Fungal Planet description sheets: 1042–1111

P.W. Crous1,2, M.J. Wingfield3, Y.-H. Chooi3, C.L.M. Gilchrist4, E. Lacey4, J.L. Pitt4, F. Roets5, W.J. Swart6, J.F. Cano-Lira7, N. Valenzuela-Lopez8, V. Hubka9,10, R.G. Shivaa11, A.M. Stchigel6, D.G. Holdom12, Z. Jurjević13, A.V. Kachalkin14,15, T. Lebel16, C. Lock12, M.P. Martin17, Y.P. Tan18, M.A. Tomashevskaya15, J.S. Vitelli12, I.G. Baseia19, V.K. Bhatt20, M.E. Smith87, D. Spadaro83, M. Spetik38, M. Sochor88, Z. Sochorová89, J.O. Sousa43, A. Morte25, V. Papp26, A. Rodriguez25, E. Rodriguez-Andrade7, K.C. Semwal27, L. Tegart28, Z.G. Abad29, A. Akulov30, P. Alvarado31, A. Alves32, J.P. Andrade33,34, F. Arenas25, C. Asenjo35, A.M. Glushakova14,56, M.F.M. Gonçalves32, M. González57, M. Gorczak58, C. Gorton59, A.L. Guarnizo25, J. Guarro7, M. Gutiérrez35, P. Hamal60, L.T. Hien61, R. Mahiques73, E.F. Malysheva49, P.A.S. Marbach53, P. Marinho74, N. Matočec69, L. Kelly67, T.N. Khanh61, K. Kislo11, L. Kiss11, A. Kubáňová9, V. Kučera88, I. Kučerová9, I. Kušan69, G. Levicán41, A. Lewis44, N.V. Liem61, K. Liimatainen45, H.J. Lim70, M.N. Lyons71, J.G. Maciá-Vicente72, V. MagañaDueñas7, R. Mahiques73, E.F. Malyshova19, P.A.S. Marbach53, P. Marinho74, N. Matočec69, A.R. McTaggart75, A. Mešić69, L. Morin63, J.M. Muñoz-Mohedano25, A. Navarro-Rodrénas24, C.P. Nicolii22, R.L. Oliveira76, E. Otsing77, C.L. Ovrebo78, T.A. Pankratov14,79, A. Paños26, A. Paz-Conde80, A. Pérez-Sierra44, C. Phorsí81, A. Pintos82, A. Pošta69, S. Prencipe83, E. Rubio84, A. Saïta85, L.S. Sales53, L. Sanhueza52, L.A. Shuttleworth44, J. Smith86, M.E. Smith87, D. Spadaro83, M. Spetik38, M. Sochor88, Z. Sochorová89, J.O. Sousa43, N. Suwannasara20, L. Tedersoo77, H.M. Than61, L.D. Thao61, Z. Tkáčec69, N. Vaghefi61, A.S. Venzhik14, A. Verbeken18, A. Vizzini92, S. Voyron46, M. Wainhouse93, A.J.S. Whalley84, M. Wrzosek95, M. Zapata96, I. Zeil-Rolfe63, J.Z. Groenewald1

