish the new strains from *S. bolithoteri*. The new species is not able to ferment galactose, is able to assimilate propane 1,2 diol and is not able to assimilate L-sorbose. Growth in the presence of 16 % NaCl, 50 % and 60 % glucose, and in the presence of 0.01 cycloheximide is negative. Nine characteristics distinguished the new strains from *S. choctaworum.* The new species is not able to ferment galactose, is not able to assimilate L-sorbose, L-arabinose and D-arabinose. Growth in the presence of 16 % NaCl, 50 % and 60 % glucose, and in the presence of 0.01 and 0.1 % of cycloheximide is negative.



Phylogenetic tree obtained by the analysis of combined ITS and LSU nrDNA sequences of *Suhomyces rilaensis* DZ3^{T} and related species using a neighbour-joining method (Kimura two-parameter model; MEGA v. 7; 100 bootstrap replicates).

Dilnora E. Gouliamova & Roumen Dimitrov, The Stephan Angeloff Institute of Microbiology, Bulgarian Academy of Sciences, 26 Acad. Georgi Bonchev, Sofia 1113, Bulgaria; e-mail: dilnorag@gmail.com & roumen.dimitrov@gmail.com


Tolypocladium flavonigrum

Fungal Planet 1175 – 19 December 2020

Tolypocladium flavonigrum Noisripoom, Tasanathai, Khonsanit & Luangsa-ard, *sp. nov.*

Etymology. Named after the colour of fresh stromata, from the Latin '*flavo'* meaning yellow, and '*nigrum'* meaning black.

Classification — *Ophiocordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Single or multiple stromata emerging directly from the ground growing on unidentified *Elaphomyces* sp., clavate, 15–30 mm long, 1–2 mm wide, yellowish green when immature, black when mature. Terminal part of the stroma fertile, capitate, yellow black to black, 2–5 mm diam. *Perithecia* crowded, ordinal in arrangement, completely immersed, elongate-ovoid, (560–)567–697(–750) × (200–)206–248(–250) µm. *Asci* cylindrical, 8-spored, (318–)330–416(–482) × 7–8 µm with thickened ascus caps, 4.5–5 × 5 µm. *Ascospores* hyaline, filiform, (310–)330–375(–395) × 1.5–2 µm, breaking into 64 cylindrical part-spores, 2–5 × 1.5–2 µm.

Culture characteristics — (Colonies developed from germinating ascospores. Ascospores germinated within 24 h on potato dextrose agar (PDA). Colonies on PDA moderately growing, funiculose, c. 10 mm diam after 3 w at 25 °C. Colonies white to smoke grey with age. Colonies reverse cream. *Conidiophores* erect, arising from vegetative hyphae. *Conidia* single-celled, hyaline, smooth, globose, 3–5 µm diam, produced in slimy heads.

Typus. Thailand, Kalasin Province, Khok Pa Si Community Forest, on *Elaphomyces* sp., underground, 14 Aug. 2013, *K. Tasanathai, W. Noisripoom & A. Khonsanit* (holotype BBH37600, culture ex-type BCC66576 = MY08887, ITS, LSU and *tef1* sequences GenBank MN338090, MN337287 and MN338495, MycoBank MB832658).

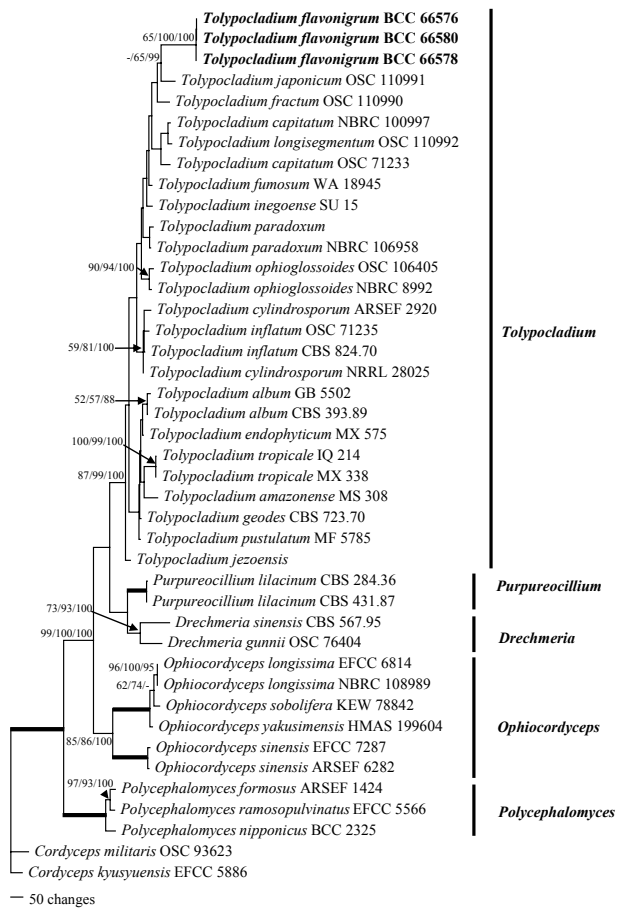
Additional material examined. Thailand, Kalasin Province, Khok Pa Si Community Forest, on *Elaphomyces* sp., underground, 14 Aug. 2013, *K. Tasanathai, W. Noisripoom & A. Khonsanit*, BBH37601, culture BCC66578, ITS, LSU and *tef1* sequences GenBank MN338091, MN337288 and MN338496; ibid. BBH37602, culture BCC66580 LSU, *tef1* and *rpb1* sequences GenBank MN337289, MN338497 and MN338494.

Notes — *Tolypocladium flavonigrum* is a rare species in Thailand found only in Khok Pa Si Community Forest*, Kalasin province.* Compared with other species occurring on *Elaphomyces* sp., *T. flavonigrum* shows similarity to *T. fractum* (Mains 1957) in the colour and shape of the fertile head as well as in the size and shape of the ascospores but differ in the size of perithecia and asci. *Tolypocladium flavonigrum* produces elongate, ovoid perithecia and asci, which are broader than *T. fractum* (500–600 × 220–260; 300–480 × 5–6 µm, respectively). *Tolypocladium japonicum* (Mains 1957) possesses a clavate fertile head and is distinct from all known species on truffles, while both *T. capitatum* (Mains 1957) and *T. longisegmentum* possess a yellowish stipe and reddish brown fertile part of the stromata, and differ mainly by the length of their part-spores: *T. longisegmentum* has the longest part-spores (40–65 × 4–5 µm) followed by *T. capitatum*, *T. japonicum* and *T. flavonigrum* (8–32 × 2.5–3; 10–18 × 2.5–4; 2–5 × 1.5–2 µm), respectively.

Colour illustrations. Type locality – a small plot in Khok Pa Si Community Forest. Stroma on *Elaphomyces* sp.; immersed, elongate ovoid perithecia; part of asci showing asci tips; ascospore; part-spores; colonies on PDA; conidiophores with conidia; conidia. Scale bars =10 mm (stromata and plate culture), 100 µm (perithecia), 10 µm (asci and ascospore), 5 µm (part-spores, conidiophores with conidia and conidia).

The results of our phylogenetic study using LSU, *tef1* and *rpb1* sequences clearly separates *T. flavonigrum* from other species.

Based on a megablast search of NCBIs GenBank nucleotide database, the LSU sequence of *Tolypocladium flavonigrum* had the highest similarity to *T. japonicum* (strain OSC 110991, GenBank DQ51876.1; Identities = 850/908 (94 %), 33 gaps (3 %)), the closest hits using the *tef1* sequence are *T. japonicum* (strain OSC 110991, GenBank DQ522330.1; Identities = 880/921 (96 %), no gaps), the closest hits using the *rpb1* sequence are *T. japonicum* (strain OSC 110991, GenBank DQ522375.1; Identities = 534/566 (94 %), 3 gaps (0 %)).



Phylogenetic tree with *T. flavonigrum* constructed from a combined dataset comprising LSU, *tef1* and *rpb1*. The phylogenetic tree was analysed using Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference. The MP analysis was conducted on the combined data set using PAUP v. 4.0b10 (Swofford 2003), adopting random addition sequences (100 replications), with gaps being treated as missing data. A bootstrap (BP) analysis was performed using the maximum parsimony criterion in 1000 replications. The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) under a GTR model, with 1000 bootstrap replicates. Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), with 5 M generations and under the same model. Numbers at the significant nodes represent MP bootstrap support values/RAxML bootstrap support values/Bayesian posterior probabilities (BPP) times 100. Thickened lines in the tree represent 99–100 % bootstrap support values and 99–100 BPP.

Supplementary material

FP1175 List of species and GenBank accessions numbers of sequences used in this study.

Kanoksri Tasanathai, Wasana Noisripoom, Artit Khonsanit & Jennifer Luangsa-ard, Plant Microbe Interaction Research Team, Bioscience and Biotechnology for Agriculture, BIOTEC, 113 Thailand Science Park, Pathum Thani 12120, Thailand; e-mail: tasanatai@biotec.or.th, wasana.noi@biotec.or.th, Artit.kho@biotec.or.th & jajen@biotec.or.th


Tuber lusitanicum

Fungal Planet 1176 – 19 December 2020

Tuber lusitanicum Ant. Rodr. & Muñoz-Mohedano, *sp. nov.*

Etymology. Referring to Lusitania, the name given by the Romans to the western region of the Iberian Peninsula, which now covers the Portuguese area below Douro river and the neighbouring regions of Spanish Extremadura.

Classification — *Tuberaceae*, *Pezizales*, *Pezizomycetes*.

