Persoonia 46, 2021: 313–528
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

ISSN (Online) 1878-9080
https://doi.org/10.3767/persoonia.2021.46.11

Fungal Planet description sheets: 1182–1283

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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: **Algeria**, *Phaeoacremonium adelophialidum* from *Vitis vinifera.* **Antarctica**, *Comoclathris antarctica* from soil. **Australia**, *Coniochaeta salicifolia* as endophyte from healthy leaves of *Geijera salicifolia*, *Eremothecium peggii* in fruit of *Citrus australis*, *Microdochium ratticaudae* from stem of *Sporobolus natalensis*, *Neocelosporium corymbiae* on stems of *Corymbia variegata*, *Phytophthora kelmanii* from rhizosphere soil of *Ptilotus pyramidatus*, *Pseudosydowia backhousiae* on living leaves of *Backhousia citriodora*, *Pseudosydowia indooroopillyensis*, *Pseudosydowia louisecottisiae* and *Pseudosydowia queenslandica* on living leaves of *Eucalyptus* sp. **Brazil**, *Absidia montepascoalis* from soil. **Chile**, *Ilyonectria zarorii* from soil under *Maytenus boaria.* **Costa Rica**, *Colletotrichum filicis* from an unidentified fern. **Croatia**, *Mollisia endogranulata* on deteriorated hardwood. **Czech Republic**, *Arcopilus navicularis* from tea bag with fruit tea, *Neosetophoma buxi* as endophyte from *Buxus sempervirens*, *Xerochrysium bohemicum* on surface of biscuits with chocolate glaze and filled with jam. **France**, *Entoloma cyaneobasale* on basic to calcareous soil, *Fusarium aconidiale* from *Triticum aestivum*, *Fusarium juglandicola* from buds of *Juglans regia*. **Germany**, *Tetraploa endophytica* as endophyte from *Microthlaspi perfoliatum* roots. **India**, *Castanediella ambae* on leaves of *Mangifera indica*, *Lactifluus kanadii* on soil under *Castanopsis* sp., *Penicillium uttarakhandense* from soil. **Italy**, *Penicillium ferraniaense* from compost. **Namibia**, *Bezerromyces gobabebensis* on leaves of unidentified succulent, *Cladosporium stipagrostidicola* on leaves of *Stipagrostis* sp., *Cymostachys euphorbiae* on leaves of *Euphorbia* sp., *Deniquelata hypolithi* from hypolith under a rock, *Hysterobrevium walvisbayicola* on leaves of unidentified tree, *Knufia hypolithi* and *Knufia walvisbayicola* from hypolith under a rock, *Lapidomyces stipagrostidicola* on leaves of *Stipagrostis* sp., *Nothophaeotheca mirabibensis* (incl. *Nothophaeotheca* gen. nov.) on persistent inflorescence remains of *Blepharis obmitrata*, *Paramyrothecium salvadorae* on twigs of *Salvadora persica*, *Preussia procaviicola* on dung of *Procavia* sp., *Sordaria equicola* on zebra dung, *Volutella salvadorae* on stems of *Salvadora persica*. **Netherlands**, *Entoloma ammophilum* on sandy soil, *Entoloma pseudocruentatum* on nutrient poor (acid) soil, *Entoloma pudens* on plant debris, amongst grasses. **New Zealand**, *Amorocoelophoma neoregeliae* from leaf spots of *Neoregelia* sp., *Aquilomyces metrosideri* and *Septoriella callistemonis* from stem discolouration and leaf spots of *Metrosideros* sp., *Cadophora neoregeliae* from leaf spots of *Neoregelia* sp., *Flexuomyces asteliae* (incl. *Flexuomyces* gen. nov.) and *Mollisia asteliae* from leaf spots of *Astelia chathamica*, *Ophioceras freycinetiae* from leaf spots of *Freycinetia*

Abstract (cont.)

banksii, *Phaeosphaeria caricis-sectae* from leaf spots of *Carex secta*. **Norway**, *Cuphophyllus flavipesoides* on soil in semi-natural grassland, *Entoloma coracis* on soil in calcareous *Pinus* and *Tilia* forests, *Entoloma cyaneolilacinum* on soil semi-natural grasslands, *Inocybe norvegica* on gravelly soil. **Pakistan**, *Butyriboletus parachinarensis* on soil in association with *Quercus baloot*. **Poland**, *Hyalodendriella bialowiezensis* on debris beneath fallen bark of Norway spruce *Picea abies*. **Russia**, *Bolbitius sibiricus* on a moss covered rotting trunk of *Populus tremula*, *Crepidotus wasseri* on debris of *Populus tremula*, *Entoloma isborscanum* on soil on calcareous grasslands, *Entoloma subcoracis* on soil in subalpine grasslands, *Hydropus lecythiocystis* on rotted wood of *Betula pendula*, *Meruliopsis faginea* on fallen dead branches of *Fagus orientalis*, *Metschnikowia taurica* from fruits of *Ziziphus jujube*, *Suillus praetermissus* on soil, *Teunia lichenophila* as endophyte from *Cladonia rangiferina*. **Slovakia**, *Hygrocybe fulgens* on mowed grassland, *Pleuroflammula pannonica* from corticated branches of *Quercus* sp. **South Africa**, *Acrodontium burrowsianum* on leaves of unidentified *Poaceae*, *Castanediella senegaliae* on dead pods of *Senegalia ataxacantha*, *Cladophialophora behniae* on leaves of *Behnia* sp., *Colletotrichum cliviigenum* on leaves of *Clivia* sp., *Diatrype dalbergiae* on bark of *Dalbergia armata*, *Falcocladium heteropyxidicola* on leaves of *Heteropyxis canescens*, *Lapidomyces aloidendricola* as epiphyte on brown stem of *Aloidendron dichotomum*, *Lasionectria sansevieriae* and *Phaeosphaeriopsis sansevieriae* on leaves of *Sansevieria hyacinthoides*, *Lylea dalbergiae* on *Diatrype dalbergiae* on bark of *Dalbergia armata*, *Neochaetothyrina syzygii* (incl. *Neochaetothyrina* gen. nov.) on leaves of *Syzygium chordatum*, *Nothophaeomoniella ekebergiae* (incl. *Nothophaeomoniella* gen. nov.) on leaves of *Ekebergia pterophylla*, *Paracymostachys euphorbiae* (incl. *Paracymostachys* gen. nov.) on leaf litter of *Euphorbia ingens*, *Paramycosphaerella pterocarpi* on leaves of *Pterocarpus angolensis*, *Paramycosphaerella syzygii* on leaf litter of *Syzygium chordatum*, *Parateichospora phoenicicola* (incl. *Parateichospora* gen. nov.) on leaves of *Phoenix reclinata*, *Seiridium syzygii* on twigs of *Syzygium chordatum*, *Setophoma syzygii* on leaves of *Syzygium* sp., *Starmerella xylocopis* from larval feed of an Afrotropical bee *Xylocopa caffra*, *Teratosphaeria combreti* on leaf litter of *Combretum kraussii*, *Teratosphaericola leucadendri* on leaves of *Leucadendron* sp., *Toxicocladosporium pterocarpi* on pods of *Pterocarpus angolensis*. **Spain**, *Cortinarius bonachei* with *Quercus ilex* in calcareus soils, *Cortinarius brunneovolvatus* under *Quercus ilex* subsp. *ballota* in calcareous soil, *Extremopsis radicicola* (incl. *Extremopsis* gen. nov.) from root-associated soil in a wet heathland, *Russula quintanensis* on acidic soils, *Tubaria vulcanica* on volcanic lapilii material, *Tuber zambonelliae* in calcareus soil. **Sweden**, *Elaphomyces borealis* on soil under *Pinus sylvestris* and *Betula pubescens*. **Tanzania**, *Curvularia tanzanica* on inflorescence of *Cyperus aromaticus*. **Thailand**, *Simplicillium niveum* on *Ophiocordyceps camponoti-leonardi* on underside of unidentified dicotyledonous leaf. **USA**, *Calonectria californiensis* on leaves of *Umbellularia californica*, *Exophiala spartinae* from surface sterilised roots of *Spartina alterniflora*, *Neophaeococcomyces oklahomaensis* from outside wall of alcohol distillery. **Vietnam**, *Fistulinella aurantioflava* on soil. Morphological and culture characteristics are supported by DNA barcodes.

Citation: Crous PW, Cowan DA, Maggs-Kölling, et al. 2021. Fungal Planet description sheets: 1182–1283. Persoonia 46: 313 – 528.
https://doi.org/10.3767/persoonia.2021.46.11.
Effectively published online: 13 July 2021 [Received: 1 May 2021; Accepted: 1 June 2021].

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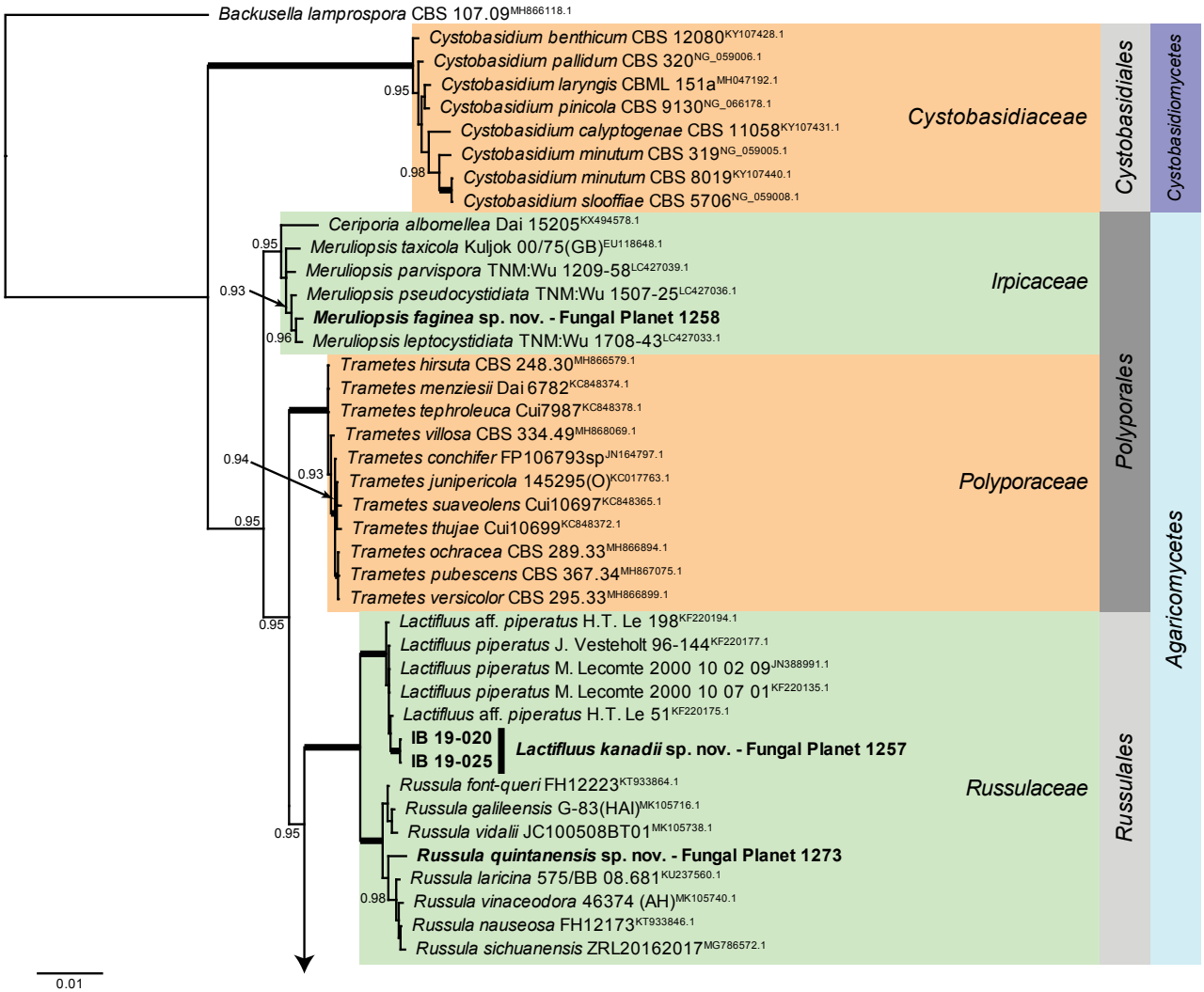
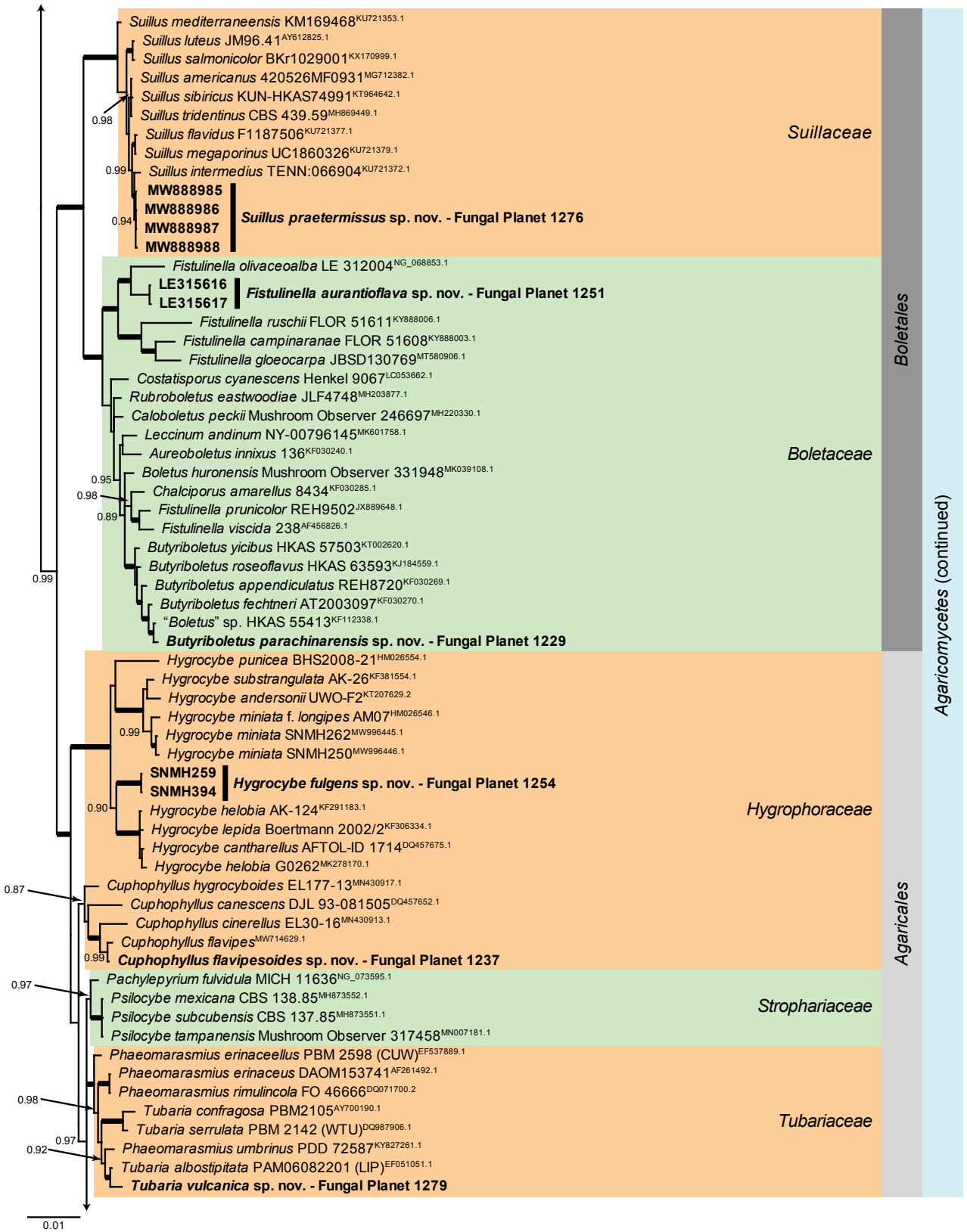
Acknowledgements Leslie W.S. de Freitas and colleagues express their gratitude to Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for scholarships provided to Leslie Freitas and for the research grant provided to André Luiz Santiago; their contribution was financed by the projects 'Diversity of *Mucoromycotina* in the different ecosystems of the Atlantic Rainforest of Pernambuco' (FACEPE–First Projects Program PPP/FACEPE/CNPq–APQ–0842-2.12/14) and 'Biology of conservation of fungi s.l. in areas of Atlantic Forest of Northeast Brazil' (CNPq/ICMBio 421241/2017-9) H.B. Lee was supported by the Graduate Program for the Undiscovered Taxa of Korea (NIBR202130202). The study of O.V. Morozova, E.F. Malysheva, V.F. Malysheva, I.V. Zmitrovich, and L.B. Kalinina 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'. The work of O. V. Morozova, L.B. Kalinina, T. Yu. Svetasheva, and E.A. Zvyagina was financially supported by Russian Foundation for Basic Research project no. 20-04-00349. E.A. Zvyagina and T.Yu. Svetasheva are grateful to A.V. Alexandrova, A.E. Kovalenko, A.S. Baykalova for the loan of specimens, T.Y. James, E.F. Malysheva and V.F. Malysheva for sequencing. J.D. Reyes acknowledges B. Dima for comparing the holotype sequence of *Cortinarius bonachei* with the sequences in his database. A. Mateos and J.D. Reyes acknowledge L. Quijada for reviewing the phylogeny and S. de la Peña-Lastra and P. Alvarado for their support and help. Vladimir I. Kapitonov and colleagues are grateful to Brigitta Kiss for help with their molecular studies. This study was conducted under research projects of the Tobolsk Complex Scientific Station of the Ural Branch of the Russian Academy of Sciences (N AAAA-A19-119011190112-5). E. Larsson acknowledges the Swedish Taxonomy Initiative, SLU Artdatabanken, Uppsala (dha.2019.4.3-13). The study of D.B. Raudabaugh and colleagues was supported by the Schmidt Science Fellows, in partnership with the Rhodes Trust. Gregorio Delgado is grateful to Michael Manning and Kamash Pillai (Eurofins EMLab P&K) for provision of laboratory facilities. Jose G. Maciá-Vicente acknowledges support from the German Research Foundation under grant MA7171/1-1, and from the Landes-Offensive zur Entwicklung Wissenschaftlich-ökonomischer Exzellenz (LOEWE) of the state of Hesse within the framework of the Cluster for Integrative Fungal Research (IPF). Thanks are also due to the authorities of the Cabañeros National Park and Los Alcornocales Natural Park for granting the collection permit and for support during field work. The study of Alina V. Alexandrova was carried out as part of the Scientific Project of the State Order of the Government of Russian Federation to Lomonosov Moscow State University No. 121032300081-7. Michał Gorczak was financially supported by the Ministry of Science and Higher Education through the Faculty of Biology, University of Warsaw intramural grant DSM 0117600-13. M. Gorczak acknowledges M. Klemens for sharing a photo of the Białowieża Forest logging site and M. Senderowicz for help with preparing the illustration. Ivona Kautmanová and D. Szabóová were funded by the Operational Program of Research and Development and co-financed with the European Fund for Regional Development (EFRD). ITMS 26230120004: 'Building of research and development infrastructure for investigation of genetic biodiversity of organisms and joining IBOL initiative'. Ishika Bera, Aniket Ghosh, Jorinde Nuytinck and Annemieke Verbeken are grateful to the Director, Botanical Survey of India (Kolkata), Head of the Department of Botany & Microbiology & USIC Dept. HNB Garhwal University, Srinagar, Garhwal for providing research facilities. Ishika Bera and Aniket Ghosh acknowledge the staff of the forest department of Arunachal Pradesh for facilitating the macrofungal surveys to the restricted areas. Sergey Volobuev was supported by the Russian Science Foundation (RSF project N 19-77-00085). Aleksey V. Kachalkin and colleagues were supported by the Russian Science Foundation (grant No. 19-74-10002). The study of Anna M. Glushakova was carried out as part of the Scientific Project of the State Order of the Government of Russian Federation to Lomonosov Moscow State University No. 121040800174-6. Tracey V. Steinrucken and colleagues were supported by AgriFutures Australia (Rural Industries Research and Development Corporation), through funding from the Australian Government Department of Agriculture, Water and the Environment, as part of its Rural Research and Development for Profit program (PRJ-010527). Neven Matočec and colleagues thank the Croatian Science Foundation for their financial support under the project grant HRZZ-IP-2018-01-1736 (ForFungiDNA). Ana Pošta thanks the Croatian Science Foundation for their support under the grant HRZZ-2018-09-7081. The research of Milan Spetik and co-authors was supported by Internal Grant of Mendel University in Brno No. IGA-ZF/2021-SI1003. K.C. Rajeshkumar thanks SERB, the Department of Science and Technology, Government of India for providing financial support under the project CRG/2020/000668 and the Director, Agharkar Research Institute for providing research facilities. Nikhil Ashtekar thanks CSIR-HRDG, INDIA, for financial support under the SRF fellowship (09/670(0090)/2020-EMR-I), and acknowledges the support of the DIC Microscopy Facility, established by Dr Karthick Balasubramanian, B&P (Plants) Group, ARI, Pune. The research of Alla Eddine Mahamedi and co-authors was supported by project No. CZ.02.1.01/0.0/0.0/16_017/0002334, Czech Republic. Tereza Tejklová is thanked for providing useful literature. A. Polhorský and colleagues were supported by the Operational Program of Research and Development and co-financed with the European fund for Regional Development (EFRD), ITMS 26230120004: Building of research and development infrastructure for investigation of genetic biodiversity of organisms and joining IBOL initiative. Yu Pei Tan and colleagues thank R. Chen for her technical support. Ernest Lacey thanks the Cooperative Research Centres Projects scheme (CRCP-FIVE000119) for its support. Suchada Mongkolsamrit and colleagues were financially supported by the Platform Technology Management Section, National Center for Genetic Engineering and Biotechnology (BIOTEC), Project Grant No. P19-50231. Dilnora Gouliamova and colleagues were supported by a grant from the Bulgarian Science Fund (KP-06-H31/19). The research of Timofey A. Pankratov was supported by the Russian Foundation for Basic Research (grant No. 19-04-00297a). Gabriel Moreno and colleagues wish to express their gratitude to L. Monje and A. Pueblas of the Department of Drawing and Scientific Photography at the University of Alcalá for their help in the digital preparation of the photographs, and to J. Rejos, curator of the AH herbarium, for his assistance with the specimens examined in the present study. Vit Hubka was supported by the Charles University Research Centre program No. 204069. Alena Kubátová was supported by The National Programme on Conservation and Utilization of Microbial Genetic Resources Important for Agriculture (Ministry of Agriculture of the Czech Republic). The Kits van Waveren Foundation (Rijksherbariumfonds Dr E. Kits van Waveren, Leiden, Netherlands) contributed substantially to the costs of sequencing and travelling expenses for M. Noordeloos. The work of B. Dima was supported by the ÚNKP-20-4 New National Excellence Program of the Ministry for Innovation and Technology from the source of the National Research, Development and Innovation Fund, and by the ELTE Thematic Excellence Programme 2020 supported by the National Research, Development and Innovation Office of Hungary (TKP2020-IKA-05). The Norwegian *Entoloma* studies received funding from the Norwegian Biodiversity Information Centre (NBIC), and the material was partly sequenced through NorBOL. Gunnhild Marthinsen and Katriina Bendiksen (Natural History Museum, University of Oslo, Norway) are acknowledged for performing the main parts of the *Entoloma* barcoding work. 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. Vladimír Ostrý was supported by the Ministry of Health, Czech Republic - conceptual development of research organization (National Institute of Public Health – NIPH, IN 75010330). Konstanze Bensch (Westerdijk Fungal Biodiversity Institute, Utrecht) is thanked for correcting the spelling of various Latin epithets.

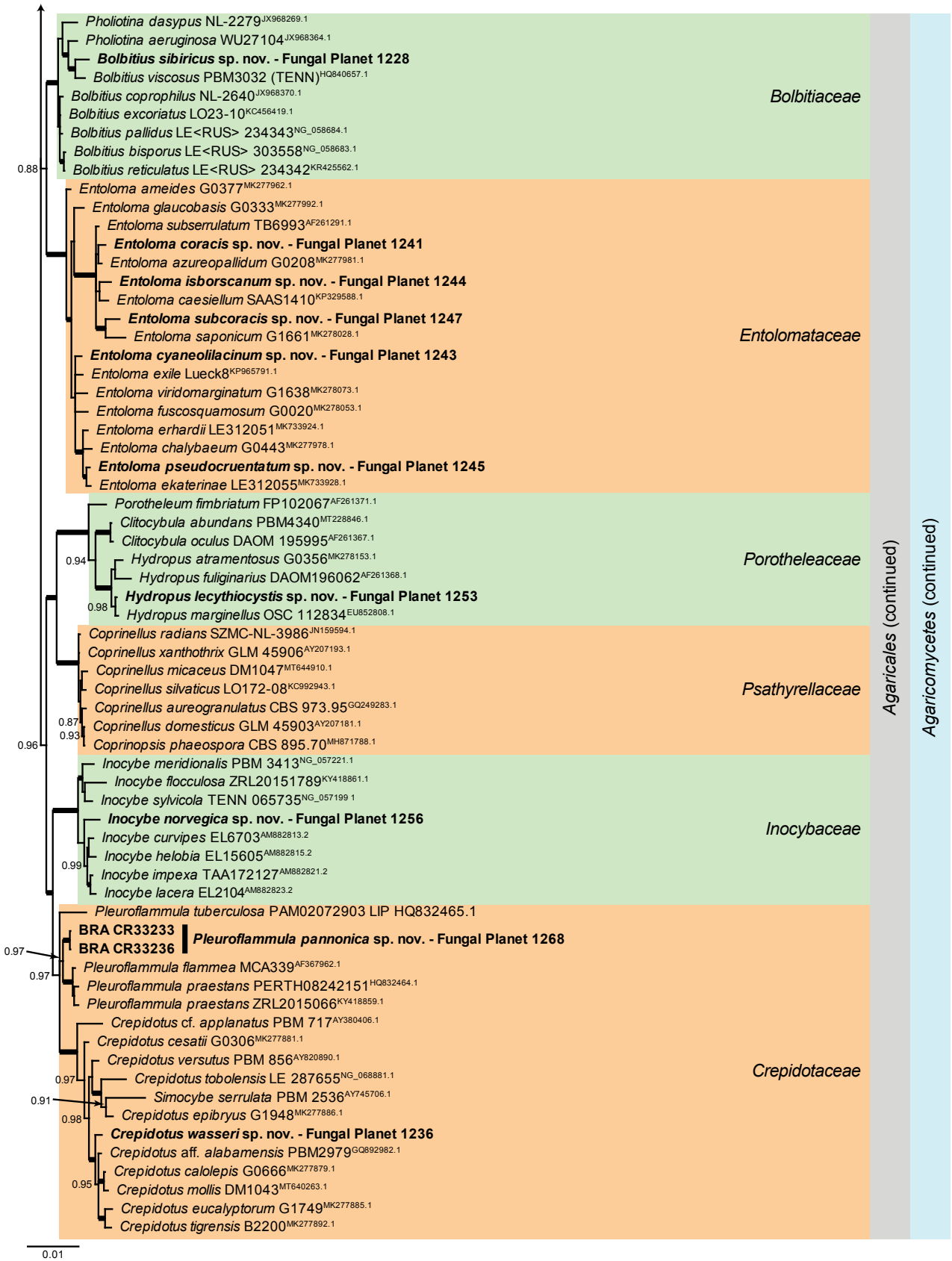


Overview *Agaricomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 279752 trees resulting from a Bayesian analysis of the LSU sequence alignment (170 sequences including outgroup; 948 aligned positions; 553 unique site patterns; 1865000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).



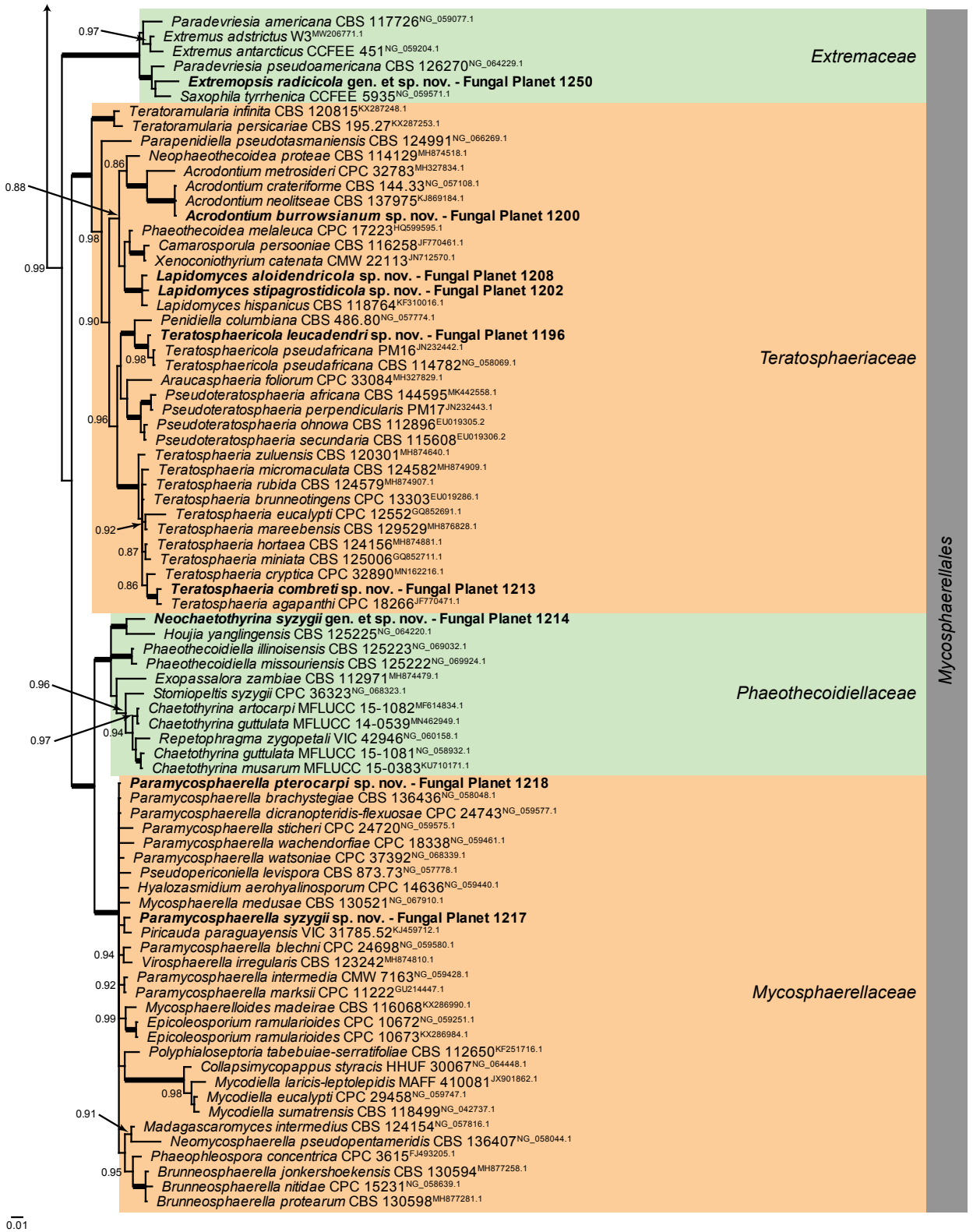
Overview *Agaricomycetes* phylogeny (cont.) – part 2



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

Overview *Dothideomycetes* (Other orders) phylogeny – part 1

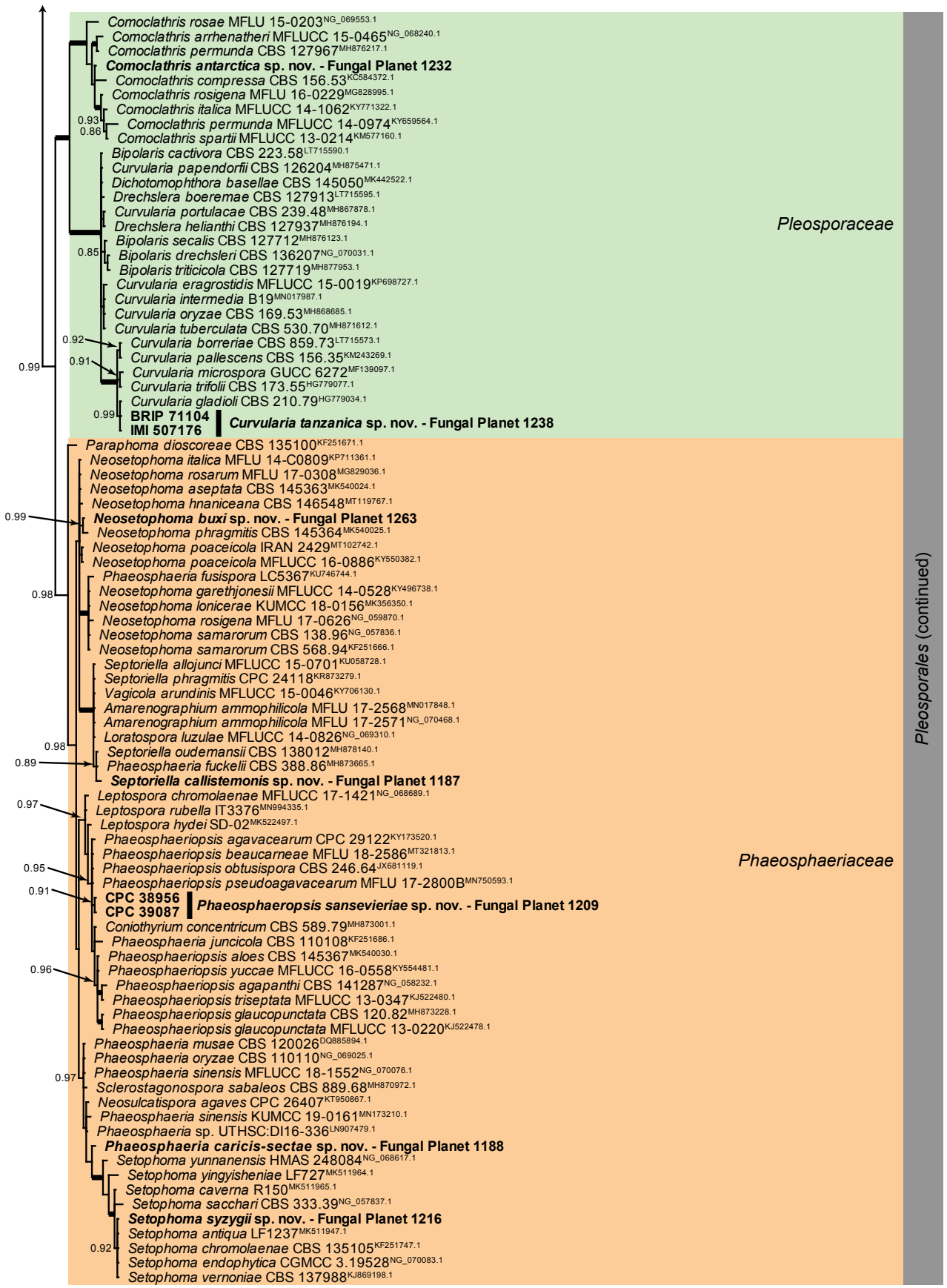
Consensus phylogram (50 % majority rule) of 56 102 trees resulting from a Bayesian analysis of the LSU sequence alignment (179 sequences including outgroup; 832 aligned positions; 378 unique site patterns; 3 740 000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 most basal branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).



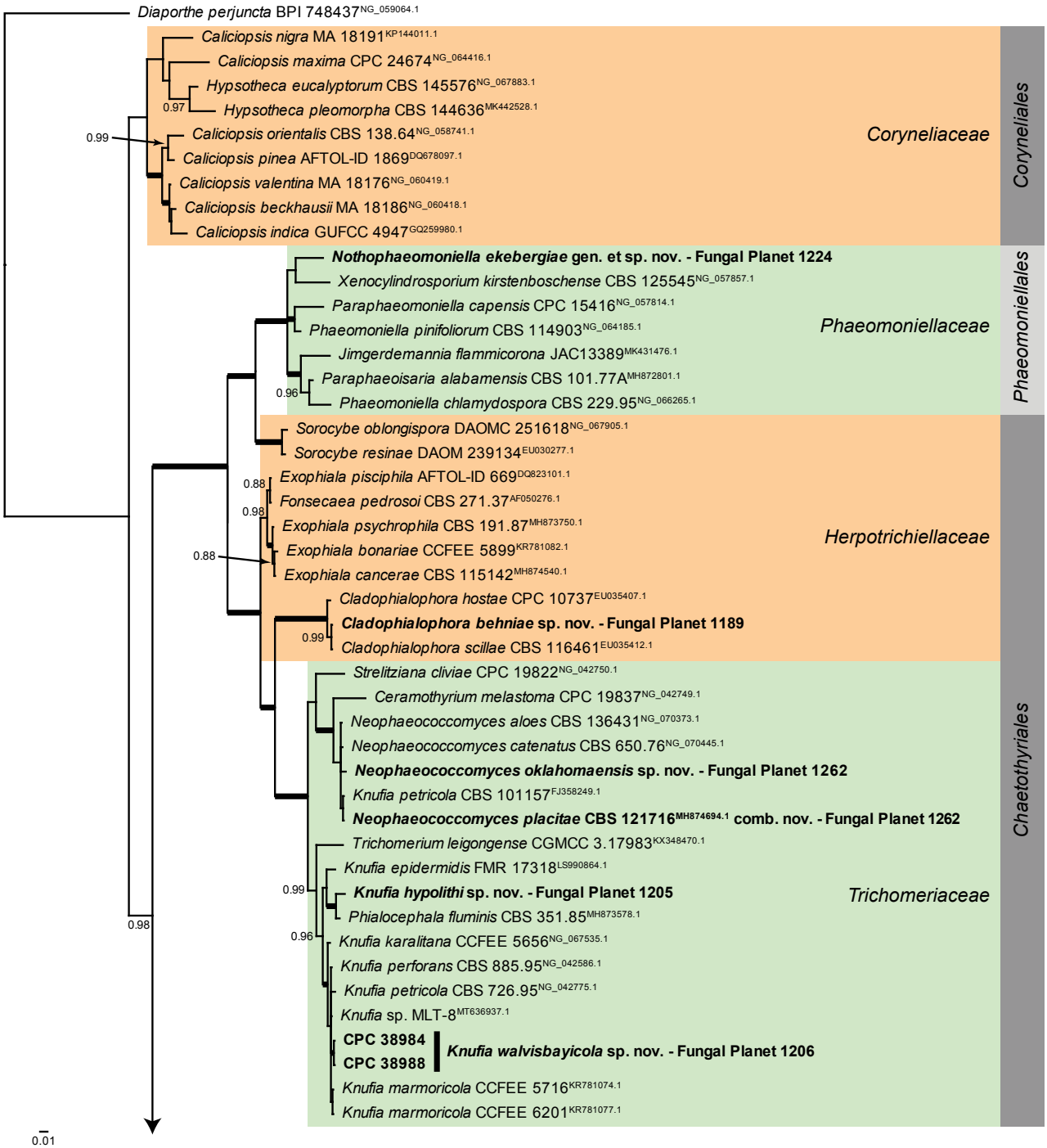
Overview *Dothideomycetes* (Other orders) phylogeny – part 2

Overview *Dothideomycetes* (*Pleosporales*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 91 128 trees resulting from a Bayesian analysis of the LSU sequence alignment (170 sequences including outgroup; 799 aligned positions; 295 unique site patterns; 6 075 000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).

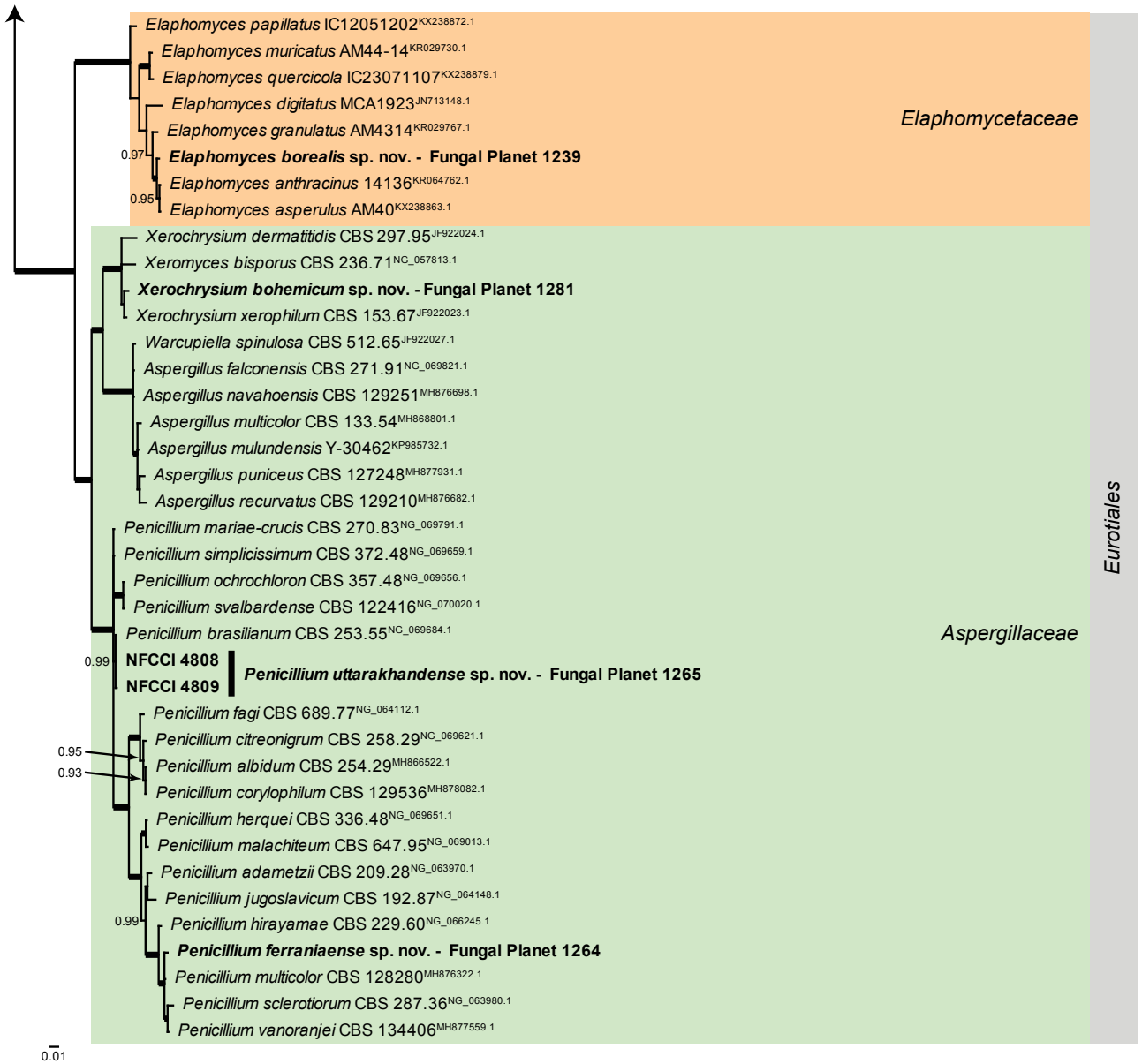


Overview *Dothideomycetes* (*Pleosporales*) phylogeny – part 2

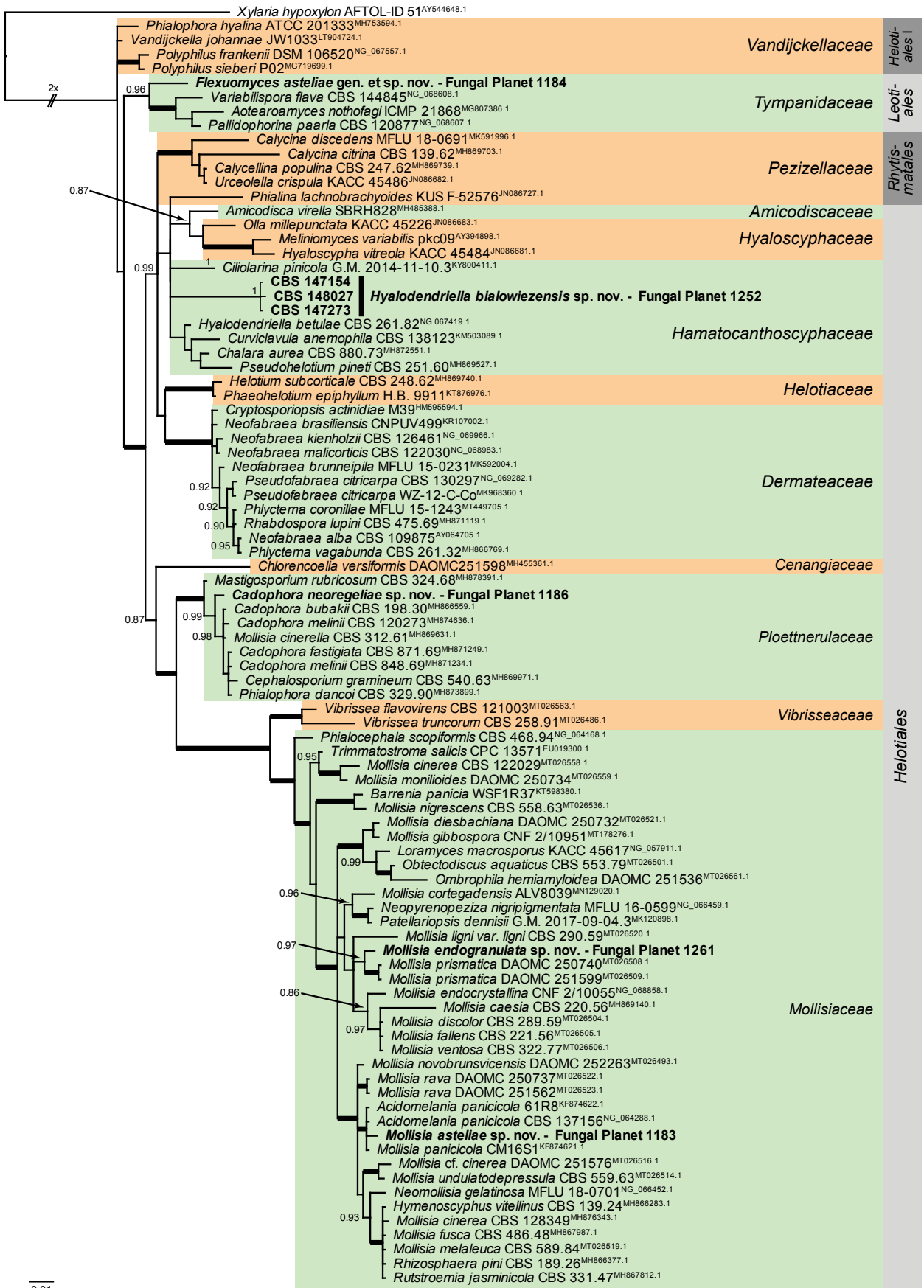


Overview *Eurotiomycetes* phylogeny – part 1

Consensus phylogram (50 % majority rule) of 146 252 trees resulting from a Bayesian analysis of the LSU sequence alignment (85 sequences including outgroup; 847 aligned positions; 357 unique site patterns; 1 010 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).



Overview *Eurotiomycetes* phylogeny – part 2

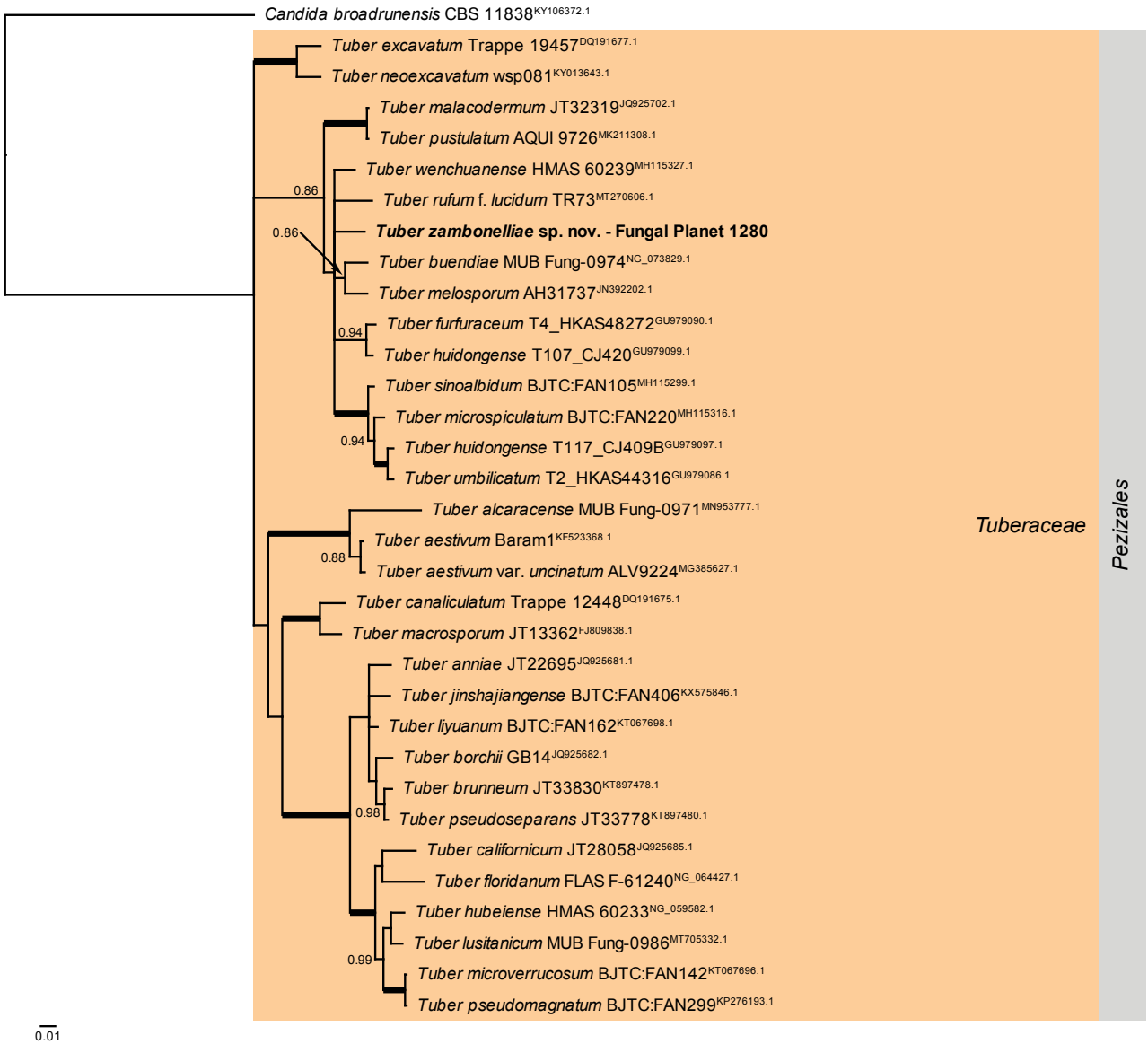


Overview *Leotiomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 408 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (90 sequences including outgroup; 826 aligned positions; 283 unique site patterns; 2 720 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 most basal branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

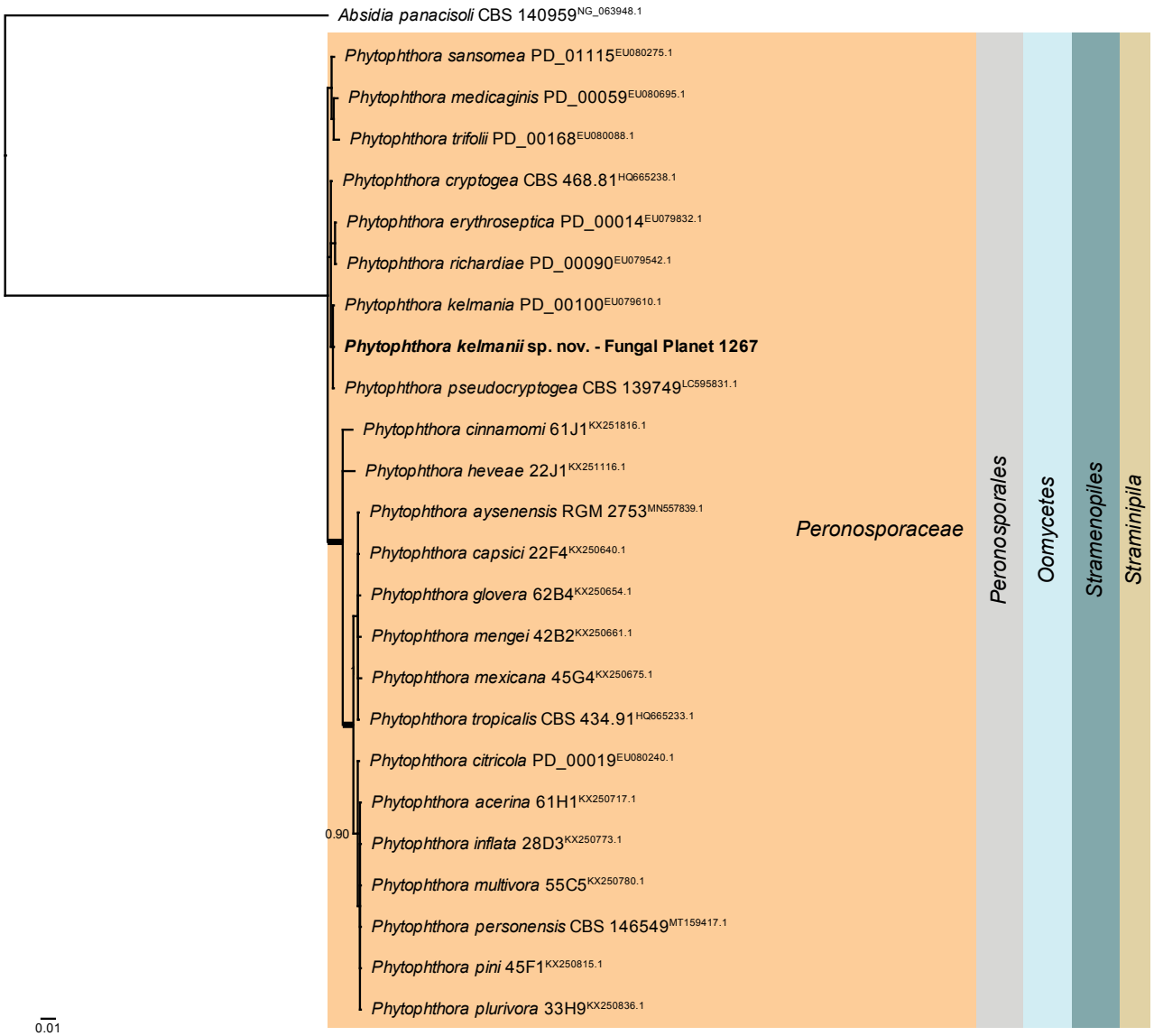
Overview *Mucoromycetes* phylogeny

Consensus phylogram (50 % majority rule) of 141 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (22 sequences including outgroup; 660 aligned positions; 319 unique site patterns; 470 000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher taxonomic classification is indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) or Fungal Planet numbers are indicated behind the species names. The tree was rooted to *Chytridium lagenaria* (GenBank FJ804156.1) 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 28129).



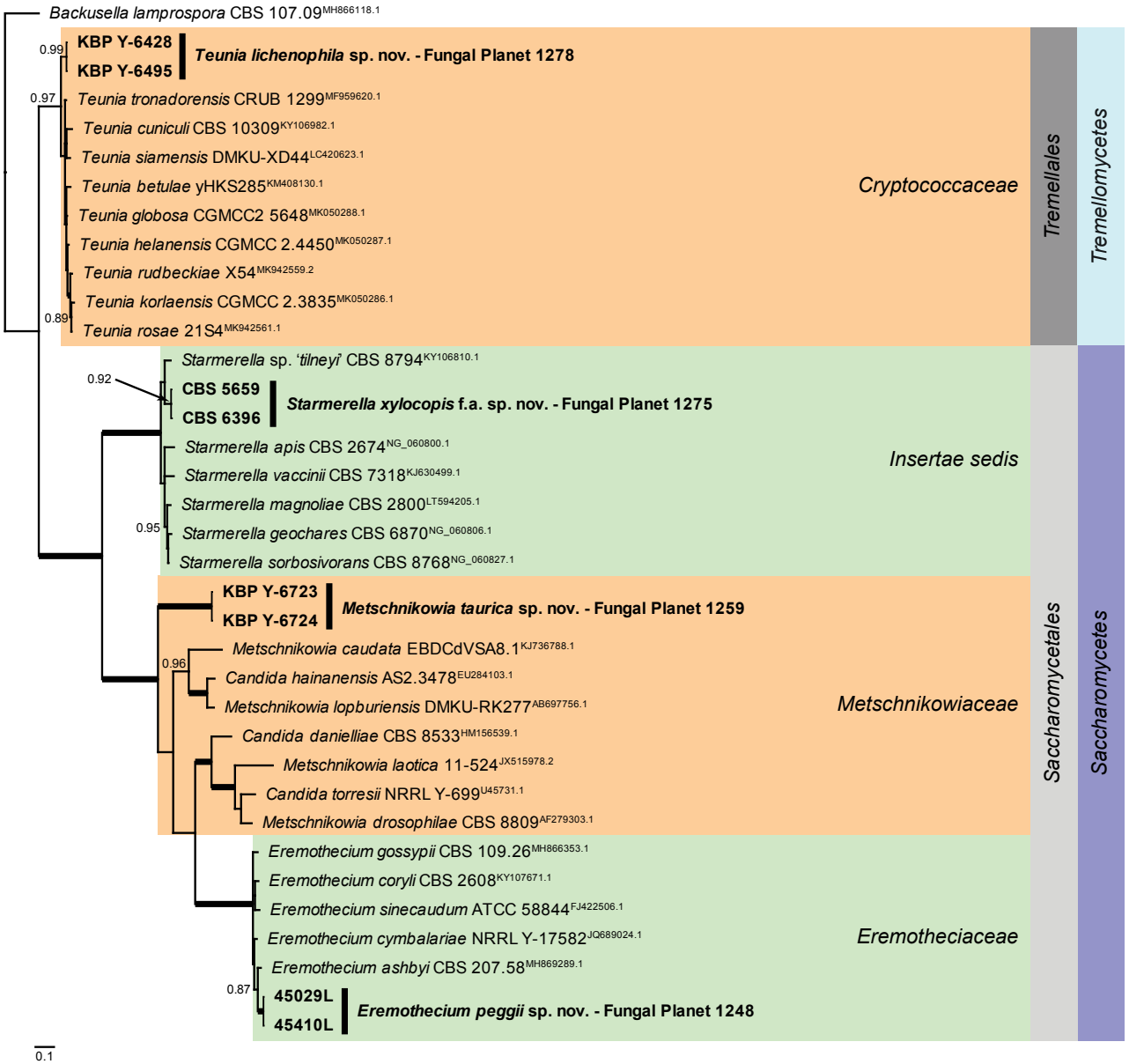
Overview *Pezizomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 87 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (33 sequences including outgroup; 792 aligned positions; 203 unique site patterns; 290 000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The family and order are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).



Overview *Phytophthora* phylogeny

Consensus phylogram (50 % majority rule) of 64 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (25 sequences including outgroup; 1 110 aligned positions; 68 unique site patterns; 215 000 generations with trees sampled every five generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher taxonomic classification is indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).

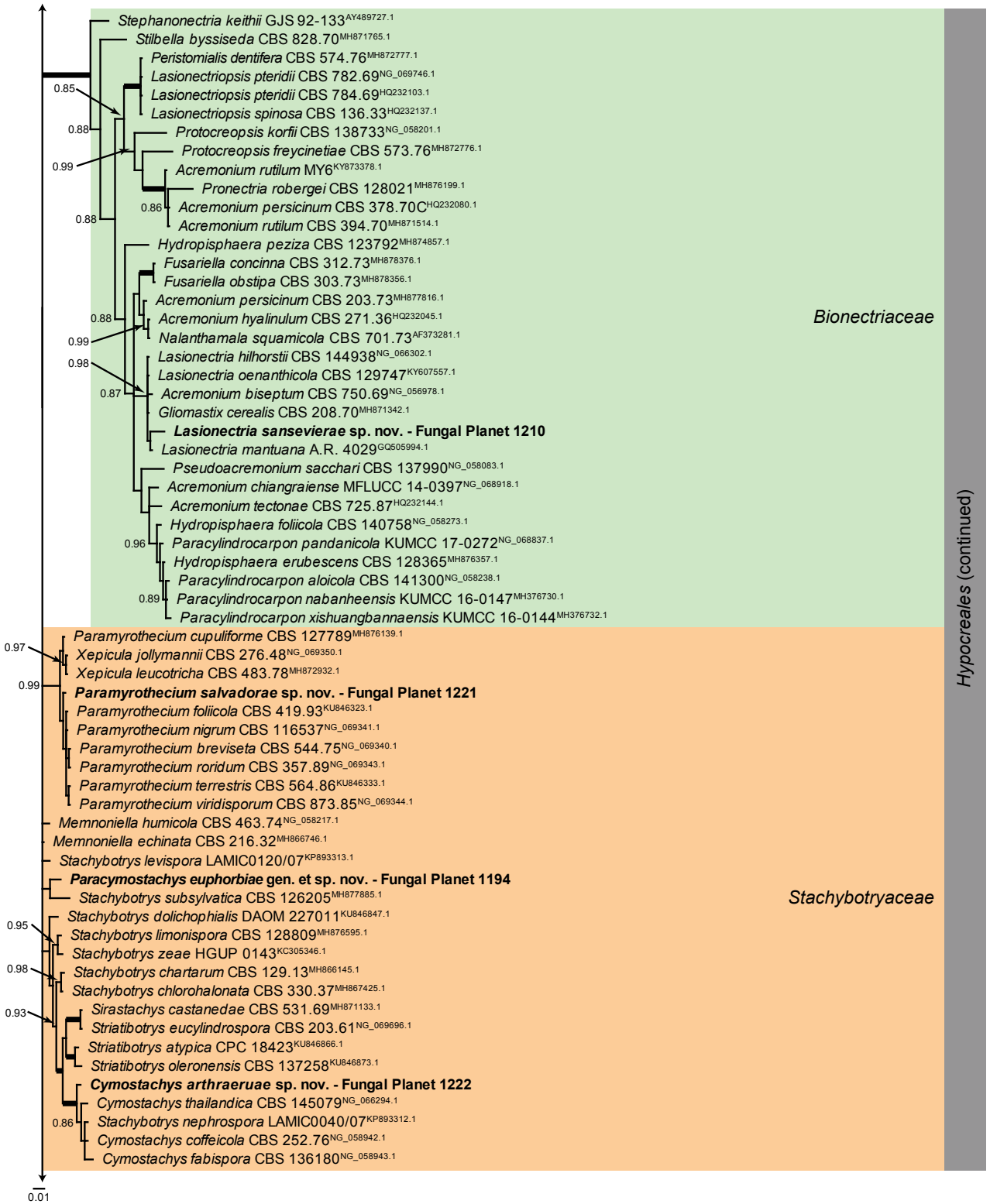


Overview *Saccharomycetes* and *Tremellomycetes* phylogeny

Consensus phylogram (50 % majority rule) of 136 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (36 sequences including outgroup; 667 aligned positions; 432 unique site patterns; 910 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The families, orders and classes are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).

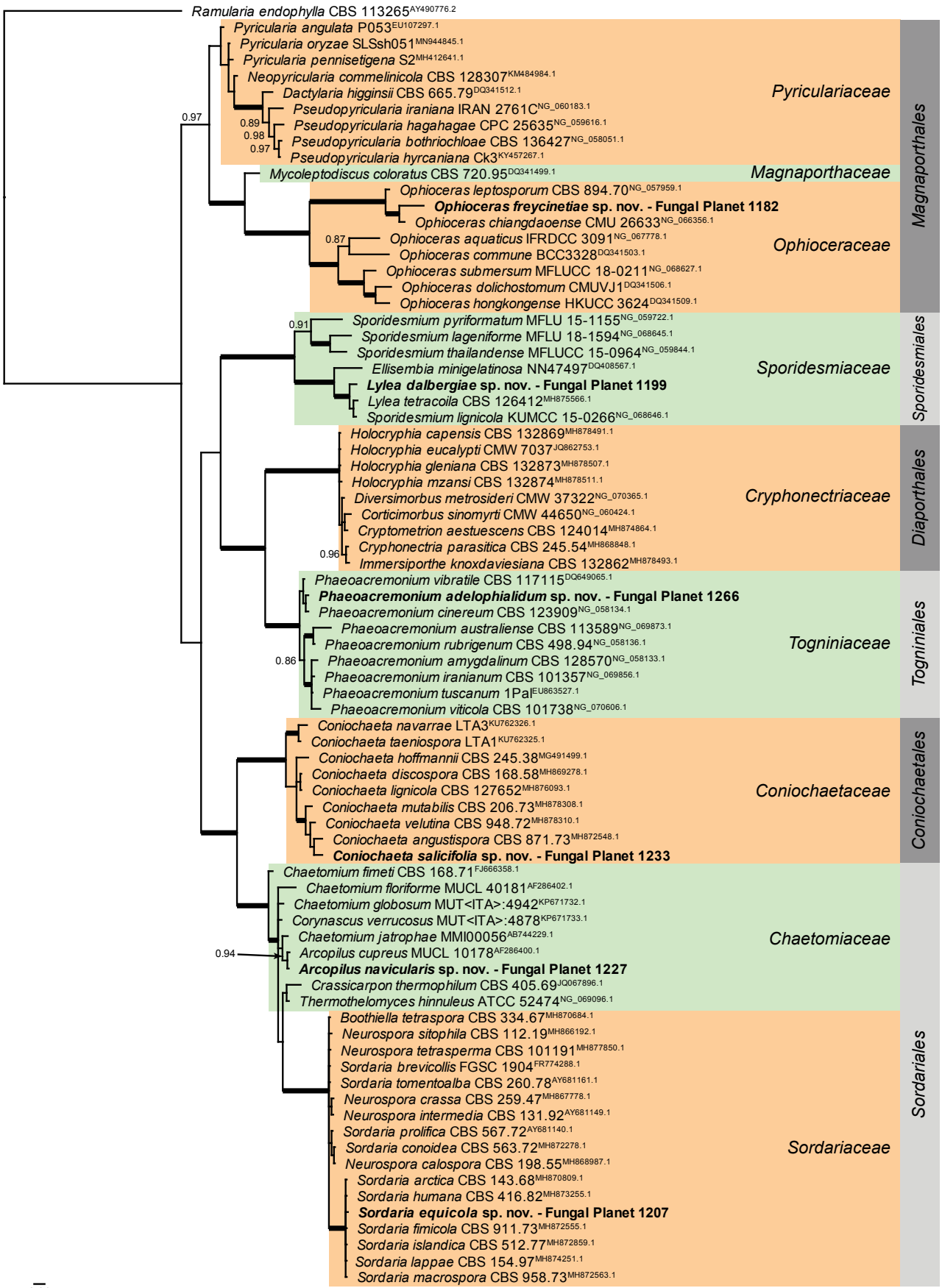
Overview *Sordariomycetes* (*Falcocladiales*, *Glomerellales* and *Hypocreales*) phylogeny – part 1

Consensus phylogram (50 % majority rule) of 846 978 trees resulting from a Bayesian analysis of the LSU sequence alignment (194 sequences including outgroup; 816 aligned positions; 310 unique site patterns; 56 465 000 generations with trees sampled every 100 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).



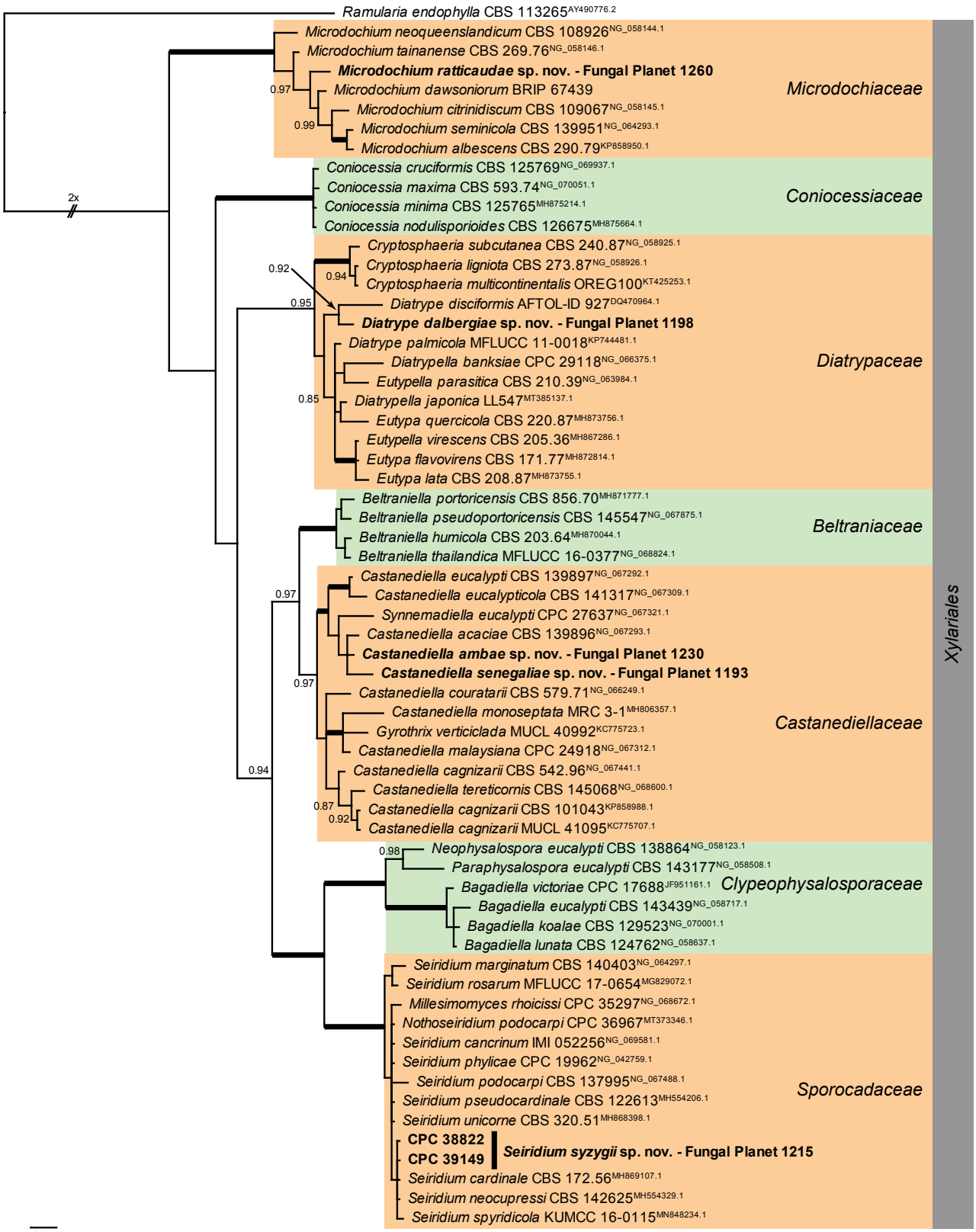
Overview *Sordariomycetes* (*Falcocladiales*, *Glomerellales* and *Hypocreales*) phylogeny (cont.) – part 2

Overview *Sordariomycetes* (*Falcocladiales*, *Glomerellales* and *Hypocreales*) phylogeny (cont.) – part 3



Overview *Sordariomycetes* (Other orders) phylogeny

Consensus phylogram (50 % majority rule) of 229 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (79 sequences including outgroup; 813 aligned positions; 293 unique site patterns; 1 530 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 28129).



Overview *Sordariomycetes* (*Xylariales*) phylogeny

Consensus phylogram (50 % majority rule) of 118 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (63 sequences including outgroup; 800 aligned positions; 192 unique site patterns; 790 000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and the order are indicated with coloured blocks to the right of the tree. Culture collection/voucher, GenBank accession (in superscript) 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 most basal branched was halved in length to facilitate layout. The alignment and tree were deposited in TreeBASE (Submission ID 28129).


Ophioceras freycinetiae

Fungal Planet 1182 – 13 July 2021

Ophioceras freycinetiae Crous, *sp. nov.*

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

Classification — *Ophioceraceae*, *Magnaporthales*, *Sordariomycetes.*

Mycelium consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells that are aggregated in clusters, forming a slimy sporodochial mass on the agar surface. *Conidiogenous cells* hyaline, smooth, elongated, ampulliform, straight to curved, phialidic with well-developed apical collarette, 10–20 × 2–3 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical, falcate, apex subobtuse, base truncate, (8–)10–12(–13) × 1–1.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface dirty white, reverse buff; on PDA surface and reverse olivaceous grey; on OA surface dirty white.

Typus. New Zealand, Manukau Domain, from leaf spots of *Freycinetia banksii* (*Pandanaceae*), 19 Mar. 2019, *C. Inglis* (holotype CBS H-24412, culture ex-type CPC 38508 = T19_02806E = CBS 146781, ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank MZ064408.1, MZ064465.1, MZ078219.1 and MZ078256.1, MycoBank MB 839493).

Notes — *Ophioceras* has globose to elongated-globose ascomata, cylindrical, 8-spored asci, and filiform, narrowly fusoid to cylindrical, septate ascospores (Tsui et al. 2001, Crous et al. 2021). *Ophioceras freycinetiae* is the first asexual morph linked to the genus. It is closely related to *O. chiangdaoense* and *O. leptosporum*, which are known only from their sexual morphs, thus precluding a morphological comparison.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pestalotiopsis mangifolia* (voucher INBio:612E, GenBank KU204609.1; Identities = 519/546 (95 %), five gaps (0 %)), *Ophioceras* sp. (strain F2020, GenBank KU747855.1; Identities = 465/490 (95 %), five gaps (1 %)) and *Microcera larvarum* (voucher INBio:658D, GenBank KU204629.1; Identities = 475/504 (94 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Ophioceras chiangdaoense* (strain CMU 26633, GenBank NG_066356.1; Identities = 827/843 (98 %), two gaps (0 %)), *Ophioceras leptosporum* (strain CBS 894.70, GenBank NG_057959.1; Identities = 825/846 (98 %), two gaps (0 %)) and *Ophioceras commune* (strain BCC3328, GenBank DQ341503.1; Identities = 785/848 (93 %), six gaps (0 %)). No significant hits were obtained when the ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. *Freycinetia banksii*. Conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

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Mollisia asteliae
& Flexuomyces asteliae

Fungal Planet 1183 & 1184 – 13 July 2021

Mollisia asteliae Crous, *sp. nov.*

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

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

Apothecia scattered, sessile with central subiculum, cup-shaped, becoming disc-shaped at maturity, outline entire, buff, outer surface buff to honey, 500–800 µm diam. Ectal excipulum at base of *textura globosa*, 200–300 µm diam near base, composed on globose to subglobose brown cells, 7–11 µm diam. *Paraphyses* cylindrical with rounded ends, at times slightly swollen, septate, branched below, thin-walled, 3–4 µm diam, with large refractive vacuole bodies, similar in length to asci. *Asci* cylindrical-clavate, stipitate, 8-spored, 45–52 × 5–7 µm, pore amyloid in Melzer's reagent. *Ascospores* biseriate to obliquely uniseriate, (7–)10–12(–13) × (2–)2.5–3(–3.5) µm, fusoid-ellipsoid to oblong, apices rounded, slightly curved to straight, aseptate, thin-walled, guttulate, some ascospores in water showing remnants of mucoid sheath in central region, disappearing at maturity.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, smooth margin, covering dish after 2 wk at 25 °C. On MEA and PDA surface hazel, reverse fuscous black; on OA surface rosy buff.

Typus. New Zealand, Auckland, Taunton Terrace, from leaf spots of *Astelia chathamica* (*Asteliaceae*), 14 Mar. 2019, *C. Inglis* (holotype CBS H-24415, culture ex-type CPC 38521 = T19_02324D = CBS 146780, ITS, LSU, *tef1* (second part) and *tub2* sequences GenBank MZ064417.1, MZ064474.1, MZ078248.1 and MZ078261.1, MycoBank MB 839494).

Notes — *Mollisia asteliae* is related to *M. panicicola*, which was described as an asexual morph, *Acidomelania panicicola* (Walsh et al. 2014), later included in *Mollisia* by Tanney & Seifert (2020). It is morphologically and phylogenetically distinct from species presently accepted in the genus (Tanney & Seifert 2020).

(notes *Mollisia asteliae* continues on Supplementary material page FP1183 & 1184)

Flexuomyces Crous, *gen. nov.*

Etymology. Name refers to the flexuous nature of its conidia.

Classification — *Tympanidaceae*, *Leotiales*, *Leotiomycetes*.

Conidiomata convex with a short stipe arising from a basal stroma of brown *textura epidermoidea*; stipe short, of brown, parallel cylindrical cells, fanning outward towards umbrella-like apex, which is pale brown, giving rise to cylindrical, hyaline conidiogenous cells that taper at apex; conidiomata brown, sessile with a crystalline mucoid conidial mass; wall of several layers of brown *textura epidermoidea. Conidiophores* septate, cylindrical, tightly aggregated; on inner plane forming a layer of phialidic *conidiogenous cells*, hyaline, smooth. *Conidia* single, hyaline, smooth, subcylindrical to acicular, multi-septate, guttulate, apex subobtuse, base truncate, conidia spirally twisted in middle with apical and basal part in different planes, widest at basal septum, tapering to truncate hilum.

Type species. Flexuomyces asteliae Crous
MycoBank MB 839495.

Flexuomyces asteliae Crous, *sp. nov.*

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

Conidiomata convex with a short stipe arising from a basal stroma of brown *textura epidermoidea*; stipe short, of brown, parallel cylindrical cells, fanning outward towards umbrella-like apex, which is pale brown, giving rise to cylindrical, hyaline conidiogenous cells that taper at apex; conidiomata brown, 200–400 µm diam, sessile with a crystalline mucoid conidial mass; wall of several layers of brown *textura epidermoidea. Conidiophores* septate, cylindrical, tightly aggregated, up to 40 µm tall, 2–3 µm diam; on inner plane forming a layer of phialidic *conidiogenous cells*, hyaline, smooth, 4–7 × 2 µm. *Conidia* single, hyaline, smooth, subcylindrical to acicular, 3–8-septate, guttulate, apex subobtuse, base truncate, conidia spirally twisted in middle with apical and basal part in different planes, 60–100 × 1.5–2 µm, widest at basal septum, tapering to truncate hilum, 1 µm diam.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, even margin, reaching 40 mm diam after 2 wk at 25 °C on MEA, but covering dish on PDA and OA. On MEA surface and reverse umber; on PDA surface and reverse chestnut; on OA surface umber with patches of buff.

Typus. New Zealand, Auckland, Taunton Terrace, from leaf spots of *Astelia chathamica* (*Asteliaceae*), 14 Mar. 2019, *C. Inglis* (holotype CBS H-24416, culture ex-type CPC 38522 = T19_02324E = CBS 146786, ITS and LSU sequences GenBank MZ064409.1 and MZ064466.1, MycoBank MB 839496).

Notes — *Flexuomyces* is related to hyphomycetous genera such as *Pallidophorina*, *Variabilispora* (Bien et al. 2020) and *Vandijckella* (Crous et al. 2017). It can easily be distinguished from those genera by its convex conidiomata with a short stipe, and multiseptate, spirally twisted conidia.

(notes *Flexuomyces asteliae* continues on Supplementary material page FP1183 & 1184)

Colour illustrations. Auckland, Taunton Terrace. Left column: *Mollisia asteliae*. Apothecia on OA; ectal excipulum; asci and paraphyses; asci and ascospores; ascospores. Right column: *Flexuomyces asteliae*. Conidiomata *in vitro*; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (sporocarps), 10 µm (all others).

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Amorocoelophoma neoregeliae
& Cadophora neoregeliae

Fungal Planet 1185 & 1186 – 13 July 2021

Amorocoelophoma neoregeliae Crous, *sp. nov.*

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

Classification — *Amorosiaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata solitary, erumpent, globose, pycnidial, brown with central ostiole, 200–350 µm diam; wall of 6–8 layers of brown *textura angularis. Conidiophores* lining the inner cavity, reduced to conidiogenous cells or with a supporting cell, branched at base, hyaline, smooth, 7–15 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical with apical taper, 7–12 × 2–2.5 µm, phialidic with periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, straight, subcylindrical, apex obtuse, base bluntly rounded, (3–)3.5–4.5(–5) × (1.5–)2(–2.5) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface olivaceous grey, reverse isabelline; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey.

Typus. New Zealand, Tauranga port, from leaf spots of *Neoregelia* sp. (*Bromeliaceae*), 22 Aug. 2019, *D. Brunt* (holotype CBS H-24438, culture ex-type CPC 38740 = T19_05712A = CBS 146820, ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank MZ064410.1, MZ064467.1, MZ078193.1 and MZ078247.1, MycoBank MB 839497).

Notes — *Amorocoelophoma neoregeliae* is related to *A. cassiae*, but distinct in that the latter has longer conidia (9–11 × 2–3 µm) (Jayasiri et al. 2019).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Hermatomyces* sp. 1-2018 (strain KZP352, GenBank LS398262.1; Identities = 671/776 (86 %), 32 gaps (4 %)), *Acrocalymma vagum* (strain 0101-2, GenBank MN540314.1; Identities = 651/778 (84 %), 38 gaps (4 %)) and *Alfoldia vorosii* (strain CBS 145501, GenBank NR_171211.1; Identities = 396/409 (97 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank NG_066307.1; Identities = 871/877 (99 %), one gap (0 %)), *Alfoldia vorosii* (strain CBS 145501, GenBank NG_068885.1; Identities = 869/877 (99 %), no gaps) and *Angustimassarina populi* (strain MFLUCC 17-1069, GenBank MF409166.1; Identities = 861/878 (98 %), two gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Opegrapha varia* (voucher KAG981017-42, GenBank AY485628.1; Identities = 833/921 (90 %), one gap (0 %)), *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank MK434894.1; Identities = 810/908 (89 %), three gaps (0 %)) and *Angustimassarina rosarum* (strain MFLUCC 17-2155, GenBank MT394678.1; Identities = 725/823 (88 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Alfoldia vorosii* (strain REF117, GenBank MK599321.1; Identities = 874/907 (96 %), no gaps), *Pseudohelminthosporium clematidis* (strain MFLUCC 17-2086, GenBank MT394627.1; Identities = 833/868 (96 %), no gaps) and *Amorocoelophoma cassiae* (strain MFLUCC 17-2283, GenBank MK360041.1; Identities = 868/907 (96 %), no gaps).

Cadophora neoregeliae Crous, *sp. nov.*

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

Classification — *Ploettnerulaceae*, *Helotiales*, *Leotiomycetes.*

Mycelium consisting of hyaline, smooth, septate, branched, 2–3 µm diam hyphae. *Conidiophores* hyaline, smooth, erect, penicillate (at times reduced to solitary phialides on hyphae), branched or not, with clusters of conidiogenous cells, terminal and intercalary, 30–90 × 2–3 µm, 2–7-septate. *Conidiogenous cells* hyaline, smooth, curved, phialidic, 7–15 × 2.5–3 µm, with visible periclinal thickening, arranged in rosettes of up to seven per conidiophore, mostly terminal. *Conidia* solitary, aseptate, globose, guttulate to granular, smooth, hyaline, 2.5–4 µm diam. *Chlamydospores* rare, terminal on hyphae, ellipsoid to subglobose, brown, smooth, guttulate, 8–12 × 6–8 µm.