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: Antarctica, Cladosporium arbuscum from marine sediment sand, Argentina, Kosmimatymyces aleutophyllus (incl. Kosmimatymyces gen. nov.) from soil, Australia, Aspergillus banksianus, Aspergillus kumbius, Aspergillus luteorubrus, Aspergillus malvicolor and Aspergillus nanangensis from soil, Erysiphe medicaginis from leaves of Medicago polymorpha, Hymenomycidiella communis on leaf litter of Eucalyptus bicostata, Lactifluus alboipicri and Lactifluus austropiperatus on soil, Macalpymyces colliae on Eriachne benthamii, Mammagoniomyces vagus on soil, Microdochium dassonoviae from leaves of Sporobolus natalensis, Neostephalotopsis nebuloides from leaves of Sporobolus elongatus, Pestalotiopsis etonensis from leaves of Sporobolus Jacquemontii, Phytophthora aysenensis, Stachmopsis pini, Venturia paralias on leaves of Eucalyptus bicostata from indoor chestnut mill, Calvatia baixaverdensis on leaf litter, Greeneria kielmeyerae on leaf spots of Kielmeyera coriacea, Chiile, Phyllophthora aysenensis on leaf litter and stem of Aristotelia chilensis, Croatia, Mollisia gibbospora on fallen branch of Fagus sylvatica, Czech Republic, Neosotaphora thalassica from Buxus sempervirens, Ecuador, Exophiala frigidotolerans from soil, Estonia, Elaphomyces tutchmi on leaf litter, France, Venturia paralias from leaves of Euphorbia paralias, India, Cortinarius baltiostrophicus and Cortinarius uhrkagharenisis on leaf litter. Indonesia, Hymenomycidiella indonesiana on Eucalyptus urophylla leaf litter, Italy, Penicillium taenius from indoor chestnut mill, Malaysia, Hemileucoglossum kalibentense on soil, Satchmopsis pini on dead needles of Pinus tecunumanii, Poland, Lecanicillium praecognitum on insects’ frass, Portugal, Neodevriesia aestuarina from saline water, Russia, Candida pellucida from Exomias pellucidus, Heterocephalessia septentrionalis as endophyte from Cladonia rangiferina, Vishniacozyma phoenicus from dates fruit, Volvariella paludosa from swamp, Slovenia, Mallophyce crassivelata on leaf litter. South Africa, Beltraniiodes podocarpis, Hamatocanthes podocarpis, Coleophaoma podocarpis and Nothoseiridium podocarpis (incl. Nothoseiridium

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute

You are free to share - to copy, distribute and transmit the work, under the following conditions:
- Attribution: You must attribute the work in the manner specified by the author or licensor (but not in any way that suggests that they endorse you or your use of the work).
- Non-commercial: You may not use this work for commercial purposes.
- No derivative works: You may not alter, transform, or build upon this work.

For any reuse or distribution, you must make clear to others the license terms of this work, which can be found at http://creativecommons.org/licenses/by-nc-nd/3.0/legalcode. Any of the above conditions can be waived if you get permission from the copyright holder. Nothing in this license impairs or restricts the author's moral rights.
Abstract (cont.)

...gen. nov.) from leaves of Podocarpus latifolius, Gyrotrichus encephalartis from leaves of Eocenefloratus sp., Paraphyton cutaneum from skin of human patient, Phacidiella asplioa from leaves of Allopopsis capensis, and Satchmopsis metrosidoni on leaf litter of Metrosideros excelsa. Spain. Cladosiphosphora cabanensia from soil, Cylindrium magnoliae from leaves of Magnolia grandiflora, Trichophoma cylindrospora (incl. Trichophoma gen. nov.) from plant debris, Tuber alcaracense in calcareous soil, Tuber buendia in calcareous soil. Thailand. Annullohypoxylon spougeii on corticated wood, Poaceaeform sp. from leaves of unknown Poaceae. UK. Dendrostauma luteum on branch lesions of Castanea sativa, Ypsilina buttongrensis from heartwood of Quercus sp. Ukraine. Mymecridium phragmetica from leaves of Phragmites australis. USA. Abadia pararepsirs from air, Junomyces californiensis (incl. Junomyces gen. nov.) from leaves of Juncus effusus, Magnusia cylindrospora from a human skin sample, Muphiila oklahomensis (incl. Muphiila gen. nov.) on outside wall of alcohol distillery, Neofabraea eucalyptorum from leaves of Eucalyptus maculanda, Diabolocovidia clausiti (incl. Diabolocovidia gen. nov.) from leaves of Serenoa repens, Paecilomyces pellucifolius from air, Pseudopezicula betulae from leaves of leaf spots of Populus tremuloides. Vietnam. Diaporthe duriogenes on branches of Durio zibethinus and Rondiomyces pseudoterram on rotten wood. Morphological and culture characteristics are supported by DNA barcodes.