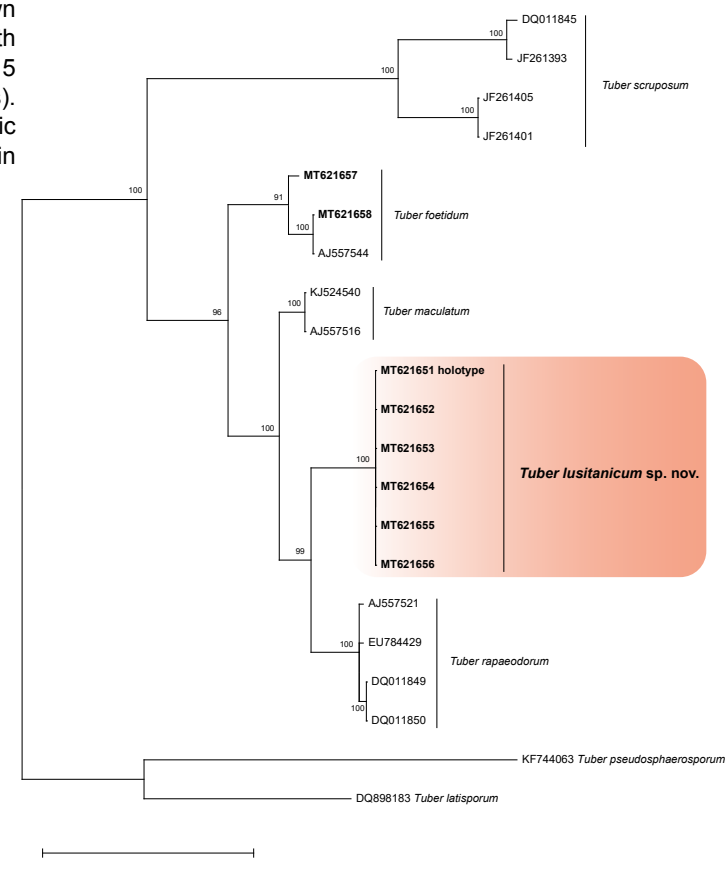
Ascomata hypogeous, 0.5–2 cm in size, subglobose, often lobed or irregular in form, solid, firm, white at first, becoming white-cream, pale yellowish, sometimes with a reddish tinge, darker at maturity, smooth. *Peridium* 300–500 µm thick, two-layered: the outermost pseudoparenchymatous, composed of subglobose or subangular cells, mostly 10–20 µm diam, yellowish, thick-walled, giving rise to hairs at the surface overlying; the inner layer composed of hyaline, thin-walled, interwoven, broad hyphae gradually intermixing into gleba. *Hairs* sparse, commonly 40–60 × 3–5 µm, hyaline, slender, tapered, setose, thick-walled, sometimes 1-septate near the base. *Gleba* whitish when immature, becoming olive brown, dark brown at maturity, marbled with numerous, thin, white veins, some veins ending in the peridium. *Odour* slight and not distinctive. *Asci* inamyloid, 50–80 × 50–60 µm, thin-walled, ellipsoid to subglobose, sessile or short-stalked, (1–)3–4(–5)-spored. *Ascospores* 19–35 × 17–28 µm, Q = 1.1–1.3, excluding ornamentation, the walls 2 µm thick, at first hyaline, becoming yellowish brown at maturity, subglobose to broadly ellipsoid, ornamented with a regular reticulum, alveoli 3–6 µm tall, 6–10 µm long, 2–5 alveolar meshes along the spore length, polygonal (5–6 sides).

Ecology & Distribution — *Tuber lusitanicum* grows in acidic soils of Extremadura dehesas associated to *Quercus* spp. in spring. Currently known only from Cáceres, Spain.

Typus. Spain, Cáceres, Rosalejo, in acidic soil, under *Quercus suber* (*Fagaceae*), 10 June 2012, *A. Rodriguez* (holotype MUB Fung-986, ITS and LSU sequences GenBank MT621651 and MT705332, MycoBank MB835881).

Additional materials examined. Spain, Cáceres, Rosalejo, under *Quercus faginea*, 10 June 2012, *J. Mohedano*, MUB Fung-987 and MUB Fung-988, ITS sequences GenBank MT621652 and MT621653; Belvís de Monroy under *Quercus suber*, 20 May 2012, *J. Mohedano*, MUB Fung-989 and MUB Fung-990, ITS sequences GenBank MT621654 and MT621655; Millanes under *Quercus suber*, 5 June 2006, *J. Mohedano*, MUB Fung-991, ITS sequence GenBank MT621656.

Notes — *Tuber lusitanicum* is a whitish truffle that clusters in the maculatum clade, and is characterised by its white-cream smooth peridium, brown gleba marbled with numerous, thin, white veins and reticulate-alveolate spores. *Tuber lusitanicum* is a sister species to *T. rapaeodorum* (88 % of similarity of ITS sequence), but *T. rapaeodorum* differs by having larger, narrower spores and thinner peridium (Ceruti et al. 2003). It also resembles *T. maculatum* (74 % of similarity of ITS sequence) but *T. maculatum* has a prosenchymatous peridium, lacking hairs and larger spores (Mello et al. 2000).



Maximum likelihood (ML) phylogenetic tree inferred from ITS sequences using RAxML-HPC v. 8 (Stamatakis 2014) on XSEDE in the CIPRES science gateway (Miller et al. 2010). GTR + G was selected as model of evolution for the analysis. The sequences obtained in the present study are highlighted in **bold**. Bootstrap support values (≥ 70 %) are indicated at the nodes. *Tuber latisporum* and *Tuber pseudosphaerosporum* were used as outgroup. The scale bar indicates the expected changes per site.

Colour illustrations. Spain, Cáceres, Rosalejo, *Quercus suber* in Extremadura dehesa where the holotype was collected. Ascocarps; mature ascospores; peridium and hairs. Scale bars = 20 µm.

Antonio Rodríguez, Justo Muñoz-Mohedano, Alfonso Navarro-Ródenas, Francisco Arenas & Asunción Morte, Departamento de Biología Vegetal (Botánica), Facultad de Biología, Universidad de Murcia, 30100 Murcia, Spain; e-mail: antonio@trufamania.com, kaerques@gmail.com, anr@um.es, f.arenasjimenez@um.es & amorte@um.es


Tylopilus subotsuensis

Fungal Planet 1177 – 19 December 2020

Tylopilus subotsuensis T.H.G. Pham, A.V. Alexandrova & O.V. Morozova, *sp. nov*.

Etymology. The epithet refers to macromorphological similarity of the new species to *Tylopilus otsuensis*.

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes*.

Basidiomata medium to large sized, boletoid. *Pileus* 30–90 mm diam, firstly hemispherical, then convex and pulvinate-flattened; fleshy; margin initially involute, then curved downwards, finally plane, not or only slightly extending beyond the tubes, surface matt, dry, slightly slimy in moist weather, firstly finely pruinose or felted, then smooth and glabrous; the colour varies from beige and pale ochraceous brown with minute olive tinge to light brown and brown (4A3–4, 4B3–4, 5C3–5, 5D4–8, 6E4–6; Kornerup & Wanscher 1978). *Hymenophore* depressed around the apex of stipe, up to 10 mm thick, thinner than the context, whitish, becoming pinkish; pores round or slightly angular, up to 1 mm diam. *Stipe* 80–120 × 10–25 mm, almost cylindrical or broadened towards the base, solid; minutely tomentose, without distinct reticulum; dry, slightly slimy in moist weather, concolorous with the pileus or slightly lighter. *Context* firm, white, unchanging or slowly yellowing in the stem base and in the areas damaged by insects. *Smell* weak, *taste* bitter. *Spores* (7.5–)9–10(–11.5) × (3–)3.5(–4.5) µm, Q = (2.2–)2.6(–3), fusoid, ellipsoid-fusoid, tapering towards the apex, inequilateral in side view, without or with weak suprahilar depression, sometimes substrangulate, hyaline in KOH, smooth. *Basidia* 23–28 × 6–9 µm, 4-spored, narrowly clavate to clavate, clampless. *Cheilocystidia* lageniform or fusoid, 29–66 × 9–15 µm, often thin-walled, with granulose content, forming sterile or heterogeneous tube edge. *Pleurocystidia* 45–72 × 10–15 µm, same as cheilocystidia. *Hymenophoral trama* divergent, boletoid. *Pileipellis* a trichoderm, made up of strongly interwoven filamentous, frequently branched yellowish hyphae 5–8 µm wide. *Stipitipellis* a caulohymenium of basidiolae-like narrowly clavate cells, 25–35 × 7–10 µm, with scattered caulobasidia. *Caulocystidia* 25–60 × 6–10 µm, lageniform, fusoid or subcylindrical. *Clamp connections* absent.

Habit, Habitat & Known distribution — Solitary, in groups or caespitose on soil in montane evergreen tropical forests. Known from Vietnam.

Typus. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar, 7 km northwest of Chu Yang Sin Mt., N12.42656° E108.36633°, 985 m alt., middle montane evergreen broadleaf forest, 18 May 2014, *A.V. Alexandrova & T.H.G. Pham* (holotype LE312534; ITS, *tef1α* and LSU sequences GenBank MW009074, MW014268 and MW009073, MycoBank MB837493).

Additional materials examined. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar, 7 km northwest of Chu Yang Sin mountain, N12.39497° E108.34823°, 1 000 m alt., middle montane evergreen mixed riparian forest, 21 Mar. 2013, *A.V. Alexandrova & T.H.G. Pham* (LE312526; *tef1α* sequence GenBank MW014271); ibid., 22 Mar. 2013, *A.V. Alexandrova & T.H.G. Pham* (LE312525; ITS and *tef1α* sequences GenBank MW009075 and MW014269); Lam Dong Province, Bao Lam District, 21 km NW of the town of Bao Loc, Loc Bac Forestry, N11.74449° E107.70647°, 1 006 m alt., 6 Apr. 2013, lower montane evergreen broadleaf forest (*Magnoliaceae, Myrtaceae, Theaceae, Lauraceae, Fagaceae, Annonaceae*), *A.V. Alexandrova & T.H.G. Pham* (LE312528; *tef1α* sequence GenBank MW014270); Gia Lai Province, K'Bang District, Son Lang Commune, Kon Chu Rang Nature Reserve, N14.50042° E108.56338°, 1 000 m alt., on soil in middle montane evergreen mixed forest, 27 May 2016, *A.V. Alexandrova* (LE312527; *tef1α* sequence GenBank MW014272).

Notes — *Tylopilus subotsuensis* is characterised by the brownish basidiomata, usually lacking distinct olivaceous or purplish tinges. *Tylopilus otsuensis,* described from Japan (Hongo 1966), is superficially similar. It is distinguished by the oblong spores, presence of distinct olivaceous tinge and reddish-brown discolouration when bruised. Long, fusoid, tapering towards the apex spores, unchanging or slightly yellowish context and lack or almost lack of olivaceous tinge in the colour of basidiomata are characteristic for the new species. Micromorphologically, due to spores and cystidia, the new species resembles *T. neofelleus* (Hongo 1973). But for the latter species the presence of a more or less pronounced purplish tinge and thin reticulum on the upper part of stipe surface is characteristic. In fact, colour variations are not a very reliable way to distinguish species in the genus *Tylopilus*. Gelardi et al. (2014b) and Wu et al. (2016) have shown with molecular evidence that the presence of a purplish tinge in basidiomata of *T. neofelleus* (including *T. microsporus*) can vary greatly from a pronounced colour to its complete absence. In the last case *T. subotsuensis* and *T. neofelleus* are almost inseparable, distinguished only by the absence of a reticulum in the apex of the stipe, slightly longer spores and wider cystidia in the new species. However, molecular data support the *T. subotsuensis* as distinct.

Colour illustrations. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, type locality. Spores, cheilocystidium; pleurocystidium; pileipellis; stipitipellis with caulocystidia (all from holotype). Pileus, basidioma in situ (from holotype); group of fasciculate basidiomata with a longitudinal section through one of them. Scale bars = 10 µm (spores and microstructures), 1 cm (basidiomata).

Supplementary material

FP1177 Phylogenetic tree derived from Bayesian analysis based on *tef1α* data. The analysis was performed under a GTR model of evolution for 3 M generations using MrBayes v. 3.2.1 (Ronquist et al. 2012). Posterior probability (PP > 0.95) values from the Bayesian analysis are shown at the nodes. The scale bar represents the expected number of nucleotide changes per site.