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

Typus. New Zealand, Tauranga port, from leaf spots of *Neoregelia* sp. (*Bromeliaceae*), 22 Aug. 2019, *D. Brunt* (holotype CBS H-24439, culture ex-type CPC 38741 = T19_05712B = CBS 146821, ITS and LSU sequences GenBank MZ064411.1 and MZ064468.1, MycoBank MB 839498).

Notes — Species of *Cadophora* (dematiaceous hyphomycetes with monophialidic conidiophores with distinct flask-shaped, hyaline collarettes, and aseptate conidia) are commonly isolated from soil, but are also known as plant pathogens or saprobes (Bien & Damm 2020, Crous et al. 2020b). *Cadophora neoregeliae* is distinguished from other species known in the genus by its globose conidia, 2.5–4 µm diam, and the production of chlamydospores in culture.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cadophora fastigiata* (strain CBS 869.69, GenBank MH859469.1; Identities = 554/569 (97 %), no gaps), *Phialophora dancoi* (strain IFM 50357, GenBank AB190869.1; Identities = 551/566 (97 %), no gaps) and *Cadophora malorum* (strain NW-FVA5175, GenBank MT561395.1; Identities = 563/579 (97 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Mollisia cinerella* (strain CBS 312.61, GenBank MH869631.1; Identities = 860/864 (99 %), no gaps), *Cadophora bubakii* (as *Phialophora bubakii*; strain CBS 198.30, GenBank MH866559.1; Identities = 860/864 (99 %), no gaps) and *Cadophora melinii* (strain CBS 120273, GenBank MH874636.1; Identities = 859/864 (99 %), no gaps).

Colour illustrations. Neoregelia sp. Left column: *Amorocoelophoma neoregeliae.* Conidiomata on PDA; conidioma with ostiole; conidiogenous cells giving rise to conidia; conidia. Right column: *Cadophora neoregeliae*. Colony sporulating on OA; conidiogenous cells; chlamydospore; conidiophore giving rise to conidia; conidia. Scale bars = 10 µm.

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Septoriella callistemonis

Fungal Planet 1187 – 13 July 2021

Septoriella callistemonis Crous, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata immersed, globose, brown, pycnidial, 250–350 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, phialidic, at times sympodial, 5–10 × 3–4 µm. *Conidia* solitary, subcylindrical, variously curved to straight, apex obtuse, base truncate, brown, smooth, guttulate, (3–)7-septate, (35–)52–65(–67) × 3 µm.

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

Typus. New Zealand, Tauranga port, from leaf spots of *Callistemon* sp. (*Myrtaceae*), 22 Aug. 2019, *C. Inglis* (holotype CBS H-24441, culture ex-type CPC 38761 = T19_05745B = CBS 146822, ITS, LSU, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064412.1, MZ064469.1, MZ078194.1, MZ078220.1 and MZ078257.1, MycoBank MB 839499).

Notes — Species of *Septoriella* are mostly saprobic or weakly aggressive pathogens of grasses, and thus the occurrence of *S. callistemonis* (on *Callistemon*) is surprizing. It is related to several known species (Crous et al. 2019b, Marin-Felix et al. 2019a) from which it can be distinguished based on conidial dimensions and septation.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria typharum* (strain CBS 305.71, GenBank KY090643.1; Identities = 582/593 (98 %), two gaps (0 %)), *Septoriella allojunci* (strain MFLUCC 15-0701, GenBank KU058718.1; Identities = 577/590 (98 %), two gaps (0 %)) and *Phaeosphaeria eustoma* (strain CBS 337.86, GenBank AJ496629.1; Identities = 568/581 (98 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Septoriella oudemansii* (strain CBS 138012, GenBank MH878140.1; Identities = 801/803 (99 %), no gaps), *Phaeosphaeria fuckelii* (strain CBS 388.86, GenBank MH873665.1; Identities = 801/803 (99 %), no gaps) and *Loratospora luzulae* (strain MFLUCC 14-0826, GenBank NG_069310.1; Identities = 800/803 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Septoriella tridentina* (strain MFLUCC 15-0474, GenBank KX891170.1; Identities = 835/893 (94 %), one gap (0 %)), *Phaeosphaeria ammophilae* (strain CBS 114595, GenBank GU371724.1; Identities = 814/876 (93 %), one gap (0 %)) and *Dactylidina dactylidis* (strain MFLUCC 14-0966, GenBank MG829253.1; Identities = 834/908 (92 %), one gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Septoriella pseudophragmitis* (strain CBS 145417, GenBank MK559452.1; Identities = 381/418 (91 %), 22 gaps (5 %)), *Septoriella hollandica* (strain CBS 145374, GenBank MK540160.1; Identities = 371/422 (88 %), 19 gaps (4 %)) and *Septoriella germanica* (strain CBS 145372, GenBank MK540159.1; Identities = 363/415 (87 %), 20 gaps (4 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Septoriella pseudophragmitis* (strain CBS 145417, GenBank MK559451.1; Identities = 309/324 (95 %), one gap (0 %)), *Septoriella hollandica* (strain CBS 145374, GenBank MK540175.1; Identities = 300/319 (94 %), one gap (0 %)) and *Alternaria eryngii* (strain EGS 41-005, GenBank JQ672007.1; Identities = 295/328 (90 %), five gaps (1 %)).

Colour illustrations. Callistemon sp. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Phaeosphaeria caricis-sectae

Fungal Planet 1188 – 13 July 2021

Phaeosphaeria caricis-sectae Crous, *sp. nov.*

Etymology. Name refers to the host *Carex secta*, which is indigenous to New Zealand.

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, solitary, immersed in agar, globose, brown to dark brown, pycnidial with central ostiole, 250–350 µm diam; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, doliiform to globose, holoblastic, 4–8 × 5–7 µm. *Conidia* solitary, subcylindrical, variously curved, apex obtuse, base truncate, guttulate, medium brown, smooth, (1–)3(–4)-septate, (20–)25–30(–36) × (2–)2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, even margin, reaching 45 mm diam after 2 wk at 25 °C. On MEA and PDA surface honey, reverse isabelline; on OA surface buff.

Typus. New Zealand, Auckland Airport, from leaf spots of *Carex secta* (*Cyperaceae*), 27 Aug. 2019, *C. Inglis* (holotype CBS H-24442, culture ex-type CPC 38771 = T19_05742B = CBS 146823, ITS, LSU, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064413.1, MZ064470.1, MZ078195.1, MZ078221.1 and MZ078258.1, MycoBank MB 839500).

Notes — *Phaeosphaeria* (based on *P. oryzae*) has *Phaeoseptoria* asexual morphs (Quaedvlieg et al. 2013). Several species of *Phaeosphaeria* occurring on *Carex* mainly from Europe and North America were treated by Shoemaker & Babcock (1989), but these are all known from their sexual morphs, making it impossible to make a morphological comparison with the asexual *P. caricis-sectae*, which occurs on *Carex secta*, a host endemic to New Zealand. Three species of *Phaeoseptoria* are known from *Carex*, namely *P. caricis* (conidia 70–80 × 7 µm, 7–10-septate), *P. caricicola* (conidia 35–55 × 4 µm, 7-septate) and *P. festucae* (conidia 50–85 × 2.8–4.8 µm, 8–11-septate (Erdoğdu & Özbek 2017), which are clearly distinct from *P. caricis-sectae.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phaeosphaeria sinensis* (strain MFLUCC 18-1552, GenBank NR_163350.1; Identities = 462/482 (96 %), one gap (0 %)), *Phaeosphaeria oryzae* (strain 9Y-G19a, GenBank MT131346.1; Identities = 496/518 (96 %), six gaps (1 %)) and *Hendersonia sabaleos* (strain CBS 889.68, GenBank MH859244.1; Identities = 518/541 (96 %), four gaps (0 %)). Closest hits using the **LSU** sequence are *Phaeosphaeria sinensis* (strain MFLUCC 18-1552, GenBank NG_070076.1; Identities = 840/844 (99 %), no gaps), *Phaeosphaeria oryzae* (strain CBS 110110, GenBank NG_069025.1; Identities = 840/844 (99 %), no gaps) and *Phaeosphaeria musae* (strain CBS 120026, GenBank DQ885894.1; Identities = 840/844 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Parastagonospora nodorum* (strain UTHSC DI16-240, GenBank LT797006.1; Identities = 831/902 (92 %), no gaps), *Didymocyrtis cladoniicola* (strain UTHSC DI16-313, GenBank LT797037.1; Identities = 808/931 (87 %), six gaps (0 %)) and *Phaeosphaeria oryzae* (strain MFLUCC 11-0170, GenBank KM434306.1; Identities = 627/679 (92 %), no gaps). 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 *Neosulcatispora strelitziae* (strain CPC 25657, GenBank KX228380.1; Identities = 434/476 (91 %), 14 gaps (2 %)), *Phaeosphaeria podocarpi* (strain CBS 138903, GenBank KP004508.1; Identities = 429/481 (89 %), 18 gaps (3 %)) and *Paraphoma vinacea* (strain UMPV001, GenBank KU176892.1; Identities = 284/320 (89 %), six gaps (1 %)).

Colour illustrations. *Carex secta*. Conidioma on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidioma), 10 µm (all others).

Supplementary material

FP1188 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Phaeosphaeriaceae* multigene (ITS / LSU) nucleotide alignment derived from that of Tennakoon et al. (2020). Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. GenBank accession (superscript; only those not listed in Tennakoon et al. 2020 are shown) and/or culture collection/voucher numbers are indicated for all species. The tree was rooted to *Leptosphaeria doliolum* (culture CBS 505.75) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 58 strains including the outgroup; 1 479 characters including alignment gaps analysed: 556 distinct patterns, 319 parsimony-informative, 92 singleton sites, 1 068 constant sites. The best models identified in IQ-TREE were: TIM2+F+I+G4 (ITS), K2P+I+G4 (LSU). The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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Cladophialophora behniae

Fungal Planet 1189 – 13 July 2021

Cladophialophora behniae Crous, *sp. nov.*

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

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

Mycelium consisting of pale brown, smooth, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* dimorphic, reduced to conidiogenous loci on hyphae, 2–10 × 1.5–2 µm, or macronematous, erect, flexuous, pale brown, smooth, subcylindrical, branched or not, up to 100 µm tall, 1.5–3 µm diam. *Conidiogenous cells* terminal or intercalary, subcylindrical, pale brown, smooth, 10–30 × 2–3 µm; 1–2 loci apical, not thickened, slightly darkened, 1–1.5 µm diam. *Ramoconidia* subcylindrical, 0–4-septate, 15–28 × 2–2.5 µm; *Conidia* occurring in branched chains, subcylindrical, pale brown, smooth, guttulate, 0–1-septate, (11–)13–15(–17) × 2–2.5 µm; hila slightly darkened, not thickened, 1–1.5 µm diam.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 13 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. South Africa, Northern Province, Tzaneen, Buffelskloof Nature Reserve, on leaves of *Behnia* sp. (*Asparagaceae*), 11 July 2019, *P.W. Crous*, HPC 3156 (holotype CBS H-24233, culture ex-type CPC 38914 = CBS 146975, ITS, LSU, *rpb1*, *tef1* (first part) and *tub2* sequences GenBank MZ064414.1, MZ064471.1, MZ078187.1, MZ078222.1 and MZ078259.1, MycoBank MB 839501).

Notes — *Cladophialophora* is characterised by aseptate, ellipsoidal to fusoid conidia arising through blastic, acropetal conidiogenesis, and arranged in branched chains (Badali et al. 2008). The conidial scars are thickened and darkened, but not refractive. *Cladophialophora behniae* is related to *C. scillae* (CBS 116461, on *Scilla peruviana*, New Zealand, conidia (5–)10–20(–35) × 1.5–3 µm, 0–1(–3)-septate; Crous et al. 2007d) but can be distinguished from the latter species based on conidium morphology.

Based on a blastn search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cladophialophora scillae* (strain CBS 116461, GenBank EU035412.1; Identities = 471/476 (99 %), no gaps), *Cladophialophora hostae* (strain CPC 10737, GenBank EU035407.1; Identities = 462/477 (97 %), one gap (0 %)) and '*Exophiala*' *eucalyptorum* (strain CBS 121638, GenBank MH863133.1; Identities = 422/499 (85 %), 28 gaps (5 %)). Closest hits using the **LSU** sequence are *Cladophialophora scillae* (strain CBS 116461, GenBank EU035412.1; Identities = 881/881 (100 %), no gaps), *Cladophialophora hostae* (strain CPC 10737, GenBank EU035407.1; Identities = 876/881 (99 %), no gaps) and *Exophiala pisciphila* (strain AFTOL-ID 669, GenBank DQ823101.1; Identities = 823/887 (93 %), seven gaps (0 %)). Closest hits using the ***rpb1*** sequence had highest similarity to *Cladophialophora scillae* (strain CBS 116461, GenBank KJ636045.1; Identities = 620/632 (98 %), no gaps), and *Capronia semiimmersa* (strain MUCL 39979, GenBank JN989449.1; Identities = 200/252 (79 %), eight gaps (3 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Distant hits obtained using the ***tub2*** sequence had highest similarity to *Cyphellophora olivacea* (strain CBS 123.74, GenBank KC455231.1; Identities = 345/446 (77 %), 25 gaps (5 %)), *Phialophora americana* (strain UAMH 10874, GenBank EU514706.1; Identities = 343/443 (77 %), 26 gaps (5 %)) and *Exophiala polymorpha* (as *Exophiala* sp. SD-2014; strain UTHSC DI14-255, GenBank LN794351.1; Identities = 266/330 (81 %), 21 gaps (6 %)).

Colour illustrations. Buffelskloof Nature Reserve. Leaves of *Behnia* sp.; conidia arranged in branched chains; conidia. Scale bars = 10 µm.

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Colletotrichum cliviigenum

Fungal Planet 1190 – 13 July 2021

Colletotrichum cliviigenum Crous, *sp. nov.*

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

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

Conidiomata acervular, erumpent, brown, 200–300 µm diam. *Conidiophores* arising from a basal stroma, hyaline, smooth, branched, subcylindrical, 2–6-septate, 60–120 × 6–9 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, phialidic, proliferating percurrently, 15–35 × 5–8 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, subcylindrical, apex obtuse, tapering at base toward truncate hilum, 2 µm diam, (18–)22–26(–30) × (6–)7–8 µm. Setae and appressoria not seen.

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 buff to honey, reverse buff.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Clivia* sp. (*Amaryllidaceae*), Nov. 2018, *P.W. Crous*, HPC 3158 (holotype CBS H-24444, culture ex-type CPC 38800 = CBS 146825, ITS, LSU, *actA*, *chs-1*, *gapdh*, *his3* and *tub2* sequences GenBank MZ064415.1, MZ064472.1, MZ078143.1, MZ078161.1, MZ078178.1, MZ078180.1 and MZ078260.1, MycoBank MB 839502).

Notes — *Colletotrichum cliviigenum* is accommodated in the *C. boninense* species complex (Damm et al. 2012b). Several species are known from *Clivia*, namely *C. cliviae* (conidia 23–28 × 5–7 µm, the Netherlands), *C. cliviicola (conidia* (11–)15.5–20.5(–26.5) × (4–)5.5–6.5(–7) µm, China), and *C. himantophylli (conidia* 14–24 × 4–4.5 µm, Czech Republic) (Damm et al. 2019). *Colletotrichum cliviigenum* can be distinguished from those species in having larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Colletotrichum boninense* (strain ICMP 17904, GenBank NR_165949.1; Identities = 588/593 (99 %), no gap), *Colletotrichum oncidii* (strain CBS 130242, GenBank MH865629.1; Identities = 588/593 (99 %), one gap (0 %)) and *Colletotrichum cymbidiicola* (strain JL-3, GenBank KX058529.1; Identities = 585/590 (99 %), no gaps). Closest hits using the **LSU** sequence are *Colletotrichum karsti* (strain CBS 130641, GenBank MH877253.1; Identities = 838/839 (99 %), no gaps), *Colletotrichum boninense* (strain CBS 130235, GenBank MH877209.1; Identities = 838/839 (99 %), no gaps) and *Colletotrichum novae-zelandiae* (strain CBS 130240, GenBank MH877051.1; Identities = 838/839 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Colletotrichum beeveri* (strain CBS 128527, GenBank JQ005519.1; Identities = 259/267 (97 %), no gaps), *Colletotrichum brassicicola* (strain CD015-1, GenBank KC859967.1; Identities = 258/267 (97 %), no gaps) and *Colletotrichum colombiense* (strain CBS 129818, GenBank JQ005522.1; Identities = 258/267 (97 %), no gaps). Closest hits using the ***chs-1*** sequence had highest similarity to *Colletotrichum boninense* (strain SJSH-Z43, GenBank MK992714.1; Identities = 271/273 (99 %), no gaps), *Colletotrichum philodendricola* (nom. inval.) (strain LZJZ1, GenBank MH105265.1; Identities = 271/273 (99 %), no gaps) and *Colletotrichum torulosum* (strain CBS 102667, GenBank JQ005339.1; Identities = 270/273 (99 %), no gaps). Closest hits using the ***gapdh*** sequence had highest similarity to *Colletotrichum boninense* (voucher HGUP HL8, GenBank MN542219.1; Identities = 532/547 (97 %), one gap (0 %)), *Colletotrichum karsti* (strain CkaCkLH20_04883, GenBank XM_038887602.1; Identities = 310/319 (97 %), no gaps) and *Colletotrichum aotearoa* (strain BRIP 62670, GenBank KU221340.1; Identities = 318/337 (94 %), no gaps). Closest hits using the ***his3*** sequence had highest similarity to *Colletotrichum boninense* (strain HJH-3, GenBank MH370543.1; Identities = 376/393 (96 %), five gaps (1 %)), *Colletotrichum cymbidiicola* (strain CBS 128543, GenBank JQ005428.1; Identities = 373/390 (96 %), five gaps (1 %)) and *Colletotrichum pseudoboninense* (nom. inval.) (strain LZJZ5, GenBank MK796580.1; Identities = 374/392 (95 %), five gaps (1 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Colletotrichum cymbidiicola* (strain HTL126, GenBank MH305540.1; Identities = 676/696 (97 %), no gaps), *Colletotrichum boninense* (strain LF644, GenBank KJ955336.1; Identities = 688/709 (97 %), no gaps) and *Colletotrichum philodendricola* (nom. inval.) (strain LZJZ1, GenBank MH105277.1; Identities = 684/708 (97 %), no gaps).

Colour illustrations. Symptomatic leaf of *Clivia* sp. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Aquilomyces metrosideri
Lake Rd
31A

Fungal Planet 1191 – 13 July 2021

Aquilomyces metrosideri Crous, *sp. nov.*

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

Classification — *Morosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata solitary, brown, globose to pyriform, 150–200 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis. Conidiophores* lining the inner cavity, reduced to conidiogenous cells or a supporting cell, branched at base, hyaline, smooth, subcylindrical, 10–15 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, subcylindrical, hyaline, smooth, phialidic, 7–10 × 2.5–3.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, subcylindrical with obtuse apex and truncate hilum, (3–)4(–5) × 1.5–2 µm.

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

Typus. New Zealand, Devonport, Lake Road, from stem and internal discolouration of *Metrosideros* sp. (*Myrtaceae*), 4 Oct. 2019, *K. Hofer* (holotype CBS H-24414, culture ex-type CPC 38517 = T19_034621 = CBS 146782, ITS, LSU, *actA* and *cmdA* sequences GenBank MZ064416.1, MZ064473.1, MZ078144.1 and MZ078162.1, MycoBank MB 839503).

Notes — *Aquilomyces metrosideri* is related to the sterile endophyte *A. patris* (CBS 135661; Knapp et al. 2015). *Aquilomyces* is known to have a *massarina*-like sexual morph (Tanaka et al. 2015).

Based on a blastn search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135661, GenBank NR_137961.1; Identities = 472/569 (83 %), 44 gaps (7 %)), *Aquilomyces rebunensis* (voucher HHUF 27556, GenBank NR_154664.1; Identities = 369/402 (92 %), five gaps (1 %)) and *Clypeoloculus towadaensis* (voucher HHUF 30145, GenBank NR_153865.1; Identities = 438/515 (85 %), 22 gaps (4 %)). Closest hits using the **LSU** sequence are *Clypeoloculus towadaensis* (strain HHUF 30145, GenBank NG_058722.1; Identities = 785/793 (99 %), no gaps), *Aquilomyces patris* (strain CBS 135661, GenBank NG_057057.1; Identities = 820/833 (98 %), four gaps (0 %)) and *Clypeoloculus microsporus* (strain HHUF 30143, GenBank NG_068960.1; Identities = 780/793 (98 %), two gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135662, GenBank KP184121.1; Identities = 224/237 (95 %), no gaps), *Exserohilum gedarefense* (strain CBS 504.90, GenBank LT838289.1; Identities = 188/258 (73 %), 21 gaps (8 %)) and *Setosphaeria rostrata* (strain BRIP 12090, GenBank LT837679.1; Identities = 184/256 (72 %), 20 gaps (7 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Aquilomyces patris* (strain CBS 135661, GenBank KP184154.1; Identities = 422/467 (90 %), four gaps (0 %)), *Darksidea delta* (strain CBS 135629, GenBank KP184144.1; Identities = 329/375 (88 %), 12 gaps (3 %)) and *Darksidea epsilon* (strain CBS 135658, GenBank KP184147.1; Identities = 327/375 (87 %), 12 gaps (3 %)).

Colour illustrations. Devonport, Lake Road, New Zealand. Conidiomata on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).

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Falcocladium heteropyxidicola
& Castanediella senegaliae

Fungal Planet 1192 & 1193 – 13 July 2021

Falcocladium heteropyxidicola Crous, *sp. nov.*

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

Classification — *Falcocladiaceae*, *Falcocladiales*, *Sordariomycetes*.

Conidiophores penicillate or sporodochial, arising from superficial mycelium or microsclerotia; stipe extensions hyaline, numerous per conidiophore, aseptate, thick-walled, 35–50 × 1.5–2 µm; arising from various positions in the conidiophore, terminating in globose vesicles, 4–5 µm diam. *Conidiophore branches*: primary branches hyaline, smooth, subcylindrical, 0–1-septate, 5–10 × 2–3 µm; secondary and tertiary branches hyaline, aseptate, 6–10 × 2–3 µm. *Conidiogenous cells* phialidic, in whorls of 2–6, ampulliform with elongated necks and periclinal thickening and minute collarettes, 6–12 × 2–3 µm. *Conidia* hyaline, smooth, aseptate, falcate, with short, acute, thick-walled apical beak, and basal appendage, (13–)15–17(–18) × (1.5–)2 µm; basal appendages on inner, shorter curve, 2–3 µm long, with rounded end; apical beak continuous with body, 1.5–2 µm long. *Chlamydospores* medium brown, smooth, globose, 8–15 µm diam, aggregating to form microsclerotia.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium and smooth, lobate margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface buff, reverse ochreous.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Heteropyxis canescens* (*Heteropyxidaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3151 (holotype CBS H-24486, culture ex-type CPC 38904 = CBS 146974, ITS, LSU, *actA* and *rpb2* sequences GenBank MZ064418.1, MZ064475.1, MZ078145.1 and MZ078196.1, MycoBank MB 839504).

Notes — *Falcocladium heteropyxidicola* is related to *F. thailandicum* (vesicles sphaeropedunculate, conidia (19–)20–23 (–24) × 1.5(–2) µm; Crous et al. 2007b, Lombard et al. 2015), but is distinguished from that species by its globose vesicles, and smaller conidia.

(notes *Falcocladium heteropyxidicola* continues on Supplementary material page FP1192 & 1193)

Castanediella senegaliae Crous, *sp. nov.*

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

Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes*.

Observed to form cupulate *conidiomata* (satchmopsis-like) on host tissue, but in culture these were weakly developed, 40–100 µm diam, brown, arising from a reduced stroma, with brown, cupulate basal layer giving rise to a dense layer of brown cells that terminate in densely packed, brown, ampulliform *conidiogenous cells*, 5–8 × 2.5–3 µm, that line the inner layer of the cupulate or sporodochial conidioma, polyblastic with minute unthickened denticles at apex. *Conidia* solitary, aggregated in clusters in buff mucoid mass, hyaline, smooth, granular, falcate, fusoid, aseptate, widest in middle, ends subobtuse, (9–)10–11(–13) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 16 mm diam after 2 wk at 25 °C. On MEA surface and reverse hazel; on PDA surface smoke grey, reverse hazel; on OA surface bay.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on dead pods of *Senegalia ataxacantha* (*Fabaceae*), Nov. 2018, *P.W. Crous*, HPC 3159 (holotype CBS H-24541, culture ex-type CPC 39095 = CBS 147077, ITS and LSU sequences GenBank MZ064451.1 and MZ064508.1, MycoBank MB 839505).

Notes — *Castanediella* is characterized by macronematous, mononematous or sporodochial, branched, brown to pale brown conidiophores, with monoblastic or polyblastic, sympodial, discrete, cylindrical to lageniform, hyaline to subhyaline conidiogenous cells, and septate, cylindrical to fusoid, hyaline conidia (Crous et al. 2015a, 2021, Hernández-Restrepo et al. 2017). *Castanediella senegaliae* is related to *C. ambae* (see FP1230 in this paper), which has erect, sporodochial conidiomata, similar to those observed in *C. senegaliae*, which also appear cupulate. Furthermore, it appears that *Synnemadiella eucalypti* (synnemata with phialidic conidiogenous cells and ellipsoid, inequilateral, aseptate conidia; Crous et al. 2016) clusters among species of *Castanediella*, suggesting that this complex requires revision.

(notes *Castanediella senegaliae* continues on Supplementary material page FP1192 & 1193)

Colour illustrations. Buffelskloof Nature Reserve. Left column: *Falcocladium heteropyxidicola*. Conidiophores giving rise to conidia; vesicles; chlamydospores; conidia. Right column: *Castanediella senegaliae*. Conidiomata on PNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 100 µm (conidiomata of *C. senegaliae*), 10 µm (all others).

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Paracymostachys euphorbiae

Fungal Planet 1194 – 13 July 2021

Paracymostachys Crous, *gen. nov.*

Etymology. Name reflects its close relationship to *Cymostachys*.

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

Conidiophores macronematous, mononematous, erect, mostly in groups, mostly unbranched, thick-walled, hyaline to pale olivaceous brown, smooth, 1–2-septate, with 4–6 conidiogenous cells radiating from the apex. *Conidiogenous cells* phialidic, clavate to elongate doliiform, smooth to slightly verrucose, olivaceous brown at the apex becoming subhyaline towards the base, with inconspicuous collarettes. Conidia in a mucoid droplet, aseptate, olivaceous brown to dark brown, thick-walled, guttulate, smooth to verrucose, fusoid, rarely subcylindrical, apex rounded, base truncate.

Type species. *Paracymostachys euphorbiae* Crous MycoBank MB 839506.

Paracymostachys euphorbiae Crous, *sp. nov.*

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

Conidiophores macronematous, mononematous, erect, solitary or in groups, mostly unbranched, thick- and smooth-walled, hyaline to pale olivaceous brown, 70–120 × 3–4 µm, 1–2-septate, with 4–6 conidiogenous cells arranged in a cluster at apex. *Conidiogenous cells* phialidic, clavate to fusoid or elongate doliiform, hyaline, becoming olivaceous brown and verruculose with inconspicuous collarettes, 7–11 × 3–5 µm. *Conidia* in a mucoid droplet, aseptate, olivaceous brown to dark brown, smooth, becoming verruculose, thick-walled, guttulate, fusoid, with rounded apex and truncate base, (7.5–)8–9(–10) × (3–)3.5–4 µm; rarely subcylindrical, up to 17 µm long. Germinating conidia dark brown, verrucose, 1-septate (constricted at septum) with polar germination, 13–17 × 6–7 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface saffron, margin umber, reverse umber; on PDA surface and reverse pale luteous; on OA surface iron-grey with buff margins.

Typus. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on leaf litter of *Euphorbia ingens* (*Euphorbiaceae*), Nov. 2018, *P.W. Crous*, HPC 3140 (holotype CBS H-24495, culture ex-type CPC 38954 = CBS 146983, ITS, LSU, *cmdA* and *rpb2* sequences GenBank MZ064419.1, MZ064476.1, MZ078163.1 and MZ078197.1, MycoBank MB 839507).

Notes — Lombard et al. (2016) distinguished several genera in *Stachybotryaceae. Paracymostachys* can be distinguished from *Cymostachys* by having smooth, primarily unbranched conidiophores, and fusoid, rarely subcylindrical conidia. *Paracymostachys euphorbiae* is distinct from *Cymostachys* species in not having fabiform to globose conidia. Furthermore, it is distinct from *S. limonispora* (conidia (6–)6.5–7.5(–9) × 3–4 µm) in lacking limoniform conidia, and from *S. phaeophialis* (conidia ellipsoidal to fusoid) in having larger conidia ((6–)6.5–7.5(–9) × 3–4 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 *Stachybotrys dolichophialis* (strain DAOM 227011, GenBank KU846734.1; Identities = 551/612 (90 %), 36 gaps (5 %)), *Stachybotrys zeae* (voucher HGUP 0143, GenBank KC305346.1; Identities = 546/611 (89 %), 37 gaps (6 %)) and *Stachybotrys microspora* (voucher HGUP 0120, GenBank KC305353.1; Identities = 545/610 (89 %), 36 gaps (5 %)). Closest hits using the **LSU** sequence are *Memnoniella echinata* (strain CBS 216.32, GenBank MH866746.1; Identities = 852/863 (99 %), one gap (0 %)), *Memnoniella humicola* (strain CBS 463.74, GenBank NG_058217.1; Identities = 813/825 (99 %), one gap (0 %)) and *Stachybotrys limonispora* (strain CBS 128809, GenBank MH876595.1; Identities = 848/863 (98 %), one gap (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Stachybotrys phaeophialis* (strain KAS 525, GenBank KU846632.1; Identities = 386/466 (83 %), 11 gaps (2 %)), *Stachybotrys dolichophialis* (strain DAOM 227011, GenBank KU846628.1; Identities = 386/466 (83 %), 11 gaps (2 %)) and *Stachybotrys subsylvatica* (strain CBS 126205, GenBank KU846634.1; Identities = 365/441 (83 %), 19 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Striatibotrys rhabdospora* (strain CBS 136395, GenBank KU846986.1; Identities = 620/719 (86 %), no gaps), *Striatibotrys eucylindrospora* (strain CBS 203.61, GenBank KU846975.1; Identities = 630/732 (86 %), no gaps) and *Stachybotrys microspora* (voucher MFLU 18-2620, GenBank MW201479.1; Identities = 534/621 (86 %), no gaps).

Colour illustrations. Mbombela, Lowveld Botanical Garden. Conidiophores with conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

Supplementary material

FP1194 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Stachybotrys* and related genera multigene (LSU / *rpb2*) nucleotide alignment derived from the datasets of Lombard et al. (2016) and Samarakoon et al. (2021). GenBank accession numbers for the sequences used can also be obtained from Lombard et al. (2016) and Samarakoon et al. (2021), except for cultures where GenBank accession numbers are indicated in superscript text and which were obtained from other studies. Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers are indicated for all species. The tree was rooted to *Calonectria ilicicola* (culture CBS 190.50) and the species described here are highlighted with coloured blocks and **bold** face. Alignment statistics: 91 strains including the outgroup; 1533 characters including alignment gaps analysed: 517 distinct patterns, 420 parsimony-informative, 70 singleton sites, 1043 constant sites. The best model identified for the entire alignment in IQ-TREE using the TESTNEWMERGE option was: TIM2+F+I+G4. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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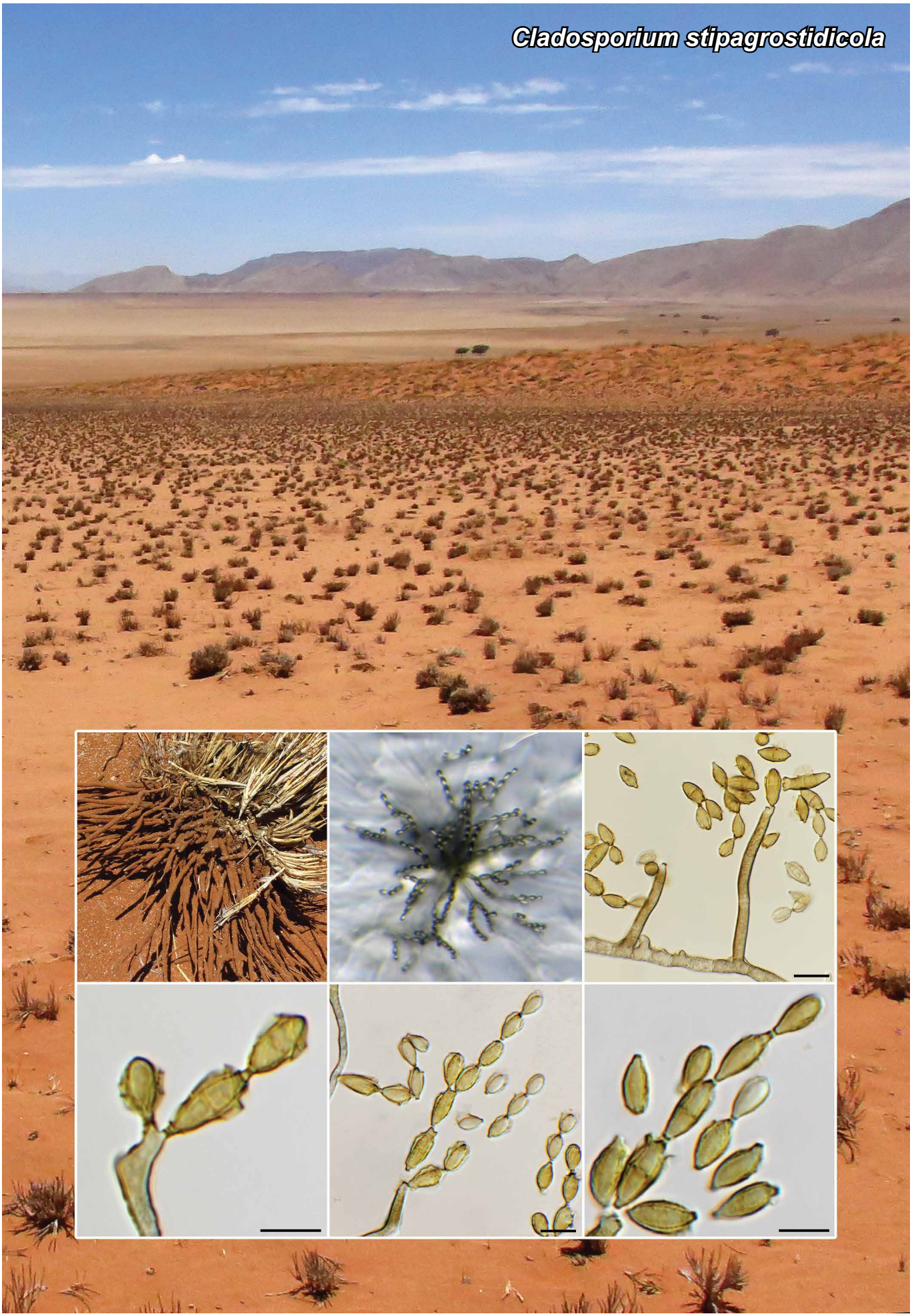
Cladosporium stipagrostidicola

Fungal Planet 1195 – 13 July 2021

Cladosporium stipagrostidicola Crous, *sp. nov.*

Etymology. Name refers to the host genus *Stipagrostis* (cf. *Stipagrostis ciliata*) from which it was isolated.

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

Mycelium consisting of pale brown to brown, finely verruculose, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells or macronematous, erect, straight to geniculate-sinuous, unbranched, subcylindrical, 10–70 × 3–4 µm, 1–4-septate, brown, smooth to verruculose. *Conidiogenous cells* integrated, terminal, subcylindrical, brown, smooth to verruculose, tapering at apex to 1–3 denticulate loci, thickened, darkened and refractive, 1.5–2 µm diam, 15–30 × 3–4 µm. *Conidia* occurring in dry, branched chains. *Secondary ramoconidia* fusoid-ellipsoid to subcylindrical, tapering at ends, golden brown, verruculose to prominently warty, 0–1(–2)-septate, 10–20 × 5–6(–7) µm; warts up to 2 µm diam; hila protruding, thickened, darkened, somewhat refractive, 1.5–2 µm diam; intermediate and terminal conidia aseptate, golden brown, verruculose to prominently warty, (8–)9–10(–11) × (4–)5(–6) µm; hila denticulate, thickened, darkened, refractive, 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, reaching 16 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. Namibia, Saagberg dunes in the Namib-Naukluft Park, east of Gobabeb Namib Research Institute, on leaves of *Stipagrostis* cf. *ciliata* (*Poaceae*), 20 Nov. 2019, *P.W. Crous*, HPC 3098 (holotype CBS H-24490, culture ex-type CPC 38936 = CBS 146978, ITS, LSU, *actA* and *tef1* (first part) sequences GenBank MZ064420.1, MZ064477.1, MZ078146.1 and MZ078223.1, MycoBank MB 839508).

Notes — *Cladosporium stipagrostidicola* resides in the *C. cladosporioides* species complex (Bensch et al. 2010, 2012, 2015, 2018), being related to *C. flabelliforme* and *C. flavovirens*. *Cladosporium flabelliforme* is distinct in having conidial chains characteristically spread in a fan-like manner, secondary ramoconidia 11–27 × (2–)2.5–3(–3.5) µm, 0(–1)-septate, small terminal conidia, obovoid or ellipsoid, 4.5–8 × 1.5–2.5 µm (Bensch et al. 2010). *Cladosporium flavovirens* is distinct from other species in that it has secondary *ramoconidia* 9–30 × 3.5–4 µm, 0–2-septate, and small terminal conidia, obovoidal to short ellipsoidal, 5–7 × 2.5–3 µm (Sandoval-Denis et al. 2016).

Colour illustrations. *Stipagrostis* tussocks in the Namib Sand Sea, Namibia. Roots of *Stipagrostis* cf. *ciliata* with rhizosheaths; conidiophores giving rise to conidial chains; ornamented conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cladosporium delicatulum* (strain CL_FF_10_con, GenBank MT548673.1; Identities = 535/535 (100 %), no gaps), *Cladosporium perangustum* (strain CL2, GenBank MT466522.1; Identities = 535/535 (100 %), no gaps) and *Cladosporium cladosporioides* (strain CBS 127759, GenBank MH864765.1; Identities = 535/535 (100 %), no gaps). Closest hits using the **LSU** sequence are *Cladosporium asperulatum* (strain CBS 126340, GenBank NG_069955.1; Identities = 877/877 (100 %), no gaps), *Cladosporium australiense* (strain CBS 125984, GenBank NG_069941.1; Identities = 877/877 (100 %), no gaps) and *Cladosporium cladosporioides* (strain CBS 127339, GenBank MH875964.1; Identities = 877/877 (100 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Cladosporium ramotenellum* (strain CBS 145592, GenBank MT223748.1; Identities = 420/437 (96 %), no gaps), *Cladosporium myrtacearum* (strain CPC 16319, GenBank KT600605.1; Identities = 405/431 (94 %), four gaps (0 %)) and *Cladosporium rugulovarians* (strain CPC 18444, GenBank KT600656.1; Identities = 486/521 (93 %), three gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Cladosporium funiculosum* (strain CPC 22298, GenBank MF473409.1; Identities = 287/328 (88 %), 12 gaps (3 %)), *Cladosporium pseudocladosporioides* (strain SL1023, GenBank MH329203.1; Identities = 284/327 (87 %), 15 gaps (4 %)) and *Cladosporium ipereniae* (strain CPC 16238, GenBank KT600491.1; Identities = 325/378 (86 %), 15 gaps (3 %)).

Supplementary material

FP1195 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Cladosporium* multigene (*actA* / *tef1*) nucleotide alignment. Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5000 ultrafast bootstrap replicates are shown at the nodes. Culture collection and GenBank accession (in superscript) numbers are indicated for all species and numbers in **bold** represent those cultures with a type status. The tree was rooted to *Cercospora beticola* (culture CBS 116456) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 67 strains including the outgroup; 661 characters including alignment gaps analysed: 429 distinct patterns, 250 parsimony-informative, 88 singleton sites, 323 constant sites. The best model identified for the entire alignment in IQ-TREE using the TESTNEWMERGE option was: TIM2+F+I+G4. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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Teratosphaericola leucadendri

Fungal Planet 1196 – 13 July 2021

Teratosphaericola leucadendri Crous, *sp. nov.*

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

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Mycelium consisting of pale brown, smooth, branched, septate, 2.5–3 µm diam hyphae. *Conidiophores* solitary, erect, branched, subcylindrical, pale brown, smooth, septate, up to 180 µm tall, 3–4 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, pale brown, smooth, 10–20 × 3–4 µm; loci sympodial, subdenticulate, 2 µm diam, slightly thickened and darkened. *Conidia* pale brown, smooth, guttulate, subcylindrical, 0–1-septate with truncate ends, occurring in dry, branched chains; ramoconidia 13–25 × 2.5–3.5 µm; conidia (12–)14–16(–17) × (2–)2.5–3 µm; hila somewhat thickened and darkened.

Culture characteristics — Colonies erumpent, spreading, with sparse to moderate aerial mycelium and smooth, lobate margin, reaching 5–7 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, Rocklands camping, on leaves of *Leucadendron* sp. (*Proteaceae*), 2 Sept. 2018, *P.W. Crous*, HPC 3052 (holotype CBS H-24504, culture ex-type CPC 38681 = CBS 146993, ITS, LSU, *actA*, *cmdA*, *tef1* (first part) and *tub2* sequences GenBank MZ064421.1, MZ064478.1, MZ078147.1, MZ078164.1, MZ078224.1 and MZ078262.1, MycoBank MB 839509).

Notes — *Teratosphaericola leucadendri* is related to *Teratosphaericola pseudafricana* (on *Eucalyptus globulus*, Zambia, CBS 114782; Quaedvlieg et al. 2014, Crous et al. 2019c). *Teratosphaericola pseudafricana* was originally described as *Mycosphaerella pseudoafricana* (Crous et al. 2006), and this is the first asexual morph linked to the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaericola pseudafricana* (strain CBS 114782, GenBank NR_154468.1; Identities = 466/492 (95 %), five gaps (1 %)), *Penidiella columbiana* (strain CBS 486.80, GenBank MH861288.1; Identities = 502/547 (92 %), 16 gaps (2 %)) and *Xenophacidiella pseudocatenata* (strain CBS 128776, GenBank NR_137066.1; Identities = 497/546 (91 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Teratosphaericola pseudafricana* (as *Teratosphaeria pseudafricana*; strain PM16, GenBank JN232442.1; Identities = 838/841 (99 %), no gaps), *Penidiella columbiana* (strain CBS 486.80, GenBank NG_057774.1; Identities = 827/841 (98 %), no gaps) and *Pseudoteratosphaeria ohnowa* (strain CBS 112896, GenBank EU019305.2; Identities = 824/843 (98 %), two gaps (0 %)). No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches. Closest hits using the ***cmdA*** sequence had highest similarity to *Teratosphaericola pseudafricana* (strain CBS 111168, GenBank KF902782.1; Identities = 367/411 (89 %), ten gaps (2 %)), *Teratosphaeria gauchensis* (strain CBS 119465, GenBank KF902726.1; Identities = 334/381 (88 %), ten gaps (2 %)) and *Teratosphaeria majorizuluensis* (strain CBS 120040, GenBank KF902733.1; Identities = 334/381 (88 %), 11 gaps (2 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Teratosphaericola pseudafricana* (strain CBS 111168, GenBank KF903370.1; Identities = 307/353 (87 %), 26 gaps (7 %)), *Pseudoteratosphaeria africana* (strain CBS 144597, GenBank MK442712.1; Identities = 198/210 (94 %), four gaps (1 %)) and *Neotrimmatostroma paraexcentricum* (strain CPC 25594, GenBank KX228378.1; Identities = 189/200 (95 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Meristemomyces frigidus* (strain CCFEE 5507, GenBank KF546749.1; Identities = 295/353 (84 %), 15 gaps (4 %)), *Teratosphaericola pseudafricana* (strain CBS 111168, GenBank KF903066.1; Identities = 225/255 (88 %), three gaps (1 %)) and *Devriesia shelburniensis* (strain CBS 115876, GenBank KF442467.1; Identities = 286/349 (82 %), 12 gaps (3 %)).

Colour illustrations. San Bushman rock art in Clanwilliam. Conidiogenous cells giving rise to branched conidial chains. Scale bars = 10 µm.

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Toxicocladosporium pterocarpi

Fungal Planet 1197 – 13 July 2021

Toxicocladosporium pterocarpi Crous, *sp. nov.*

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

Classification — *Cladosporiaceae*, *Cladosporiales*, *Dothideomyecetes.*

Mycelium consisting of pale brown to brown, smooth to warty, septate, branched, 2–3 µm diam hyphae. *Conidiophores* macronematous, erect, flexuous, branched, brown, thick-walled, subcylindrical, smooth to finely verruculose with large guttules, 60–130 × 3–4 µm. *Conidiogenous cells* integrated, terminal and intercalary, subcylindrical, brown, smooth to finely verruculose, 10–20 × 3–3.5 µm; loci darkened, thickened, refractive, 2–3 µm diam. *Conidia* occurring in dry, branched chains, subcylindrical to narrowly fusoid-ellipsoid, thick-walled, brown, verruculose, 0–1-septate; primary ramoconidia 13–25 × 3–3.5 µm; hila 2–3 µm diam; secondary ramoconidia 15–22 × 3–3.5 µm, with 1–2 apical loci; intercalary and terminal conidia (10–)13–15(–17) × 2.5–3 µm; hila thickened, darkened and refractive, 1.5–2 µm diam.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 17 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on pods of *Pterocarpus angolensis* (*Fabaceae*), Nov. 2018, *P.W. Crous*, HPC 3137 (holotype CBS H-24483, culture ex-type CPC 38890 = CBS 146971, ITS, LSU, *actA*, *rpb2* and *tub2* sequences GenBank MZ064422.1, MZ064479.1, MZ078148.1, MZ078198.1 and MZ078263.1, MycoBank MB 839510).

Notes — Crous et al. (2007a) introduced the genus *Toxicocladosporium* to accommodate cladosporium-like fungi with distinct, dark, thick-walled conidial septa, and lacking the typical coronate *Cladosporium* scar type. *Toxicocladosporium pterocarpi* is related to *T. chlamydosporum* (on *Eucalyptus camaldulensis*, Madagascar; terminal conidia 6–7(–9) × 2.5(–3) µm, forming chlamydospores in culture; Crous et al. 2009), from which it is morphologically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Toxicocladosporium chlamydosporum* (strain CBS 124159, GenBank MH863361.1; Identities = 545/549 (99 %), no gaps), *Toxicocladosporium protearum* (strain CBS 126499, GenBank NR_152321.1; Identities = 541/545 (99 %), one gap (0 %)) and *Toxicocladosporium velox* (strain CBS 124159, GenBank NR_155890.1; Identities = 518/522 (99 %), no gaps). Closest hits using the **LSU** sequence are *Toxicocladosporium chlamydosporum* (strain CBS 124157, GenBank NG_069916.1; Identities = 864/866 (99 %), no gaps), *Toxicocladosporium pseudoveloxum* (strain CBS 128777, GenBank JF499868.1; Identities = 864/866 (99 %), no gaps) and *Toxicocladosporium pini* (strain CBS 138005, GenBank KJ869217.1; Identities = 845/847 (99 %), no gaps). No significant hits were obtained when the ***actA*** sequence was used in blastn and megablast searches. Closest hits using the ***rpb2*** sequence had highest similarity to *Toxicocladosporium protearum* (strain CPC 15254, GenBank LT799786.1; Identities = 783/847 (92 %), one gap (0 %)), *Toxicocladosporium chlamydosporum* (strain CPC 15736, GenBank LT799779.1; Identities = 776/837 (93 %), no gaps) and *Toxicocladosporium pini* (strain CPC 23639, GenBank LT799784.1; Identities = 772/838 (92 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Toxicocladosporium pini* (strain CBS 138005, GenBank KY706603.1; Identities = 349/395 (88 %), 14 gaps (3 %)), *Toxicocladosporium velox* (strain CBS 124159, GenBank KY706609.1; Identities = 342/393 (87 %), 10 gaps (2 %)) and *Toxicocladosporium chlamydosporum* (strain CBS 124157, GenBank KY706598.1; Identities = 339/390 (87 %), ten gaps (2 %)).

Colour illustrations. *Pterocarpus angolensis* growing in Buffelskloof Nature Reserve. Conidiophores; conidiogenous cells giving rise to branched conidial chains. Scale bars = 10 µm.

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Diatrype dalbergiae
& Lylea dalbergiae

Fungal Planet 1198 & 1199 – 13 July 2021

Diatrype dalbergiae Crous, *sp. nov.*

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

Classification — *Diatrypaceae*, *Xylariales*, *Sordariomycetes.*

Ascomata brown, erumpent, in tight clusters on host tissue, punctiform with elongated neck, 200–500 µm diam; ascomata overmature, asci and ascospores not seen. On PNA: *Conidiomata* pycnidial, immersed, brown, subglobose, 200–300 µm diam; wall of 3–4 layers of pale brown *textura angularis. Conidiophores* hyaline, smooth, subcylindrical, branched, 1–4-septate, 20–40 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, subcylindrical with slight apical taper, phialidic, apex 1 µm diam, lacking flared collarette, 12–20 × 2–2.5 µm. *Conidia* solitary, hyaline, smooth, aseptate, sickle-shaped, widest in middle, apex subobtuse, base truncate, (15–)18–22(–25) × 1.5(–2) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface and reverse isabelline; on PDA surface and reverse umber; on OA surface buff.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on bark of *Dalbergia armata* (*Fabaceae*), Nov. 2018, *P.W. Crous*, HPC 3147 (holotype CBS H-24531, culture ex-type CPC 38900 = CBS 147068, ITS, LSU and *tub2* sequences GenBank MZ064448.1, MZ064505.1 and MZ078274.1, MycoBank MB 839511).

Notes — The phylogeny of the *Diatrypaceae* requires revision, as the present phylogeny does not correlate with the morphology (De Almeida et al. 2018). *Diatrype dalbergiae* is only known from its asexual morph, making a comparison with sexual morphs impossible. Based on its similarity to known species such as *D. disciformis* and *D*. *palmicola*, it is therefore placed in the genus *Diatrype*.

(notes *Diatrype dalbergiae* continues on Supplementary material page FP1198 & 1199)

Lylea dalbergiae Crous, *sp. nov.*

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

Classification — *Sporidesmiaceae*, *Sporidesmiales*, *Sordariomycetes.*

Mycelium consisting of septate, branched, hyaline to pale brown, smooth, 1.5–3 µm diam hyphae. *Conidiophores* micronematous, erect, solitary or aggregated, inconspicuous, subcylindrical, forming from superficial hyphae, hyaline to pale brown, smooth, unbranched, 3–8-septate, 50–120 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, monoblastic, subcylindrical, hyaline to pale brown, smooth, 15–30 × 3–4 µm, forming unbranched conidial chains; loci 1 µm diam, not thickened nor darkened. *Conidia* in unbranched, dry chains, acrogenous, acropetal, in long flexuous chains, subcylindrical, ends subobtuse, thick-walled, guttulate, hyaline becoming medium brown, smooth, (1–)2(–4)-distoseptate, (17–)23–31(–48) × (5–)6–6.5(–7) µm; scars 1 µm diam, not thickened nor darkened; conidia attached via narrow isthmus, thus frequently remaining attached for long periods.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 2–3 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey with diffuse reddish pigment; on PDA surface and reverse olivaceous grey; on OA surface olivaceous grey with diffuse red pigment.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on *Diatrype dalbergiae* on bark of *Dalbergia armata* (*Fabaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3147 (holotype CBS H-24509, culture ex-type CPC 38960 = CBS 147004, ITS and LSU sequences GenBank MZ064423.1 and MZ064480.1, MycoBank MB 839512); CBS H-24510, CPC 38961 = CBS 147005, ITS and LSU sequences GenBank MZ064424.1 and MZ064481.1.

Notes — Morgan-Jones (1975) established *Lylea* with *L. catenulata* as the type species. *Lylea* is characterised by forming catenate, distoseptate conidia on monoblastic conidiogenous cells. *Lylea dalbergiae* is related to *L. tetracoila* (conidia 3–4-distoseptate, (17.5–)20–40(–65) × (3–)4–5.5(–7) µm; Holubová-Jechová 1978), but distinct in that it has shorter conidia. It is also distinct from other species in the genus (Xia et al. 2014). *Lylea dalbergiae* was isolated as a mycophylic fungus, growing on ascomata of *Diatrype dalbergiae* (see FP1198 on top of this page) on bark of *Dalbergia armata.*

(notes *Lylea dalbergiae* continues on Supplementary material page FP1198 & 1199)

Colour illustrations. *Dalbergia armata*. Left column: *Diatrype dalbergiae.* Ascomata; ostiolar region; conidiogenous cells giving rise to conidia; conidia. Right column: *Lylea dalbergiae.* Conidial chains on SNA; conidia. Scale bars = 300 µm (ascomata of *D. dalbergiae*), 10 µm (all others).

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Acrodontium burrowsianum

Fungal Planet 1200 – 13 July 2021

Acrodontium burrowsianum Crous, *sp. nov.*

Etymology. Named for John and Sandy Burrows, two remarkable botanists who are instrumental in maintaining the Buffelskloof Research Centre, Mbombela, South Africa.

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Mycelium consisting of hyaline, septate, branched, smooth, 1–1.5 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* pale brown, smooth, thin-walled, subulate to slightly ampulliform, at times with basal septum, flexuous, proliferating sympodially and forming a rachis in upper region, (15–)20–30(–40) × 2–3 µm with multiple loci, slightly thickened, not darkened. *Conidia* hyaline, thin-walled, smooth, solitary, aseptate, ellipsoid, apex obtuse, 3–4 × 1.5–2 µm; hilum slightly thickened, not darkened.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface smoke grey, reverse isabelline; on OA surface smoke grey with diffuse hazel pigment.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of unidentified *Poaceae*, 23 Nov. 2018, *P.W. Crous*, HPC 3155 (holotype CBS H-24507, culture ex-type CPC 38912 = CBS 147002, ITS, LSU, *actA*, *gapdh*, *his3*, *rpb2* and *tef1* (first part) sequences GenBank MZ064425.1, MZ064482.1, MZ078149.1, MZ078179.1, MZ078181.1, MZ078199.1 and MZ078225.1, MycoBank MB 839513).

Notes — *Acrodontium* was introduced by De Hoog (1972), with type species *A. crateriforme* (CBS 144.33; conidia (3–)3.5–4.5(–5) × (1.5–)2–3(–4) µm. The genus was recently revised by Videira et al. (2016), who resolved its higher order phylogeny as belonging to *Teratosphaeriaceae*. *Acrodontium burrowsianum* is related to *A. crateriforme*, but has smaller conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Acrodontium crateriforme* (strain CBS 144.33, GenBank NR_152320.1; Identities = 457/459 (99 %), no gaps), *Pseudocercosporella fraxini* (strain LCM 896.01, GenBank MF495428.1; Identities = 547/549 (99 %), no gaps) and *Acrodontium neolitseae* (strain CBS 137975, GenBank NR_168148.1; Identities = 543/548 (99 %), no gaps). Closest hits using the **LSU** sequence are *Acrodontium crateriforme* (strain CBS 144.33, GenBank NG_057108.1; Identities = 859/859 (100 %), no gaps), *Acrodontium neolitseae* (strain CBS 137975, GenBank KJ869184.1; Identities = 843/843 (100 %), no gaps) and *Neophaeothecoidea proteae* (strain CBS 114129, GenBank MH874518.1; Identities = 850/880 (97 %), two gaps (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 25894, GenBank KX287559.1; Identities = 521/530 (98 %), no gaps), *Ramularia lethalis* (strain CPC 25910, GenBank KX287754.1; Identities = 453/500 (91 %), eight gaps (1 %)) and *Pantospora chromolaenae* (strain CBS 145563, GenBank MK876459.1; Identities = 467/523 (89 %), 11 gaps (2 %)). Closest hits using the ***gapdh*** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 25894, GenBank KX288124.1; Identities = 507/516 (98 %), no gaps), *Teratoramularia persicariae* (strain CPC 11408, GenBank KX288384.1; Identities = 281/314 (89 %), no gaps) and *Ramularia calcea* (strain CBS 101613, GenBank KP894547.1; Identities = 295/337 (88 %), four gaps (1 %)). Closest hits using the ***his3*** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 11519, GenBank KX288728.1; Identities = 316/323 (98 %), one gap (0 %)), *Ramularia major* (strain CPC 12542, GenBank KX288922.1; Identities = 303/330 (92 %), 11 gaps (3 %)) and *Ramularia cynarae* (strain CPC 25897, GenBank KX288847.1; Identities = 303/330 (92 %), 11 gaps (3 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Acrodontium crateriforme* (strain CBS 840.71, GenBank KX288402.1; Identities = 843/847 (99 %), no gaps), *Teratosphaeria sieberi* (strain CPC 32099, GenBank MH327872.1; Identities = 380/478 (79 %), eight gaps (1 %)) and *Teratosphaeria henryi* (strain CBS 145539, GenBank MK876492.1; Identities = 377/477 (79 %), six gaps (1 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Acrodontium crateriforme* (strain CPC 11509, GenBank GU384425.1; Identities = 266/275 (97 %), no gaps).

Colour illustrations. Unidentified *Poaceae* at Buffelskloof Nature Reserve. Conidiogenous cells on SNA; conidia. Scale bars = 10 µm.

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Bezerromyces gobabebensis

Fungal Planet 1201 – 13 July 2021

Bezerromyces gobabebensis Crous, *sp. nov.*

Etymology. Name refers to the Gobabeb Namib Research Institute, Namibia.

Classification — *Bezerromycetaceae*, *Bezerromycetales*, *Dothideomycetes.*

Ascomata separate, pseudothecial, globose, brown, 200–300 µm diam, covered in brown setae, flexuous, septate, verruculose with obtuse ends, up to 300 µm tall, 5–7 µm diam at base; wall of 6–8 layers of brown *textura angularis. Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, anastomosing, 2.5–3 µm diam, hyphae-like. *Asci* bitunicate, 8-spored, subcylindrical to slightly clavate with a well-defined ocular chamber and foot cell, 80–100 × 18–20 µm. *Ascospores* bi- to triseriate, fusoid-ellipsoid, ends subobtuse, constricted at septum just above median, and widest above this septum, transversely 3–6-septate, 2–4 oblique and vertical septa; initially hyaline, becoming brown with age, guttulate, (23–)28–31(–35) × (8–)9 µm.

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

Typus. Namibia, Gobabeb Namib Research Institute, on leaves of unidentified succulent, growing in gravel plains of Central Namib Desert, 20 Nov. 2019, *P.W. Crous*, HPC 3097 (holotype CBS H-24489, culture ex-type CPC 38934 = CBS 146977, ITS, LSU and *tef1* (second part) sequences GenBank MZ064426.1, MZ064483.1 and MZ078249.1, MycoBank MB 839514).

Notes — *Bezerromyces gobabebensis* clusters as a new species sister to a clade along with *Xiliomyces brasiliensis* (sterile *Dothideomycetes*) and species of *Bezerromyces* (Bezerra et al. 2017). Based on these data, and the morphology of *B. gobabebensis*, we have chosen to expand the circumscription of *Bezerromyces* to also include the genus *Xiliomyces*. A new name is proposed below, because the epithet *brasiliensis* is already occupied.

Bezerromyces pseudobrasiliensis Crous, *nom. nov.* MycoBank MB 839515

Basionym. *Xiliomyces brasiliensis* J.D.P. Bezerra et al., Mycol. Progr. 16: 304. 2016 ‘2017’.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Bezerromyces pernambucoensis* (strain URM7412, GenBank KX470391.1; Identities = 510/542 (94 %), 11 gaps (2 %)), *Bezerromyces brasiliensis* (strain CBS 141545, GenBank NR_153463.1; Identities = 510/542 (94 %), 11 gaps (2 %)) and *Xiliomyces brasiliensis* (strain CBS 141536, GenBank NR_153464.1; Identities = 508/542 (94 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Bezerromyces pernambucoensis* (strain URM7412, GenBank KX518624.1; Identities = 803/810 (99 %), two gaps (0 %)), *Xiliomyces brasiliensis* (strain CBS 141536, GenBank NG_069377.1; Identities = 788/795 (99 %), two gaps (0 %)) and *Bezerromyces brasiliensis* (strain CBS 141545, GenBank NG_069376.1; Identities = 801/809 (99 %), two gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Xiliomyces brasiliensis* (strain URM7413, GenBank KX518633.1; Identities = 428/439 (97 %), no gaps), *Bezerromyces pernambucoensis* (strain URM7412, GenBank KX518632.1; Identities = 424/439 (97 %), no gaps) and *Bezerromyces brasiliensis* (strain URM7411, GenBank KX518631.1; Identities = 424/439 (97 %), no gaps).

Colour illustrations. Namib Desert. Ascomata on OA; asci and pseudoparaphyses; ascospores. Scale bars = 300 µm (ascomata), 10 µm (all others).

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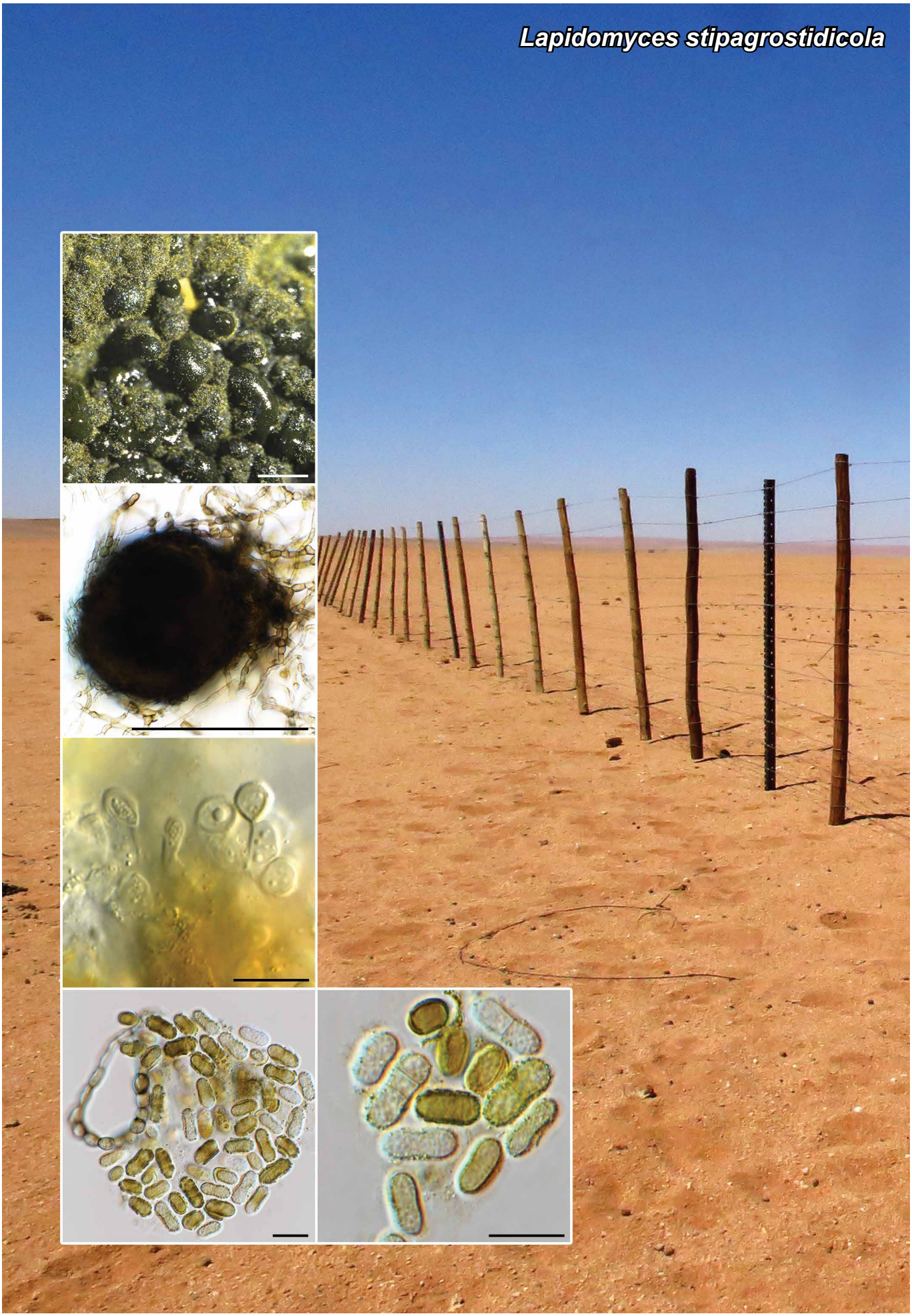
Lapidomyces stipagrostidicola

Fungal Planet 1202 – 13 July 2021

Lapidomyces stipagrostidicola Crous, *sp. nov.*

Etymology. Name refers to the host genus *Stipagrostis* cf. *ciliata* from which it was isolated.

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Conidiomata pycnidial, brown, erumpent, 50–300 µm diam with central ostiole exuding a brown mucoid conidial mass. *Conidiophores* reduced to conidiogenous cells lining inner cavity. *Conidiogenous cells* phialidic, hyaline, smooth, doliiform to ovoid, 4–5 × 3.5–5 µm. *Conidia* occurring in unbranched chains, encased in a mucoid sheath encapsulating the conidiogenous cell and conidial chain, medium brown, verruculose, prominently warty, initially joined via a narrow isthmus, ellipsoid to subcylindrical with obtuse ends, 0(–3)-septate, (9–)11–13(–17) × (4–)5–6(–7) µm.

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

Typus. Namibia, boundary fence of Namib-Naukluft Park, east of Gobabeb Namib Research Institute, on leaves of *Stipagrostis* cf. *ciliata* (*Poaceae*), 20 Nov. 2019, *P.W. Crous*, HPC 3098 (holotype CBS H-24491, culture ex-type CPC 38938 = CBS 146979, ITS, LSU, *rpb2* and *tub2* sequences GenBank MZ064427.1, MZ064484.1, MZ078200.1 and MZ078264.1, MycoBank MB 839516).

Notes — *Lapidomyces* was established for a genus of dematiaceous hyphomycetes. Although the present species was isolated having a cladosporium-like morphology *in vivo*, it only formed a coelomycetous synasexual morph *in vitro*. It is related to *Lapidomyces hispanicus*, a sterile hyphomycete with dark brown hyphae, constricted at their septa (Egidi et al. 2014, Crous et al. 2019b).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Lapidomyces hispanicus* (strain CBS 118355, GenBank NR_144960.1; Identities = 448/471 (95 %), six gaps (1 %)), *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 509/543 (94 %), nine gaps (1 %)) and *Camarosporula persooniae* (strain CBS 116258, GenBank JF770449.1; Identities = 513/549 (93 %), 13 gaps (2 %)). Closest hits using the **LSU** sequence are *Lapidomyces hispanicus* (strain CBS 118764, GenBank KF310016.1; Identities = 759/764 (99 %), no gaps), *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599595.1; Identities = 827/843 (98 %), two gaps (0 %)), *Xenoconiothyrium catenata* (strain CMW 22113, GenBank JN712570.1; Identities = 831/849 (98 %), two gaps (0 %)) and *Camarosporula persooniae* (strain CBS 116258, GenBank JF770461.1; Identities = 829/849 (98 %), two gaps (0 %)). Distant hits obtained using the ***rpb2*** sequence had highest similarity to *Capnodium salicinum* (strain CBS 131.34, GenBank KT216553.1; Identities = 196/255 (77 %), 12 gaps (4 %)), *Lecanosticta jani* (strain Guat.267.44.N1, GenBank MK015342.1; Identities = 211/280 (75 %), 11 gaps (3 %)) and *Lecanosticta brevispora* (strain CMW46503, GenBank MK015309.1; Identities = 189/248 (76 %), nine gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Lapidomyces hispanicus* (strain TRN500, GenBank KF546778.1; Identities = 315/383 (82 %), five gaps (1 %)), *Petrophila incerta* (strain TRN139b, GenBank KF546769.1; Identities = 305/372 (82 %), 16 gaps (4 %)) and *Cladosporium sphaerospermum* (strain 18ESMA010, GenBank MT881938.1; Identities = 293/357 (82 %), 21 gaps (5 %)).

Colour illustrations. Namib Desert, eastern boundary fence of the Namib-Naukluft Park. Conidiomata on SNA; conidioma; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Hysterobrevium walvisbayicola

Fungal Planet 1203 – 13 July 2021

Hysterobrevium walvisbayicola Crous, *sp. nov.*

Etymology. Name refers to Walvis Bay, Namibia, the coastal town where it was collected.

Classification — *Hysteriaceae*, *Hysteriales*, *Dothideomycetes.*

Conidiomata pycnidial, brown, subglobose with central ostiole, 200–300 µm diam (larger on OA than on MEA), exuding a pink to creamy conidial mass. *Conidiophores* subcylindrical, hyaline, smooth, branched, 1–3-septate, 15–60 × 1.5–2 µm, some branches sterile, appearing as paraphyses. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, 7–20 × 1.5–2 µm, phialidic. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical with obtuse ends, aseptate, straight, 3–5 × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface ochreous with patches of umber, reverse ochreous; on OA surface ochreous to umber.

Typus. Namibia, Walvis Bay, on leaves of unidentified tree, 19 Nov. 2019, *P.W. Crous*, HPC 3128 (holotype CBS H-24508, culture ex-type CPC 38948 = CBS 147003, ITS, LSU and *tef1* (first part) sequences GenBank MZ064428.1, MZ064485.1 and MZ093619.1, MycoBank MB 839517).

Notes — *Hysterobrevium walvisbayicola* is a phoma-like coelomycetous fungus that clusters in a complex of *Dothideomycetes* characterised by hysterothecial ascomata, namely *Gloniopsis*, *Hysterobrevium* and *Rhytidhysteron*. Although taxa in this complex are not known by their asexual morphs, Boehm et al. (2009) did record a coelomycetous asexual morph for *Hysterobrevium mori*. For the present, this species is best accommodated in *Hysterobrevium*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Gloniopsis calami* (strain MFLUCC 10-0927, GenBank MN608546.1; Identities = 449/480 (94 %), 11 gaps (2 %)), *Rhytidhysteron rufulum* (strain CFE-147, GenBank MN653261.1; Identities = 441/471 (94 %), 12 gaps (2 %)) and *Gloniopsis leucaenae* (strain MFLUCC 17-2425, GenBank NR_163334.1; Identities = 426/456 (93 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Hysterodifractum partisporum* (voucher HUEFS 42865, GenBank NG_060652.1; Identities = 884/907 (97 %), two gaps (0 %)), *Hysterobrevium mori* (strain GKM 1214, GenBank GQ221895.1; Identities = 880/906 (97 %), one gap (0 %)) and *Gloniopsis subrugosa* (strain SMH557, GenBank GQ221896.1; Identities = 879/906 (97 %), one gap (0 %)). Distant hits obtained using the ***tef1*** sequence had highest similarity to *Gloniopsis subrugosa* (strain GKM 1214, GenBank GU397336.1; Identities = 401/499 (80 %), 22 gaps (4 %)) and *Hysterobrevium mori* (strain GKM 1013, GenBank GU397338.1; Identities = 402/500 (80 %), 31 gaps (6 %)).

Colour illustrations. Flamingos at Walvis Bay lagoon. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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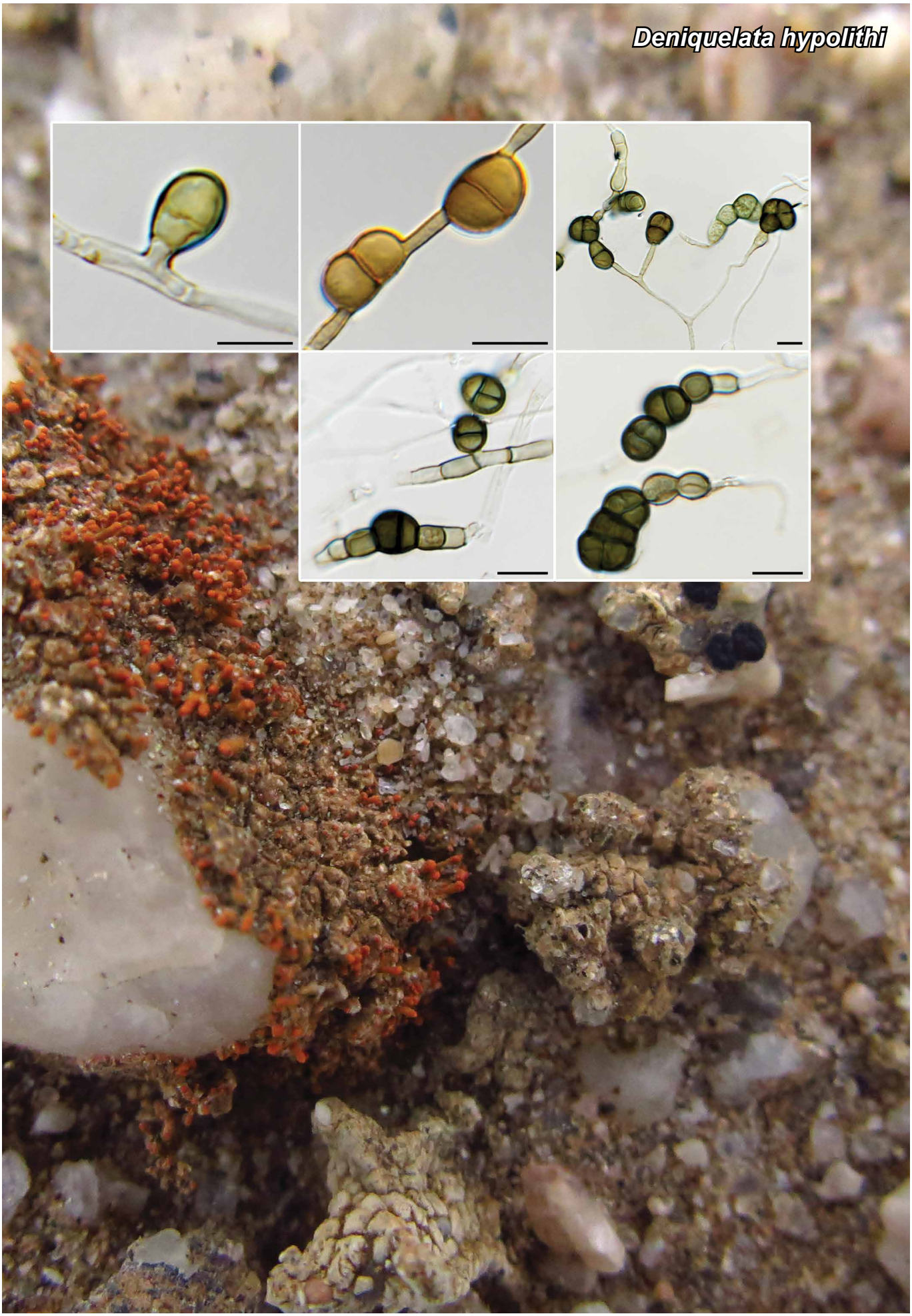
Deniquelata hypolithi

Fungal Planet 1204 – 13 July 2021

Deniquelata hypolithi Crous, *sp. nov.*

Etymology. Name refers to the fact that it was isolated from a hypolith, under a rock.

Classification — *Didymosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Mycelium consisting of pale olivaceous to subhyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* when present reduced to conidiogenous cells, erect, pale brown, subcylindrical, 4–20 × 3–4 µm. *Conidia* as intercalary chains in hyphae, or terminal on conidiogenous cells, solitary, or in short chains disarticulating at maturity, or hyphae disintegrate, leaving conidial propagules which are alternaria-like in appearance. *Conidia* brown, smooth, thick-walled, subglobose to pyriform to ellipsoid, guttulate, with 1–3 transverse and 0–2 vertical or oblique septa, (7–)10–12(–17) × (7–)9–10(–11) µm.

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 smoke grey, reverse umber to isabelline.

Typus. Namibia, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, *P.W. Crous*, HPC 3101 (holotype CBS H-24500, culture ex-type CPC 38968 = CBS 146988, ITS, LSU, *actA*, *rpb2* and *tef1* (second part) sequences GenBank MZ064429.1, MZ064486.1, MZ078150.1, MZ078201.1 and MZ078250.1, MycoBank MB 839518).

Notes — *Deniquelata* was established for a genus of *Dothideomycetes* with pseudothecia giving rise to bitunicate asci with pseudoparaphyses and brown, muriform ascospores (Ariyawansa et al. 2013). *Deniquelata hypolithi* is the first asexual morph linked to a species of *Deniquelata.*

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Deniquelata barringtoniae* (strain MFLUCC 11-0422, GenBank NR_111779.1; Identities = 669/691 (97 %), 13 gaps (1 %)), *Deniquelata quercina* (strain 1050-SAB SA5 1, GenBank MT820404.1; Identities = 649/681 (95 %), 14 gaps (2 %)) and *Didymocrea leucaenae* (strain MFLUCC 17-0896, GenBank NR_164298.1; Identities = 477/523 (91 %), 14 gaps (2 %)). Closest hits using the **LSU** sequence are *Deniquelata quercina* (strain 1050-SAB SA5 1, GenBank MT808605.1; Identities = 789/799 (99 %), one gap (0 %)), *Deniquelata barringtoniae* (strain MFLUCC 16-0271, GenBank MH260291.1; Identities = 805/816 (99 %), four gaps (0 %)) and *Neokalmusia thailandica* (strain MFLUCC 16-0399, GenBank KY706131.1; Identities = 778/814 (96 %), three gaps (0 %)). Distant hits obtained using the ***actA*** sequence had highest similarity to *Parastagonospora nodorum* (strain LDN03-Sn4, GenBank CP022803.1; Identities = 457/505 (90 %), five gaps (0 %)), *Setosphaeria rostrata* (strain BRIP 11426, GenBank LT837589.1; Identities = 474/534 (89 %), 15 gaps (2 %)) and *Setosphaeria minor* (strain BRIP 14612, GenBank LT837609.1; Identities = 471/531 (89 %), nine gaps (1 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Deniquelata vittalii* (strain PUFD39, GenBank MF168942.1; Identities = 744/823 (90 %), no gaps), *Didymocrea leucaenae* (strain MFLUCC 17-0896, GenBank MK434905.1; Identities = 733/823 (89 %), no gaps) and *Pseudopithomyces karoo* (strain MUCL 9365, GenBank LK936424.1; Identities = 766/905 (85 %), four gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudopithomyces entadae* (strain MFLUCC 17-0917, GenBank MK360083.1; Identities = 889/920 (97 %), no gaps), *Tremateia murispora* (strain GZCC 18-2787, GenBank MK986482.1; Identities = 902/934 (97 %), no gaps) and *Tremateia chromolaenae* (strain MFLUCC 17-1425, GenBank MT235778.1; Identities = 882/915 (96 %), two gaps (0 %)). The *tef1* sequences of CPC 38988 and 38984 differ by a single substitution (935/936 (99 %)).

Colour illustrations. Quartz stones with lichen and hypolith growth. Hyphae giving rise to conidia. Scale bars = 10 µm.

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Knufia hypolithi

Fungal Planet 1205 – 13 July 2021

Knufia hypolithi Crous, *sp. nov.*

Etymology. Name refers to the fact that it was isolated from a hypolith, under a quartz stone.

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of pale brown, smooth, septate, branched, 2–3 µm diam hyphae. *Chlamydospore-like propagules* intercalary, but commonly as terminal ends of hyphae, subcylindrical to ovoid-ellipsoid, dark brown, smooth-walled, with 3 to numerous constricted transverse septa, and several vertical or oblique septa, 15–80 × 10–25 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, reaching 18 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. Namibia, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, *P.W. Crous*, HPC 3101 (holotype CBS H-24503, culture ex-type CPC 38987 = CBS 146991, ITS and LSU sequences GenBank MZ064430.1 and MZ064487.1, MycoBank MB 839519).

Additional materials examined. Namibia, Walvis Bay, from hypolith under a rock, 19 Nov. 2019, *P.W. Crous*, cultures CPC 38983, 38985, ITS and LSU sequences GenBank MZ064431.1–MZ064432.1 and MZ064488.1–MZ064489.1.

Notes — *Knufia* is ecologically diverse, including species that are rock-inhabiting (Tsuneda et al. 2011), lichenicolous (Untereiner et al. 2011), opportunistic human pathogens (Li & Chen 2010), insect associates (He et al. 2013) and plant pathogens (Tsuneda & Currah 2005). *Knufia hypolithi* is related to '*Phialocephala*' *fluminis*, from which it is morphologically and phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Phialocephala fluminis* (strain WPF-48-12G, GenBank KT000162.1; Identities = 544/551 (99 %), five gaps (0 %)), *Phialocephala fluminis* (strain CBS 351.85, GenBank MH861889.1; Identities = 594/619 (96 %), nine gaps (1 %)) and *Knufia perfecta* (strain IRAN 2553C, GenBank MF062036.1; Identities = 519/562 (92 %), 21 gaps (3 %)). The ITS sequences of CPC 38983, 38985 and 38987 are identical (616/616 nucleotides). Closest hits using the **LSU** sequence are *Phialocephala fluminis* (strain CBS 351.85, GenBank MH873578.1; Identities = 845/855 (99 %), two gaps (0 %)), *Knufia perforans* (strain CBS 885.95, GenBank NG_042586.1; Identities = 827/845 (98 %), two gaps (0 %)) and *Knufia* sp. MV-2018 (strain MLT-8, GenBank MT636937.1; Identities = 817/836 (98 %), two gaps (0 %)). The LSU sequences of CPC 38983, 38985 and 38987 are identical (814/814 nucleotides).

Colour illustrations. Quartz stones and pebbles with lichen and hypolith growth. Hyphae giving rise to chlamydospore-like propagules. Scale bars = 10 µm.