Article info
Received: 1 April 2020; Accepted: 30 May 2020; Published: 29 June 2020.
63 CSIRO Health and Biosecurity, GPO Box 1700, Canberra, ACT 2601, Australia.
64 Federal and Rural University of Rio de Janeiro, Seropedica, Rio de Janeiro, Brazil.
65 CSIRO European Laboratory, Campus International de Baillarguet, Montferrier sur lez 34980, France.
66 Tobolsk Complex Scientific Station of the Ural Branch of the Russian Academy of Sciences, 626152, 15 Academic Yuri Osipov Str., Tobolsk, Russia.
67 Department of Agriculture and Fisheries, Queensland Government, Toowoomba 4350, Queensland, Australia.
68 Plant Science and Biodiversity Centre, Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 9, 845 23, Bratislava, Slovakia.
69 Ruđer Bošković Institute, Bijenička cesta 54, 10000 Zagreb, Croatia.
70 Environmental Microbiology Lab, Dept. of Agricultural Biological Chemistry, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 61186, Korea.
71 Ecosystem Science, Department of Biodiversity, Conservation and Attractions, Kensington 6151, Western Australia.
72 Institute of Ecology, Evolution and Diversity, Goethe University Frankfurt, Max-von-Laue-Str. 13, 60438, Frankfurt am Main, Germany.
73 C/ Dr. Climent, 26, E-46837, Quatretonda, València, Spain.
74 Departamento de Biología Celular e Genética, Universidade Federal do Rio Grande do Norte, Natal, Rio Grande do Norte, Brazil.
75 Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane 4102, Australia.
76 Centro de Ciências, Universidade Federal do Rio Grande do Norte, Av. Senador Salgado Filho, 3000, 59072-970 Natal, RN, Brazil.
77 Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai St., 51005 Tartu, Estonia.
78 Department of Biology, University Central Oklahoma Edmond, Oklahoma, 73034 USA.
79 S.N. Winogradsky Institute of Microbiology, Research Center of Biotechnology of the Russian Academy of Sciences, 119071, Moscow, Russia.
80 Agropocio Micologica Berguedana, carrera Vall-Ter 791, apto. correos 6, 17455, Girona, Spain.
81 Biology programme, Faculty of Science, Nahkon Phanom University, Nahkon Phanom, 48000, Thailand.
82 Interdisciplinary Ecology Group, Universitat de les Illes Balears, ctra. de Valldemossa Km 7.5, 07122 Illes Balears, Spain.
83 University of Turin - Department of Agricultural Forestry and Food Sciences, Largo Paolo Braccini 2, 10095, Grugliasco, Turin, Italy.
84 José Cueto 3 5B, 33401 Avilés, Spain.
85 Department of Agricultural, Food and Forest Sciences, University of Palermo, Viale delle Scienze, Palermo, 90128, Italy.
86 School of Forest Resources and Conservation, University of Florida, Gainesville, FL 32611-0410 USA.
87 Department of Plant Pathology & Florida Museum of Natural History, 2527 Fillfield Hall, Gainesville FL 32611, USA.
88 Centre of the Region Haná for Biotechnological and Agricultural Research, Crop Research Institute, Šlechtitělů 29, 78371, Olomouc, Czech Republic.
89 Department of Botany, Faculty of Science, Palacký University Olomouc, Šlechtitělů 27, 78371, Olomouc, Czech Republic.
90 Department of Microbiology, Faculty of Science, Srinakharinwirot University, Bangkok, 10110 Thailand.
91 Campus Ledeganck, Ghent University, Belgium.
92 Institute for Sustainable Plant Protection (IPSP) – CNR, Viale P.A. Mattioli 25, 10125, Torino, Italy.
93 Organisms and Environment Research Division, School of Biosciences, Cardiff University, Cardiff, UK.
94 School of Pharmacy and Biomolecular Sciences, Liverpool John Moores, Byrom Street, Liverpool, L3 3AF, UK.
95 Botanic Garden, Faculty of Biology, University of Warsaw, Aleje Ujazdowskie 4, 00-479 Warsaw, Poland.
96 Servicio Agrícola y Ganadero, Laboratorio Regional Chillán, Unidad de Fitopatología, Claudio Arrau 738, Chillán, Código Postal 3800773, Chile.