Thi Ha Giang Pham, Joint Russian-Vietnamese Tropical Research and Technological Center, Hanoi, Vietnam; e-mail: giangvietnga@gmail.com
Alina V. Alexandrova, Lomonosov Moscow State University (MSU), Faculty of Biology, 119234, 1, 12 Leninskie Gory Str., Moscow, Russia / Joint Russian-Vietnamese Tropical Research and Technological Center, Hanoi, Vietnam; e-mail: alexandrova@mail.bio.msu.ru
Olga V. Morozova, Komarov Botanical Institute of the Russian Academy of Sciences, 197376, 2 Prof. Popov Str., Saint Petersburg, Russia; e-mail: OMorozova@binran.ru


Veloboletus limbatus

Fungal Planet 1178 – 19 December 2020

Veloboletus limbatus Fechner & Halling, *gen.* & *sp. nov.*

Etymology. *Velo-* (veil) + *boletus* (genus of *Boletaceae*); limbus- (edge, rim, margin referring to the obvious veil remnant edge at the base of stipe).

Classification — *Boletaceae*, *Boletales*, *Agaricomycetes*.

Pileus (3–)6.5–9 cm broad, convex to plano-convex, dry, finely appressed squamulose, with squamules brown to deep reddish brown or reddish brown, overlying a dull red disc, dull yellow to bright yellow or dirty yellowish at margin, staining blue, with even or rarely a sterile projecting margin attached at stipe when young to form limbate rim on stipe base. *Flesh* pale yellow to pale lemon yellow, 1–2 cm thick, staining blue when exposed, with mild *odour* and slowly unpleasant to nearly bitter *taste*. *Hymenophore* adnexed to depressed around stipe, with tubes bright yellow to bright greenish yellow (2A–B7,6; Kornerup & Wanscher 1983), sometimes hardly bluing when young or staining blue-green when bruised at first, with pores olive yellow (3C8) to olive brown, then pores becoming brown. *Stipe* (4.5–)6.5–9.5 cm long, (1.5–)2–2.7(–5) cm broad, dry, terete or slightly flattened, equal to subclavate to clavate, sometimes with a pinched base, with a clearly defined limbate rim and tapering to base below that; surface bright lemon yellow above and heavily pruinose to subfloccose or fibrillose streaked, matted toward base, fading to whitish with age, pale pinkish red with fine appressed to suberect deep red to brown squamules below limbate rim (as in pileus), staining blue; interior solid, yellow, staining blue, with yellow (4B8) basal mycelium.
Basidiospores 9.6–15.2 × 3.5–4.9 µm, x = 12.43 × 4.30 µm, Q = 2.89, n = 100, p = 5, smooth, subfusoid to ellipsoid, hyaline to pale yellow in KOH, hyaline to rarely weakly dextrinoid in Melzer's. *Basidia* 18–40 × 8–12 µm, 4-sterigmate, clavate, hyaline, inamyloid. *Pileus trama* interwoven with hyaline, thin-walled hyphae, 4–15.6(–20) µm broad. *Tube trama* boletoid and divergent, becoming gelatinised with age, with hyphae 4–15.6(–20) µm broad, hyaline in KOH and Melzer's. *Pleurocystidia* 32–41.6 × 8.8–12 µm clavate, thin walled, inamyloid. *Cheilocystidia* 8–34.4 × 6.4–10.4 µm obclavate to clavate, inamyloid, thin-walled. *Pileipellis* a trichodermium, composed of erect to suberect cylindrical elements, 3.2–9.6 µm broad, smooth, thin-walled, hyaline to occasionally very slightly dextrinoid. *Stipitipellis* a fragile and indistinct layer of cylindric to clavate elements, 3.2–12 µm long, smooth, thin-walled, inamyloid, hyaline. *Clamp connections* absent.

Habitat & Distribution — Solitary to gregarious on soil or sand under *Allocasuarina* sp., *Eucalyptus* sp., and *Eucalyptus grandis*. At present, known in Queensland from the Tablelands west of Cairns southward to Fraser Island and the southern border of the state in the mountains west of the Gold Coast. In the months February to March, June.

Typus. Australia, Queensland, Wide Bay District, Great Sandy National Park, Fraser Island, Kingfisher Bay, S25°23'35.7" E153°1'50.7", 8 m, 10 June 2009, *R.E. Halling 9228* (holotype BRI AQ0794331, isotype NY 1393645; *rpb2*, *atp6*, *tef1* and LSU sequences GenBank MT747397, MT747398, MN413636 and MN393700, MycoBank MB832369 (genus), MB832370 (species)).

Notes — BLAST searches were conducted against the NCBIs GenBank nucleotide database for each of the six novel sequences using megablast in the blastn suite (Johnson et al. 2008). The results based on percent identity indicated consistent placement of *Veloboletus limbatus* in the subfamily *Xerocomoideae* (family *Boletaceae*). This was corroborated by a series of phylogenetic analyses of individual genes with selections of exemplars from across the *Boletaceae* (especially *Xerocomoideae*), *Paxillaceae*, and *Suillaceae*. A concatenated analysis of *tef1* and LSU was also done in this manner (see Supplement material FP1178). These analyses were conducted with MrBayes v. 3.2.7A (Ronquist et al. 2012) on the CIPRES REST API (Miller et al. 2015). In all cases, *Veloboletus limbatus* was consistently placed within a highly-supported *Xerocomoideae* (Bayesian posterior probability (bpp) = 1). With *tef1* and LSU, where more than one specimen of *V. limbatus* was available, the genus was fully supported (bpp = 1) in the individual and concatenated analyses. Though we were able to infer that *Veloboletus* belongs within subfamily *Xerocomoideae*, no clear sister group to *Veloboletus* was apparent.

As far as we know, there are no other members of the *Boletaceae* with a distinctive and conspicuous squamulose, universal veil rupturing to form an obvious limbate rim. That and the conspicuous cyanescence are diagnostic. *Xerocomoideae* is globally diverse and contains a number of iconic mushroom groups, including for example, *Boletellus*, *Aureoboletus*, *Phylloporus*, *Pulchroboletus*, *Heimioporus*, and *Xerocomus* s.str. It is notable that *Veloboletus limbatus* has a universal veil. According to the terminology of Clémençon (2012), *V. limbatus* exhibits a cleistometablema. Several other epigeous stipitate-pileate *Xerocomoideae* exhibit veils that could be interpreted as universal (*Boletellus ananas*, *B. ananiceps, B. emodensis, B. deceptivus, B. singeri*, *Aureoboletus longicollis*), but in those species, the portion of the veil nearest the stipe is not physically connected to the stipe tissue. In *B. singeri* and *A. longicollis*, the veil can separate from the pileus margin and form an annular appendage. *Alessioporus ichnusanus*, a *Xerocomoideae* from southern Europe, is described as leaving a velar remnant on the stipe of mature fruiting bodies due to mixangiocarpic development (Gelardi et al. 2014a). Based on the combination of morphological features alone, we hypothesize the uniqueness of the taxon merits generic recognition. Clearly, the need for further exploration and collection of *Boletales* in Australasia, which harbours a diverse and unique mycota, is required. Future fieldwork or herbarium-based studies may uncover a sister group to *Veloboletus* or reveal additional species in the genus.

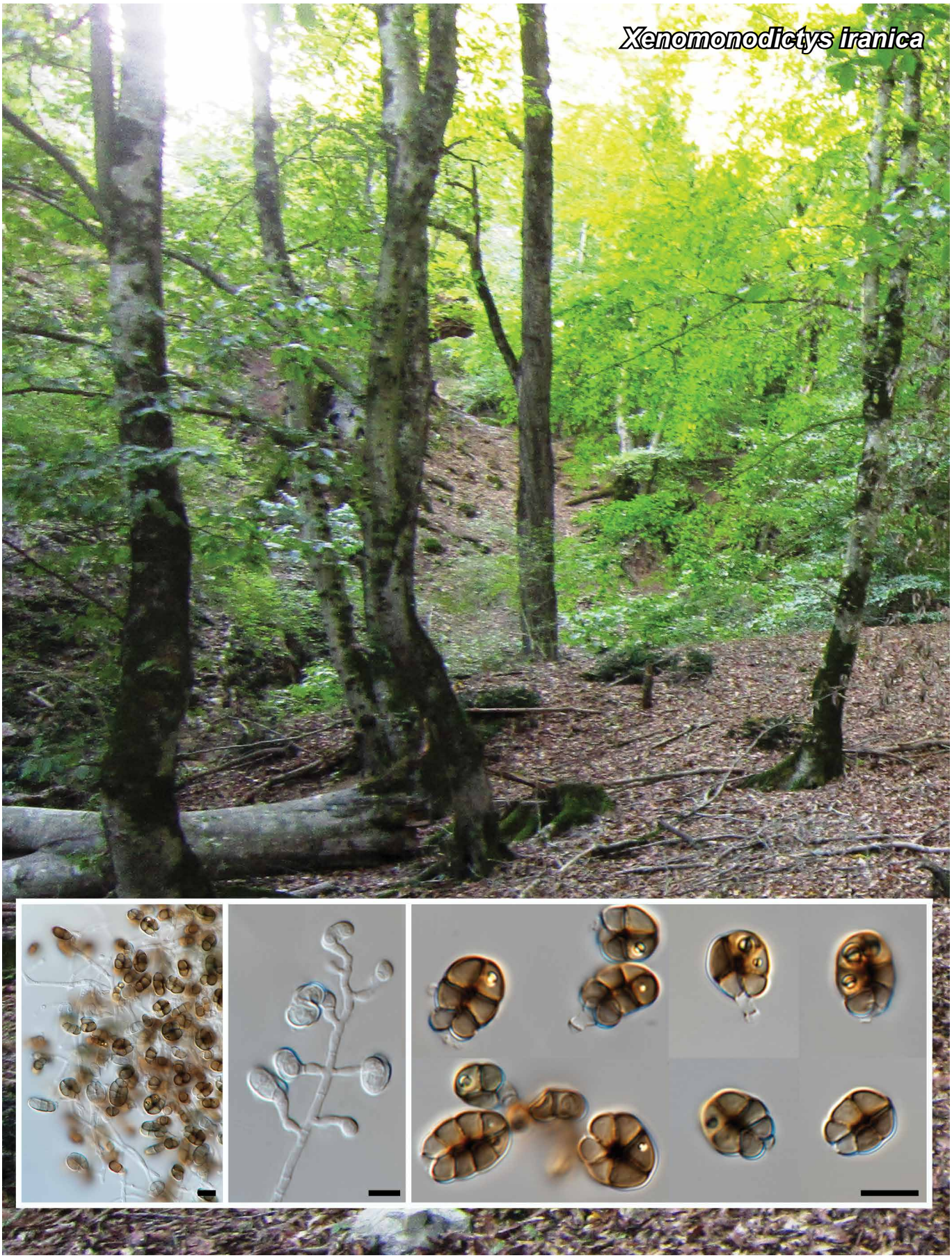
Colour illustrations. Sclerophyll vegetation with *Eucalyptus* and *Allocasuarina* at Camp Milo of the Cooloola Sandmass near Fraser Island. Stipitipellis; basidiospores; pileipellis; holotype (REH9228); solitary basidiome (REH8746); sectioned basidiome (REH8917) showing universal veil attachment (arrows). Scale bars = 1 cm (entire basidiomes), 0.5 cm (sectioned basidiome); 10 µm (spores and stipitipellis), 40 µm (pileipellis).

Supplementary material

FP1178-1 Additional materials examined.