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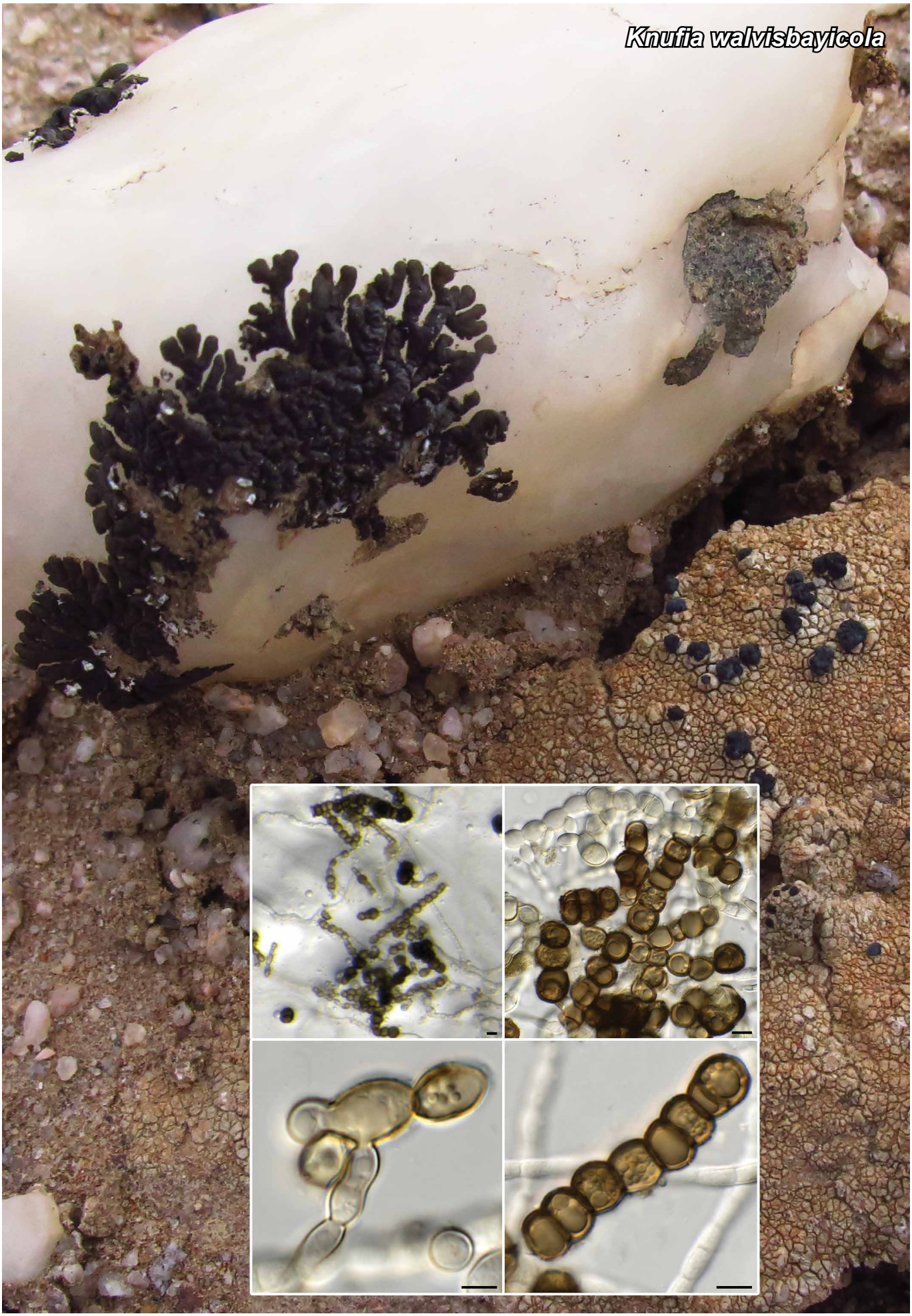
Knufia walvisbayicola

Fungal Planet 1206 – 13 July 2021

Knufia walvisbayicola Crous, *sp. nov.*

Etymology. Name refers to Walvis Bay, Namibia, where it was collected.

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Mycelium consisting of pale to dark brown hyphae, smooth, septate, branched, frequently constricted at septa, 3–4 µm diam. *Conidia* chlamydospore-like propagules, medium to dark brown, subcylindrical to elongated ellipsoid-ovoid, brown, warty, guttulate, thick-walled, with 2 to numerous transverse and 1–6 oblique or vertical septa, (20–)35–80(–170) × (9–)11–18(–30) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 8 mm diam after 2 wk at 25 °C. On MEA surface and reverse umber; on PDA surface and reverse olivaceous grey; on OA surface umber.

Typus. Namibia, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, *P.W. Crous*, HPC 3101 (holotype CBS H-24501, culture ex-type CPC 38988 = CBS 146989, ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank MZ064433.1, MZ064490.1, MZ078188.1, MZ078251.1 and MZ078265.1, MycoBank MB 839520).

Additional material examined. Namibia, Walvis Bay, from hypolith under a quartz stone, 19 Nov. 2019, *P.W. Crous*, HPC 3101, culture CPC 38984 = CBS 146990, ITS, LSU, *rpb1*, *tef1* (second part) and *tub2* sequences GenBank MZ064434.1, MZ064491.1, MZ078189.1, MZ078252.1 and MZ078266.1.

Notes — *Knufia walvisbayicola* is related to *K. marmoricola* (from marble stone, Vatican City; endoconidia 4.4–5.0 µm diam; Isola et al. 2016), from which it is phylogenetically and morphologically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 38988 had highest similarity to *Knufia marmoricola* (strain PiN-A2, GenBank KY887804.1; Identities = 483/505 (96 %), nine gaps (1 %)), *Knufia petricola* (strain 2Y43B, GenBank MT126632.1; Identities = 464/486 (95 %), ten gaps (2 %)) and *Knufia perforans* (strain CBS 885.95, GenBank NR_121502.1; Identities = 569/596 (95 %), nine gaps (1 %)). The ITS sequences of CPC 38988 and 38984 differ by an extra thymine nucleotide at two alignment positions (624/626 (99 %)). Closest hits using the **LSU** sequence of CPC 38988 are *Knufia* sp. MV-2018 (strain MLT-8, GenBank MT636937.1; Identities = 850/852 (99 %), no gaps), *Knufia marmoricola* (strain CCFEE 5716, GenBank KR781074.1; Identities = 855/858 (99 %), no gaps) and *Knufia perforans* (strain CBS 885.95, GenBank NG_042586.1; Identities = 855/858 (99 %), no gaps). The LSU sequences of CPC 38988 and 38984 are identical (796/796 (100 %)). Closest hits using the ***rpb1*** sequence of CPC 38988 had highest similarity to *Knufia* sp. LS-2015b (strain CGMCC 3.17226, GenBank KP226509.1; Identities = 565/593 (95 %), no gaps), *Knufia petricola* (strain CBS 726.95, GenBank KC978743.1; Identities = 575/631 (91 %), no gaps) and *Glyphium elatum* (strain CBS 268.34, GenBank FJ941902.1; Identities = 479/518 (92 %), no gaps). The *rpb1* sequences of CPC 38988 and 38984 are identical (682/682 (100 %)). Closest hits using the ***tef1*** sequence of CPC 38988 had highest similarity to *Knufia* sp. LS-2015b (strain CGMCC 3.17301, GenBank KP175012.1; Identities = 881/917 (96 %), no gaps), *Knufia petricola* (strain A95, GenBank MT859426.1; Identities = 895/953 (94 %), no gaps) and *Knufia epidermidis* (strain CGMCC 3.17300, GenBank KP175014.1; Identities = 837/918 (91 %), two gaps (0 %)). Distant hits obtained using the ***tub2*** sequence of CPC 38988 had highest similarity to *Phialophora americana* (strain CBS 102234, GenBank KU306351.1; Identities = 207/253 (82 %), nine gaps (3 %)), *Knufia peltigerae* (strain CGMCC 3.17283, GenBank KP226562.1; Identities = 173/204 (85 %), two gaps (0 %)) and '*Anthracinomyces ramosus*' (strain CGMCC 3.16367, GenBank KP226556.1; Identities = 175/207 (85 %), three gaps (1 %)). The *tub2* sequences of CPC 38988 and 38984 differ with three independent substitutions (573/576 (99 %)).

Colour illustrations. Quartz stone and pebbles with lichen and hypolith growth. Hyphae giving rise to chlamydospore-like propagules. Scale bars = 10 µm.

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Sordaria equicola

Fungal Planet 1207 – 13 July 2021

Sordaria equicola Crous, *sp. nov.*

Etymology. Name refers to the substrate from which it was isolated, on zebra (*Equus zebra hartmannae*) dung.

Classification — *Sordariaceae*, *Sordariales*, *Sordariomycetes.*

Mycelium consisting of smooth, pale brown, branched, septate, 1.5–2 µm diam hyphae. *Conidiophores* solitary, erect, arising from superficial hyphae, bearing a mucoid, crystalline conidial mass, subcylindrical, pale brown, smooth, branched, septate, appearing tuft-like, with numerous lateral branches, 3–4 µm diam, up to 80 µm tall. *Conidiogenous cells* integrated, terminal and intercalary, occurring throughout conidiophore as small phialidic openings, 1 µm diam, up to 0.5 µm tall, inconspicuous collarettes, not flared, conidiogenous cells 3–10 µm long, 3–4 µm diam. *Conidia* solitary, hyaline, smooth, aseptate, pyriform, apex subobtuse, base truncate, (3–)4(–4.5) × (2–)2.5(–3) µm.

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

Typus. Namibia, Gravel plains north-east of Gobabeb - Namib Research Institute, on zebra (*Equus zebra hartmannae*) dung, 20 Nov. 2019, *P.W. Crous*, HPC 3103 (holotype CBS H-24504, culture ex-type CPC 38993 = CBS 146992, ITS, LSU, *actA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064435.1, MZ064492.1, MZ078151.1, MZ078202.1, MZ078226.1 and MZ078267.1, MycoBank MB 839522).

Notes — *Sordaria* produces perithecia with asci containing eight uniseriate ascospores that are obovoid or subglobose, aseptate, smooth-walled, dark brown to black, pitted, reticulate or striate, with various appendages or sheaths (Guarro et al. 2012). *Sordaria equicola* is related to *S. fimicola*, a species commonly found in the feces of herbivores. *Sordaria equicola* is only known from its asexual morph, making a morphological comparison with other species impossible.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sordaria fimicola* (strain KoRLI047353, GenBank MN341415.1; Identities = 569/573 (99 %), one gap (0 %)), *Asordaria humana* (strain CBS 416.82, GenBank MH861509.1; Identities = 569/573 (99 %), one gap (0 %)) and *Sordaria macrospora* (strain CBS 346.62, GenBank MH858175.1; Identities = 569/573 (99 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Sordaria lappae* (strain CBS 154.97, GenBank MH874251.1; Identities = 807/808 (99 %), no gaps), *Asordaria humana* (strain CBS 416.82, GenBank MH873255.1; Identities = 807/808 (99 %), no gaps) and *Sordaria islandica* (strain CBS 512.77, GenBank MH872859.1; Identities = 807/808 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Sordaria macrospora* (strain k-hell, GenBank XM_024655553.1; Identities = 398/405 (98 %), no gaps), *Neurospora crassa* (strain OR74A, GenBank XM_011396324.1; Identities = 394/405 (97 %), no gaps) and *Neurospora tetrasperma* (strain FGSC 2508, GenBank XM_009849372.1; Identities = 393/405 (97 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Sordaria fimicola* (strain CBS 723.96, GenBank DQ368647.1; Identities = 844/882 (96 %), no gaps), *Neurospora pannonica* (strain TRTC51327, GenBank AY780185.1; Identities = 863/902 (96 %), no gaps) and *Sordaria clematidis* (voucher MFLU 16-2138, GenBank MT394717.1; Identities = 803/842 (95 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Pseudoneurospora* sp. (strain FMR 12156, GenBank HG326875.1; Identities = 447/494 (90 %), 15 gaps (3 %)), *Pseudoneurospora amorphoporcata* (strain CBS 626.80, GenBank FR774344.1; Identities = 440/487 (90 %), 16 gaps (3 %)) and *Neurospora pannonica* (strain FGSC 7221, GenBank FR774377.1; Identities = 425/483 (88 %), 17 gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Asordaria tenerifae* (strain CBS 264.86, GenBank AY681206.1; Identities = 447/480 (93 %), three gaps (0 %)), *Pseudoneurospora amorphoporcata* (strain CBS 626.80, GenBank FR774294.1; Identities = 436/469 (93 %), seven gaps (1 %)) and *Sordaria lappae* (strain CBS 154.97, GenBank AY681205.1; Identities = 448/482 (93 %), eight gaps (1 %)).

Colour illustrations. Zebras (*Equus zebra hartmannae*) in Namib Desert. Zebra dung; hyphae giving rise to conidia on SNA. Scale bars = 10 µm.

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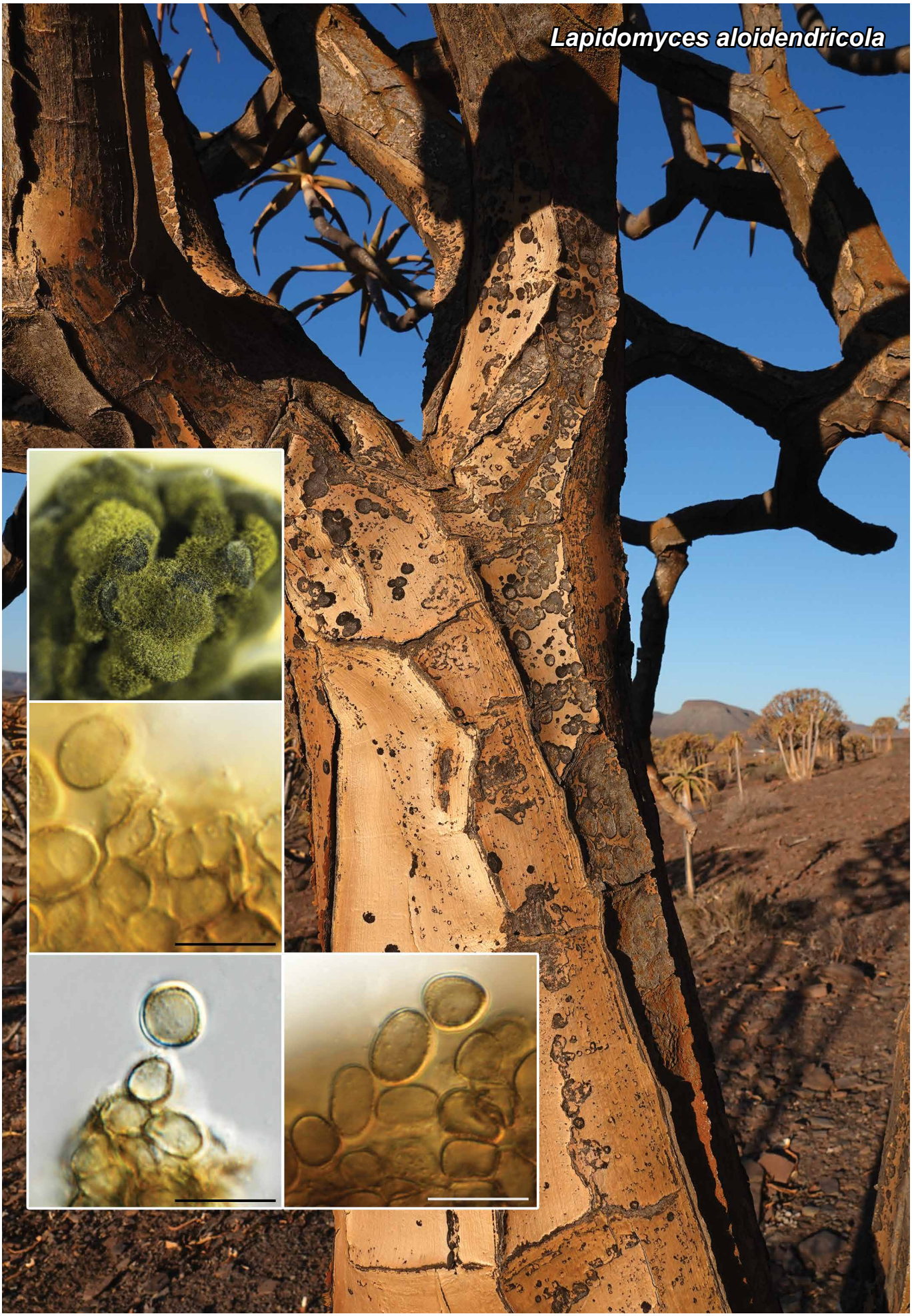
Lapidomyces aloidendricola

Fungal Planet 1208 – 13 July 2021

Lapidomyces aloidendricola Crous, *sp. nov.*

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

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes.*

Mycelium consisting of brown, finely verruculose, septate, branched, 3–6 µm diam hyphae, aggregating into a dense brown sporodochial stroma; upper layer developing brown cells, 4–7 × 4–6 µm with minute pores giving rise to solitary conidia. *Conidia* dry, ellipsoid to ovoid, brown, finely verruculose, aseptate (rarely 1-septate), (7–)8–10(–12) × 6(–7) µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse aerial mycelium and lobate, even margin, reaching 7 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron-grey.

Typus. South Africa, Northern Cape Province, Nieuwoudtville, as epiphyte on brown stem of *Aloidendron dichotomum* (*Asphodelaceae*), Nov. 2018, *P.W. Crous*, HPC 3038 (holotype CBS H-24480, culture ex-type CPC 38703 = CBS 146968, ITS, LSU, *rpb2* and *tub2* sequences GenBank MZ064436.1, MZ064493.1, MZ078203.1 and MZ078268.1, MycoBank MB 839523).

Notes — *Lapidomyces aloidendricola* is closely related to *L. hispanicus* (isolated from rocks in Spain), a sterile hyphomycete with dark brown hyphae, constricted at their septa (Egidi et al. 2014). Morphologically and phylogenetically, *L. aloidendricola* represents a distinct species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Fungal sp. (strain TRN453, GenBank AY843151.1; Identities = 464/467 (99 %), no gaps), *Lapidomyces hispanicus* (strain CBS 118355, GenBank NR_144960.1; Identities = 453/468 (97 %), three gaps (0 %)) and *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 508/536 (95 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599595.1; Identities = 831/844 (98 %), four gaps (0 %)), *Xenoconiothyrium catenata* (strain CMW 22113, GenBank JN712570.1; Identities = 833/849 (98 %), two gaps (0 %)) and *Neophaeothecoidea proteae* (strain CBS 114129, GenBank MH874518.1; Identities = 852/869 (98 %), no gaps). Distant hits obtained using the ***rpb2*** sequence had highest similarity to *Zasmidium eucalyptorum* (strain CBS 118500, GenBank MF951702.1; Identities = 377/492 (77 %), eight gaps (1 %)), *Zymoseptoria tritici* (strain ST99CH_3D1, GenBank LT854276.1; Identities = 349/455 (77 %), ten gaps (2 %)) and *Constantinomyces oldenburgensis* (strain T2.4, GenBank LT976528.1; Identities = 618/855 (72 %), 34 gaps (3 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Lapidomyces hispanicus* (strain TRN500, GenBank KF546778.1; Identities = 338/407 (83 %), seven gaps (1 %)), *Cladosporium sphaerospermum* (strain UBOCC-A-101110, GenBank KJ596619.1; Identities = 344/415 (83 %), 20 gaps (4 %)) and *Cladosporium salinae* (strain EXF-322, GenBank EF101403.1; Identities = 396/496 (80 %), 32 gaps (6 %)).

Colour illustrations. Aloidendron dichotomum. Colony on SNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

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Phaeosphaeriopsis sansevieriae
& Lasionectria sansevieriae

Fungal Planet 1209 & 1210 – 13 July 2021

Phaeosphaeriopsis sansevieriae Crous, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata red-brown, globose, 80–300 µm diam, with central ostiole (40–60 µm diam), frequently densely aggregated; wall of 6–8 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform, phialidic, 5–7 × 5–6 µm. *Conidia* solitary, aseptate, golden brown, verruculose, ellipsoid to subcylindrical with obtuse ends, (5–)6(–7) × 3–4 µm.

Culture characteristics — Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse buff.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Sansevieria hyacinthoides* (*Ruscaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3143 (holotype CBS H-24496, culture ex-type CPC 38956 = CBS 146984, ITS, LSU and *rpb2* sequences GenBank MZ064438.1, MZ064495.1 and MZ078204.1, MycoBank MB 839524).

Additional material examined. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Sansevieria hyacinthoides* (*Ruscaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3143 (CBS H-24540, culture CPC 39087 = CBS 147076, ITS, LSU and *rpb2* sequences GenBank MZ064439.1, MZ064496.1 and MZ078205.1).

Notes — *Phaeosphaeriopsis* was introduced by Câmara et al. (2003) to accommodate several paraphaeosphaeria-like taxa. *Phaeosphaeriopsis sansevieriae* formed only an asexual morph in culture. It is closely related to *P. obtusispora* (ascospores 17–22 × 5–6 µm, on leaves *Yucca gloriosa*, Argentina; Câmara et al. 2003), but is phylogenetically distinct from that species.

(notes *Phaeosphaeriopsis sansevieriae* continues on Supplementary material page FP1209 & 1210)

Lasionectria sansevieriae Crous & L. Zhao, *sp. nov.*

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

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

Mycelium consisting of hyaline, smooth, 2.5–3.5 µm diam hyphae. *Conidiophores* solitary to aggregated, erect, flexuous, subverticillate, up to 100 µm tall, 1–3-septate. *Conidiogenous cells* terminal and intercalary, subcylindrical to aculeate, 20–50 × 2.5–3(–4) µm, phialidic with periclinal thickening with minute flared collarette, 1 µm long. *Conidia* solitary, aggregated in mucoid droplet, smooth, hyaline, aseptate, fusoid-ellipsoid to subcylindrical, straight, apex subobtuse, base truncate, granular, (6–)7–7.5(–8) × (2.5–)3 µm.

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

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Sansevieria hyacinthoides* (*Ruscaceae*), Nov. 2018, *P.W. Crous*, HPC 3143 (holotype CBS H-24485, culture ex-type CPC 38898 = CBS 146973, ITS, LSU and *tef1* (first part) sequences GenBank MZ064437.1, MZ064494.1 and MZ078227.1, MycoBank MB 839525).

Notes — *Lasionectria sansevieriae* is related to *L. mantuana*, *L. hilhorstii*, *Nectriopsis lecanodes* and *Acremonium cereale* (Lombard et al. 2015), but is phylogenetically and morphologically distinct, being an acremonium-like taxon in the *Bionectriaceae*. Further research is currently underway to redefine genera in the family.

(notes *Lasionectria sansevieriae* continues on Supplementary material page FP1209 & 1210)

Colour illustrations. *Sansevieria hyacinthoides*. Left column: *Phaeosphaeropsis sansevieriae.* Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Right column: *Lasionectria sansevieriae.* Conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata of *P. sansevierae*), 10 µm (all others).

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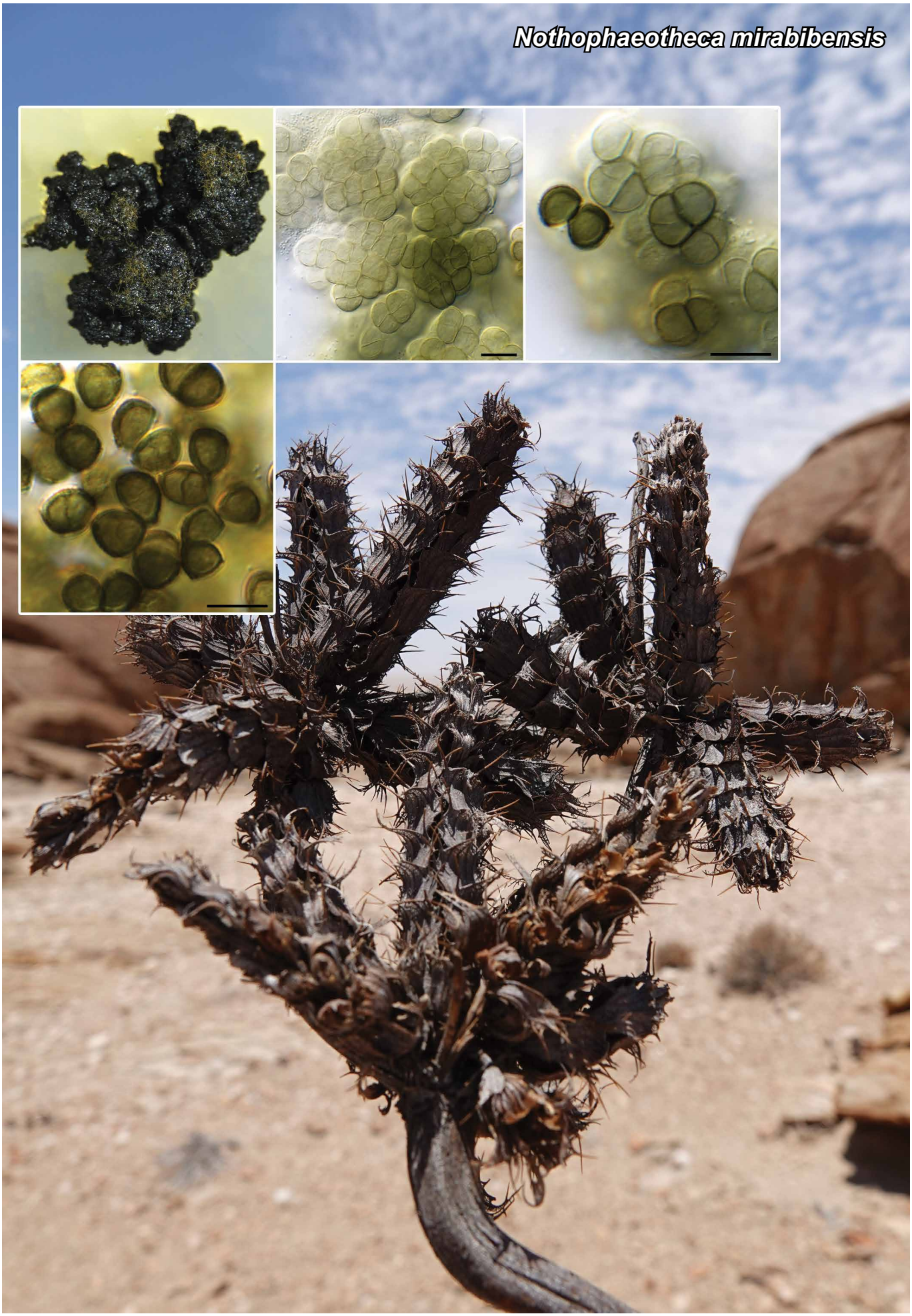
Nothophaeotheca mirabibensis

Fungal Planet 1211 – 13 July 2021

Nothophaeotheca Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Neophaeotheca*.

Classification — *Neophaeothecaceae*, *Neophaeothecales*, *Dothideomycetes.*

Mycelium consisting of smooth, hyaline to green-brown, septate, branched hyphae that give rise to microsclerotia, green-brown, globose to ellipsoid, 20–120 µm diam, containing endoconidia, globose, ellipsoid, green-brown, verruculose, muriformly septate, initially in clusters of 2–6, eventually disarticulating into solitary, globose-ellipsoid *conidia*, thick-walled, verruculose to warty, 0–1-septate, ellipsoid-globose, (7–)8–9 × (6–)7–8 µm.

Type species. Nothophaeotheca mirabibensis Crous
MycoBank MB 839526.

Nothophaeotheca mirabibensis Crous, *sp. nov.*

Etymology. Name refers to the collection site, namely the Mirabib inselberg in the Namib Desert, Namibia.

Mycelium consisting of smooth, hyaline to green-brown, septate, branched hyphae that give rise to microsclerotia, green-brown, globose to ellipsoid, 20–120 µm diam, containing endoconidia, globose, ellipsoid, green-brown, verruculose, muriformly septate, initially in clusters of 2–6, eventually disarticulating into solitary, globose-ellipsoid *conidia*, thick-walled, verruculose to warty, 0–1-septate, ellipsoid-globose, (7–)8–9 × (6–)7–8 µm.

Culture characteristics — Colonies erumpent, surface folded, with sparse aerial mycelium and lobate, uneven margin, reaching 6 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reserve iron-grey.

Typus. Namibia, Gobabeb Namib Research Institute, Mirabib, on persistent inflorescence remains of *Blepharis obmitrata* (*Acanthaceae*), 19 Nov. 2019, *P.W. Crous*, HPC 3109 (holotype CBS H-24492, culture ex-type CPC 38944 = CBS 146980, ITS, LSU, *actA*, *tef1* (first part) and *tef1* (second part) sequences GenBank MZ064440.1, MZ064497.1, MZ078152.1, MZ078228.1 and MZ078253.1, MycoBank MB 839527).

Notes — *Nothophaeotheca* is related to *Neophaeotheca*, which is known to form a dematiaceous hyphomycetous morph with endoconidia. Two species of *Neophaeotheca* are presently known from twigs and leaves of *Salicornia meyeriana* in South Africa, and the humidifier of an air-conditioning system in Belgium (Abdollahzadeh et al. 2020). Although morphologically similar, *Nothophaeotheca* is phylogenetically distinct from *Neophaeotheca*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neophaeotheca salicorniae* (strain CPC 27406, GenBank NR_145401.1; Identities = 508/563 (90 %), 26 gaps (4 %)), *Neophaeotheca triangularis* (strain CBS 471.90, GenBank NR_137142.1; Identities = 417/459 (91 %), 21 gaps (4 %)) and *Phaeothecoidea melaleuca* (strain CPC 17223, GenBank HQ599594.1; Identities = 465/545 (85 %), 22 gaps (4 %)). Closest hits using the **LSU** sequence are *Neophaeotheca triangularis* (strain CBS 471.90, GenBank NG_057776.1; Identities = 839/856 (98 %), one gap (0 %)), *Neophaeotheca salicorniae* (strain CBS 141299, GenBank NG_058237.1; Identities = 813/834 (97 %), one gap (0 %)) and *Fumagospora capnodioides* (strain CBS 131.34, GenBank EU019269.1; Identities = 823/860 (96 %), four gaps (0 %)). No significant hits were obtained when the ***actA*** and ***tef1*** sequences were used in blastn and megablast searches.

Colour illustrations. Inflorescence remains of *Blepharis obmitrata*. Colony on SNA; hyphae giving rise to endoconidia. Scale bars = 10 µm.

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Preussia procaviicola

Fungal Planet 1212 – 13 July 2021

Preussia procaviicola Crous, *sp. nov.*

Etymology. Isolated from dung of *Procavia capensis* (rock rabbit).

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

Ascomata pseudothecial, globose to pyriform, 200–300 µm diam, smooth, black, central ostiolata; wall of 6–8 layers of brown *textura angularis. Pseudoparaphyses* filiform, hyaline, smooth, 3–4 µm diam, anastomosing, constricted at septa, hyphae-like. *Asci* 8-spored, bitunicate, cylindrical-clavate, stipitate, with ocular chamber, 85–170 × 20–25 µm. *Ascospores* biseriate, cylindrical with obtuse ends, becoming dark brown, guttulate, transversely 3-septate, prominently constricted at septa, two middle cells equal in length, 7.5–9 µm long, end cells 11–14 µm long; germ slits oblique, gelatinous sheath not persistent, (32–)35–40(–42) × (7–)8–9 µm.

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

Typus. Namibia, Gobabeb Namib Research Institute, Mirabib, on dung of *Procavia capensis*, 19 Nov. 2019, *P.W. Crous*, HPC 3110 (holotype CBS H-24493, culture ex-type CPC 38946 = CBS 146981, ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank MZ064441.1, MZ064498.1, MZ078229.1 and MZ078269.1, MycoBank MB 839528).

Notes — *Preussia procaviicola* was isolated from the same dung sample as *P. procaviae* (Crous et al. 2020a), although the latter is only known from its asexual morph. *Preussia procaviicola* is close to *P. intermedia* (ascospores 3-septate, 48–59 × 9.5–11.5 µm; Guarro et al. 2012), but morphologically distinct from that species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Preussia africana* (strain A54, GenBank KX611037.1; Identities = 515/539 (96 %), seven gaps (1 %)), *Sporormiella intermedia* (strain 18THES003, GenBank MT856402.1; Identities = 498/522 (95 %), four gaps (0 %)) and *Preussia lignicola* (strain KoRLI046140, GenBank MN341249.1; Identities = 509/535 (95 %), seven gaps (1 %)). Closest hits using the **LSU** sequence are *Preussia intermedia* (strain CBS 364.69, GenBank MH878451.1; Identities = 875/877 (99 %), one gap (0 %)), *Preussia minipascua* (voucher UPS:Kruys 306, GenBank GQ203745.1; Identities = 868/876 (99 %), one gap (0 %)) and *Preussia persica* (strain GLMC 447, GenBank MT156301.1; Identities = 841/849 (99 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Preussia procaviae* (strain CPC 38861, GenBank MW173126.1; Identities = 370/484 (76 %), 44 gaps (9 %)), *Synfenestella sorbi* (strain FRa, GenBank MK357595.1; Identities = 224/253 (89 %), three gaps (1 %)) and *Parafenestella alpina* (strain C198, GenBank MK357574.1; Identities = 225/256 (88 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Preussia lignicola* (strain 18ALIC002, GenBank MT671880.1; Identities = 385/444 (87 %), 17 gaps (3 %)), *Sporormiella intermedia* (strain 18THES003, GenBank MT881987.1; Identities = 375/441 (85 %), ten gaps (2 %)) and *Preussia procaviae* (strain CPC 38861, GenBank MW173141.1; Identities = 340/389 (87 %), nine gaps (2 %)).

Colour illustrations. Mirabib, typical habitat of the rock rabbit in the Namib Desert. Asci and ascospores. Scale bars = 10 µm.

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Teratosphaeria combreti

Fungal Planet 1213 – 13 July 2021

Teratosphaeria combreti Crous, *sp. nov.*

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

Classification — *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Ascomata not associated with leaf spots, but occurring on leaf litter; pseudothecial, amphigenous, dark brown, erumpent, 50–80 µm diam, with central ostiole; wall of 3–4 layers of brown *textura angularis*. *Asci* 8-spored, stipitate, fasciculate, bitunicate, obovoid, with narrow ocular chamber, 23–29 × 5–6 µm. *Ascospores* multiseriate, guttulate, fusoid-ellipsoid, widest above septum, not constricted at median septum, thick-walled, without mucoid sheath, hyaline, smooth, 7–8 × 2.5–3 µm; ascospores germinating from both ends, with germ tubes parallel to the long axis, swelling at median septum, remaining hyaline, 5–7 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, PDA and OA surface and reverse olivaceous grey.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaf litter of *Combretum kraussii* (*Combretaceae*), Nov. 2018, *P.W. Crous*, HPC 3145 (holotype CBS H-24497, culture ex-type CPC 38958 = CBS 146985, ITS, LSU, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064442.1, MZ064499.1, MZ078165.1, MZ078206.1, MZ078230.1 and MZ078270.1, MycoBank MB 839530).

Notes — *Teratosphaeria combreti* is related to *T. agapanthi* (on *Agapanthus* spp., ascospores (17–)18–20(–21) × 4.5–5 (–6) µm; Crous et al. 2011, 2020b). Both species occur on host plants indigenous to South Africa. Morphologically, however, they can easily be distinguished based on their ascospore dimensions.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teratosphaeria agapanthi* (strain CBS 129192, GenBank NR_169894.1; Identities = 507/531 (95 %), one gap (0 %)), *Teratosphaeria hortaea* (strain CBS 124156, GenBank MH863358.; Identities = 498/537 (93 %), nine gaps (1 %)) and *Teratosphaeria considenianae* (strain CPC 15009, GenBank MN162031.1; Identities = 489/528 (93 %), six gaps (1 %)). Closest hits using the **LSU** sequence are *Teratosphaeria agapanthi* (strain CPC 18266, GenBank JF770471.1; Identities = 879/882 (99 %), no gaps), *Teratosphaeria hortaea* (strain CBS 124156, GenBank MH874881.1; Identities = 871/879 (99 %), no gaps) and *Teratosphaeria miniata* (strain CBS 125006, GenBank GQ852711.1; Identities = 837/845 (99 %), no gaps). Distant hits obtained using the ***cmdA*** sequence had highest similarity to *Austroafricana parva* (strain CPC 12249, GenBank KF902533.1; Identities = 287/304 (94 %), no gaps), *Penidiella columbiana* (strain CBS 486.80, GenBank KF902594.1; Identities = 285/305 (93 %), no gaps) and *Euteratosphaeria verrucosiafricana* (strain CBS 118497, GenBank KF902541.1; Identities = 281/305 (92 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Teratosphaeria cryptica* (strain CBS 111663, GenBank KX348101.1; Identities = 691/871 (79 %), 15 gaps (1 %)), *Teratosphaeria sieberi* (strain CPC 32099, GenBank MH327872.1; Identities = 690/871 (79 %), 19 gaps (2 %)) and *Teratosphaeria stellenboschiana* (strain CBS 125215, GenBank MF951743.1; Identities = 682/868 (79 %), 13 gaps (1 %)). Distant hits using the ***tef1*** sequence had highest similarity to *Teratosphaeria corymbiicola* (strain CBS 146047, GenBank MN556823.1; Identities = 291/365 (80 %), 26 gaps (7 %)), *Teratosphaeria pseudocryptica* (strain CPC 29430, GenBank MN162366.1; Identities = 280/353 (79 %), 20 gaps (5 %)) and *Teratosphaeria fibrillosa* (strain CBS 121707, GenBank KF903305.1; Identities = 284/357 (80 %), 32 gaps (8 %)).Closest hits using the ***tub2*** sequence had highest similarity to *Teratosphaeria gracilis* (strain CBS 145090, GenBank MK047583.1; Identities = 438/530 (83 %), 27 gaps (5 %)), *Teratosphaeria dunnii* (strain CBS 145548, GenBank MK876504.1; Identities = 433/537 (81 %), 22 gaps (4 %)) and *Teratosphaeria henryi* (strain CBS 145539, GenBank MK876505.1; Identities = 431/536 (80 %), 29 gaps (5 %)).

Colour illustrations. *Combretum kraussii*. Leaf spot with ascomata; asci with ascospores; ascospores; germinating ascospores. Scale bars = 10 µm.

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Neochaetothyrina syzygii

Fungal Planet 1214 – 13 July 2021

Neochaetothyrina Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Chaetothyrina*.

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

Leaf spots absent, saprobic. *Ascomata* hypophyllous, superficial on leaf tissue, brown, developing beneath a brown mycelial layer, globose, cupulate when dry, surface of brown *textura epidermoidea*, wall of 2–3 layers of brown *textura angularis*; outer wall of ascomata forming brown, radiating superficial hyphae, branched, septate, anastomosing, with mucoid sheath, constricted at septa; hyphopodia not seen. *Setae* arising from outer wall of ascoma, dark brown, verruculose to warty, thick-walled, flexuous, multi-septate, tapering to subobtuse apex, at times also arising from superficial mycelium surrounding ascoma, with basal T-cell, slightly swollen. *Pseudoparaphyses* hyaline, smooth, cellular, constricted at septa, anastomosing. *Asci* arranged in basal layer, obovoid to broadly ellipsoid, bitunicate, 8-spored, with apical chamber. *Ascospores* multiseriate, hyaline, smooth, thick-walled, guttulate, granular, fusoid-ellipsoid, straight or curved, apex subobtuse, tapering to obtuse base, constricted at median septum, widest above septum, encased in mucoid sheath.

Type species. Neochaetothyrina syzygii Crous
MycoBank MB 839531.

Neochaetothyrina syzygii Crous, *sp. nov.*

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

Leaf spots absent, saprobic. *Ascomata* hypophyllous, superficial on leaf tissue, brown, developing beneath a brown mycelial layer, globose, 100–200 µm diam, cupulate when dry, surface of brown *textura epidermoidea*, wall of 2–3 layers of brown *textura angularis*; outer wall of ascomata forming brown, radiating superficial hyphae, branched, septate, anastomosing, with mucoid sheath, constricted at septa, 3–6 µm diam; hyphopodia not seen. *Setae* arising from outer wall of ascoma, dark brown, verruculose to warty, thick-walled, flexuous, 4–15-septate, tapering to subobtuse apex, 3–4 µm diam, up to 300 µm long, 7–10 µm diam at base, at times also arising from superficial mycelium surrounding ascoma, with basal T-cell, slightly swollen. *Pseudoparaphyses* hyaline, smooth, cellular, constricted at septa, anastomosing, 3–4 µm diam. *Asci* arranged in basal layer, obovoid to broadly ellipsoid, bitunicate, 8-spored, with apical chamber, 5–6 µm diam, 30–40 × 20–25 µm. *Ascospores* multiseriate, hyaline, smooth, thick-walled, guttulate, granular, fusoid-ellipsoid, straight or curved, apex subobtuse, tapering to obtuse base, constricted at median septum, widest above septum, encased in mucoid sheath, (16–)17–18(–22) × (5–)6(–7) µm. Ascospores germinating from both ends, becoming brown and verruculose, swollen and distorted, 7–8 µm diam, but not developing additional septa in ascospore.

Culture characteristics — Colonies erumpent, with sparse aerial mycelium and smooth, lobate margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

Typus. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on leaves of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3157 (holotype CBS H-24537, culture ex-type CPC 39051 = CBS 147073, ITS, LSU and *rpb2* sequences GenBank MZ064443.1, MZ064500.1 and MZ078207.1, MycoBank MB 839532).

Colour illustrations. *Syzygium cordatum*. Ascomata on leaf surface with setae; setae; asci and ascospores; germinating ascospores. Scale bars = 200 µm (ascomata), 10 µm (all others).

Notes — When freshly collected leaves colonised by *Neochaetothyrina syzygii* are incubated in moist chambers, ascomata develop within 1 wk. However, the upper wall is a covering membrane of hyphae, that easily separates during slide preparation, leaving a layer of near naked asci embedded in a brown mucilaginous mass. *Neochaetothyrina* is reminiscent of *Chaetothyrina* (Hongsanan et al. 2017), but the latter species lacks superficial hyphae and setae.

Neochaetothyrina syzygii was also compared to *Chaetothyrium syzygii* (on *Syzygium cordatum*, Kwazulu-Natal, PREM 33103), but the latter had hyaline, fusoid ascospores that become brown and 3-septate at maturity, 20 × 6–7 µm. Furthermore, *Asterina syzygii* (on *Syzygium gerrardi*, Woodbush, Limpopo Province, PREM 17755) had 1-septate, slightly constricted, brown, finely verruculose ascospores, 27.5–35 × 14–17 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Chaetothyrina guttulata* (strain MFLUCC 14-0539, GenBank MN462949.1; Identities = 412/481 (86 %), 23 gaps (4 %)), *Xenosonderhenia syzygii* (strain MEFC132, GenBank MK732144.1; Identities = 354/399 (89 %), 17 gaps (4 %)) and *Pseudosasa guanxianensis* (clone 8, GenBank KT006327.1; Identities = 353/399 (88 %), 17 gaps (4 %)). Closest hits using the **LSU** sequence are *Chaetothyrina artocarpi* (strain MFLUCC 15-1082, GenBank MF614834.1; Identities = 802/823 (97 %), one gap (0 %)), *Chaetothyrina guttulata* (strain MFLUCC 14-0539, GenBank MN462949.1; Identities = 830/852 (97 %), one gap (0 %)) and *Houjia yanglingensis* (strain CBS 125225, GenBank NG_064220.1; Identities = 835/860 (97 %), one gap (0 %)). Distant hits using the ***rpb2*** sequence had highest similarity to *Houjia pomigena* (strain CBS 125224, GenBank MF951422.1; Identities = 640/801 (80 %), two gaps (0 %)), *Hyalocercosporidium desmodii* (strain CBS 142179, GenBank MF951503.1; Identities = 660/880 (75 %), 26 gaps (2 %)) and *Stromatoseptoria castaneicola* (strain CBS 102322, GenBank MF951681.1; Identities = 665/888 (75 %), 24 gaps (2 %)).

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Seiridium syzygii

Fungal Planet 1215 – 13 July 2021

Seiridium syzygii Crous, *sp. nov.*

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

Classification — *Sporocadaceae*, *Xylariales*, *Sordariomycetes.*

Conidiomata stromatic, separate, globose, immersed to erumpent, black, up to 300 µm diam, unilocular; walls of 3–6 layers of brown *textura angularis. Conidiophores* lining the inner cavity, subcylindrical, unbranched or branched below, hyaline, 1–3-septate, smooth, up to 40 µm long. *Conidiogenous cells* discrete, integrated, subcylindrical, 7–13 × 2.5–3 µm, with several percurrent proliferations near apex. *Conidia* fusoid, wall smooth, not constricted at septa, 5-septate with central pore, guttulate, (24–)25–28(–31) × 8(–10) µm, wall 1.5 µm thick, with appendages; basal cell obconic, subhyaline to pale brown with a single, unbranched central appendage, 5–12 µm; apical cell broadly conical to bluntly rounded, subhyaline to pale brown with central appendage, unbranched, 5–12 µm.

Culture characteristics — Colonies flat, spreading, with moderate aerial mycelium and lobate, smooth margin, reaching 35 mm diam after 2 wk at 25 °C. On MEA surface pale grey olivaceous, reverse sienna in middle, umber in outer region; on PDA surface and reverse grey olivaceous; on OA surface olivaceous grey.

Typus. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on twigs of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3149 (holotype CBS H-24543, culture ex-type CPC 39149 = CBS 147078, ITS and LSU sequences GenBank MZ064444.1 and MZ064501.1, MycoBank MB 839533).

Additional material examined. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on twigs of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3149 (CBS H-24482, culture CPC 38822 = CBS 146970, ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank MZ064445.1, MZ064502.1, MZ078231.1 and MZ078271.1).

Notes — *Seiridium syzygii* has conidia that are similar to those of *S. podocarpi* (on *Podocarpus latifolius*, South Africa, (23–)25–28(–30) × (8–)9–10 µm; Crous et al. 2014a, Bonthond et al. 2018), but it has shorter conidiophores and conidiogenous cells, and is also phylogenetically distinct from the latter species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 39149 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank NR_156589.1; Identities = 584/588 (99 %), no gaps), *Seiridium camelliae* (strain MFLUCC 12-0647, GenBank NR_158886.1; Identities = 525/534 (98 %), three gaps (0 %)) and *Seiridium cancrinum* (strain CBS 226.55, GenBank NR_160577.1; Identities = 567/597 (95 %), nine gaps (1 %)). The ITS sequences of CPC 39149 and 38822 differ by a single substitution (586/587 (99 %)). Closest hits using the **LSU** sequence of CPC 39149 are *Seiridium cardinale* (strain CBS 172.56, GenBank MH869107.1; Identities = 877/877 (100 %), no gaps), *Seiridium neocupressi* (strain CBS 142625, GenBank MH554329.1; Identities = 834/834 (100 %), no gaps) and *Nothoseiridium podocarpi* (strain CPC 36967, GenBank MT373346.1; Identities = 869/870 (99 %), no gaps). The LSU sequences of CPC 39149 and 38822 are identical (849/849 (100 %)). Closest hits using the ***tef1*** sequence of CPC 38822 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 501/540(93 %), five gaps (0 %)), *Seiridium eucalypti* (strain CBS 343.97, GenBank LT853196.1; Identities = 474/545 (87 %), 23 gaps (4 %)) and *Seiridium kartense* (as *Seiridium* sp. GB-2017a; strain CBS 142629, GenBank LT853197.1; Identities = 468/542 (86 %), 18 gaps (3 %)). Closest hits using the ***tub2*** sequence of CPC 38822 had highest similarity to *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 667/710 (94 %), six gaps (0 %)), *Seiridium cupressi* (strain CMW18607, GenBank DQ926979.1; Identities = 290/312 (93 %), two gaps (0 %)) and *Seiridium persooniae* (strain CBS 143445, GenBank MG386163.1; Identities = 367/403 (91 %), four gaps (0 %)).

Colour illustrations. Leaves of *Syzygium cordatum*. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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Setophoma syzygii

Fungal Planet 1216 – 13 July 2021

Setophoma syzygii Crous, *sp. nov.*

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

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

Conidiomata pycnidial, globose, brown, 150–250 µm diam, multilocular, aggregated in a brown stroma with several apical ostioles, oozing a crystalline mucoid mass; outer surface covered in brown, flexuous setae, subcylindrical, brown, base verruculose, septate, up to 70 µm tall, 3–4 µm diam, terminating in obtuse ends. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, 5–7 × 3–4 µm, phialidic with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, aseptate, subcylindrical, ends obtuse, slightly curved, (3–)4–5 × (2–)2.5 µm.

Culture characteristics — Colonies flat, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface and reverse olivaceous grey, outer region apricot; on PDA surface and reverse isabelline in centre, outer region rosy buff; on OA surface brown vinaceous with patches of rosy buff.

Typus. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on leaves of *Syzygium* sp. (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3166 (holotype CBS H-24488, culture ex-type CPC 38921 = CBS 146976, ITS, LSU and *tub2* sequences GenBank MZ064446.1, MZ064503.1 and MZ078272.1, MycoBank MB 839534).

Colour illustrations. Lowveld Botanical Garden. Conidioma on OA; setae; conidiogenous cells giving rise to conidia; conidia. Scale bars = 250 µm (conidioma), 10 µm (all others).

Notes — *Setophoma* is characterised by having setose conidiomatal pycnidia, phialidic conidiogenous cells and hyaline, ellipsoidal to subcylindrical, aseptate conidia (De Gruyter et al. 2010, Quaedvlieg et al. 2013, Liu et al. 2019). *Setophoma syzygii* is related to *S. chromolaenae* (on *Chromolaena odorata*, Brazil, conidia (4.5–)5–6(–7) × (2–)2.5(–3) µm; Quaedvlieg et al. 2013), but is morphologically and phylogenetically distinct from that species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Setophoma chromolaena* (strain AM01, GenBank KM246158.1; Identities = 564/565 (99 %), no gaps), *Setophoma vernoniae* (strain CBS 137988, GenBank NR_168153.1; Identities = 573/583 (98 %), no gaps) and *Setophoma caverna* (strain LF2095, GenBank MK511927.1; Identities = 491/508 (97 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Setophoma vernoniae* (strain CBS 137988, GenBank KJ869198.1; Identities = 883/883 (100 %), no gaps), *Setophoma endophytica* (strain CGMCC 3.19528, GenBank NG_070083.1; Identities = 882/882 (100 %), no gaps) and *Setophoma antiqua* (as *Setophoma* sp. FL-2019a; strain LF1237, GenBank MK511947.1; Identities = 882/882 (100 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Setophoma vernoniae* (strain CBS 137988, GenBank MK540177.1; Identities = 501/530 (95 %), two gaps (0 %)), *Setophoma endophytica* (strain LC3163, GenBank MK525020.1; Identities = 481/523 (92 %), eight gaps (1 %)), *Setophoma antiqua* (strain LC6595, GenBank MK525000.1; Identities = 466/504 (92 %), seven gaps (1 %)) and *Setophoma chromolaenae* (strain CBS 135105, GenBank KF252728.1; Identities = 274/295 (93 %), one gap (0 %)).

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Paramycosphaerella syzygii

Fungal Planet 1217 – 13 July 2021

Paramycosphaerella syzygii Crous, *sp. nov.*

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

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

On SNA. *Mycelium* consisting of pale brown, smooth, septate, branched, 1.5–2.5 µm diam hyphae. *Conidiophores* 0–2-septate, brown, smooth, erect, branched or not, subcylindrical, 15–50 × 4–5 µm. *Conidiogenous cells* integrated, terminal and intercalary, brown, smooth, subcylindrical, 10–20 × 4–5 µm, proliferating sympodially with 1–3 loci, thickened, darkened, refractive, 2–3 µm diam. *Conidia* solitary, brown, smooth, guttulate, obclavate, apex subobtuse, straight to slightly curved, 2–6-septate, (35–)50–70(–90) × (3–)4–4.5 µm; scars thickened, darkened, refractive, 2–3 µm diam.

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

Typus. South Africa, Mpumalanga, Mbombela, Lowveld Botanical Garden, on leaf litter of *Syzygium cordatum* (*Myrtaceae*), Nov. 2018, *P.W. Crous*, HPC 3157 (holotype CBS H-24499, culture ex-type CPC 38964 = CBS 146987, ITS, LSU, *actA*, *cmdA*, *tef1* (first part) and *tub2* sequences GenBank MZ064447.1, MZ064504.1, MZ078153.1, MZ078166.1, MZ078232.1 and MZ078273.1, MycoBank MB 839535).

Notes — *Paramycosphaerella syzygii* forms a passalora-like asexual morph in culture. On the host tissue, however, it formed synnemata, which were absent in culture. Videira et al. (2017) commented that *Paramycosphaerella* was heterogeneous, and although most species were known by their sexual morphs, some had zasmidium- or pseudocercospora-like asexual morphs. Phylogenetically and morphologically, *P. syzygii* is distinct from other species described in the genus.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella dicranopteridis* (strain TNM 3953, GenBank NR_155639.1; Identities = 478/507 (94 %), five gaps (0 %)), *Paramycosphaerella blechni* (strain CPC 24698, GenBank NR_155663.1; Identities = 478/513 (93 %), ten gaps (1 %)) and *Mycosphaerella rosigena* (strain CBS 330.51, GenBank GU214632.1; Identities = 476/511 (93 %), nine gaps (1 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 859/866 (99 %), no gaps), *Hyalozasmidium aerohyalinosporum* (strain CPC 14636, GenBank NG_059440.1; Identities = 838/846 (99 %), no gaps), *Virosphaerella irregularis* (strain CBS 123242, GenBank MH874810.1; Identities = 843/853 (99 %), no gaps) and *Piricauda paraguayensis* (strain VIC 31785.52, GenBank KJ459712.1; Identities = 790/795 (99 %), no gaps). Closest hits using the ***actA*** sequence had highest similarity to *Mycosphaerella musae* (strain CIRAD-AUS, GenBank MW070780.1; Identities = 536/601 (89 %), 15 gaps (2 %)), *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556790.1; Identities = 544/614 (89 %), 23 gaps (3 %)) and *Paramycosphaerella marksii* (strain CBS 110750, GenBank KF903404.1; Identities = 486/544 (89 %), seven gaps (1 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF902788.1; Identities = 328/367 (89 %), ten gaps (2 %)), *Septoria steviae* (strain NCSep12, GenBank MH532378.1; Identities = 278/304 (91 %), no gaps) and *Nothopassalora personata* (strain IRAN 3479C, GenBank MN422408.1; Identities = 283/312 (91 %), no gaps). No significant hits were obtained when the ***tef1*** and ***tub2*** sequences were used in blastn and megablast searches.

Colour illustrations. *Syzygium cordatum*. Conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.

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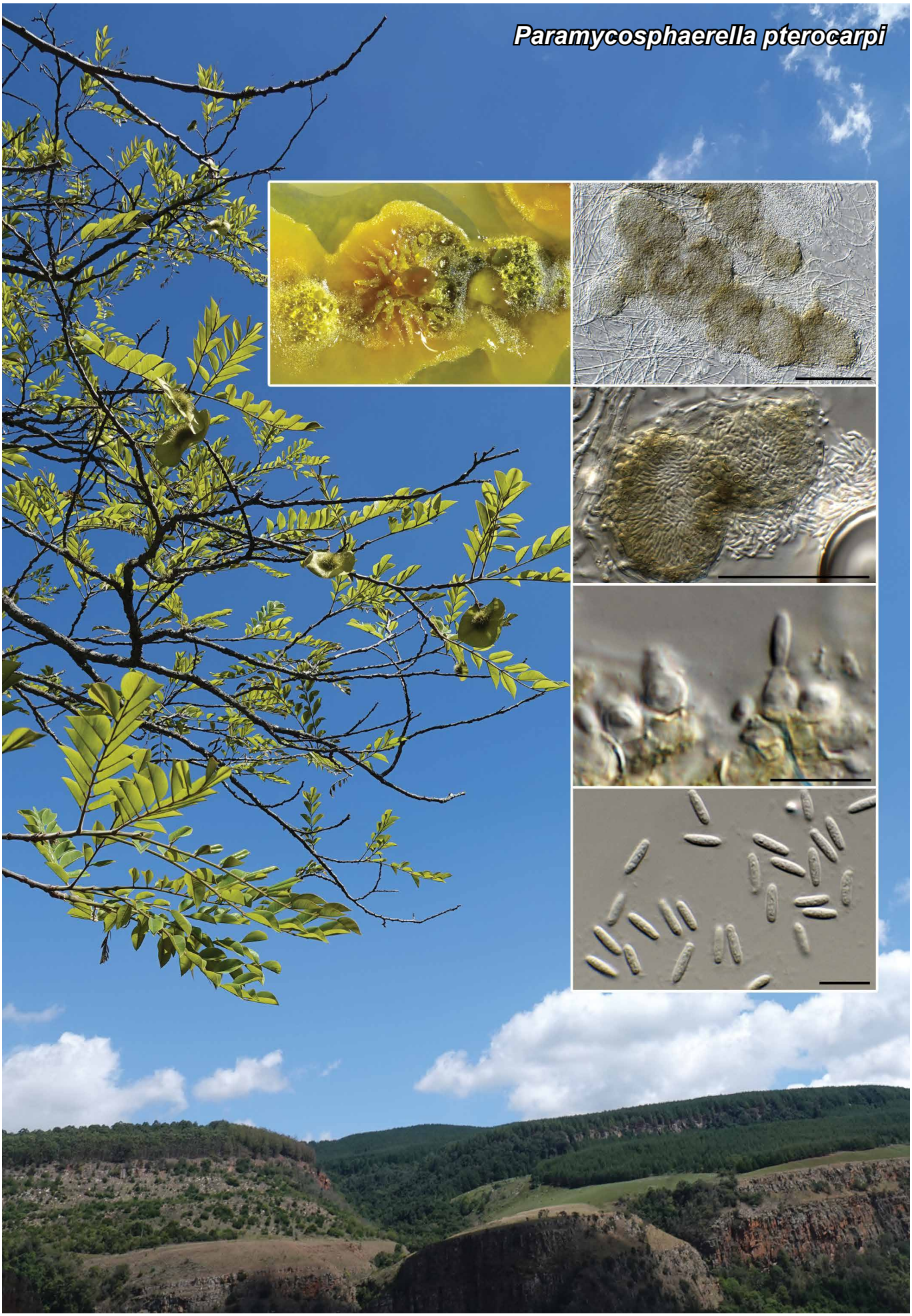
Paramycosphaerella pterocarpi

Fungal Planet 1218 – 13 July 2021

Paramycosphaerella pterocarpi Crous, *sp. nov.*

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

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

On SNA: *Conidiomata* solitary, erumpent, subglobose, brown, 30–100 µm diam with central ostiole, solitary or in chains, linked by a brown stroma; wall of 2–4 layers of brown *textura angularis. Conidiophores* reduced to conidiogenous cells, in dense clusters, hyaline, smooth to pale brown, verruculose, ampulliform, 3–6 × 2.5–3 µm, phialidic with periclinal thickening, with age developing percurrent proliferations. *Conidia* exuding from conidioma in mucoid droplets, aseptate, smooth, hyaline, subcylindrical, guttulate to granular, apex subobtuse, base truncate, (4–)6–7 × (1.5–)2 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with moderate aerial mycelium and smooth, lobate margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA surface and reverse greenish olivaceous with patches of pale mouse grey; on PDA surface and reverse luteous with patches of greenish olivaceous; on OA surface pale mouse grey.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Pterocarpus angolensis* (*Fabaceae*), Nov. 2018, *P.W. Crous*, HPC 3137 (holotype CBS H-24535, culture ex-type CPC 39035 = CBS 147071, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064449.1, MZ064506.1, MZ078154.1, MZ078167.1, MZ078208.1, MZ078233.1 and MZ078275.1, MycoBank MB 839536).

Colour illustrations. Buffelskloof Nature Reserve. Conidiomata on PDA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 100 µm (conidiomata), 10 µm (all others).

Notes — *Paramycosphaerella pterocarpi* is related to *Paramycosphaerella watsoniae* (conidia aseptate, fusoid-ellipsoid, (3.5–)4–5(–6) × 2 µm; Crous et al. 2019d), but can be distinguished based on its morphology, and phylogeny.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NR_166341.1; Identities = 520/528 (98 %), one gap (0 %)), *Paramycosphaerella sticheri* (strain CPC 24720, GenBank NR_155660.1; Identities = 485/511 (95 %), two gaps (0 %)) and *Paramycosphaerella wachendorfiae* (strain CPC 18338, GenBank NR_156547.1; Identities = 481/516 (93 %), eight gaps (1 %)). Closest hits using the **LSU** sequence are *Paramycosphaerella brachystegiae* (strain CBS 136436, GenBank NG_058048.1; Identities = 864/866 (99 %), no gaps), *Paramycosphaerella watsoniae* (strain CPC 37392, GenBank NG_068339.1; Identities = 846/848 (99 %), no gaps) and *Paramycosphaerella dicranopteridis-flexuosae* (strain CPC 24743, GenBank NG_059577.1; Identities = 805/808 (99 %), one gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556790.1; Identities = 552/584 (95 %), five gaps (0 %)), *Mycosphaerella musae* (strain CIRADCOK 003, GenBank MW070786.1; Identities = 524/580 (90 %), five gaps (0 %)) and *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF903466.1; Identities = 491/538 (91 %), four gaps (0 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556795.1; Identities = 405/428 (95 %), no gaps), *Hyalozasmidium aerohyalinosporum* (strain CBS 125011, GenBank KF902788.1; Identities = 269/294 (91 %), no gaps) and *Nothopassalora personata* (strain IRAN 3479C, GenBank MN422408.1; Identities = 278/309 (90 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Paramycosphaerella watsoniae* (strain CBS 146064, GenBank MN556814.1; Identities = 733/793 (92 %), no gaps), *Virosphaerella pseudomarksii* (strain CBS 123241, GenBank MF951686.1; Identities = 679/864 (79 %), 26 gaps (3 %)) and *Mycosphaerelloides madeirae* (strain CBS 115936, GenBank KX288443.1; Identities = 635/824 (77 %), ten gaps (1 %)). Distant hits obtained using the ***tef1*** sequence had highest similarity to *Mycosphaerella musae* (strain CIRAD-MTQ 1241, GenBank MW071103.1; Identities = 315/381 (83 %), 24 gaps (6 %)), *Brunneosphaerella nitidae* (strain CPC 15231, GenBank JN712581.1; Identities = 313/380 (82 %), 30 gaps (7 %)) and *Brunneosphaerella protearum* (strain CPC 18328, GenBank JN712585.1; Identities = 307/378 (81 %), 27 gaps (7 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Paramycosphaerella intermedia* (strain CBS 114356, GenBank KF902845.1; Identities = 275/329 (84 %), 12 gaps (3 %)), *Paramycosphaerella marksii* (strain CBS 110920, GenBank KF902848.1; Identities = 270/328 (82 %), ten gaps (3 %)) and *Zasmidium podocarpi* (strain CBS 142529, GenBank KY979930.1; Identities = 307/383 (80 %), 21 gaps (5 %)).

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Volutella salvadorae

Fungal Planet 1219 – 13 July 2021

Volutella salvadorae Crous, *sp. nov.*

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

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

Conidiophores dimorphic. Subverticillium-like conidiophores erect, solitary, at times aggregated into synnemata, subcylindrical, smooth, unbranched or branched below, 3–8-septate, 100–200 × 3–4 µm. *Conidiogenous cells* phialidic, hyaline, smooth, subcylindrical with apical taper, arranged in 2–3 whorls, 10–25 × 2–3 µm, with apical flared collarette, 1–2 µm long. *Conidia* solitary, cylindrical, apex obtuse, base tapering abruptly to truncate hilum, hyaline, smooth, guttulate, (6–)10–12(–15) × 2(–2.5) µm. *Conidiomata* sporodochial, white, with mucoid conidial mass, arising from submerged hyphae, forming a layer of branched, 2–3-septate conidiophores, subcylindrical, hyaline, smooth, 20–35 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, doliiform, phialidic with minute marginal frill, 6–11 × 3–4 µm. *Setae* arising throughout conidioma within conidiogenous apparatus, replacing phialides on conidiophore, thick-walled, hyaline, smooth, flexuous, sparingly septate, tapering to acutely rounded apex, 50–150 × 2.5–3 µm.

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

Typus. Namibia, Walvis Bay, on stems of *Salvadora persica* (*Salvadoraceae*), 20 Nov. 2019, *P.W. Crous*, HPC 3120 (holotype CBS H-24534, culture ex-type CPC 39017 = CBS 147070, ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064450.1, MZ064507.1, MZ078155.1, MZ078168.1, MZ078209.1, MZ078234.1 and MZ078276.1, MycoBank MB 839537).

Colour illustrations. Walvis Bay, Namibia. Conidiophores on PNA and SNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Notes — *Volutella salvadorae* is related to several species of *Volutella* (see Gräfenhan et al. 2011), including *V. consors* (setae 250–260 µm long, conidia (4.5–)5–7(–13) × 1.5–2.5(–3) µm; Samuels 1977), from which it is phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Volutella consors* (strain CBS 139.79, GenBank KM231768.1; Identities = 544/566 (96 %), two gaps (0 %)), *Lauriomyces sakaeratensis* (voucher SFC 01642, GenBank KX649976.1; Identities = 547/571 (96 %), nine gaps (1 %)) and *Volutella citrinella* (strain DAOM 226720, GenBank HQ897821.1; Identities = 543/567 (96 %), five gaps (0 %)). Closest hits using the **LSU** sequence are *Volutella ciliata* (strain CBS 127312, GenBank MH875955.1; Identities = 796/803 (99 %), no gaps), *Volutella rosea* (strain CBS 128258, GenBank KM231634.1; Identities = 796/803 (99 %), no gaps) and *Volutella roseola* (strain CBS 377.55, GenBank MH869058.1; Identities = 792/800 (99 %), one gap (0 %)). Closest hits using the ***actA*** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231160.1; Identities = 615/669 (92 %), ten gaps (1 %)), *Volutella ciliata* (strain CBS 483.61, GenBank KM231163.1; Identities = 609/693 (88 %), 34 gaps (4 %)) and *Volutella rosea* (strain CBS 128258, GenBank KM231162.1; Identities = 610/695 (88 %), 35 gaps (5 %)). Closest hits using the ***cmdA*** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231333.1; Identities = 495/621 (80 %), 26 gaps (4 %)), *Volutella ciliata* (strain CBS 483.61, GenBank KM231336.1; Identities = 356/436 (82 %), 15 gaps (3 %)) and *Volutella rosea* (strain CBS 128258, GenBank KM231335.1; Identities = 358/439 (82 %), 19 gaps (4 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Volutella citrinella* (strain DAOM 226720, GenBank HQ897770.1; Identities = 724/829 (87 %), two gaps (0 %)), *Volutella consors* (strain CBS 328.77, GenBank HQ897716.1; Identities = 722/828 (87 %), no gaps) and *Volutella ciliata* (strain CBS 426.52, GenBank MH936691.1; Identities = 706/837 (84 %), six gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM231898.1; Identities = 383/476 (80 %), 28 gaps (5 %)), *Thelonectria jungneri* (strain G.J.S.10-127, GenBank KJ022367.1; Identities = 236/270 (87 %), 13 gaps (4 %)) and *Lanatonectria flavolanata* (strain 5622, GenBank HM054073.1; Identities = 233/267 (87 %), 14 gaps (5 %)). Closest hits using the ***tub2*** sequence had highest similarity to *Volutella consors* (strain CBS 122767, GenBank KM232025.1; Identities = 547/650 (84 %), 28 gaps (4 %)), *Volutella rosea* (strain CBS 128258, GenBank KM232027.1; Identities = 415/486 (85 %), 23 gaps (4 %)) and *Gliocladiopsis indonesiensis* (strain CBS 116090, GenBank JQ666132.1; Identities = 409/481 (85 %), 28 gaps (5 %)).

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Neocelosporium corymbiae

Fungal Planet 1220 – 13 July 2021

Neocelosporium corymbiae Crous, *sp. nov.*

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

Classification — *Neocelosporiaceae*, *Neocelosporiales*, *Dothideomycetes.*

Colonies erumpent, forming sporodochia with radiating hyphae. *Mycelium* consisting of brown, smooth, thick-walled, 5–7 µm diam hyphae encased in mucoid sheath; hyphae aggregate to form a brown stroma that gives rise to sporodochia. *Conidiogenous cells* integrated on hyphae and on stroma, reduced to loci, phialidic with pore slightly darkened and flared, 2–4 µm diam, cells 5–10 µm long. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid, thick-walled, guttulate, apex obtuse, tapering to truncate hilum, 1.5–2 µm diam, with age becoming medianly 1-septate, brown, encased in mucoid sheath, (8–)10–11(–13) × (3.5–)4(–5) µm.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and smooth, even margin, reaching 4 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse brown vinaceous.

Typus. Australia, New South Wales, Dyraaba, private plantation, on stems of *Corymbia variegata* (*Myrtaceae*), Nov. 2015, *A.J. Carnegie*, HPC 3216 (holotype CBS H-24548, culture ex-type CPC 39297 = CBS 147080, ITS and LSU sequences GenBank MZ064452.1 and MZ064509.1, MycoBank MB 839538).

Notes — *Neocelosporium corymbiae* is closely related to *N. eucalypti* (on *Eucalyptus cyanophylla*, Mildura, Mungo National Park, primary conidia 5–12 × 3–5 µm, becoming brown, thick-walled and swollen with age; Crous et al. 2018a), but is morphologically and phylogenetically distinct from the latter species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neocelosporium eucalypti* (strain CBS 145086, GenBank NR_164293.1; Identities = 559/578 (97 %), two gaps (0 %)), *Celosporium larixicola* (strain L3-1, GenBank FJ997287.1; Identities = 495/544 (91 %), 11 gaps (2 %)) and *Perusta inaequalis* (strain CBS 118271, GenBank NR_144958.1; Identities = 467/514 (91 %), 12 gaps (2 %)). Closest hits using the **LSU** sequence are *Neocelosporium eucalypti* (strain CBS 145086, GenBank NG_066297.1; Identities = 850/865 (98 %), one gap (0 %)), *Celosporium larixicola* (strain L3-1, GenBank FJ997288.1; Identities = 800/835 (96 %), five gaps (0 %)) and *Muellerites juniperi* (strain CBS 339.73, GenBank MH877745.1; Identities = 825/864 (95 %), six gaps (0 %)).

Colour illustrations. Eucalypt forest. Colonies on SNA; hyphae with conidiogenous loci; conidia. Scale bars = 10 µm.

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Paramyrothecium salvadorae

Fungal Planet 1221 – 13 July 2021

Paramyrothecium salvadorae Crous, *sp. nov.*

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

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

Conidiomata sporodochial with green mucoid conidial mass, stromatic, superficial, cupulate, separate or gregarious, 30–120 µm diam. *Setae* arising from stroma, hyaline, smooth, 5–10-septate, straight to flexuous, 100–200 × 2.5–3 µm; apices subacutely rounded. *Conidiophores* penicillate with branched conidiogenous apparatus; stipes hyaline, smooth, subcylindrical, septate, 20–40 × 3–4 µm; primary branches aseptate, smooth, 10–20 × 2.5–3 µm; secondary branches aseptate, smooth, 5–10 × 2.5–3 µm, terminating in a whorl of 3–6 *conidiogenous cells*, phialidic, subcylindrical, hyaline, 8–15 × 2–2.5 µm, smooth, straight to curved with conspicuous collarettes and periclinal thickening. *Conidia* aseptate, hyaline to olivaceous, subcylindrical, (8–)10–12(–13) × 2–2.5 µm, with obtuse ends.

Culture characteristics — Colonies flat, spreading, surface with concentric zone lines, with moderate aerial mycelium and smooth, even margin, reaching 38 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff.

Typus. Namibia, Walvis Bay, on twigs of *Salvadora persica* (*Salvadoraceae)*, 20 Nov. 2019, *P.W. Crous*, HPC 3120 (holotype CBS H-24538, culture ex-type CPC 39071 = CBS 147074, ITS, LSU, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank MZ064453.1, MZ064510.1, MZ078210.1, MZ078254.1 and MZ078277.1, MycoBank MB 839539).

Notes — *Paramyrothecium salvadorae* is related to *P. roridum* (conidia subcylindrical to ellipsoidal, (5–)6.5–7.5(–8) × 2 µm; Lombard et al. 2016), from which it is morphologically and phylogenetically distinct.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Paramyrothecium roridum* (as *Myrothecium roridum*; strain MA-20, GenBank JF724152.1; Identities = 579/584 (99 %), three gaps (0 %)), *Paramyrothecium terrestris* (strain CBS 564.86, GenBank NR_145078.1; Identities = 574/581 (99 %), one gap (0 %)) and *Myrothecium lachastrae* (strain IMI 273160, GenBank AY254159.1; Identities = 570/578 (99 %), two gaps (0 %)). Closest hits using the **LSU** sequence are *Paramyrothecium nigrum* (strain CBS 116537, GenBank NG_069341.1; Identities = 811/812 (99 %), no gaps), *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846323.1; Identities = 811/812 (99 %), no gaps) and *Paramyrothecium viridisporum* (strain CBS 873.85, GenBank NG_069344.1; Identities = 810/812 (99 %), no gaps). Closest hits using the ***rpb2*** sequence had highest similarity to *Paramyrothecium* sp. (strain MU6, GenBank MN397961.1; Identities = 682/714 (96 %), no gaps), *Paramyrothecium roridum* (strain CBS 372.50, GenBank KU846362.1; Identities = 671/714 (94 %), no gaps) and *Paramyrothecium foliicola* (strain CBS 419.93, GenBank KU846355.1; Identities = 668/714 (94 %), no gaps). Closest hits using the ***tef1*** sequence had highest similarity to *Paramyrothecium roridum* (as *Myrothecium roridum*; strain 781, GenBank JF724132.1; Identities = 430/435 (99 %), no gaps), *Striaticonidium cinctum* (as *Myrothecium cinctum*; strain ATCC 22270, GenBank AY489605.1; Identities = 440/451 (98 %), no gaps) and *Myrothecium inundatum* (strain IMI 158855, GenBank AY489626.1; Identities = 434/454 (96 %), no gaps). Closest hits using the ***tub2*** sequence had highest similarity to *Paramyrothecium roridum* (strain AGR1reis1, GenBank MH824740.1; Identities = 287/293 (98 %), no gaps), *Paramyrothecium foliicola* (strain CBS 113121, GenBank KU846411.1; Identities = 278/293 (95 %), no gaps) and *Paramyrothecium terrestris* (strain CBS 564.86, GenBank KU846420.1; Identities = 277/294 (94 %), one gap (0 %)).

Also see the phylogenetic tree provided with the supplementary material FP1194.

Colour illustrations. Namib Desert, with mycologists in the distance. Sporodochial conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

FP1221 Consensus phylogram (50 % majority rule) obtained from the maximum likelihood analysis with IQ-TREE v. 1.6.12 (Nguyen et al. 2015, Kalyaanamoorthy et al. 2017, Hoang et al. 2018) of the *Paramyrothecium* and related genera multigene (ITS / *tub2* / *cmdA* / *rpb2*) nucleotide alignment derived from the datasets of Lombard et al. (2016). GenBank accession numbers for the sequences used can also be obtained from Lombard et al. (2016). Bootstrap support values (> 69 % shown; only values > 94 % are significant) from 5 000 ultrafast bootstrap replicates are shown at the nodes. Culture collection numbers are indicated for all species and numbers in **bold** represent those cultures with a type status. The tree was rooted to *Fusarium sambucinum* (culture CBS 146.95) and the species described here is highlighted with a coloured block and **bold** face. Alignment statistics: 47 strains including the outgroup; 2 415 characters including alignment gaps analysed: 900 distinct patterns, 651 parsimony-informative, 252 singleton sites, 1 512 constant sites. The best model identified for the entire alignment in IQ-TREE using the TESTNEWMERGE option was: TIM2+F+I+G4. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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Cymostachys arthraeruae

Fungal Planet 1222 – 13 July 2021

Cymostachys arthraeruae Crous, *sp. nov.*

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

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

Mycelium consisting of hyaline, smooth, irregular, 3–5 µm diam hyphae, at times forming swollen, thick-walled chains of chlamydospore-like structures, 7–9 µm diam. *Conidiophores* erect, solitary or in groups, unbranched, subcylindrical, 1(–2)-septate, 30–110 × 3–4 µm, upper cell becoming verruculose, and isabelline in colour, bearing a whorl of 3–6 conidiogenous cells. *Conidiogenous cells* clavate, phialidic, isabelline to dark brown and verruculose at apex, becoming paler so towards base, with minute collarettes. *Conidia* aseptate, guttulate, broadly ellipsoid to slightly obovoid (to subcylindrical on OA), finely verruculose, surface with continuously sigmoid striations, isabelline, apex obtuse, tapering to truncate hilum, 8–9(–11) × (6–)7–8(–10) µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 50 mm diam after 2 wk at 25 °C. On MEA surface sepia to hazel, reverse sepia; on PDA surface cinnamon with patches of isabelline, reverse cinnamon; on OA surface isabelline.

Typus. Namibia, Walvis Bay, on *Arthraerua leubnitziae (Amaranthaceae)*, 20 Nov. 2019, *P.W. Crous*, HPC 3127 (holotype CBS H-24549, culture ex-type CPC 39335 = CBS 147081, ITS, LSU, *rpb2*, *tef1* (first part) and *tef1* (second part) sequences GenBank MZ064454.1, MZ064511.1, MZ078211.1, MZ078235.1 and MZ078255.1, MycoBank MB 839540).

Notes — Morphologically, *Cymostachys arthraeruae* is closest to *C. coffeicola* (conidia fabiform, smooth to verrucose, (7–)7.5–8.5(–10) × (5–)5.5–6.5(–7) µm; Lombard et al. 2016), from which it is distinct in having larger conidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Memnoniella oenanthes* (strain IBT 9473, GenBank KX690115.1; Identities = 489/498 (98 %), no gaps), *Cymostachys coffeicola* (strain CPC 25009, GenBank KU846053.1; Identities = 503/513 (98 %), three gaps (0 %)) and *Stachybotrys nephrospora* (strain Stanep1907, GenBank KF626486.1; Identities = 478/488 (98 %), one gap (0 %)). Closest hits using the **LSU** sequence are *Cymostachys coffeicola* (strain CBS 252.76, GenBank MH872746.1; Identities = 871/876 (99 %), one gap (0 %)), *Stachybotrys nephrospora* (strain LAMIC0040/07, GenBank KP893312.1; Identities = 871/876 (99 %), two gaps (0 %)) and *Cymostachys thailandica* (strain CBS 145079, GenBank NG_066294.1; Identities = 871/877 (99 %), three gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Cymostachys fabispora* (strain MUCL 39004, GenBank KU846082.1; Identities = 680/719 (95 %), no gaps), *Cymostachys thailandica* (strain CBS 145079, GenBank MK047546.1; Identities = 775/822 (94 %), no gaps) and *Cymostachys coffeicola* (strain CBS 252.76, GenBank KU846081.1; Identities = 677/719 (94 %), no gaps). Closest hits using the ***tef1*** (first part) sequence had highest similarity to *Cymostachys coffeicola* (strain CBS 252.76, GenBank KU846097.1; Identities = 272/325 (84 %), 23 gaps (7 %)), *Cymostachys thailandica* (strain CBS 145079, GenBank MK047566.1; Identities = 272/326 (83 %), 24 gaps (7 %)) and *Striatibotrys eucylindrospora* (strain CBS 949.72, GenBank KU847079.1; Identities = 258/311 (83 %), 17 gaps (5 %)). Closest hits using the ***tef1*** (second part) sequence had highest similarity to *Striatibotrys eucylindrospora* (as *Stachybotrys eucylindrospora*; strain UAMH 7122, GenBank DQ676617.1; Identities = 764/790 (97 %), two gaps (0 %)), *Stachybotrys microspora* (strain UAMH 7747, GenBank DQ676619.1; Identities = 759/790 (96 %), two gaps (0 %)) and *Stachybotrys chlorohalonata* (voucher MFLU 18-1638, GenBank MN200279.1; Identities = 753/789 (95 %), no gaps).

Colour illustrations. Namib Desert with long-lived, fog-dependent *Arthraerua leubnitziae* (pencil bush). Conidiophores; conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

Supplementary material

Also see the phylogenetic tree provided with the supplementary material FP1194.

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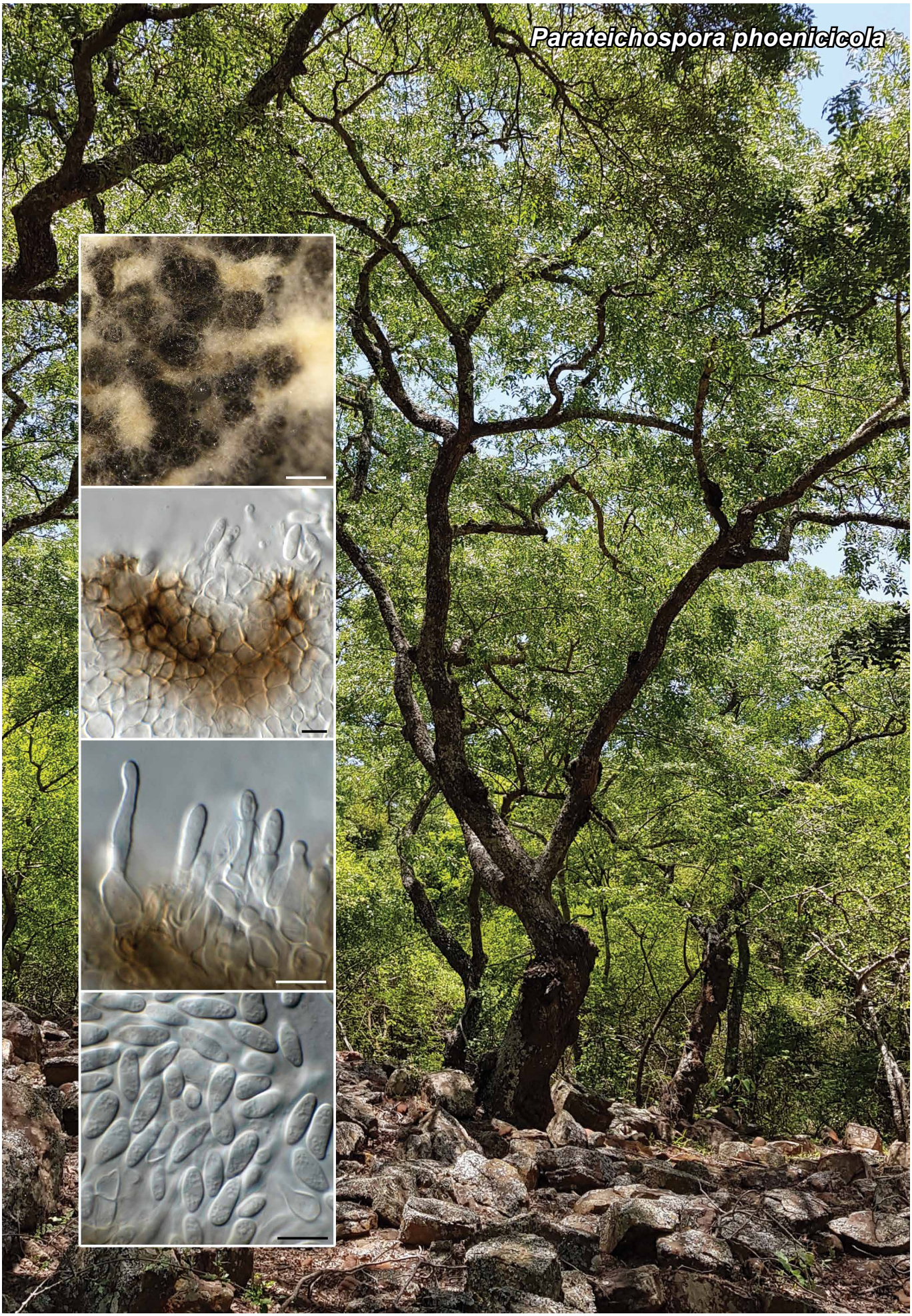
Parateichospora phoenicicola

Fungal Planet 1223 – 13 July 2021

Parateichospora Crous, *gen. nov.*

Etymology. Name refers to its close relationship to *Teichospora*.