Acknowledgements Nuttilka Suwannasi and colleagues thank Mongkol Kamsook for the photograph of the Phu Khiao Wildlife Sanctuary; the study was partially supported by IFS, NRCT and CGL2015-67459-P projects. The study of John I. Pitt and colleagues was funded in part by the Cooperative Research Centres Projects scheme (CRCPF/VE000119), Canberra, Australia. Financial support was provided to Renan L. Oliveira and Renato J. Ferreira by the Coordination of Improvement of Higher Level Personnel (CAPES), and to Iuri G. Baseia, Paulo S. M. Lúcio and Maria P. Martin by the National Council for Scientific and Technological Development (CNPq) under CNPq-Universal 2016 (409960/2016-0) and CNPq-visitoring research (407474/2013-7). This study of Aleksey V. Kachalkin and colleagues was supported by the Russian Science Foundation (grant No. 19-74-10002). Jose G. Maciá-Vicente acknowledges support from the German Research Foundation under grant MAT1717/1-1, and thanks the authorities of the Cabañeros National Park, especially A. Gómez Manzanque to collect the permission and for support during the sampling. Loreto Sanhueza thanks the support of Fondo de Desarrollo to la Publicación (FDP PEP i-2019076), Universidad Mayor. Carlos Gil-Durán thanks doctoral fellowship CONICYT-PFCHA/Doctorado Nacional/2014-63140056. Gloria Levician thanks grant INACH RT_31-16 from Chilean Antarctic Institute. Renato Chávez thanks DICYT-USACH and project INACH RG_03-14. The study of Bálint Dima was partly supported by the ELTE Institutional Excellence Program supported by the National Research, Development and Innovation Office (NKFIH-1157-8/2019-DT) in Hungary, Kamal C. Semwal and Vinod K. Bhatt are grateful to the Uttarakhand State Council for Science and Technology (UCOST), Dehradun, Uttarakhand, India for the financial support under the project no. UCS&T/R&D/LIS-1/12-13/4912, entitled Collection, Identification, Documentation of Wild Edible and Medicinal Mushrooms of Garhwal Himalaya of Uttarakhand. The study of Ernesto Rodríguez-Andrade, Nicomedes Valenzuela-Lopez and colleagues was supported by the Spanish Ministerio de Economía y Competitividad, grant CGL2017-88094-P. Coordenación de Aperfeiçoamento de Pessoal de Nível Superior (CAPES-Brazil) are thanked for the scholarships awarded to Julmar Freitas-Neto, and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq, Brazilian agency) for providing financial support for the Projeto Pesquisador Visitante Especial (PVE - 407474/2013-7). The Smithsonian Tropical Research Institute is thanked for granting permission to collect on the Barro Colorado Nature Monument. The study of Hyang Burnm Lee and colleagues was supported by the Graduate Program for the Undiscovered Taxa of Korea, funded by NIBR of the Ministry of Environment (MDE) of Korea. Viktor Kučera and colleagues collected material under the permit no. NCCD.907.4.J(LD).13-337 issued by the Sarawak Forestry Department. Financial support was provided by grant agency VEGA (project 2/00619/2019) to Viktor Kučera and by an internal grant from Palacký University (IGA-PrF-2020-003) to Zuzana Sochorová. Michal Sochor was supported by grant no. R004/18 from Ministry of Agriculture, the Czech Republic. Zuzana Sochorová thanks Habibah Saleh for cooperation. Teresa Lebel and Lachlan Tegart thank the curation staff at RBGV, PERTH and BRI for their help with loans and processing of collections, Geoff Lay, Matt Barrett and Fan Guard for the background images, Vanessa Ryan for assistance with photos. Lachlan Tegart was funded through a Willis Summer student internship at the Royal Botanic Gardens Victoria. Australasian Biological Resources Study (RFL217-63) and Bioplatforms Australia funding supported part of this research. Thank you also to Matthew Barrett for providing sequences and collection