FP1178-2 Bayesian phylogram of selected *Boletales*, especially subfam. *Xerocomoideae*.

Roy E. Halling, Institute of Systematic Botany, New York Botanical Garden, 2900 Southern Blvd, Bronx, NY 10458-5126, USA; e-mail: rhalling@nybg.org
Nigel Fechner, Queensland Herbarium, Mt Coot-tha Road, Toowong, Brisbane, Queensland 4066, Australia; e-mail: nigel.fechner@des.qld.gov.au
Naveed Davoodian, National Herbarium, Royal Botanic Gardens Victoria, South Yarra, Victoria 3141, Australia; e-mail: naveed.davoodian@rbg.vic.gov.au


Xenomonodictys iranica

Fungal Planet 1179 – 19 December 2020

Xenomonodictys Hern.-Restr., Karimi, Alizadeh & Tajick Ghanbary, *gen. nov.*

Etymology. From the Greek 'Xenos' indicating strangeness and the related genus *Monodictys*, referring to a variant of the genus *Monodictys*.

Classification — *Sporormiaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiophores micronematous, hyaline to subhyaline, mostly reduced to conidiogenous cells arising from the mycelium. *Conidiogenous cells* hyaline to subhyaline, cylindrical. *Conidia* multicellular, composed by brown cells of different tones, usually with basal cell paler than the rest.

Type species. Xenomonodictys iranica Hern.-Restr., Karimi, Alizadeh & Tajick Ghanbary.

MycoBank MB837750.

Xenomonodictys iranica Hern.-Restr., Karimi, Alizadeh & Tajick Ghanbary, *sp. nov.*

Etymology. Name refers to the country where this fungus was collected, Iran.

Mycelium composed of hyaline to brown, smooth, septate, 1–2 µm wide hyphae. *Conidiophores* micronematous, hyaline to subhyaline, mostly reduced to conidiogenous cells arising from the mycelium. *Conidiogenous cells* hyaline to subhyaline, cylindrical, 3–9 × 1–2 µm. *Conidia* 10–15 × 7–9 µm, base 1–2 µm, subglobose to ellipsoidal, multicellular, composed of up to 10, smooth, brown cells, each cell 3–5 µm diam, usually in two rows, with basal cell paler than the rest. Conidial secession rhexolythic.

Culture characteristics — Colonies in oatmeal agar (OA) at 25 °C reaching 40 mm after 3 wk, cottony to velvety, with moderate aerial mycelium, olivaceous grey to mouse grey, margin entire to fimbriate; reverse olivaceous grey. On potato dextrose agar (PDA) after 2 wk reaching 45 mm, greyish to black.

Typus. Iran, Mazandaran, Pol sefid, (N36°3'27.99" E53°5'57.84"), on wood of *Fagus orientalis* (*Fagaceae*), 11 May 2015, *O. Karimi* A2FC200 (holotype CBS H-24521, culture ex-type CBS 147181, ITS and LSU sequences GenBank MW175368.1 and MW175406.1, MycoBank MB837751).

Notes — *Monodictys* is a large genus with 69 names presently registered in Index Fungorum. Morphologically it is characterised by multicellular, brown conidia borne on micronematous conidiophores. Based on DNA sequence data, species of *Monodictys* have in the past been allocated to several genera in *Dothideomycetes* and *Sordariomycetes*. *Monodictys putredinis*, the type species, is the asexual morph of *Ohleria brasilensis* (*Melanommataceae*) which resides in *Pleosporales* together with *Paramonodictys* (*Parabambusicolaceae*), *Pleomonodictys* (*Pleomonodictydaceae*) and *Xenomonodictys* (*Sporormiaceae*). Other species (as asexual morphs) have been connected with *Tubeufia* (*Tubeufiaceae*) and *Aquastroma* (*Parabambusicolaceae*) in *Dothideomycetes* (Day et al. 2006, Velmurugan et al. 2013, Tanaka et al. 2015, Hernández-Restrepo et al. 2017, Vu et al. 2019). In *Sordariomycetes*, however, monodictys-like species are placed in the genera *Dematiosporium*, *Ascotaiwania* (*Savoryellalceae*), *Neomonodictys* (*Pleurotheciaceae*), *Trichocladium* (*Chaetomiaceae*), and *Nereiospora* (*Microascales*) (Mouzouras & Jones 1985, Hernández-Restrepo et al. 2017, Réblová et al. 2020). Furthermore, in *Helotiales*, a monodictys-like species has been accommodated as the asexual morph of *Hyaloshypha monodictys* (Hosoya & Huhtinen 2002). *Xenomonodictys* is therefore introduced as a new genus for a monodictys-like taxon phylogenetically related to *Preussia terricola.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pleospora iqbalii* (GenBank NR_160118.1; Identities = 486/546 (89 %), 28 gaps (5 %)), and *Preussia fleischhakii* (GenBank MH474379.1; Identities = 484/549 (88 %), 18 gaps (3 %)). Closest hits using the **LSU** sequence are *Preussia terricola* (GenBank GQ203725.1; Identities = 820/845 (97 %), one gap (0 %)), *Pleospora iqbalii* (GenBank MH871062.1; Identities = 819/847 (97 %), five gaps (0 %)), and *Neomassarina chromolaenae* (GenBank NG_068715.1; Identities = 817/845 (97 %), two gaps (0 %)).

Colour illustrations. Farim Forest near the city of Pol Sefid, Mazandaran Province, Iran. Conidiophores and conidia; conidia. Scale bars = 20 µm (conidiophores), 10 µm (all others).

Margarita Hernández-Restrepo, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: m.hernandez@wi.knaw.nl
Omid Karimi & Mohammad Ali Tajick Ghanbary, Department of Plant Protection, Faculty of Agronomy, Sari Agricultural Sciences and Natural Resources University, Sari, Iran; e-mail: karimiomid18@gmail.com & mycology2@gmail.com
Alireza Alizadeh, Department of Plant Protection, Faculty of Agriculture, Azarbaijan Shahid madani University, Tabriz, Iran; e-mail: alizadeh.al2008@gmail.com


Cortinarius indopurpurascens
RCS 2442

Fungal Planet 1180 – 19 December 2020

Cortinarius indopurpurascens Dima, Semwal, Brandrud, V. Papp, & V.K. Bhatt, *sp. nov*.

Etymology. The epithet refers to the occurrence in India and the close relationship with *Cortinarius purpurascens*.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 45–65 mm diam, convex to plano-convex, then applanate, margin uplifted with age, surface sticky to glutinous, glabrous, with a few darker, hygrophanous spots or radial streaks, initially pale bluish grey (Methuen 12B3–12C3) with an ochraceous tinge at disc, then becoming somewhat ochraceous brown from centre (6C6, 6D8–6C5). *Lamellae* emarginate, crowded, bifurcate towards margin, up to 7 mm broad, lamellulae of various lengths, bright purple, amethyst to reddish lilac tinge (15A6, 15C5–14B5), turning darker purplish when bruised. *Stipe* 50–70 × 10–17 mm, cylindrical with a 17–24 mm wide roundish marginated bulb at the base, concolorous with lamellae, purple to amethyst (15A6–15C5), reddish lilac tinged (14B5) when mature or bruised. Few remnants of cortina present at the upper half. Universal veil at bulb margin thin and indistinct. *Context* purplish. *Odour* honey-like, especially when bruised. *Taste* not recorded. *Spore print* cocoa brown (6E7). *Basidiospores* (9.3–)9.7–10.3(–10.9) × (5.2–)5.4–5.7(–5.9) µm, av. = 9.9 × 5.5 µm, Q = (1.6–)1.7–1.8(–1.9), Qav = 1.75, n = 60, (ellipsoid to) subamygdaloid, strongly verrucose, with discrete, hardly interconnected warts. *Basidia* 4-spored, 26–33 × 6–8 µm, clavate.

Habitat & Distribution — Solitary to caespitose, occurring among leaf litter of the evergreen banj oak *Quercus leucotrichophora*, on humicolous soil, in temperate broadleaved, Himalayan mid-elevation forests, dominated by mainly *Q. leucotrichophora, Myrica esculenta* with scattered *Rhododendron arboreum* trees.

Typus. India, Uttarakhand, Pauri Garhwal, Mundneshwar, 1820 m asl, N29°01'5" E78°44'32", 12 Aug. 2015, *K.C. Semwal* (holotype KCS 2442, ITS sequence GenBank MW135432, MycoBank MB837766).

Additional materials examined. India, Uttarakhand, Pauri Garhwal, Phedhkal, 1880 m asl, N30°16'36" E78°85'42", 17 Aug. 2015, *K.C. Semwal*, KCS 2467, ITS sequence GenBank MW135431; Dandapani, 1900 m asl, 28 July 2015, *K.C. Semwal*, KCS 2529, ITS sequence GenBank MW135430.

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Mundneshwar, type locality. Spores and basidiomata (from KCS 2442, holotype). Scale bar = 10 µm (spores).

Notes — *Cortinarius indopurpurascens* belongs to the sect. *Purpurascentes* based on morphological and molecular (nrDNA ITS and LSU regions) data. The species in this section are characterised by basidiomata with purplish lilac tinges mainly in young stages of development, surfaces and context becoming purplish-lilac on bruising, especially on the lamellae, a positive Lugol reaction in the context, moderate to strong honey-like smell, and ellipsoid to subamygdaloid, distinctly-strongly verrucose spores (Saar et al. 2014, Soop et al. 2019). The nrDNA ITS sequences of the three studied *C. indopurpurascens* specimens are identical and form a well-supported monophyletic group within sect. *Purpurascentes* closely related to the European *C. purpurascens*, and to an undescribed *Cortinarius* species from North America (see Supplementary Material FP1180). It differs by 9–10 nucleotide and indel positions (98.5–98.3 % similarity) from *C. purpurascens* and 6–8 nucleotide and indel position (99–98.7 % similarity) from *Cortinarius* sp.

In morphology *C. indopurpurascens* is most similar to the mainly European *C. purpurascens* and *C. collocandoides*; both species may possess strong lilac-purplish tinges on the basidiomata, and show a distinctly marginate bulb. According to material seen, *C. indopurpurascens* seems to be a paler species, being pale bluish grey when young, a colour reminding more of *C. porphyropus* (a more distant relative with non-marginated bulb), than of *C. purpurascens*. With regard to microcharacters, the European species have significantly smaller spores (*C. purpurascens*: av. = 8 × 4.9 µm and *C. collocandoides*: av. = 9.2 × 5.4 µm vs *C. indopurpurascens*: 9.9 × 5.5 µm). Furthermore, among the five European species in this section (Saar et al. 2014), all taxa have smaller and broader spores than those of *C. indopurpurascens*. Ecologically, *C. indopurpurascens* seems to be associated with the Himalayan, evergreen *Quercus leucotrichophora*, whereas, the closely related, mainly European *C. purpurascens* is associated with a wide range of trees, including oaks, but normally do not occur under (Mediterranean) evergreen oaks. It should be noted that *C. purpurascens* also follows the coniferous boreal-taiga belt into Asian Siberia, but here it is known only from *Pinus sylvestris* forests (pers. obs.), and it is highly unlikely that *C. indopurpurascens* and *C. purpurascens* have an overlapping distribution.