Classification — *Teichosporaceae*, *Pleosporales*, *Dothideomycetes*.

Conidiomata pycnidial, solitary to aggregated, brown, globose, ostiolate, with or without long neck; wall of 6–8 layers of hyaline to pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform, proliferating percurrently at apex. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, becoming brown with age, ellipsoid, apex subobtuse, tapering to truncate hilum.

Type species. *Parateichospora phoenicicola* Crous
MycoBank MB 839541.

Parateichospora phoenicicola Crous, *sp. nov.*

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

Conidiomata pycnidial, solitary to aggregated, brown, globose, 250–300 µm diam, ostiolate, with long neck *in vivo*, but absent *in vitro*; wall of 6–8 layers of hyaline to pale brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining inner cavity, hyaline, smooth, ampulliform, proliferating percurrently at apex, 7–20 × 4–5 µm. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, becoming brown with age, ellipsoid, apex subobtuse, tapering to truncate hilum, (8–)9–11(–12) × (3.5–)4–4.5(–5) µm.

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

Typus. South Africa, Northern Province, Limpopo, Gundani, Miombo, on leaves of *Phoenix reclinata* (*Arecaceae*), 18 Dec. 2015, *J. Roux*, HPC 3247 (holotype CBS H-24552, culture ex-type CPC 39351 = CBS 147084, ITS, LSU, *rpb2* and *tef1* (first part) sequences GenBank MZ064455.1, MZ064512.1, MZ078212.1 and MZ078236.1, MycoBank MB 839542).

Notes — *Parateichospora* resides in *Teichosporaceae*, several genera of which have similar phoma-like asexual morphs (Crous et al. 2018b, Phukhamsakda et al. 2020). Presently *Parateichospora* is monotypic, and only known from its asexual morph.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Teichospora quercus* (strain CBS 143396, GenBank NR_159069.1; Identities = 432/490 (88 %), ten gaps (2 %)), *Teichospora mariae* (strain C136, GenBank KU601581.1; Identities = 487/571 (85 %), 26 gaps (4 %)) and *Teichospora kingiae* (strain CPC 29104, GenBank NR_154656.1; Identities = 485/569 (85 %, 24 gaps (4 %)). Closest hits using the **LSU** sequence are *Misturatosphaeria minima* (strain ANM 933, GenBank GU385195.1; Identities = 855/879 (97 %), two gaps (0 %)), *Teichospora quercus* (strain CBS 143396, GenBank NG_067335.1; Identities = 831/856 (97 %), two gaps (0 %)) and *Teichospora proteae* (strain CBS 122675, GenBank EU552117.1; Identities = 837/863 (97 %), three gaps (0 %)). Closest hits using the ***rpb2*** sequence had highest similarity to *Teichospora rubriostiolata* (strain C158x, GenBank KU601597.1; Identities = 628/743 (85 %), two gaps (0 %)), *Flabellascoma fusiforme* (strain MFLUCC 18-1019, GenBank MT878452.1; Identities = 496/647 (77 %), 22 gaps (3 %)) and *Flabellascoma minimum* (strain KT 2040, GenBank LC312591.1; Identities = 499/657 (76 %), 22 gaps (3 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Teichospora melanommoides* (strain MP5, GenBank KU601610.1; Identities = 361/440 (82 %), 22 gaps (5 %)), *Teichospora rubriostiolata* (strain C158x, GenBank KU601608.1; Identities = 363/443 (82 %), 23 gaps (5 %)) and *Teichospora pusilla* (strain C140, GenBank KU601605.1; Identities = 360/444 (81 %), 26 gaps (5 %)).

Colour illustrations. Forest at Gundari, Miombo. Conidiomata on OA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).

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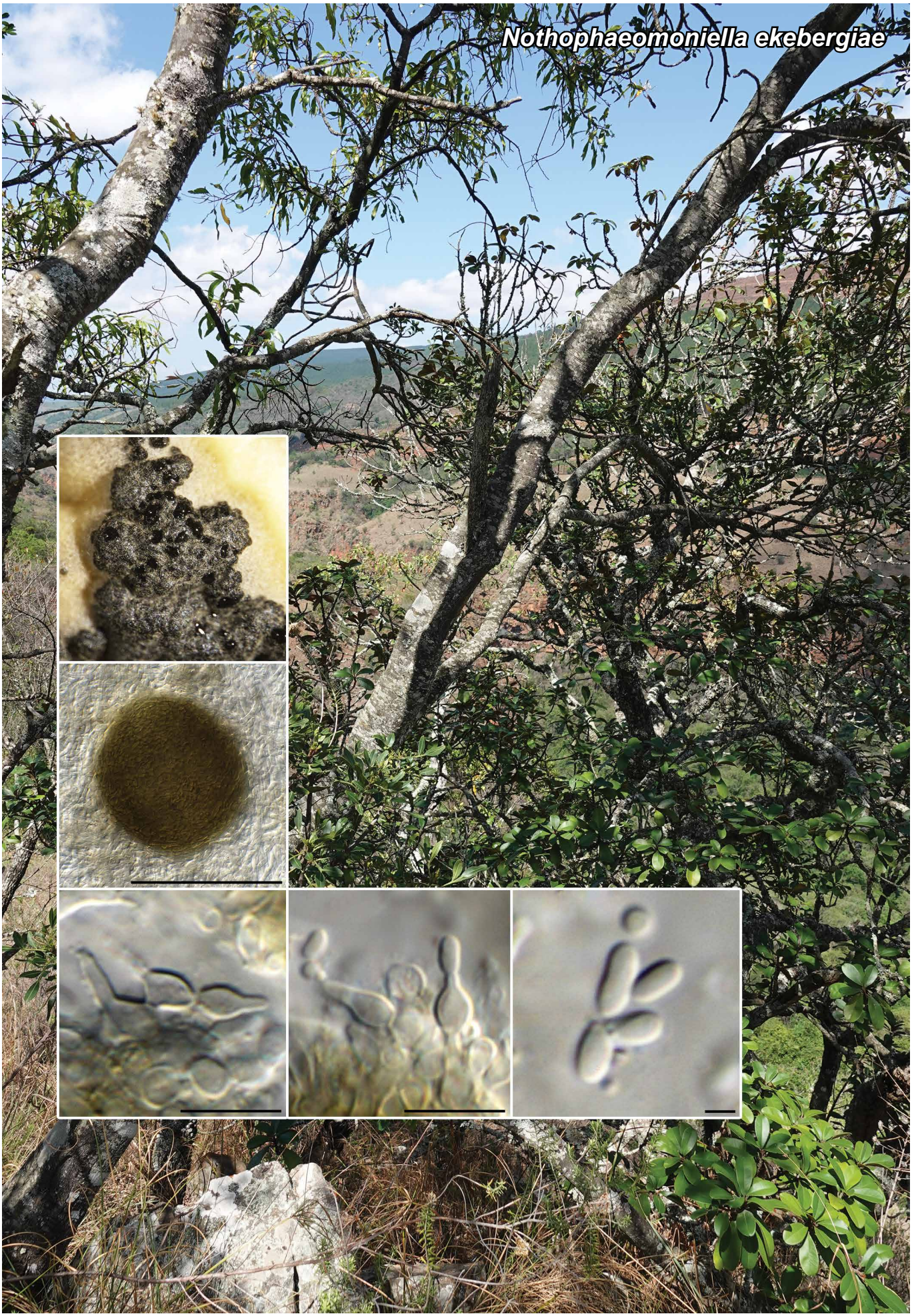
Nothophaeomoniella ekebergiae

Fungal Planet 1224 – 13 July 2021

Nothophaeomoniella Crous, *gen. nov.*

Etymology. Name refers to its morphological similarity to *Phaeomoniella*.

Classification — *Phaeomoniellaceae*, *Phaeomoniellales*, *Eurotiomycetes.*

Conidiomata pycnidial, black, globose, with central ostiole, separate or aggregated; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, ampulliform, lining inner cavity, hyaline to pale brown, smooth, phialidic. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid.

Type species. Nothophaeomoniella ekebergiae Crous
MycoBank MB 839543.

Nothophaeomoniella ekebergiae Crous, *sp. nov.*

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

Conidiomata pycnidial, black, globose, 80–150 µm diam, with central ostiole; wall of 6–8 layers of brown *textura angularis*; occurring as separate conidiomata on SNA and OA, but aggregated, immersed in a continuous black stroma on MEA. Sporulating poorly on OA: *conidiophores* reduced to conidiogenous cells, ampulliform, lining inner cavity, hyaline to pale brown, smooth, phialidic, 5–8 × 2–3 µm. *Conidia* solitary, aseptate, hyaline, smooth, ellipsoid, 3–4 × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading, surface folded, with sparse aerial mycelium, and even, lobate margins, reaching 10 mm diam. On MEA surface and reverse olivaceous grey, with buff margin; on PDA surface dull green with margin buff, reverse buff; on OA surface dull green with margin buff.

Typus. South Africa, Mpumalanga, Mbombela, Buffelskloof Nature Reserve, on leaves of *Ekebergia pterophylla* (*Meliaceae*), 23 Nov. 2018, *P.W. Crous*, HPC 3136 (holotype CBS H-24750, culture ex-type CPC 39341 = CBS 147178, ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank MZ064456.1, MZ064513.1, MZ078237.1 and MZ078278.1, MycoBank MB 839544).

Notes — *Nothophaeomoniella* is related to '*Phaeomoniella*' *pinifoliorum*, which also represents a genus distinct from *Phaeomoniella*, typified by *P. chlamydospora* (Crous & Gams 2000, Crous et al. 2015a). A new genus is thus introduced to accommodate this species, isolated from leaves of *Ekebergia pterophylla*, and forming a coelomycetous morph in culture. The *Phaeomoniellales* was recently treated by Kraus et al. (2020).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Vredendaliella oleae* (as *Phaeomoniellales* sp. CS-2020a; strain CBS 146757, GenBank MT791073.1; Identities = 471/498 (95 %), ten gaps (2 %)), *Aequabiliella effusa* (strain P6, GenBank MK801313.1; Identities = 450/482 (93 %), ten gaps (2 %)) and *Aequabiliella palatina* (strain JKI-Ap36, GenBank MH999506.1; Identities = 445/482 (92 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Phaeomoniella pinifoliorum* (strain CBS 114903, GenBank NG_064185.1; Identities = 838/882 (95 %), seven gaps (0 %)), *Xenocylindrosporium kirstenboschense* (strain CBS 125545, GenBank NG_057857.1; Identities = 813/862 (94 %), eight gaps (0 %)) and *Paraphaeoisaria alabamensis* (strain CBS 101.77A, GenBank MH872801.1; Identities = 792/845 (94 %), 13 gaps (1 %)). No significant hits were obtained when the ***tef1*** sequence was used in blastn and megablast searches. Distant hits obtained using the ***tub2*** sequence had highest similarity to *Vredendaliella oleae* (strain CBS 146757, GenBank MW017334.1; Identities = 275/323 (85 %), two gaps (0 %)), *Aequabiliella palatina* (strain JKI-Ap36, GenBank MK070469.1; Identities = 247/308 (80 %), 13 gaps (4 %)) and *Moristroma palatinum* (strain JKI-Au02, GenBank MK070475.1; Identities = 254/319 (80 %), 16 gaps (5 %)).

Colour illustrations. *Ekebergia pterophylla* tree in Buffelskloof Nature Reserve. Conidiomata in black stroma on MEA; separate conidioma on SNA; conidiogenous cells giving rise to conidia; conidia. Scale bars = 300 µm (conidioma), 10 µm (conidiogenous cells), 2 µm (conidia).

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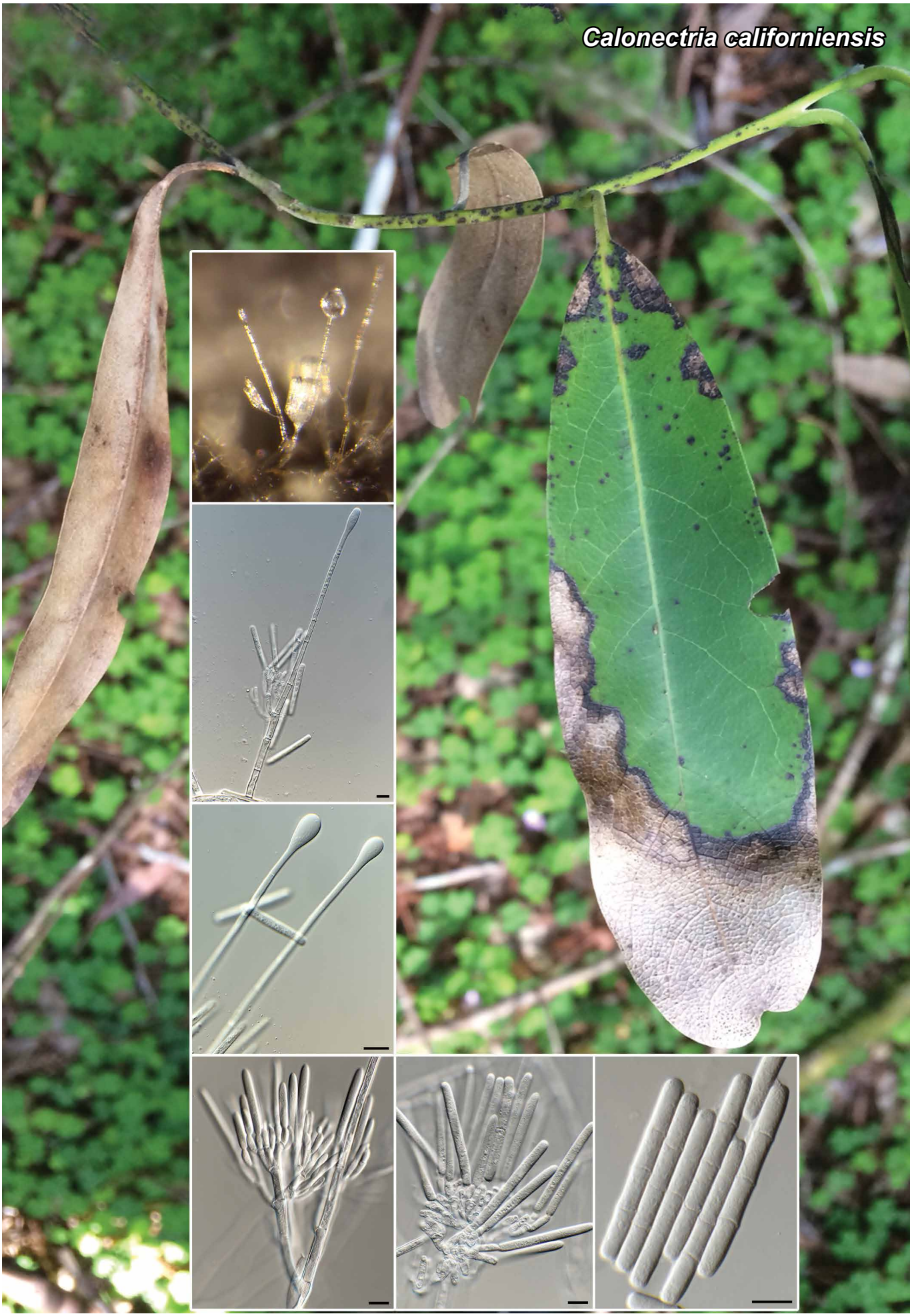
Calonectria californiensis

Fungal Planet 1225 – 13 July 2021

Calonectria californiensis Crous & Roon.-Lath., *sp. nov*.

Etymology. Name refers to the state of California, USA, where this fungus was collected.

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

Macroconidiophores comprised of a stipe, a penicillate arrangement of fertile branches, a stipe extension, and a terminal vesicle. *Stipe* septate, hyaline at base, smooth, 40–100 × 6–7 µm. *Conidiogenous apparatus* with primary branches aseptate or 1-septate, 15–50 × 4–5 µm; secondary branches aseptate, 8–14 × 3.5–4 µm, each terminal branch producing 2–4 phialides; phialides doliiform to reniform, hyaline, aseptate, 8–10 × 3–4 µm, apex with minute periclinal thickening and inconspicuous collarette; stipe extensions septate, straight to flexuous, 100–190 µm long, 3–4 µm wide at apical septum, terminating in ellipsoid to obpyriform to pyriform vesicle, (7–)8–9(–10) µm diam. *Conidia* cylindrical, rounded at both ends, straight, (41–)47–52(–58) × (4.5–)5–5.5(–6) µm, (1–)3-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Chlamydospores* dark brown, thickened, globose, 10–12 µm diam, formed in sparse chains throughout the medium.

Culture characteristics — Colonies flat, spreading, with sparse to moderate aerial mycelium and lobate, smooth margin, reaching 30 mm diam after 7 d at 25 °C. On MEA and PDA surface sienna to umber, reverse umber in centre, sienna in outer region. On OA sienna on surface.

Typus. USA, California, Sonoma County, Guerneville, on leaves of *Umbellularia californica* (*Lauraceae*), 5 May 2015, *S. Rooney-Latham*, CDFA267 (holotype CBS H- 24751, culture ex-type CPC 29621 = CBS 147604, LSU, *actA*, *cmdA*, *his3*, *tef1* (first part) and *tub2* sequences GenBank MZ064514.1, MZ078156.1, MZ078169.1, MZ078182.1, MZ078238.1 and MZ078279.1, MycoBank MB 839545).

Additional material examined. USA, California, Sonoma County, Guerneville, on leaves of *U. californica*, 5 May 2015, *S. Rooney-Latham*, CPC 29619, ITS, LSU, *actA*, *cmdA*, *his3*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064457.1, MZ064515.1, MZ078157.1, MZ078170.1, MZ078183.1, MZ078213.1, MZ078239.1 and MZ078280.1; ibid., CPC 29620, ITS, LSU, *actA*, *cmdA*, *his3*, *tef1* (first part) and *tub2* sequences GenBank MZ064458.1, MZ064516.1, MZ078158.1, MZ078171.1, MZ078184.1, MZ078240.1 and MZ078281.1; ibid., CPC 29622, ITS, LSU, *actA*, *cmdA*, *his3*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank MZ064459.1, MZ064517.1, MZ078159.1, MZ078172.1, MZ078185.1, MZ078214.1, MZ078241.1 and MZ078282.1.

Notes — Brayford & Chapman (1987) reported a wilting disease of *Laurus nobilis* on the Isles of Scilly, and later on *Arbutus andrachnoides* and *Gaultheria shallon* in West Devon, UK. Lechat et al. (2010) linked this disease to a new species, *Calonectria lauri* (validated by Liu et al. 2020), which was reported from leaves of *Ilex aquifolium* in France and the Netherlands, and roots of *Buxus sempervirens* in Belgium. *Calonectria lauri* is sister to *C. californiensis* described in the present study. Although the two species can be distinguished in that *C. lauri* has conidia that are somewhat larger, (45–)55–68(–73) × (4–)5–6(–7) µm, they are best separated based on their DNA phylogeny.

Colour illustrations. Symptomatic leaves of *Umbellularia californica*. Conidiophores with stipe extensions on SNA; vesicles; penicillate conidiogenous apparatus; conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT359736.1; Identities = 534/534 (100 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT359683.1; Identities = 533/534 (99 %), no gaps) and *Calonectria tunisiana* (now synonym of *Calonectria pseudomexicana*; strain CAL-EU2, GenBank MT345681.1; Identities = 531/534 (99 %), no gaps). The ITS sequences of CPC 29619, 29620 and 29622 are identical (533/533 (100 %)). Closest hits using the **LSU** sequence are *Calonectria lauri* (strain CMW 23682 (R), GenBank MT359496.1; Identities = 821/821 (100 %), no gaps), *Calonectria penicilloides* (strain CMW 23696 (R), GenBank MT359559.1; Identities = 819/821 (99 %), no gaps) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT359498.1; Identities = 819/821 (99 %), no gaps). The LSU sequences of CPC 29619, 29620, 29621 and 29622 are identical (781/781 (100 %)). Closest hits using the ***actA*** sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335043.1; Identities = 221/221 (100 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT334992.1; Identities = 213/222 (96 %), one gap (0 %)) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335045.1; Identities = 214/222 (96 %), one gap (0 %)). The *actA* sequences of CPC 29619, 29620, 29621 and 29622 are identical (559/559 (100 %)). Closest hits using the ***cmdA*** sequence of CPC 29619 are *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335275.1; Identities = 654/662 (99 %), no gaps), *Calonectria citri* (strain CMW 23675 (R), GenBank MT335222.1; Identities = 627/663 (95 %), two gaps (0 %)) and *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335277.1; Identities = 618/662 (93 %), no gaps). The *cmdA* sequences of CPC 29619, 29620 and 29622 are identical (662/662 (100 %)). Closest hits using the ***his3*** sequence of CPC 29619 had highest similarity to *Calonectria lauri* (strain CMW 23682 (R), GenBank MT335515.1; Identities = 399/415 (96 %), no gaps), *Calonectria leucothoes* (strain CMW 30977 (R), GenBank MT335517.1; Identities = 387/419 (92 %), ten gaps (2 %)) and *Calonectria citri* (strain CMW 23675 (R), GenBank MT335462.1; Identities = 372/415 (90 %), four gaps (0 %)). The *his3* sequences of CPC 29619, 29620, 29621 and 29622 are identical (412/412 (100 %)).

(text continues on Supplementary material page FP1225)

Supplementary material

FP1225 Consensus phylogram (50 % majority rule) of 9752 trees resulting from a Bayesian analysis of the *Calonectria* multigene (*actA* / *cmdA* / *his3* / ITS / LSU / *rpb2* / *tef1* / *tub2*) sequence alignment (45 sequences including outgroup; 5068 aligned positions; 96 / 310 / 192 / 69 / 59 / 253 / 282 / 308 unique site patterns, respectively; 65000 generations with trees sampled every 10 generations) using MrBayes v. 3.2.7a (Ronquist et al. 2012). The alignment is derived from the dataset of Liu et al. (2020) and methodology used and GenBank accession numbers of the reference sequences can be found in the same reference. 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 tree was rooted to *Curvicladiella cignea* (culture CBS 109167) and the species described here is highlighted with a coloured block and **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID 28129).

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Absidia montepascoalis

Fungal Planet 1226 – 13 July 2021

Absidia montepascoalis L.W.S. Freitas, Hyang B. Lee, T.T.T. Nguyen, M.O. Cruz & A.L. Santiago, *sp. nov.*

Etymology. Refers to the Reserve Parque Nacional e Histórico do Monte Pascoal from where the species was isolated.

Classification — *Cunninghamellaceae*, *Mucorales*, *Mucoromycetes.*

Mycelium with hyaline to pale brown *rhizoids*, slightly branched, commonly finger-like or lobular, 25–240 × 2.5–7 µm. *Stolons* hyaline to pale brown, irregularly septate, with septa commonly observed near the origin of sporangiophores, smooth-walled, 5–10 µm diam. *Sporangiophores* pale brown, arising along the pale brown *stolons* or terminal, single or in whorls of 4–6(–7), simple or branched, with branches shorter or longer than the main sporangiophore, with slightly incrusted wall, (45–)120–325(–400) × 4–8 µm; some branches may re-branch up to five times with a septum below the sporangium. *Sporangia* pale brown, pyriform, smooth-walled, 25–40 × 21.5–35 µm, with a funnel-shaped (short or long) apophysis, 5–15 × 11–21.5 µm. *Columellae* hyaline to brownish grey, mostly subglobose, some hemispherical, and fig-shaped, smooth-walled, frequently with one projection, less commonly with two or rarely three projections on its surface, 9.5–25 × 10–30 µm diam, or without projections on the largest columellae; *collar* distinct or absent. *Projections* cylindrical, conical, some bulbous at distal end, and some may show a constriction on its apical portion, 2.5–5.5 × 1.5–5 µm. These projections may arise separated at the base or fork. *Sporangiospores* hyaline, short cylindrical, slightly constricted in the centre, smooth-walled, 3–5 × 1.5–3 µm. *Chlamydospores* present in aerial hyphae, globose, 5–10 µm diam, subglobose and ovoid, 7–15 × 6–15 µm. *Zygospores* not observed.

Culture characteristics & cardinal temperatures for growth — Colony initially white, becoming pale grey after 5 d at 25 °C on PDA; reverse cream, wave zonate. On MEA: at 10 °C no growth; at 15 °C 4 cm in 96 h and poor sporulation; at 20 °C 5.5 cm in 96 h with good sporulation; at 25 °C 7 cm in 96 h with excellent sporulation; at 30 °C 9 cm in 96 h with excellent sporulation; at 35 °C 4 cm in 96 h with good sporulation; at 40 °C no growth. On PDA: at 10 °C no growth; 15 °C 3.5 cm in 96 h with poor sporulation; at 20 °C 5.5 cm in 96 h with good sporulation; at 25 °C 7 cm in 96 h with excellent sporulation; at 30 °C 9 cm in 96 h with excellent sporulation; at 35 °C 4 cm in 96 h with good sporulation; at 40 °C no growth.

Typus. Brazil, Reserve Parque Nacional e Histórico do Monte Pascoal, Itamaraju, Bahia state, S16°53'00.6" W39°24'37.7", soil, 9 Aug. 2018, *L.W.S Freitas* (holotype CNUFC HT19001, culture ex-type CNUFC B190023 = URM 8218, ITS and LSU sequences MW473494 and MW561560, MycoBank MB 838694).

Colour illustrations. Fragment of Atlantic Forest at the biological Reserve Parque Nacional e Histórico do Monte Pascoal, located in the State of Bahia, Brazil. Sporangiophore with sporangium; sporangiophore with columella and one (constricted) projection on its surface; sporangiophore with columella and two projections on its surface; sporangiophore with columella and one (fork) projection on its surface; sporangiophore with columella and one projection on its surface; branched sporangiophore with sporangium and columellae; sporangiospores. Scale bars = 25 µm.

Notes — The ITS and LSU phylogenetic trees showed that *A. montepascoalis* is a new species related to *A. bonitoensis*, but also close to *A. anomala*, *A. multispora* and *A. jindoensis.* The morphological characteristics differ among these species. *Absidia montepascoalis* presents rare swellings (on MEA at 25, 30 and 35 °C), and abortive sporangia are never formed. However, sporangiospores of *A. montepascoalis* are exclusively cylindrical. In contrast, *A. bonitoensis* produces sporangiophores commonly with one or more randomly distributed swellings, as well as some sporangiophores with abortive sporangia that bear a new sporangiophore. In addition, *A. bonitoensis* produces globose to subglobose and rarely cylindrical sporangiospores (Lima et al. 2020). *Absidia multispora* produces sporangiophores arranged singly or in whorls of two to four, with the formation of occasional abortive sporangia, and sporangiospores are of varied shapes such as globose, subglobose, ellipsoid, short cylindrical, ellipsoidal and irregular (Cordeiro et al. 2020), whereas *A. montepascoalis* produces sporangiophores in whorls of up to seven, and does not form abortive sporangia. Sporangiospores are typically cylindrical and slightly constricted at the centre. *Absidia anomala* can be differentiated from *A. montepascoalis* as the former produces sporangiophores singly and in whorls of two, and only one projection can be observed at the columellae. The colony is purple to violet and azygospores are produced (Hesseltine & Ellis 1964). *Absidia jindoensis* is morphologically different from *A. montepascoalis* as it has 2–6(–8) sporangiophores in a whorl, hemispherical columellae, sometimes subglobose, commonly with one projection on its surface, and sporangiophores cylindrical with rounded ends (Wanasinghe et al. 2018).

Supplementary material

FP1226 Maximum likelihood (ML) tree obtained from the ITS sequence of *A. montepascoalis* and sequences retrieved from GenBank. Bayesian inference (BI) and Maximum likelihood analyses were performed using MrBayes v. 3.2 (Ronquist et al. 2012) and PhyML v. 3.0 (Guindon & Gascuel 2003), respectively. Bayesian posterior probabilities (BYPP) ≥ 0.9 and bootstrap values for maximum likelihood (MLBS) ≥ 70 % are placed above the branches (MLBS/BYPP). Support values lower than 0.9 and 70 % are marked with '*', and absent are marked with '–'. The bar indicates the expected number of substitutions per position. Ex-type, ex-isotype, and ex-neotype strains are marked with superscript 'T', 'IT' and 'NT', respectively. *Cunninghamella phaeospora* CBS 692.68 and *C. vesiculosa* CBS 989.96 were used as outgroups.

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Arcopilus navicularis

Fungal Planet 1227 – 13 July 2021

Arcopilus navicularis Kubátová, V. Ostrý & Hubka, *sp. nov.*

Etymology. Name reflects its boat-shaped ascospores.

Classification — *Chaetomiaceae*, *Sordariales*, *Sordariomycetes.*

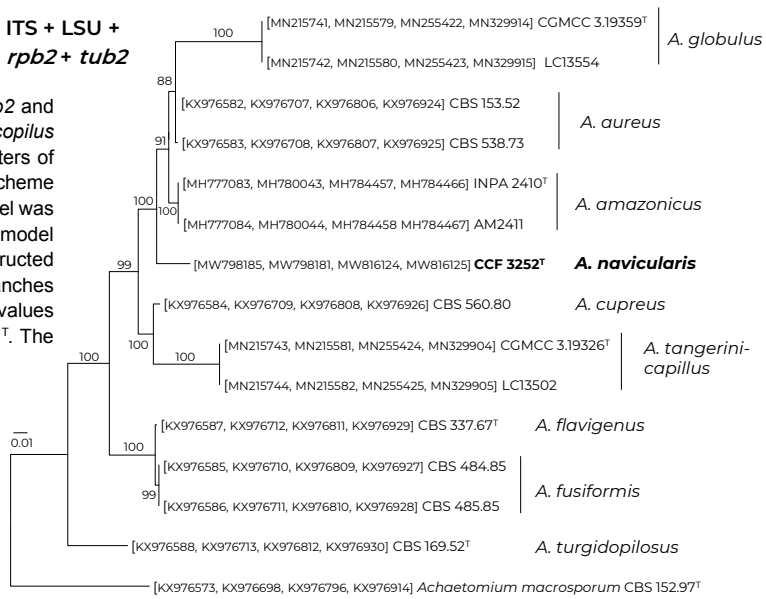
Micromorphology (on oatmeal agar; OA): *Ascomata* superficial, ostiolate, subglobose or ovate, c. 130–200 µm diam, with brown walls of *textura angularis*. *Ascomatal hairs* pale green or greenish olivaceous in reflected light. *Terminal hairs* septate, warty, undulated at apices, brown to grey, 5–6.5 µm diam near the base, 2–2.8 µm diam at the tip. *Lateral hairs* straight or inequilaterally undulated. *Asci* clavate, 8-spored, about 30–37 × 9–12 µm. *Ascospores* dark brown, broadly navicular in side view, 7.2–8.8 × 4.5–5.5 µm (mean ± standard deviation: 8.0 ± 0.4 × 4.9 ± 0.3), lemon-shaped seen from above, 7.2–8.8 × 5.5–6.1 µm (8.0 ± 0.4 × 5.7 ± 0.2), with two apical germ pores. *Asexual morph* unknown. On PCA at 37 °C after 7 d, amorphous crystals in pigmented zone of agar were observed, about 5–7 µm diam.

Culture characteristics — (at 25 °C after 7 d, in darkness): Colonies on potato carrot agar (PCA) 32–37 mm diam, olivaceous in the centre due to formation of ascomata, finely filamentous and pale towards the edges, with pale vinaceous exudates diffusing into the medium around the colonies; reverse dark grey-vinaceous in the centre, pink-grey towards the edges; ascomata maturing after 14 d. Colonies on OA 39–41 mm diam; the appearance of colonies similar to those on PCA, but the pigmentation is more pronounced, and the colonies form more abundant aerial mycelium; ascomata maturing later than on PCA. Colonies on malt extract agar (MEA) 35–38 mm diam, with pinkish white aerial mycelium, wine red exudates diffusing into the medium, reverse dark ruby; ascomata not formed after 7 d. Colonies on PCA at 37 °C after 7 d 18–20 mm diam.

Typus. Czech Republic, Brno, tea bag with fruit tea (lemons, rose hips and apple pulp), Nov. 2001, *V. Ostrý* (holotype PRM 954081, isotype PRC 295, culture ex-type CCF 3252 = CBS 147158, ITS, LSU, *rpb2* and *tub2* sequences GenBank MW798185, MW798181, MW816124 and MW816125, MycoBank MB 839209).

Notes — *Arcopilus navicularis* shares an identical ITS and LSU region with *A. aureus*, *A. amazonicus* and *A. globulus*. BLAST analysis with the *rpb2* sequences showed 96–96.5 % similarity with the latter three mentioned species, while the *tub2* gene showed only 87–87.5 % similarity.

The strain CCF 3252 was originally identified as *Chaetomium aureum* (Kubátová 2006), currently *Arcopilus aureus*. The latter has similar pigmentation of ascomatal hairs, but differs in ascospore shape. *Arcopilus cupreus*, *A. amazonicus* and *A. globulus* have similar shaped ascospores to *A. navicularis*, but their ascospores are slightly larger. *Arcopilus cupreus* differs moreover by red or orange-red hairs in reflected light, and *A. amazonicus* has smaller ascomata and yellow mature hairs (Ames 1949, Von Arx et al. 1986, Wang et al. 2016, Raza et al. 2019, Sousa et al. 2020).



A best scoring maximum likelihood tree based on the ITS, LSU, *rpb2* and *tub2* genes shows the relationships of *A. navicularis* with other *Arcopilus* species. The dataset contained 15 taxa and a total of 2054 characters of which 421 were variable and 297 parsimony-informative. Partitioning scheme and substitution models for analyses were as follows: the HKY+I model was proposed for the ITS region; TrNef model for the LSU region; TrN+G model for the *RPB2* gene; and K80+I for the *tub2* gene. The tree was constructed with IQ-TREE v. 1.4.4 (Nguyen et al. 2015). Support values at branches were obtained from 1 000 bootstrap replicates; only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by the superscript T. The tree is rooted with *Achaetomium macrosporum*.

Colour illustrations. Fruit tea (lemons, rose hips and apple pulp). Fourteen-day-old colonies on OA, PCA, and MEA; ascomata (stereoscopic dissecting microscope); ascoma, hairs (scanning electron microscopy, SEM), asci, ascospores in light microscopy and SEM. Scale bars = 100 µm (ascoma), 10 µm (others).

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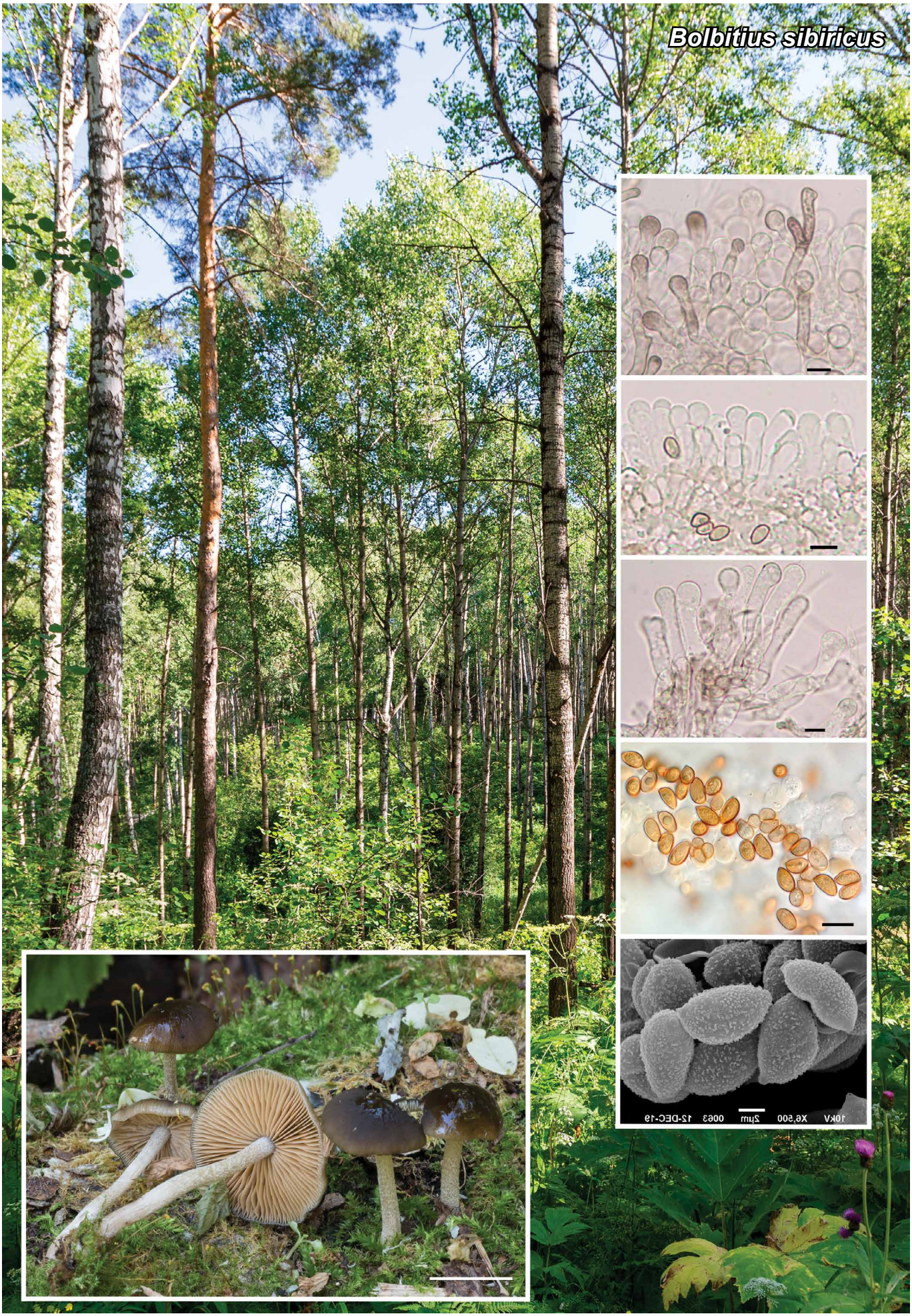

Bolbitius sibiricus
10kV X6,500 2µm 0023 12-DEC-19

Fungal Planet 1228 – 13 July 2021

Bolbitius sibiricus Bulyonk., E.F. Malysheva & L.B. Kalinina, *sp. nov*.

Etymology. The name refers to the geographic region – Siberia, where the species was discovered.

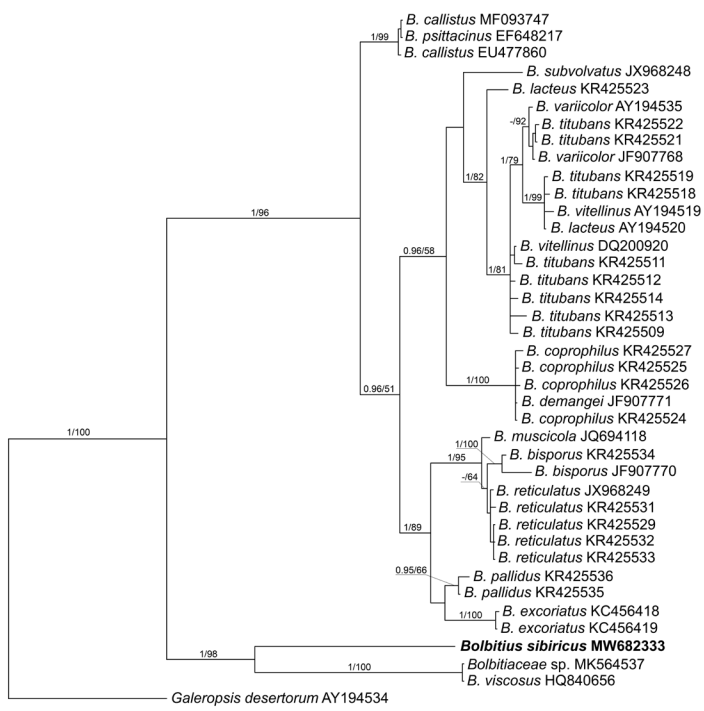
Classification — *Bolbitiaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps small to medium-sized. *Pileus* 8–23 mm diam, at first hemispherical or convex, becoming plano-convex without distinct umbo, with incurved, often undulating striate margin; hygrophanous; surface glabrous, viscid, wrinkled at centre, smoked oak brown (080 30 26) or beech brown (070 30 20), olive black (080 30 10) at centre and bamboo yellow (080 60 40) at margin (all colour codes of macroscopic features are given following the RAL DESIGN colour range system). *Lamellae* narrowly adnate, crowded, with lamellulae, slightly ventricose, natural rice beige (080 80 20) to ash yellow (075 80 40) or orient yellow (075 80 50), edge even or somewhat serrulate, concolorous or slightly paler. *Stipe* 25–40 × 2–4 mm, cylindrical, fragile, hollow, whitish to lemon ice cream yellow (095 90 30), entirely pruinose. *Context* thin, whitish. *Smell* and *taste* not distinctive. *Basidiospores* 7.3–9.5 × 4.0–5.0 µm, Q = 1.60–2.00, Qav = 1.80, n = 40, broadly ellipsoid or slightly flattened and amygdaliform in side view, yellow-brown in KOH, slightly thick-walled, with prominent central germ-pore; distinctly punctate under the compound microscope and verrucose under scanning electron microscope (SEM) – entirely covered with numerous isolated papillae. *Basidia* predominantly 4-spored, sporadically 1–2-spored, 20–27 × 8–10 µm, broadly clavate, surrounded by similar-shaped scarce pseudoparaphyses. *Cheilocystidia* numerous, 24.5–41.5 × 5.2–8.0 µm, subcylindrical or cylindrical with obtuse to subcapitate apex, hyaline or slightly brownish, thin-walled. *Pleurocystidia* absent. *Pileipellis* hymeniform, composed of 15–50 × 10–20 µm, broadly clavate or subglobose and globose elements, in chains, thick-walled, almost hyaline or greyish brown. *Pileocystidia* rather numerous, represented by cylindrical, often with subcapitate or capitate apex, or narrowly clavate elements, 30–55 × 5–10 µm, weakly to strongly pigmented with intracellular greyish brown and granular pigment, thick-walled. *Stipitipellis* a cutis, containing fascicles of *caulocystidia*, 37–63(–83) × 5.5–11.0 µm, subcylindrical, cylindrical or narrowly clavate, sometimes irregular-shaped and septate, hyaline, slightly thick-walled. *Clamp-connections* present and numerous in all parts of basidiocarp.

Habitat & Distribution — Growing in small groups on a moss covered rotting trunk of aspen (*Populus tremula*). So far known only from type locality.

Typus. Russia, vicinity of Novosibirsk, 'Academic Town', mixed aspen-birch forest, ravine slope, N54°48'49.1603" E83°08'35.2283", on fallen trunk of *Populus tremula*, 7 July 2019, *T. Bulyonkova* (holotype LE 313563, ITS and LSU sequences GenBank MW682333 and MW682334, MycoBank MB 839016).

Notes — *Bolbitius sibiricus* is characterised by its glutinous-viscid and dark olive-brown pileus, pale stipe, subcylindrical or cylindrical cheilo- and caulocystidia, numerous pileocystidia, ornamented basidiospores, and lignicolous habitat. Morphologically it resembles *B. viscosus* originally described from North America (Watling 1975), but in addition to genetic differences (a dissimilarity of nrITS sequences of up to 19 %) it differs from the latter by having slightly larger basidiocarps, more cylindrical cheilocystidia, not clavate and longer caulocystidia (vs 14–33 µm in *B. viscosus*), and the presence of numerous pileocystidia. Another *Bolbitius* species with basidiospores ornamented under SEM, the North American *B. callistus*, can easily be distinguished from the new species by its conspicuously coloured basidiocarps with green, yellow and reddish tints, fusiform cheilocystidia, differently shaped pileocystidia and the absence of clamp-connections (Watling 1987).



Phylogenetic nrITS topology from Bayesian analysis performed with MrBayes v. 3.2.5 software (Ronquist et al. 2012) with 5 M generations under GTR+G model, showing relationships of *Bolbitius* species, with *Galeropsis desertorum* as outgroup. Maximum likelihood (ML) analysis was performed on RAxML server v. 1.0.0 (https://raxml-ng.vital-it.ch/#/) with 100 rapid bootstrap replicates. Support values (Bayesian posterior probability/ML bootstrap) are given above the branches. All tips are labelled with taxon name and GenBank accession number. The newly generated sequence is in **bold**.

Colour illustrations. Russia, Novosibirsk region, mixed forest in the vicinities of Novosibirsk, where the holotype was collected. From top to bottom: pileipellis elements, cheilocystidia, caulocystidia, basidiospores under compound microscope and SEM; and mature basidiocarps (all from holotype). Scale bar = 1 cm (basidiocarps), 10 µm (microstructures).

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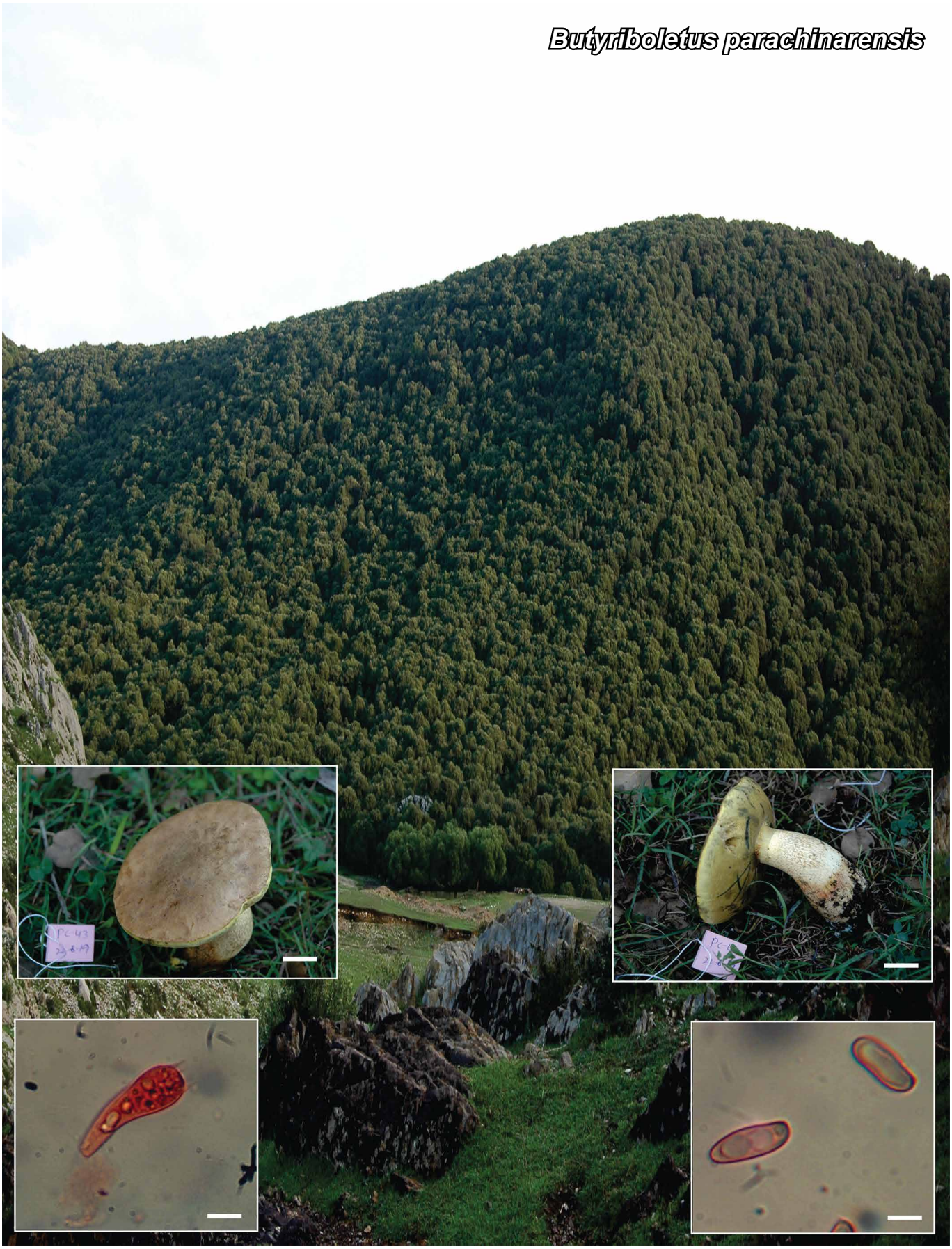
Butyriboletus parachinarensis

Fungal Planet 1229 – 13 July 2021

Butyriboletus parachinarensis Naseer, Davoodian & Khalid, *sp. nov.*

Etymology. Named for its type locality, Parachinar (Pakistan).

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

Pileus 9.7–10.5 cm broad, convex to plano-convex, pale brown with small dark brown patches, surface dry and glabrous, margin entire. *Context* pale yellow, firm. *Hymenophore* pale to bright yellow, dark yellow at maturity, pore surface more or less concolorous with the tubes, turning dark blue quickly when bruised. *Stipe* about 7.5 cm in length, 3.5 cm at base, tapering upward to 2.2 cm thick at apex, subclavate to clavate, creamy yellow, reticulated, reticulation brown over most of the upper half, reticulated areas around base and apex with red or yellow colouration. *Basidiospores* 10.3–13.9 × 4.7–5.5(–5.9) µm, av. = 11.9 × 5.1 µm, Q = 1.7–2.8, Qav = 2.4, fusoid, thin-walled, smooth, pale brown or yellowish in 5 % KOH, dark olive brown in mass. *Basidia* 24.9–39.4 × 10.3–13.8 µm, av. = 32.8 × 11.8 µm, clavate to broadly clavate, thick-walled, four-spored, densely guttulate, hyaline in 5 % KOH. *Cheilocystidia* 10.9–60.3 × 5.9–11.3 µm, av. = 31.1 × 7.7 µm, lageniform, thin-walled, hyaline in 5 % KOH. *Pileipellis* an interwoven trichodermium, elements 2.5–4.6 µm diam, av. = 3.4 µm, septate, branched, thin-walled, hyaline in 5 % KOH. *Clamp connections* absent.

Habitat & Distribution — Currently known only from the type locality, in association with *Quercus baloot* (*Fagaceae*).

Typus. Pakistan, Khyber Pakhtunkhwa Province, Kurram District, Parachinar, 22 Aug. 2019, *A. Naseer* AS-PC43 (holotype LAH 36760, partial LSU and ITS sequences GenBank MT825244 and MT825245, MycoBank MB 839366).

Notes — *Butyriboletus parachinarensis* is distinguished based on morphology and the distinctness of partial ITS and LSU sequences. *Butyriboletus sanicibus* from China is similar based on BLAST comparison of our partial ITS sequence (97.04 % identity) but is known to have a larger pileus with an incurved margin and a pore surface that is slightly greenish with age (Arora & Frank 2014). Furthermore, *B. sanicibus* has subfusoid basidiospores with an average Q value of 2.8 while *B. parachinarensis* has fusoid basidiospores with an average Q value of 2.4. *Butyriboletus yicibus* from China is similar based on BLAST comparison of our partial LSU sequence (97.24 % identity) but can be distinguished from *B. parachinarensis* by its more gracile stature and tendency to stain blue-grey rather than blue when bruised (Arora & Frank 2014). *Butyriboletus yicibus* can have a longer stipe (up to 15 cm) than *B. parachinarensis*.

Colour illustrations. Stands of *Quercus baloot* around Parachinar. Holotype (AS-PC43); basidiome, top view; basidiome, side view showing hymenophore bruising blue; basidium; spore. Scale bars = 1 cm (basidiomes), 5.2 µm (basidium), 1.65 µm (spore).

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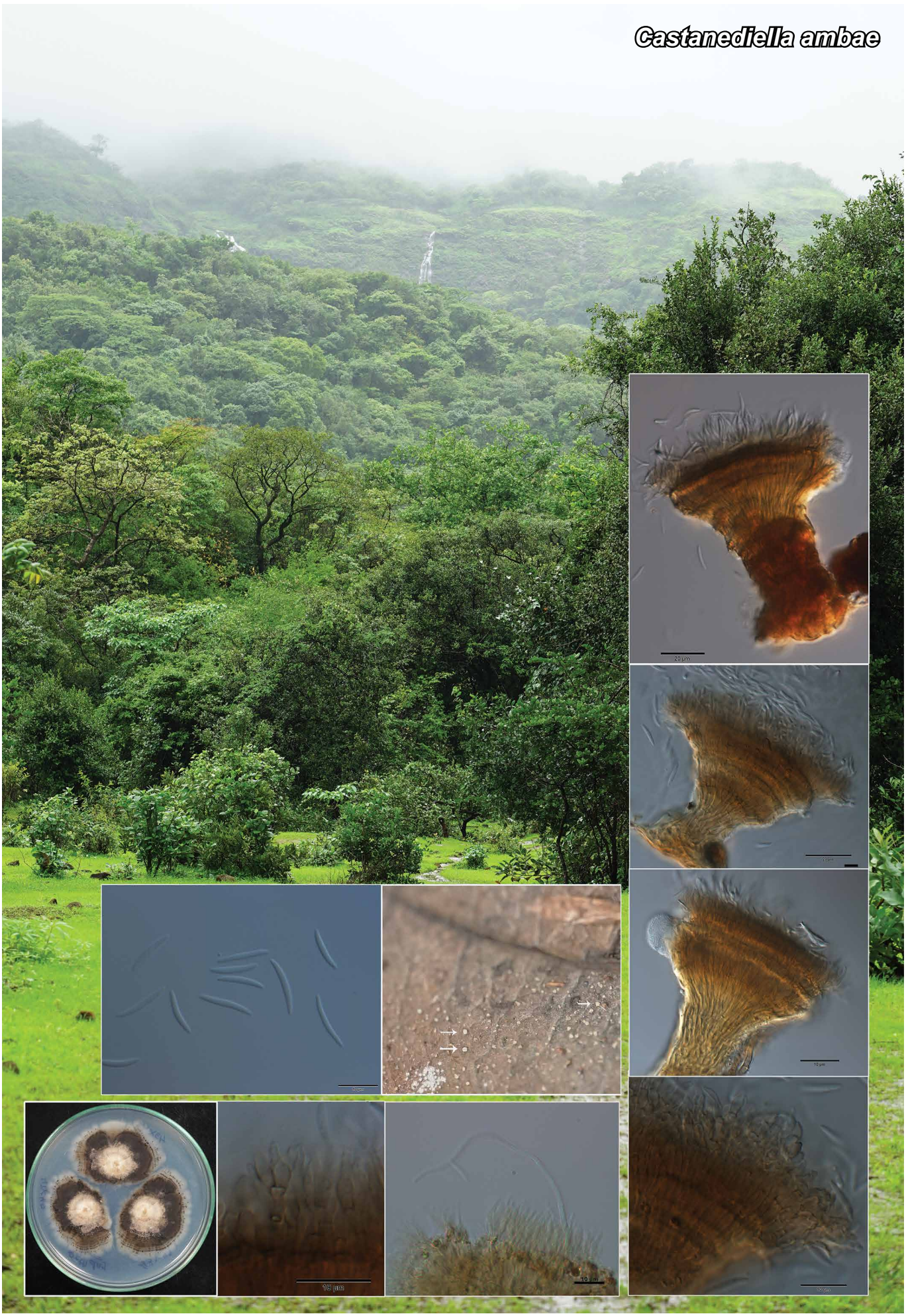

Castanediella ambae

Fungal Planet 1230 – 13 July 2021

Castanediella ambae Rajeshk., Crous, J.Z. Groenew., S. Fatima, S. Lad, *sp. nov.*

Etymology. Named after 'amba' meaning Mango tree in Marathi language, the host of the fungus.

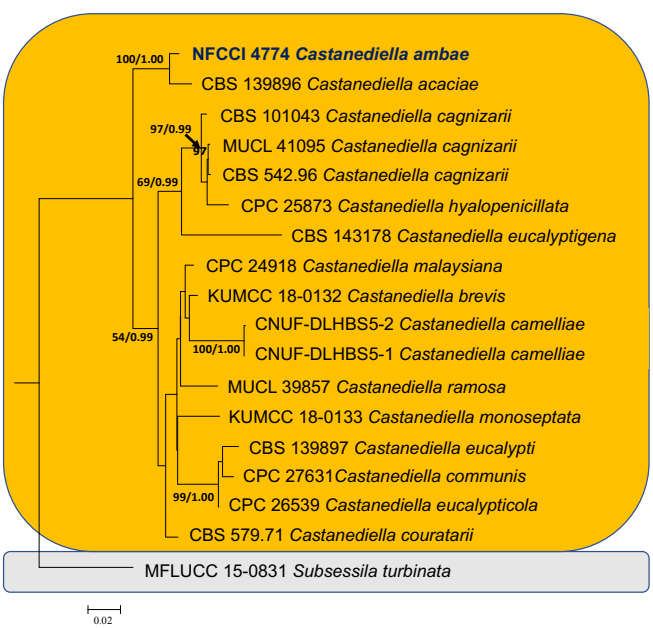
Classification — *Castanediellaceae*, *Xylariales*, *Sordariomycetes*.

On decaying leaves of *Mangifera indica*: Mycelium pale to dark brown, immersed, septate, hyphae 2–3.5 µm diam. *Conidiomata* sporodochial, scattered, erumpent, starting as a penicillate tuft of conidiophores with central attachment point, expanding lateral and apical, becoming densely branched, but with central attachment, stipitate, 20–80 µm diam, 35–120 µm high. *Setae* rare, hyaline, flexuous or undulate with obtuse tips, attached to the base of the sporodochia, up to 87 µm long and 2–2.5 µm wide. *Conidiophores* subcylindrical, densely branched, multiseptate, medium to dark brown, smooth. *Conidiogenous cells* terminal and intercalary, ampulliform, pale brown, smooth, apex truncate, polyblastic, phialidic?, 7–10.5 × 2–2.8 µm. *Conidia* solitary, hyaline, smooth, falcate with subobtuse or acute ends, 0–2-guttulate, (8–)9.5–15.5(–19) × 1.5–1.8(–2) µm.

Culture characteristics — (on malt extract agar at 25 ± 2 °C after 1 mo): Colonies floccose or umbonate at centre, grey (5E1) to brownish orange (5C4) (Kornerup & Wanscher 1978), velutinous or immersed, dark brownish grey (5F2) to dark grey (5F1); reverse dark brownish grey (5F2) to dark grey (5F1), colonies reaching 40–50 mm diam.

Typus. India, Tamhini Ghats, Tamhini village, on leaves of *Mangifera indica* (*Anacardiaceae*), 23 July 2018, *K.C. Rajeshkumar* (holotype AMH 10211, cultures ex-type NFCCI Raj18 = NFCCI 4774, ITS and LSU sequences GenBank MN660236 and MN660235, MycoBank MB 833316).

Notes — Morphologically, *C. ambae* resembles *C. acaciae* (Crous et al. 2015a), having sporodochial conidiomata compared to all other species of *Castanediella*. However, the sporodochia in *C. ambae* are smaller in width and slightly longer than those of the type species *C. acaciae*. The presence of hyaline, flexuous setae with obtuse tips arising from the base of the sporodochia, is another unique feature of *C. ambae*. Furthermore, conidia are marginally longer in *C. ambae* in comparison to those of *C. acaciae*. Phylogenetic analyses based on combined ITS and LSU sequence data resulted in a unique clade for the sporodochial *Castanediella* species, *C. acaciae* and *C. ambae* from other taxa in *Castanediella*. The new species form a fully supported (100 % bootstrap support, posterior probability = 1.00) clade with *C. acaciae*. Based on a megablast (type BLASTn) search of NCBIs GenBank nucleotide database, the closest hits using the **LSU** sequence are *C. acaciae* (GenBank KR476763; Identities = 844/848 (99 %), no gaps), *C. cagnizarii* (GenBank MH874222; Identities = 837/848 (99 %), no gaps) and *C. eucalypti* (GenBank KR476758; Identities = 837/851 (98 %), three gaps (0 %)). Closest hits using the **ITS** sequence had highest similarity to *C. acaciae* (GenBank NR_137985; Identities = 506/526 (96 %), five gaps (0 %)), *C. tereticornis* (GenBank NR_161116; Identities = 487/532 (92 %), eight gaps (1 %)) and *C. cagnizarii* (GenBank MH862597; Identities = 481/530 (91 %), ten gaps (1 %)).



Phylogram generated from a maximum likelihood (ML) analysis based on LSU and ITS sequence data representing the genus *Castanediella* in RAxML v. 8.2.12 (Stamatakis 2014). Related sequences are taken from Lin et al. (2019). Eighteen strains are included in the combined analyses which comprise 1363 characters and 530 characters for LSU and ITS, respectively, after alignment. *Subsessila turbinata* (KX762288, KX762289) was used as the outgroup taxon. Single-gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis performed in siMBa (Mishra & Thines 2014). The best scoring RAxML tree with a final likelihood value of -3866.720205 is presented. The matrix had 256 distinct alignment patterns, with 7.71 % undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.253765, C = 0.209910, G = 0.261361, T = 0.274964; substitution rates AC = 1.675661, AG = 3.141033, AT = 2.412224, CG = 0.281419, CT = 6.326033, GT = 1.000000; gamma distribution shape parameter α = 1.214174. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 50 % and Bayesian posterior probability clade credibility values greater than 0.95 (BPP; the rounding of values to 2 decimal proportions) from Bayesian-inference analysis (siMBa) labelled on the nodes (MLBS/BPP). The newly generated sequence is indicated in **bold**.

Colour illustrations. Habitat forest area near Tamhini village. Sporodochia (right column): conidia; conidiomata on *Mangifera indica* (upper row); colonies on MEA; conidiogenous cells; hyaline seta (lower row). Scale bars = 10 µm.

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Colletotrichum filicis

Fungal Planet 1231 – 13 July 2021

Colletotrichum filicis Damm & Baroncelli, *sp. nov.*

Etymology. Named after the host plant, a fern, Latin = *filix*.

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

Sexual morph not observed. *Asexual morph* on synthetic nutrient-poor agar medium (SNA) (microscopic preparations in clear lactic acid, with 30 measurements per structure). *Vegetative hyphae* 1–6.5 µm diam, hyaline to pale brown, smooth-walled, septate, branched. *Conidiomata* not developed, conidiophores formed directly on hyphae. *Setae* not observed. *Conidiophores* hyaline, smooth-walled, septate, branched. *Conidiogenous cells* hyaline smooth-walled, cylindrical to ampulliform, 6–18 × 2.5–4 µm, opening 1–1.5 µm diam, collarette 1 µm long, periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, cylindrical to clavate, sometimes slightly constricted in the middle, with both ends slightly acute or one end round, (13–)15–19(–22) × (3.5–)4–5(–5.5) µm, mean ± SD = 16.9 ± 2.0 × 4.5 ± 0.4 µm, L/W ratio = 3.7. *Appressoria* single or in loose groups, medium brown, smooth-walled, subglobose to ellipsoidal, undulate or entire edge, (5.5–)6.5–10(–14) × (5–)6–8(–8.5) µm, mean ± SD = 8.2 ± 1.8 × 6.8 ± 1.0 µm, L/W ratio = 1.2.

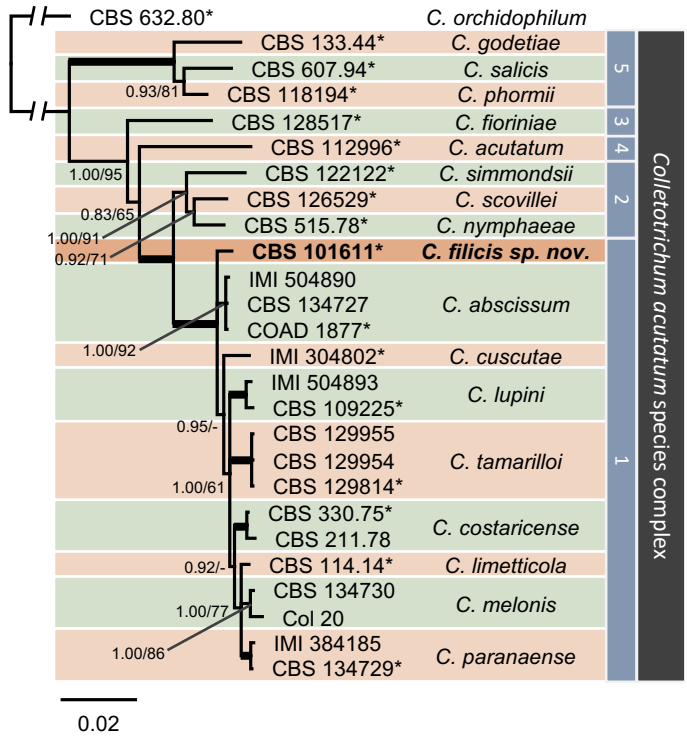
Asexual morph on Anthriscus stem. *Conidiomata* acervular, conidiophores formed on pale brown, angular basal cells, 3–7 µm diam. *Setae* not observed. *Conidiophores* hyaline to pale brown, smooth-walled to verruculose, septate, branched, up to 70 µm long. *Conidiogenous cells* hyaline to pale brown, smooth-walled, cylindrical, 9–21.5 × 3–4 µm, opening 1–1.5 µm diam, collarette 1–1.5 µm long, periclinal thickening visible. *Conidia* hyaline, smooth-walled, aseptate, straight, clavate to cylindrical with both ends acute, (14–)16.5–20(–23.5) × (4–)4.5–5(–5.5) µm, mean ± SD = 18.3 ± 1.8 × 4.6 ± 0.3 µm, L/W ratio = 4.0.

Culture characteristics — Colonies on SNA flat with entire margin, hyaline, buff to pale honey, SNA medium, filter paper and *Anthriscus* stem partly covered with thin floccose white aerial mycelium and orange acervuli, reverse same colours; 21–22.5 mm in 7 d (28.5–31.5 mm in 10 d). Colonies on oatmeal agar flat with entire margin; surface covert with granular to floccose white to pale olivaceous grey aerial mycelium and apricot acervuli, reverse buff to rosy buff, apricot to fuscous black in the centre; 20–22.5 mm in 7 d (30–31.5 mm in 10 d). Conidia in mass orange to apricot.

Typus. Costa Rica, from an unidentified fern (*Pteridophyta*), unknown collection date and collector (deposited in CBS collection Feb. 1999 by *P. Lafeber*), (holotype CBS H-20817, culture ex-type CBS 101611, LSU sequence GenBank MW724319, other sequences from Damm et al. 2012a, MycoBank MB 839338).

Notes — Based on blastn searches on NCBI GenBank, the ITS sequence of strain CBS 101611 is identical with that of *C. scovillei*, including its ex-type strain and with strain CBS 129820 from *Passiflora* in Colombia (Damm et al. 2012a), but also with strains from fronds of *Rumohra adiantiformis* (leatherleaf fern) with anthracnose from Costa Rica (Schiller et al. 2006) and Florida, USA (MacKenzie et al. 2009). Phylogenies inferred from concatenated ITS, *chs-1*, *tub2*, *act*, *his3* and *gapdh* sequences placed the fungus in clade 1 of the *C. acutatum* species complex (Damm et al. 2012a, this study), where it forms a distinct single-strain lineage.

The species can be distinguished with *act*, *gapdh*, *his3* and *tub2* sequences, best with *act* and *tub2*. The closest matches with the *act* and *tub2* sequences were with 99 % identity (two nucleotides difference) several *Colletotrichum* strains including the ex-type strains of *C. limetticola*, *C. lupini* and *C. paranaense* (Nirenberg et al. 2002, Bragança et al. 2016, Damm et al. 2012a), and *Colletotrichum* sp. CBS 129810 from tamarillo in Colombia, respectively, while the ex-type strain closest to the *tub2* sequence was three nucleotides different to that of *C. tamarilloi* (Damm et al. 2012a). The closest matches to the *gapdh* and *his3* sequences were with 99 % identity (one nucleotide difference) strains of *C. abscissum*, including its ex-type (Crous et al. 2015a), and strains CBS 129820 and CBS 129821 from *Passiflora* in Colombia as well as *C. costaricense* strain CBS 211.78 (Damm et al. 2012a), respectively. The *gapdh* sequence of *C. filicis* differs from those of the strains from leatherleaf fern in Florida (MacKenzie et al. 2009) in two or four nucleotides, respectively; they are therefore unlikely to be conspecific.



Phylogenetic tree of the *Colletotrichum acutatum* species complex obtained with MrBayes v. 3.2.7 (Ronquist & Huelsenbeck 2003) inferred from a concatenated ITS (511bp), *chs-1* (242), *tub2* (492), *act* (245), *his3* (339) and *gapdh* (257) sequence alignment with *C. orchidophilum* CBS 632.80 as outgroup (sequences from Damm et al. 2012a, Crous et al. 2015a, Bragança et al. 2016, Dubrulle et al. 2020). Bayesian posterior probability (BPP) and maximum likelihood bootstrap support (BS) values above 0.8 and 50 % are shown at the nodes; thicker branches indicate values of 1 and 100 %, respectively. Bootstrap support values have been calculated based on 1 000 replicates under maximum likelihood using RAxML v. 8.2.11 (Stamatakis 2014). * indicates ex-holotype, ex-neotype and ex-epitype strains. Clades of Damm et al. (2012a) are indicated in blue blocks.

Colour illustrations. Waterfall on the Osa Peninsula, Costa Rica (photo by O. Spilke). Conidioma; conidiophores; appressoria; conidia; conidiophores. Scale bars = 10 µm.

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Comoclathris antarctica

Fungal Planet 1232 – 13 July 2021

Comoclathris antarctica Ł. Istel, J. Pawłowska & Wrzosek, *sp. nov.*

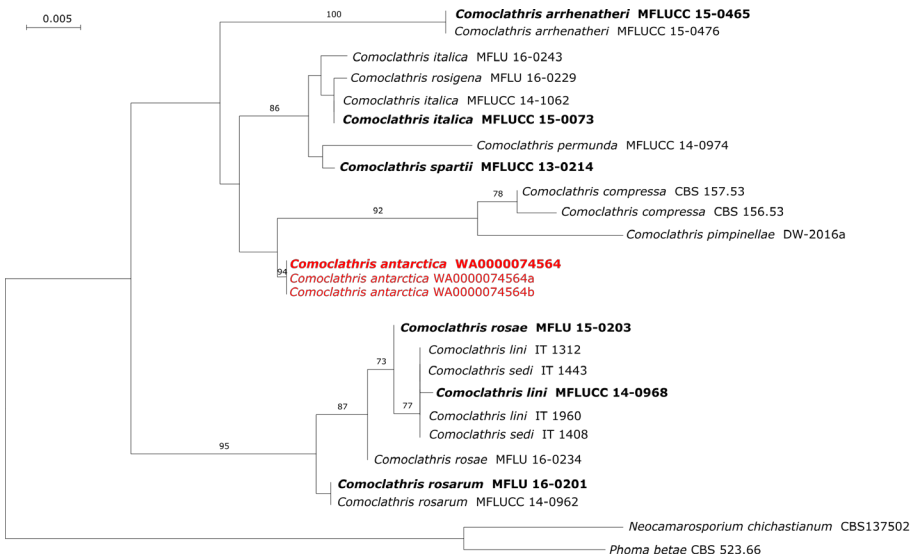
Etymology. The specific epithet 'antarctica' refers to the isolation locality – Antarctica.

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

Colonies: On potato glucose agar (PGA) after 7 d of growth at 24 °C reaching 2.58 cm (± 0.34 cm) diam. Initially sterile, pink in the centre, becoming orange at the colony edge. Reverse orange to dark brown. Aerial hyphae and ascocarps appear after 6 wk of incubation at 4 °C. *Ascocarps* perithecial, separate or in groups, dark brown to almost black, strongly enclosed in aerial hyphae, ovoid to spherical, 339 (± 103) × 299 (± 97) µm, without distinct ostiole, 51–116 µm diam; neck very short, up to 26 µm long; operculum semispherical, flattened, 102–197 × 97–182 × 24 µm; perithecial hyphae dark; wall of 2–3 cell layers. *Asci* bitunicate, mostly 8-spored, 72–84 × 18–26 µm, immature asci shorter (~ 60 µm), cylindrical to clavate, bitunicate with a rounded apex. *Ascospores* lanceolate to ovoid, clavate, yellow to pale brown, elongated, asymmetrical with a blunt apex, muriformly, with 6–8 transvers septa, consisting of 10–17 cells, apical cell not divided, 31 (± 2) × 13.5 (± 1) µm.

Typus. Antarctica, King George Island, 50 m from the front of Sphinx Glacier, coordinates S62°11'36.3" W58°27'18", isolated from soil sample using Warcup method on Minimal Media with 0.01 % diesel oil, 21 Mar. 2018, *Ł. Istel* (holotype WA0000074564 – dried specimen, culture ex-type CBS 147272, ITS and LSU sequences GenBank MW040594 and MW040597, MycoBank MB 837527).

Notes — The genus *Comoclathris* was described by Clements (1909). In 2015 the genus was placed in the *Pleosporales* by Ariyawansa et al. (2015). Currently, the genus consists of 41 registered names in MycoBank. However, data on only 10 species are represented in GenBank. The type species of the genus is *C. lanata*, which lacks ITS nrDNA sequence data. Ariyawansa et al. (2014) used sequences of two strains of *C. compressa* (CBS 157.53 and CBS 156.57) as reference. Those two strains together create a well-supported clade inside *Pleosporaceae* but outside the *Alternaria* complex. The morphological characteristic features of the genus are the presence of operculate perithecia, and asymmetrical, muriform, strongly divided ascospores (Shoemaker & Babcock 1992, Wanasinghe et al. 2018) and the isolate described here represents these features. The main characteristic that differentiates *C. antarctica* from another species in the genus is the 6–8 transversal ascospore septa. Additionally, *Comoclathris* representatives were never observed before in Antarctica. The rDNA sequences of ITS and LSU regions of *C. antarctica* are showing the highest similarity (95 % and 97 % respectively) to *C. spartii* (GenBank KM557160.1). However, *C. spartii* is saprobic on *Spartium junceum* and has smaller ascocarps (Crous et al. 2014b). The main morphological difference between *C. antarctica* and *C. compressa* is in the number of ascospore septa. *Comoclathris antarctica* has 6–8 transverse septa while ascospores of *C. compressa* only have three septa (Shoemaker & Babcock 1992). *Comoclathris antarctica* is the most similar to *C. arctica* based on morphology. However, *C. arctica* has much smaller ascocarps (~ 200 µm diam) and larger asci, being up to 120 µm long (Shoemaker & Babcock 1992).



Maximum Likelihood (RAxML-ng v. 0.9.0 BETA; Kozlov et al. 2019) phylogenetic tree based on the combined ITS and LSU nrDNA sequences data (GTR+FC+G4m+B model, 1228 sites, Final LogLikelihood = -2508.6, AICc score: 5156.8, BIC score: 5486.6, bootstrap replicates = 1000) of selected representatives of the genus *Comoclathris*. The novel species is in red bold text, ex-type strains are in bold, the branch support values over 70 % are shown. The scale bar indicates the expected number of changes per site.

Colour illustrations. Collection site (photo by H. Galera). Top left: colony after 7 d of incubation on PGA medium (sterile); perithecium with perithecial hairs; ascospores; ascospores in ascus; immature ascospores in ascus (photos by M. Wrzosek). Scale bars = 20 µm.

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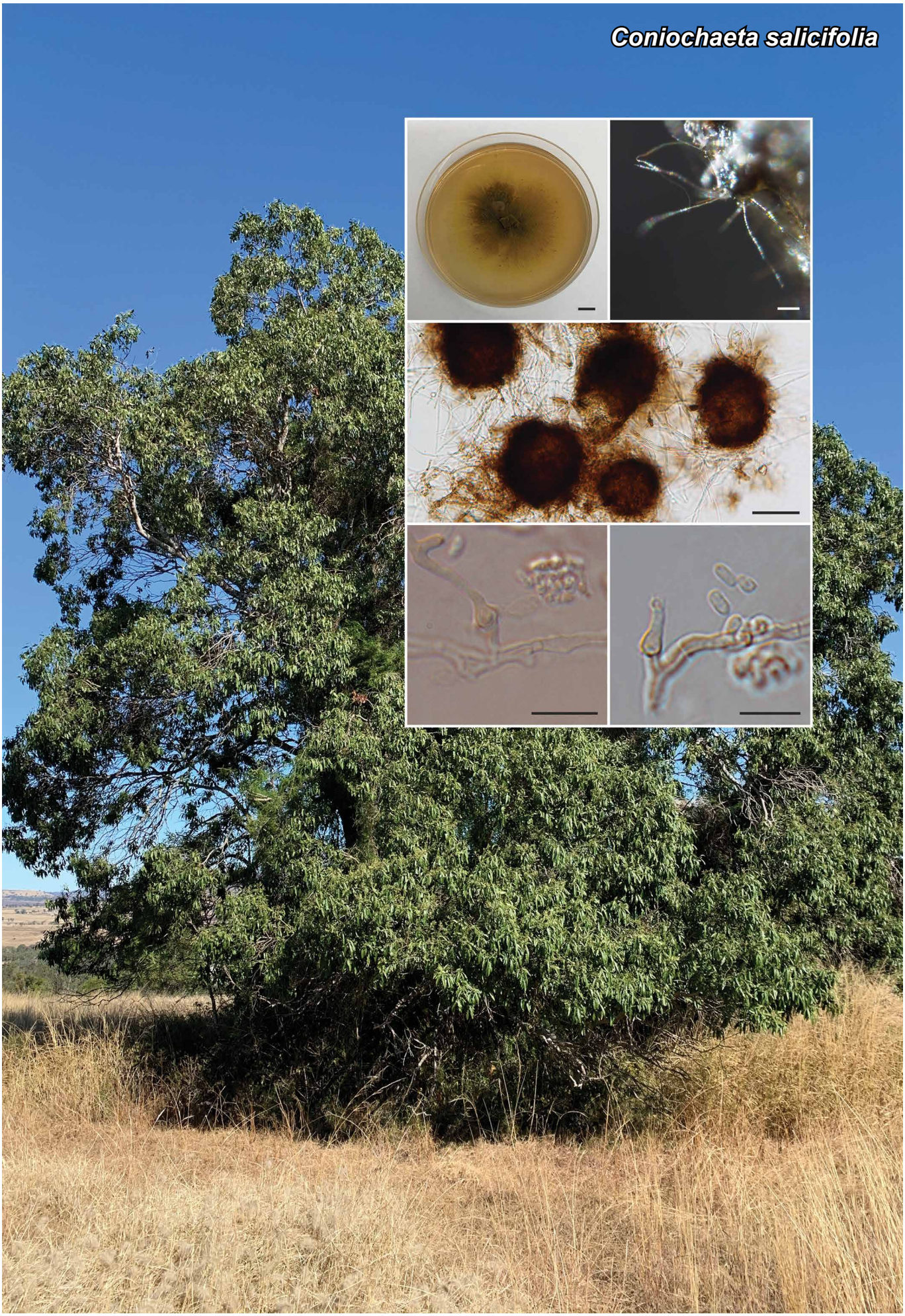

Coniochaeta salicifolia

Fungal Planet 1233 – 13 July 2021

Coniochaeta salicifolia A.B. Sharma & Dearnaley, *sp. nov.*

Etymology. Name refers to the host plant from which it was isolated, *Geijera salicifolia*.

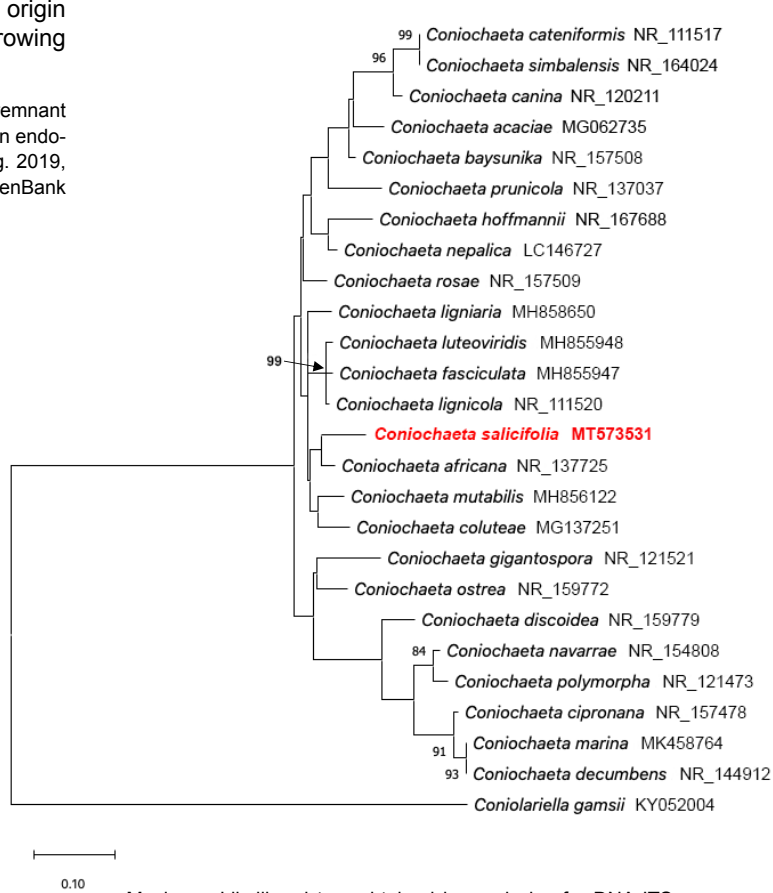
Classification — *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

Ascomata perithecial, on and adjacent to sterilised grapevine stems on synthetic nutrient-poor agar media, dark-brown to black, subglobose, 99–154 µm diam (av. 121 µm); outer wall of brown *textura angularis*; some ascomata with central ostiole. *Setae* straight or curved, hyaline, smooth-walled, cylindrical, tapering to a round tip, 117–545 × 2 µm (av. 232 × 2 µm). *Asci* and *ascospores* not seen. *Lecythophora* asexual morph: *Conidiophores* formed directly on hyphae, mostly reduced to conidiogenous cells, 2–23 × 1–3 µm (av. 12 × 2 µm). *Conidiogenous cells* variable, with apical collarette or rounded ends, hyaline, 2–14 × 1–3 µm (av. 7 × 2 µm). Sporulation abundant. *Conidia* hyaline, aseptate, clustered in heads on the ends of conidiogenous cells, ellipsoidal with round ends, 4–6 × 2–3 µm (av. 5 × 2 µm). Vegetative hyphae 2 µm diam, hyaline; *chlamydospores* absent.

Culture characteristics — Colonies on potato dextrose agar flat, slow growing; surface glistering without aerial hyphae; margins irregular; raw umber and orange-citrine at the origin with white spots and lemon chrome margin indicating growing zone; 1.9 cm diam after 2 wk dark incubation at 23 °C.

Typus. Australia, Queensland, Baxter's Hill, Gowrie Junction, remnant dry rainforest, S27°29'7" E151°52'41", altitude 570 m, isolated as an endophyte from healthy leaves of *Geijera salicifolia* (*Rutaceae*), 20 Aug. 2019, *A.B. Sharma* (holotype BRIP 71282a, ITS and LSU sequences GenBank MT573531 and MT525302, MycoBank MB 836228).