information for Northern Territory material for this project. Jonathan Martin and Jessica Malka are thanked for providing specimens for this research. Funding for sequencing (USF) was provided by the Cooley and Lakela Foundation Funds. Michal 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 and Ministry of Science and Higher Education grant no. DI204012344. Michal Gorczak would also like to thank Malgorzata Klemes for sharing a photo of Bialowieża Forest logging site. Marta Wrozek was partially supported by National Science Centre, Poland, grant 2016/23/682/16SU2890897. Ditte Bandini (Wiesenbach, Germany) is thanked for providing useful information on Malloctye pallidomentosum. Ivana Kušan, Neven Matočec, Ana Pošta, Ždenko Tkáč, and Armin Melič are grateful to Croatian Science Foundation for their financial support under the project grant HRZZ-IP-2018-01-1736 (ForFungiDNA) and Public Institution Paklenica National Park for their fieldwork support. Ana Pošta thanks Croatian Science Foundation for their support under the grant HRZZ-2018-09-7081. Vit Hubka was supported by the project BIOCEV (CZ.1.05/1.1.00/2019-0109) provided by the Ministry of Education, Youth and Sports of CR and ERDF and by the Charles University Research Centre grant No. 204089. Micael F.M. Gonçalves and Artur Alves acknowledge financial support from the Portuguese Foundation for Science and Technology (FCT) to CESAM (UIDB50017/2020+UIDP/50017/2020) and the PhD grant of M. Goncalves (SFRH/BD/129020/2017). Milan Spetík and colleagues were supported by the Czech Republic, project No. TJ02000096. Ivana Kučerová was supported by the Charles University Grant Agency (grant No. GAUK 80518). Petr Hamal was supported by the grant of the Czech Ministry of Health (AZV 17–31269A). Anna Kiyashko expresses appreciation to Olga V. Morozova and Ekaterina F. Malyshova for valuable comments. The research of Anna Kiyashko, Anna Fedosova and Ekaterina Malyshova was done using equipment of The Core Facilities Center ‘Cell and Molecular Technologies in Plant Science’ at the Komarov Botanical Institute RAS (St.-Petersburg, Russia) as a part of the research project of the Komarov Botanical Institute (AAAA-A19-11920890079-6). The study of Vladimir I. Kapitonov was conducted under research projects of Tobolsk Complex Scientific Station of the Ural Branch of the Russian Academy of Sciences (NAAAA-A19-11901190112-5). The research of T.A. Pankratov has been supported by the Russian Foundation for Basic Research (grant No. 19-04-00297a). 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/F/16) for financial support. Gavin C. Hunter and colleagues acknowledge the Australian Government via the Rural Industries Research and Development Corporation and the NSW Government through its Environmental Trust for financial support. The authors also acknowledge the valuable contributions of John Scott (CSIRO) who laid the foundation underpinning this research. Matthew E. Smith’s participation was supported by the USDA-NIFA McIntire-Stennis project 1011527. The study of Claire Lock, Joseph S. Vitelli and colleagues was supported by AgriFutures Australia, through funding from the Australian Government Department of Agriculture, Water and the Environment as part of its Rural R&D for Profit program (PRJ 15-02-005) and Queensland Department of Agriculture and Fisheries, New South Wales Department of Primary Industries, NSW Weed Biocontrol Taskforce, Bundaberg Regional Council, Gladstone Regional Council and HQPlantations Pty Ltd. Peter Johnston was supported through the Manaki Whenua Systematics Portfolio with funding from the Science and Innovation Group of the New Zealand Ministry of Business, Innovation and Employment.
Overview Tremellomycetes and Agaricomycetes phylogeny  part 1