Supplementary material

FP1180 Phylogenetic tree of *Cortinarius* sect. *Purpurascentes* derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTR-GAMMA substitution model for the partitioned (ITS1-5.8S-ITS2) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values are shown at the nodes (BS > 70 %). Sequences of the new species are highlighted in blue.

Bálint Dima, Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; e-mail: cortinarius1@gmail.com
Kamal C. Semwal, Department of Biology, College of Sciences, Eritrea Institute of Technology, Mai Nafhi, Asmara, Eritrea; e-mail: kamalsemwal@gmail.com
Tor Erik Brandrud, Norwegian Institute for Nature Research, Gaustadalléen 21, NO-0349 Oslo, Norway; e-mail: tor.brandrud@nina.no
Viktor Papp, Institute of Horticultural Plant Biology, Szent István University, H-1518, Budapest, Hungary; e-mail: agaricum@gmail.com
Vinod K. Bhatt, Navdanya, 105, Rajpur Road, Dehradun, Uttarakhand, India; e-mail: vinodkbhatt@gmail.com


Cortinarius glaucoelotus
1 cm

Fungal Planet 1181 – 19 December 2020

Cortinarius glaucoelotus Brandrud, Dima, Krisai, Ballarà & Peintner, *sp. nov*.

Etymology. Name refers to bluish (glaucous) tinges on stipe and resemblance to *C. elotus* sensu Moser.

Classification — *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

Pileus 35–60(–80) mm diam, hemispherical, then planoconvex, glutinous, glabrous, often with coarse, radial innately fibrillose structure near margin, centre sometimes with whitish patches of universal veil remnants; initially olivaceous brown, often with greenish grey tinge at margin, more ochraceous brown-buff to brown at centre, exposed parts often becoming oxidised to warmer red-brown, even chestnut brown with age. *Lamellae* emarginate, 4–8 mm broad, greyish to faintly wax yellow-ochre tinged, paler towards margin, later greyish brown, edge even to slightly serrulate. *Stipe* 25–60 × 10–17 mm, with a distinctly (but not very broad) marginate bulb (bulb up to 27 mm wide), whitish, with a distinct and sometimes persistent lilac-amethyst zone at apex, with age brownish. Universal veil on bulb margin sparse, viscid, often difficult to distinguish from stipe surface, whitish (bluish tinges not seen), cortina abundant, whitish, soon brown from spores. *Context* whitish to cream, some with pale ochre grey hygrophanous streaks at stipe apex, cortex lilac at stipe apex, a few with vivid saffron yellow spots in base of bulb. *Odour* distinctly raphanoid (to earthy). *Taste* mild. *Spore print* dark (rusty) brown. *Basidiospores* (9.8–)10.9–11.9(–12.7) × (6.4–)6.7–7.5(–7.8) µm, av. = 11.40 × 7.07 µm, Q = (1.4–)1.5–1.7(–1.8), Qav = 1.61 (type collection; n = 67); range of MVs from all collections 11.4–12.1 × 7.0–7.7 µm, av. = 11.81 × 7.37 µm, Qav = 1.60; distinctly citriform to amygdaloid, strongly and coarsely, net-like verrucose, suprahilar plage indistinct, apiculus smooth. *Basidia* 4-spored, 9–11 µm wide. *Pileipellis* simplex, with gradual transition from erect-entangled-sinuous, gelatinous, very narrow, 2–3 µm wide, pale yellow hyphae at surface, to more repent-parallel, slightly wider (3–4(–5)) µm hyphae basally. The basal epicutis with pale yellow brown hyphae, sometimes more strongly yellow to yellow brown, with some hyphae filled with amorphous-oleiferous golden brown pigment, pigment sometimes in lumps like staples of coins, hyphae sometimes forming subparallel, interconnected bundles. A few thicker (6–7 µm wide) hyphae with faintly thicker walls are sometimes seen basally, some of these might be distinctly zebra-striped encrusted.

Chemical reactions — KOH 20–30 % negative (slightly brownish) on pileipellis and bulb margin.

Habitat & Distribution — In calcareous *Abies* dominated forests, as well as calcareous *Picea* and *Pinus* forests. Very rare, but widely distributed in montane Europe (Pyrenees - The Alps - Caucasus), and into Asian Siberia. Result of nrDNA ITS sequencing verified the species from NE Spain (with *Pinus nigra* and *P. sylvestris*), E Austria (with *Abies alba* and some *Picea abies*), Russian W Caucasus (with *Abies nordmanniana* and some *Picea orientalis*) and Altai (Russian Siberia; with *Picea obovata*).

Colour illustrations. Austria, Schneebergdörfl, WU 42513, type locality. Spores and basidiomata (from WU 42513, holotype). Scale bar = 10 µm (spores).

Typus. Austria, Lower Austria, Schneebergdörfl , 780 m asl, N47°46'45" E15°52'13", 9 Oct. 2017, *T.E. Brandrud, I. Krisai-Greilhuber & H. Voglmayr* (holotype TEB898-17 (O), isotypus WU 42513, ITS sequence GenBank MW135358, MycoBank MB837764).

Additional materials examined. Austria, Lower Austria, Schneebergdörfl NW, 9 Oct. 2017, *T.E. Brandrud, I. Krisai-Greilhuber* & *H. Voglmayr*, WU 42455 / TEB898b-17 (O), ITS sequence GenBank MW135357. – Russia, Altai republic, Chuya river (Katun), NW of Uagan Unus, 22 Aug. 2001 (as '*C. elotus*'), *M.M. Moser* (IB 2001/0090), ITS-LSU sequence GenBank EU056953; Karachay-Cherkessia Republic (NW Caucasus), Kuzgych river, Arkhyz W, 10 Oct. 2016, *T.E. Brandrud & T. Svetasheva*, TEB 635-16 (LE), ITS sequence GenBank MW135356. – Spain, Berguedà, Espunyola Can Gomira, 700–900 m asl, 8 Nov. 2014, *J. Ballarà,* JB-8525-14, ITS sequence GenBank MW135354.

Notes — *Cortinarius glaucoelotus* belongs to the Humolentes clade (within the Calochroi lineage), where it has a sister position to *C. pseudoglaucopus* and *C. praetermissus*. *Cortinarius pseudoglaucopus* is distributed both in Europe and North America, and shows a slight phylogeographical differentiation between these regions. The nrDNA ITS sequences generated from *C. glaucoelotus* differ from sequences of European *C. pseudoglaucopus* by 9–12 nucleotide and indel positions (98.35–98.02 % similarity). The two species have overlap in their distribution and similar habitat requirements: both are occurring in calcareous coniferous forests, but *C. glaucoelotus* is possibly more associated with *Abies* spp. They are co-occurring in W Caucasus and found in the same area and same kind of forests in E Austria and NE Spain. Morphologically, *C. glaucoelotus* and *C. pseudoglaucopus* are very similar, characterised e.g. by their initially olive brown pilei. Based on the material seen so far, it seems that *C. glaucoelotus* can be distinguished from *C. pseudoglaucopus* by the beautiful lilac-amethyst narrow zone at the stipe apex when young. However, we do not know if this lilac apex colour is constant. The bluish pigments in *C. pseudoglaucopus* are very variable, sometimes the stipe and context can be bluish-violet tinged when young, and the veil and bulb margin are often violaceous spotted when young. These bluish variants have usually rather dark pileus colours, as already indicated by Moser (1961). The bluish tinges on the bulb margin including the veil have not thus far been seen in *C. glaucoelotus*. It is also possible that *C. glaucoelotus* on average has more olive greenish tinges on the pileus margin when (very) young, but this needs further confirmation.

(text continues on Supplementary material page FP1181)

Supplementary material

FP1181 Phylogenetic tree of the Humolentes clade within sect. *Calochroi* derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2, partial nrLSU and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTRGAMMA substitution model for the partitioned (ITS1-5.8S-ITS2 and LSU) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values are shown at the nodes (BS > 70 %). Sequences generated for this study are highlighted in **bold** face.

Bálint Dima, Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; e-mail: cortinarius1@gmail.com
Tor Erik Brandrud, Norwegian Institute for Nature Research, Gaustadalléen 21, NO-0349 Oslo, Norway; e-mail: tor.brandrud@nina.no
Irmgard Krisai-Greilhuber, Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Wien, Austria; e-mail: irmgard.greilhuber@univie.ac.at
Josep Ballarà, C/ Tossalet de les Forques, 44, E-08600, Berga, Catalonia, Spain; e-mail: josep.cortinarius@gmail.com
Ursula Peintner, Institute of Microbiology, University of Innsbruck, Technikerstrasse 25, 6020 Innsbruck, Austria; e-mail: Ursula.Peintner@uibk.ac.at

REFERENCES

Anisimova M, Manuel G., Dufayard J-F, et al. 2011. Survey of branch support methods demonstrates accuracy, power, and robustness of Fast Likelihood-based approximation schemes. Systematic Biology 60: 685–699.

Antonín V, Ryoo R, Ka K-H, et al. 2014. Three new species of Crinipellis and one new variety of Moniliophthora (Basidiomycota, Marasmiaceae) described from the Republic of Korea. Phytotaxa 170: 86–102.

Arauzo S, Iglesias P. 2014. La familia Geoglossaceae ss. str. en la península Ibérica y la Macaronesia. Errotari 11: 166–259.

Attili-Angelis D, Duarte APM, Pagnocca FC, et al. 2014. Novel Phialophora species from leaf-cutting ants (tribe Attini). Fungal Diversity 65: 65–75.

Australian Plant Pest Database, online database, (accessed 06 August 2020). https://appd.ala.org.au/appd-hub/search#tab_simpleSearch.

Baral H-O. 1987. Lugol's solution / IKI versus Melzer's reagent: hemiamyloidity, a universal feature of the ascus wall. Mycotaxon 29: 399–450.

Basiewicz M, Weiss M, Kogel K-H, et al. 2012. Molecular and phenotypic characterization of Sebacina vermifera strains associated with orchids, and the description of Pirformospora williamsii sp. nov. Fungal Biology 116: 204–213.

Baten MA, Mingzhu L, Motohashi K, et al. 2015. Two new species, Phytopythium iriomotense sp. nov. and P. aichiense sp. nov., isolated from river water and water purification sludge in Japan. Mycological Progress 14: 1–12.

Bezerra JDP, Sandoval-Denis M, Paiva LM, et al. 2017. New endophytic Toxicocladosporium species from cacti in Brazil, and description of Neocladosporium gen. nov. IMA Fungus 8: 77–97.

Bon M. 1984. Novitates – Combinaisons et taxons nouveaux. Documents Mycologiques 14 (53): 6.

Borchsenius F. 2009. FastGap 1.2. Department of Bio-sciences, Aarhus University, Denmark. http://www.aubot.dk/FastGap_home.htm.

Brasier CM, Sanchez-Hernandez E, Kirk SA. 2003. Phytophthora inundata sp. nov., a part heterothallic pathogen of trees and shrubs in wet or flooded soils. Mycological Research 107: 477–484.

Braun U, Crous PW, Nakashima C. 2015. Cercosporoid fungi (Mycosphaerellaceae) 3. Species on monocots (Poaceae, true grasses). IMA Fungus 6: 25–97.