Notes — Members of *Coniochaeta* are characterised by dark-brown to black, globose or subglobose perithecia, longitudinal germ slits in dark ascospores and a phialidic asexual morph (Nasr et al. 2018, Harrington et al. 2019). *Coniochaeta* spp. occur as endophytes and human and plant pathogens (Damm et al. 2010, Khan et al. 2013, Xie et al. 2015). A number of bioactive compounds have been isolated from members of the genus including coniochaetone and coniosetin (Wang et al. 1995, Segeth et al. 2003). *Coniochaeta salicifolia* is distinct on BLAST searches from *C. africana* (ITS GenBank MH863095, 94 % over 542 bp) and *C. navarrae* (ITS GenBank NR_154808, 93 % similarity over 375 bp). *Coniochaeta salicifolia* differs morphologically from *C. africana* by its white and long setae (up to 545 µm). The LSU sequence of *C. salicifolia* has 98 % similarity to *C. rosae* (over 819 bp; GenBank NG_066204).



Maximum Likelihood tree obtained by analysis of nrDNA ITS sequences from *C. salicifolia* (**bold**) and related *Coniochaetales* species in GenBank. Phylogenetic analysis was conducted in MEGA v. 10 (Kumar et al. 2018a) using ClustalW for alignment (652 bp in the final dataset) and Kimura 2 parameters, Gamma distribution and 1 000 bootstrap re-samplings to build the tree. Bootstrap values less than 70 % are not shown. *Coniolariella gamsii* (*Xylariaceae*) was used as an outgroup to root the tree.

Colour illustrations. Geijera salicifolia at Baxter's Hill, Gowrie Junction, Queensland, Australia. Colony of *Coniochaeta salicifolia* on PDA; perithecium showing setae; cluster of perithecia; conidial cluster; conidiogenous cell and conidia. Scale bars = 1 cm (Petri dish), 100 µm (perithecium), 50 µm (perithecia), 10 µm (conidiogenous cells and conidia).

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Cortinarius bonachei

Fungal Planet 1234 – 13 July 2021

Cortinarius bonachei J.D. Reyes, *sp. nov.*

Etymology. Named after J.M. Bonache, a dear friend, and after a lagoon of the same name, where this species was collected.

Classification — *Cortinariaceae*, *Cortinariales*, *Agaricomycetes*.

Pileus 25–45(–50) mm diam, brown dark (Séguy 1936; 696, 701) becoming brown (694, 695), at first conical campanulate, later convex with a persistent obtuse and low umbo. *Margin* first incurved, straight, later extended. *Surface* dry, hygrophanous, matt and finely innate-fibrillose, sometimes with white veil remnants. *Lamellae* 4–5 mm diam, medium spaced, adnate to sinuate, brown when young (694, 695), paler at the edge (705), with lamellulae. *Stipe* 35–50 × 4–6 mm, cylindrical, subbulbous towards the base (8 mm diam). *Surface* fibrillose, with whitish fibrils on a pink background. *Context* reddish brown on the pileus, and lighter reddish brown towards the base of the stipe. *Odour* and *taste* indistinct. *Basidiospores* (6.3–)6.6–7.7(–8.7) × (4.2–)4.5–5.4(–6) µm; Q = (1.3–)1.34–1.6(–1.7); n = 60 spores; Mv = 7.2 × 5 µm; Qv = 1.5; Ve = 93; obovoid-subamygdaliform, strongly verrucose, isolated, most prominent at the apex. *Basidia* tetrasporic, 30–40 × 6–9 µm. *Lamellar edge* fertile or without true cystidia, with scattered basidioliform banal cells, 7–8 µm. *Pileipellis* composed of hyphae narrow, 6–8 µm. *Clamp connections* present in all tissues.

Macrochemical reactions — KOH slightly brownish. Guaiac negative.

Habitat — *Quercus ilex* in calcareous soils.

Typus. Spain, Jaén, Siles, Laguna de Bonache, 1 200 m a.s.l., with *Quercus ilex* in calcareous soils, 16 Nov. 2006, *J.D. Reyes* (holotype JA-9576, isotype JDRG16110607, ITS sequence GenBank MW752900, MycoBank MB 839008).

Notes — Different public nucleotide databases were consulted using the blastn algorithm: GenBank, UNITE and BOLD, comparing the generated holotype sequence with the closest species of *Cortinarius* subg. *Telamonia*, differing with *C. roseocastaneus* (GenBank NR131866) in seven nucleotides and eight indels. *Cortinarius roseobasilis* (GenBank NR153059) in eight nucleotides and 11 indels and *C. fulvopaludosus* (GenBank NR154868)) in six nucleotides and 17 indels, 95.59–96.95 % similarity.

Morphological characters distinguish *C. bonachei* from related species: *C. roseocastaneus* has a very dark brown to blackish brown pileus, dark brown lamellae, and less verrucose basidiospores. Ecological characters distinguish *C. bonachei* from *C. fulvopaludosus*, a species associate with conifers (*Abies*, *Picea* and *Pinus* spp.) and deciduous hosts such as *Betula*, *Alnus* and *Salix* spp., in forests of Northern Europe. *Cortinarius roseobasalis*, an American species, is linked to *Quercus garryana*.

Colour illustrations. Spain, Jaén, Siles, Sierra Segura, Cazorla y las Villas Natural Park, forest of *Q. ilex* subsp. *ballota*, where the holotype of *Cortinarius bonachei* was collected (JA-9576). Basidiomata correspond with the holotype; basidiospores. Scale bar = 10 µm.

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Cortinarius brunneovolvatus

Fungal Planet 1235 – 13 July 2021

Cortinarius brunneovolvatus A. Mateos & J.D. Reyes, *sp. nov.*

Etymology. The first part of the epithet ('*brunneo*') refers to the general brown colour of the basidiomata, the second part ('*volvatus*') refers to the fact that it is provided with a veil covering the stipe in the form of a volva.

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

Basidiomata of medium size, growing gregarious to fasciculate, with a sordid appearance ven when young. *Pileus* 50–70(–90) mm diam, convex to plano-convex when young, flat to depressed in developed specimens, with a broad obtuse umbo and wavy margin, incurved at first but later straight, sometimes somewhat incised; cuticle reddish brown (Séguy 1936: 146), dark (126) to sordid (177), a bit hygrophanous, with a large amount of white veil in the centre and fibrillose remnants towards the margin, which is somewhat exceeding. *Lamellae* spaced, widely spaced at maturity, emarginate, with abundant short and long lamellulae, up to 10 mm thick, with a wavy and sometimes somewhat serrate edge; beige when young (190) but soon reddish brown (187, 191). *Stipe* 50–70(–120) × 10–15 mm, cylindrical to claviform, with a bulbous base up to 25 mm thick, recurved, with a fibrillose surface presenting white velar remnants in the lower half, more abundant at the base and finally disappearing elsewhere, with silver fibrils at the apex; reddish brown, paler towards the top (202, 187). *Context* firm, reddish brown in the centre of the pileus (161), paler towards the top of the stipe (162), greyish brown towards the base (200), *odour* slightly earthy, *taste* not remarkable. *Exsiccatae*: pileus sordid brown to dark greyish brown, especially in the centre; stipe brownish grey. *Macrochemical reactions*: KOH, on cuticle dark brown, on flesh somewhat brownish at the pileus and subnull elsewhere; Guaiac, ++ rather fast. *Basidiospores* ellipsoid to subamygdaliform, with ornaments consisting of evenly distributed isolated warts of medium height and thickness, (8–)8.9–*9.5*–10.3(–11.3) × (4.9–)5.5–*6.1*–6.7(–7.5) µm; Q = (1.4–)1.5–*1.6*–1.7(–1.8); n = 80; Vm = 189 µm^3, sometimes with large central oil droplets. *Lamellar edge* fertile or without true cystidia, with scattered basidioliform banal cells. *Hymenophoral trama* consisting of 3–10 µm wide cylindrical hyphae, with greyish parietal pigment and sometimes with vacuolar pigmentation. *Basidia* claviform, tetrasporic, 25–35 × 8–10 µm, with stigmata 2–4 µm long. *Pileipellis* consisting of a duplex cutis (Type 1 according to Bidaud et al. 2004). *Epicutis* formed by a thin layer of radial hyphae of (3–)4–8(–14) µm, with few free and hardly differentiated tips, and greyish brown parietal incrusted pigment. *Subcutis* well differentiated from the epicutis, consisting of a layer of subcellular elements of 17–23 µm diam, with brownish parietal pigmentation. *Clamp connections* present in all tissues.

Habitat & Distribution — Gregarius and caespitose, in large groups among leaf litter of *Quercus ilex* subsp. *ballota*, on rich calcareous soils, in Mediterranean sclerophyllous mountain forest in Sierra Mágina, Subbetic System (southern Iberian Peninsula), consisting of *Q. ilex* subsp. *ballota*, *Q. coccifera* and *Pinus* spp. The existence of an ITS sequence in GenBank (HQ204636.1) of ectomycorrhizal communities in a Mediterranean forest ecosystem dominated by *Quercus ilex* which is almost identical to that obtained in the present study indicates the presence of *C. brunneovolvatus* in the *Q. ilex* forests of France.

Typus. Spain, Jaén, Cambil, Parque Natural Sierra Mágina, Gibralberca, N37°40'45.74" W3°29'8.26", 1 240 m a.s.l., gregarious growth, under *Quercus ilex* subsp. *ballota* in calcareous soil, 7 Dec. 2012, *A. Mateos* (holotype AMI 3752, ITS sequence GenBank MW752903, MycoBank MB 839028).

Additional materials examined. Spain, Jaén, Cambil, Parque Natural Sierra Mágina, Gibralberca, 1 200 m a.s.l., fasciculate growth, under *Quercus ilex* subsp. *ballota* in calcareous soil, on 7 Dec. 2012, *A. Mateos*, AMI 3751, ITS sequence GenBank MW752904; ibid., 21 Dec. 2012, gregarious growth, *J.D.D. Reyes*, JDRG2112200101, ITS sequence GenBank MW752905.

Phylogeny — The final alignment included 663 bp of which 153 were variable and 108 were parsimoniously informative among 31 sequences (three newly generated, 28 retrieved from public databases). For the elimination of ambiguously aligned sites, this alignment was optimised in GBlocks (Castresana 2000) with the least restrictive parameters resulting in 501 positions, of which 376 were conserved, 125 variable, 89 parsimoniously informative and 36 singletons. JModeltest v. 2.1.4 (Darriba et al. 2012) was used to select the best nucleotide substitution model, using the Akaike Information Criterion (AIC, Akaike 1974) analysis. The GTR+I+G model was selected. Maximum likelihood (ML) and Bayesian inference (BI) analyses were performed using Geneious v. 6.1.7. Supporting statistical nodes in the ML analyses were inferred from 1 000 bootstrap replicates. Phylogenetic trees were drawn with FigTree v. 1.4, and finally adapted in Adobe Illustrator CS5.

Notes — *Cortinarius brunneovolvatus* has as characteristic morphological characters, chestnut-brown colour of its basidiomata, the large amount of white veil remnants on the pileus and thickly covering bulbous base of stipe, and its ellipsoid to subamygdaliform spores with medium-sized ornaments. However, these features are present also in several species of *Telamonia* s.lat. and, more specifically, in the sections *Brunnei*, *Sordescens* and *Lanigeri* (Brandrud et al. 1989, 1992, 1994, 1998, Melot 1990, Bidaud et al. 2002, 2009), as well as other species in section *Bovini* where *C. brunneovolvatus* is nested, based on phylogenetic analyses, as well as morphological evidence representing the type species *C. bovini* ((Brandrud et al. 2012: pl. E20, Niskanen et al. 2013). Section *Bovini* (Moser & Horak 1975), underwent several modifications by its original author (Moser 1978, 1983, 2001, Moser et al. 1995), who included several European and South American species, one North American species (*C. pseudobovinus*) and others from the Southern Hemisphere. Subsequently, Bidaud et al. (2009) added some new species and suggested several other modifications.

(text continues on Supplementary material page FP1235)

Colour illustrations. Spain, Cambil, Sierra Mágina Natural Park, forest of *Q. ilex* subsp. *ballota*, where the holotype of *Cortinarius brunneovolvatus* was collected (AMI 3752). Basidiomata in upper photo correspond with the holotype; middle photo corresponds with AMI 3751 and the bottom photo is JDRG2112200101; holotype basidiospores. Scale bar = 10 µm.

Supplementary material

FP1235-1 Key to the related species of section *Bovini.*

FP1235-2 Phylogram depicting the evolutionary relationships of *Cortinarius brunneovolvatus* and its relatives based on ITS sequence data.

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Crepidotus wasseri

Fungal Planet 1236 – 13 July 2021

Crepidotus wasseri Kapitonov, Biketova, Zmitr. & Á. Kovács, *sp. nov*.

Etymology. The name refers to the 75th anniversary of Professor Solomon P. Wasser, a famous agaricologist, and organizer of research on cryptogamic botany in the USSR, Ukraine, and Israel, as well as the founder and Editor-in-Chief of the International Journal of Medicinal Mushrooms.

Classification — *Crepidotaceae*, *Agaricales*, *Agaricomycetes*.

Type material is presented as a group of four basidiomes at different stages of their development. *Pileus* small, of pleurotoid habit, hemispherical or cupulate when young, campanulate with kidney-shaped underside outline when mature, 2–10 mm diam, dorsally attached, with inrolled margin, not hygrophanous, felted-tomentose, white when fresh, staying ivory creamish after drying. *Gills* not frequent, of two levels, 2–8 mm long, c. 0.3 mm wide, with white, minutely fimbriate *edge*, young white, later pale cinnamon near the centre. *Stipe* absent; dorsal *attachment zone* white, subtomentose. *Flesh* thin (c. 0.2 mm thick), white, not hygrophanous; *odour* and *taste* not recorded. *Spore print* cinnamon-buff. *Basidiospores* (6.5–)7.1–8.6(–9.0) × (4.5–)4.8–5.5(–5.9) µm, av. = 7.8 × 5.2 µm, Q = (1.36–)1.43–1.64(–1.77), $Q_{av.}$ = 1.52 (n = 50), obovate, somewhat abaxially flattened, entirely smooth, thick-walled, pale cinnamon, with globules-rich contents, CB+, IKI–. *Basidia* (21.6–)24.0–28.6 (–30.8) × (6.7–)7.2–10.0(–10.4) µm, av. = 26.6 × 8.6 µm (n = 30), clavate, (2–)4-spored, clamped at the base. *Cheilocystidia* numerous, (33.1–)37.1–59.6(–74.0) × (3.9–)4.6–7.3(–8.4) µm, av. = 47.2 × 5.9 µm (n = 50), narrowly lageniform, with elongated base and narrow tip, in some cases simply septate at the base. *Pleurocystidia* especially not differentiated. *Pileipellis* a trichoderm consisting of simple-septate hyphae, 3.5–5.8 (–6.3) µm diam, *terminal cells* (pileocystidia) narrowly lageniform, (42.2–)54.8–83.0(–93.2) × (4.2–)4.5–7.4(–8.8) µm (n = 20). *Pigment* lacking. *Clamp connections* abundant in the internal tissues, but invisible in the pileipellis.

Habitat & Distribution — Growing gregarious on wood debris of *Populus tremula*. Uncommon in the studied area. So far known only from Russia.

Typus. Russia, Tyumen Region, Tobolsky District, vicinity of Belaya village, Betuleto-Tremuletum variiherbosum, on debris of *Populus tremula*, N58°16'36" E68°41'40", 26 Sept. 2019, *V.I. Kapitonov* (holotype LE 287679, ITS and nrLSU sequences GenBank MW722981 and MW723022, MycoBank MB 839123).

Additional material examined. *Crepidotus caspari*: Russia, Novgorod, on *Salix* sp. wood, 21 Aug. 1999, *O.V. Morozova* (LE 227999, ITS sequence GenBank MW722982).

Colour illustrations. Russia, Tyumen Region, Tobolskiy district, Betuleto-Tremuletum variiherbosum, where the holotype was collected. Top: basidiomes *in situ*; median: pileipellis with terminal elements; bottom left: cheilocystidia; bottom right: basidia; on the right: basidiospores (all from holotype). Scale bars = 5 mm (basidiomes), 10 µm (pileipellis and cheilocystidia), 5 µm (basidia and basidiospores).

Notes — *Crepidotus wasseri* could be well characterised by a combination of characters such as: 1) small basidiomes; 2) completely smooth basidiospores; 3) narrowly lageniform elements along the gills edge as well as the pileus upperside; and 4) invisible clamp connections in the pileipellis hyphae. The latter feature, although it was partially visible in some pileipellis photos of *Crepidotus volubilis* (Kumar et al. 2018a), was generally not reported for the genus *Crepidotus* as a whole (whose representatives were characterised either by the complete absence of clamp connections, or by their presence in all tissues), but it was reported quite regularly, e.g., for entolomataceous fungi (e.g., Jančovičova & Adamčik 2012). As shown in the molecular phylogram, *C. wasseri* represents a distinct and rather distant clade from neighbouring species clades, forming a basal lineage to the *C. palodensis*-*C. subverrucisporus* complex. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequences were Uncultured *Basidiomycota* 4S1_A12 (GenBank EU489965.1; Identities = 819/881 (93 %), 18 gaps (2 %)) and Uncultured fungus FDBC50 (GenBank JQ247381.1; Identities = 818/884 (93 %), 18 gaps (2 %)). The closest hits using the **LSU** sequence *C.* aff. *alabamensis* (GenBank GQ892982.1; Identities = 1347/1368 (98 %), no gaps) and *C. mollis* (GenBank DQ986293; Identities = 1346/1368 (98 %), no gaps).

Other morphologically similar species with minute basidiomes (see Supplementary material FP1236-1) bear only superficial similarities with *C. wasseri* in various aspects, e.g., lageniform cheilocystidia (*C. epibryus*, *C. lagenicystis*), or smooth basidiospores (*C. autochtonus*, *C. epibryus*).

Supplementary material

FP1236-1 Differentiating characters of phylogenetically (top section) and morphologically (bottom section) related *Crepidotus* species.

FP1236-2 Maximum likelihood tree of *Crepidotus wasseri* sp. nov. and closely related species. Analysis of the nrDNA ITS region was conducted using MEGA X software (Kumar et al. 2018b) employing the GTR+G model with 1000 bootstrap replicates. Another measure of branch support was estimated through Bayesian Inference using MrBayes v. 3.2.6 (Ronquist et al. 2012) under the same model for 2.5 M replicates. Posterior probability values ≥ 0.7 and bootstrap support values ≥ 50 % are shown at the nodes. The new species is indicated in **bold**, holotypes indicated with asterisk (*). Two-letter country codes (ISO 3166-1 alpha-2) reflecting origin of specimens are given.

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Cuphophyllus flavipesoides

Fungal Planet 1237 – 13 July 2021

Cuphophyllus flavipesoides J.B. Jordal & E. Larss., *sp. nov.*

Etymology. Refers to its morphological similarity of *Cuphophyllus flavipes*.

Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata clitocybioid. *Pileus* 15–40(–50) mm diam, as young conical to plano-convex with a broad and blunt umbo and incurved margin, later becoming more plane, with age sometimes becoming slightly depressed and with somewhat undulating and lobed margin. Lubricous to subviscid, sometimes translucently striate at margin up to 2/3 towards the centre, hygrophanous, as young grey violet or ash grey to greyish brown to brown, with a violaceous tint, dark at centre, paler towards the margin and with age discolouring to pale grey to grey violet. *Lamellae* short to deeply decurrent, arcuate, distant to subdistant, lamellae that reach the stipe = 30–40(–50), interspaced with lamellulae, a few furcate, intervening, first whitish to greyish, when greyish with paler margin, with age pale greyish. *Stipe* 30–65 × 3–7 mm, cylindrical and usually thickest at the apex or upper half, tapering and often bending towards the base, dry, matt, fibrillose lengthwise, pale, whitish grey, at the base normally pale yellow, up to 1/3 of the stipe. *Context* concolorous. *Smell* weak, indistinct, *taste* mild.

Micro-morphological characters measured from dried material dehydrated in 3 % KOH and ammoniacal Congo red solution. *Spores* (5.5–)7.0–7.3(–8.8) × (4.2–)5.2–5.4(–6.1) µm, n = 117, av. 7.2 × 5.3 µm, Q = 1.34–1.39, subglobose to ellipsoid, often lacrimoid, with a distinct and often oblique apiculus, hyaline, white in deposit, non-amyloid. *Basidia* 35–54 × 7.5–9 µm, 2–4-spored observed, sterigmata 5–6.5 µm. *Lamellar trama* irregular interwoven, made up of cylindrical hyphae, 5.5–7 µm wide and 30–60 µm long, some branched and inflated. *Pileipellis* an ixocutis, 50–110 µm thick with radially interwoven hyphae, 3–6 µm wide, 30–60 µm long, incrusted with finely granular pigments. Hyphae in subpellis interwoven, 7–10 µm wide, 40–55 µm long, with inflated end cells up to 20 µm wide. *Clamp connections* frequent in all tissues.

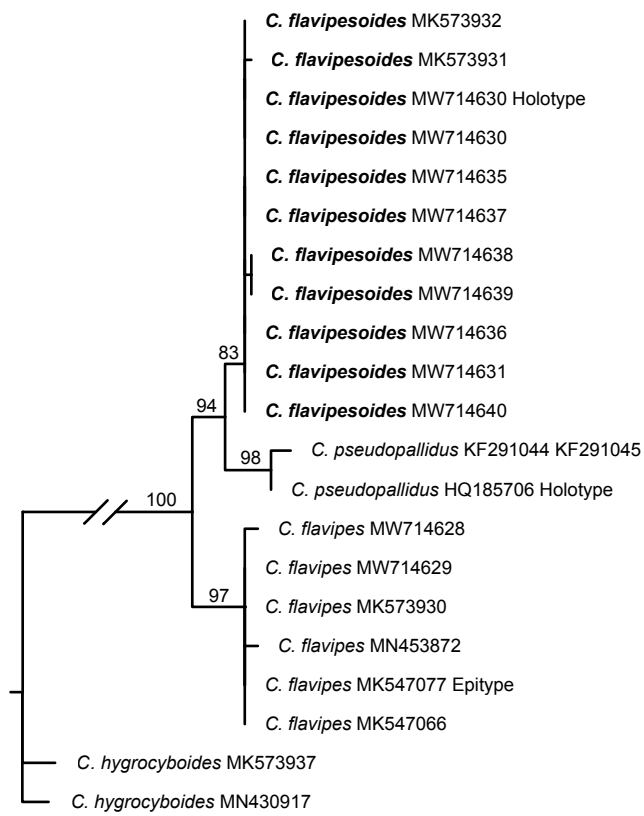
Ecology & Distribution — Associated with nutrient poor semi-natural grasslands, among mosses, herbs and grasses, with the soil ranging from rather acid to (rarely) moderately calcareous. Confirmed distribution so far from Norway, Sweden and Denmark.

Typus. Norway, Vestland, Alver, Lygra (Utluro), 25 m a.s.l., in semi-natural grassland pasture, 3 Sept. 2019, *J.B. Jordal*, JBJ19-013 (holotype OF-258322, isotype GB-0207610, ITS-LSU sequence GenBank MW714630, MycoBank MB 839261).

Notes — *Cuphophyllus flavipesoides* belongs in a complex of closely related and morphologically similar species. In macro- and micromorphology it is very similar to *C. flavipes*. On average we find that the spores in *C. flavipes* are more subglobose with the average measurements 7.1 × 5.6 µm, and Q = 1.22–1.27, compared to the average in *C. flavipesoides*, 7.2 × 5.3 µm, Q = 1.34–1.39. In Voitk et al. (2020) an average value for the spores of the selected epitype of *C. flavipes* was measured to Q = 1.2. The two species differ in ITS1 sequence data by four substitutions and four single bp insertion/deletion events, in the ITS2 by six substitutions and three single bp insertion/deletion events. The sequences in the *C. flavipesoides* clade are homogenous, suggesting an independent evolutionary lineage.

Based on the sequence data available, the two species differ somewhat in geographic distribution where *C. flavipes* seems to be more common in southern Europe and confirmed from Italy, Austria, Germany, UK, Denmark, SW Norway and S Sweden, whereas *C. flavipesoides* has a more northern distribution range and is confirmed from Norway, Sweden and Denmark and is most common in the northern/boreal areas. However, the two species overlap and co-occur in some areas in southern parts of Scandinavia.

Cuphophyllus pseudopallidus is also closely related and resembles *C. flavipesoides*, but it differs in morphology by having a pale beige brown (ecru-drab) to pale greyish pileus colour and ivory yellow lamellae, a stipe that is glabrous, striate and white-shining, and somewhat smaller spores (Hesler & Smith 1963, Voitk et al. 2020). So far only known from North America and Japan.



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *C. flavipesoides* to *C. flavipes* and *C. pseudopallidus*. Bootstrap support values are indicated on branches. *Cuphophyllus flavipesoides* is marked in **bold** and the holotype is indicated.

Colour illustrations. *Cuphophyllus flavipesoides* habitat in semi-natural grassland, from the type locality in Vestland, Alver, Lygra, Norway. *In situ* basidiomata of the holotype; hymenium and basidiospores of the holotype (OF-258322). Scale bars = 10 µm for spores, 20 µm for hymenium.

Supplementary material

FP1237 Additional materials examined.

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Curvularia tanzanica

Fungal Planet 1238 – 13 July 2021

Curvularia tanzanica Y.P. Tan, Dhileepan, Ntandu, Kurose & R.G. Shivas, *sp. nov.*

Etymology. Name refers to Tanzania, the country from which it was collected.

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

Hyphae pale brown, smooth or verruculose, branched and septate, up to 3–6 µm wide. *Conidiophores* erect, straight to flexuous, geniculate towards apex, brown, smooth, septate, 50–110 × 3–4 µm, lateral or terminal, unbranched or sparingly branched. *Conidiogenous cells* intercalary and terminal, brown, smooth to minutely verruculose, polytretic with darkened scars. *Conidia* cylindrical to narrowly ellipsoidal, straight, rounded at the apex, 21–32 × 8–12 µm, 3(–4)-distoseptate, brown to dark brown, end cells paler than others, third cell from base sometimes larger and darker than others; *hila* conspicuous, protuberant, thickened, darkened, 2–3 µm wide.

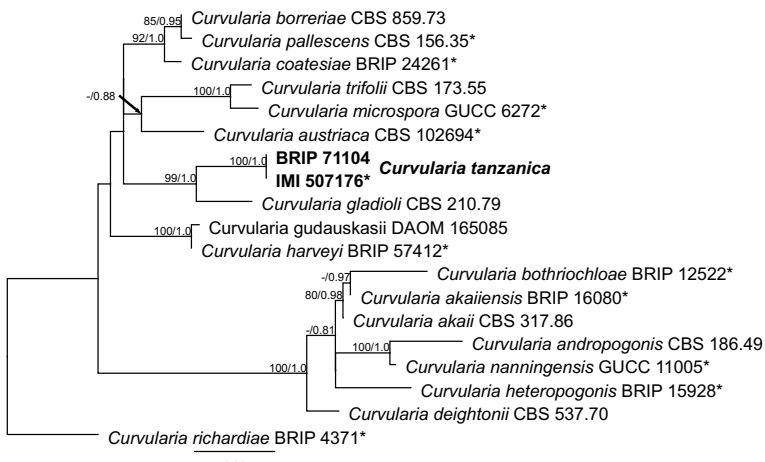
Culture characteristics — Colonies on potato dextrose agar approx. 4 cm diam after 7 d at 25 °C, surface with little aerial mycelium, dark brown to black.

Typus. Tanzania, Korogwe, Msambiasi, S05°07'57" E038°23'10", on inflorescence of *Cyperus aromaticus* (*Cyperaceae*), 22 Dec. 2019, *J.E. Ntandu*, *K. Dhileepan*, *M.D.E. Shivas & R.G. Shivas* (holotype BRIP 71771, culture ex-type IMI 507176, ITS, LSU and *gapdh* sequences GenBank MW396857, MW396841 and MW388669, MycoBank MB 838305).

Additional material examined. Tanzania, Korogwe, Msambiasi, S05°07'57" E038°23'10", from inflorescence of *Cyperus aromaticus* (*Cyperaceae*), 22 Dec. 2019, *J.E. Ntandu*, *K. Dhileepan*, *M.D.E. Shivas* & *R.G. Shivas*, BRIP 71104, ITS, LSU and *gapdh* sequences GenBank MW396856, MW396840 and MW388668.

Notes — *Curvularia tanzanica* is only known from collections on *Cyperus aromaticus* (syn: *Kyllinga polyphylla*) (*Cyperaceae*) in Tanzania. *Curvularia tanzanica* was discovered while searching for plant pathogens on *C. aromaticus* in its native range in equatorial Africa. The aim of the surveys was to find plant pathogens that may have potential for the biological control of *C. aromaticus* in northern Queensland, Australia, where the sedge has become an invasive weed in pastures and sugar cane crops. *Curvularia tanzanica* colonised the floral parts of *C. aromaticus* that superficially resembled the darkened crustose inflorescences of *Sporobolus* spp. (*Poaceae*) covered (and sometimes destroyed) by certain species of *Curvularia* spp. (Luttrell 1976, Alcorn 1982, Tan et al. 2018).

The multilocus phylogenetic analysis of the ITS and *gapdh* loci placed *C. tanzanica* sister to *C. gladioli* strain CBS 210.79. Based on a blastn search, *C. tanzanica* differs from *C. gladioli* in ITS (GenBank LT631345; Identities 558/565 (99 %), no gaps) and *gapdh* (GenBank LT715802; Identities 531/540 (98 %), no gaps). Morphologically, *C. tanzanica* has straight conidia, which differentiates it from *C. gladioli* (illustrated in Parmelee (1956) as *C. trifolii* f. sp. *gladioli*) with curved conidia (the third cell from the base is swollen and convex on one side).



Phylogenetic tree of selected *Curvularia* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS and *gapdh*). Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Curvularia richardiae* was used as outgroup. Novel taxon is indicated in **bold**. Ex-type strains are marked with an asterisk (*).

Colour illustrations. Kunjithapatham Dhileepan in sedgeland, eastern Tanzania. Inflorescence of *Cyperus aromaticus* colonised by *Curvularia tanzanica*; conidiophores; conidia. Scale bars = 1 mm (inflorescence), 10 µm (others).

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Elaphomyces borealis

Fungal Planet 1239 – 13 July 2021

Elaphomyces borealis Jeppson & E. Larss., *sp. nov*.

Etymology. Name refers to its distribution in boreal regions.

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

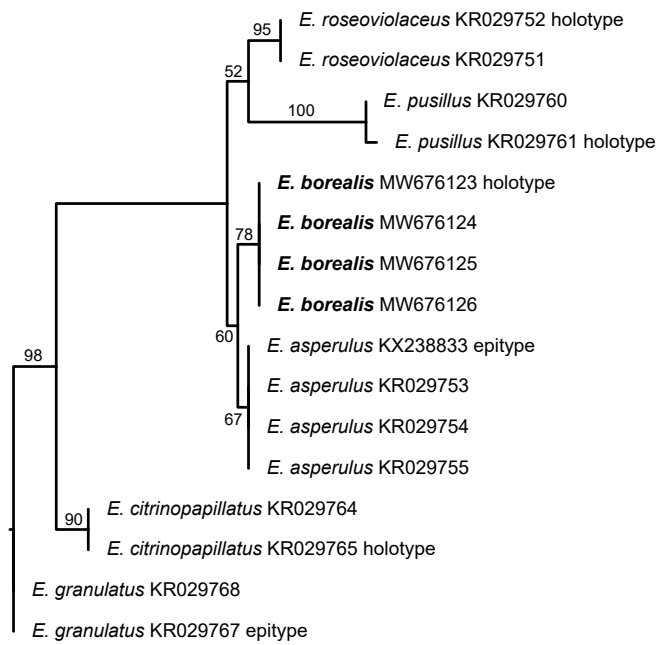
Ascomata subglobose, 1–3 cm diam. *Peridial* surface first yellowish brown to orange brown, with age greyish brown with a covering of dense small pyramidal papillae, in places fragile and more or less farinaceous, found solitary or in small groups, no conspicuous hyphal mat or hyphal crust present. *Cortex* of hyaline to yellowish compacted parallel bundles of regularly septate hyphae, 2–4 µm diam, towards the gleba more loosely interwoven and moderately ramified hyphae, 3–5 µm diam. *Papillae* more strongly yellow pigmented and constructed of intricately interwoven hyphae. *Peridium* in section fresh up to 3 mm diam, pale pink to violaceous pink, often with slight orange tinges, consisting of hyaline hyphae, 2–5 µm diam, towards the gleba partly covered with abundant extracellular grains of reddish brown pigments. *Gleba* immature whitish greenish with hyaline hyphae and rounded, thick-walled, 2–2.5 µm diam, pedunculate asci 40–50 µm diam containing 5–8 ascospores, mature gleba dark brown to black. *Ascospores* globose, 35–45 µm in KOH incl. ornamentation, 25–30 µm in Hoyer's medium, with a dense ornamentation of straight to slightly curved spines, 1–2.5 µm long, forming an inconspicuous cheetah pattern with scarce and narrow 'pathways'. High proportion of ascospores collapsing when mounted in KOH 3 %. Considerably smaller, 14–20 µm, and more pigmented spores, interpreted as aborted spores, are abundantly present among the normal ascospores.

Ecology & Distribution — Associated with *Picea abies*, *Pinus sylvestris* and *Betula pubescens* in boreal and subalpine forest habitats. It has a more northern distribution range than *E. asperulus* and *E. granulatus*, and to date it has only been recorded in Central Sweden, but is likely to occur also in suitable habitats in neighbouring countries.

Typus. Sweden, Härjedalen, Tännäs, Mittådalen, subalpine woodland under *Pinus sylvestris* and *Betula pubescens*, 760 m a.s.l., N62.698857° E12.684028°, 25 Aug. 2020, *E. Larsson*, *D. Gustafsson & M. Jeppson 11239* (holotype GB-0207608, ITS-LSU sequence GenBank MW676123, MycoBank MB 839018).

Additional material examined. *Elaphomyces borealis*: Sweden, Dalarna, Järna, Noret, mesic coniferous woodland, under *Pinus sylvestris* and *Picea abies*, 260 m a.s.l., N60.564776° E14.425721°, 22 Aug. 2020, *E. Larsson*, *D. Gustafsson & M. Jeppson 11199* (GB-0207607, ITS-LSU sequence GenBank MW676125); ibid., *11204*, *11205*, *11206*; Härjedalen, Tännäs, Mittådalen, subalpine woodland under *Betula pubescens* and *Pinus sylvestris*, 760 m a.s.l., 25 Aug. 2020, *E. Larsson*, *D. Gustafsson & M. Jeppson 11232*, *11233*, *11236*, *11238*; Härjedalen, Tännäs, Vivallen, mesic coniferous woodland under *Picea abies* and *Betula pubescens*, 670 m a.s.l., 26 Aug. 2020, *E. Larsson*, *D. Gustafsson & M. Jeppson 11249* (GB-0207605, ITS-LSU sequence GenBank MW676124); ibid., *E. Larsson 86-20* (GB-0207609, ITS-LSU sequence GenBank MW676126).

Notes — *Elaphomyces borealis* belongs in a complex of morphologically similar species in subsect. *Elaphomyces*. It is most closely related to *E. asperulus* for which an epitype was selected by Paz et al. (2017), and the recently described species *E. roseoviolaceus* and *E. pusillus* (Molia et al. 2020). It differs morphologically from *E. asperulus* in ascospore ornamentation, abundance of aborted spores, and the orange tone of the peridium. *Elaphomyces pusillus* also has a northern boreal distribution range and occurs in similar habitats but differs in having smaller ascomata and pink to slightly violaceous peridium in section, and smaller spores. *Elaphomyces roseoviolaceus* is associated with richer and calcareous coniferous mixed forests and has dark pink to bluish violaceous peridium in section and somewhat smaller spores.



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

Colour illustrations. *Elaphomyces borealis* forest habitat from the type locality in Härjedalen, Sweden. Ascomata; ascospores in side view and surface view and smaller abortive spores (holotype). Scale bars = 10 mm (ascomata), 10 µm (ascospores).

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Entoloma ammophilum

Fungal Planet 1240 – 13 July 2021

Entoloma ammophilum G.M. Jansen, Dima, Noordel. & Vila, *sp. nov.*

Etymology. Referring to the habitat on sandy soil (from ἄμμος, Greek, – sand, and φιλέω, Greek, – to like).

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 10–20(–35) mm diam, convex to convex flattened, umbilicate, not distinctly hygrophanous, dark brown or grey brown with blackish brown centre, deeply translucently striate up to centre, minutely squamulose at centre, more or less glabrous towards margin. *Lamellae*, L = about 30, l = 3–5, deeply emarginate, ventricose, pink with eroded, concolorous edge. *Stipe* 30–50 × 1–2 mm, cylindrical, bicolored, steel-blue in lower part, brown above, polished. *Smell* and *taste* not noted. *Spores* heterodiametrical, 9.5–11.5 × 7–8.5 µm, av. 10.4 × 7.8 µm, Q = 1.1–1.55, Qav = 1.25, regularly 5–7-angled. *Basidia* 4-spored, clavate, up to 45 × 15 µm, clampless. *Lamella edge* fertile, cystidia absent. *Pileipellis* a cutis at margin, trichoderm-like at centre, made up of clavate terminal elements, up to 20 µm wide. *Pigment* intracellular-granular, brown. *Clamp connections* absent in all tissues.

Habitat & Distribution — Terrestrial on sandy soil, in small groups in moist dune valley with *Salix repens* on calcareous sandy-clayey soil, or in sandy soil of riverbanks, under *Populus nigra* and *Alnus glutinosa*. Known from the Netherlands and Spain.

Typus. The Netherlands, Prov. Zeeland, Dreischor, 22 Oct. 2016, *G.M. Jansen* C160-4418 (holotype L0608224, ITS sequence GenBank MW934591, MycoBank MB 839221).

Additional material examined. Spain, Barcelona, Vallès Oriental, Can Romegosa, Sant Fost de Campsentelles, alt. 140 m, 24 Oct. 2010, under *Populus nigra* and *Alnus glutinosa*, on sandy soil, *F. Caballero* & *J. Vila*, SFC 101024-05 (L0607606, ITS sequence GenBank MW934592).

Notes — *Entoloma ammophilum* has a characteristic dark brown or brown grey pileus and a polished, bicoloured stipe. It differs from *E. glaucobasis*, which frequently occurs in the same habitat, by the polished nature of the stipe, and fertile lamellae edge. Furthermore, *E. glaucobasis* is phylogenetically rather distant in the /Griseocyaneum clade. Within the /Sarcitulum clade, this species resembles *E. montanum*, which may superficially look similar, but differs clearly in having a sterile, often brown coloured lamella edge, and alpine or boreal distribution.

Colour illustrations. The Netherlands, Prov. Zeeland, Dreischor (type locality). Spores and pileipellis (from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

Supplementary material

FP1240 Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. Analysis was performed in PhyML v. 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. ML bootstrap support values are shown at the nodes (BS > 50 %).

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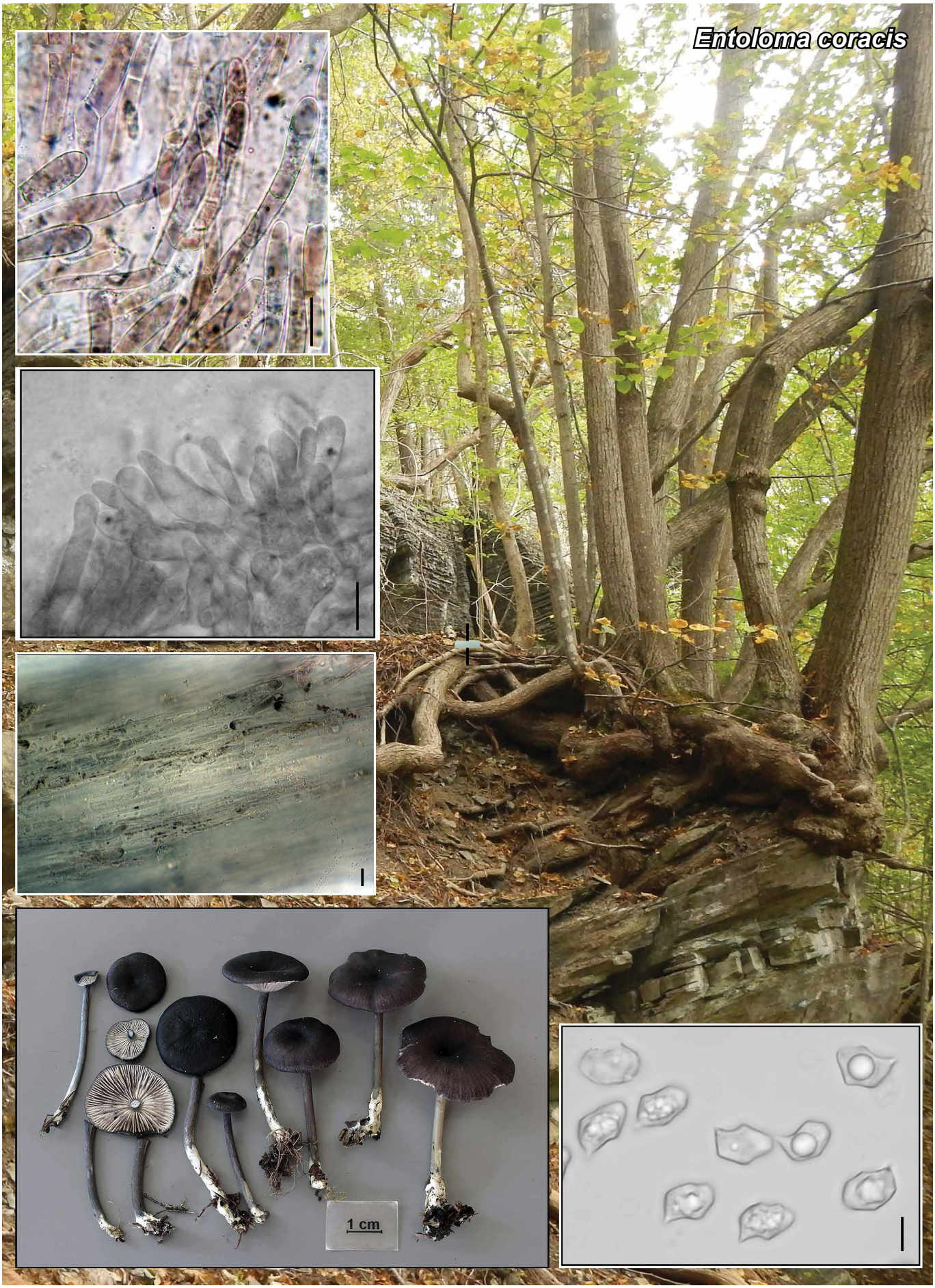
Entoloma coracis
1 cm

Fungal Planet 1241 – 13 July 2021

Entoloma coracis Brandrud, Dima, Noordel., G.M. Jansen & Vila, *sp. nov*.

Etymology. The epithet refers to the dark blackish to violaceous black colour of the basidiomata, like plumage of a raven (*Corvus corax*).

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 10–35 mm, hemispherical to convex expanding plano-convex with involute then deflexed margin, with depressed, rarely umbilicate centre, not hygrophanous, not translucently striate, initially very dark blackish to violaceous black, with age the bluish tinges fade away, leaving the pileus very dark brownish black, violaceous black or porphyry brown, uniformly coloured, not or slightly pallescent on maturing, entirely tomentose and staying so during development or breaking up in small squamules. *Lamellae*, L = 20–30, l = 1–3, moderately distant, adnate-emarginate or with decurrent tooth, segmentiform to subventricose, white, then with pale pink tinge, with irregular, usually with concolorous edge; rarely spotted black from the start, or becoming spotted blackish with age. *Stipe* 20–80 × 3–7 mm, relatively long and stout, initially violaceous grey, fading to pale bluish grey, sometimes developing a lilac-pink tinge, much paler than the pileus, not polished, but covered with blue to violaceous longitudinal fibrils, sometimes scaly-flocculose at apex, especially in rainy conditions, fibrils with same colour or contrastingly darker than background, with abundant white basal mycelium. *Context* white. *Smell* insignificant, *taste* not recorded. *Spores* 8.5–12.5 × 5.5–7.5 µm, av. 9.5–11 × 6–6.5 µm, Q = 1.3–1.7, Qav = 1.3–1.4, heterodiametrical, with 5–7 rather pronounced and sharp angles. *Basidia* 4-spored, claviform, 28.5–41 × 8–13.5 µm, clampless. *Lamella edge* sterile, consisting of a strand of hyphae with clustered cheilocystidia (serrulatum-type) with rather pronounced often somewhat tapering cheilocystidia, 5–15 µm wide, usually not pigmented, but occasionally becoming bluish black with age. *Hymenophoral trama* regular, made up of cylindrical to inflated hyphae, 11–25 µm wide. *Pileipellis* a cutis with transitions to a trichoderm, of clavate, septate, terminal elements, 50–110 × 8–19 µm. *Pigment* intracellular, brown. *Brilliant granules* sparse to abundant. *Clamp connections* absent.

Habitat & Distribution — Saprotrophic, calciphilous or acidophilous. In Norway mainly in open, calcareous *Pinus* and *Tilia* forests, but also in naturally open, steppe-like, thermophilous grassland/shrubland on shallow-soil limestone rocks, and once also recorded in grassland and shrub vegetation on limestone. In South Europe in Mediterranean thermophilous areas, under *Quercus ilex*, *Cistus monspeliensis* or *Pinus halepensis*, also known in the Canary Islands, on woods with *Laurus novocanariensis*, *Pinus radiata* and *Cistus symphytifolius*. Known from Norway, France, Spain and Austria, but certainly more widespread in Europe.

Colour illustrations. Norway, Telemark, Porsgrunn, Frierflogene NR, calcareous dry grassland/margin of calcareous pine forest (type locality). Spores, cheilocystidia, pileipellis, stipitipellis (all from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

Typus. Norway, Telemark, Porsgrunn, Frierflogene NR, near bridge, calcareous, dry grassland/margin of calcareous pine forest, 14 Sept. 2019, *T.E. Brandrud*, *B. Dima & R. Solvang*, TEB 381-19 (holotype O-F-256850, ITS and LSU sequences GenBank MW934571 and MW934251, MycoBank MB 839222).

Additional materials examined. Austria, Tirol, Ehrwald, 28 Aug. 2018, *Rainer Wald* (L0608002, ITS sequence GenBank MW934578). – France, Dordogne, Sanilhac, route de Lafaye, on soil with *Mycenella bryophila*, 241 m a.s.l., 6 Nov. 2019, *G. Eyssartier* (GE 19027, ITS sequence GenBank MW934581). – Norway, Nordland, Alstahaug, Altra, 10 m a.s.l., calcareous pasture, 18 Sept. 2004, *D. Pettersen*, *A.B. Stærnes*, *J.B. Jordal*, *A. Knutsen* & *P. Fadnes* (O-F-67255, ITS sequence GenBank MW934572); Trøndelag, Snåsa, Bergsåsen Nature Reserve, calcareous pine forest, 2 Sept. 2009, *E. Bendiksen* & *K. Bendiksen* KB&EB51/09 (O-F-252053, ITS sequence GenBank MW934574); Steinkjer, Kvam, Aunvolltangen, 60 m a.s.l., old calcareous *Picea* forest, 3 Sept. 2010, *H. Holien* & *T.E. Brandrud*, *U.-B. Bøe*, *A. Molia* HH 57/10 (O-F-293335, ITS sequence GenBank MW934575); Telemark, Bamble, Baneåsen Nature Reserve, calcareous *Tilia* forest, 7 Sept. 2015, *B. Dima* & *T.E. Brandrud* TEB 244-15 (O-F-251952, ITS sequence GenBank MW934573); Bamble, Røsskleiva Nature Reserve SE, in calcareous *Fraxinus-Corylus* forest, 8 Sept. 2015, *T.E. Brandrud* & *B. Dima* TEB 279-15 (O-F-254580, ITS sequence GenBank MW934576); Porsgrunn, Blekebakken Nature Reserve, calcareous *Pinus* forest, 25 Sept. 2015, *T.E. Brandrud* & *B. Dima* TEB 557-15 (O-F-254614, ITS sequence GenBank MW934577); Vestfold, Larvik, Løvallåsen, calcareous grassland, 9 Oct. 2013, *T. Læssøe* & *A. Molia* AM-245ø-2013 (O-F-21892, ITS sequence GenBank MW934579). – Spain, Girona, Can Cofi, 1 June 2013, *P. Carbo* 20130601 (L0608020, ITS sequence GenBank MW934580).

Notes — *Entoloma coracis* is one of the *E. corvinum* look-alikes, with its very dark, opaque, tomentose pileus, white lamellae, and fibrous stipe. *Entoloma aranense* is a sister species of *E. coracis*, less robust, paler, with a lilac-bluish tinged pileus when young, later brown and fibrillose, and a typical subalpine-alpine habitat. Microscopically the differences are minimal. *Entoloma porphyrogriseum* is also closely related, but differs, e.g., in smaller spores, and not so persistently dark pileus. Phylogenetically (see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240), these three species are rather distant from *E. corvinum* s.str., as we now interpret it, and they differ from *E. coracis*, morphologically by the narrower, more sharply angled spores, the serrulatum-type lamella edge, and the habitat. *Entoloma corvinum* is an alpine species, like the similar *E. erhardii*, which differs by having smaller spores, and a polished stipe.

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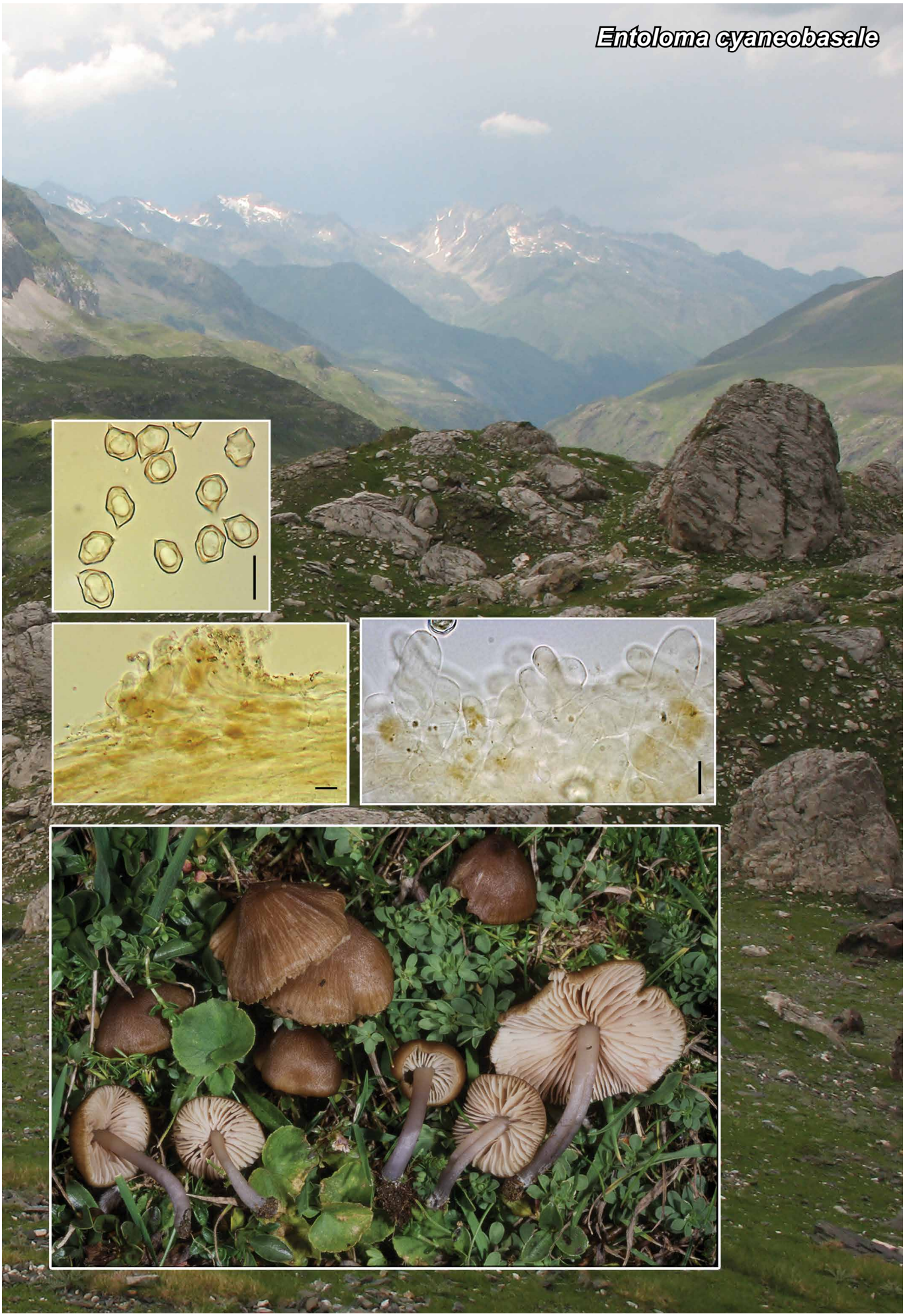
Entoloma cyaneobasale

Fungal Planet 1242 – 13 July 2021

Entoloma cyaneobasale Corriol, Dima & Noordel., *sp. nov*.

Etymology. The epithet refers to the blue colour in the base of the stipe (from '*cyaneus*', Greek – dark blue, and '*basis*', Greek – base).

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 20–40 mm diam, campanulate to convex with incurved margin, then bluntly conico-convex to convex with more or less lobed margin, brown (near 7.5YR3/4) then brown-yellow (10 YR 5.4; Munsell 1954), darker at centre, distinctly hygrophanous (drying to 10 YR 7/3), nearly opaque with only slight striation at margin, entirely fibrillose to sub-squamulose. *Lamellae* rather distant, deeply emarginate, straight to ventricose, whitish, then pink, with slightly eroded, brown edge. *Stipe* up to 45 × 4.5 mm, cylindrical, or quite often compressed with groove, initially blue-grey at base (2.5 / PB), and pale greyish at apex (10 YR 7–6/2), typically bicoloured, quickly fading, nearly polished, but with fine fibrillose striation over whole length, with white mycelial base. *Context* whitish. *Smell* and *taste* not noted. *Spores* (9–)9.5–11(–11.5) × (7–)7.5–8.5(–9) µm, av. 10 × 8 µm, Q = (1.1–)1.15–1.4, Qav = 1.3, shortly heterodiametrical, with 6–8 weak angles, thick-walled, with granular content. *Basidia* 22–30 × 10–12 µm, 4-spored, shortly cylindrico-clavate to ventricose, with 3–4 µm long sterigmata, clampless. *Lamellae edge* sterile, of serrulatum-type, made up of septate cheilocystidia, with terminal elements 35–55 × 9–13 µm, with brown, intracellular pigment. *Pleurocystidia* not observed. *Subhymenium* branched. *Pileipellis* a trichoderm, with clavate terminal elements, often in clusters, with brown, diffuse, intracellular pigment. *Subpellis* with concentrated brown intracellular pigment, with abundant brilliant granules and mixed with refringent lactiferous hyphae. *Clamp connections* absent.

Habitat & Distribution — Terrestrial in alpine snowbed on basic to calcareous soil, together with *Dryas* and *Salix* species. Known from France and Italy.

Typus. France, Pyrenées-Atlantiques, Eaux-Bonnes, cirque du Plaa Ségouné, Gourette, 2400 m a.s.l., 30 Aug. 2002, *G. Corriol* (holotype GC02083008 in BBF, ITS sequence GenBank MW934560, MycoBank MB 839223).

Additional materials examined. Italy, Trentino-Alto Adige, Passo dello Stelvio/Stilfser Joch, near Berghotel Franzenshöhe, alpine grassland with *Dryas* and *Salix* spp., 2200 m a.s.l., 30 July 2018, *B. Dima*, DB-2018-07-30-1 (ITS sequence GenBank MW934561).

Notes — *Entoloma cyaneobasale* falls within the /Mediterraneense clade (see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240). In the field, these collections were readily identified as *E. glaucobasis* on account of the bicoloured stipe. However, the spores are smaller, the stipe is more polished, and it has a lamella edge of the serrulatum-type with brown pigment. *Entoloma glaucobasis* is also phylogenetically distant, and belongs to the /Griseocyaneum clade.

Colour illustrations. France, Pyrenee-Atlantiques, Eaux-Bonns, cirque du Plaa Ségouné à Gourette, 2400 m a.s.l., calcareous alpine snowbeds on the northern slope of Pyrenees. Spores; cheilocystidia; pileipellis; stipitipellis (all from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

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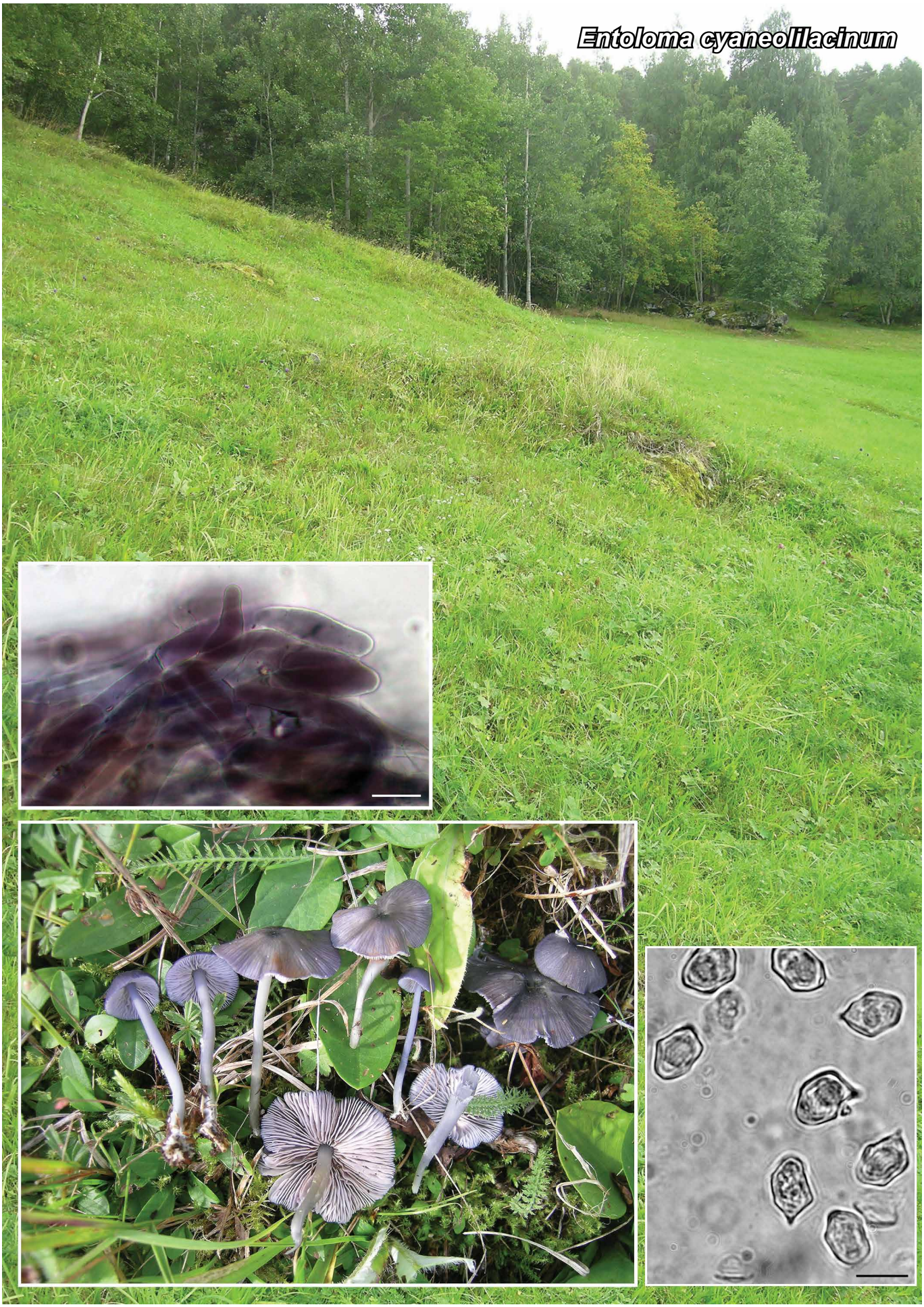
Entoloma cyaneolilacinum

Fungal Planet 1243 – 13 July 2021

Entoloma cyaneolilacinum Noordel., J.B. Jordal, Brandrud & Dima, *sp. nov*.

Etymology. The epithet refers to the colours of the basidiocarps, from '*cyaneus'*, Greek, – blue, and '*lilacinus'* – lilac.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 10–25 mm, conico-convex or campanulate-conical, slightly expanding, finally plano-convex, with deflexed then straight margin, not distinctly hygrophanous, deep blue then paler lilac-blue with a slightly darker spot at centre, deeply translucently striate, at first finely radially fibrillose to faintly tomentose, breaking up in small squamules in central part, radially fibrillose to almost smooth towards margin. *Lamellae* moderately distant, deeply emarginate, ventricose, white or with a faint bluish tinge, contrasting with blue pileus and stipe, with entire, concolorous edge. *Stipe* 30–50 × 2–3 mm, cylindrical, deep blue then lilac-blue, concolorous with margin of pileus or paler, glabrous, smooth, polished, with some white mycelium at base, once observed with yellow (discoloured?) mycelium. *Smell* and *taste* not indicated. *Spores* (7.5–)8.0–10.0(–11.0) × 6.0–8.5 µm, av. 8.5–9.5 × 6.5–8.0 µm, Q = 1.2–1.6, Qav = 1.4, heterodiametrical, 5–7-angled in side-view. *Basidia* 30–50 × 8–12 µm, 4-spored, clampless. *Lamella* edge fertile. *Cystidia* absent. *Hymenophoral trama* regular, made up of inflated elements, up to 20 µm wide. *Pileipellis* a transition between a cutis and a trichoderm, made up of clavate terminal elements, 22–75 × 10–25 µm with brownish intracellular pigment. *Brilliant granules* present, but not abundant. *Clamp connections* absent.

Habitat & Distribution — In semi-natural grasslands and in deciduous woodlands with *Betula*, *Corylus*, *Fraxinus* and *Quercus*. Verified with sequenced collections from Norway and The Netherlands, also reported from Germany.

Typus. Norway, Møre og Romsdal, Stranda, Liabygda, Ansok, N62.3137° E7.0236° (± 7 m), 310 m a.s.l., seminatural grassland (meadow), on the ground, 2 Sept. 2009, *J.B. Jordal*, JBJ09-E02 (holotype O-F-252009, ITS and LSU sequences GenBank MW934582 and MW934252, MycoBank MB 839224).

Additional materials examined. Norway, Møre og Romsdal, Sunndal, Jordalsgrenda, Kalvhusvøttu, 60 m a.s.l., seminatural grassland (meadow), 14 Sept. 2004, *J.B. Jordal*, *M.E. Noordeloos* & *G. Gulden* (O-F-177981, ITS sequence GenBank MW934584); ibid., 20 Sept. 2019, JBJ19-049 (O-F-256792, ITS sequence GenBank MW934586); Rogaland, Stavanger, Rennesøy, Askje, V-side, c. 60 m a.s.l., in semi-natural pasture, 3 Oct. 2006, *J.I. Johnsen* & *J.B. Jordal* (O-F-361225, ITS sequence GenBank MW934587); Vindafjord, Alnåsen west, 129 m a.s.l., west-faced deciduous forest, 5 Sept. 2008, *J.B. Jordal*, JBJ08-E02 (O-F-252007, ITS sequence GenBank MW934585). – The Netherlands, Prov. Utrecht, Soesterberg, former airfield, 30 Sept. 2019, *M.E. Noordeloos*, *P.J. Keizer* & *J. v. Dongen* (L0607898, ITS sequence GenBank MW934583).

Notes — The delicate lilac-blue colour of the basidiocarps as well as the small spores and fertile lamella edge are distinctive for *E. cyaneolilacinum*. It was treated as *E. lepiotosme* in Noordeloos (2004). However, there are considerable discrepancies with the protologue, describing a species with a blackish brown, virgate pileus, reminiscent of a species of *Inocybe*, a fibrillose stipe surface, a strong smell like that of *Lepiota cristata*, and larger spores. The lectotype of *Rhodophyllus lepiotosmus* failed for DNA sequencing. Considering the conflict with the protologue and the lack of molecular data, it was decided to describe the present taxon here as a species in its own right. Morphologically, *E. cyaneolilacinum* resembles *E. violaceoviride*, which has a sterile, brown pigmented lamella edge and often some greenish tinges in the basidiocarp, and has a distant phylogenetic position. *Entoloma cruentatum*, also phylogenetically distant (see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240), has similar spores and fertile lamella edge, but often turns orange-yellow when bruised at the base of the stipe.

Colour illustrations. Norway, Møre og Romsdal, Stranda, Liabygda, Ansok, seminatural grassland, type locality. Spores, cheilocystidia, pileipellis, stipitipellis (all from holotype); Basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

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Entoloma isborscanum

Fungal Planet 1244 – 13 July 2021

Entoloma isborscanum O.V. Morozova, Noordel., Dima, G.M. Jansen & Reschke, *sp. nov*.

Etymology. Named after Izborsk (*Isborscum*, Lat.), a village in the Pskov Region of Russia, one of the oldest Russian towns, type locality and *Entoloma* hot spot.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 15–35 mm diam, hemispherical, with slightly depressed centre, then expanding to convex or plano-convex with slightly umbilicate centre, with deflexed then straight margin, not hygrophanous or in the pileus margin only, not translucently striate or up to 1/3 of radius, radially fibrillose-squamulose all over, more densely in the centre, white background is visible between fibrils, brownish yellow, yellowish brown or light brown, darker in centre (5C5–8, 5D5–8; Kornerup & Wanscher 1978), in old and drying specimens radially cracking, showing white underground. *Lamellae* moderately distant, adnate-emarginate, decurrent with short tooth, whitish, pale or greyish, becoming pinkish grey, with irregular, concolorous, whitish or brownish edge. *Stipe* 20–70 × 2–3 mm, cylindrical or slightly broadened towards the base, minutely distinctly longitudinally striate, completely greyish blue (20B3–4, 20C3–4), greyish brown, bluish on the base only or completely yellow-brown, concolorous with the pileus (5C5–8, 5D5–8), white tomentose at the base. *Context* white, brownish under the surface. *Smell* pleasantly sweet or indistinct, *taste* unpleasant, nitrous. *Basidiospores* 8–12 × 6–7.5 µm, av. 9–10.5 × 6–7.5 µm, Q = (1.15–)1.3–1.7, Qav = 1.35–1.5, heterodiametrical, with 5–7 distinct angles in side-view, sometimes with some large spores up to 14 × 7 µm with indistinct angles from 1–2-spored basidia. *Basidia* 32–35.5 × 9.5–10.5 µm, 1–4-spored, narrowly clavate to clavate, sometimes with broadened walls, clampless. *Lamella edge* sterile of the 'serrulatum'-type. *Cheilocystidia* 40–90 × 9–25 µm, as terminal elements of the hyphae arising from the subhymenium, clavate, broadly clavate or cylindrical, sometimes septate, sometimes with intracellular pigment, brownish in KOH. *Hymenophoral trama* regular, 4–20 µm wide, cylindrical hyphae. *Pileipellis* a cutis with transition to a trichoderm of cylindrical hyphae, 5–12 µm wide with cylindrical or inflated to ellipsoid or ovoid terminal elements, 48–105 × 12–32 µm, and intracellular, sometimes agglutinate pigment, brown in KOH. *Caulocystidia* as ascending bundled, cylindrical to slightly inflated terminal elements of the stipitipellis hyphae. *Clamp connections* absent.

Habit & Distribution — In small groups on soil on calcareous grasslands. Known from Denmark, Germany, the Netherlands, and Russia (European part).

Colour illustrations. Russia, Pskov region, Pechorsky district, Izborsk village, foot of the Truvor hillfort, calcareous grassland (type locality). Spores, cheilocystidia, pileipellis, caulocystidia (all from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

Typus. Russia, Pskov region, Pechorsky district, Izborsk village, foot of the Truvor hillfort, on calcareous grassland, N57.717702° E27.854764°, 24 Aug. 2011, *O. Morozova* (holotype LE 302088, ITS and LSU sequences GenBank MW934566 and MW934253, MycoBank MB 839225).

Additional materials examined. Denmark, Jylland, Begtrup Røn, 26 Aug. 2011, *R. Ejrnæs* (C, DMS167798, ITS sequence GenBank MW934570). – Germany, Baden-Württemberg, Heimberg, near Schloßböckelheim, 27 Oct. 2017, *W. Prüfert* (M-0141378, ITS sequence GenBank MW934565). – Russia, Pskov region, Pechorsky district, Izborsk village, foot of the Truvor hillfort, on calcareous grassland, 24 Aug. 2011, *O. Morozova*, LE 312486, ITS sequence GenBank MW934564; ibid., 12 Sept. 2020, *O. Morozova*, LE 312679, ITS sequence GenBank MW934569. – The Netherlands, Prov. Limburg, Nijswiller-Noord, 14 Aug. 2019, *F.* & *R. Salzmann*, L0607743, ITS sequence GenBank MW934568; ibid., 21 Aug. 2019, L0607927, ITS sequence GenBank MW934567; ibid., 2 Oct. 2019, L0607719, ITS sequence GenBank MW934563; ibid., 16 Oct. 2019, L0607718, ITS sequence GenBank MW934562.

Notes — *Entoloma isborscanum* is characterised by a squamulose yellowish brown pileus, a bluish or brownish blue, longitudinally striate stipe, rather small spores with distinct 5–7 angles, and a sterile lamella edge consisting of large clavate cheilocystidia arising from the subhymenium. Superficially it resembles *E. griseocyaneum*, which differs by the absence of cheilocystidia and smaller spores, or *E. glaucobasis*, which possesses larger, almost nodulose spores (Noordeloos 1992). The holotype specimen was published in Morozova et al. (2015) as *E. exile*, but this species is sufficiently more slender with distinct greenish glaucous tinges in the stipe. Also see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240.

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Entoloma pseudocruentatum
1 cm

Fungal Planet 1245 – 13 July 2021

Entoloma pseudocruentatum Noordel., Brandrud, G.M. Jansen, Dima & Læssøe, *sp. nov.*

Etymology. The epithet refers to the erroneously applied name *Entoloma cruentatum* for this species.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata small to medium-sized, collybioid. *Pileus* 15–25 mm diam, convex to flattened-convex, later, when maturing, from flattened to somewhat depressed in the centre, never umbonate; slate blue grey with slight violaceous tinge, deeply translucently striate, innately radially fibrillose, not squamulose at centre, margin somewhat crenulate. *Lamellae* adnate, bluish grey when young. *Stipe* 30–40 × 2–4 mm, similar in colour to the pileus or paler, polished, with white to yellow or orange-yellow basal tomentum. *Context* thin, pale grey bluish. *Smell* indistinct. *Taste* not known. *Basidiospores* 8.5–10.0 × 6.0–7.5 µm, av. 9.1 × 6.8 µm, heterodiametrical, with 5–7 angles in side-view. *Basidia* 28–34 × 9.5–12.5 µm, clavate, 4-spored, clampless. *Lamella edge* fertile, cheilocystidia absent. *Pileipellis* a cutis of cylindrical hyphae, 3.5–9 µm wide, with a transition to a trichoderm at centre of clavate elements, 12–30 µm wide. *Pigment* blue to grey-blue, clotted granular and diffusely intracellular. Stipitipellis cylindrical hyphen 3.5–8.5 µm wide with grey blue clotted granular and diffuse intracellular pigment. *Clamp connections* absent in all tissues.

Habitat & Distribution — Saprotrophic, in groups on nutrient poor (acid) soil, in a regularly mown, species-rich grassland of an old airbase (holotype) and on rich grassland (Denmark), herb/grass-rich *Fraxinus-Quercus* forest (Norway).

Typus. The Netherlands, Prov. Utrecht, Soesterberg, former airfield, 30 Sept. 2019, *M.E. Noordeloos*, *P.J. Keizer* & *J.V. Dongen* (holotype L0607915, ITS and LSU sequences GenBank MW934588 and MW934254, MycoBank MB 839227).

Additional materials examined. Denmark, Favrholt, in semi-natural grassland, on shady slope with *Plantago lanceolata* and *Succisa pratensis*, 19 Aug. 2008, *T. Læssøe*, TL-13373 (C, DMS-730741; ITS sequence GenBank MW934590). – Norway, Telemark, Drangedal, Malfjell S, 31 Aug. 2015, in rich, somewhat calcareous grass-herb vegetation in open *Fraxinus-Quercus* forest, *T.E. Brandrud*, TEB 188-15 (O-F-251951; ITS sequence GenBank MW934589).

Notes — *Entoloma pseudocruentatum* was interpreted as *E. cruentatum* by Noordeloos (1987, 2004), as similar to *E. chalybaeum*, with a fertile lamella edge, a glaucous-blue stipe, with the base frequently discolouring yellowish or pale orange. However, there are now reasonable doubts as whether the original diagnosis of Quélet (1886) actually refers to the same species. *Entoloma cruentatum* is described as a species with a more or less conical to umbonate, lilac-blue pileus, and a stipe with glaucous bluish stipe with a strong reddening at base. Kühner & Romagnesi (1953) considered it a dubious species, probably in subg. *Nolanea*. Another option could be that *E. cruentatum* represents a form of *E. exile*, a species with rather variable pileus shape and colour, and often a reddening stipe base. The concept of Noordeloos (1984) was based on a collection from Scotland, which has many characters in common with the species described here. For this reason, we describe *Entoloma cruentatum* sensu Noordeloos (1984) as a new species. Also see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240.

Colour illustrations. The Netherlands, Prov. Utrecht, Soesterberg, former airfield (type locality, photo credit P.J. Keizer). Basidiomata (left from holotype, right from TEB188-15); spores, cheilocystidia, pileipellis, stipitipellis (all from holotype). Scale bars = 1 cm (habit), 10 µm (spores), 5 µm (pileipellis and stipitipellis).

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Entoloma pudens
10 mm

Fungal Planet 1246 – 13 July 2021

Entoloma pudens Noordel., G.M. Jansen, M.v.d. Vegte & Dima, *sp. nov*.

Etymology. The epithet refers to the modest size of the species.

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata small-sized, omphalioid. *Pileus* 12–18 mm diam, convex with straight or slightly crenulate margin, umbilicate, hygrophanous, deeply translucently striate up to centre, dark brown with obscure sepia-brown centre, finely scaly-virgate, particularly at central part. *Lamellae* distant, L = 12, l = 1–3, arcuate-deeply decurrent, pale brown with pinkish hue, with concolorous, entire edge. *Stipe* 35–30 × 1–1.5 mm, slightly broadened towards apex, pale horn brown, glabrous, polished. *Smell* and *taste* indistinct. Spores 9.5–13 × 6.5–8.5 µm, av. 11.3–11.5 × 7.6–8.2 µm, Q = 1.2–1.7, Qav 1.4–1.5, heterodiametrical, rather regularly 5–7-angled. *Basidia* 28–53 × 11–11.5 µm, 4-spored, clampless. *Lamella* edge fertile, *cystidia* absent. *Pileipellis* a cutis of broad hyphae with transitions to a trichoderm, made up of clavate elements, up to 25 µm wide, with both intracellular and incrusting pigment. *Clamp connections* absent.

Habitat & Distribution — Gregarious on plant debris, amongst grasses and *Sphagnum* in unfertilized hayfield. Known only from the type locality in The Netherlands.

Typus. The Netherlands, Prov. Gelderland, Groesbeek, de Bruuk, 17 Sept. 2018, *Marjon v.d. Vegte* & *G. Jansen* C173-6268 (holotype L0608054, ITS and LSU sequences GenBank MW934594, MycoBank MB 839226).

Additional material examined. The Netherlands, Prov. Gelderland, Groesbeek, de Bruuk, 2 Sept. 2018, *G. Jansen*, C173-6195 (L0607607, not sequenced).

Notes — This small omphalioid species was initially identified as *Entoloma nigellum* sensu Orton (1960), a concept accepted by Noordeloos (2004). The Dutch specimens are very likely the same as Orton's with their dark, translucently striate pileus, distant, decurrent lamellae, polished stipe, large spores and clampless hyphae. However, when comparing the original diagnosis of this poorly known species it became clear that Quélet's *Eccilia nigella* (Quélet 1886) strongly deviates in habit, in having a not translucent, almost black pileus, and a dark stipe, which sometimes has a bluish tinge. It is therefore rather questionable whether we can adopt the epithet '*nigellum'* for our taxon. Quélet's species could well stand for another, dark coloured species in the /Rusticoides clade and type material is not existent. For the time being, it therefore seems prudent to consider *Eccilia nigellum* as a *nomen dubium*. *Entoloma subpusillum* is similar, differing in having a non-translucent, not glabrous but uneven-rugulose pileal surface. Two other apparently similar species, viz., *E. pseudonigellum* and *E. rickenelliformis*, differ both in having a dark, not translucent pileus, differently sized and shaped spores, and abundant clamp-connections. The type sequence of *E. pseudonigellum* cluster distantly, in the /Undati clade, while DNA sequencing of the type of *E. rickenelliformis* proved unsuccessful. Several questions therefore remain unanswered in this group. *Entoloma pudens* is described as new, based on well-annotated material and molecular sequence data (see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240).

Colour illustrations. The Netherlands, Groesbeek, de Bruuk, unfertilised hayfield, type locality. Spores, cheilocystidia, pileipellis, stipitipellis (all from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

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Entoloma subcoracis

Fungal Planet 1247 – 13 July 2021

Entoloma subcoracis O.V. Morozova, Noordel. & Dima, *sp. nov*.

Etymology. The epithet refers to the resemblance of *Entoloma coracis* due to its black colour, like a raven (*Corvus corax*).

Classification — *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata medium-sized, collybioid. *Pileus* 10–35 mm diam, hemispherical or abruptly conical with central depression, hardly expanding, with deflexed margin, not hygrophanous, translucently striate almost up to the centre, initially uniformly blackish blue (21F5–8; Kornerup & Wanscher 1978), discolouring to bluish grey (21F3–4), minutely radially fibrillose-squamulose all over. *Lamellae* moderately distant, adnate-emarginate, segmentiform to narrowly ventricose, white, contrasting with the pileus surface, becoming pink, with irregular, serrulate concolorous edge. *Stipe* 30–70 × 1.5–3 mm, cylindrical, sometimes twisted, slightly longitudinally striate, minutely squamulose, especially in the upper part, concolorous with pileus or a little paler (up to 21F3–4), white tomentose at base. *Context* white, greyish under the surface. Smell indistinct, taste not reported. *Basidiospores* 9.5–11 × 6.5–8 µm, av. 10.0 × 7.0 µm, Q = 1.3–1.5, Qav = 1.4; heterodiametrical, with 5–7 angles in side-view, relatively simple. *Basidia* 32–38 × 10–12 µm, 4-spored, narrowly clavate to clavate, clampless. *Lamella edge* sterile. *Cheilocystidia* 37–80 × 8.5–13.5 µm, composed of 3–4 elements, terminal cells mostly lageniform or fusiform, sometimes cylindrical or narrowly clavate, colourless. *Pileipellis* cutis with transition to a trichoderm of cylindrical to slightly inflated hyphae 8–20 µm wide with inflated terminal elements and dark intracellular pigment, brownish in KOH. *Caulocystidia* 35–100 × 5.5–10 µm, as chains of cylindrical or inflated elements, usually with tapered terminal cells. Brilliant granules present. *Clamp connections* absent.

Habitat & Distribution — In small groups on soil in subalpine grasslands. Known from Russia (Caucasus).

Typus. Russia, Karachaevo-Cherkesia Republic, Teberda Nature Reserve, Arkhyz site, near the waterfall, N43.558889° E41.301389°, alt. 1 390 m a.s.l., 17 Aug. 2009, *O. Morozova* (holotype LE312483, ITS and LSU sequences GenBank MW934593 and MW934255, MycoBank MB 839228).

Notes — *Entoloma subcoracis* belongs to the form-group of *E. corvinum* s. auct. including taxa such as *E. coracis* (also described in present paper) and *E. porphyrogriseum* characterised by blackish blue basidiocarps. *Entoloma subcoracis* is characterised by the voluminous cheilocystidia, and fusiform, septate caulocystidia. The characteristic large cystidia are shared with the North American *E. subcorvinum* (Hesler 1967, Noordeloos 1988). Both species seem, however, to be geographically separated. Unfortunately, no DNA sequence data are available for the holotype of *E. subcorvinum*. Also see the phylogenetic tree for *E. ammophilum* in Supplementary material FP1240.

Colour illustrations. Russia, Karachaevo-Cherkesia Republic, Teberda Nature Reserve, Arkhyz site, near the waterfall, type locality (photo credit E. Malysheva). Spores, cheilocystidia, pileipellis, caulocystidia (all from holotype); basidiomata *in situ* (holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

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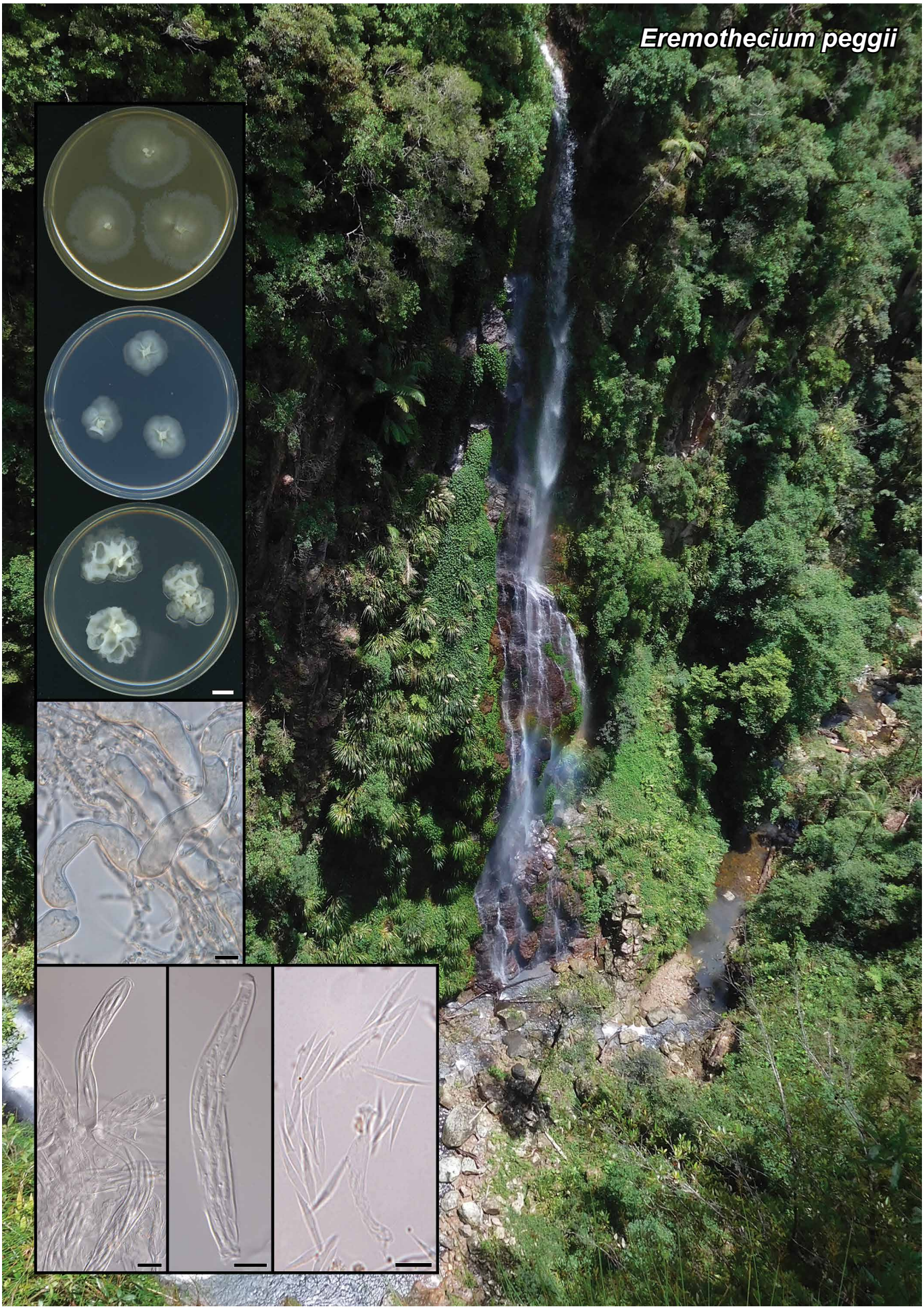

Eremothecium peggii

Fungal Planet 1248 – 13 July 2021

Eremothecium peggii R.G. Shivas, Marney, Cunningt. & Y.P. Tan, *sp. nov.*

Etymology. Named after Kenneth G. Pegg, an eminent Australian plant pathologist, from whose garden the fungus was first collected.