Consensus phylogram (50% majority rule) of 416252 trees resulting from a Bayesian analysis of the LSU sequence alignment (122 sequences including outgroup; 745 aligned positions; 487 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Backussella 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 S26166).

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Overview Tremellomycetes and Agaricomycetes phylogeny (cont.) part 2
Overview Saccharomycetes phylogeny

Consensus phylogram (50 % majority rule) of 198751 trees resulting from a Bayesian analysis of the LSU sequence alignment (29 sequences including outgroup; 520 aligned positions; 197 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The family, order and class are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Backusella lamprospora (GenBank MH866118.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).
Overview Dothideomycetes phylogeny part 1

Consensus phylogram (50 % majority rule) of 138,002 trees resulting from a Bayesian analysis of the LSU sequence alignment (101 sequences including outgroup; 816 aligned positions; 351 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Diaporthe perjuncta (GenBank NG_059064.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).
Overview Eurotiomycetes phylogeny

Consensus phylogram (50% majority rule) of 109 502 trees resulting from a Bayesian analysis of the LSU sequence alignment (82 sequences including outgroup, 826 aligned positions; 273 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Dipartho 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 S26166).
Overview Geoglossomycetes, Lecanoromycetes and Pezizomycetes phylogeny

Consensus phylogram (50 % majority rule) of 21002 trees resulting from a Bayesian analysis of the LSU sequence alignment (45 sequences including outgroup; 784 aligned positions; 310 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families, orders and classes are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Saccharomyces cerevisiae (GenBank Z73326.1) 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 S26166).
Overview Leotiomycetes phylogeny part 1

Consensus phylogram (50 % majority rule) of 634,502 trees resulting from a Bayesian analysis of the LSU sequence alignment (116 sequences including outgroup; 839 aligned positions; 328 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Xylaria hypoxylon (GenBank AY544648.1) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in bold face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).
Overview Leotiomycetes phylogeny part 2
Overview Cunninghamellaceae phylogeny

Consensus phylogram (50% majority rule) of 97,502 trees resulting from a Bayesian analysis of the LSU sequence alignment (18 sequences including outgroup; 616 aligned positions; 278 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher order taxonomic classification is indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Chytridium lagenaria (GenBank FJ804156.1) 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 S26166).
Overview Phytophthora phylogeny

Consensus phylogram (50 % majority rule) of 337,502 trees resulting from a Bayesian analysis of the LSU sequence alignment (19 sequences including outgroup; 1,284 aligned positions; 63 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. The higher order taxonomic classification is indicated with coloured blocks to the right of the tree. GenBank accession or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Absidia panacisoli (GenBank NG_063948.1) and the taxonomic 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 S26166).
Overview Sordariomycetes phylogeny part 1

Consensus phylogram (50% majority rule) of 684 002 trees resulting from a Bayesian analysis of the LSU sequence alignment (132 sequences including outgroup; 786 aligned positions; 296 unique site patterns) using MrBayes v. 3.2.7a (Ronquist et al. 2012). Bayesian posterior probabilities (PP) > 0.84 are shown at the nodes and thickened lines represent nodes with PP = 1.00. The scale bar represents the expected changes per site. Families and orders are indicated with coloured blocks to the right of the tree. GenBank accession and/or Fungal Planet numbers are indicated behind the species names. The tree was rooted to Ramularia endophylla (GenBank AY490776.2) and the taxonomic novelties described in this study for which LSU sequence data were available are indicated in **bold** face. The alignment and tree were deposited in TreeBASE (Submission ID S26166).
Overview Sordariomycetes phylogeny (cont.) part 2
Phacidiella alsophilae
Fungal Planet 1042 – 29 June 2020

**Phacidiella alsophilae** Crous, sp. nov.

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

**Classification —** *Stictidaceae*, *Ostroplecs*, *Lecanoromycetes*.

*Conidiomata* pycnidial, erumpent, hyaline on SNA and OA, solitary or aggregated, globose, up to 300 μm diam; wall of 3–6 layers of hyaline *textura angularis*; exuding a creamy conidial mass. *Conidiophores* lining the inner cavity, subcylindrical, smooth, hyaline, 0–1-septate, giving rise to 1–2 conidiogenous cells, 4–10 × 2–3 μm. *Conidiogenous cells* terminal, smooth, subcylindrical to doliform, proliferating sympodially at apex, 5–10 × 2–3 μm. *Conidia* solitary, hyaline, smooth, subcylindrical, flexuous, apex obtuse, base truncate, (60–)90–135(–150) × (2–)2.5(–3) μm, 15–25-septate, disarticulating into phragmospores, cylindrical with truncate ends, 4–7 μm long; flexuous conidia enclosed in mucoid sheath, 1–1.5 μm diam.