Braun U, Hill CF. 2002. Some new micromycetes from New Zealand. Mycological Progress 1: 19–30.

Burgess TI, Simamora A, White D, et al. 2018. New species from Phytophthora Clade 6a: evidence for recent radiation. Persoonia 41: 1–17.

Buyck B. 2000. Le genre Cantharellus en Europe. Bulletin de la Société Mycologique de France 116: 91–1378.

Buyck B, Hofstetter V. 2011. The contribution of tef-1 sequences for species delimitation in the Cantharellus cibarius complex in the southeastern USA. Fungal Diversity 49: 35–46.

Ceruti A, Fontana A, Nosenzo C. 2003. Le specie europee del genere Tuber. Una revision storica. Museo Regionale di Scienze Naturali, Torino.

Chaverri P, Liu M, Hodge KT. 2008. A monograph of the entomopathogenic genera Hypocrella, Moelleriella, and Samuelsia gen. nov. (Ascomycota, Hypocreales, Clavicipitaceae), and their aschersonia-like anamorphs in the Neotropics. Studies in Mycology 60: 1–66.

Chevenet F, Brun C, Bañuls A-L, et al. 2006. TreeDyn: towards dynamic graphics and annotations for analyses of trees. BMC Bioinformatics 7: 439.

Clémençon H. 2012. Cytology and plectology of the hymenomycetes. 2nd ed. Cramer, Stuttgart.

Corner EHJ. 1994. Agarics in Malesia II Mycenoid. Beihefte zur Nova Hedwigia 109: 1–271.

Crous PW. 2002. Taxonomy and pathology of Cylindrocladium (Calonectria) and allied genera. APS Press.

Crous PW, Braun U, Schubert K, et al. 2007a. Delimiting Cladosporium from morphologically similar genera. Studies in Mycology 58: 33–56.

Crous PW, Decock C, Schoch CL. 2001. Xenocylindrocladium guianense and X. subverticillatum, two new species of hyphomycetes from plant debris in the tropics. Mycoscience 42: 559–566.

Crous PW, Groenewald JZ. 2016. They seldom occur alone. Fungal Biology 120: 1392–1415.

Crous PW, Groenewald JZ. 2017. The genera of fungi – G 4: Camarosporium and Dothiora. IMA Fungus 8: 131–152.

Crous PW, Groenewald JZ, Shivas RG. 2011. Fungal Planet description sheets: 69–91. Persoonia 26: 108–156.

Crous PW, Luangsa-ard JJ, Wingfield MJ, et al. 2018a. Fungal Planet description sheets: 785–867. Persoonia 41: 238–417.

Crous PW, Mohammed C, Glen M, et al. 2007b. Eucalyptus microfungi known from culture. 3. Eucasphaeria and Sympoventuria genera nova, and new species of Furcaspora, Harknessia, Heteroconium and Phacidiella. Fungal Diversity 25: 19–36.

Crous PW, Schumacher RK, Akulov A, et al. 2019a. New and interesting fungi. 2. Fungal Systematics and Evolution 3: 57–134.

Crous PW, Schumacher RK, Wingfield MJ, et al. 2018b. New and interesting fungi. 1. Fungal Systematics and Evolution 1: 169–215.

Crous PW, Shivas RG, Quaedvlieg W, et al. 2014. Fungal Planet description Sheets: 214–280. Persoonia 32: 184–306.

Crous PW, Shivas RG, Wingfield MJ, et al. 2012. Fungal Planet description sheets: 128–153. Persoonia 29: 146–201.

Crous PW, Wingfield MJ, Burgess TI, et al. 2017a. Fungal Planet description sheets: 625–715. Persoonia 39: 270–467.

Crous PW, Wingfield MJ, Burgess TI, et al. 2018c. Fungal Planet description sheets: 716–784. Persoonia 40: 240–393.

Crous PW, Wingfield MJ, Burgess TI. 2017b. Fungal Planet description sheets: 558–624. Persoonia 38: 240–384.

Crous PW, Wingfield MJ, Cheewangkoon R, et al. 2019b. Foliar pathogens of eucalypts. Studies in Mycology 94: 125–298.

Crous PW, Wingfield MJ, Chooi Y-H, et al. 2020a. Fungal Planet description sheets: 1042–1111. Persoonia 44: 301–459.

Crous PW, Wingfield MJ, Lombard L, et al. 2019c. Fungal Planet description sheets: 951–1041. Persoonia 43: 223–425.

Crous PW, Wingfield MJ, Schumacher RK, et al. 2020b. New and interesting fungi. 3. Fungal Systematics and Evolution 6: 157–231.

Da Cruz ACR, Gusmão LFP, Castañeda-Ruíz RF. 2007. Conidial fungi from the semi-arid Caatinga biome of Brazil. Subramaniomyces pulcher sp. nov. and notes on Sporidesmium circinophorum. Mycotaxon 102: 25–32.

Daranagama DA, Camporesi E, Liu XZ, et al. 2016. Tristratiperidium microsporum gen. et sp. nov. (Xylariales) on dead leaves of Arundo plinii. Mycological Progress 15: 8.

Darriba D, Taaboada GL, Doallo R, et al. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nature Methods 9: 772.

Das K, Atri NS, Buyck B. 2013. Three new species of Russula (Russulales) from Sikkim (India). Mycosphere 4: 722–732.

Das K, Rossi W, Leonardi M, et al. 2018. Fungal Biodiversity Profiles 61–70. Cryptogamie, Mycologie 39: 381–418.

Day MJ, Gibas CFC, Fujimura KE, et al. 2006. Monodictys arctica, a new hyphomycete from the roots of Saxifraga oppositifolia collected in the Canadian High Arctic. Mycotaxon 98: 261–272.

De Beer ZW, Duong TA, Barnes I, et al. 2014. Redefining Ceratocystis and allied genera. Studies in Mycology 79: 187–219.

De Hoog GS, Vicente VA, Najafzadeh MJ, et al. 2011. Waterborne Exophiala species causing disease in cold-blooded animals. Persoonia 27: 46–72.

De Hoog GS, Weenink XO, Gerrits van den Ende AHG. 1999. Taxonomy of the Phialophora verrucosa complex with the description of two new species. Studies in Mycology 43: 107–122.

DeCock C, Hennebert GL, Crous PW. 1997. Nectria serpens sp. nov. and its hyphomycetous anamorph Xenocylindrocladium gen. nov. Mycological Research 101: 786–790.

Deighton FC. 1967. Studies on Cercospora and allied genera. II. Passalora, Cercosporidium and some species of Fusicladium on Euphorbia. Mycological Papers 112: 1–80.

Dennis RWG. 1952. Lepiota and allied genera in Trinidad, British West Indies. Kew Bulletin 7: 459–500.

Dereeper A, Guignon V, Blanc G, et al. 2008. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research 36 (Web Server issue), W465–W469.

Durand EJ. 1908. The Geoglossaceae of North America. Annales Mycologici 6: 387–477.

Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research 32: 1792–1797.

Fries EM. 1836–1838. Epicrisis systematis mycologici seu synopsis Hymenomycetum. Uppsala, Sweden.

Gams W. 1971. Cephalosporium-artige Schimmelpilze (Hyphomycetes). Fischer, Stuttgart.

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

Garnica S, Weiß M, Oertel B, et al. 2009. Phylogenetic relationships in Cortinarius, section Calochroi, inferred from nuclear DNA sequences. BMC Evolutionary Biology 9: 1.

Garzon LM, Rueda LJ, Celis AM, et al. 2019. Exophiala psychrophila: a new agent of chromoblastomycosis. Medical Mycology Case Reports 23: 31–33.

Gelardi M, Simonini G, Ercole E, et al. 2014a. Alessioporus and Pulchroboletus (Boletaceae, Boletineae), two novel genera for Xerocomus ichnusanus and X. roseoalbidus from the European Mediterranean basin: molecular and morphological evidence. Mycologia 106: 1168–1187.