Classification — *Eremotheciaceae*, *Saccharomycetales*, *Saccharomycetes*.

Mycelium composed of filamentous hyphae, budding cells lacking. *Hyphae* coenocytic without true septa, undulate or straight walls, with abundant localized dense cytoplasmic regions, 2–9 µm wide, branches often at right angles, hyaline. *Asci* form directly from hyphae, mostly intercalary and aligned in chains, occasionally terminal or lateral, with a narrow base 3–5 µm wide, when immature cytoplasmic contents distinctively concave at base and separate from hyphal cytoplasm, irregularly sinuous to clavate-cylindrical, rounded at apex, hyaline, (20–)40–75(–120) × 8–18 µm, with 16 or 32 ascospores, splits irregularly. *Ascospores* acicular, straight or slightly curved, 15–21 × 1.5–2 µm, hyaline, widest at a narrow faint hyaline band near the middle, narrow to a truncate base less than 0.5 µm wide, arranged in the ascus in two (or four) opposed bundles of eight spores with apices pointed at the poles, germinate by a perpendicular or oblique germ tube at swollen mid-point.

Culture characteristics — On malt yeast extract peptone glucose agar after 4 wk in the dark at 25 °C, colonies 2–3.5 cm diam, flat, dull, dry, translucent, margin filamentous and irregular, raised, tenacious in their consistency.

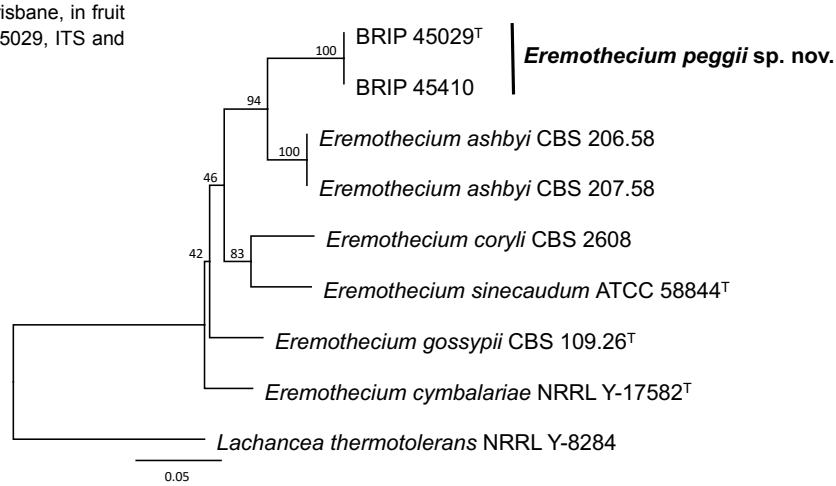
Typus. Australia, Queensland, Brisbane, in fruit of *Citrus australis*, 12 July 2004, *K.G. Pegg* (holotype BRIP 45029, culture ex-type BRIP 45029, ITS and LSU sequences GenBank MW442983 and MW442985, MycoBank MB 838410).

Additional material examined. Australia, Queensland, Brisbane, in fruit of *Citrus australis*, 26 July 2004, *K.G. Pegg* (culture BRIP 45029, ITS and LSU sequences GenBank MW442982 and MW442984).

Colour illustrations. Sub-tropical rainforest, Lamington National Park. Colonies of *E. peggii* on V8 agar (top), potato dextrose agar (middle) and malt yeast extract peptone glucose agar (bottom) after 4 wk in the dark at 25 °C; hyphae differentiating into asci, asci; ascus, ascospores. Scale bars = 1 cm (top), other = 10 µm.

Notes — The *Eremotheciaceae* is a monophyletic group of species that have needle-shaped ascospores (Kurtzman 1995). *Eremothecium* contains five species, *E. ashbyi*, *E. coryli*, *E. cymbalariae*, *E. gossypii* and *E. sinecaudum*, that are characterised by acicular ascospores (https://theyeasts.org, Kurtzman & Robnett 2003). One of these, *E. coryli*, has been associated with fruit dry rot in cultivated and indigenous *Citrus* in Australia (Shivas et al. 2005). During that study, *Eremothecium peggii* was isolated from fruit with dry rot of *Citrus australis* (Dooja, round lime), which is native to subtropical rainforest in New South Wales and Queensland, Australia. All species of *Eremothecium* are considered as plant pathogens, although the pathogenicity of *E. peggii* as the cause of fruit dry rot has not been demonstrated.

Based on a BLASTn search of NCBI GenBank nucleotide database, the closest hit against **LSU** sequences ex-type specimens were *E. cymbalariae* (strain NRRL Y-17582, GenBank NR_042628.1, Identities 854/884 (97 %), Gaps = 4 (0 %)); *E. sinecaudum* (strain ATCC 58844, GenBank XR_001930265.1, Identities 867/898 (97 %), Gaps = 5/898 (0 %)); and *E. gossypii* (strain CBS 109.26, GenBank NG_063967.1, Identities 863/899 (96 %), Gaps = 5/899 (0 %)). The closest hit against **ITS** sequences ex-type specimens was *Kluyveromyces aestuarii* (ex-type strain CBS 4438; GenBank NR_165976.1; Identities 208/218 (95 %), Gaps = 1 (0 %)).



Phylogenetic tree of *Eremothecium* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS and LSU). Analyses were performed on the Geneious v. 11.1.2 platform (Biomatters Ltd.) using RAxML v. 8.2.11 (Stamatakis 2014) and MrBayes v. 3.2.6 (Ronquist & Huelsenbeck 2003), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the nodes (bs/pp). *Saccothecium rubi* and *S. sepincola* were used as outgroups. Novel taxa are indicated in **bold**. Ex-type strains are marked with T.

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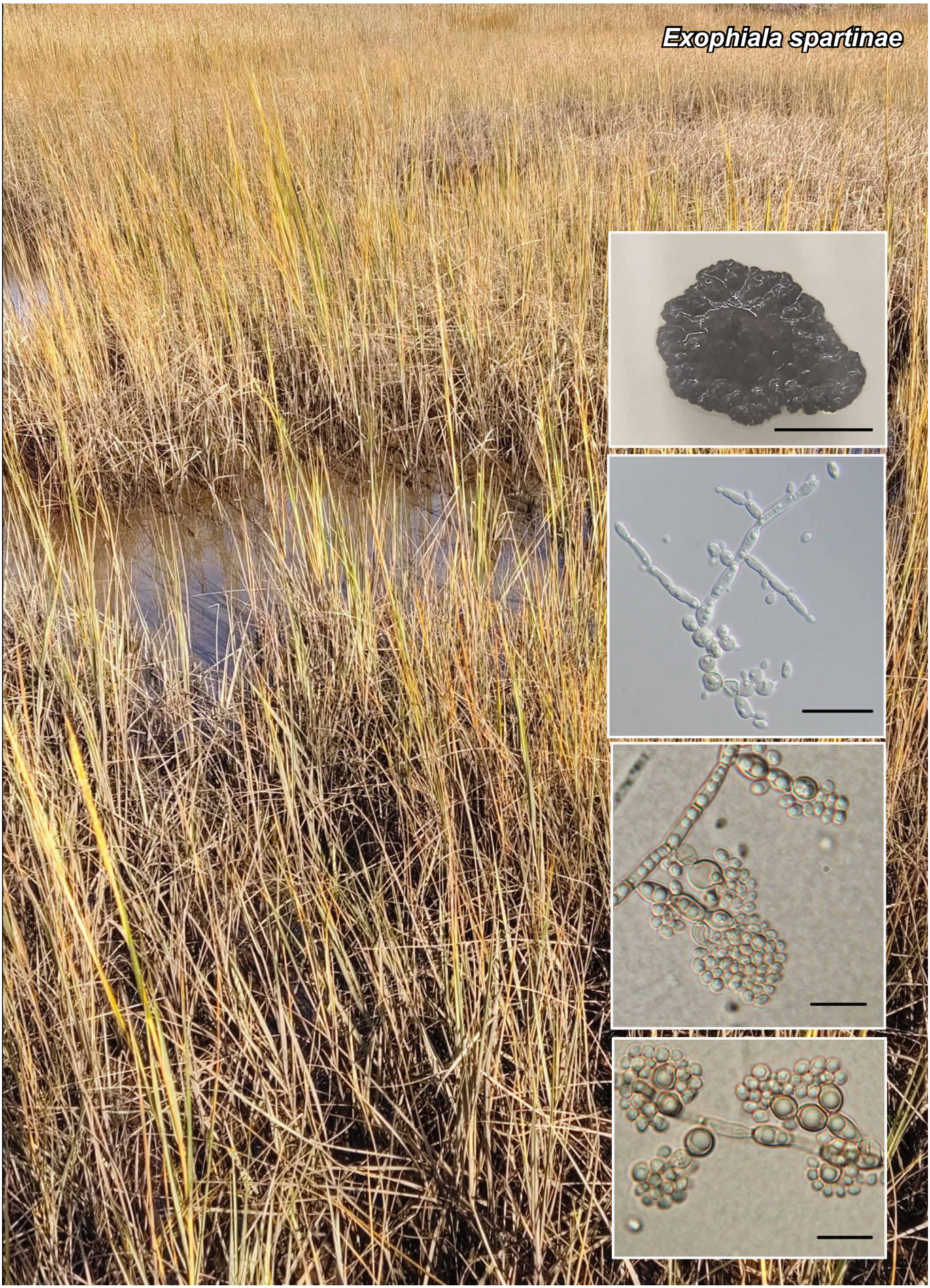

Exophiala spartinae

Fungal Planet 1249 – 13 July 2021

Exophiala spartinae Raudabaugh, Gunsch, & A.N. Mill., *sp. nov.*

Etymology. Named after the host species, *Spartina alterniflora*.

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

Mycelium on agar black, slimy texture containing pigmented yeast cells and pseudomycelium, large non-budding yeast cells purplish black, 4–4.5 × 6–6.5 µm, pseudomycelium purplish black, cells 2–3 × 10–12 µm. Mycelium submerged in agar pale brown, smooth, branched, septate, 3–4 µm wide hyphae. *Conidiophores* purplish brown, branched or unbranched, typically one or two subglobose to broadly ellipsoidal basal cells 3.5–5 × 4.5–7 µm, guttulate. *Conidiogenous cells* intercalary or terminal, purplish brown, broadly ellipsoidal to obpyriform, 3.5–5 × 4.5–7 µm, polyblastic. *Conidia* smooth, ellipsoidal, aseptate, purplish brown, 2–3 × 3–3.5 µm.

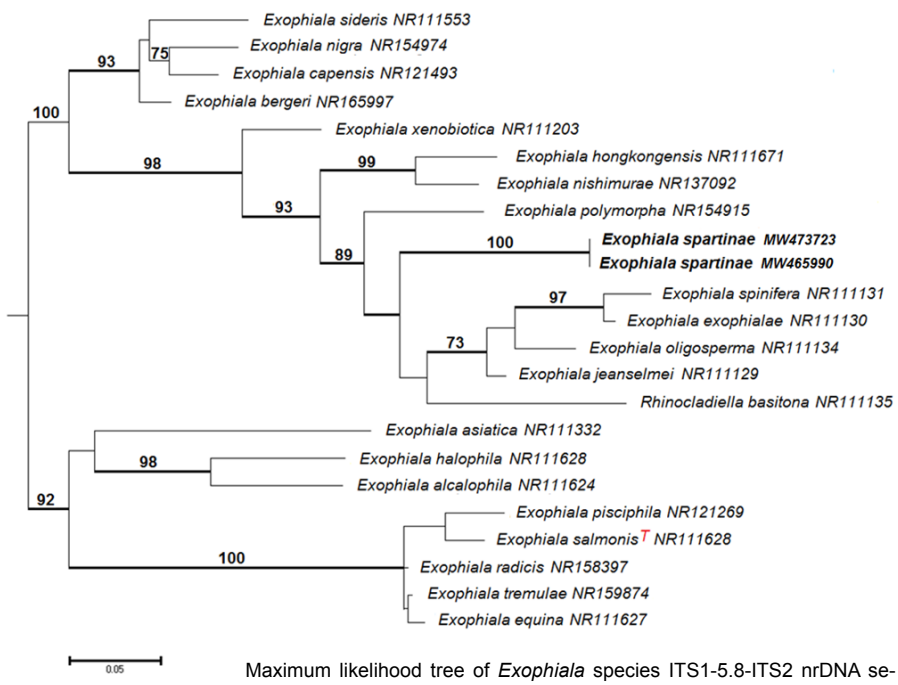
Culture characteristics — Colonies on malt extract agar and potato dextrose agar umbonate on surface, black, dry to moist, margin undulate, reaching 8–15 mm diam after 10 d at 20 °C, reverse purplish black without diffusible pigment.

Habitat & Distribution — Isolated from surface sterilised roots of *Spartina alterniflora* from saltwater marsh. Known only from Virginia, USA.

Typus. USA, Virginia, Chesapeake County, from sterilised *Spartina alterniflora* (*Poaceae*) root tissue in saltwater marsh, 36.7926, -76.2898, c. 1 m a.s.l., 13 Nov. 2019, *D. Raudabaugh*, B6-6-NF (holotype ILLS00121429, culture ex-type B6-6-NF-C = CBS 147266, ITS sequence GenBank MW473723, MycoBank MB 838321).

Additional material examined. USA, Virginia, Chesapeake County, from sterilized *S. alterniflora* root tissue in saltwater marsh, 36.7928, -76.2898, c. 1 m a.s.l., 13 Nov. 2019, *D. Raudabaugh*, B4-7-NF (ILLS00121430, ITS sequence GenBank MW465990).

Notes — *Exophiala spartinae* was isolated using nitrogen free medium (Kurtzman et al. 2011) from two separate *S. alterniflora* plants. Phylogenetic analyses of ITS nrDNA sequences employing Maximum Likelihood and Bayesian criteria and implementing Gblocks suggest that the closest taxa to *E. spartinae* are *E. oligosperma*, *E. jenselmei*, *E. spinifera*, *E. exophialae*, and *Rhinocladiella basitona*. This species is distinguished by its subglobose to broadly ellipsoidal conidiophore cells, which consist of one to three cells with a terminal conidiogenous cell. *Exophiala spinifera* (NR111131) was the closest nrITS BLASTn match (90 %) against the entire *E. spartinae* ITS sequence.



Maximum likelihood tree of *Exophiala* species ITS1-5.8-ITS2 nrDNA sequences generated using RAxML v. 8.2.10 (Stamatakis 2014) on the CIPRES v. 3.3 portal (Miller et al. 2010). Bootstrap support values ≥ 70 % are shown above branches. Thickened branches indicate Bayesian posterior probabilities ≥ 95 %. *Exophiala spartinae* is identified in **bold**. The type species of *Exophiala* is *E. salmonis* and identified by ᵀ. All *Exophiala* sequences obtained from type specimens.

Colour illustrations. *Spartina alterniflora* growing in a salt-water marsh in Virginia, USA. Colony growing on PDA; yeast cells and pseudomycelium; mycelium with lipid guttules, conidiophores, conidiogenous cells, and conidia; branched conidiophore. Scale bars = 5 mm (culture), 20 µm (pseudomycelium), 10 µm (conidiophores, conidiogenous cells, conidia).

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Extremopsis radicicola

Fungal Planet 1250 – 13 July 2021

Extremopsis G. Delgado & Maciá-Vicente, *gen. nov.*

Etymology. Named after its close phylogenetic relationship with the genus *Extremus*.

Classification — *Extremaceae*, *Mycosphaerellales*, *Dothideomycetes*.

Mycelium colonising root-associated soil and isolated on culture media from surface-sterilised roots of living plants. Chlamydospores present, terminal or intercalary, solitary, in chains or forming clusters, variable in shape, 0–1-septate.

Type species. Extremopsis radicicola G. Delgado & Maciá-Vicente MycoBank MB 838931.

Extremopsis radicicola G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology. Name refers to the roots of the host plant from which the fungus was isolated.

Mycelium composed of hyaline, subhyaline to pale brown, branched, septate hyphae, 2–3.5 µm wide. *Chlamydospores* present, abundant, terminal or intercalary, solitary, in short chains of up to 8 or forming more or less dense clusters, globose, subglobose, ellipsoidal, pyriform or elongated, subhyaline to pale brown, smooth, thin-walled that may become brown, thick-walled, 0–1-septate and smooth to verruculose, dark brown when forming large clusters, (3–)4–11(–13) × 2.5–8(–10) µm.

Culture characteristics — Colonies on malt extract agar (MEA) slow growing, reaching 9–13 mm diam after 3 wk at 25 °C, velvety, grey to dark grey or blackish grey, raised 1–2 mm at the centre, with or without a concentric ring around the raised centre, margin entire, reverse black, no exudates. On potato dextrose agar (PDA) reaching 10–14 mm diam, dark grey olivaceous, slightly raised at the centre, margin slightly diffuse, reverse black olivaceous. On modified cellulose agar (MCA) very slow growing, reaching 6–8 mm diam, dark grey, grey at the centre, flat, margin irregular, diffuse, reverse black. Cultures sterile, chlamydospores abundant.

Typus. Spain, Ciudad Real, Cabañeros National Park, from root-associated soil in a wet heathland ('trampal'), N39°20'58.5" W4°21'38.6", 725 m a.s.l., isolated from surface-sterilised, asymptomatic roots of an *Arabidopsis thaliana* plant inoculated with soil and grown under controlled conditions, 19 Apr. 2018, coll. *J.G. Maciá-Vicente*, isol. 20 June 2018, *J.G. Maciá-Vicente*, P6446 (holotype stored in a metabolically inactive state CBS 147117, culture ex-type CBS 147117, ITS and LSU sequences GenBank MN310191 and MN308483, MycoBank MB 838946).

Notes — The family *Extremaceae* includes fungi that are ecologically highly diverse ranging from extremophilic, rock inhabiting and acidophilic members such as *Extremus*, the generic type, to lichenicolous, epiphyllous, endophytic, saprobic or plant pathogenic genera (Quaedvlieg et al. 2014). The new genus *Extremopsis* is introduced to accommodate sterile strains of a root endophyte isolated from surface-sterilised, asymptomatic roots of plants used as bait inoculated with root-associated soil. The three strains of *E. radicicola* did not sporulate in any of the different culture media used including MEA, PDA, MCA or Water Agar supplemented with wooden toothpicks, but they produced abundant chlamydospores in all media. Their ITS and partial LSU sequences were nearly identical except for a single gap at position 128 of alignment in the case of the ITS of both CBS 147117 and P6514, and two bp differences in the LSU of the latter. Phylogenetically, they form a strongly supported monophyletic group in *Extremaceae* sister to the genus *Extremus* but with low support. Moreover, although originally identified as '*Devriesia*' sp., they group distant from *Devriesia* s.str. in *Teratosphaeriaceae* represented by *D. staurophora*, the generic type (Meng et al. 2017). Interestingly, two other strains also named '*Devriesia*' sp., NG_p52, isolated during a study of gene expression of fungal nitrate reductases in agricultural soils from Austria (Gorfer et al. 2011); and MI63, isolated from soil in Germany, grouped within the *Extremopsis* clade and seem conspecific with *E. radicicola*, expanding the known distribution of the genus from southern Spain to other localities across Europe.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of *Extremopsis radicicola* (CBS 147117) using the **ITS** sequence are '*Devriesia*' sp. NG_p52 (GenBank HQ115717.1; Identities = 232/232 (100 %), no gaps), '*Devriesia*' sp. MI63 (GenBank MW268825.1; Identities = 230/232 (99 %), no gaps) and a melanised limestone ascomycete CR-2004 TRN80 (GenBank AY559340.1; Identities = 222/232 (96 %), two gaps (0 %)). The closest hits using the **LSU** sequence are '*Devriesia*' sp. NG_p52 (GenBank: HQ115717.1; Identities = 488/490 (99 %), no gaps), *Extremus adstrictus* (GenBank KF310022.1; Identities = 527/539 (98 %), two gaps (0 %)) and '*Devriesia*' sp. OTU56 TS-2013 (GenBank AB808449.1; Identities = 521/535 (97 %), two gaps (0 %)).

Colour illustrations. Wet heathland ('trampal') in the Cabañeros National Park, Ciudad Real, Spain. Colonies on MEA; chlamydospores solitary or in chains; cluster of chlamydospores; mycelium. Scale bars = 10 µm (chlamydospores), 5 µm (mycelium).

Supplementary material

FP1250-1 Additional materials examined.

FP1250-2 Maximum likelihood (ML) phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences of strains of *Extremopsis* and related genera showing their placement within *Extremaceae*. The new genus is enclosed in a coloured box and strains newly obtained in this study are in **bold**. ML and Bayesian analyses were performed using RAxML v. 8.2.12 (Stamatakis 2014) and MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003), respectively, on the CIPRES Science Gateway server (Miller et al. 2010). Maximum likelihood analysis employed the rapid bootstrapping algorithm with the GTRCAT model and 1 000 bootstrap iterations. Numbers above branches represent bootstrap support values ≥ 70 %. Bayesian inference consisted of two independent runs of 10 M generations sampled every 100th generation and the first 25 % of trees discarded as burn-in. Bayesian posterior probabilities ≥ 0.95 are indicated by thickened branches. *Myriangium hispanicum* (CBS 247.33) and *Elsinoe phaseoli* (CBS 165.31) were used as outgroup. The alignment and trees were deposited in TreeBASE (study 27826).

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Fistulinella aurantioflava

Fungal Planet 1251 – 13 July 2021

Fistulinella aurantioflava T.H.G. Pham, A.V. Alexandrova & O.V. Morozova, *sp. nov*.

Etymology. The epithet refers to bright yellow colour of the basidiomata and orange margin of tubes, from Latin '*aurantius*' (orange) and '*flavus*' (yellow).

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

Basidiomata medium sized, boletoid. *Pileus* 25–50 mm diam, hemispherical to convex; the surface is mucous to sticky when wet, smooth; the edge overhanging the hymenophore, even, strongly inflexed in young basidiomata; yellow, bright yellow or yellow-orange to orange and dark orange (3A6–8, 4A6–8, 4B5–6; Kornerup & Wanscher 1978). *Hymenophore* poroid, adnate-emarginate, decurrent with a short tooth on the stipe, slightly depressed around the apex of the stipe, 3–8 mm thick, 1.5–2 times thicker than the context; tubes yellowish to cream, do not change colour if damaged; the pores are rounded to angular, 0.5–1 mm diam, with bright orange drops of exudate on the margin. *Stipe* 40–90 × 3–7 mm, cylindrical, fusiform or slightly widening towards the base, pale yellow with orange dots above (drops of exudate), bright yellow below the annular zone (if present), smooth, mucous to sticky, solid in upper part, becomes hollow in the lower part. *Context* yellowish, not changing in the pileus and in the upper part of the stipe, in the lower half turns slightly blue. *Smell* weak, *taste* not reported. *Basidiospores* (10–)11.5–12.5(–14) × (3.5–)4(–4.5) µm, Q = (3.0–)3.1(–3.3), fusiform or nearly cylindrical with weak suprahilar depression in lateral projection, fusiform in the ventral projection, from yellowish to brownish yellow in KOH, smooth. *Basidia* 24–36 × 7–10 µm, 4-spored, clavate. *Cheilocystidia* 45–70 × 4–6 µm, forming a sterile margin, cylindrical, flexuous, thin-walled, with pale yellow content. *Pleurocystidia* 35–75 × 5–10 µm, fusiform or narrowly lageniform, with bright yellow or yellow-brown contents. *Hymenophoral trama* divergent, boletoid. *Pileipellis* ixotrichoderm, consisting of yellowish or brownish, cylindrical gelatinised intertwined hyphae, 2.5–5 µm wide with both yellow-brown intracellular and additionally incrusting pigments, and scattered dermatocystidia, 10–25 × 3–4 µm. *Stipitipellis* is a cutis of hyaline parallel hyphae, 2–5 µm thick. *Caulocystidia* 68–130 × 11–16 µm, in the form of cylindrical, septate hairs with narrowly clavate end cells, sometimes diverticulate. *Clamp connections* absent.

Typus. Vietnam, Dak Lak Province, Kon Ka Kinh National Park, 35 km east of the city of Kon Tum Ayun, N14.217129° E108.310132°, 1220 m a.s.l., on slopes on a tropical mountain polydominant soil forest with the participation of representatives of the families *Anacardiaceae*, *Fagaceae*, *Meliaceae*, *Myrtaceae* and *Theaceae*, 16 May 2016, *A.V. Alexandrova* (holotype LE 315616, ITS, LU and mtSSU GenBank sequences MW784159, MW760388 and MW776411, MycoBank MB 839260).

Additional materials examined. Vietnam, Dak Lak Province, Krong Bong District, Chu Yang Sin National Park, Krong Kmar Commune, 7 km north-west of Chu Yang Sin Mt, N12.421139° E108.373722°, 1196 m a.s.l., on the soil on the trail in the mountain primary evergreen polydominant tropical forest, 28 May 2014, *A.V. Alexandrova* & *T.H.G. Pham* (LE 315617, ITS, LSU and mtSSU GenBank sequences MW784160, MW760389 and MW776412).

Notes — *Fistulinella aurantioflava* is characterised by a bright yellow colouration of basidiomata, a smooth, strongly glutinous surface of pileus and stipe in a wet state, a strongly involved pileus margin, covering the hymenophore of young basidiomata, and a wide hymenophore. Microscopically, smooth fusiform, almost cylindrical spores and lageniform pleurocystidia with yellow content are characteristic. Due to macromorphological features, *F. aurantioflava* resembles *Pulveroboletus curtisii*, described from North America and distributed there. However, the surface of the pileus of the true *Pulveroboletus* species is pulverulent, and distinct pileal margin veil covers the hymenophore when young. Contrary, the strongly glutinous covering of the pileus and stipe makes our species similar to representatives of the pink-spored genus *Fistulinella* (*Austroboletoideae*), originally described based on a species from Cameroon (Hennings 1901). Preliminary molecular analyses suggested this genus to be polyphyletic. Vasco-Palacios et al. (2014), Magnago et al. (2017) and Gelardi et al. (2021) showed that American species of *Fistulinella* cluster in a statistically strongly supported separate clade with respect to those described from Australia, New Zealand and Asia. However, molecular analyses are required on the generic type, the African taxon *F. staudtii* to clarify the delimitation of *Fistulinella* s.str.

According to the data of the phylogenetic analysis, our specimens are nested within the /Austroboletoideae clade, close to *Austroboletus*, *Veloporphyrellus* and the Asian branch of *Fistulinella*. Despite the presence of some morphological differences (the absence of a pronounced pink colour of the spores, the presence of yellow-coloured pleurocystidia, and the unusual bright yellow colour of basidiomata), we attribute this species to the genus *Fistulinella*.

Fistulinella aurantioflava differs from *Pulveroboletus curtisii* (the systematic position of which also requires clarification) by its smaller and narrower spores ((10–)11.5–12.5(–14) × (3.5–)4(–4.5) µm vs (10.5–)11.2–15(–19) × 4.3–6.5 µm (Singer 1947)), the presence of a bluish discolouration in the lower part of the stem, and geographical distribution. In the GenBank database *Pulveroboletus curtisii* is represented only by mtSSU and LSU sequences. Our sequences of these markers are very distant from them (mtSSU: 5.35 %; LSU: 7.29–7.39 %).

Colour illustrations. Vietnam, Dak Lak Province, Kon Ka Kinh National Park (type locality). Spores, cheilocystidium; pleurocystidium; pileipellis; stipitipellis with caulocystidia (all from holotype); young basidioma *in situ*, hymenophore with orange drops in the tube edges (LE 315617); longitudinal section through the basidioma (from holotype). Scale bars = 1 cm (basidiomata), 10 µm (spores and microstructures).

Supplementary material

FP1251 Phylogenetic tree derived from Bayesian analysis, based on ITS1-5.8S-ITS2 data. Analysis was performed under 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 added at the nodes. The scale bar represents the number of nucleotide changes per site. Sequences derived from type material is indicated with (T) and the tree was rooted to two sequences of *Gyroporus*.

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Hyalodendriella bialowiezensis

Fungal Planet 1252 – 13 July 2021

Hyalodendriella bialowiezensis Gorczak, *sp. nov.*

Etymology. Name refers to the Białowieża Primeval Forest where it was collected.

Classification — *Hamatocanthoscyphaceae*, *Helotiales*, *Leotiomycetes.*

On cornmeal agar (CMA): *Conidiophores* initially simple, later branching laterally, arborescent, usually with 2–4 branches, sometimes with secondary branches, 4–8 cells in main axis (av. = 5.5), conidiogenous cells mostly with single apical locus, infrequently 2–3 loci present. *Conidiophores* with distinctly wider and shorter cells than vegetative mycelium, with thicker cell walls, (30.5–)36–52.5(–57.5) (av. = 44) µm long × 2.5–3.5(–4) (av. = 3) µm wide. Rarely simple conidiophores forming as lateral branches on hyphae 1–2 cells, forming unbranched chain of conidia. *Conidia* formed in basipetal chains, infrequently 2–4 spores detach connected. *Conidia* hyaline, smooth or very finely verrucose, granular, aseptate, distinctly apiculate, limoniform, ellipsoidal or oval, (3.5–)5–7.5(–10) (av. = 6.2) µm long × (1.5–)2–2.5(–4) (av. = 2.3) µm wide. *Ramoconidia* derived from detached cells of branchlets of upper conidiophores present in older cultures, more irregular, angular and elongated, sometimes apiculate, (5.5–)7–11.5(–15) (av. = 9.1) µm long × (1.5–)2–3(–4) (av. = 2.6) µm wide. *Vegetative hyphae* smooth, hyaline, thin-walled, regularly septate, 1–2 (av. = 1.7) µm wide; rarely, larger, thin-walled, globose cells present.

Culture characteristics — (in darkness, 20 ± 2 °C). On oatmeal agar (OA) colonies dense, margin irregular, undulating, elevated in the centre, initially creamy, later beige, slightly orange in the centre in older colonies, with very sparse patches of white, low aerial mycelium, reaching 2(–2.5) cm in 2 mo. On potato dextrose agar (PDA) and malt extract agar (MEA) averse creamy, yellowish in older cultures, reverse yellowish, reaching 1.5(–2) cm in 2 mo. On cornmeal agar (CMA) cultures tiny, with white, snow-like, fluffy aerial mycelium, vegetative mycelium sparse and thin. On CMA radiating needle-like crystals were noted on the surface of the mycelium, 20–40 (av. = 31) µm diam.

Typus. Poland, Podlaskie Voivodeship, Białowieża Forest, forest division 366B, near Teremiski, on debris beneath fallen bark of Norway spruce *Picea abies* previously infected with European spruce bark beetle *Ips typographus*, 22 Nov. 2018, *M. Gorczak* (holotype WA0000074527, ex-type culture MGC 152A = CBS 148027,, ITS, SSU, LSU, *tef1-α*, *rpb1* and *rpb2* sequences GenBank MW004162, MW004159, MW009815, MW013798, MW811184 and MW013801, MycoBank MB 839246).

Notes — *Hyalodendriella bialowiezensis* is similar to subhyaline cladosporium-like fungi – *Hyalodendriella betulae*, *Rachicladosporium*, *Hormiactis*, and members of obsolete genus *Hyalodendron* (now in *Ramularia* and *Apiotrichum*). However, conidia of *H. bialowiezensis* do not have coronate scars (like *Ramularia* or true *Cladosporium*), and are always aseptate (unlike *Hormiactis*). Moreover, conidiophores and conidia of *H. bialowiezensis* are consistently hyaline, while abovementioned taxa are at least partially subhyaline or brownish. Young terminal limoniform conidia of *H. bialowiezensis* sometimes detach in chains still connected with thin thread of not fully divided cell wall in a manner similar to *Oidiodendron griseum*. Although *H. bialowiezensis* is related to apothecia-forming *Helotiales*, no associated sexual morph was recorded.

Hyalodendriella betulae and *H. bialowiezensis* have very similar limoniform conidia with distinctly apiculate ends, that in both cases are formed in chains. However, in case of *H. bialowiezensis* conidia are significantly larger (5–7 µm long, in *H. betulae* 0.5–1 µm) (Crous et al. 2007a). Conidiophores of *H. bialowiezensis* correspond with macroconidiophores (or type B conidiophores) of *H. betulae* in having, albeit rarely, conidiogenous cells with multiple loci (up to three in *H. bialowiezensis*). Interestingly in both species undetached conidia seem to elongate from the conidiophores in some cases. While they remain attached to microconidiophores of *H. betulae*, they infrequently break up as ramoconidia in *H. bialowiezensis*.

Hyalodendriella is placed either in *Pezizellaceae*, *Helotiales* (Johnston et al. 2019) or in *Hamatocanthoscyphaceae*, which in the classification of Ekanayaka et al. (2019) does not belong to *Helotiales* s.str.

Based on a megablast search of NCBIs GenBank nucleotide database the most similar, identified fungal sequences belong to *Hyalodendriella betulae* strain CBS 261.82 (LSU sequence, 96 % identity), *Chalara constricta* and *Chalara hughesii* (SSU sequences, 95 % identity). ITS sequences of *H. bialowiezensis* are distantly similar to other *Helotiales* (90 % identity to *Xenopolyscytalum* and various unidentified *Hyaloscyphaceae* sequences for ITS).

The maximum likelihood tree was constructed with RAxML-NG (Kozlov et al. 2019) on a partitioned alignment including SSU, 5.8S and LSU rDNA, mtSSU and protein coding *tef1-α*, *rpb1*, *rpb2*, *β-tub* and *mcm7* sequences, being an excerpt of the combined datasets of Han et al. (2014) and Johnston et al. (2019). The dataset contained 35 taxa and a total of 7 873 characters of which 1 919 were variable. Bootstrap support values at branches were obtained by generating 1 000 bootstrap replicates. The tree is rooted with *Leotia lubrica* belonging to *Leotiales*.

Colour illustrations. Białowieża Primeval Forest logging site, Poland (photo M. Klemens). Two-month-old colonies of *H. bialowiezensis* on PDA (left) and OA (right); conidiophores with visible young lateral branches and chains of limoniform conidia; various spores including irregular ramoconidia and undivided chains of limoniform spores. Scale bars = 20 µm.

Supplementary material

FP1252-1 Additional materials examined.

FP1252-2 The best scoring maximum likelihood tree calculated from 9 molecular markers shows *H. bialowiezensis* and closest related *Helotiales*. Only bootstrap support values ≥ 70 % are shown.

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Hydropus lecythiocystis

Fungal Planet 1253 – 13 July 2021

Hydropus lecythiocystis E.F. Malysheva & Malysheva, *sp. nov*.

Etymology. The name refers to the shape (lecythiform) of cheilocystidia.

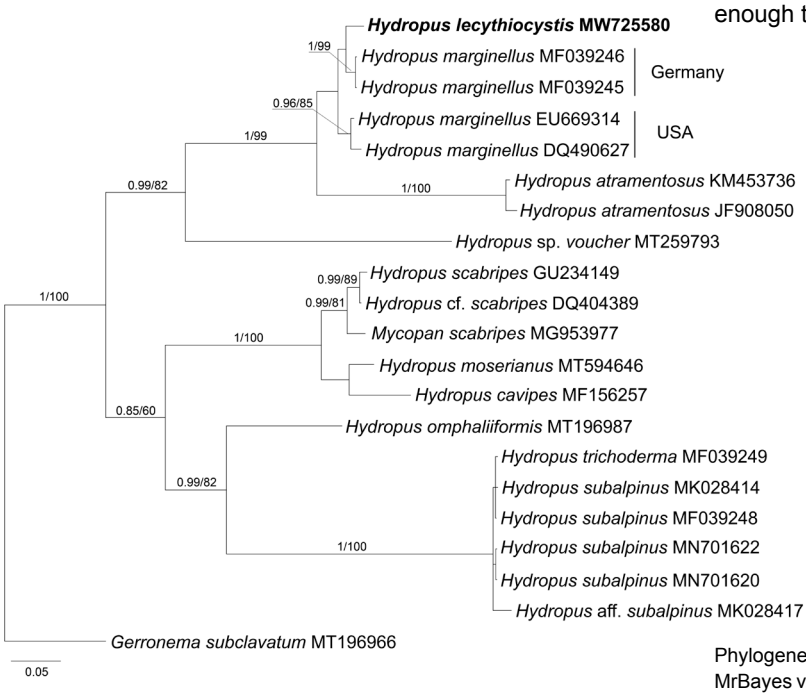
Classification — *Porotheleaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps small to medium-sized, collybioid or omphalioid. *Pileus* 12–30 mm diam, applanate or subinfundibuliform, with flattened or without umbo, with undulating and scarcely striate margin; hygrophanous; surface pruinose to subvelutinous, saruk grey (07 05 10), huckleberry brown (070 40 20) or arable brown (070 40 30), with beech brown (070 30 20) or mineral brown (070 30 10) centre, with a touch of olive (all colour names of macroscopic features are given following the RAL DESIGN colour range system). *Lamellae* crowded, decurrent, with lamellulae, slightly ventricose, pastel sand (080 80 10) or micaceous light grey (080 80 05), edge even or somewhat serrulate, concolorous. *Stipe* 20–35 × 2–2.5 mm, cylindrical, ash gold (070 50 20) at upper part and beech brown (070 30 20) at base, slightly pruinose. *Context* thin, whitish. *Smell* and *taste* not distinctive. *Basidiospores* (6.0–)6.7–8.0(–10.2) × 3.7–5.0 µm, Q = 1.60–2.00, Qav = 1.70, n = 50, subcylindrical or dacryoid, often slightly allantoid, hyaline in KOH, thin-walled; amyloid. *Basidia* predominantly 2-spored, sporadically 1-spored, 20–32 × 4.5–6 µm, narrowly clavate. *Cheilocystidia* abundant, 34–59 × 9–18(–27) µm, utriform, broadly lageniform with subcapitate apex, some proportion almost lecythiform with broad capitula, intermixed with broadly clavate, urniform or subcylindrical ones, hyaline, thin-walled. *Pleurocystidia* absent. *Pileipellis* a clavicutis, with dense layer of broadly clavate, cylindrical, subglobose, pyriform or broadly utriform pileocystidia, 41.5–72 × 15–28.5 µm, weakly to strongly pigmented with intracellular greyish brown pigment, slightly thick-walled. *Stipitipellis* a cutis, containing fascicles of *caulocystidia*, (45–)53–77(–106) × 11–26 µm, broadly clavate, utriform, subcylindrical or lageniform, hyaline, slightly thick-walled. *Clamp connections* present.

Habitat & Distribution — Growing in small groups or solitary on rotted wood of *Betula pendula*. So far known only from type locality.

Typus. Russia, Krasnoyarsk Territory, Sayano-Shushenskiy State Biospheric Nature Reserve, the mouth of the Sarly River, N52°09'55.5" E92°18'43.9", floodplain birch forest, on rotted wood of *Betula pendula*, 16 Aug. 2020, *V. Malysheva* (holotype LE 313638, ITS and LSU sequences GenBank MW725580 and MW760390, MycoBank MB 839059).

Notes — *Hydropus lecythiocystis* is characterised by its pruinose and dark greyish brown pileus with slight touch of olive, cheilocystidia of variable shape with presence of lecythiform elements, 2-spored basidia, predominantly subcylindrical, allantoid or dacryoid, amyloid basidiospores, and lignicolous habitat. Based on morphological characters it resembles *H. marginellus* (Bas 1999, Læssøe 2008), but differs from the latter by having concolorous lamellae edge, exclusively 1–2-spored basidia, shorter cheilocystidia with present of distinctive lageniform ones with subcapitate apex, and growing on wood of deciduous trees. Phylogenetically, *H. lecythiocystis* and *H. marginellus* turned out to be closely related species. In the phylogenetic tree, *H. lecythiocystis* formed a branch close to European collections of *H. marginellus* but not to North American ones. However, the dissimilarity of their nrITS sequences reaches more than 2 %, and together with strong micromorphological differences, it is enough to consider them as different species.



Phylogenetic nrITS topology from Bayesian analysis was performed with MrBayes v. 3.2.5 software (Ronquist et al. 2012) with 6 M generations under GTR+G model, showing relationships of *Hydropus* species, with *Gerronema subclavatum* as outgroup. Maximum likelihood analysis was performed on RAxML server v. 1.0.0 (https://raxml-ng.vital-it.ch/#/) with 100 rapid bootstrap replicates. Support values (PP/BS) are given above the branches. All tips are labelled with taxon name and GenBank accession number. The newly generated sequence is in **bold**.

Colour illustrations. Russia, Yenisei river basin in Sayano-Shushenskiy Reserve. From top to bottom: pileipellis elements, basidiospores, cheilocystidia, caulocystidia; and mature basidiocarps (all from holotype). Scale bar = 1 cm (basidiocarps), 10 µm (microstructures).

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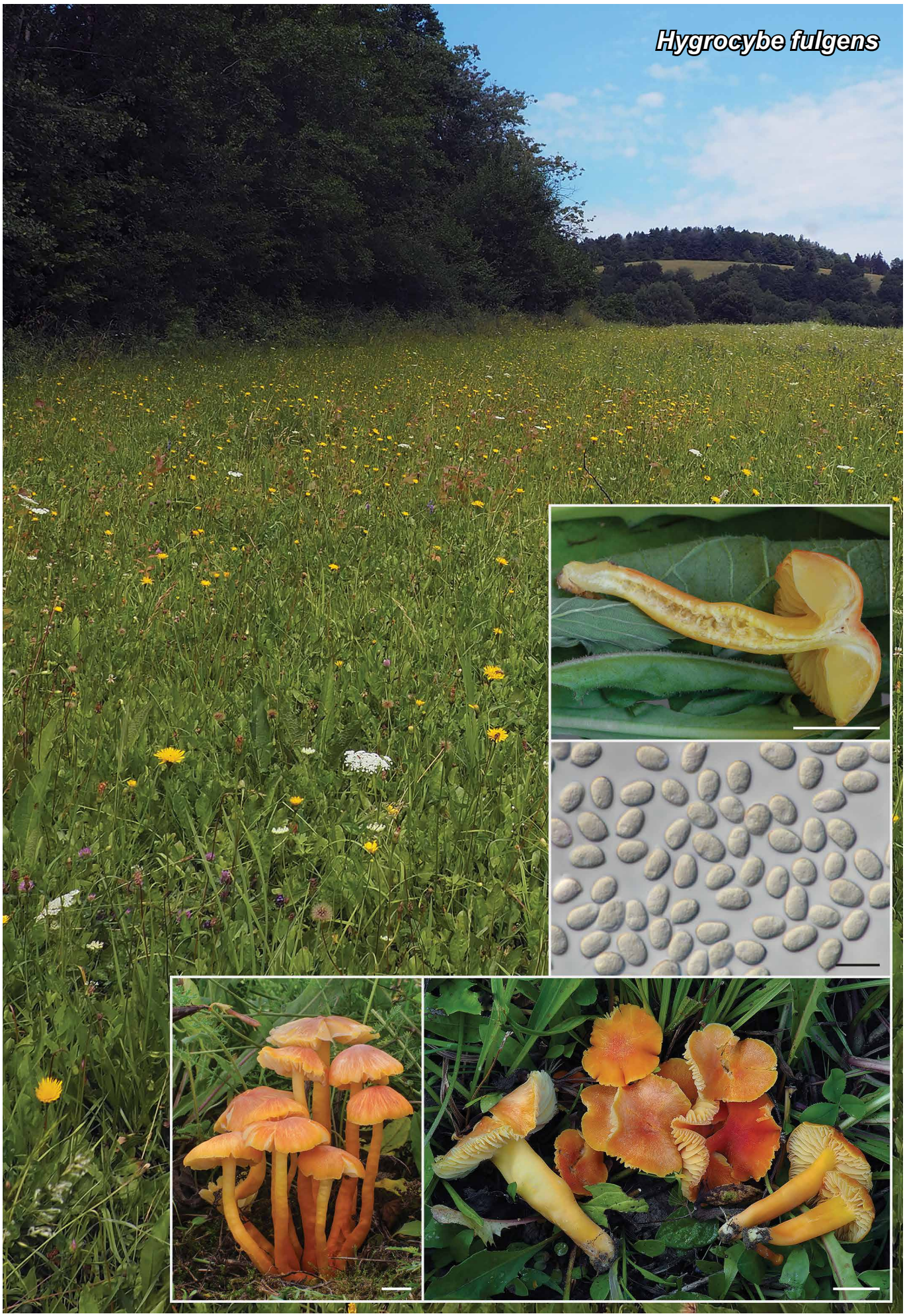
Hygrocybe fulgens

Fungal Planet 1254 – 13 July 2021

Hygrocybe fulgens Fuljer, Kautmanová & Boertm., *sp. nov.*

Etymology. The name reflects the shiny colour of the basidiomata.

Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

Pileus 14–65 mm diam, at first hemispherical, broadly convex, later more or less applanate with depressed centre, brittle; surface finely squamulose, squamules concolorous or paler, sometimes smooth, dry, orange, yellowish orange or reddish (Pantone 1505C, Pantone 2018C, Pantone 716C) (Pantone Color Finder 2021; https://www.pantone.com/color-finder/2021-C), often with a slightly scarlet red centre (Pantone 2028C). *Stipe* 25–60 × 2.5–18 mm, terete or compressed, often attenuated downwards, brittle, hollow; surface smooth, sometimes finely fibrillose, dry, matt or silky sheen, golden yellow, yellow, yellowish orange, orange (Pantone 7406C to Pantone 7414C), sometimes paler at the top (Pantone 130C). *Lamellae* broadly adnate, ventricose, brittle, distant; surface smooth, paler than pileus and stipe, almost whitish at first, becoming yellowish or pale orange (Pantone 127C to Pantone 130C), sometimes with salmon hue; edges often paler. *Context* yellowish white (Pantone 127C to Pantone 130C), sometimes more orange or orange red in pileus and base of stem (Pantone Orange 021C), unchanging when cut. *Smell* and *taste* insignificant. *Spore print* white. *Basidiospores* smooth, non-amyloid, sometimes with one big vacuole, ellipsoid to oblong, (6.6–)7.1–9.9(–10.2) × (4.5–)4.8–6.3(–6.9) µm, Q = 1.3–1.9 (Lm = 8; Wm = 5.55; Qm = 1.54), 130 spores from three basidiomata measured from the holotype (BRACR 32958). *Basidia* 38–55 × 5–8 µm (excluding sterigmata), clavate, predominately 4-spored, relatively long with long attenuated base, *sterigmata* elongate, 4–7 µm long. *Cystidia* absent. *Pileipellis* as a trichoderm, with more or less clavate (inflated) terminal elements, hyphae sometimes septate and connected with a clamp, predominately short, (29–)32–103(–145) × (5.2–)6.3–13.1(–15) µm. *Stipitipellis* as a cutis, hyphae sometimes septate and clamped, predominately short, (28–)32–110(–111) × (3.8–)4.2–8.7(–9.1) µm. *Gill trama* subregular, with cells (42–)46–120(–145) × (8.5–)9.7–18(–19) µm.

Distribution & Habitat — Known from Slovakia, probably more widespread but overlooked and misidentified. Growing gregarious, solitary or scattered in mowed grasslands, mowed parks, on neutral to slightly calcareous soils. From July to September (–October).

Typus. Slovakia, Javorníky Mts, Sádky, Petrovice, N49°15'21.73" E18°32'7.77", alt. 359 m, mowed grassland (south-facing, fertilised in the past), in association with *Leontodon hispidus*, *Trifolium pratense*, *Agrostis capilaris*, *Fragaria vesca*, *Daucus carota*, *Agrimonia eupatoria*, *Symphytum officinale*, *Plantago major*, *Trisetum flavescens*, *Trifolium repens*, etc., on bare soil, 30 Aug. 2019, *F. Fuljer & I. Fuljer* (holotype BRACR 32958, ITS and LSU sequences GenBank MW471672 and MW471670, BOLD ITS sequence FULGE001-20, MycoBank MB 839238).

Colour illustrations. Mowed grassland in Petrovice village (Javorníky Mts, Slovakia), where the typus (holotype) was collected. Type specimens *in situ*, cross section of the sporocarp (Photo credit F. Fuljer); basidiospores. Scale bars = 10 mm (fruitbodies), 10 µm (spores).

Additional materials examined. Slovakia, Javorníky Mts, Sádky, Petrovice, N49°15'21.73" E18°32'7.77", alt. 359 m, mowed meadow (south-facing), in association of *Leontodon hispidus*, *Trifolium pratense*, *Agrostis capilaris*, *Fragaria vesca*, *Daucus carota*, *Agrimonia eupatoria*, *Symphytum officinale*, *Plantago major*, *Trisetum flavescens*, *Trifolium repens*, etc., on bare soil, 8 Sept. 2020, *F. Fuljer*, BRACR 32959; Beskydske predhorie Basin, Snina town, city park near the Vihorlat hotel, N48°59'21.4" E22°09'39.1", alt. 220 m, in moss and grass,10 Sept. 2020, *J. Pavlík*, BRACR 33659, ITS and LSU sequences GenBank MW471671 and MW471669, BOLD ITS sequence FULGE002-20.

Notes — *Hygrocybe fulgens* is characterised by a dry, squamulose applanate pileus, dry, smooth and broad stipe, pileipellis a trichoderm, ellipsoid to oblong spores, and by a size and colour of whole sporocarps, which are usually orange yellow, often with golden yellow stipe and darker (almost scarlet red) central part of pileus. Due to these features, this species fits well with the concept of the subgenus *Pseudohygrocybe* section *Coccineae* and subsection *Squamulosae* (Lodge et al. 2014). Based on macromorphological features, the most similar species to *Hygrocybe fulgens* are *H. calciphila*, *H. miniata*, *H. reidii* and *H. substrangulata*. *Hygrocybe calciphila*, differs by typical subglobose to broadly ellipsoid spores and smaller basidiomata. Macroscopically, *H. fulgens* and *H. calciphila* are very similar, but sporocarps of *H. fulgens* are mostly much larger and robust. *Hygrocybe miniata* is characterised by triangular or pear-shaped spores, pileus without darker central part and also by a thinner stipe (usually to 5 mm broad). *Hygrocybe reidii* is another macroscopically similar species to *H. fulgens*, differing by a honey-like smell and smooth, orange-red coloured pileus. *Hygrocybe substrangulata* differs from other mentioned *Hygrocybe* species by much larger spores (up to 14.5 µm) and sometimes decurrent lamellae (Boertmann 2010). All above mentioned species grow in central Europe in the unimproved, sometimes grazed or mowed grasslands with *Nardus stricta* or *Agrostis* spp., but *H. fulgens* was found in a different type of grassland, where *Leontodon hispidus* was a dominant plant.

In the maximum likelihood tree based on the ITS sequences *H. fulgens* is positioned on a separate branch close to the clade of subsection *Squamulosae*, which is consistent with the results of macro- and micro-character observations.

Supplementary material

FP1254 Subtree of the maximum likelihood tree obtained from the analysis of ITS sequences of *Hygrocybe* subgenera *Hygrocybe* and *Pseudohygrocybe*. The alignment was performed with ClustalW and the Tamura-Nei model was used for the phylogenetic analysis (Tamura & Nei 1993). Bootstrap support values are indicated at the nodes. The original analysis involved 66 nucleotide sequences, 21 of them are implemented in the subtree. There were a total of 700 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018a).

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Ilyonectria zarorii

Fungal Planet 1255 – 13 July 2021

Ilyonectria zarorii Sand.-Den. & Giraldo López, *sp. nov.*

Etymology. In honour of Prof. Luis Zaror, prominent Chilean mycologist and writer; active promoter of medical technology and mycology in South America, and long-time inhabitant of Teja island, where this species was first collected.

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

Conidiophores of two types: a) solitary, erect or prostrate, arising laterally from aerial and substrate mycelium, commonly formed on dense and twisted hyphal ropes, septate, 33.5–482 µm long, unbranched or sparsely, irregularly branched, bearing terminal and solitary conidiogenous cells; or b) densely packed in sporodochia, formed on the substrate surface, simple, rarely branched, bearing terminal single conidiogenous cells or whorls of up to three conidiogenous cells; *conidiogenous cells* monophialidic, subcylindrical to cylindrical, gently tapering towards apex, with inconspicuous periclinal thickening and short, flared apical collarettes, those formed on aerial conidiophores 24–58.5 µm long, 2.5–4 µm at the widest point; phialides on sporodochial conidiophores 20–27 µm long, 2.5–3.5 µm at the widest point. *Microconidia* rarely observed, formed on aerial conidiophores, 0(–1)-septate, subglobose, ellipsoid to long clavate, (8–)10–15(–16) × (3–)4–5.5 µm (av. = 12.2 × 4.6 µm). *Macroconidia* produced abundantly on aerial and sporodochial conidiophores, 1–2(–3)-septate, cylindrical with both ends more or less obtusely rounded, straight or slightly curved; 1-septate conidia: (16.5–)20.5–28.5(–32) × (4.5–)5.5–6.5(–7) µm (av. 24.5 × 6 µm); 2-septate conidia: (26–)29–35(–41.5) × 5–7(–8) µm (av. 32.4 × 6.3 µm); 3-septate conidia: (28–)30–39(–40.5) × 6–7.5 µm (av. 34.6 × 6.8 µm); overall: (16.5–)23.5–34(–41.5) × (4.5–)5.5–7(–8) µm (av. 28.9 × 6.2 µm). *Chlamydospores* rarely produced, doliiform, subglobose to globose, 7–14 µm diam, thick- and smooth-walled, terminal or intercalary; solitary, in short chains or forming sparse clusters, hyaline at first, quickly becoming golden yellow to brown.

Culture characteristics — Colony on malt extract agar (MEA) reaching 48–58 mm diam in 7 at 24 °C. Surface initially flat and velvety, peach, scarlet to red (colour notation from Rayner 1970), later becoming cupulate and cottony with abundant white to pale peach aerial mycelium, margin filiform. Reverse red, rust or brown with radial patches of amber to brown diffusible pigments.

Typus. Chile, Los Ríos Region, Valdivia, Teja Island, proximities of the Universidad Austral de Chile, from soil under *Maytenus boaria*, 26 Dec. 2018, *A. Giraldo* & *N. Sandoval-Giraldo* (holotype CBS H-24561, culture ex-type CBS 147179 = CPC 37835, ITS, LSU, *his3*, *tef1* and *tub2* sequences GenBank MW114893, MW114944, MW119259, MW119261 and MW119263, MycoBank MB 837768).

Colour illustrations. Chile, young *Maytenus boaria* ('maitén'; photo by M. Sandoval-Sáez). Aerial and sporodochial (inset) conidiophores; chlamydospores and conidia of various sizes and septation. Scale bars = 20 µm (black), 10 µm (white).

Additional material studied. Chile, Los Ríos Region, Valdivia, Teja Island, proximities of the Universidad Austral de Chile, from soil under *Maytenus boaria*, 26 Dec. 2018, *A. Giraldo* & *N. Sandoval*, CBS 147180 = CPC 37837, ITS, LSU, *his3*, *tef1* and *tub2* sequences GenBank MW114894, MW114945, MW119260, MW119262 and MW119264.

Notes — *Ilyonectria zarorii* is phylogenetically and morphologically related to *I. crassa* and *I. pseudodestructans*, all species characterised by similar conidiophores and conidia, with marked predominance of macroconidia in both types of conidiophores (Cabral et al. 2012). *Ilyonectria crassa*, however, produces flask-shaped sporodochial phialides and its macroconidia are smaller, cylindrical, straight and present a prominent basal hilum. *Ilyonectria pseudodestructans* differs from *I. zarorii* by forming more clavate macroconidia and slender microconidia.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ***his3*** sequence had highest similarity to *I. pseudodestructans* (strain CBS 117824, GenBank JF735562.1; Identities = 443/447 (99 %), no gaps) and *I. crassa* (strain CBS 139.30, GenBank JF735534.1; Identities = 442/447 (99 %), no gaps). Closest hits using the **ITS** sequence are *I. panacis* (strain CBS 129079, GenBank MH865176.1; Identities = 420/420 (100 %), no gaps) and *I. crassa* (strain ICMP 14372, GenBank MH497565.1; Identities = 420/420 (100 %), no gaps). Closest hits using the **LSU** sequence had highest similarity to *I. coprosmae* (strain CBS 126772, GenBank MH875672.1; Identities = 813/829 (98 %), three gaps (0 %)), *I. panacis* (strain CBS 129079, GenBank MH876614.1; Identities = 811/829 (98 %), three gaps (0 %)) and *I. cyclaminicola* (strain CBS 302.93, GenBank NG_069249.1; Identities = 810/829 (98 %), three gaps (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *I. pseudodestructans* (strain CPC 13534, GenBank JF735749.1; Identities = 473/474 (99 %), one gap (0 %)), *I. pseudodestructans* (strain CBS 117812, GenBank JF735750.1; Identities = 473/477 (99 %), four gaps (0 %)) and *Ilyonectria* sp. (strain CBS 120370, GenBank JF735728.1; Identities = 471/475 (99 %), two gaps (0 %)). Closest hits using the ***tub2*** sequence had highest similarity to *I. panacis* (strain CDC-N-9a, GenBank JF735424.1; Identities = 492/498 (99 %), no gaps), *I. pseudodestructans* (CBS 117812, GenBank JF735418.1; Identities = 490/498 (98 %), no gaps) and *I. crassa* (strain CBS 158. 31, GenBank JF735394.1; Identities = 489/498 (98 %), no gaps).

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Inocybe norvegica

Fungal Planet 1256 – 13 July 2021

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

Etymology. Refers to Norway where the first collection was found.

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

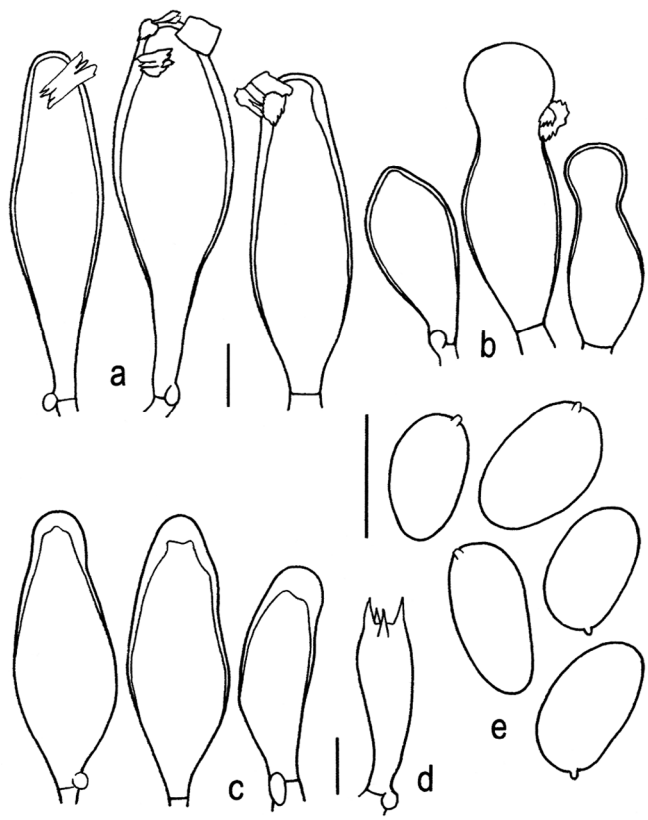
Pileus 8–17 mm diam, hemispherical, later plano-convex, sometimes indistinctly umbonate, whitish, pale brown to brown around centre, towards margin greyish brown to brown, subtomentose-smooth around centre, towards margin coarsely fibrillose, subsquamulose to recurvately squamulose, margin not rimulose, often with indistinct velipellis. *Lamellae* moderately crowded, to 4 mm broad, broadly adnate, some emarginate with decurrent tooth, at first pale greyish brown, then grey-brown, ochraceous to ochraceous brown; edge fimbriate, pale to brownish. *Stipe* 20–38 × 1–3 mm, equal to slightly bulbous but without bulb, grey-brown, brown, black-brown especially in middle part, not pruinose, longitudinally woolly-fibrillose, often coarsely so, part of fibrils silvery pale. *Cortina* greyish, rather abundant in young basidiomes. *Context* pale brown, often with reddish tint, shiny in stipe, cortex rather dark reddish brown. *Smell* faint, indistinct to slightly acidulous. *Basidiospores* (9.9–)10.5–*11.7*–12.9(–13.5) × (6.0–)6.3–*6.8*–7.4(–7.7) µm, Q = (1.5–)1.55–*1.71*–1.9(–2.0) (*n* = 140), smooth, subamygdaliform, subellipsoid to subphaseoliform, some minimally angular, with obtuse apex, often with indistinct germ-pore, rather dark, yellow-brown, rather thick-walled. *Basidia* (24–)28–*30*–35(–40) × (9–)10–*11*–13(–14) µm (*n* = 80), subclavate to clavate, 4-spored. *Pleurocystidia* (48–)54–*61*–74(–78) × (12–)13–*17*–20(–22) µm (*n* = 80), fusiform to subclavate, sometimes indistinctly capitate, with up to 2 µm thick, colourless to slightly yellow wall, crystalliferous at apex. *Cheilocystidia* (33–)35–*49*–67(–70) × (10–)11–*16*–24(–28) µm (*n* = 62), more variable than pleurocystidia, often brown. *Paracystidia* (16–)19–*23*–27(–30) × (9–)10–*13*–17(–18) µm (*n* = 21), rather scarce, often pyriform, colourless to brown. *Caulocystidia* at stipe apex only, (29–)33–*46*–58 × 10–*15*–22(–25) µm (*n* = 43), cauloparacystidia few. *Clamp connections* present.

Ecology & Distribution — Associated with *Salix* spp. and *Betula pubescens* subsp. *czerepanovii* in open areas on somewhat calcareous sandy soils. Basidiomata so far only known from the subalpine zone of Norway and alpine zone of Sweden, where it grew amongst *Salix herbacea*. In addition, ITS sequence data generated from soil samples in a locality in the alpine zone shows that it also occurs in Austria.

Typus. Norway, Hedmark, Folldal, Liamælan near Gravbekkli bru, in subalpine moor-like area on gravelly soil with *Betula pubescens* subsp. *czerepanovii*, *B. nana* and *Salix* spp., amongst mosses and lichens, 820 m a.s.l., 21 Aug. 2012, *J. Vauras* 29084F, *S. Jacobsson* & *E. Larsson* EL109-12 (holotype TUR-A 198408, ITS-LSU sequence GenBank MW617340; isotypes GB-0207604, AH, O, MycoBank MB 838947).

Additional materials examined. Norway, Troms, Storfjord, NW of Helligskogen along E8, subalpine area on gravelly ground with *Betula pubescens* subsp. *czerepanovii* and *Salix* spp., 310 m a.s.l., 20 Aug. 2017, *E. Larsson* EL172-17 and *J. Vauras*, GB-0207603, TUR-A 208752, ITS-LSU sequence GenBank MW617339; ibid., 21 Aug. 2017, *E. Larsson* & *J. Vauras*, EL193-17, GB-0207602. – Sweden, Lule lappmark, Jokkmokk, Padjelanta NP, Sorjosjaure, alpine area on calcareous ground, among *Salix herbacea*, 830 m a.s.l., 17 Aug. 2016, *J. Vauras*, TUR-A 204346, ITS-LSU sequence GenBank MW617341.

Notes — *Inocybe norvegica* belongs in the *I. lacera* group. It is a rather small species characterised by hemispherical pileus which is subsquamulose to recurvately squamulose and often with indistinct velipellis. Microscopically it shows rather dark and ellipsoid spores, often with indistinct germ-pore. *Inocybe helobia* (Kuyper 1986, Bandini et al. 2020) grows like *I. norvegica* with *Salix* and has similarly dark spores, but they are more amygdaliform and angular, and with larger average Q (1.9–2.3 vs 1.7 in *I. norvegica*). Further, it has pleurocystidia with often acute apex and thicker and mostly more yellow walls, and grows mainly in moist habitats. *Inocybe impexa* (Kuyper 1986) is another species with rather darker spores. It is stouter and has larger spores, with larger average Q (2.0–2.3). It grows on sandy seashores, but also in inland sand-pits, and even in alpine localities with *Salix herbacea.* Other smooth-spored taxa of the *Inocybe lacera* group (*I. lacera*, *I. lacera* var. *heterosperma* and *I. pluppiana*) have paler spores.



Inocybe norvegica. Drawing of micro-morphological characters from the holotype (TUR-A 198408). a. Pleurocystidia; b. cheilocystidia; c. caulocystidia; d. basidium; e. spores. Scale bars = 10 µm.

Colour illustrations. *Inocybe norvegica* habitat in the subalpine zone with *Betula pubescens* subsp. *czerepanovii* and *Salix* spp. shrubs, Folldal, Hedmark, Norway. *In situ* basidiomata and cross-sections of the holotype (TUR-A 198408); cheilocystidia and basidiospores of isotype (GB-0207604). Scale bars = 20 µm (cheilocystidia), 10 µm (spores).

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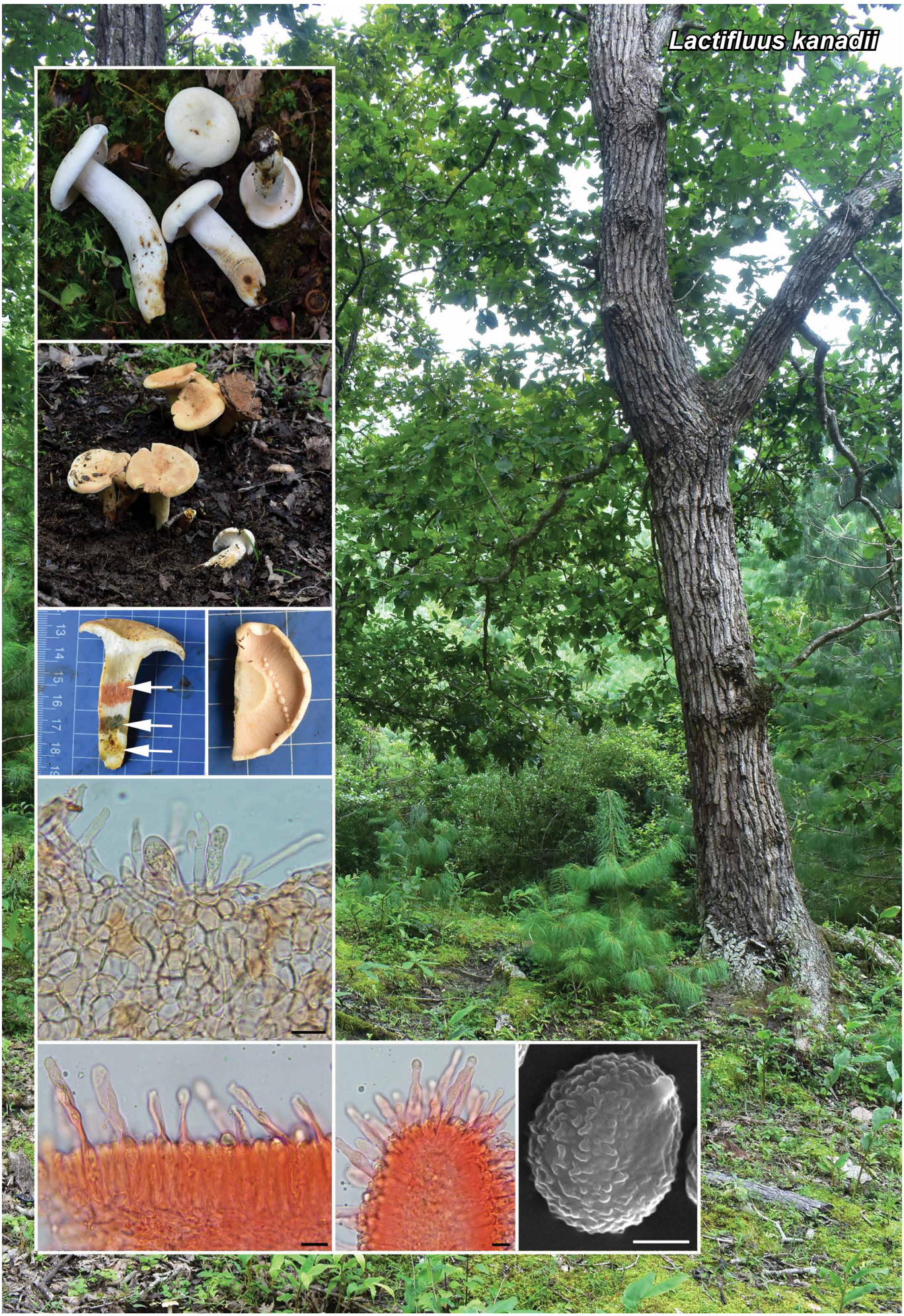
Lactifluus kanadii

Fungal Planet 1257 – 13 July 2021

Lactifluus kanadii I. Bera, A. Ghosh, Nuytinck & Verbeken, *sp. nov.*

Etymology. In honour of Dr Kanad Das for his invaluable contribution to the systematics of *Russulaceae* in the Indian Himalayan Region.

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

Pileus 30–85 mm diam, hemispheric to convex when young, gradually becoming planoconvex with a broad shallow depressed centre; surface moist, smooth, velvety, faintly rugulose towards the margin, yellowish white (1A2) and paler, with some irregular darker spots, but turning orange white to pale orange (5A2–4) to ochraceous and darker on bruising and even brownish on maturity; cracked at several places towards the margin in mature basidiomata; margin entire, incurved when young, remaining incurved through maturity. *Lamellae* adnate to subdecurrent, close to rather crowded (20 L+l /cm at pileus margin), dichotomously forked; lamellulae present in 3–4 series; yellowish white (2–3A2); edge entire, smooth, concolorous. *Stipe* 25–95 × 15–30 mm, central, cylindrical but sometimes twisted near the base; surface velvety, strongly rugulose locally; concolorous to the pileus, when bruised turning pale orange to light orange (5A3–4) to ochraceous and darker. *Context* thick in pileus and stipe, yellowish white (1–2A2), almost immediately turning pale orange on bruising, greyish green (1D4) in guaiac, orange (5A6–7) in $FeSO_4$ and immediately yellowish in KOH. *Latex* yellowish white, copious, unchanging on cut lamellae. *Taste* very acrid. *Odour* fruity. *Spore print* not recorded.

Basidiospores 5.8–*6.7*–8.2(–9.1) × 4.7–*5.6*–6.7 µm, n = 30, Q = 1.04–*1.19*–1.32(–1.44), usually globose to ellipsoid; ornamentation amyloid, up to 0.6 µm high, composed of isolated irregular warts which are sometimes aligned or connected by lower lines but never forms any reticulation; suprahilar spot inamyloid. *Basidia* 39–56.8 × 9.0–11.8 µm, clavate to subclavate, 4-spored; sterigmata 2–3 × 1.4–2 µm. *Pleuromacrocystidia* abundant, 47–69 × 5.4–9 µm, emergent up to 32 µm, cylindrical to subcylindrical with rounded, subfusoid to subcapitate apices, thin-walled; content dense, granular to crystalline. *Pleuropseudocystidia* abundant, 2.5–3 µm wide, emergent up to 12 µm, cylindrical, with rounded apex. *Lamellae edge* fertile with basidia, basidioles and cystidia. *Cheilomacrocystidia* abundant, 45–61 × 4.6–6.6 µm, emergent up to 40 µm, subcylindrical with rounded, subfusoid to subcapitate apices, thin-walled; content dense, granular to crystalline. *Subhymenium* up to 20 µm thick, cellular. *Hymenophoral trama* composed of lactifers and few nests of sphaerocytes connected with hyphae. *Pileipellis* a trichoepithelium, up to 136 µm thick; suprapellis composed of ascending elements, 15.4–22.1 × 2.7–3.8 µm, cylindrical to subfusiform, septate; subpellis multicellular composed of isodiametric cells of 8.6–12.8 × 4.0–11.1 µm; pileocystidia present, 22–26.5 × 5–10 µm, cylindrical to subcylindrical, content dense, crystalline. *Stipitipellis* a trichoepithelium, up to 52.2 µm thick; suprapellis composed of septate ascending elements arising from distinct multicellular subpellis of mostly isodiametric cells; caulocystidia present, 16–26 × 5.5–6.6 µm, mostly cylindrical, content dense, crystalline. *Clamp connections* absent in all tissues.

Colour illustrations. India, Arunachal Pradesh, Bebar Thanka, West Kameng, temperate broadleaf forest. *Lactifluus kanadii* (IB 19-020, holotype); macrochemical test with $FeSO_4$, Guaiac and KOH on stipe context; latex on the cut lamellae; transverse section through pileipellis; pleuromacrocystidia; cheilomacrocystidia; SEM of basidiospore. Scale bars = 10 µm (all others), 2 µm (basidiospore).

Sporocarp characteristics — *Lactifluus kanadii* differs from the other members of *L.* sect. *Piperati* due to the clear change of basidiomata colour from yellowish white when young to pale orange to ochraceous and darker to even brownish on maturity and when bruising, the trichoepithelium nature of pileipellis and stipitipeliis and in sequence data of the nrITS, LSU and *rpb2* markers.

Typus. India, Arunachal Pradesh, Bebar Thanka, Dirang, West Kameng, under *Castanopsis* sp. (*Fagaceae*) in temperate broadleaf forest, 4 Aug. 2019, *I. Bera*, IB 19-020 (holotype CAL 1826, ITS, LSU and *rpb2* sequences GenBank MW295837, MW295839 and MW354672, MycoBank MB 838371).

Additional material examined. India, Arunachal Pradesh, Namchu, Dirang, West Kameng, under *Castanopsis* sp. (*Fagaceae*) in temperate broadleaf forest, 6 Aug. 2019, *I. Bera*, IB 19-025, CAL 1827, ITS, LSU and *rpb2* sequences GenBank MW295838, MW295840 and MW354673.

Notes — The combination of macro- and micromorphological characters like the smooth, yellowish white, firm sporocarp, crowded lamellae, yellowish white, copious, latex, acrid tasting context and two-layered pileipellis with the hyphal suprapellis and the cellular subpellis with pileocystidia undoubtedly place *L. kanadii* in *L.* subg. *Lactifluus* sect. *Piperati* (Hesler & Smith 1979, Heilmann-Clausen et al. 1998, De Crop et al. 2014). In the field, it can be misidentified as *L. piperatus* (as the name has been misapplied several times to many lookalike specimens worldwide), but *L. kanadii* easily distinguishes itself due to its much smaller pileus (30–85 mm diam), striking colour change of the basidiomata from the yellowish white in young sporocarps to light orange to ochraceous and darker and even brownish on maturity, its context that immediately turns yellowish in KOH, much thicker pileipellis (up to 137 µm thick) and the trichoepithelial nature of both the pilei- and stipitipellis. Morphologically, *L. glaucescens* can also be confused with *L. kanadii*. But *L. glaucescens* can be distinguished on account of its latex turning greenish on drying, subglobose to ellipsoid basidiospores (Q = 1.05–*1.26*–*1.33*–1.45) with much shorter ornamentation (up to 0.2 µm high), longer pleuromacrocystidia (60–90 × 7–10 µm) and cheilomacrocystidia (55–70 × 7–9 µm) (Heilmann-Clausen et al. 1998).

The Indian species *Lactifluus dwaliensis* (originally described as *Lactarius dwaliensis*) can easily be distinguished from *L. kanadii* due to its much more robust and larger sporocarps (pileus 84–130 mm diam, stipe 50–145 × 17–30 mm), rather distant lamellae and latex turning greenish yellow on exposure (Das et al. 2003, Verbeken et al. 2012).

(text continues on Supplementary material page FP1257)

Supplementary material

FP1257 Maximum Likelihood (ML) phylogram inferred from raxmlGUI v. 2.0 (Edler et al. 2021) based on concatenated three-locus (nuc rDNA ITS, nrLSU and *rpb2*) sequences of *Lactifluus*. Bootstrap support values (> 70 %) obtained from the Maximum Likelihood (ML) analysis are shown above or below the branches at nodes. Sequences derived from the novel Indian species *Lactifluus kanadii* (vouchers IB 19-020 and IB 19-025) are presented in blue and bold font.

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Meruliopsis faginea

Fungal Planet 1258 – 13 July 2021

Meruliopsis faginea Volobuev & Ismailov, *sp. nov.*

Etymology. Name refers to the host genus *Fagus* on which wood this fungus was collected.

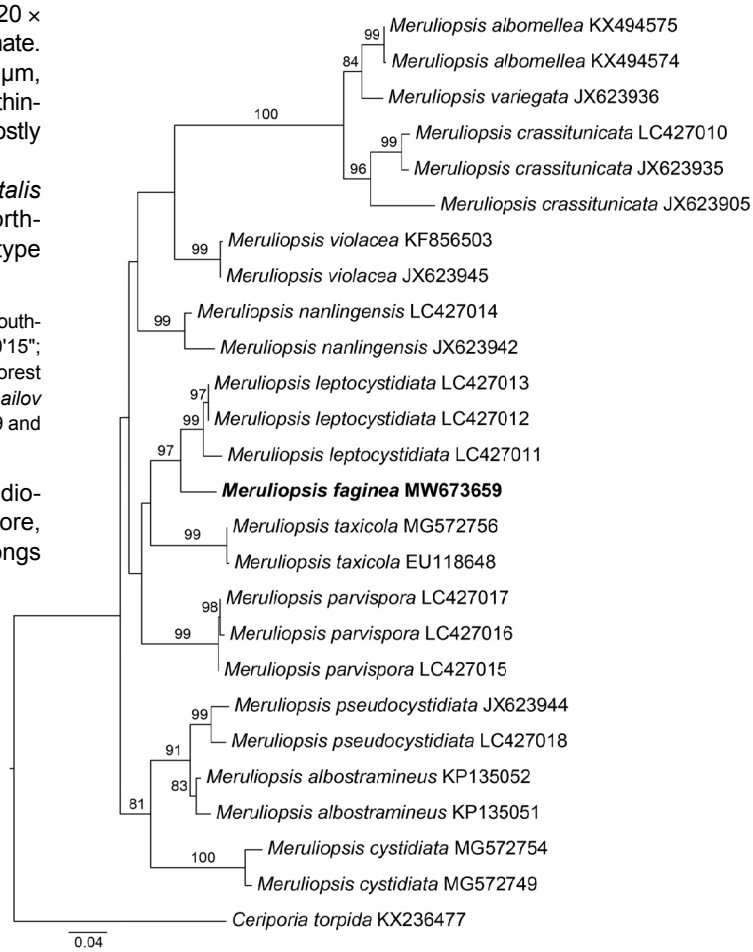
Classification — *Irpicaceae*, *Polyporales*, *Agaricomycetes*.

Basidiomata annual, resupinate, poroid, separable to slightly adnate, effuse, brittle when dry, up to 1 mm thick and 3 cm wide. Margin white, well-distinguished, up to 2 mm wide, thinning out, cottony to fimbriate. *Pore surface* pale greyish brown with light pinkish brown tints and yellowish beige close to the edge. *Pores* 3–4 per mm, round to angular and slightly elongate, with entire dissepiments. Subiculum thin, white to cream, soft and cottony, up to 0.5 mm thick. Tube layer concolorous with pore surface. *Hyphal system* monomitic; generative hyphae simple-septate. Subicular and tramal hyphae 3–4.5 µm diam, hyaline, slightly to distinctly thick-walled, encrusted with numerous sandy-like crystals, occasionally ampullate, strongly ramified, loosely interwoven, often branched at right angles. Subhymenial hyphae up to 2.5–3 µm diam, hyaline, thin-walled, smooth, compactly interwoven. *Cystidia* 25–35 × 3.5–4.5 µm, rather common, thin-walled, not encrusted, partly projecting above the hymenium up to 15 µm long, almost cylindrical to fusoid. *Basidia* 16–20 × 4.5–5 µm, clavate, with a simple septum at the base, 4-sterigmate. *Basidiospores* (3.9–)4.0–4.9(–5.3) × (1.9–)2.0–2.3(–2.4) µm, *n* = 30, L = 4.37, W = 2.15, Q = 1.83–2.29, smooth, hyaline, thin-walled, suballantoid to ellipsoid, inamyloid, non-dextrinoid, mostly with one oil drop.

Habitat & Distribution — On dead fallen *Fagus orientalis* branches, in a beech forest of piedmont Dagestan (North-Eastern Caucasus, Russia). Hitherto only known from the type locality.

Typus. Russia, Republic of Dagestan, Tabasaransky District, 1850 m southwestward from the Yersi settlement, 690 m a.s.l., N42°00'02" E48°00'15"; on fallen dead branches of *Fagus orientalis* (*Fagaceae*) in beech forest without any herbal undergrowth, 12 Sept. 2020, *S. Volobuev* & *A. Ismailov* (holotype LE F-334408, ITS and LSU sequences GenBank MW673659 and MW673660, MycoBank MB 839242).

Notes — *Meruliopsis faginea*, having resupinate basidiocarps with a greyish to pinkish brown poroid hymenophore, monomitic hyphal system and simple-septate hyphae, belongs to the genus *Meruliopsis*, distinguished as a well-supported clade in a recent three-gene phylogenetic study (Chen et al. 2020). Our Maximum Likelihood analysis of ITS sequences showed that *M. faginea* forms a neighbouring branch to *M. leptocystidiata*, and according to a BLAST search of NCBIs GenBank nucleotide databases the similarity of these sequences is insufficient to consider *M. faginea* and *M. leptocystidiata* conspecific. The comparison results of the newly generated nrITS sequence of *M. faginea* with *M. leptocystidiata* sequences are as follows: GenBank LC427013; Identities = 517/552 (94 %), 17 gaps (3 %); LC427012; Identities = 511/546 (94 %), 17 gaps (3 %); LC427012; Identities = 551/603 (91 %), 27 gaps (4 %). Moreover, *M. faginea* has larger basidiospores (mostly 4–4.9 × 2–2.3 µm vs 3–4 × 1.5–2 µm in *M. leptocystidiata*), wider pores and a more intensive colour of the pore surface. Morphologically, *M. faginea* is close to *M. violacea* in shape and size of spores, as well as hyphal structure, but the latter species differs by having violet or purple violet tints of the pore surface and lacking cystidia.