Gelardi M, Vizzini A, Ercole E, et al. 2014b. New collection, iconography and molecular evidence for Tylopilus neofelleus (Boletaceae, Boletoideae) from southwestern China and the taxonomic status of T. plumbeoviolaceoides and T. microsporus. Mycoscience 56: 373–386.
Gomes RR, Vicente VA, De Azevedo CMPS, et al. 2016. Molecular epidemiology of agents of human chromoblastomycosis in Brazil with the description of two novel species. PLoS Neglected Tropical Diseases 10 (11): e0005102.
Guarro J, Gene J, Stchigel AM, et al. 2012. Atlas of soil ascomycetes. CBS Biodiversity Series 10. Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands.
Guevara-Suarez M, García D, Cano-Lira JF, et al. 2020. Species diversity in Penicillium and Talaromyces from herbivore dung, and the proposal of two new genera of penicillium-like fungi in Aspergillaceae. Fungal Systematics and Evolution 5: 39–75.
Guindon S, Dufayard JF, Lefort V, et al. 2010a. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Systematic Biology 59: 307–321.
Guindon S, Lethiec F, Duroux P, et al. 2010b. PHYML online – a web server for fast maximum likelihood-based phylogenetic inference. Nucleic Acids Research 33 (Web Server issue): W557–W559.
Hakelier N. 1967. Three new Swedish species of Geoglossum. Svensk Botanisk Tidskrift 61: 419–424.
Heilmann-Clausen J, Verbeken A, Vesterholt J. 1998. The genus Lactarius. Fungi of Northern Europe Vol 2.
Hernández-Restrepo M, Gené J, Castañeda-Ruiz RF, et al. 2017. Phylogeny of saprobic microfungi from Southern Europe. Studies in Mycology 86: 53–97.
Herrera M, Bandala VL, Montoya L. 2018. Cantharellus violaceovinosus, a new species from tropical Quercus forests in eastern Mexico. MycoKeys 32: 91–109.
Hesseltine CW, Fennell DI. 1955. The genus Circinella. Mycologia 47: 193–212.
Hongo T. 1966. Notulae Mycologicae (5). Memoirs of the Faculty of Education, Shiga University. Natural Science (Otsu) 16: 57–62.
Hongo T. 1973. Enumeration of the Hygrophoraceae, Boletaceae and Strobilomycetaceae. Mycological reports from New Guinea and the Solomon Islands (16–21). Bulletin of the National Science Museum (Tokyo) 16: 537–557.
Hosoya T, Huhtinen S. 2002. Hyaloscyphaceae in Japan (7): Hyaloscypha albohyalina var. monodictys var. nov. Mycoscience 43: 405–409.
Houbraken J, Kocsubé S, Visagie CM, et al. 2020. Classification of Aspergillus, Penicillium, Talaromyces and related genera (Eurotiales): an overview of families, genera, subgenera, sections, series and species. Studies in Mycology 95: 5–169.
Huelsenbeck JP, Ronquist F. 2001. MrBayes: Bayesian inference of phylogenetic trees. Bioinformatics 17: 754–755.
Jaklitsch WM, Voglmayr H. 2012. Phylogenetic relationships of five genera of Xylariales and Rosasphaeria gen. nov. (Hypocreales). Fungal Diversity 52: 75–98.
Johnson M, Zaretskaya I, Raytselis Y, et al. 2008. NCBI BLAST: a better web interface. Nucleic Acids Research 36 (suppl_2): W5–W9.
Johnston PR, Quijada L, Smith CA, et al. 2019. A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. IMA Fungus 10: 1.
Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20: 1160–1166.
Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30: 772–780.
Kearse M, Moir R, Wilson A, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28: 1647–1649.
Kerekes JF, Desjardin DE. 2009. A monograph of the genera Crinipellis and Moniliophthora from Southeast Asia including a molecular phylogeny of the nrITS region. Fungal Diversity 37: 101–152.
Kirk PM. 1982. New or interesting microfungi IV. Dematiaceous hyphomycetes from Devon. Transactions of the British Mycological Society 78: 55–74.
Kirk PM. 1983. New or interesting microfungi IX. Dematiaceous hyphomycetes from Esher Common. Transactions of the British Mycological Society 80: 449–467.
Klaubauf S, Tharreau D, Fournier E, et al. 2014. Resolving the polyphyletic nature of Pyricularia (Pyriculariaceae). Studies in Mycology 79: 85–120.
Ko WH, Ann PJ. 1985. Phytophthora humicola, a new species from soil of a citrus orchard in Taiwan. Mycologia 77: 631–636.
Kornerup A, Wanscher JH. 1967. Methuen Handbook of Colour. Methuen & Co Ltd, London, England.
Kornerup A, Wanscher JH. 1978. Methuen Handbook of Colour, 3rd ed. Eyre Methuen, London.
Kornerup A, Wanscher JH. 1983. Methuen Handbook of Colour, 3rd ed. Eyre Methuen, Ltd., London.
Kumar S, Stecher G, Li M, et al. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Molecular Biology and Evolution 35: 1547–1549.
Kumar S, Stecher G, Tamura K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Molecular Biology and Evolution 33: 1870–1874.
Kurtzman CP. 2001. Six new anamorphic ascomycetous yeasts near Candida tanzawaensis. FEMS Yeast Research 1: 177–185.
Kurtzman CP, Robnett CJ, Blackwell M. 2016. Description of Teunomyces gen. nov. for the Candida kruisii clade, Suhomyces gen. nov. for the Candida tanzawaensis clade and Suhomyces kilbournensis sp. nov. FEMS Yeast Research 16: 1–9.
Kušan I, Matočec N, Antonić O, et al. 2014. Biogeographical variability and re-description of an imperfectly known species Hamatocanthoscypha rotundispora (Helotiales, Hyaloscyphaceae). Phytotaxa 170: 1–12.
Kušan I, Matočec N, Mešić A, et al. 2015. A new species of Thecotheus from Croatia with a key to the known species with apiculate spores. Sydowia 67: 51–63.
Lanfear R, Frandsen PB, Wright AM, et al. 2016. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Molecular Biology and Evolution 4: 772–773.
Leigh JW, Bryant D. 2015. POPART: full-feature software for haplotype network construction. Methods in Ecology and Evolution 6: 1110–1116.
Li GJ, Hyde KD, Zhao RL, et al. 2016. Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 78: 1–237.
Li GJ, Zhao Q, Zhao D, et al. 2013. Russula atroaeruginea and R. sichuanensis spp. nov.from southwest China. Mycotaxon 124: 173–188.
Liu YJ, Whelen S, Hall BD, 1999. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Molecular Biology and Evolution 16: 1799e1808.
Lombard L, Houbraken J, Decock C, et al. 2016. Generic hyper-diversity in Stachybotriaceae. Persoonia 36: 156–246.
Lombard L, Van der Merwe NA, Groenewald JZ, et al. 2015. Generic concepts in Nectriaceae. Studies in Mycology 80: 189–245.
Lorch JM, Lindner DL, Gargas A, et al. 2013. A culture-based survey of fungi in soil from bat hibernacula in the eastern United States and its implications for detection of Geomyces destructans, the causal agent of bat white nose syndrome. Mycologia 105: 237–252.
Maas Geesteranus RA, Horak E. 1995. Mycena and related genera from Papua New Guinea and New Caledonia. Bibliotheca Mycologica 159: 143–329.
Maciá-Vicente JG, Glynou K, Piepenbring M. 2016. A new species of Exophiala associated with roots. Mycological Progress 15: 18.
Madrid H, Hernández-Restrepo M, Gené J, et al. 2016. New and interesting chaetothyrialean fungi from Spain. Mycological Progress 15: 1179–1201.
Mains EB. 1957. Species of Cordyceps parasitic on Elaphomyces. Bulletin of the Torrey Botanical Club 84: 243–251.
Man in't Veld WA, Rosendahl KC, Brouwer H, et al. 2011. Phytophthora gemini sp. nov., a new species isolated from the halophilic plant Zostera marina in the Netherlands. Fungal Biology 115: 724–732.
Man in't Veld WA, Rosendahl KC, Van Rijswick PC, et al. 2019. Multiple Halophytophthora spp. and Phytophthora spp. including P. gemini, P. inundata and P. chesapeakensis sp. nov. isolated from the seagrass Zostera marina in the Northern hemisphere. European Journal of Plant Pathology 153: 341–57.
Marin-Felix Y, Groenewald JZ, Cai L, et al. 2017a. Genera of phytopathogenic fungi: GOPHY 1. Studies in Mycology 86: 99–216.
Marin-Felix Y, Hernández-Restrepo M, Crous PW. 2020. Multi-locus phylogeny of the genus Curvularia and description of ten new species. Mycological Progress 19: 559–588.
Marin-Felix Y, Senwanna C, Cheewangkoon R, et al. 2017b. New species and records of Bipolaris and Curvularia from Thailand. Mycosphere 8: 1556–1574.
Marincowitz S, Crous PW, Groenewald JZ, et al. 2008. Microfungi occurring on Proteaceae in the fynbos. CBS Biodiversity Series 7: 1–166.
Massimo NC, Nandi Devan MM, Arendt KR, et al. 2015. Fungal endophytes in aboveground tissues of desert plants: infrequent in culture, but highly diverse and distinctive symbionts. Microbial Ecology 70: 61–76.
Matheny PB, Swenie RA. 2018. The Inocybe geophylla group in North America: a revision of the lilac species surrounding I. lilacina. Mycologia 110: 618–634.
Matsushima T. 1971. Microfungi of the Solomon Islands and Papua-New Guinea. Published by the author, Kobe.

McLeod A, Botha WJ, Meitz JC, et al. 2009. Biodiversity of Pythium species in South African agricultural systems. Mycological Research 113: 933–951.
Mello A, Vizzini A, Longato S, et al. 2000. Tuber borchii versus Tuber maculatum: neotype studies and DNA analyses. Mycologia 92: 326–331.
Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees, In: Proceedings of the Gateway Computing Environments Workshop (GCE), 14 Nov. 2010, New Orleans, LA: 1–8.
Miller MA, Schwartz T, Pickett BE, et al. 2015. A RESTful API for access to phylogenetic tools via the CIPRES science gateway. Evolutionary Bioinformatics 11: EBO-S21501.
Miller OK Jr, Lodge DJ, Baroni TJ. 2000. New and interesting ectomycorrhizal fungi from Puerto Rico, Mona, and Guana Islands. Mycologia 92: 558–570.
Minh BQ, Nguyen MAT, Von Haeseler A. 2013. Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30: 1188–1195.
Minnis AM, Lindner DL. 2013. Phylogenetic evaluation of Geomyces and allies reveals no close relatives of Pseudogymnoascus destructans, comb. nov., in bat hibernacula of eastern North America. Fungal Mycology 117: 638–649.
Minter DW, Cannon PF. 2015. Geoglossum cookeanum. IMI Descriptions of Fungi and Bacteria, No. 204, Sheet 2031.
Molia A, Larsson E, Jeppson M, et al. 2020. Elaphomyces section Elaphomyces (Eurotiales, Ascomycota) – taxonomy and phylogeny of North European taxa, with the introduction of three new species. Fungal Systematics and Evolution 5: 283–300.
Morgan-Jones G. 1975. Notes on Hyphomycetes. VIII. Lylea, a new genus. Mycotaxon 3: 129–132.
Moser M. 1961 '1960'. Die Gattung Phlegmacium (Schleimköpfe). Die Pilze Mitteleuropas, Band IV. Klinkhardt, Germany.
Mouzouras R, Jones EBG. 1985. Monodictys pelagica, the anamorph of Nereiospora cristata (Halosphaeriaceae). Canadian Journal of Botany 63: 2444–2447.
Müller E, Von Arx JA. 1962. Die Gattungen der didymosporen Pyrenomyceten. Beiträge zur Kryptogamenflora der Schweiz 11: 1–922.
Munsell. 1975. Munsell Soil Colour Charts. Macbeth, Baltimore.
Munsell AH, Munsell Color (Firm). 2000. Munsell soil color charts. New Windsor, NY: Munsell Color.
Nagy LG, Desjardin DE, Vágvölgyi C, et al. 2013. Phylogenetic analyses of Coprinopsis section Lanatuli and Atramentarii identify multiple species within morphologically defined taxa. Mycologia 105: 112–124.
Najafzadeh MJ, Vicente VA, Feng P, et al. 2018. Rapid identification of seven waterborne Exophiala species by RCA DNA padlock probes. Mycopathologia 183: 669–677.
Nakase T, Itoh M, Takematsu A, et al. 1988. Candida tanzawaensis, a new species of yeast isolated from moss collected in Japan. Transactions of the Mycological Society of Japan 29: 331–338.
Nannfeldt JA. 1942. The Geoglossaceae of Sweden (with regard also to the surrounding countries). Arkiv för Botanik 30A: 1–67.
Nguyen LT, Schmidt HA, Von Haeseler A, et al. 2015. IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32: 268–274.
Nishikawa J, Nakashima C. 2020. Japanese species of Alternaria and their species boundaries based on host range. Fungal Systematics and Evolution 5: 197–281.
Oberwinkler F. 1964. Intrahymeniale Heterobasidiomyceten: Fruchtkörperlose Sebacina-Sippen und ihre systematische Stellung. Nova Hedwigia 7: 489–499.
Okonechnikov K, Golosova O, Fursov M, et al. 2012. Unipro UGENE: A unified bioinformatics toolkit. Bioinformatics 28: 1166–1167.
Paden JW. 1971. Three new species of Eupenicillium from soil. Mycopathologia et Mycologia Applicata 43: 259–268.
Palmer JM, Kubatova A, Novakova A, et al. 2014. Molecular characterization of a heterothallic mating system in Pseudogymnoascus destructans, the fungus causing white-nose syndrome of bats. G3: Genes, Genomes, Genetics 4: 1755–1763.
Paz A, Bellanger JM, Lavoise C, et al. 2017. The genus Elaphomyces (Ascomycota, Eurotiales): a ribosomal DNA-based phylogeny and revised systematics of European 'deer truffles'. Persoonia 38: 197–239.
Peck CH. 1985. Gymnascella. Mycotaxon 24: 68–93.
Pegler DN. 1983. Agaric flora of the Lesser Antilles. Kew Bulletin Additional Series 9: 1–668.
Petch T. 1906. Descriptions of new Ceylon fungi. Annals of the Royal Botanic Gardens Peradeniya 3: 1–10.
Pitt J. 1980. The genus Penicillium and its teleomorphic states Eupenicillium and Talaromyces. Academic Press, London.
Pordel A, Khodaparast SA, McKenzie EHC, et al. 2017. Two new species of Pseudopyricularia from Iran. Mycological Progress 16: 729–736.
Raithelhuber J. 1974. Hongos argentinos. Tomo I. Buenos Aires: Compañía Impresora Argentina.
Rayner RW. 1970. A Mycological Colour Chart. Commonwealth Mycological Institute, Kew and British Mycological Society.
Réblová M, Hernández-Restrepo M, Fournier J, et al. 2020. New insights into the systematics of Bactrodesmium and its allies and introducing new genera, species and morphological patterns in the Pleurotheciales and Savoryellales (Sordariomycetes). Studies in Mycology 95: 415–466.
Réblová M, Untereiner WA, Réblová K. 2013. Novel Evolutionary lineages revealed in the Chaetothyriales (Fungi) based on multigene phylogenetic analyses and comparison of ITS secondary structure. PLoS One 8 (5): e63547.
Rehner SA, Buckley E. 2005. A Beauveria phylogeny inferred from nuclear ITS and EF1-α sequences: evidence for cryptic diversification and links to Cordyceps teleomorphs. Mycologia 97: 84–98.
Riess K, Oberwinkler F, Bauer R, et al. 2014. Communities of endophytic Sebacinales associated with roots of herbaceous plants in agricultural and grassland ecosystems are dominated by Serendipita herbamans sp. nov. PLoS ONE 9: E94676.
Roberts P. 1993. Exidiopsis species from Devon, including the new segregate genera Ceratosebacina, Endoperplexa, Microsebacina, and Serendipita. Mycological Research 97: 467–478.
Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574.
Ronquist F, Teslenko M, Van der Mark P, et al. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biolology 61: 539–542.
Ryberg M, Nilsson RH, Kristiansson E, et al. 2008. Mining metadata from unidentified ITS sequences in GenBank: a case study in Inocybe (Basidiomycota). BMC Evolutionary Biology 8: 50.
Saar G, Brandrud TE, Dima B, et al. 2014. Cortinarius untergattung Phlegmacium sektion Purpurascentes in Europa. Journal des JEC 16: 140–161.
Samson RA. 1972. Notes on Pseudogymnoascus, Gymnoascus and related genera. Acta Botanica Neerlandica 21: 517–527.
Samson RA, Yilmaz N, Houbraken J, et al. 2011. Phylogeny and nomenclature of the genus Talaromyces and taxa accommodated in Penicillium subgenus Biverticillium. Studies in Mycology 70: 159–183.
Sánchez-García M, Cifuentes-Blanco J, Matheny PB. 2013. Revisión taxonómica del género Melanoleuca en México y descripción de especies nuevas. Revista Mexicana de Biodiversidad 84 (supplemento micologia): 111–127.
Sandoval-Denis M, Gené J, Sutton DA, et al. 2016. Redefining Microascus, Scopulariopsis and allied genera. Persoonia: Molecular Phylogeny and Evolution of Fungi. 36: 1–36.
Sarnari M.1998. Monografia illustrate del genere Russula in Europa. Tromo Primo, Italy.
Sarwar S, Aziz T, Hanif M, et al. 2019. Russula swatica: A new species of Russula based on molecular, light microscopy, and scanning electron microscopy analyses from Swat Valley of Khyber Pakhtunkhwa province of Pakistan. Microscopy Research and Technique 82: 1700–1705.
Saxena AS, Mukerji KG. 1970. Fungi of Delhi XV. Lophotrichus indicus sp. nov. Acta Botanica Neerlandica 19: 722–726.
Seifert K, Morgan-Jones G, Gams W, et al. 2011. The genera of Hyphomycetes. CBS Biodiversity Series no. 9: 1–997. Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands.
Silvestro D, Michalak I. 2012. raxmlGUI: a graphical front-end for RAxML. Organisms Diversity and Evolution 12: 335–337.
Singer R. 1942. A monographic study of the genera Crinipellis and Chaetocalathus. Lilloa 8: 441–534.
Singer R. 1955. Type Studies on Basidiomycetes. VIII. Sydowia 9: 367–431.
Singer R, Digilio APL. 1951. Pródromo de la Flora Agaricina Argentina. Lilloa 25: 5–461.
Singtripop C, Hongsanan S, Li J, et al. 2016. Chaetothyrina mangiferae sp. nov., a new species of Chaetothyrina. Phytotaxa 255: 21–33.
Soop K, Dima B, Cooper JA, et al. 2019. A phylogenetic approach to a global supraspecific taxonomy of Cortinarius (Agaricales) with an emphasis on the southern mycota. Persoonia 42: 261–290.
Stamatakis A. 2014. RAxML Version 8: A tool for phylogenetic analysis and postanalysis of large phylogenies. Bioinformatics 30: 1312–1313.
Stamatakis A. 2015. Using RAxML to infer phylogenies. Current Protocols in Bioinformatics 51: 6.14.1–6.14.14.
Stecher G, Tamura K, Kumar S. 2020. Molecular Evolutionary Genetics Analysis (MEGA) for macOS. Molecular Biology and Evolution 37: 1237–1239.
Stevenson JA. 1975. Fungi of Puerto Rico and the American Virgin Islands. Contribution of the Reed Herbarium 23: 1–743.
Suh S-Q, McHugh JV, Blackwell M. 2004. Expansion of the Candida tanzawaensis yeast clade: 16 novel Candida species from basidiocarp-feeding beetles. International Journal of Systematic and Evolutionary Microbiology 54: 2409–2429.

Summerbell RC, Gueidan C, Guarro J, et al. 2018. The protean acremonium. A. sclerotigenum/egyptiacum: Revision, food contaminant, and human disease. Microorganisms 6: 88.
Swofford DL. 2002. PAUP*: Phylogenetic Analysis Using Parsimony (*and other methods). Version 4.0b10. Sunderland, Massachusetts: Sinauer Associates.
Swofford DL. 2003. PAUP* 4.0b10. Phylogenetic Analysis Using Parsimony (*and other methods). Version 4. Sinauer Associates, Sunderland, MA, USA.
Tamura K, Stecher G, Peterson D, et al. 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725–2729.
Tanaka K, Hirayama K, Yonezawa H, et al. 2015. Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 82: 75–136.
Tanney JB, Douglas B, Seifert KA. 2016. Sexual and asexual states of some endophytic Phialocephala species of Picea. Mycologia 108: 255–280.
Tanney JB, Seifert KA. 2020. Mollisiaceae: An overlooked lineage of diverse endophytes. Studies in Mycology 95: 293–380.
Taylor JE, Crous PW. 2001. Morphological variation and cultural characteristics of Coniothyrium leucospermi associated with leaf spots of Proteaceae. Mycoscience 42: 265–271.
Thorn RG, Kim JI, Lebeuf R, et al. 2017. The golden chanterelles of Newfoundland and Labrador: a new species, a new record for North America, and a lost species rediscovered. Botany 95: 547–560.
Trifinopoulos J, Nguyen L-T, Von Haeseler A, et al. 2016. W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research: 44 (W1): W232–W235.
Tsuneda A, Hambleton S, Currah RS. 2004. Morphology and phylogenetic placement of Endoconidioma, a new endoconidial genus from trembling aspen. Mycologia 96: 1128–1135.
Uljé CB. 2005. Coprinus. In: Noordeloos ME, Kuyper TW, Vellinga EC (eds), Flora Agaricina Neerlandica 6: 22–109. Taylor & Francis, Boca Raton.
Van der Plaats-Niterink AJ. 1981. Monograph of the genus Pythium. Studies in Mycology 21: 1–242.
Varghese KI, Rao VG. 1980 '1979'. Forest microfungi I. Subramaniomyces, a new genus of hyphomycetes. Kavaka 7: 83–85.
Velmurugan S, Prasannakumar C, Manokaran S, et al. 2013. DNA barcodes for marine fungal identification and discovery. Fungal Ecology 6: 408–418.
Videira SIR, Groenewald JZ, Nakashima C, et al. 2017. Mycosphaerellaceae – chaos or clarity? Studies in Mycology 87: 257–421.
Visagie CM, Houbraken J, Frisvad JC, et al. 2014. Identification and nomenclature of the genus Penicillium. Studies in Mycology 78: 343–371.
Vu D, Groenewald M, De Vries M, et al. 2019. Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154.
Wanasinghe DN, Hyde KD, Jeewon R, et al. 2017. Phylogenetic revision of Camarosporium (Pleosporineae, Dothideomycetes) and allied genera. Studies in Mycology 87: 207–256.
Warcup JH, Talbot PHB. 1967. Perfect states of Rhizoctonias associated with orchids. New Phytologist 66: 631–641.
Watling R, Gregory NM. 1986. Observations on the boletes of the Cooloola Sandmass, Queensland and notes on their distribution in Australia. Proceedings of the Royal Society of Queensland 97: 97–128.
Weir BS, Johnston PR, Damm U. 2012. The Colletotrichum gloeosporioides species complex. Studies in Mycology 73: 115–180.
Weiss M, Waller F, Zuccaro A, et al. 2016. Sebacinales – one thousand and one interactions with land plants. New Phytologist 211: 20–40.
Wendt L, Sir EB, Kuhnert E, et al. 2018. Resurrection and emendation of the Hypoxylaceae, recognised from a multigene phylogeny of the Xylariales. Mycological Progress 17: 115–154.
White TJ, Bruns T, Lee S, et al. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, et al. (eds), PCR protocols: A guide to methods and applications: 315–322. Academic Press, Inc., New York.
Whitehead MR, Catullo RA, Ruibal M, et al. 2017. Evaluating multilocus Bayesian species delimitation for discovery of cryptic mycorrhizal diversity. Fungal Ecology 26: 74–84.
Wijayawardene NN, Hyde KD, Bhat DJ, et al. 2015. Additions to brown spored coelomycetous taxa in Massarinae, Pleosporales: introducing Phragmocamarosporium gen. nov. and Suttonomyces gen. nov. Cryptogamie, Mycologie 36: 213–224.
Woudenberg JHC, Hanse B, Van Leeuwen GCM, et al. 2017. Stemphylium revisited. Studies in Mycology 87: 77–103.
Woudenberg JHC, Seidl MF, Groenewald JZ, et al. 2015. Alternaria section Alternaria: Species, formae speciales or pathotypes? Studies in Mycology 82: 1–21.
Wu G, Li YC, Zhu XT, et al. 2016. One hundred noteworthy boletes from China. Fungal Diversity 81: 25–188.
Yilmaz N, Visagie CM, Houbraken J, et al. 2014. Polyphasic taxonomy of the genus Talaromyces. Studies in Mycology 78: 175–341.
Zheng J, Lu YF, Liu XJ, et al. 2017. Cyberlindnera xishuangbannaensis f.a., sp. nov., a yeast isolated from rotting wood. International Journal of Systematic and Evolutionary Microbiology 67: 5051–5055.
Zwickl DJ. 2006. Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD dissertation, The University of Texas at Austen.