Phylogenetic tree derived from a Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 data. The analysis was performed in the IQ-TREE Web Server (Trifinopoulos et al. 2016) with 1000 ultrafast bootstrap replicates. Maximum Likelihood bootstrap support values > 80 % are shown above branches. The new species is shown in **bold** face. The scale bar represents the expected number of nucleotide changes per site.

Colour illustrations. Beech forest in the vicinity of the Yersi settlement (Dagestan, Russia). Basidiocarp; cystidia and spores (all from holotype). Scale bars = 1 cm (basidiocarp), 10 µm (cystidia), 5 µm (spores).

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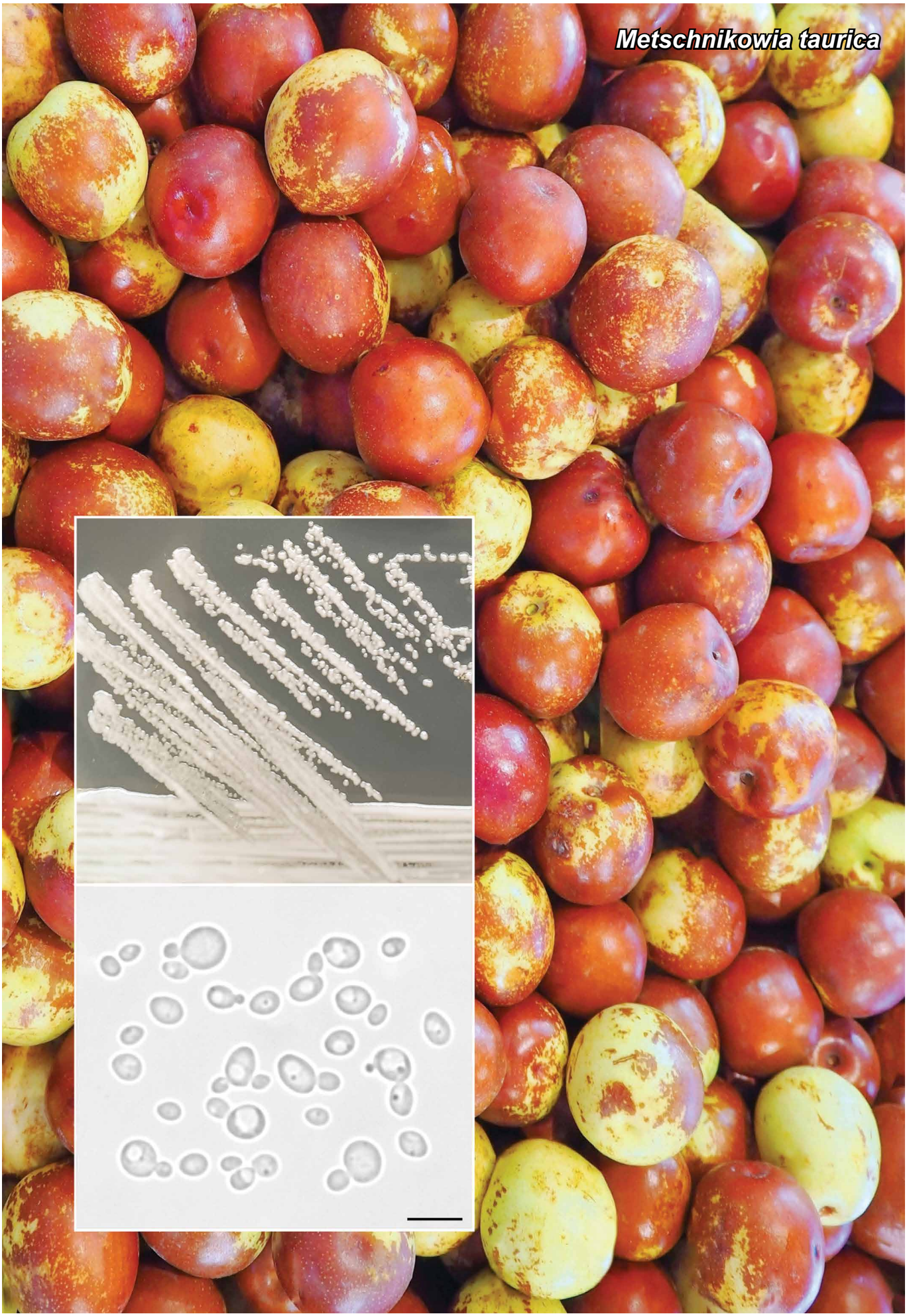

Metschnikowia taurica

Fungal Planet 1259 – 13 July 2021

Metschnikowia taurica Kachalkin, A.M. Glushakova & M.A. Tomashevskaya, *sp. nov.*

Etymology. From the Latin *Tauria* (Crimea), referring to the region where this species was found.

Classification — *Metschnikowiaceae*, *Saccharomycetales*, *Saccharomycetes*.

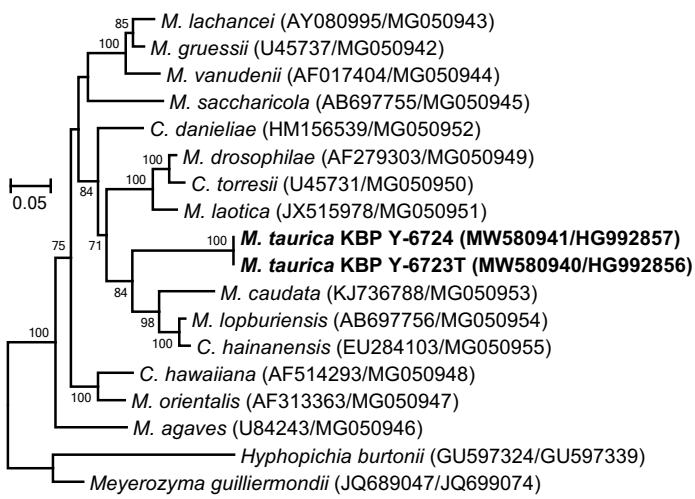
On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 23 °C, *streak* is white to cream, flat with a smooth surface, glistening, butyrous in texture with a slightly irregular margin. *Cells* are subglobose and ovoid (1.5–3.5 × 2–4 µm), and occur singly or in pairs, dividing by multilateral budding with one or two buds per cell. *Ascospores*, *pseudohyphae* and *true hyphae* not observed during 6 wk at 23 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, potato dextrose agar (PDA), cornmeal agar (CMA), McClary acetate agar and V8 juice agar. Fermentation of glucose is positive, but negative for D-galactose, sucrose, maltose, lactose and raffinose. Glucose, sucrose, trehalose (weak), maltose, melezitose, methyl alpha-D-glucoside (weak), cellobiose, salicin, L-sorbose, ethanol, D-mannitol, D-glucitol, succinic acid (weak), 2-keto-D-gluconate and arbutin are assimilated; no growth occurs on inulin, raffinose, melibiose, galactose, lactose, soluble starch, L-rhamnose, D-xylose, L-arabinose, D-arabinose, D-ribose, methanol, glycerol, erythritol, ribitol, galactitol, *myo*-inositol, DL-lactic acid, citric acid, D-glucosamine, 5-keto-D-gluconate and D-glucuronate. Assimilation of nitrogen compounds: positive for ammonium sulfate, cadaverine and L-lysine, and negative for potassium nitrate and D-glucosamine. Growth on vitamin-free medium and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth on MEA with 10 % NaCl, and 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 38 °C.

Typus. Russia, Alushta, from fruits of *Ziziphus jujube* (*Rhamnaceae*) bought on local market, Oct. 2020, *A.M. Glushakova*, B-4 (holotype KBP Y-6723, preserved in a metabolically inactive state; ex-type culture VKM Y-3063 = DSM 112138 = CBS 16717, ITS, D1/D2 domains of LSU nrDNA and *tef1* sequences GenBank MW579432, MW580940 and HG992856, MycoBank MB 838986).

Colour illustrations. Russia, Alushta, the jujube fruits on local market. *Metschnikowia taurica* KBP Y-6723: growth of yeast colonies and yeast cells on GPYA (after 7 d at 23 °C). Scale bar = 5 µm.

Additional material examined. Russia, Alushta, from fruits of *Z. jujube* bought on local market, Oct. 2020, *A.M. Glushakova*, KBP YE-1682 = KBP Y-6724, ITS, D1/D2 domains of LSU nrDNA and *tef1* sequences GenBank MW579433, MW580941 and HG992857.

Notes — During a survey of endophytic yeast biodiversity, two conspecific and asexual yeast strains belonging to the genus *Metschnikowia* were isolated from internal tissues of jujube fruits. Many new species of *Metschnikowia* have been isolated before from plant-insects associations (Lachance 2016). The nrDNA sequences of studied strains have a number of nucleotide substitutions and indels between described species. Based on a blastn search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence is *Metschnikowia caudata* (CBS 13651^T, GenBank KM233175; Identities = 236/287 (82 %), 16 gaps (5 %)); using the **LSU** sequence these are *Candida hainanensis* (AS2.3478^T, GenBank EU284103; Identities = 290/326 (89 %), 12 gaps (3 %)) and *C. touchengensis* (CBS 10585^T, GenBank EU284103; Identities = 310/355 (87 %), 14 gaps (3 %)); using ***tef1*** it is *C. hainanensis* (NRRL Y-48715, GenBank MG050955; Identities = 817/850 (96 %), no gaps). Results of the phylogenetic analysis of the LSU and *tef1* combined dataset as proposed by Kurtzman et al. (2018) suggest that studied strains belong to a new species closest to the *M. caudata* clade, including both asexual and sexual yeasts. *Metschnikowia taurica* sp. nov. differs from the phylogenetically closest species by 4–12 physiological characteristics. Among common distinctions, the new species is not able to assimilate glycerol and no growth in the presence of 10 % NaCl.



Maximum likelihood (ML) tree of *Metschnikowia taurica*, the *M. caudata* clade and some closely related species obtained from the combined analysis of LSU and *tef1* genes. The alignment included 1 091 bp and was performed with MAFFT v. 7 (Katoh et al. 2019). The Kimura two-parameter model with a gamma distribution of invariant sites was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). The novel species is highlighted with **bold** font.

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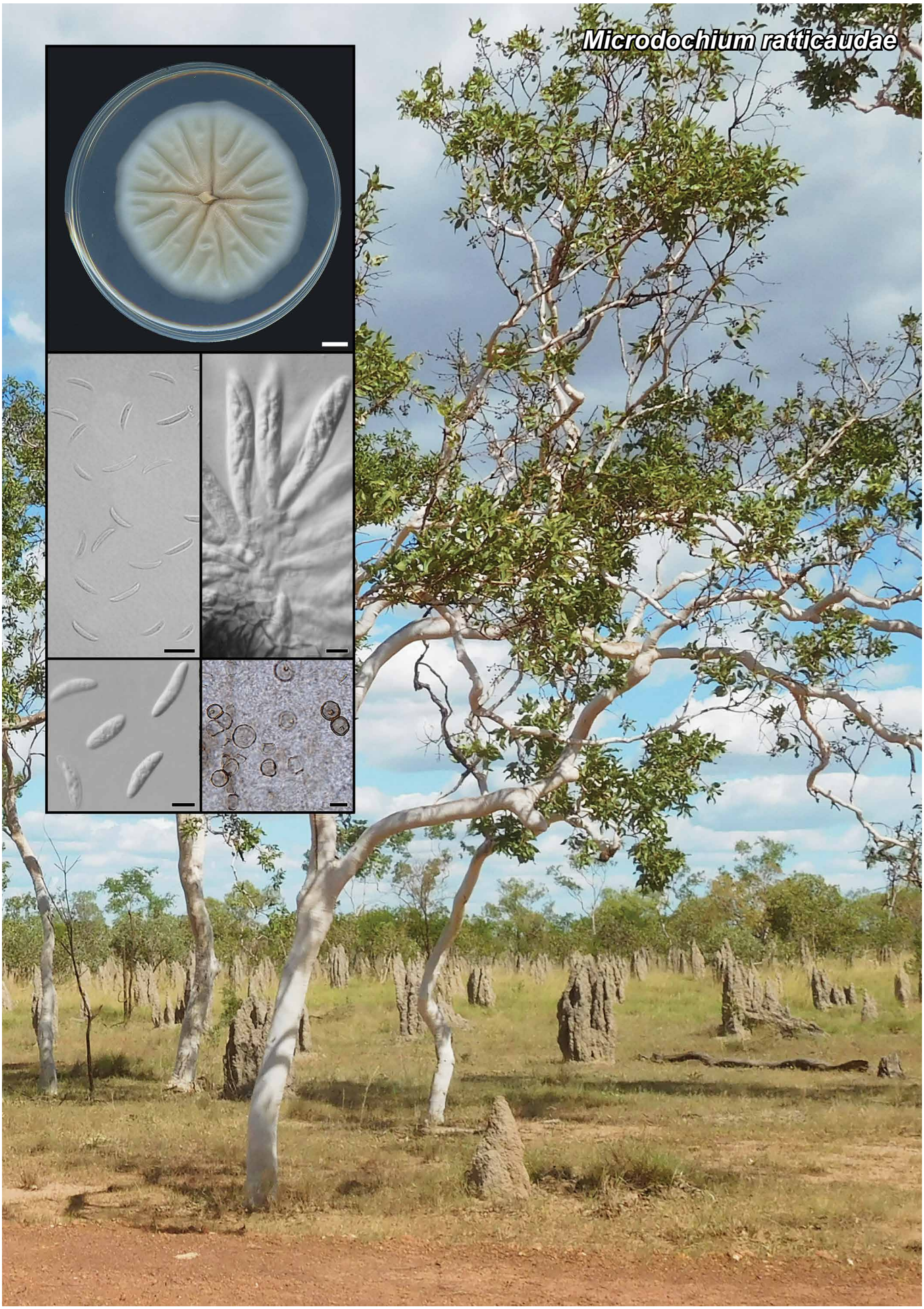

Microdochium ratticaudae

Fungal Planet 1260 – 13 July 2021

Microdochium ratticaudae Steinrucken, Vitelli, Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. After the common name of the host plant, giant rat's tail grass, from which the fungus was collected.

Classification — *Microdochiaceae*, *Xylariales*, *Sordariomycetes*.

Mycelium immersed and superficial. *Sporodochia* slimy, buff, aggregated, indistinct. *Conidiophores* undifferentiated. *Conidiogenous cells* indistinct from hyphae, terminal, solitary. *Conidia* fusoid, falcate, 7–11 × 1.5–2.5 µm, acute at the apex and narrowed at the base, hyaline, aseptate. *Chlamydospores* abundant, subglobose or cylindrical, terminal, solitary or in short chains, 7–12 µm diam, with a conspicuous germ pore, pale to olivaceous brown. *Ascomata* perithecial superficial, solitary, subspherical, 100–160 µm diam, pale brown, paraphysate. *Asci* basal, 50–75 × 10–14 µm, narrowly clavate, with eight ascospores, short stipitate. *Ascospores* fusoid to navicular, 14–24 × 4–7 µm, aseptate, hyaline, smooth.

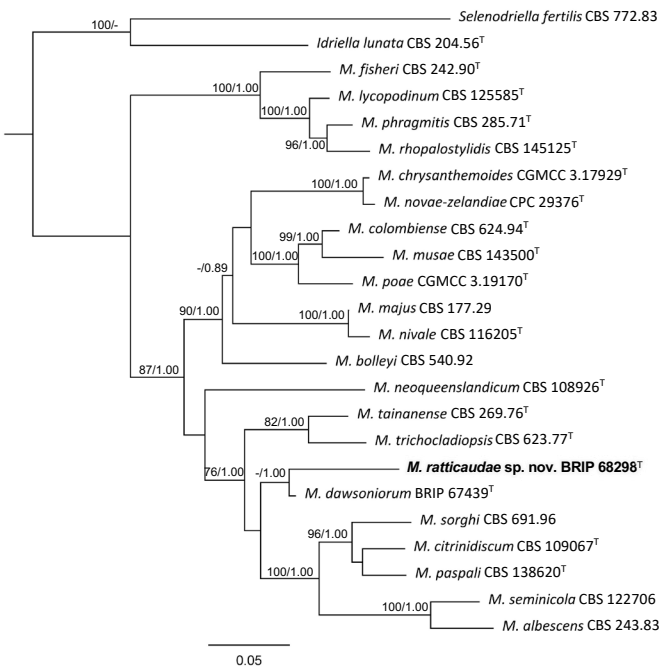
Culture characteristics — Colonies on oatmeal agar (OA) and potato dextrose agar (PDA) ± 6 cm diam after 10 d at 25 °C, surface flat, rugose, rosy buff to buff, margin entire.

Typus. Australia, Queensland, Taunton, Williams Way, S24°26'58.0" E151°47'05.6", from stem of *Sporobolus natalensis* (*Poaceae*), 15 May 2018, *J.S. Vitelli* (holotype BRIP 68298, includes ex-type culture, ITS, LSU and *rpb2* sequences GenBank MW481661, MW481666 and MW626890, MycoBank MB 838488).

Notes — *Microdochium ratticaudae* was discovered during a survey in Australia for fungi on leaves and stems of introduced giant rat's tail grasses (*Sporobolus natalensis* and *S. pyramidalis*), which have become weedy in pastures. *Microdochium ratticaudae* is currently under investigation by us as a potential biological control agent for these exotic grasses in Queensland. The genus *Microdochium* contains about 50 species, with several that are plant pathogens of grasses (Hernández-Restrepo et al. 2016, Liang et al. 2019, Marin-Felix et al. 2019b).

A multilocus phylogenetic analysis of the ITS, LSU and *rpb2* loci placed *M. ratticaudae* in a monophyletic branch sister to *M. dawsoniorum*, and close relatives of *M. albescens*, *M. citrinidiscum*, *M. paspali*, *M. seminicola* and *M. sorghi*.

A blastn search of NCBIs GenBank shows that the closest hits using the **ITS** sequence were *M. trichocladiopsis* (GenBank KP858998; Identities 493/516 (96 %), seven gaps (1 %)), *M. tainanense* (GenBank NR_145248; Identities 491/515 (95 %), seven gaps (1 %)) and *M. dawsoniorum* (GenBank MK966337; Identities 497/526 (94 %), ten gaps (1 %)). A blastn search of NCBIs GenBank shows that the closest hits using the **LSU** sequence were *Sporothrix sclerotialis* (GenBank MH872840; Identities 852/864 (99 %), two gaps (0 %)), *M. tainanense* (GenBank KP858931; Identities 853/860 (99 %), one gap (0 %)) and *M. bolleyi* (GenBank MH869857; Identities 849/864 (98 %), three gaps (0 %)). A blastn search of NCBIs GenBank shows that the closest hits using the ***rpb2*** sequence were *M. albescens* (GenBank KP859103; Identities 710/839 (85 %), no gaps) and *M. bolleyi* (GenBank LT990643; Identities 743/891 (83 %), no gaps).



Phylogenetic tree of *Microdochium* species based on maximum likelihood analysis of a combined multilocus alignment (ITS, LSU and *rpb2*). Analyses were performed on the Geneious Prime ® 2021.0.3 platform (Biomatters Ltd.) using RAxML v. 8.2. (Stamatakis 2014) and MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. Branch lengths are proportional to distance. RAxML bootstrap (bs) values greater than 70 % and Bayesian posterior probabilities (pp) greater than 0.8 are given at the branches (bs/pp). *Selenodriella fertilis* and *Idriella lunata* were used as outgroups. The novel taxon is indicated in **bold**. Ex-type strains are marked with T.

Colour illustrations. Central Queensland (photo credit M.D.E. Shivas). Colony on PDA; conidia; asci; ascospores; chlamydospores. Scale bars = 1 cm (Petri dish), 10 µm (all others).

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Mollisia endogranulata

Fungal Planet 1261 – 13 July 2021

Mollisia endogranulata Matočec, I. Kušan, Pošta, Mešić & Tkalčec, *sp. nov.*

Etymology. Named after the granular matter found in ectal excipular cells.

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

Ascomata apothecial, plate-shaped when young, becoming richly lobed when fully mature, superficial, sessile, irregular from above, *(1.7–)2–4 mm diam, solitary or few apothecia merged together, thin-fleshed in relation to size. Hymenium white to pale beige or pale grey, wrinkled; margin sharp, whitish, smooth, entire, lobed, ex-rolled in maturity; excipular surface pale brown from apothecial base to the upper flank, smooth. Basal hyphae not visible. *Hymenium* *95–115 µm thick. *Asci* cylindrical with conical-subtruncate apex, *77.8–107 × 6.6–7.7 µm, *pars sporifera* *41.4–48.9 µm, 8-spored, base pleurorhynchous, arising from repetitive croziers, apical apparatus refractive and readily visible already in water, in Lugol's solution (IKI) apical ring medium to strongly amyloid (2–3bb) of *Calycina*-type. *Ascospores* cylindrical to elongated ellipsoid when slightly heteropolar or vestigiiform-pisciod to subscutuliform when strongly heteropolar, nearly straight to slightly bent, 1-celled, *8.9–*11.5*–14.7(–15.2) × (2.9–)3–*3.6*–4.2(–4.3) µm, n = 60, *Q = 2.4–*3.2*–4, hyaline, smooth, uninucleate, freshly ejected without sheath, biseriate inside *asci, without lipid bodies (LBs) to sparsely guttulate, when overmature and just germinated remaining aseptate, LBs regularly present, 1–1.7 µm diam; in IKI and brilliant cresyl blue (CRB) sporoplasm unstained. *Paraphyses* subcylindrical, tapered at apex, widest in the middle part, apical cell *(35.3–)43–75.1 × (2.6–)2.9–4.6 µm, †2–3.2 µm wide, straight, simple, *at first containing long series of mutually compressed nummuliform, strongly refractive vacuolar bodies (VBs), coalescing only in old apothecia into a single or several cylindrical VBs, wall thin and hyaline; in KOH without yellow reaction; in IKI VBs not stained, in CRB turquoise blue to deep blue, immediately collapse after adding KOH. *Subhymenium* *17–21 µm thick, hyaline, richly beset with highly repetitive croziers, composed of hyaline densely packed epidermoid and shortly cylindrical cells, *2–4.7 µm wide. *Medullary excipulum* *70–85 µm thick at the middle flank, *37–48.5 µm at the upper flank, composed of rather compact hyaline *textura porrecta-intricata*, cells *2.7–4.5 µm wide, devoid of crystals and KOH-soluble cytoplasmic bodies. *Ectal excipulum* *42–66 µm thick at the middle flank, *45–62 µm at the upper flank, composed of *textura globulosa-angularis*, cells *7–25.7 × 5–19.5 µm, †6–18.2 × 4–12.5 µm, in the inner part walls hyaline, in the outer part thickened, ochre-brownish, *0.6–0.8 µm thick. Outermost cells of the upper flank contain single VB, while inner cells and nearly all cells of middle and lower flank contain resistant excipular granules (REG), i.e., single to few fixed, subhyaline and moderately refractive, KOH resistant granules, bluish grey in CRB and greyish pink in CRB+KOH, but not stained by IKI, 2.5–4.2 µm diam; excipulum devoid of true intra- or intercellular crystals. *Marginal tissue* *30–34 µm thick, hairless, composed of hyaline cylindrical cells resembling paraphyses, running perpendicularly towards the surface, terminal cells cylindrical-clavate, thin-walled, *11–16.7 × 3.7–7 µm, containing single refractive hyaline VB. *Subicular hyphae* completely reduced.

Culture characteristics — Colonies after 40 d in the dark at 20 °C on wort agar (2 % sucrose) 7.5–12.6 mm diam, pulvinate, inconspicuously papillate, with whitish grey covering, woolly aerial hyphae; margin radially diffuse, hyaline; underlying layer more compact, hazel brown, partially visible near margin; reverse sienna ochre to dull cinnamon grey, but pale cinnamon orange diffuse pigmentation present in substratal broad zone around colonies. Exudate drops absent. Large stellate-dendritic sulphur yellow and small orange fibrillar-fasciculate crystalloids abundantly formed around the colony edge. Conidiogenesis absent even within 2.5 mo. Aerial, covering loosely woven hyphae hyaline to subhyaline; underlying hyphae ± compact, porrectoid, subhyaline to pale ochre, but becoming substromatal, epidermioid and with slightly thickened walls in old cultures; all hyphae thin-walled, smooth, septate, branched, rich in LBs, *1.9–3.5 µm wide, wall *(0.2–)0.3–0.4 µm, often producing loops with trapped brown matter. Conidiophores and conidia absent. Asterisk (*) denotes living and cross (†) dead state. Ascus amyloidity is termed after Baral (1987), spore shape after Kušan et al. (2014), and wort agar is prepared after Fassatiová (1986).

Distribution & Habitat — Known so far only from the type locality in the Konavle area, Croatia. Type collection was found on deteriorated, previously treated and introduced hardwood lying in litter on the forest floor, under a dense canopy in the evergreen thermo-Mediterranean forest.

Typus. Croatia, Dubrovnik-Neretva County, Konavle area, 330 m S-SW from the Ljuta river spring, N42°32'12.5" E18°22'43.5", 70 m a.s.l., on deteriorated hardwood, in a forest of *Laurus nobilis*, with *Ligustrum vulgare*, *Smilax aspera*, *Asparagus* sp. and *Hedera helix*, 20 Dec. 2020, *I. Kušan*, (holotype CNF 2/11126, ex-type culture CBS 147847, ITS, LSU and *rpb1* sequences GenBank MW711783, MW729399 and MW725302, MycoBank MB 839046).

Notes — According to our phylogenetic analysis, *Mollisia endogranulata* belongs to the *M. endocrystallina*-*M. prismatica* clade within the *Mollisia* s.str. species group. This clade is characterised by lignicolous and apothecial species having relatively pale, often creamy white to pale grey hymenium (yellow to greenish grey in *M. ventosa*), ± concolorous with marginal areas, and with overall relatively paler pigmentation

(text continues on Supplementary material page FP1261)

Colour illustrations. Croatia, Konavle area, forest of *Laurus nobilis* near the Ljuta river spring (type locality). Apothecia; upper excipular flank texture in *H_2O; marginal texture in *H_2O; ectal excipular cells displaying REGs in *H_2O and †KOH; REGs in *CRB (two pictures) and †CRB+KOH; freshly ejected mature ascospores in *H_2O; ascus with crozier and mature asci in *H_2O, *CRB, †IKI; paraphyses in *H_2O and *CRB; 60 d old colony on wort agar with aggregation of stellate-dendritic crystals (upper left corner); part of stellate-dendritic crystal mass (left) and fibrillar-fasciculate crystalloid (right); hyphal loop and end-cells of aerial mycelium. Scale bars = 5 mm (apothecia, colony), 0.5 mm (aggregation of stellate-dendritic crystals), 50 µm (upper excipular flank, fibrillar-fasciculate crystalloid), 10 µm (all other microscopic elements).

Supplementary material

FP1261 Phylogenetic tree obtained from a maximum likelihood analysis based on concatenated ITS and LSU sequences of Mollisia endogranulata and related species.

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Neophaeococcomyces oklahomaensis

Fungal Planet 1262 – 13 July 2021

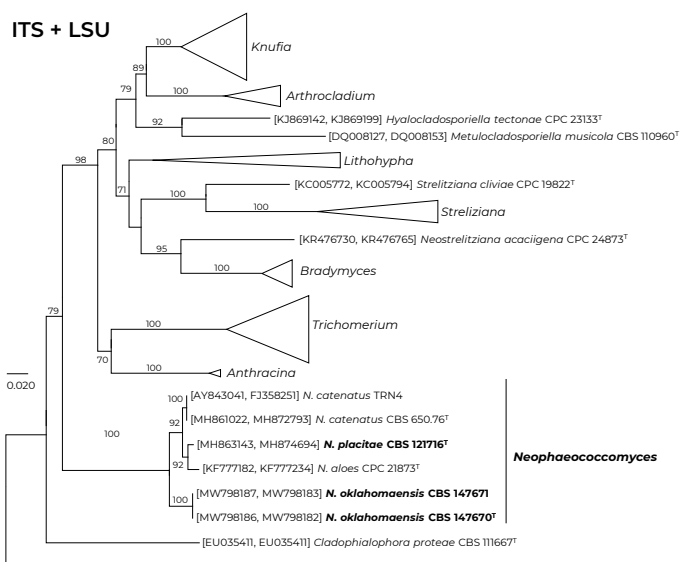
Neophaeococcomyces oklahomaensis Jurjević & Hubka, *sp. nov.*

Etymology. Name refers to the state in the USA where the species was collected, Oklahoma.

Classification — *Trichomeriaceae*, *Chaetothyriales*, *Eurotiomycetes.*

Micromorphology (on malt extract agar; MEA): *Hyphae* pale olivaceous to olivaceous brown, thick-walled, 4–7 µm diam, smooth, septate, occasionally anastomosing. *Conidia* forming from swollen arthric or blastic cells that vary in the shape from commonly globose to moniliform nearly cylindrical, smooth, (4–)5–7(–8) × 4–7(–8) µm diam, occasionally cells remain attached, forming unbranched or branched chains, lacks distinctive conidiophores.

Culture characteristics — (in darkness, 25 °C after 21 d): Colonies on MEA 10–12 mm diam, velvety to near smooth, olivaceous black to black (R46; Ridgway 1912), abruptly rising 5–6 mm, radially moderate deep to deep sulcate near wrinkled, irregularly lobed margin, exudate absent, soluble pigments absent, reverse olivaceous black to black. Colonies on Czapek yeast autolysate agar (CYA) 8–10 mm diam, similar appearance to MEA. Colonies on potato dextrose agar (PDA) 8–10 mm diam, velvety to near smooth, olivaceous black to black (R46), radially lightly sulcate, exudate absent, soluble pigments absent, reverse black. Colonies on corn meal agar (CMA) 9–11 mm diam, velvety, chaotura drab to olivaceous black (R46), rising c. 3 mm, exudate absent, soluble pigments in dark brown shades, reverse olivaceous black. Colonies on oatmeal agar (OA) 9–11 mm diam, similar appearance to MEA. Colony diam (in mm after 21 d) at 20 °C/30 °C; MEA 9–10/10–11; CYA 5–6/8–9; PDA 6–9/5–9; CMA 4–6/5–6; OA 7–9/9–10; no growth at 35 °C.



Colour illustrations. Outside wall of alcohol distillery. Conidia and conidiophores on MEA (all from 21-d-old cultures at 25 °C); *Neophaeococcomyces oklahomaensis* colonies on MEA (top to bottom 20 °C, 25 °C, 30 °C). Scale bars = 10 µm.

Typus. USA, Oklahoma, McAlester, East side of building, swab from outside wall of alcohol distillery, 20 Jan. 2016, *Ž. Jurjević* (holotype CBS H-24763, culture ex-type CBS 147670 = EMSL 3312 = CCF 6565, ITS, LSU and SSU sequences GenBank MW798186, MW798182 and MW798179, MycoBank MB 839076).

Additional materials examined. USA, Oklahoma, McAlester, East side of building, swab from outside wall of alcohol distillery, 20 Jan. 2016, *Ž. Jurjević* (culture CBS 147671 = EMSL 3313 = CCF 6566, ITS and LSU sequence GenBank MW798187 and MW798183).

Notes — BLAST analysis with the ITS sequence of *N. oklahomaensis* showed greatest similarity with *N. placitae* (~94.1 %), *N. catenatus* (93.7 %) and *N. aloes* (~92.9 %).

Neophaeococcomyces oklahomaensis commonly produces globose to moniliform conidia, (4–)5–7(–8) × 4–7(–8) µm diam, compared to ellipsoidal to globose conidia in *N. aloes*, 4–7 × 3.5–6.5 µm diam, globose in *N. catenatus*, 5–9 µm diam, and narrowly ellipsoidal with obtuse apex and subtruncate base in *N. placitae*, (4–)5–6 × 3–4 µm diam.

Rock inhabiting fungi are dispersed through the diversity of the *Trichomeriaceae* and accommodated mostly in genera *Anthracina*, *Bradymyces*, *Knufia* and *Lithohypha* (Hubka et al. 2014, Isola et al. 2016, Sun et al. 2020). The genus *Neophaeococcomyces* was erected by Crous et al. (2015b) to accommodate the epiphytic *N. aloes* and the rock-inhabiting / airborne *N. catenatus.* Here we describe another rock-inhabiting member of the genus, *N. oklahomaensis*, and transfer the epiphytic species, *Exophiala placitae* (Crous et al. 2007c), to *Neophaeococcomyces.* The phenotypic differentiation of species and genera of rock-inhabiting fungi across different orders and families is almost impossible due to convergent evolution associated with adaptations to identical extreme environments. Reliable differentiation is possible only by means of molecular methods.

Neophaeococcomyces placitae (Crous & Summerell) Hubka & Jurjević, *comb. nov.* — MycoBank MB 839245

Basionym. Exophiala placitae Crous & Summerell, Fungal Planet no. 17. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands. 2007.

A best scoring maximum likelihood tree based on the ITS and LSU regions shows the relationships of *N. oklahomaensis* with other species and genera in *Trichomeriaceae*. The dataset contained 53 taxa and a total of 1546 characters of which 569 were variable. Partitioning scheme and substitution models for analyses were as follows: the GTR+I+G model was proposed for the ITS1 and ITS2; K80+I for the 5.8 region and TrNef+I+G for the LSU region. The tree was constructed with IQ-TREE v. 1.4.4 (Nguyen et al. 2015). Support values at branches were obtained from 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by superscript ^{T} and the taxonomic novelties in **bold** text. The tree is rooted with *Bacillicladium* species.

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Neosetophoma buxi

Fungal Planet 1263 – 13 July 2021

Neosetophoma buxi Spetik, Eichmeier, Pecenka, Gramaje & Berraf-Tebbal, *sp. nov*.

Etymology. Named after *Buxus*, the host genus from which the fungus was collected.

Classification — *Phaeosphaeriaceae*, *Pleosporales*, *Dothideomycetes.*

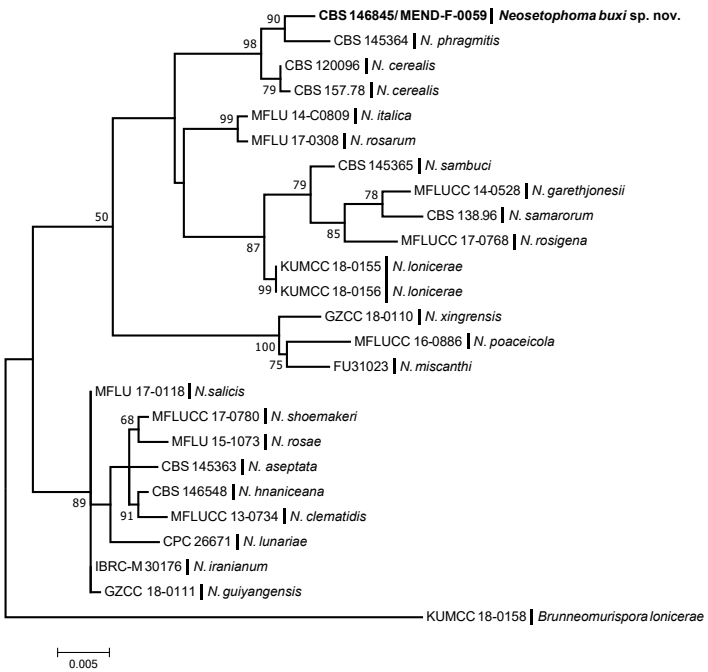
Conidiomata 60–110 µm high, 120–140 µm diam, pycnidial, separate, dark to pale brown, globose, subepidermal, unilocular, thin-walled, papillate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, doliiform to ampulliform, determinate, hyaline. *Conidia* (7.01–)8.46–9.81 (–12.03) × (1.99–)2.7–3.01(–3.23) µm, av. ± S.D. 9.56 ± 0.8 × 2.89 ± 0.41 µm, ellipsoidal to fusoid, individually hyaline to pale brown at maturity as a mass, aseptate, thin and smooth-walled.

Culture characteristics — Colonies on potato dextrose agar (PDA) reaching 25.5 mm diam at 25 °C after 10 d, margin semi-regular, erumpent, floccose, white to brown; reverse olivaceous. On malt extract agar (MEA) reaching 34.3 mm diam after 10 d, entire margin, with a moderate amount of aerial dirty-white mycelium and greyish white from reverse. Colony on oatmeal agar (OA) reaching 35 mm diam after 10 d, margin regular, floccose, dirty white in outer ring grey olivaceous towards to the centre, white in centre.

Typus. Czech Republic, Moutnice, isolated as endophyte from inner wood of *Buxus sempervirens* (*Buxaceae*), Sept. 2018, *M. Spetik* (holotype CBS H-24476, ex-type culture CBS 146845 = MEND-F-0059, ITS, LSU, *tef1-α* and *rpb2* sequences GenBank MW621494, MW620993, MW628871 and MW628872, MycoBank MB 838923).

Notes — In the phylogenetic analysis based on ITS and LSU sequences, *N. buxi* formed a branch sister to *N. phragmitis* with high bootstrap support (ML = 90/100). *Neosetophoma buxi* can be easily distinguished from *N. phragmitis* by size of conidia (7.01–)8.46–9.81(–12.03) × 2.7–3.01 µm in *N. buxi* vs (3–)4–5(–6) × 2 µm in *N. phragmitis.* Moreover, *N. buxi* produce smaller conidiomata 120–140 µm diam vs 180–200 µm diam in *N. phragmitis*.

Based on a megablast search of NCBIs nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Pleosporales* sp. (strain MI247, GenBank MW268974.1; Identities = 565/566 (99 %), one gap (0 %)), *Pleosporales* sp. (strain FL11-3, GenBank KX641956.1; Identities = 553/553 (100 %), no gaps) and *Neosetophoma* sp. (strain ZMGL13, GenBank MT446157.1; Identities = 561/567 (99 %), one gap (0 %)). The closest hits using the **LSU** sequence had the highest similarity to *Neosetophoma samarorum* (strain CBS 139.96, GenBank GQ387579.1; Identities = 1 027/1 029 (99 %), one gap (0 %)), *Pseudodiplodia* sp. (strain CBS 255.86, GenBank EU754201.1; Identities = 1 027/1 029 (99 %), one gap (0 %)) and *Dothideomycetes* sp. (strain R20I3, GenBank MK503569.1; Identities = 1 022/1 024 (99 %), one gap (0 %)); closest hits using the ***rpb2*** sequence are *Neosetophoma cerealis* (strain CBS 518.74, GenBank MT223692.1; Identities = 791/834 (95 %), no gaps), *Neosetophoma* sp. 1 (strain UTHSC:DI16-283, GenBank LT797026.1; Identities = 790/888 (89 %), no gaps) and *Neosetophoma* sp. 1 (strain UTHSC:DI16-191, GenBank LT796991.1; Identities = 788/886 (89 %), no gaps). The closest hits using the ***tef1-α*** sequence had the highest similarity to *Neosetophoma phragmitis* (strain CBS 145364, GenBank MK540148.1; Identities = 242/269 (70 %), no gaps), *Diederichomyces ficuzzae* (strain CBS 128019, GenBank KP170673.1; Identities = 213/272 (78 %), 28 gaps (10 %)) and *Parastagonospora novozelandica* (strain T15-06960B, GenBank MK540151.1; Identities = 208/270 (77 %), 13 gaps (4 %)).



Maximum likelihood tree generated from the combined analysis of ITS and LSU sequences data. Alignment comprised 25 ingroup isolates belonging to 22 *Neosetophoma* species and one outgroup taxon (*Brunneomurispora lonicerae* KUMCC 18-0158). The obtained *Neosetophoma* isolate formed a branch sister to *N. phragmitis* with high bootstrap support (ML = 90/100). The isolate was considered to be the newly described species named here as *Neosetophoma buxi* sp. nov. Maximum likelihood bootstrap support values less than 50 % are not shown. The tree was built using MEGA v. 7.0 (Kumar et al. 2016). The alignment and tree are available in TreeBASE (Submission ID: 27824).

Colour illustrations. Chateau Lednice, Czech Republic. Culture on MEA; conidiogenous cells; conidia. Scale bars = 10 µm.

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Penicillium ferraniaense

Fungal Planet 1264 – 13 July 2021

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

Etymology. Latin, name refers to Ferrania, the city where the type was isolated.

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

Conidiophores monoverticillate, minor portion with a singular additional branch that exceeds the length of the main axis. *Stipes* hyaline, smooth, short, 50–80 × 2–3.5 µm, vesiculate, 2.5–5 µm. *Phialides* ampulliform, 5–9 per stipe, 7–10 × 2–3 (8.7 ± 1.1 × 2.6 ± 0.3) µm. *Conidia* smooth-walled, hyaline to greenish, subglobose to broadly ellipsoidal, 2.5–3(–3.5) × 2–2.5 (2.8 ± 0.2 × 2.3 ± 0.1) µm. *Ascomata* or *sclerotia* not observed.

Culture characteristics — Czapek yeast extract agar (CYA): Colonies radially sulcate, elevated in centre; margin slightly irregular; mycelium white; texture velvety, slightly floccose in centre; sporulation moderate; soluble pigments absent; exudates present as small, hyaline droplets, predominantly present in centre; conidia *en masse* greyish green; reverse pastel yellow, pale orange to orange white at margin. Malt extract agar (MEA): Colonies radially sulcate, flat; margin irregular, umbonate; mycelium white; texture velvety; sporulation moderate, intensifying towards to centre, absent at edge; soluble pigments absent; exudates absent; conidia *en masse* greyish green; reverse brown in centre, pale brown at edge. Yeast extract sucrose agar (YES): Colonies randomly sulcate (radial and concentric), slightly elevated; margins entire; mycelium white or pale yellow; texture velvety; sporulation weak to moderate in centre, absent at margin; soluble pigment absent; exudates absent; conidia *en masse* greyish green; reverse pale yellow to yellowish white, golden yellow in centre. Dichloran 18 % glycerol agar (DG18): Colonies with concentric rings in centre, radially sulcate towards margin, flat and slightly sunken in centre; margins slightly irregular; mycelium white or pale yellow; texture velvety; sporulation weak; soluble pigments absent; exudates absent; conidia *en masse* greyish green; reverse pale yellow to golden yellow. Oatmeal agar (OA): Colonies non-sulcate, plane, low; margins entire; mycelium white or yellow; texture velvety; sporulation moderate in centre, absent at margin; soluble pigments absent; exudates present as small hyaline droplets. Creatine agar (CREA): poor growth, acid production moderate to good, base production absent.

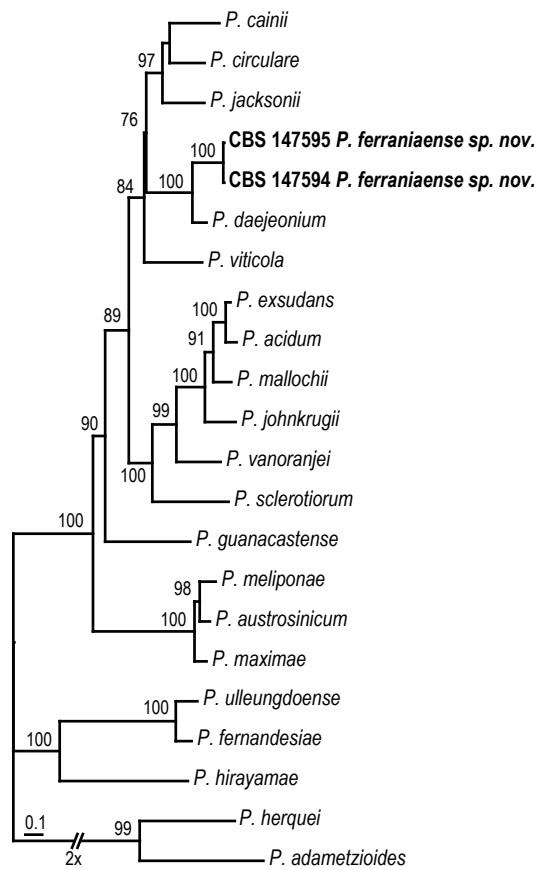
Colony diam, 7 d, in mm — CYA 25–28; CYA 30 °C 16–20; CYA 37 °C no growth; MEA 25–28; DG18 18–22; YES 21–23; OA 22–25; CREA 12–17.

Typus. Italy, Savona, Valle Bormida, Ferrania (Cairo Montenotte), from 1-d-mature compost pile made of 1 : 1 (w : w) anaerobic digestate, and green and brown waste, 15 Mar. 2018, *S. Di Piazza* (holotype CBS H-24757, culture ex-type CBS 147595 = DTO 400-D8, ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank MW694951, MW694939, MW689336, MW689338 and MW689340; MycoBank MB 839119).

Additional material examined. Italy. Valle Bormida, Ferrania (Cairo Montenotte), from anaerobic-digestate (compost), 16 Mar. 2018, *S. Di Piazza*, culture CBS 147594 = DTO 400-B2, ITS, *BenA*, *CaM* and *RPB2* sequences MW694952, MW689337, MW689339 and MW689341.

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 bar = 10 µm.

Notes — A homology search of ITS, *BenA*, *CaM* and *RPB2* sequences of *P. ferraniaense* CBS 147595 against an in-house reference sequence database containing data of all accepted *Penicillium* species (Houbraken et al. 2020), retrieved *P. daejeonium* (ITS, 99.3 %; *BenA*, 97.1 %; *CaM*, 95.6 %) as most similar species; no *RPB2* reference sequences of *P. daejeonium* are present on GenBank or in the in-house reference sequence database. The close relationship between *P. ferraniaense* and *P. daejeonium* is confirmed by phylogenetic analysis. Phylogenetic analysis also shows that *P. ferraniaense* belongs to ser. *Sclerotiorum* of sect. *Sclerotiorum*. Like other sect. *Sclerotiorum* species, the conidiophores of *P. ferraniaense* are also predominantly monoverticillate (in contrast to the biverticillate conidiophores of ser. *Herqueorum* species) and the strains do not produce coloured, soluble pigments (in contrast to ser. *Adametziorum* species). Compared to *P. daejeonium*, *P. ferraniaense* grows more slowly on CYA (25–28 vs 36–41 mm), MEA (25–28 vs 30–35 mm) and YES (21–23 vs 33–36 mm), and is able to grow on CYA incubated at 30 °C.



Maximum likelihood tree of *Penicillium* strains belonging to sect. *Sclerotiorum* ser. *Sclerotiorum* based on 1739 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 herquei* and *P. adametzioides* were used as outgroup. The scale bar indicates the expected number of substitutions per site.

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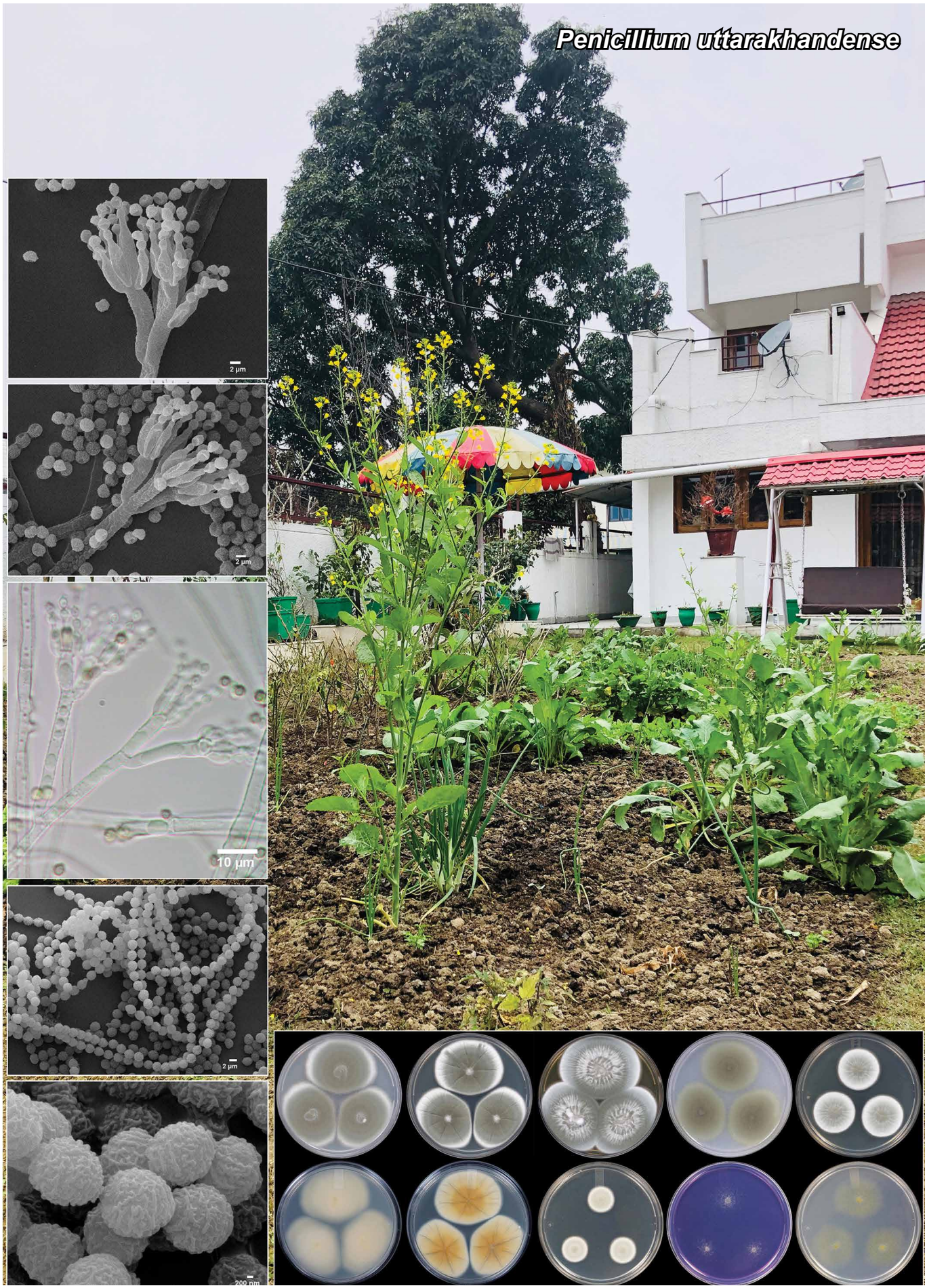

Penicillium uttarakhandense
2 µm
2 µm
10 µm
2 µm
200 nm

Fungal Planet 1265 – 13 July 2021

Penicillium uttarakhandense Rajeshk., N. Ashtekar, Visagie, G. Anand & Yilmaz, *sp. nov.*

Etymology. Latin, *uttarakhandense*, named after the state Uttarakhand, India, where this species was collected.

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

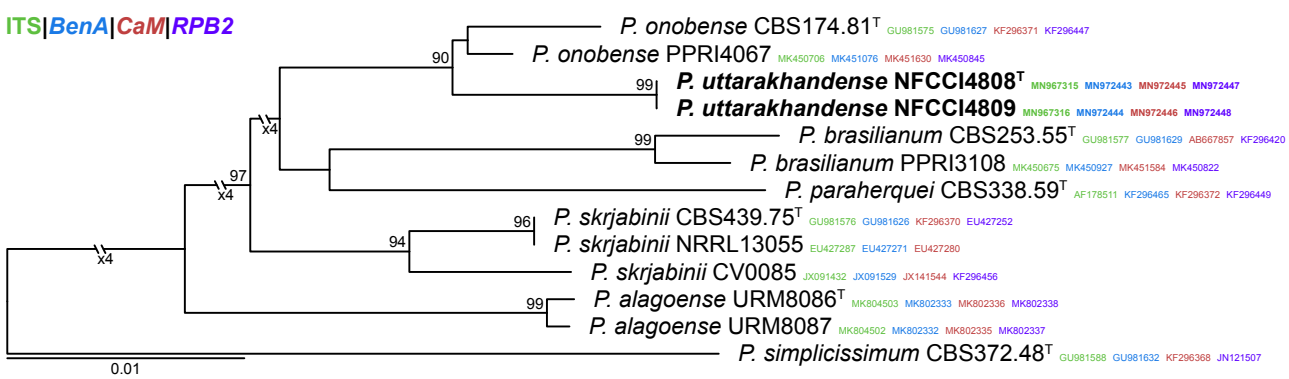
Conidiophores divaricate and biverticillate. *Stipes* finely roughened to verruculose, 160–370 × 2.5–4.5 µm. *Metulae* in verticils of 2–4, asymmetrical, 10–12(–18) × 2.5–3.5 µm. *Phialides* ampulliform, in verticils of 2–5 per metula, 7.5–10.5(–14) × 2.5–4 µm. *Conidia* globose to subglobose, 3–3.5 × 2.5–3 µm, finely roughened to roughened to verruculose, borne in long disordered chains.

Culture characteristics (25 °C, 7 d, in darkness) — Colonies on Czapek yeast autolysate agar (CYA) 34–42 mm diam, margin regular, conidia *en masse* dense, olive grey (1E2; Kornerup & Wanscher 1978) centrally, towards periphery pale grey (1B1), texture velutinous, with slight radial sulcations, exudates clear, soluble pigments absent, reverse golden yellow (4C6) centrally, with pale yellow (3A3) margin. Colonies on malt extract agar (MEA) 34–42 mm diam, margin regular, conidia *en masse* dense, dull green (24E4), texture floccose, exudates clear, soluble pigments absent, reverse light yellow (3A5) centrally, yellowish white (3A2) towards periphery. Colonies on CYA with 5 % NaCl (CYAS) 23–24 mm diam, margin regular, conidia *en masse* moderately dense, yellowish grey (3C2) to greyish green (29D5), texture velutinous, exudates absent, soluble pigments absent, reverse white (1A1). Colonies on oatmeal agar (OA) 31–33 mm diam, margin regular, conidia *en masse* moderately dense, dull green (24E4), texture velutinous, exudates absent, soluble pigments absent, reverse white (1A1). Colonies on Czapek's agar (CZ) 32–37 mm diam, margin irregular, conidia *en masse* moderately dense, yellowish white (1A2), texture velutinous, exudates absent, soluble pigments absent, reverse white (1A1). Colonies on dichloran 18 % glycerol agar (DG18) 11–13 mm diam, margin regular, conidia *en masse* sparse, greenish grey (29B2), texture velutinous, exudates absent, soluble pigments absent, reverse pale yellow (3A3). Colonies on yeast extract sucrose agar (YES) 49–52 mm diam, margin regular, conidia *en masse* moderately dense, greenish grey (29B2) to dull green (29E4), texture velutinous, sulcate, exudates colourless, soluble pigments absent, reverse greyish yellow (4B6) to pale yellow (4A3). Colonies on creatine sucrose agar (CREA) 30–32 mm diam, acid production absent.

Typus. India, Uttarakhand, Dehradun, from garden soil, 23 June 2018, *A. Garima & K.C. Rajeshkumar* (holotype AMH 10225, culture ex-type NFCCI 4808, ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank MN967315, MT026706, MN972443, MN972445 and MN972447, MycoBank MB 834093).

Additional material examined. India, Uttarakhand, Dehradun, from garden soil, 23 June 2018, *A. Garima & K.C. Rajeshkumar*, NFCCI 4809; ITS, LSU, *BenA*, *CaM* and *RPB2* sequences GenBank MN967316, MT026707, MN972444, MN972446 and MN972448.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using ***BenA*** were *P. onobense* (GenBank GU981627; Identities = 449/456 (98 %), no gaps), *P. brasilianum* (GenBank GU981629; Identities = 442/456 (97 %), one gap (0 %)) and *P. skrjabinii* (GenBank GU981626; Identities = 443/458 (97 %), two gaps (0 %)). These species are classified in sect. *Lanata-Divaricata*. This relationship was confirmed with a multigene phylogeny. Morphological comparison between *P. uttarakhandense* and *P. onobense* revealed that the new species have slightly longer stipes (up to 370 µm vs up to 300 µm) and has globose to subglobose conidia with roughened to verruculose ornamentation, compared to the elliptical to subglobose conidia with roughening in spiral bands of *P. onobense* (Ramírez & Martínez 1981).



Combined phylogeny of *P. uttarakhandense* and its close relatives, based on ITS, *BenA*, *CaM* and *RPB2*. Aligned data sets (MAFFT v. 7.450; Katoh & Standley 2013) were analysed using Maximum Likelihood analysis (IQ-TREE v. 1.6.12; Nguyen et al. 2015). Bootstrap support values (≥ 80 %) are given above supported 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. simplicissimum*.

Colour illustrations. Anand's home garden at Dehradun, Uttarakhand. Bottom row. Colonies on MEA (obverse, reverse), CYA (obverse, reverse), YES, DG18, OA, CREA, CYAS, CZ (obverse). Left column. Biverticillate (SEM) and divaricate penicilli; conidia; conidial chain (SEM); conidia (SEM).

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Phaeoacremonium adelophialidum

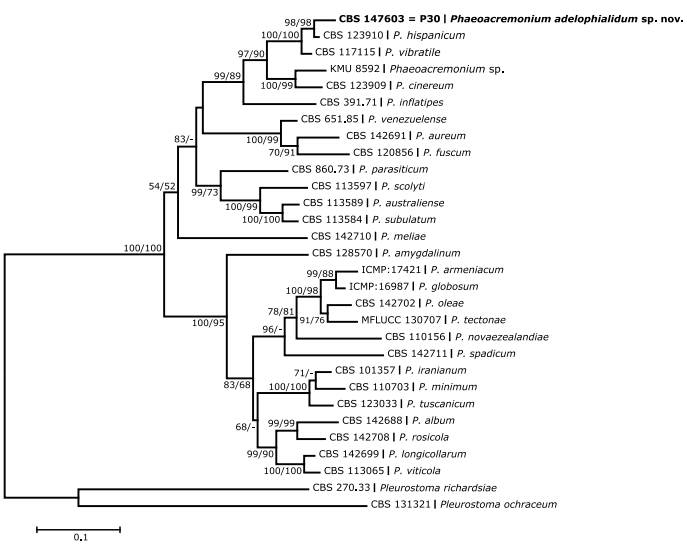
Fungal Planet 1266 – 13 July 2021

Phaeoacremonium adelophialidum Mahamedi, Spetik, Eichmeier & Berraf-Tebbal, *sp. nov.*

Etymology. Latin, In reference to the predominance of the adelophialides.

Classification — *Togniniaceae*, *Togniniales*, *Sordariomycetes*.

Mycelium consisting of branched, septate hyphae that occur singly or in bundles of up to four; subhyaline to medium brown and smooth. *Conidiophores* mostly of short to medium length, branched or unbranched, arising from aerial or submerged hyphae, erect to flexuous, ending with lateral phialides, or occasionally in a single terminal phialide, subhyaline to pale brown, darker brown towards the tip, smooth to verruculose, (4–)8–12(–27) × (2–)2.5–3(–3.5) µm. *Conidiogenous cells* terminal or lateral, arising directly from the mycelium or integrated on conidiophores, smooth, hyaline to medium brown, mostly monophialidic, frequently rejuvenating to form chains of phialides, collarettes inconspicuous; type I phialides predominant, mostly elongated ampulliform or navicular, attenuated at the base, (4–)6–7.5(–11) × (2–)2.5–3(–3.5) µm, av. ± S.D of 30 phialides = 5.5 ± 1 × 2 ± 0.3 µm; type II phialides navicular or subcylindrical, tapering towards the apex (8–)10–11(–14) × (2–)2.5–3(–3.5) µm, av. ± S.D. of 30 phialides = 10.5 ± 2 × 3 ± 0.5 µm; type III phialides mostly subcylindrical, occasionally navicular, tapering towards the apex (10–)15.5–20(–34.5) × (1.5–)2–2.5(–3) µm, av. ± S.D. of 30 phialides = 18 ± 7 × 2.5 ± 0.4 µm. *Conidia* on aerial mycelium hyaline, aseptate, oval to subglobose, (2.5–)3–4(–4.5) × (1.5–)2–2.5(–3) µm, av. ± S.D. of 30 conidia = 3.4 ± 0.4 × 2 ± 0.2 µm; on agar surface hyaline, aseptate, mostly cylindrical to allantoid, (4–)6–7(–8) × 1–1.5(–2) µm, av. ± S.D. of 30 conidia = 6 ± 1.4 × 2 ± 0.3 µm, also ovoid to subglobose, identical to the ones formed on aerial parts.



Phylogenetic relationships of *Phaeoacremonium* species based on combined *tub2* and *actA* partial sequence data using the Maximum likelihood (ML) and maximum parsimony (MP) methods, under MEGA v. 7.0 (Kumar et al. 2016). *Pleurostoma richardsiae* (CBS 270.33) and *Pl. ochraceum* (CBS 131321) were used as outgroup. The dataset consisted of 903 characters of which 540 were variable. The heuristic search of the 422 parsimony-informative characters resulted in 1 000 replicates has generated seven parsimonious trees through 1 405 steps with CI = 0.49, RI = 0.63 and HI = 0.51. ML and MP analyses produced trees with essentially identical topologies. The ML tree with ML/MP bootstrap values presented at the nodes is available in TreeBASE (Submission ID: 27892).

Colour illustrations. *Vitis vinifera* showing trunk diseases symptoms in Algerian vineyard. Type I phialides; type II phialides; type III phialides; conidiophores with percurrent rejuvenation; conidia. Scale bars = 10 µm.

Culture characteristics — Colonies reaching a radius of 3 mm after 8 d at 25 °C. Minimum temperature for growth 10 °C, optimum 25 °C, maximum 37 °C. Colonies on MEA flat, mostly fealty with very little aerial mycelium, margin entire, after 16 d colonies vinaceous buff (Rayner 1970) becoming buff, similar in the reverse. Colonies on PDA flat, short woolly to fealty, with entire to lobate margin, after 16 d vinaceous buff, fawn in centre, similar in reverse. Colonies on OA flat, fealty with very little aerial mycelium, appearing yeast-like, with entire margin, after 8 and 16 d colonies rosy buff, similar in reverse.

Typus. Algeria, Tipaza, isolated from *Vitis vinifera* (cv. Cinsault) with necrosis and black streakings, July 2007, *A. Berraf-Tebbal* (holotype BRNU 677815, culture ex-type CBS 147603 = P30, ITS, LSU, *act*A and *tub2* sequences GenBank MW689543, MW689544, HQ604996 and HQ605019, MycoBank MB 839124).

Notes — *Phaeoacremonium* species have a worldwide distribution and a wide host range, including woody plants, humans and arthropods (Mostert et al. 2006). According to Gramaje et al. (2015) and Spies et al. (2018), 29 *Phaeoacremonium* species are known only from grapevine. Phylogenetically, *P. adelophialidum* is closely related to *P. vibratile* and *P. hispanicum.* It was previously identified as *P. hispanicum* (Berraf-Tebbal et al. 2011). Based on a megablast search of NCBI nucleotide database, the closest hits using the ***actA*** sequence had the highest similarity to *P. hispanicum* (GenBank HQ700716.1; Identities = 255/261 (98 %), no gaps), *P. vibratile* (GenBank DQ649064.1; Identities = 249/262 (95 %), two gaps (0 %)) and *P. hispanicum* (GenBank FJ517156.1; Identities = 226/236 (96 %), two gaps (0 %)). The closest hits using the ***tub2*** sequence had the highest similarity to *P. hispanicum* (GenBank HQ700715.1; Identities = 622/636 (98 %), one gap (0 %)), *P. hispanicum* (GenBank FJ517164.1; Identities = 535/549 (97 %), one gap (0 %)) and *P. vibratile* (GenBank DQ649063.1; Identities = 525/550 (95 %), three gaps (0 %)); closest hits using the **ITS** sequence are *P. hispanicum* (GenBank KR909191.1; Identities = 585/586 (99 %), no gaps), *P. hispanicum* (GenBank NR_136058.1; Identities = 584/586 (99 %), no gaps) and *P. hispanicum* (GenBank MH863327.1; Identities = 582/584 (99 %), no gaps). The closest hits using the **LSU** sequence had the highest similarity to *P. sphinctrophorum* (GenBank NG_057746.1; Identities = 1 193/1 251 (95 %), 12 gaps (0 %)), *P. sphinctrophorum* (GenBank DQ173152.1; Identities = 1 165/1 215 (96 %), 12 gaps (0 %)) and *P. vibratile* (GenBank DQ649065.1; Identities = 1 169/1 222 (96 %), 13 gaps (1 %)).

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Phytophthora kelmanii

Fungal Planet 1267 – 13 July 2021

Phytophthora kelmanii Z.G. Abad, J.A. Abad, T.I. Burgess & Mostowf., *sp. nov.*

Etymology. Named to honour Dr Arthur Kelman, Emeritus Professor at the Department of Plant Pathology, North Carolina State University, USA and mentor of Jorge and Gloria Abad during their work at NCSU. Arthur Kelman (11 Dec. 1918 – 29 June 2009) was one of the most influential plant pathologists of the twentieth century. He was a member of the National Academy of Sciences for his pioneering contributions to the study of phytobacteriology and received numerous awards including Fellow of the International Society of Plant Pathology, American Phytopathological Society, the American Association for the Advancement of Science and the American Academy of Microbiology.

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

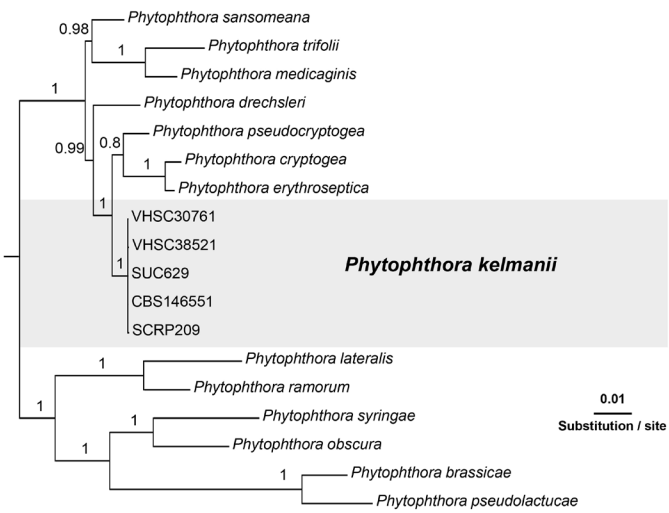
Sporangia produced on V8 agar and carrot agar (CA) flooded with both distilled water and non-sterile soil extract; terminal, borne on unbranched sporangiophores or in loose sympodia, non-papillate, predominantly ovoid, sometime broad obpyriform, rarely ellipsoid or pyriform; 46 ± 11.0 × 31 ± 4.9 µm (overall range 26–75 × 21–49 µm), length/breadth ratio of 1.5 ± 0.2. *Sporangial proliferation* in chains of internally proliferating sporangia, both nested and extended. *Hyphal swellings* common, in small clusters, various shapes, 11 ± 2.7 µm (overall range 4–15 µm). *Chlamydospores* common, globose, thin-walled, 14 ± 5.1 µm (overall range 6.5–30 µm). *Gametangia* were rarely produced in dual cultures (heterothallic). *Oogonia* smooth-walled, globose, golden to brown, 39 ± 4.5 µm (isolates ranged from 27–44 µm). *Oospores* were both predominantly plerotic to slightly aplerotic, av. 36 ± 4 µm (isolates ranged from 24–40 µm). Oospore walls wavy, av. 2.4 ± 0.9 µm, oospore wall index 0.34. *Antheridia* were amphigenous, monoclinous, spherical to ellipsoidal, ranged from 13–24 µm in length (av. 18.5 ± 1.7 µm) and 9–20 µm in breadth (av. 15.5 ± 1.7 µm). *Hyphae* were hyaline, normally non-septate, 4–5 µm wide. Minimum, optimum and maximum temperatures for growth were 4 °C, 25 °C and 37.5 °C, respectively. Radial growth rate on CA in the dark at 25 °C was 9.0 ± 1.1 mm/d.

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

Typus. Australia, Western Australia, Armadale, baited from rhizosphere soil of *Ptilotus pyramidatus*, 2016, *G. Hardy* (holotype MURU 485, culture ex-type CBS 146551, ITS, *Btub*, *hsp90*, *coxI*, *nadh1* and LSU sequences GenBank MT210487, MT210491, MT210495, MT210499, MT210503 and MT210486, MycoBank MB 838760).

Additional materials examined. Australia, Western Australia baited from rhizosphere soil of *Xanthorrhea pressii*, 27 May 2014, culture VHS30761; ibid., rhizosphere soil of *Salvia rosmarinus*, 10 Oct. 2018, collected by Department of Biosecurity, Conservation and Attractions, culture VHS38521. – USA, unknown substrate, 1992, collector unknown, culture SUC629; California, baited from rhizosphere soil of *Juglans nigra*, 1995, collector unknown, culture SCRP209.

Notes — Isolates of *Phytophthora kelmanii* constitute a well-supported monophyletic group sharing a common ancestor with a clade consisting of *P. pseudocryptogea* (Safaiefarahani et al. 2015), *P. cryptogea* (Pethybridge & Lafferty 1919) and *P. erthroseptica* (Pethybridge 1913). These species together with *P. drechsleri* (Tucker 1931), *P. sansomeana* (Hansen et al. 2009), *P. medicaginis* (Hansen & Maxwell 1991) and *P. trifolii* (Hansen & Maxwell 1991) clustered within clade 8a of the *Phytophthora* phylogeny (Yang et al. 2017). In a multigene phylogeny of the ITS, *Btub*, *hsp90*, *cox*I and *nadh1* gene regions, *P. kelmanii* differs from its closest sister taxon, *P. pseudocryptogea*, by 1.3 %. Morphologically, *P. kelmanii* is similar to other species in clade 8a, producing terminal, typically ovoid, persistent, non-papillate sporangia, and it is also a high-temperature tolerant *Phytophthora* species. The IDphy online resource was used for close evaluation of *P. kelmanii* and related species (Abad et al. 2019). Isolates of *P. kelmanii* are heterothallic similarly to *P. pseudocryptogea*, *P. cryptogea* and *P. drechsleri*, however, four of the five isolates examined were sterile and did not produce any oospores in dual cultures. In addition many oospores aborted after the formation of the oospore wall. Unlike *P. pseudocryptogea*, *P. cryptogea*, *P. erthroseptica* and *P. drechsleri*, *P. kelmanii* produced small chlamydospores on agar. *Phytophthora kelmanii* frequently forms small clustered hyphal swellings in culture media, water and soil solution cultures which is a typical character of the species. *Phytophthora kelmanii* was first isolated in 1989 from *Abies fraseri*, *Salvia officinalis* and *Picea abies* in North Carolina, USA (Abad et al. 2002). Thereafter it has frequently been isolated from firs, herbaceous ornamentals, and even agriculturally important trees such as walnut, around the world.



Bayesian inference tree based on a concatenated ITS, *Btub*, *hsp90*, *cox*I and *nadh1* sequence alignment showing the placement of *Phytophthora kelmanii* in *Phytophthora* Clade 8. The tree was generated in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) using the GTR substitution model. The posterior probability values are shown at the nodes. The tree was rooted to *P. citrophthora* (not shown) and the novel species is shown in **bold** font and a shaded box. See Yang et al. 2017 for isolate code and GenBank accession numbers of reference sequence.

Colour illustrations. *Xanthorrhoea* sp., a host of *Phytophthora kelmanii*. Typical ovoid sporangia in loose sympodia; sporangia with internal proliferation; aborted oogonium with amphigenous antheridium; mature aplerotic oospore with wavy walls; small chlamydospore; hyphal swellings; uniform colony on carrot-agar; mass of hyphal swellings typical of the species. Scale bar = 80 µm (hyphal swellings), 20 µm (others).

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Pleuroflammula pannonica

Fungal Planet 1268 – 13 July 2021

Pleuroflammula pannonica Polhorský, Kautmanová & Szabóová, *sp. nov*.

Etymology. Named after its occurrence in Slovak pannonian oak groves.

Classification — *Crepidotaceae*, *Agaricales*, *Agaricomycetes*.

Basidiomata scattered to subgregarious. *Pileus* (0.5–)1–2.3 (–3) mm diam, convex, becoming plano-convex, pale brown, amber brown to deep rust brown, moderately hydrophobic, dry, non-striate, minutely scurfy. *Veil* scanty, only visible on young basidiocarps at the margin, evanescent, appendiculate, fibrillose, white to pale brown. *Lamellae* widely spaced, 4–12, lamellulae 1–6, whitish, finally orange-brown from mature basidiospores, adnexed; edge white, serrated from cheilocystidia agglutinated into teeth-like projections. *Stipe* (0.3–)0.5–1(–1.5) × 0.15–0.5 mm, slightly to strongly eccentric, sometimes central, cylindrical, slightly enlarged towards the pileus, concolorous with pileus, fibrillose in its entirety, sometimes longitudinally striate. *Basidia* 18–29 × 5–8.3 µm, 4-spored, cylindrical to slender-clavate, indistinctly clamped. *Basidioles* 12–24 × 5–8.4 µm, slender- to broadly-clavate. *Basidiospores* (6.4–)8–9.3(–10) × (4.3–)5.2–6(–6.7) µm, Q 1.3–1.9, obovoid or ellipsoid, smooth, rust brown, ± thick-walled, wall 0.4–0.8 µm thick; lipid content granular in living spores, coalescing in dead spores into larger guttule(s); 1, 2-nucleate; germ pore often visible. *Cheilocystidia* 20–40 × 2.2–3.7 µm, distinct, variable, narrowly lageniform to cylindrical, flexuous, hyaline or containing orange-brown pigment, smooth, often agglutinated into fascicles, exceptionally apically forked, apex rounded, tapering or slightly capitate. *Pleurocystidia* absent. *Pileipellis* a cutis, composed of interwoven hyphae, 1.7–4.3 µm wide. *Pigment* intercellular, granulose or amorphous, abundant, ochre to deep orange-brown, partially dissolving in KOH solution. *Clamp connections* present.

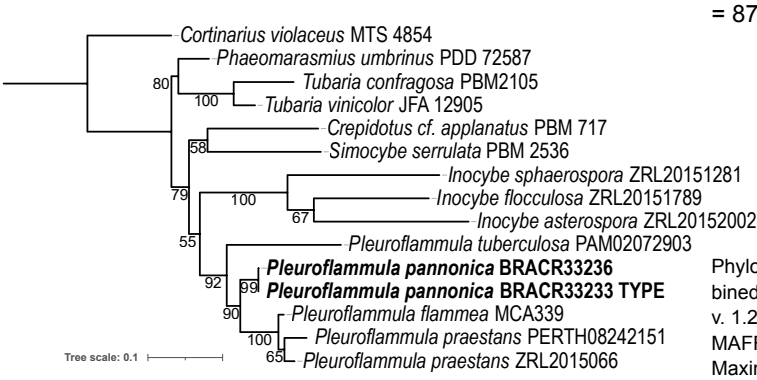
Ecology — Growing on fallen, dead *Quercus* sp. branches, on ± loose bark or on undecayed wood, not in contact with soil, 0.3–1 m above ground, in lowland, xerothermophilous pannonian oak groves with *Acer campestre*, *Cornus mas* and *Ulmus minor*. Phenology: VI–I, presumably throughout the year in case of good conditions. Geology: loess and sandy sediments.

Typus. Slovakia, Bratislava, Senec, Martinský les, corticated branches of *Quercus* sp. (*Fagaceae*), N48.25466° E17.38976°, alt. 152 m, 18 Oct. 2020, *A. Polhorský* (holotype BRA CR33236, ITS and LSU sequences GenBank MW726639 and MW726637, MycoBank MB 839244).

Additional materials examined. Slovakia, Bratislava, Senec, Martinský les, decorticated branches of *Quercus* sp., N48.25114° E17.3788°, alt. 156 m, 21 June 2020, *A. Polhorský*, BRA CR33233, ITS and LSU sequences GenBank MW726640 and MW726638; ibid., 20 Aug. 2020, *A. Polhorský*, BRA CR33234; ibid., corticated branches of *Quercus* sp., N48.25689° E17.38271°, alt. 156 m, 4 Sept. 2020, *A. Polhorský*, BRA CR33235; ibid., decorticated branch of *Quercus* sp., N48.25662° E17.36758°, alt. 171 m, 22 Jan. 2021, *A. Polhorský*, BRA CR33774; Podunajské Biskupice, Topoľové Hony, bark of cf. *Quercus*, N48.08129° E17.20171°, alt. 132 m, 18 May 2019, *A. Polhorský*, unpreserved.

Notes — Ovoid, thick-walled, rust brown basidiospores, cylindrical cheilocystidia, eccentric stipe, indistinct but present veil and orange-brown pigment dissolving in KOH agree well with the generic concept of *Pleuroflammula* and distinguishes it from morphologically similar genera (*Crepidotus*, *Phaeomarasmius*, *Pholiota*, *Simocybe*) (Horak 1978, 2018). Most of the c. 20 described species are known from the USA, but several other species are only from countries in the Southern Hemisphere (Chile, Brazil, South Africa, Indonesia, Papua New Guinea, Australia and New Zealand). Presently the only known species from Europe were cosmopolitan-appearing *P. ragazziana* (Gierczyk & Kubiński 2019) and *P. tuberculosa* (Horak 1986). From European taxa, *P. pannonica* superficially resembles small members of the genus *Phaeomarasmius*, e.g., *P. rimulincola* and *P. siquieri* (Salom & Esteve-Raventós 2011), but differs in KOH-soluble pigment, not encrusted cheilocystidia and smaller spores. This new species represents the smallest member of the genus next to *P. minutula* (pileus 2–6 mm diam), which differs in more persistent veil, broader cheilocystidia (4–7 µm) and growth on living bark of *Populus* (Smith & Hesler 1968).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of BRA CR33236 were *P. croceosanguinea* (strain TFB8631, GenBank KY559341; Identities = 540/583 (92 %), 16 gaps (2%)), *P. flammea* (AFTOL-ID 1381, GenBank DQ494685; Identities = 507/578 (88 %), 26 gaps (4 %)) and *P. praestans* (PBM3461, GenBank HQ832450; Identities = 519/597 (87 %), 36 gaps (6 %)). Closest hits using the **LSU** sequence of BRA CR33236 are *P. flammea* (MCA339, GenBank AF367962; Identities = 874/893 (98 %), no gaps), *Pleuroflammula* sp. (OKM24609, GenBank AF208533; Identities = 873/893 (98 %), no gaps) and *P. praestans* (PBM3461, GenBank HQ832464; Identities = 873/893 (98 %), no gaps).



Phylogenetic tree based on the Maximum Likelihood analysis from the combined ITS-LSU sequence alignment. Analyses were done on the Phylosuite v. 1.2.2 platform (Zhang et al. 2020). The alignment was performed with MAFFT v. 7 (Katoh & Standley 2013) and manually checked and trimmed. Maximum Likelihood phylogenies were inferred using IQ-TREE 2 (Nguyen et al. 2015) under the model automatically selected by IQ-TREE for 5000 ultrafast (Minh et al. 2013) bootstraps. Bootstrap support values are given at the nodes. *Cortinarius violaceus* was used as an outgroup. The novel taxon is indicated in **bold**. Scale bar on the tree indicates the expected number of changes per site.

Colour illustrations. Martinský les oak grove. Young and mature basidiomata; cheilocystidia; basidiospores. Scale bars = 0.5 mm (basidiomata), 10 µm (microstructures).

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Pseudosydowia backhousiae,
Pseudosydowia indooroopillyensis,
Pseudosydowia louisecottisiae
& Pseudosydowia queenslandica

Fungal Planet 1269–1272 – 13 July 2021

Pseudosydowia backhousiae R.G. Shivas, Marney & Y.P. Tan, *sp. nov.*

Etymology. Refers to *Backhousia*, a myrtaceous genus that includes the host plant from which the fungus was isolated.

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

Mycelium comprised of branched, septate, smooth, hyaline, 2–5 mm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary, producing conidia on minute lateral or terminal projections, cylindrical to ampulliform, hyaline, 7–12 × 3–5 µm. *Conidia* solitary, subglobose to ellipsoidal or obovoid, (2–)4–7(–10) × 2.5–4 µm, aseptate, apex rounded, base narrowed, hyaline, smooth.

Culture characteristics — Colonies on potato dextrose agar (PDA) after 4 wk at 25 °C reaching 5 cm diam, flat, pale rosy buff, copious conidial ooze covers the central part, without aerial mycelium, margin entire; reverse buff.

Typus. Australia, Queensland, Brisbane, Chapel Hill, on living leaves of *Backhousia citriodora* (*Myrtaceae*), 28 Aug. 2001, *T.S. Marney* (holotype BRIP 28243, includes ex-type culture, ITS sequence GenBank MW443073, MycoBank MB 838438).

Pseudosydowia indooroopillyensis R.G. Shivas, Marney & Y.P. Tan, *sp. nov.*

Etymology. Refers to the Brisbane suburb of Indooroopilly, from where the fungus was isolated.

Mycelium comprised of branched, septate, smooth, hyaline, 2.5–3.5 mm wide hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary, producing conidia on minute lateral or terminal projections, cylindrical, hyaline, 7–15 × 2.5–5 µm. *Conidia* solitary, subglobose to ellipsoidal, 4–7(–9) × 3–5 µm, aseptate, apex rounded, larger cells often papillate at base, hyaline, smooth.

Culture characteristics — Colonies on PDA after 4 wk at 25 °C reaching 5 cm diam, flat, leathery, pale rosy vinaceous, without aerial mycelium, margin entire; reverse rosy vinaceous.

Typus. Australia, Queensland, Brisbane, Indooroopilly, on living leaves of *Eucalyptus* sp. (*Myrtaceae*), 13 Sept. 2001, *T.S. Marney* (holotype BRIP 28248, includes ex-type culture, ITS and LSU sequences GenBank MW443076 and MW443081, MycoBank MB 838439).

Additional materials examined. Australia, Queensland, Brisbane (Indooroopilly), on living leaves of *Eucalyptus* sp., 13 Sept. 2001, *T.S. Marney TSM040*, culture BRIP 28246 (ITS sequence GenBank MW443074); ibid., culture BRIP 28247 (ITS and LSU sequences GenBank MW443075 and MW443080).

Pseudosydowia louisecottisiae Marney, *sp. nov.*

Etymology. Named for Louise Cottis, in appreciation of her support for T.S. Marney's mycological endeavours. "Every little breeze seems to whisper Louise."

Mycelium comprised of branched, septate, smooth, hyaline, 2.5–5 mm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary, producing conidia on minute lateral or terminal projections, cylindrical, hyaline, 7–15 × 2.5–5 µm. *Conidia* solitary, clavate or obovoid, 5–9(–10) × 2.5–4.5 µm, aseptate, apex rounded, base narrowed and sometimes papillate, hyaline, smooth.

Culture characteristics — Colonies on PDA after 4 wk at 25 °C reaching 4 cm diam, flat, pale buff with irregular pale to dark cinnamon patches in the central part, without aerial mycelium, copious conidial ooze covers the central part, margin entire; reverse buff at margin becoming honey in central part.

Typus. Australia, Queensland, Brisbane, Indooroopilly, on living leaves of *Eucalyptus* sp. (*Myrtaceae*), 13 Sept. 2001, *T.S. Marney* (holotype BRIP 28185, includes ex-type culture, ITS sequence GenBank MW443072, MycoBank MB 838440).

Additional materials examined. Australia, Queensland, Brisbane (Chapel Hill), on living leaves of *Backhousia citriodora*, 28 Aug. 2011, *T.S. Marney TSM004*, culture BRIP 28157 (ITS and LSU sequences GenBank MW443070 and MW443078); ibid., *TSM006*, culture BRIP 28159 (ITS and LSU sequences GenBank MW443071 and MW443079).

Pseudosydowia queenslandica R.G. Shivas, Marney & Y.P. Tan, *sp. nov.*

Etymology. Refers to the Australian state of Queensland, where the fungus was isolated.

Mycelium comprised of branched, septate, smooth, hyaline, 2.5–4 mm wide hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary, producing conidia on minute lateral or terminal projections, cylindrical, hyaline, 10–15 × 2.5–3.5 µm. *Conidia* solitary, subglobose to ellipsoidal, 5–10 × 3–4.5 µm, aseptate, apex rounded, hyaline, smooth.

Culture characteristics — Colonies on PDA after 4 wk at 25 °C reach 5 cm diam, flat, leathery, rosy buff, without aerial mycelium, margin entire; reverse pale rosy buff.

Typus. Australia, Queensland, Brisbane, Indooroopilly, on living leaves of *Eucalyptus* sp. (*Myrtaceae*), 13 Sept. 2001, *T.S. Marney* (holotype BRIP 28249, includes ex-type culture, ITS and LSU sequences GenBank MW443077 and MW443082, MycoBank MB 838441).

(text continues on Supplementary material page FP1269–1272)

Colour illustrations. Eucalypt woodland, central Queensland. *Pseudosydowia backhousiae* colony, hyphae and conidia (top row); *Pseudosydowia indooroopillyensis* colony, hyphae and conidia (second row); *Pseudosydowia louisecottisiae* colony, hyphae and conidia (third row); *Pseudosydowia queenslandica* colony, hyphae and conidia (bottom row). Scale bars = 1 cm (colonies), 10 µm (others).

Supplementary material

FP1269–1272 Phylogenetic tree of *Pseudosydowia* species based on a maximum likelihood analysis of a combined multilocus alignment (ITS and LSU).

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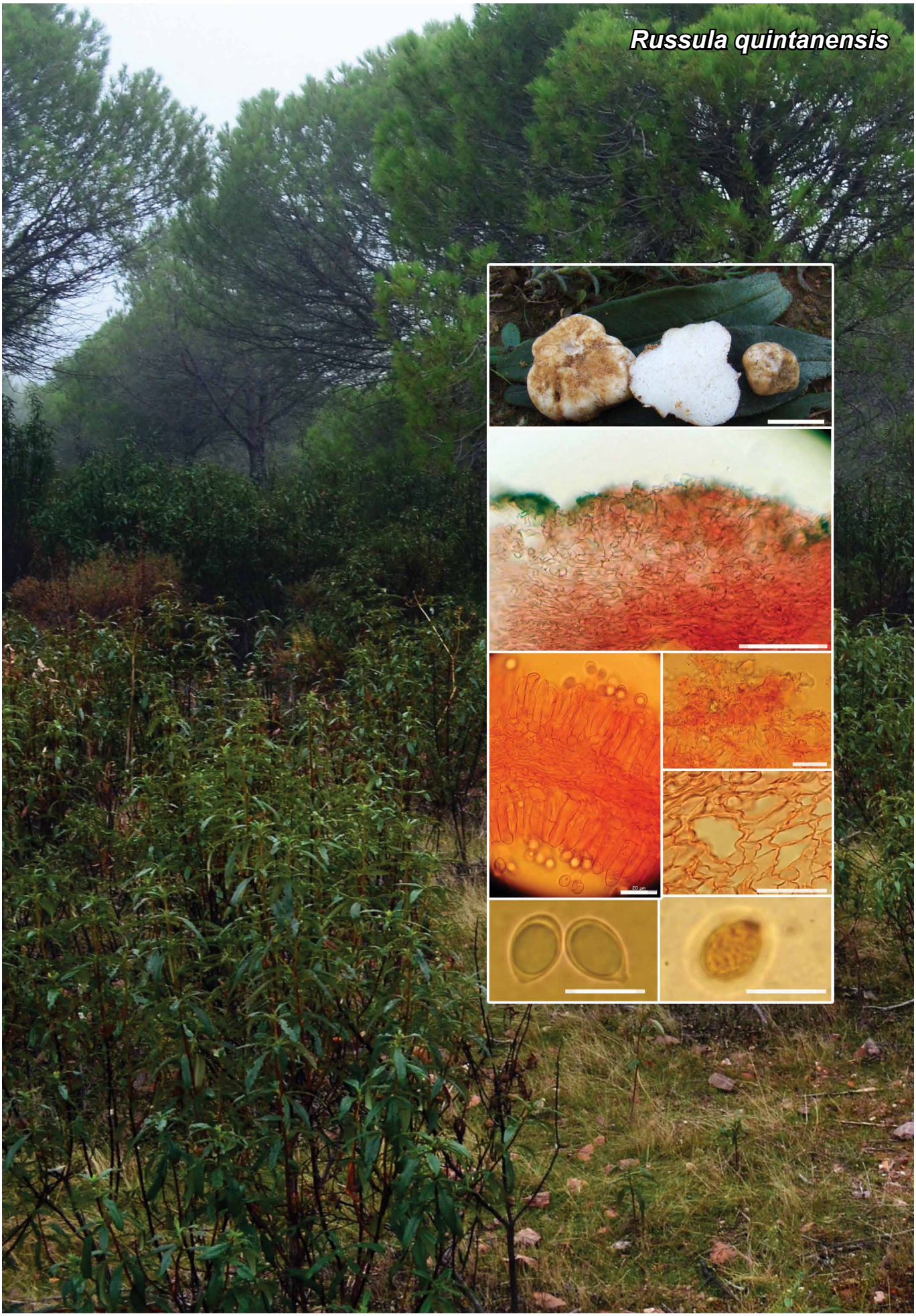
Russula quintanensis

Fungal Planet 1273 – 13 July 2021

Russula quintanensis M. Romero & P. Alvarado, *sp. nov.*

Etymology. The epithet refers to Quintana de la Serena (Extremadura, Spain), where the holotype was collected.

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

Basidiomata angiocarpic (gasteroid), irregularly globose to subglobose, sometimes also flattened or lobed, 0.5–2.8 cm diam, sometimes attached to the substrate with a small sterile base. *Peridium surface* dry, smooth to slightly tomentose, with soil debris adhered, first white, turning pale ochre with exposure and handling, pale brown to brown with whitish patches with age. Several specimens have areas where the peridium is lost, and the hymenium cells are exposed. *Gleba* loculated, composed of mostly sinuose, long and narrow cells, but occasionally also circular; pearly white in colour in young specimens, turning cream white to light brown with age, sometimes presenting dark brown spots. *Columella* absent, but sometimes presenting a base of sterile tissue with a small linear projection into the gleba. *Smell* slightly acidic or fruity when found, then inconspicuous. *Reactions*: negative to KOH, guaiac or ferrous sulphate in peridium and gleba. *Peridium* 70–150 µm; formed of: 1) peridiopellis reduced to a few compressed septate hyphae 2–3 µm diam parallel with the surface, with plates of brownish pigment; 2) subpellis prosenchymatic, composed of entangled septate hyphae 3–6 µm diam, frequently angled and bifurcated, looking subgelatinised, as well as longer and narrower hyphae 2–3.5 µm diam abundant near the hymenium; 3) subhymenium pseudoparenchymatic, formed of 1–3 rows of polyhedric to globose hyphae measuring 6–10 × 8–15 µm. *Trama* narrow, subgelatinised, formed of parallel hyphae 2.5–5 µm diam. Spherocytes 8–15 µm diam, frequent in the innermost peridium layers and trama, forming cords or sometimes rosettes. *Clamp connections* not observed. *Basidia* abundant, cylindric to claviform, tetrasporic or sometimes bisporic, 35–45 × 8–10 µm. *Basidioles* claviform, 30–40 × 8–9 µm. *Basidiospores* measuring (7.5–)8–9.5(–10) × (5.5–)6–7(–7.5) µm, av. 8.5 × 6.5 µm, Q = (1.2–)1.3–1.5(–1.6), average Q = 1.4 (*n* = 25); ellipsoid, heterotropic, with a small hylar appendix, smooth in water under compound microscope, with a large central droplet; not changing in KOH, amyloid in Melzer reagent, after staining with Melzer and sulphovanillin spores look minutely warted and partially subreticulated, warts are 0.1–0.2 µm high, mostly isolated but some of them coalesce forming small ridges. *Paraphysoid cells* abundant, resembling basidioles, 1–2-septate. *Cystidia* not observed.

Habitat — Solitary or in small groups. Fruits between November and March. Hypogeous or semihypogeous in acidic soils near *Cistus ladanifer* with or without *Pinus pinea* or *Quercus ilex*.

Typus. Spain, Extremadura, Badajoz, Quintana de la Serena, Sierra de los Pajaritos, below ground near *Cistus ladanifer* and *Pinus pinea*, 7 Feb. 2016, *M. Romero* (holotype FCO-Fungi 26, ITS, LSU and *rpb2* sequences GenBank MW077679, MW077681 and MW086478; ibid., isotype MRG378, MycoBank MB 837957).

Additional materials examined. Spain, Extremadura, Badajoz, Aldea de la Guarda, below ground near *Cistus ladanifer* and *Quercus ilex*, 14 Jan. 2019, *M. Romero* (paratype FCO-Fungi 27, ITS and LSU sequences GenBank MW077680, MW077682; duplicate MRG529); ibid., 18 Mar. 2018, *M. Romero* (MRG475); Badajoz, Quintana de la Serena, Fuente Quemada, below ground near *Cistus ladanifer* and *Genista scorpius*, 28 Feb. 2018, *M. Romero* (MRG462); Badajoz, Quintana de la Serena, Sierra Agalla, below ground near *Cistus ladanifer*, *Quercus ilex* and *Genista scorpius*, 15 Jan. 2019, *M. Romero* (paratype FCO-Fungi 28; duplicate MRG532); ibid., below ground near *Cistus ladanifer* and *Genista scorpius*, 4 Dec. 2008, *M. Romero* (MRG177); ibid., 19 Dec. 2018, *M. Romero* (MRG521); Badajoz, Quintana de la Serena, Sierra de los Pajaritos, below ground near *Cistus ladanifer* and *Pinus pinea*, 16 Nov. 2018, *M. Romero* (MRG512).

Notes — *Russula quintanensis* differs from other sequestrate species of *Russula* because of its angiocarpic (gasteroid) basidiomata, loculated gleba without a columella, and its ellipsoid spores 8.5 × 6.5 µm on average (Q = 1.4) ornamented with very small warts 0.1–0.2 µm high that sometimes coalesce forming small ridges. The closest matches in public databases to the LSU and *rpb2* sequences obtained come from specimens identified as *R. cessans*, *R. laricina*, *R. maculata*, *R. nauseosa* and others (about 97 % similarity of LSU, 96 % similarity of *rpb2*). Phylogenetic analysis based on ITS, LSU and *rpb2* confirms that *R. quintanensis* is nested within subsect. *Laricinae* (see Supplementary material FP1273). Other sequestrate species have been found in this subsection before (Vidal et al. 2019), such as *Russula galileensis*, *R. sichuanensis*, *R. subloculata* and *R. vinaceodora*, but they all have pseudoangiocarpic (secotioid) basidiomata. *Russula californica* turns ocherish orange in the gleba with KOH, has subglobose spores 9–12 × 7.5–9 µm ornamented with larger warts 0.25–0.5 µm wide, and cystidia. *Russula monticola* has globose to subglobose spores, 9.5–12 × 10–12.5 µm, ornamented with isolated or coalescing warts, 0.5–1.1 µm high. *Russula setigera* has a trichoderm peridiopellis, abundant cystidia, and globose spores 8–10(–11) µm ornamented with an incomplete reticulum. Finally, *R. vidalii* has also a trichoderm peridiopellis, abundant macrocystidia, and subglobose spores 9–11(–13) µm ornamented with warts 0.5–1 µm high. *Russula andaluciana* (Moreno-Arroyo et al. 2002) can be found in the same habitats and season, but differs from *R. quintanensis* because of its remarkable smell, as well as its globose to subglobose basidiospores ornamented with spines 0.3 µm high forming a reticulum.

Colour illustrations. *Pinus pinea* forest with *Cistus ladanifer* at Sierra de los Pajaritos (Extremadura, Spain). Basidiomata; peridium; opposed hymenium layers with subhymenium; peridiopellis, spherocytes; spores in water; spores in Melzer + sulphovanillin. Scale bars = 1 cm (basidiomata), 50 µm (peridium), 20 µm (hymenium, peridiopellis and spherocytes), 10 µm (spores).

Supplementary material

FP1273 P50 % majority rule consensus phylogram obtained in MrBayes from 7 500 sampled trees after the analysis of a combined alignment of ITS rDNA, 28S rDNA and *rpb2* sequences of *Russula* s.str. Nodes were annotated if supported by ≥ 0.95 Bayesian PP (left) or ≥ 70 % ML BP (right).

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Simplicillium niveum

Fungal Planet 1274 – 13 July 2021

Simplicillium niveum Mongkols., Noisrip. & Luangsa-ard, *sp. nov.*

Etymology. From the Latin '*niveus*', referring to white mycelium of the fungus on the host.

Classification — *Cordycipitaceae*, *Hypocreales*, *Sordariomycetes*.

Mycophylic on *Ophiocordyceps camponoti-leonardi* (*Ophiocordycipitaceae*) attached to unidentified dicotyledonous leaves of forest plants. *Mycelium* white. Conidial structures consisting of erect conidiophores usually arising from prostrate mycelium, verticillate with phialides in whorls of two to five on each branch. *Conidiogenous cells* phialides, gradually tapering from base to the apex, 10–20.5(–25) × 1–2 µm. *Conidia* hyaline, oblong-ellipsoidal or ellipsoidal, smooth, aseptate, 3–4.5(–6) × 1–2 µm, aggregated in heads at the apex of phialides. *Sexual morph* not observed.

Culture characteristics — Colonies initiated from germinating conidia. Conidia germinated within 24 h on potato dextrose agar (PDA). Colonies reaching 8–12 mm diam after 7 d at 25 °C. Colonies compact with white mycelium, reverse uncoloured. Conidia and reproductive structures not observed.

Typus. Thailand, Nam Nao National Park, on *Ophiocordyceps camponoti-leonardi* (*Ophiocordycipitaceae*) on underside of unidentified dicotyledonous leaf, 24 Nov. 2016, *S. Mongkolsamrit*, *K. Tasanathai*, *P. Srikitikulchai*, *S. Wongkanoun*, *U. Pinruan & R. Promharn* (holotype BBH 42334, culture extype BCC 83036, ITS, LSU, *tef1* and *rpb1* sequences GenBank MW620992, MW621499, MW603488 and MW603489, MycoBank MB 838772).

Notes — Species in *Simplicillium* have been reported occurring on a broad spectrum of hosts and substrates, such as insects, plants, rusts, soil, decaying wood, calcareous rock (Zare & Gams 2001, Liu & Cai 2012, Nonaka et al. 2013, Zhang et al. 2017, Chen et al. 2019). *Simplicillium lanosoniveum* has been reported as both an endophytic and hyperparasitic fungus (Baiswar et al. 2014, Wei et al. 2019). The gross macromorphology of the natural samples of *S. niveum* closely resembles *S. lanosoniveum* (Wei et al. 2019) by producing white hyphae on decayed *O. camponoti-leonardi* (Kobmoo et al. 2012), but *O. unilateralis* (Wei et al. 2019) was the host reported for the latter. Both species produce phialides with aggregated conidia on the host surface. However, the micromorphological characters in *S. niveum* differ from *S. lanosoniveum* in having verticillate conidiophores with phialides in whorls, whereas *S. lanosoniveum* produces solitary phialides along its hyphae. Results of the molecular phylogenetic study strongly support and separate *S. niveum* from other known species.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to Fungal sp. (clone PdIM07-69, GenBank MG920352.1; Identities = 501/536 (93 %), 15 gaps (2 %)) and *Simplicillium* sp. (strain fgcc1, GenBank LC033905.1; Identities = 497/537 (93 %), 15 gaps (2 %)). Closest hits using the **LSU** sequence had highest similarity to *Acremonium* sp. (strain NORIE7, GenBank MK913356.1; Identities = 1 192/1 204 (99 %), one gap (0 %)) and *Lecanicillium* sp. (strain VS6320, GenBank KU342077.1; Identities = 1 192/1 204 (99 %), one gap (0 %)). Closest hits using the ***tef1*** sequence are *Blackwellomyces lateris* (as *Blackwellomyces* sp. YX-2018a, voucher MFLU 18-0663, GenBank MK069471.1; Identities = 885/949 (93 %), three gaps (0 %)) and *Blackwellomyces cardinalis* (strain OSC 93609, GenBank DQ522325.1; Identities = 880/942 (93 %), two gaps (0 %)). Closest hits using the ***rpb1*** sequence are *Beauveria gryllotalpidicola* (strain BCC26300, GenBank MK632184.1; Identities = 494/601 (82 %), four gaps (0 %)) and *Beauveria malawiensis* (strain BCC17613, GenBank HQ880896.1; Identities = 494/601 (82 %), four gaps (0 %)).

Colour illustrations. Forest in Thailand. Fungi on host; side view of sample showing white hyphae of *S. niveum* on decayed *Ophiocordyceps camponoti-leonardi* body and leg; conidiophores and phialides in whorls and conidia; culture derived from conidia on PDA (sporulation absent). Scale bars = 10 mm (culture), 2 mm (*O. camponoti-leonardi*), 20 µm (phialides), 10 µm (conidia).

Supplementary material

FP1274-1 Phylogenetic tree derived from a Bayesian analysis based on a combined dataset comprising ITS and LSU sequences. The data was analysed using Bayesian inference (BI) and Maximum likelihood (ML). Bayesian phylogenetic inference was calculated with MrBayes v. 3.2.7a (Ronquist et al. 2012), with 3 M generations and under the GTR+I+G model. The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) on XSEDE in the CIPRES portal (www.phylo.org). Numbers at the significant nodes represent Bayesian posterior probabilities (BPP) / RAxML bootstrap support values (ML-BS). Thickened lines in the tree represent fully supported branches (BPP = 1, ML-BS = 100). The new species is shown in **bold** font and a coloured box. GenBank accession numbers are provided in the supplementary table (FP1274-2).

FP1274-2 List of species and GenBank accession numbers of sequences used in this study.

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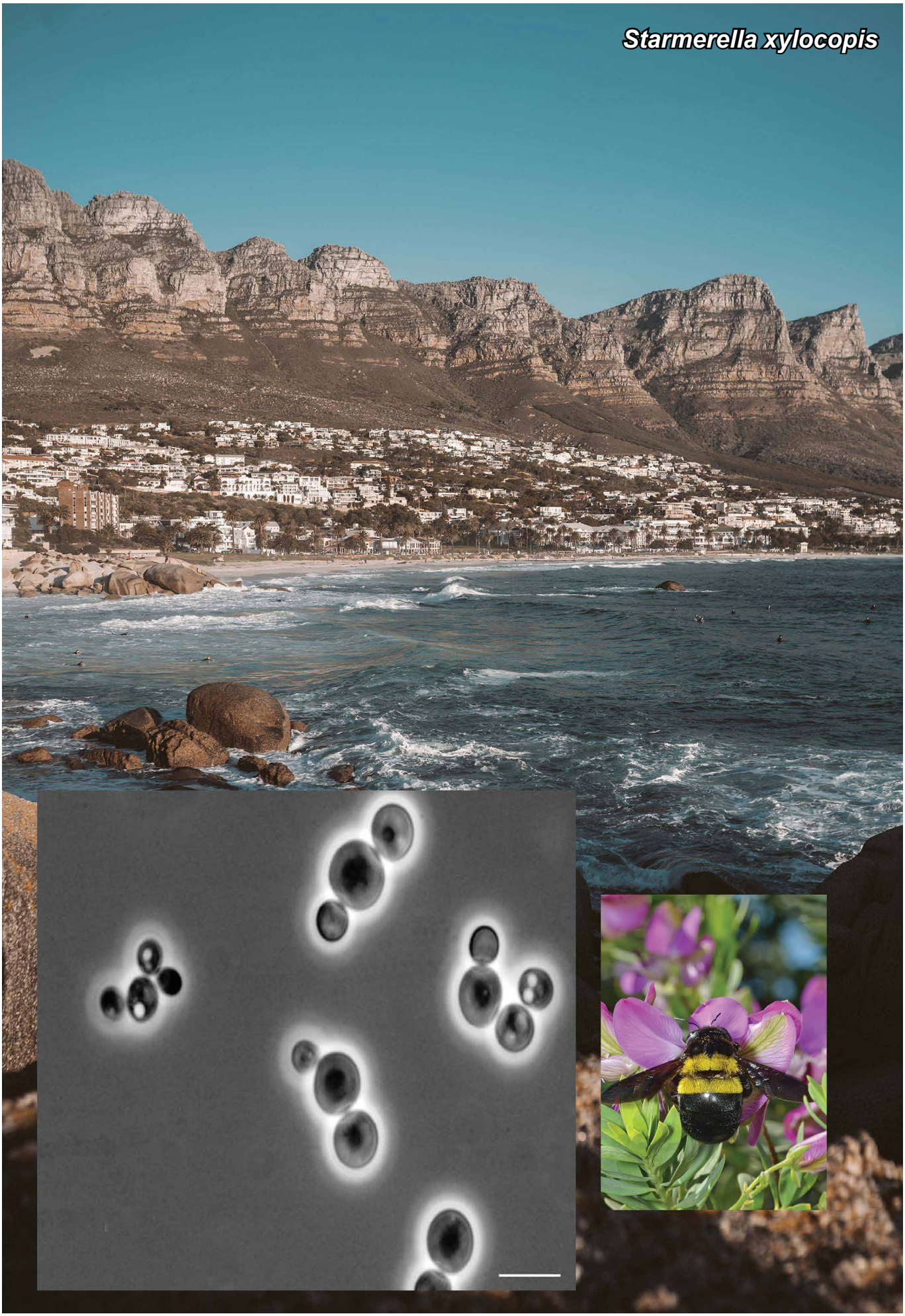

Starmerella xylocopis

Fungal Planet 1275 – 13 July 2021

Starmerella xylocopis Gouliamova, Dimitrov, M. Groenew., M.T. Sm. & Boekhout, *sp. nov.*

Etymology. *Xy-lo-co-pis*, referring to the host *Xylocopa caffra* from which this species was isolated.

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

After 7 d at 25 °C in 4 % glucose broth, the cells are subglobose to globose, 3–5.8 × 2.9–5.2 µm, occurring singly or in clusters. A thin sediment and a ring are present. *Asexual reproduction* occurs by multilateral budding, but with the majority of cells having a single bud on a broad base. Short chains of adhering yeast cells may be present. On malt extract, yeast extract agar (MEA) yeast cells have a similar morphology and are ellipsoid, broadly ellipsoid, subglobose, and usually with one conspicuous vacuole. After 7 d at 25 °C the *colony* on glucose, yeast extract, pepton agar (GYPA) and MEA is 5 cm diam, flat, with the centre slightly raised, smooth, shiny, cream-beige, with fine faint transverse striations and an entire margin. The colony on GYPA is slightly paler. Dalmau plate culture after 10 d on morphology agar did not show pseudohyphae or true hyphae. *Ascospore production* was not detected on yeast extract, malt extract, pepton, dextrose agar (YMA), 5 % MEA, McClary acetate agar and undiluted V8 agar as single and mixed cultures.

Physiological profiles of two new strains

Fermentation — D-glucose (w,d), sucrose (w,d), α,α trehalose (w,d) are fermented. Galactose, maltose, lactose and raffinose are not fermented.

Carbon assimilation — D-glucose, D-galactose (-,d), L-sorbose, D-glucitol, D-mannitol, D-glucono-1,5-lactone, D-gluconate, succinate (d,+), citrate, glycerol, D-ribose (d) and *α,α*-trehalose (d), ribitol (-,d), 2 keto-D-gluconate (-,d), are assimilated. D-glucosamine, D-xylose, L-arabinose, D-arabinose, L-rhamnose, maltose, methyl-*α*-glucoside, sucrose, cellobiose, salicin, arbutin, melibiose, lactose, raffinose, melezitose, inulin, soluble starch, erythritol, xylitol, L-arabinitol, galactitol, myo-inositol, D-glucuronate, D-galacturonate, propane-1,2-diol, butane-2,3-diol, quinic acid, D-glucarate, D-galactonate, DL-lactate, ethanol and methanol are not assimilated.

Nitrogen assimilation — Nitrate (+,+), nitrite (+,+), ethylamine (+,+), L-lysine (+,+) and cadaverine (+,+) are assimilated. Creatine, creatinine, N-acetyl-glucosamine and imidazole are not assimilated.

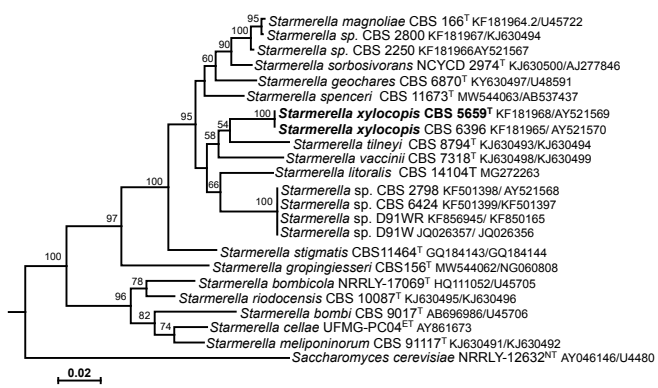
Other tests — Growth without all vitamins is negative. Growth without only myo-inositol (+,+), pantothenate (+,+), pyridoxine (+,+) niacin (+,+) and PABA (+,+) is positive. Growth without biotin, thiamin, biotin and thiamin, pyridoxine and thiamin is negative. Growth in presence of 0.01 % and 0.1 % cycloheximide is delayed (-,d) and negative, respectively. Grow in medium containing 10 % NaCl (+,+), 16 % NaCl (+,w/v), 50 % and 60 % glucose is positive. Growth at 25 °C, 30 °C and at 35 °C is positive. Growth at 37 °C is negative. Starch production, urea and DBB tests are negative.

Colour illustrations. South Africa, Camps Bay (photo credit T. Elliott, pexels.com). Morphology of cells of *Starmerella xylocopis* CBS 5659^{T} in 5 % glucose broth after 1 wk; female *Xylocopa caffra*, foraging for nectar and pollen, Gifberg, Western Cape Province, South Africa (photo credit S. Marshall, University of Guelph, Canada). Scale bar = 5 µm.

Typus. South Africa, from larval feed of an Afrotropical bee *Xylocopa caffra* (*Apidae*, *Hymenoptera*), *J.P. van der Walt*, date unknown (holotype CBS 5659 culture preserved in a metabolically inactive state (lyophilised), culture ex-type CBS 5659 = JCM 9436, ITS and LSU nrDNA sequences GenBank KF181968 and AY521569, MycoBank MB 807733).

Additional material examined. South Africa, from the larval pabulum of *Xylocopa scioensis*, *J.P. van der Walt*, culture CBS 6396 = JCM 1452 = JCM 1806 = VKM Y-1692, ITS and LSU nrDNA sequences GenBank KF181965 and AY521570.

Notes — S*tarmerella* includes 48 yeast species (http://www.indexfungorum.org; search date 08.04.2021) that are associated with flowering plants and related insects, mainly stingless bees (Lachance 2011). Two novel *Starmerella* strains associated with carpenter bees, CBS 5659 and CBS 6396, were isolated and deposited to the CBS yeast collection by J.P. van der Walt in 1960 and 1980, respectively. The two strains are conspecific (99 % sequence similarity in LSU: one subst. and 100 % sequence similarity in ITS nrDNA). Phylogenetic analysis using combined sequences of ITS and LSU nrDNAsequences of the novel strains and closely related yeasts belonging to the *Starmerella* clade placed the two strains within the subclade of *S. tilneyi* CBS 8794^{T} and *S. vaccinii* CBS 7318^{T} as a sister branch. Pairwise sequence analysis from a multiple alignment showed that the new strains have 92.3 % sequence similarity (626 identical nt., 49 subst., 26 gaps) with *S. tilneyi* and 91.3 % sequence similarity (619 identical nt., 50 subst., 25 gaps) with *S. vaccinii*. Comparison of the physiological properties confirmed the distinction of the new strains from the closely related yeast species *S. tilneyi* and *S. vaccinii.* The novel strains can be distinguished from *S. tilneyi* based on nine physiological characteristics. The strains can assimilate D-ribose, *α,α*-trehalose, ribitol and cannot assimilate inulin, xylitol and N-acetyl-glucosamine. Unlike *S. tilneyi* the strains are able to assimilate nitrate and nitrite and are not able to grow on medium without vitamins. Ten physiological characteristics discriminate the new strains from *S. vaccinii*. The strains can assimilate D-ribose, *α,α*-trehalose and ribitol. The strains are not able to assimilate sucrose, cellobiose, salicin, arbutin, raffinose and xylitol. Unlike *S. vaccinii*, the novel strains are not able to grow at 37 °C.



Phylogenetic tree obtained by the analysis of combined ITS and LSU nrDNA sequences of *Starmerella xylocopis* CBS 5659^{T} and related species using a neighbour-joining method (Kimura two-parameter model; MEGA v. 7; 100 bootstrap replicates).

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Suillus praetermissus

Fungal Planet 1276 – 13 July 2021

Suillus praetermissus Zvyagina & Svetash., *sp. nov.*

Etymology. '*Praetermissus*' means overlooked, neglected. The epithet refers to the fact that a common species of edible harvested mushroom has so far been considered under the name of another species.

Classification — *Suillaceae*, *Boletales*, *Agaricomycetes*.

Mature basidiomata boletoid. *Pileus* 5–10 cm diam, convex, flattening with age, margin floccose-appendiculate with mucous flakes at least when young. Surface copiously viscid in wet weather, glabrous, first evenly olivaceous-yellow, then darker, brownish, with thin grey-brown innately radial streaks. *Pores* angular, big and different in size, sinuate, greyish yellow, later dirty olive yellow, *tubes* concolorous or a bit lighter. *Context* fleshy, yellow with olivaceous tint. *Stipe* cylindrical, central, 0.8–1 cm broad, 7–10 cm long, covered with ash grey dots both above ring and below. Ring double, olivaceous mucous in upper part and whitish cotton-like in lower part. *Context* yellow with olive tint in young specimens and brownish in old ones. *Taste* distinctly acid, especially on the slime cap surface. *Basidiospores* 8.1–11.2(–12.4) × 3.0–4.0(–4.2) µm, Q = 2.3–3.2(–3.5), ellipsoid, ovoid, inequilateral in profile, moderately thick-walled, pale brown, smooth. *Basidia* 22–29 × 6.4–7.9 µm, clavate to subclavate, hyaline or with yellowish brown context in KOH. *Cystidia* 38–82 × 4.1–8.6 µm, cylindrical and slightly widened to clavate in upper part, with brown context in KOH or sometimes hyaline, arranged in fascicles. *Pileipellis* ixocutis, consisting of hyphae, 3–5 µm broad.

Habitat & Distribution — In groups, mainly in moist conifer and mixed forests among mosses, mycorrhizal with *Pinus* subsect. *Strobus.* Russia (Northern Urals, Western and Eastern Siberia), Mongolia, China and Japan. Quite common edible mushroom harvested by local people.

Typus. Russia, Altai Republic, Turochakskiy rayon, vicinities of Yaylyu, cordon Chelyush, mixed delta forest with *Alnus viridis* subsp. *fruticosa*, *Betula* sp., *Larix sibirica*, *Pinus sibirica*, *P. sylvestris*, *Salix* sp., N51.41° E87.79°, 28 Aug. 2018, *T. Svetasheva* (holotype LE312659, ITS and LSU sequences GenBank MW432521 and MW888987, MycoBank MB 838637).

Additional materials examined. Mongolia, Selenga aimag, Mandal sum, Khonin Nuga Biostation of the Mongolian State University, Sanste, N49.15° E107.30°, mixed forests with *Abies sibirica*, *Pinus sibirica*, 29 July 2008, *A. Alexandrova*, LE 235742. – Russia, Khanty-Mansy autonomous okrug, Gornopravdinsk, N60.03° E69.96°, mixed forest with *Abies sibirica*, *Picea abies* and *Pinus sibirica*, 21 Aug. 2009, *A. Baykalova*, LE312654, ITS sequence GenBank KU059565; Khanty-Mansy autonomous okrug, Ugut, N60.50° E74.05°, mixed forest with *Betula pendula* and *Pinus sibirica*, 19 Aug. 2019, *E. Zvyagina*, LE312653, ITS and LSU sequences GenBank MW432520 and MW888986; Khanty-Mansy autonomous okrug, Ugut, N60.50° E74.05°, cutting site in mixed forest with *Pinus sibirica* and *P. silvestris*, *E. Zvyagina*, LE312652, ITS sequence GenBank MW432519; Tomsk Region, Orlovka, N56.88° E84.67°, edge of the transit bog, under *Pinus sibirica*, 22 Aug. 2018, *T. Svetasheva & A. Dahlberg*, LE312660, ITS and LSU sequences GenBank MW432522 and MW888988; Altai Republic, Turochakskiy rayon, Yaylyu, N51.77° E87.60°, mixed forests with *Betula* sp., *Abies sibirica* and *Pinus sibirica*, 15 Aug. 2008, *A. Kovalenko*, LE312655, ITS sequence GenBank MK568020.

Colour illustrations. Mixed forest with *Pinus sibirica* at holotype specimen's location, Altai Republic, Russia. Holotype basidiomata; cystidia; spores; pileipellis section. Scale bars = 10 µm.

Notes — The olive yellow cap and ash grey dots on the stipe surface, as well as larger spores, distinguish *S. praetermissus* from the closest species of the *Suillus acidus* group. According to phylogenetic analysis, the nearest species is *S. subalutaceus*, p-distance is 1.8 %, 12 nucleotide substitutions per 666 alignment positions of ITS1-5.8S-ITS2. According to a microscopic examination of the type specimen of *S. subalutaceus* (MICH 50221) carried out by E. Zvyagina, its spores are much shorter with the same width. The cap surface of *S. subalutaceus* is 'pinkish-buff' (Smith & Thiers 1964). *Suillus subalutaceus* forms mycorrhiza with two-needle pines (Nguyen et al. 2016), while the new taxon *S. praetermissus* is associated with five-needle pines. In our study all examined specimens were collected under *Pinus sibirica*. However, for specimens and mycorrhizal samples from Japan, of which sequences were used in the phylogenetic tree, an association with *P. corayensis* and *P. pumila* was also noted. *Suillus subalutaceus* is an American species, while *S. praetermissus* has an Asian distribution.

Supplementary material

FP1276 ITS rDNA phylogenetic tree obtained with MrBayes v. 3.2.5 (Ronquist & Huelsenbeck 2003) under GTR+I+G model for 10 M generations on the partial ITS sequence alignment (445 nucleotides including alignment gaps). The GenBank accession numbers are indicated after species names. Novel species is indicated in a **bold** font in the green box. Support values are indicated on the branches (posterior probabilities). Scale bar = 0.4 expected substitutions per site. The alignment and tree were deposited in TreeBASE (study S27683).

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Tetraploa endophytica

Fungal Planet 1277 – 13 July 2021

Tetraploa endophytica G. Delgado & Maciá-Vicente, *sp. nov.*

Etymology. Referring to the endophytic lifestyle of the fungus.

Classification — *Tetraplosphaeriaceae*, *Pleosporales*, *Dothideomycetes*.

Root endophyte isolated on culture media from surface-sterilised roots of living plants. Mycelium composed of hyaline, subhyaline, pale brown to brown, branched, septate, smooth or finely verruculose to locally verrucose hyphae, (1.5–)2–3(–3.5) µm wide, sometimes with swellings 5–7 µm wide or covered with more or less rounded, clear to brown exudates, often with intercalary or rarely terminal, short, somewhat irregular geniculations having slightly darkened lateral shoulders, forming loops or aggregated in tightly packed, brown to dark brown cords, up to 135 µm wide.

Culture characteristics — Colonies on malt extract agar (MEA) moderately fast growing, reaching 16–25 mm diam after 2 wk at 25 °C, dark grey, floccose at the centre with visible mycelial cords, margin dull white, more or less diffuse, reverse dull grey. On potato dextrose agar (PDA) reaching 23–25 mm diam, velvety or somewhat cottony, whitish grey, depressed at the centre and cottony, grey and secreting amber colour exudate droplets, margin entire, reverse reddish brown. On modified cellulose agar (MCA) reaching 15–17 mm diam, flat, somewhat cottony at the centre, grey, margin diffuse, reverse dull grey. Cultures sterile.

Typus. Germany, Baden-Württemberg, Setzingen, endophytic in roots of *Microthlaspi perfoliatum* (*Brassicaceae*) growing in a grassland, N48°33'00.0" E10°07'12.0", 481 m a.s.l., isolated from surface-sterilised, asymptomatic roots of a wild plant, 12 June 2013, coll. *K. Glynou & J.G. Maciá-Vicente*, isol. *K. Glynou*, P6086 (holotype and culture ex-type permanently preserved in a metabolically inactive state CBS 147114, ITS, LSU and *tef1* sequences GenBank KT270279, MW659165 and MW659821, MycoBank MB 839006).

Notes — *Tetraploa* species are characterised by distinct, brown, smooth or verrucose conidia composed of four columns of 2–6 cells, each one terminating in a septate, setiform appendage that tend to diverge apically from one another and are borne on monoblastic conidiogenous cells (Ellis 1971, Whitton et al. 2012). They are linked to massarina-like sexual morphs and are currently placed in their own pleosporalean family, *Tetraplosphaeriaceae*, along with other genera having appendiculate, tetraploa-like asexual morphs (Tanaka et al. 2009). Some members of *Tetraploa* are ubiquitous and they mostly occur on leaves or stems of monocotyledons such as bamboo, but also on various dicotyledons. However, there are very few reports of them as endophytes and only the widespread *T. aristata* has been isolated from *Opuntia ficus-indica* (*Cactaceae*) (Rashmi et al. 2019). *Tetraploa endophytica* was isolated during an extensive sampling for root endophytic fungi across Europe (Glynou et al. 2016), and it is the first *Tetraploa* species described as a sterile, root endophyte. Our strain did not sporulate in any of the different culture media used including MEA, PDA, MCA or Water Agar supplemented with wooden toothpicks. Phylogenetically, it clustered with a *Tetraploa* sp. strain P1501, represented only by an ITS sequence (GenBank KY987533.1), which is also a root endophyte isolated from *Polygonum chinense* (*Polygonaceae*) in China (Liu et al. 2017), and probably conspecific. Another root endophyte, *Tetraploa* sp. strain M1403, isolated from *Stellaria media* (*Caryophyllaceae*) also during the study of Liu et al. (2017), grouped sister to our strain but without support. It occurs in a strongly supported group with the ex-type strain of *T. sasicola* and an isolate of this species obtained from a root of wild *Vaccinium* sp., suggesting that some *Tetraploa* taxa are possibly well adapted to the root endophytic lifestyle.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence of *Tetraploa endophytica* (CBS 147114) are *Tetraploa* sp. (strain P1501 as *Tetraplosphaeria* sp., GenBank KY987533.1; Identities = 511/512 (99 %), no gaps), *Tetraploa* sp. (strain M1403 as *Tetraplosphaeria* sp., GenBank KY987520.1; Identities = 483/510 (95 %), 11 gaps (2 %)) and *Tetraploa sasicola* (as *Tetraplosphaeria sasicola*, GenBank KX440178.1; Identities = 491/519 (95 %), 11 gaps (2 %)). Closest hits using the **LSU** sequence are *Tetraploa* sp. (strain KT 1684, GenBank AB524628.1; Identities = 955/959 (99 %), one gap (0 %)), *Tetraploa sasicola* (GenBank NG_042329.1; Identities = 951/959 (99 %), one gap (0 %)) and *Tetraploa dwibahubeeja* (GenBank NG_068929.1; Identities = 949/958 (99 %), one gap (0 %)). Closest hits using the ***tef1*** sequence had highest similarity to *Tetraploa yunnanensis* (GenBank MT954406.1; Identities = 705/749 (94 %), no gaps), *Brunneofusispora sinensis* (GenBank MH395329.1; Identities = 694/751 (92 %), four gaps (0 %)) and *Ernakulamia cochinensis* (GenBank MT954373.1; Identities = 690/750 (92 %), two gaps (0 %)).

Colour illustrations. Grassland near Setzingen, where the sample was taken. Colonies on MEA, surface and reverse view; mycelium with hyphal loops; hyphal cord and loop; hypha covered with exudate droplets; finely verruculose hypha. Scale bars = 5 µm.

Supplementary material

FP1277-1 Maximum likelihood (ML) phylogenetic tree obtained from concatenated ITS and LSU rDNA sequences of *Tetraploa* species showing the position of *T. endophytica* within the genus. The final alignment consisted of 37 sequences and 1 309 positions including the outgroups, 514 from the ITS alignment and 795 from the LSU. Maximum likelihood and Bayesian inference analyses were conducted using RAxML v. 8.2.12 (Stamatakis 2014) and MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003), respectively, on the CIPRES Science Gateway server (Miller et al. 2010). The ML analysis employed the rapid bootstrapping algorithm using the GTRCAT model and 1 000 bootstrap iterations. Bayesian inference consisted of two independent runs of 10 M generations sampled every 100th generation and the first 25 % of trees discarded as burn-in. Bootstrap support values ≥ 70 % and Bayesian posterior probabilities ≥ 0.95 are indicated by numbers close to nodes and thickened branches, respectively. The tree is rooted with *Ernakulamia cochinensis* (PRC 3992) and *Quadricrura bicornis* (CBS 125427). The novel *Tetraploa* species is highlighted in **bold**. The alignment and trees were deposited in TreeBASE (study 27855).

FP1277-2 List of strains included in this study and their GenBank accession numbers.

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Teunia lichenophila

Fungal Planet 1278 – 13 July 2021

Teunia lichenophila Kachalkin, M.A. Tomashevskaya & T.A. Pankratov, *sp. nov.*

Etymology. Named for its association with lichens.

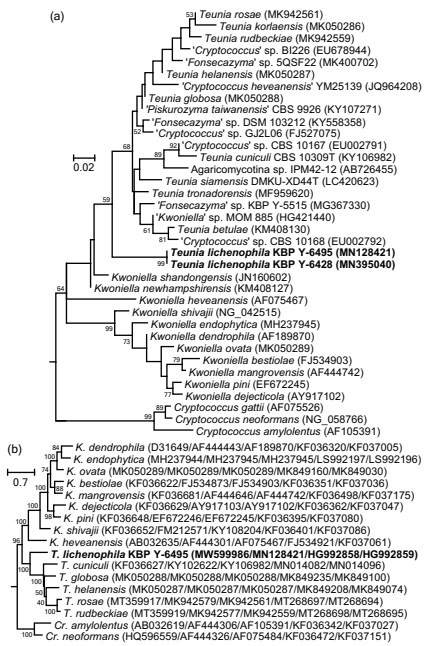
Classification — *Cryptococcaceae*, *Tremellales*, *Tremellomycetes*.

On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 21 °C, *streak* is yellowish cream, shiny and mucoid, with an entire margin. *Cells* are subglobose to globose (3–6 × 4–7 µm), occur singly or in pairs, dividing by polar budding. *Sexual structures*, *pseudohyphae*, *true hyphae* and *ballistoconidia* have not been observed during 6 wk at 21 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, potato dextrose agar (PDA), cornmeal agar (CMA), McClary acetate agar. Glucose is not fermented. Glucose, galactose (weak), sucrose, maltose, trehalose, cellobiose, raffinose (weak), melezitose, D-xylose, L-arabinose (weak), D-arabinose, L-rhamnose, ethanol, glycerol, ribitol, galactitol, D-mannitol, D-glucitol, methyl alpha-D-glucoside, salicin, DL-lactic acid (weak), citric acid (weak), D-glucuronate, 2-keto-D-gluconate and arbutin are assimilated; no growth occurs on L-sorbose, melibiose, lactose, inulin, soluble starch, D-ribose, D-glucosamine, erythritol, succinic acid, *myo*-inositol, 5-keto-D-gluconate and methanol. Assimilation of nitrogen compounds: positive for ammonium sulfate and L-lysine, and negative for potassium nitrate and cadaverine. Growth on vitamin-free medium is positive. Growth on 50 % w/w glucose / yeast extract (0.5 %) agar, on MEA with 10 % NaCl, and with 0.01 % and 0.1 % cycloheximide is negative. Starch-like compounds are not produced. Diazonium blue B colour and urease reactions are positive. Maximum growth temperature is 25 °C.

Typus. Russia, Tyumen Oblast, Pokachi, isolated as endophyte from *Cladonia rangiferina* (*Cladoniaceae*), July 2018, *T.A. Pankratov & A.V. Kachalkin*, 1184b (holotype KBP Y-6495, preserved in a metabolically inactive state, ex-type cultures VKM Y-3062 = DSM 112086 = CBS 16716, ITS-D1/D2 domains of LSU nrDNA, SSU, *tef1* and *rpb1* sequences GenBank MN128421, MW599986, HG992859 and HG992858, MycoBank MB 838989).

Additional materials examined. Russia, Nadym, isolated as endophyte from *C. stellaris*, July 2017, *T.A. Pankratov & A.V. Kachalkin*, KBP Y-6428, ITS and D1/D2 domains of LSU nrDNA sequence GenBank MN395040; Altai Krai, isolated from *C. rangiferina*, July 2019, *T.A. Pankratov & A.V. Kachalkin*, KBP Y-6613, ITS and D1 domain of LSU nrDNA sequence GenBank MW675809.

Notes — During a survey of yeast biodiversity associated with *Cladonia* lichens, three yeast strains that are conspecific based on ITS sequence data were isolated. Based on a blastn search of NCBIs GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Kwoniella bestiolae* (strain P-14, GenBank KY366237; Identities = 425/450 (94 %), five gaps (1 %)), but this result differs from the ex-type strain *K. bestiolae* (CBS 10118^{T}, GenBank NR_111373; Identities = 475/577 (82 %), 35 gaps (7 %)); other best hits using the ITS sequence are '*Fonsecazyma*' sp. from *Teunia* clade (DSM 103212, GenBank KY558358; Identities = 379/438 (87 %), 19 gaps (4 %)) and *K. ovata* (CGMCC 2.3439^{T}, GenBank MK050289; Identities = 372/430 (87 %), 17 gaps (3 %)). The closest hit using the **LSU** sequence is *T. helanensis* (CGMCC 2.4450^{T}, GenBank MK050287; Identities = 495/513 (96 %), two gaps (0 %)), using **SSU** it is *T. korlaensis* (CGMCC 2.3835^{T}, GenBank MK050286; Identities = 1 656/1 675 (99 %), one gap (0 %)), using ***tef1*** it is *T. rudbeckiae* (CGMCC 2.5840^{T}, GenBank MT268695; Identities = 437/480 (91 %), 11 gaps (2 %)) and using ***rpb1*** the number of nucleotide substitutions was considerable – without hits with *Teunia* and *Kwoniella*. In agreement with results of the recent analysis of the genus *Teunia* (Wang et al. 2020), the phylogenetic position of the new species is demonstrated using the LSU rDNA phylogeny. Results of the analysis suggest that strains KBP Y-6495 and KBP Y-6428 belong to a new species, which occupies a basal position in the *Teunia* clade. Because the new species was distantly related to other species of the genus, a multi-locus phylogenetic analysis of concatenated sequences of ribosomal genes (SSU, ITS and LSU) and two protein-coding regions (*rpb1* and *tef1*) was performed. The *Teunia* clade and the strain KBP Y-6495 received strong support in the analysis. *Teunia lichenophila* sp. nov. is distinguished from the closest (according to the multi-locus phylogenetic analysis) species *T. cuniculi* by more than 10 physiological tests.



Maximum likelihood (ML) trees of *Teunia lichenophila* sp. nov. and (a) related strains, species and genera obtained from the LSU sequence data with a hidden outgroup containing *Fonsecazyma mujuensis* and (b) representatives from genera *Teunia* and *Kwoniella* with a hidden outgroup containing *Vishniacozyma victoriae* and *V. carnescens* obtained from the combined analysis of SSU, ITS, LSU, *rpb1* and *tef1* genes. The alignments included 552 bp and 3 423 bp, respectively, and were performed with MAFFT v. 7 (Katoh et al. 2019). The General Time Reversible model with a gamma distribution and invariant sites was used as the best nucleotide substitution model. The phylogenetic analysis was conducted in MEGA v. 6 (Tamura et al. 2013). The novel species is indicated in **bold** font.

Colour illustrations. Russia, Tyumen Oblast, Pokachi, *Cladonia* lichen ground cover. *Teunia lichenophila* KBP Y-6495: growth of yeast colonies and yeast cells on MEA (after 7 d at 21 °C). Scale bar = 5 µm.

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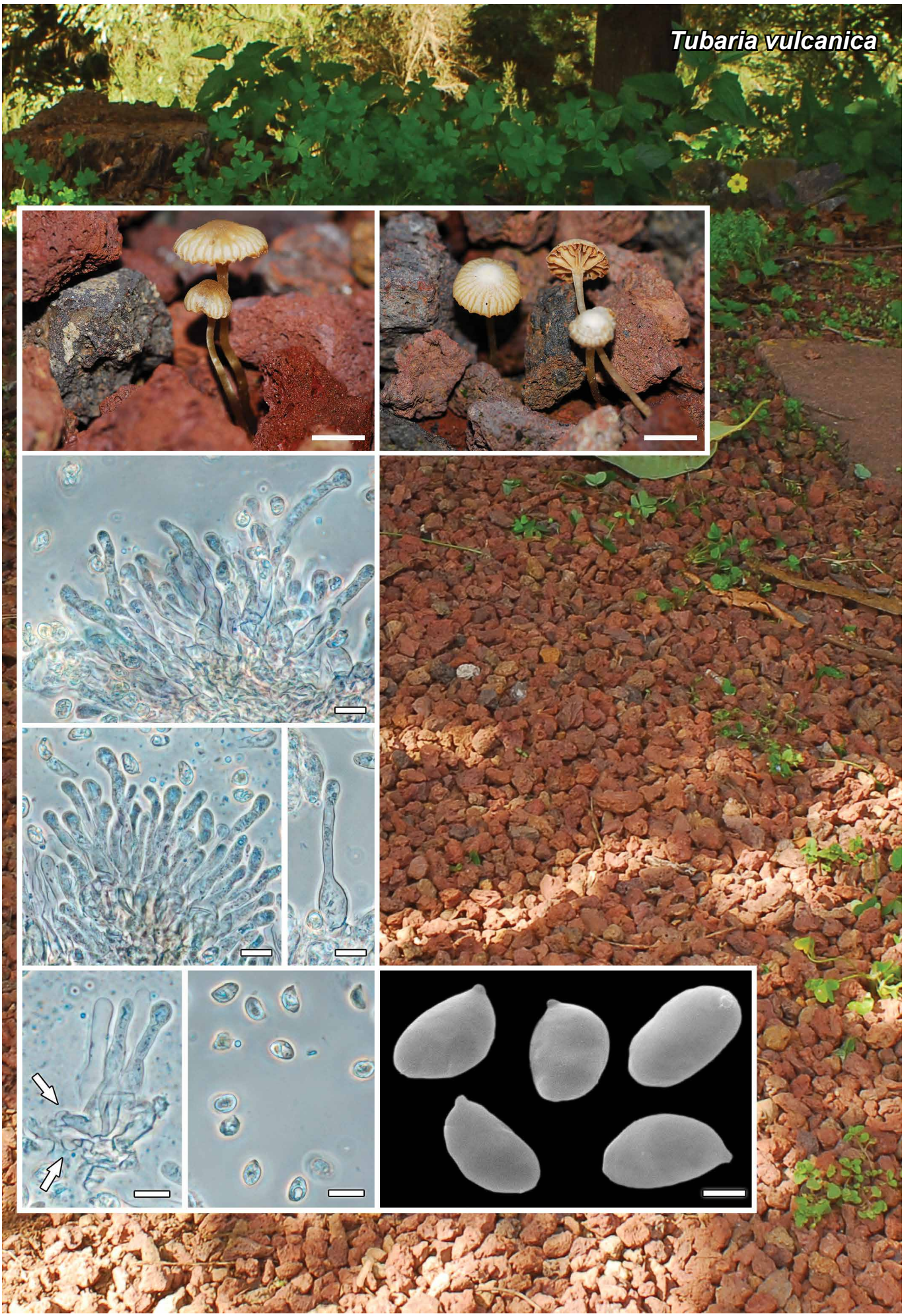
Tubaria vulcanica

Fungal Planet 1279 – 13 July 2021

Tubaria vulcanica G. Moreno, Bañares & P. Alvarado, *sp. nov.*

Etymology. Name reflects its occurrence on volcanic lapilli material.

Classification — *Tubariaceae*, *Agaricales*, *Agaricomycetes*.

Basidiocarps annual, with a central stipe. *Cap* 0.3–0.8 mm, paraboloid-subcampanulate, then convex, plano-convex, sometimes subapplanate, striate up to the umbo when moist (mature basidiomes), tawny-honey in colour, pale brown in the centre, slightly furfuraceous-micaceous, margin with remnants of a white veil when young. *Gills* (lamellae = 14–16; lamellulae = 10–12), adnate to decurrent, distant, first concolorous with the cap, then beige or rusty, edge paler and flocculose, excedent (usually exceeding the margin which then appears denticulate). *Stem* 15–30 × 1 mm, almost equal or slightly narrowed downwards, flexuous, concolorous with the cap or paler, apex pruinose. *Odour* not distinctive. *Basidia* (2–)4-spored, 18–25(–30) × 7–8 µm, sterigmata up to 5 µm long. *Spores* 6.5–8.8(–9) × 4.4–6 µm, av. 5.3–7.7 µm Q_{av} = 1.4 (n = 20, holotype), amygdaliform to ellipsoid, smooth, with lipid vacuoles, frequently collapsing. *Cheilocystidia* (lamellae edge sterile), lageniform to tibiiform, rarely narrowly lageniform or narrowly cylindrical, 31–68 × 4.5–10 µm length × width; neck cylindrical (2.5–3.5 µm wide), elongate; apex inflated, usually subcapitate to capitate (up to 7 µm wide). *Caulocystidia* present, similar to cheilocystidia. *Pleurocystidia* absent. *Pileipellis* composed of cylindrical hyphae (4–9(–13) µm thick) with occasional short or inflated elements, as well as short, broadly cylindrical to lanceolate or obtuse terminal cells, not incrusted. *Clamps* present.

Habitat & Distribution — Gregarious on volcanic lapilii material (on fragments 5–10 mm) used for domestic pavement.

Typus. Spain, Canary Islands, Tenerife, Barranco de Las Lajas (T.M. Tacoronte), N28°27'58.46" W16°23'11.76", 780 m, on volcanic lapilli material in an anthropic (domestic) environment in the edge of the Monteverde vegetation, 21 Jan. 2018, *Á. Bañares & O. Bermúdez* (holotype TFC Mic. 25407, ITS, LSU and *rpb2* sequences GenBank MW662647, MW662646 and MW672100; isotype in AH 49172, MycoBank MB 838918).

Additional material examined. Spain, Canary Islands, Tenerife, Barranco de Las Lajas (T.M. Tacoronte), N28°27'58.46" W16°23'11.76", 780 m, on volcanic lapilli material in an anthropic (domestic) environment in the edge of the Monteverde vegetation, 13 Dec. 2020, TFC Mic. 25408.

Notes — The genus *Tubaria* is actually included in the family *Tubariaceae*, along with *Flammulaster*, *Phaeomarasmius* and *Phaeomyces* (Vizzini 2008, Vizzini et al. 2019). *Tubaria vulcanica* is characterised by its smooth, amygdaliform to ellipsoid spores, and lageniform to tibiiform cheilocystidia. Its basidiomes were found growing directly on volcanic lapilli material used for gardening or pavement in the Canary Islands. Following Bon (1992), *T. vulcanica* could be included in sect. *Pallidosporae* because of its lamellae of pallid colour when young, and thin walled, amygdaliform and not pigmented spores. Its LSU rDNA sequence is close to one identified as *Tubaria albostipitata* (GenBank EF051051, 98.24 % similar), but the new species has a differently coloured stipe, larger spores and cheilocystidia, and pileipellis with much broader elements. ITS rDNA is 97.55 % similar to one sequence obtained from forest soil litter in Arkansas, USA (GenBank MK234224) and *rpb2* is 84 % similar to several undetermined sequences of *Tubaria* sp. (GenBank MH618217, HQ839738, MH618216).

Colour illustrations. Spain, Islas Canarias. Tenerife, Barranco Las Lajas, pyroclastic fragments (lapilli) where the holotype was collected. Basidiomata; cheilocystidia; clamps; spores under LM; spores under SEM (from the holotype). Scale bars = 0.5 cm (basidiomata), 10 µm (cheilocystidia and spores under LM), 2.5 µm (spores under SEM).

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Tuber zambonelliae

Fungal Planet 1280 – 13 July 2021

Tuber zambonelliae Ant. Rodr. & Morte, *sp. nov.*

Etymology. Named after Alessandra Zambonelli, from the University of Bologna, mycologist and specialist in hypogeous fungi and mycorrhizae, for her outstanding contribution to the knowledge of *Tuber* spp.

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

Ascomata hypogeous, 0.5–2 cm diam, subglobose, pale brown, smooth, minutely pruinose. *Peridium* 100–200(–300) µm thick, composed of hyaline, agglutinated, interwoven hyphae (intricate texture). *Gleba* firm, solid, whitish at first, becoming pale to dark brown at maturity, marbled with numerous, branching, white and dark veins. *Odour* pleasant. *Asci* inamyloid, 60–70 × 40–50 µm excluding stalk, pyriform to clavate or subglobose, with a long or short stalk arising from a crozier, 10–40 µm long, walls 1–2 µm thick, 1–4(–5)-spored. *Ascospores* 22–45 × 16–26 µm, Q = 1.4–1.9, excluding ornamentation, at first hyaline, yellowish brown at maturity, ellipsoidal to ovoid, ornamented with short spines, 1–2 µm long, often connected by lower ridges, making the ornamentation an irregular and incomplete spiny reticulum.

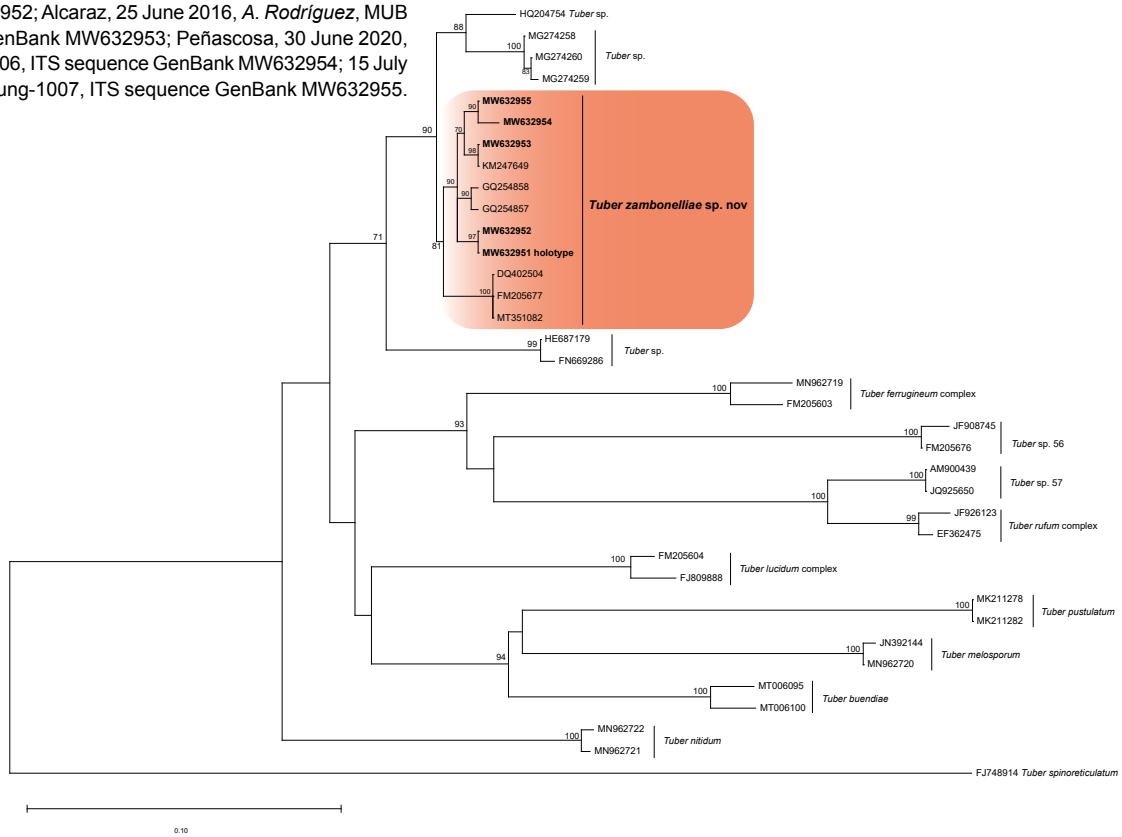
Ecology & Distribution — *Tuber zambonelliae* grows in Mediterranean *Quercus ilex* subsp. *ballota* forests, in limestone mountains of the south of the Iberian Peninsula, 1 000–1 300 m in altitude. The species occurs in spring and summer.

Typus. Spain, Albacete, Masegoso, in calcareous soil, in *Quercus ilex* subsp. *ballota* forest (*Fagaceae*), 15 June 2020, *E. Buendía* (holotype MUB Fung-995, ITS and LSU sequences GenBank MW632951 and MW642207, MycoBank MB 838904).

Additional materials examined. Spain, Albacete, Masegoso, in *Quercus ilex* subsp. *ballota* forest, 18 June 2016, *A. Rodríguez*, MUB Fung-740, ITS sequence GenBank MW632952; Alcaraz, 25 June 2016, *A. Rodríguez*, MUB Fung-741, ITS sequence GenBank MW632953; Peñascosa, 30 June 2020, *A. Rodríguez*, MUB Fung-1006, ITS sequence GenBank MW632954; 15 July 2020, *A. Rodríguez*, MUB Fung-1007, ITS sequence GenBank MW632955.

Notes — *Tuber zambonelliae* is a pale brown truffle that clusters in the rufum clade, and is characterised by its smooth peridium, brown gleba marbled with white and dark veins and spiny-reticulate spores. *Tuber zambonelliae* resembles *Tuber nitidum*, but in addition to genetic differences, *T. nitidum* differs by having a basal cavity, peridium with cellular structure in the outermost layer and smaller spores with separate and shorter spines (Ceruti et al. 2003). *Tuber requienii* also resembles *Tuber zambonelliae* but it has a papillose peridium and lacking dark veins (Tulasne & Tulasne 1851).

Maximum likelihood (ML) phylogenetic tree of the *T. rufum* clade inferred from ITS sequences, using RAxML-HPC v. 8 (Stamatakis 2014) on XSEDE in the CIPRES science gateway (Miller et al. 2010). GTR + G selected as model of evolution for analysis. The sequences obtained in the present study are highlighted in **bold** and the novel species with a coloured box. Bootstrap support values (≥ 70 %) are indicated at the nodes. *Tuber spinoreticulatum* (GenBank FJ748914) was used as outgroup. The scale bar indicates the expected changes per site. Species hypotheses for undescribed species (*Tuber* sp. followed by numbers) follow the conventions of Bonito et al. (2010).



Colour illustrations. Spain, Alcaraz mountain range (Albacete), Mediterranean *Quercus ilex* subsp. *ballota* forest. Ascocarps; mature ascospores. Scale bar = 20 µm.

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Xerochrysium bohemicum

Fungal Planet 1281 – 13 July 2021

Xerochrysium bohemicum Kubátová & Hubka, *sp. nov.*

Etymology. Named after the region where the fungus was collected.

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

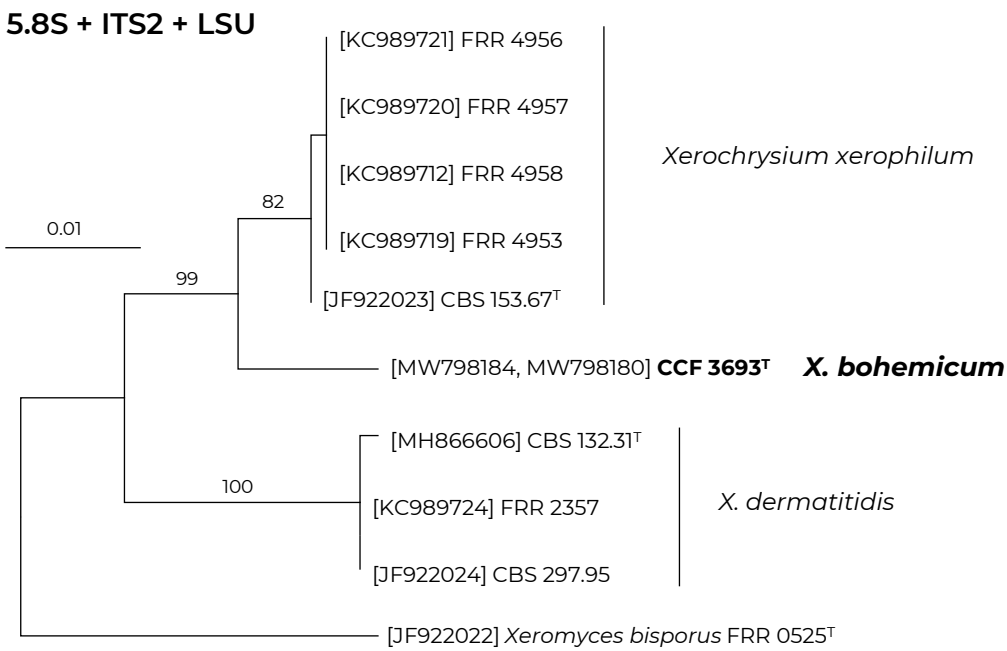
Micromorphology (on malt extract yeast extract 50 % glucose agar; MY50G): *Hyphae* hyaline, 2–10 µm diam (mean ± standard deviation: 5.7 ± 1.6), later transforming into arthroconidia; lateral and terminal aleurioconidia abundant. All conidia hyaline, with thick, smooth wall. *Arthroconidia* of variable shape and size, cylindrical, doliiform, ovoid to globose, 4.3–14 × 3.1–10 µm. *Lateral aleurioconidia* sessile or borne on short cylindrical, funnel-shaped or swollen pedicels, subglobose to globose. *Terminal aleurioconidia* pyriform, subglobose to globose. Size of lateral and terminal conidia similar, 5.7–12.2 × 5–10 µm (av. ± SD 7.4 ± 1.3 × 6.6 ± 1). No sexual morph observed.

Culture characteristics (at 25 °C after 7/14 d, in darkness) — Colonies on MY50G 16–18/38–42 mm diam, velutinous, mycelium whitish, margins fimbriate, sporulation heavy, reverse uncoloured, later yellowish to brownish in the centre. Colonies on malt extract 20 % sucrose agar (MA20S) 4–5/14 mm diam, velutinous, mycelium dense, white, sporulation heavy, reverse uncoloured, later brownish in the centre. Colony diam (in mm after 7 d) at 15 °C on MY50G 2–3 and on MA20S no growth; at 20 °C on MY50G 10–11 and on MA20S 2; at 30 °C on MY50G 21–24 and on MA20S 2. Optimum temperature for growth is 25–30 °C. Growth on malt extract agar (MEA) is very restricted and absent on Czapek yeast extract agar (CYA). No growth at 37 °C.

Typus. Czech Republic, Prague, surface of biscuits with chocolate glaze and filled with jam (similar to Jaffa cakes), 2007, *J. Jirešová* (holotype PRM 954080, culture ex-type CCF 3693 = CBS 147157, ITS and LSU sequences GenBank MW798184 and MW798180, MycoBank MB 839239).

Notes — BLAST analyses with the ITS and LSU region of *Xerochrysium bohemicum* showed greatest similarity with isolates of *X. xerophilum* (~94.8 % / ~99.4 %), *X. dermatitidis* (~93.8 % / ~98.4 %) and *Xeromyces bisporus* (~89.6 % / ~98.2 %).

Xerochrysium bohemicum is morphologically similar to *X. dermatitidis* and *X. xerophilum*, but grows more rapidly. *Xerochrysium bohemicum* and *X. xerophilum* differ from *X. dermatitidis* by almost complete differentiation of vegetative hyphae into intercalary arthroconidia (Pitt et al. 2013).



A best scoring maximum likelihood tree based on the region containing 5.8S, ITS2 and LSU sequences. The dataset contained 15 taxa and a total of 1 402 characters of which 79 were variable and 21 parsimony-informative. The tree was constructed with IQ-TREE v. 1.4.4 (Nguyen et al. 2015), substitution model TN+F+I was used. Support values at branches were obtained from 1 000 bootstrap replicates; only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by superscript T. The tree is rooted with *Xeromyces bisporus*.

Colour illustrations. Biscuits with chocolate glaze and filled with jam. Fourteen-day-old colonies on MY50G and MA20S (6 cm Petri dish); conidiophores and conidia (scanning electron microscopy, phase contrast, differential interference contrast). Scale bars = 10 µm.

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Fusarium juglandicola

Fungal Planet 1282 – 13 July 2021

Fusarium juglandicola L. Lombard & Crous, *sp. nov*.

Etymology. From the Latin *iuglandis*, walnut, referring to the substrate that this fungus was isolated from.

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

Conidiophores on aerial mycelium 10–95 µm tall, unbranched or rarely irregularly or sympodially branched and proliferating, bearing terminal single phialides or whorls of 2–3 phialides, commonly reduced to solitary conidiogenous cells borne laterally on hyphae; *aerial conidiogenous cells* monophialides, subulate to subcylindrical, smooth- and thin-walled, 11–33 × 3–5 µm, proliferating percurrently, periclinal thickening and collarettes often inconspicuous or absent. *Aerial microconidia* not observed. *Sporodochial conidiophores* 18–24 µm tall, irregularly branched, bearing terminal solitary or whorls of 2–3 phialides. *Sporodochial conidiogenous cells* monophialidic, doliiform, subulate to subcylindrical, smooth- and thin-walled, (8–)10–14(–17) × 3–4.5(–6) µm. *Sporodochial conidia* straight to moderately curved, tapering towards the basal part, apical cell more or less equally sized than the adjacent cell, curved to hooked; basal cell well-developed, foot-shaped, rarely papillate, (1–)3–4(–5)-septate, hyaline, thin- and smooth-walled: 1-septate conidia: 41–44 × 4–5 µm; 3-septate conidia: (37–)39.5–44.5(–47) × (4–)4.5–5.5(–6) µm (av. 42 × 5 µm); 4-septate conidia: (41–)42–48(–53) × (4–)4.5–5.5(–6) µm (av. 45 × 5 µm); 5-septate conidia: (45–)47–51(–53) × (4–)4.5–5.5(–6) µm (av. 49 × 5 µm), overall: (37–)41.5–48.5(–53) × (4–)4.5–5.5 (–6) µm (av. 45 × 5 µm). *Chlamydospores* not observed.

Culture characteristics — Colonies on potato dextrose agar reaching 25–45 mm diam at 25 °C after 7 d. Surface white to pale luteus, flat, woolly to cottony with radial patches of white aerial mycelium, margin regular and filiform. Reverse white to pale luteus. On oatmeal agar pale luteus, flat, membranous, margin regular. Reverse pale luteus.

Typus. France, Rhone-Alps region, from bud of *Juglans regia* (*Juglandaceae*), 2017, *P. Nodet* (holotype CBS H-24770, culture ex-type CBS 147773 = CPC 37962 = UBOCC-A-119001, ITS, LSU, *CaM*, *rpb1*, *rpb2* and *tef1* sequences GenBank MZ064461.1, MZ064519.1, MZ078174.1, MZ078190.1, MZ078215.1 and MZ078243.1, MycoBank MB 839621).

Additional materials examined. France, from *Juniperus* sp. (*Cupressaceae*), 2001, LUBEM collector, culture CBS 147774 = CPC 37956 = UBOCC-A-101147, ITS, LSU, *CaM*, *rpb2* and *tef1* sequences GenBank MZ064462.1, MZ064520.1, MZ078175.1, MZ078216.1 and MZ078244.1; from eggs, 2002, LUBEM collector culture CBS 147775 = CPC 37957 = UBOCC-A-102014, ITS, LSU, *CaM*, *rpb1*, *rpb2* and *tef1* sequences GenBank MZ064463.1, MZ064521.1, MZ078176.1, MZ078191.1, MZ078217.1 and MZ078245.1.

Notes — *Fusarium juglandicola* was repeatedly isolated from walnut (fruits or flower buds), and based on *tef1* sequences, initially considered closely related to *F. lateritium*. Later, these isolates were considered much closer to *F. salinense*. Following this reclassification, a re-examination of some strains (UBOCC collection) initially classified as closely related to *F. lateritium*, revealed several strains also related to *F. salinense*, which were included in the present study.

Fusarium juglandicola nested within the *F. citricola* species complex. Similar to *F. celtidicola*, *F. citricola* and *F. salinense*, this slow-growing species only forms monophialidic conidiogenous cells in culture, and produces up to 5-septate sporodochial conidia (Sandoval-Denis et al. 2018, Shang et al. 2018). However, *F. juglandicola* is easily distinguished from *F. celtidicola*, *F. citricola* and *F. salinense* by the lack of aerial microconidia and absence of chlamydospore formation. Additionally, *F. juglandicola* does not produce red pigments when incubated under continuous white light as has been reported for the other three species in this complex (Sandoval-Denis et al. 2018, Shang et al. 2018).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Fusarium lateritium* (strain BBA 65248, GenBank AF310980.1; Identities = 571/572 (99 %), no gaps), *Fusarium tricinctum* (strain 05009, GenBank MG274297.1; Identities = 570/572 (99 %), no gaps) and *Fusarium citricola* (strain CPC 27813, GenBank LT746246.1; Identities = 570/572 (99 %), no gaps). Closest hits using the **LSU** sequence are *Fusarium lateritium* (strain CBS 253.61, GenBank MH869608.1; Identities = 897/898 (99 %), no gaps), *Fusarium lateritium* (strain CBS 189.31, GenBank MH866630.1; Identities = 896/897 (99 %), no gaps) and *Fusarium equiseti* (strain CBS 125827, GenBank MH875256.1; Identities = 897/899 (99 %), no gaps). Closest hits using the ***CaM*** sequence are *Fusarium avenaceum* (strain p12.56.2016, GenBank MK547650.1; Identities = 561/611 (92 %), eight gaps (1 %)), *Fusarium flocciferum* (strain NRRL 45999, GenBank GQ505401.1; Identities = 539/579 (93 %), seven gaps (1 %)) and *Fusarium* sp. (strain NRRL 36147, GenBank GQ505389.1; Identities = 530/576 (92 %), eight gaps (1 %)). Closest hits using the ***rpb1*** sequence are *Fusarium salinense* (strain CPC 26457, GenBank LT46285.1; Identities = 714/738 (97 %), one gap (0 %)), *Fusarium pietersiae* (strain CBS 143231, GenBank MG386138.1; Identities = 699/738 (95 %), one gap (0 %)) and *Fusarium flocciferum* (strain NRRL 45999, GenBank HM347195.1; Identities = 651/686 (95 %), no gaps). Closest hits using the ***rpb2*** sequence are *Fusarium salinense* (strain IT 2345, GenBank MT212199.1; Identities = 886/902 (98 %), no gaps), *Fusarium citricola* (strain CPC 27813, GenBank LT746311.1; Identities = 880/902 (98 %), no gaps) and *Fusarium flocciferum* (strain NRRL 52714, GenBank MH582363.1; Identities = 832/857 (97 %), no gaps). Closest hits using the ***tef1*** sequence are *Fusarium* sp. (strain ICMP 1793, GenBank MG857157.1; Identities = 643/643 (100 %), no gaps), *Fusarium citricola* (strain CPC 27069, GenBank LT746195.1; Identities = 632/646 (98 %), five gaps (0 %)) and *Fusarium lateritium* (strain MAFF 235344, GenBank AB674281.1; Identities = 629/646 (97 %), seven gaps (1 %)).

Colour illustrations. *Juglans regia* with fruit growing in France (photo credit P. Nodet). Sporodochia on carnation leaf agar; aerial conidiophores and lateral monophialides on aerial mycelium on SNA; sporodochial conidia. Scale bars = 10 µm.

Supplementary material

FP1282 & 1283 The maximum likelihood consensus tree inferred from the combined *rpb1*, *rpb2* and *tef1* sequence alignment using RAxML v. 8.2.9 (Stamatakis 2014).

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Fusarium aconidiale

Fungal Planet 1283 – 13 July 2021

Fusarium aconidiale L. Lombard & Crous, *sp. nov*.

Etymology. Name refers to an absence of aerial microconidia produced in culture by this fungus.

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

Conidiophores on aerial mycelium 30–115 µm tall, unbranched or rarely irregularly or sympodially branched and proliferating, bearing terminal single phialides or whorls of 2–3 phialides, commonly reduced to solitary conidiogenous cells borne laterally on hyphae; *aerial conidiogenous cells* monophialides, subulate to subcylindrical, smooth- and thin-walled, 14–28 × 3–5 µm, proliferating percurrently, periclinal thickening and collarettes often inconspicuous or absent. *Aerial microconidia* not observed. *Sporodochial conidiophores* 23–38 µm tall, irregularly branched, bearing terminal solitary or whorls of 2–3 phialides. *Sporodochial conidiogenous cells* monophialidic, doliiform, subulate to subcylindrical, smooth- and thin-walled, (11–)13–17(–21) × 3–5 µm. *Sporodochial conidia* straight to moderately curved, tapering towards the basal part, apical cell more or less equally sized than the adjacent cell, curved to hooked; basal cell well-developed, foot-shaped, rarely papillate, 3(–5)-septate, hyaline, thin- and smooth-walled: 3-septate conidia: (36–)41–49(–53) × 4–5 µm (av. 45 × 4 µm); 4-septate conidia: 46–52(–56) × 4–5 µm (av. 49 × 5 µm); 5-septate conidia: 52–60(–61) × 5–6 µm (av. 56 × 5 µm), overall: (36–)42–53(–61) × (4–)4.5–5.5(–6) µm (av. 47 × 5 µm). *Chlamydospores* not observed.

Culture characteristics — Colonies on potato dextrose agar reaching 15–40 mm diam at 25 °C after 7 d. Surface white to rosy buff, flat, woolly to cottony with radial patches of white aerial mycelium, margin regular and filiform. Reverse white to pale rosy buff. On oatmeal agar pale rosy buff, flat, membranous, margin effuse. Reverse colourless.

Typus. France, from *Triticum aestivum* (*Poaceae*), 2008, *A. Weill* (holotype CBS H-24769, culture ex-type CBS 147772 = CPC 37959 = UBOCC-A-109005, ITS, LSU, *CaM*, *rpb1*, *rpb2* and *tef1* sequences GenBank MZ064464.1, MZ064522.1, MZ078177.1, MZ078192.1, MZ078218.1 and MZ078246.1, MycoBank MB 839622).

Notes — *Fusarium aconidiale* is phylogenetically closely related to *F. celtidicola* and *F. juglandicola* in the *F. citricola* species complex (FCCSC; Sandoval-Denis et al. 2018, Shang et al. 2018). Similar to *F. juglandicola*, this species does not produce red pigment under continuous white light nor any chlamydospores or aerial microconidia, distinguishing it from other members of the FSSCS. However, *F. aconidiale* produces predominantly 3-septate sporodochial conidia and much less frequently 4- and 5-septate sporodochial conidia compared to *F. juglandicola*.

Colour illustrations. *Triticum aestivum* field in South Africa (photo credit G. van Coller). Sporodochia on carnation leaf agar; aerial conidiophores and lateral monophialides on aerial mycelium on SNA; sporodochial conidia. Scale bars = 10 µm.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the **ITS** sequence had the highest similarity to *Fusarium lateritium* (strain BBA 65248, GenBank AF310980.1; Identities = 584/588 (99 %), one gap (0 %), *Cordyceps sinensis* (strain SANMEI, GenBank AB067719.1; Identities = 583/588 (99 %), no gaps) and *Fusarium lateritium* (strain HMA-1, GenBank GU480949.1; Identities = 582/588 (99 %), one gap (0 %). Closest hits using the **LSU** sequence are *Fusarium lateritium* (strain CBS 253.61, GenBank MH869608.1; Identities = 897/898 (99 %), one gap (0 %)), *Fusarium lateritium* (strain CBS 189.31, GenBank MH866630.1; Identities = 896/897 (99 %), no gaps) and *Fusarium equiseti* (strain CBS 125827, GenBank MH875256.1; Identities = 897/899 (99 %), no gaps). Closest hits using the ***CaM*** sequence are *Fusarium flocciferum* (strain NRRL 45999, GenBank GQ505401.1; Identities = 539/579 (93 %), seven gaps (1 %)), *Fusarium avenaceum* (strain p12.56.2016, GenBank MK547650.1; Identities = 550/598 (92 %), seven gaps (0 %)) and *Fusarium* sp. (strain NRRL 36147, GenBank GQ505389.1; Identities = 530/576 (92 %), eight gaps (1 %)). Closest hits using the ***rpb1*** sequence are *Fusarium salinense* (strain CPC 26457, GenBank LT46285.1; Identities = 674/700 (96 %), one gap (0 %)), *Fusarium pietersiae* (strain CBS 143231, GenBank MG386138.1; Identities = 658/700 (94 %), one gap (0 %)) and *Fusarium flocciferum* (strain NRRL 45999, GenBank HM347195.1; Identities = 629/667 (94 %), no gaps). Closest hits using the ***rpb2*** sequence are *Fusarium salinense* (strain IT 2345, GenBank MT212199.1; Identities = 888/902 (98 %), no gaps), *Fusarium citricola* (strain CPC 27813, GenBank LT746311.1; Identities = 882/902 (98 %), no gaps) and *Fusarium citricola* (strain CPC 27805, GenBank LT746310.1; Identities = 882/902 (98 %), no gaps). Closest hits using the ***tef1*** sequence are *Fusarium* sp. (strain ICMP 5227, GenBank MG857225.1; Identities = 642/642 (100 %), no gaps), *Fusarium* sp. (strain ICMP 5661, GenBank MG857291.1; Identities = 633/646 (98 %), seven gaps (1 %)) and *Fusarium* sp. (strain ICMP 1793, GenBank MG857157.1; Identities = 633/646 (98 %), seven gaps (1 %)).

Supplementary material

FP1282 & 1283 The maximum likelihood consensus tree inferred from the combined *rpb1*, *rpb2* and *tef1* sequence alignment using RAxML v. 8.2.9 (Stamatakis 2014). The robustness of the analysis was evaluated by bootstrap support (BS) with the number of bootstrap replicates automatically determined by the software. The combined sequence dataset included 19 ingroup taxa with *Fusarium heterosporum* (CBS 391.68) as outgroup. The dataset consisted of 4 177 characters including gaps. Additionally, MrBayes v. 3.2.1 (Ronquist & Huelsenbeck 2003) was used for BI to generate phylogenetic trees under optimal criteria for each locus. A Markov Chain Monte Carlo (MCMC) algorithm of four chains was initiated in parallel from a random tree topology with the heating parameter set at 0.3. The MCMC analysis lasted until the average standard deviation of split frequencies was below 0.01 with trees saved every 1 000 generations. The first 25 % of saved trees were discarded as the 'burn-in' phase and posterior probabilities (PP) were determined from the remaining trees. Support values (BS & PP values) are indicated at the branches. The scale bar indicates 0.04 expected changes per site.

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