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

**Typus.** SOUTHERN AFRICA, Western Cape Province, Krynson, on leaves of *Alsophila capensis* (= *Cyathea capensis*) (Cyatheaceae), Nov. 2018, M.J. Wingfield, HPC 2701 (holotype CBS H-24233, culture ex-type CPC 37041 = CBS 146134; ITS and LSU sequences GenBank MT373361.1 and MT373344.1, MycoBank MB835393).

Notes — *Phacidiella alsophilae* is related to *P. podocarpi* (conidia 1-septate, (7–)8–10(–12) × (2–)2.5(–3) μm; Crous et al. 2014), although they are morphologically distinct. Because the type species of *Phacidiella*, *P. salicina* (conidia aseptate, on twigs of *Salix viminalis*, Finland), is presently not known from culture, the phylogenetic relationships between species in the genus remains unresolved. *Phacidiella alsophilae* and *P. podocarpi* are thus tentatively retained in *Phacidiella*.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Phacidiella podocarpi* (strain CBS 138904, GenBank NR_137394.1; identities = 558/614 (91 %), 10 gaps (1 %)), *Fitzroyomyces cyperi* (strain CBS 143170, GenBank MG386047.1; identities = 626/729 (86 %), 16 gaps (2 %)), and *Fitzroyomyces cyperacearum* (voucher MFLU 16-0695b, GenBank MK499349.1; identities = 626/731 (86 %), 22 gaps (3 %)). Closest hits using the LSU sequence were *Phacidiella podocarpi* (strain CBS 138904, GenBank NG_058118.1; identities = 904/930 (97 %), 10 gaps (1 %)), *Stictis radiata* (voucher Palice (ESS 21520), GenBank:AY300864.1; identities = 754/783 (96 %), no gaps), and *Carestiella socia* (strain GG2437a, GenBank AY661682.1; identities = 793/826 (96 %), 3 gaps (0 %)).

**Colour illustrations.** Unfolding leaf of *Alsophila capensis*. Conidiomata on OA; conidiogenous cells giving rise to conidia. Scale bars = 10 μm.

---

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

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

Francois Roets, Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch 7600, South Africa; e-mail: fr@sun.ac.za

Wijnand J. Swart, Department of Plant Sciences (Division of Plant Pathology), University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa; e-mail: Swartwj@ufs.ac.za

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Poaceascoma filiforme
**Poaceascoma filiforme** Crous, sp. nov.

**Etymology.** Name refers to its characteristic filiform ascospores.

**Classification.** — Lentitheciaceae, Pleosporales, Dothideomycetes.

Ascomata developing on OA, immersed in agar, globose, brown. 80–140 μm diam, with smooth wall and central ostiole; wall of 2–4 layers of brown textura angularis. Pseudoparaphyses intermingled among asci, hyphae-like, hyaline, smooth, septate, anastomosing, 2–3 μm diam. Asci bitunicate, subcylindrical, apex obtuse with small apical chamber, base truncate, stipitate, 80–140 × 8–10 μm. Ascospores multiseriate in asci, spirally twisted, hyaline, smooth, filiform, subcylindrical with obtuse ends, guttulate, 70–120 × 2–2.5 μm.

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

**Typus.** THAILAND, Chiang Mai, Unknown Poaceae, 2008, P.W. Crous (holotype CBS H-24361, culture ex-type CPC 33467 = CBS 146689; ITS, LSU, rpb2, tef1 and tub2 sequences GenBank MT373362.1, MT373345.1, MT375098.1, MT375108.1 and MT375118.1, MycoBank MB835395).

Notes — Poaceascoma was introduced by Phookamsak et al. (2015) to accommodate a genus of saprobic ascomycetes on Poaceae with setose ascomata and filiform ascospores. Although *P. filiforme* lacks setae, its spirally twisted, filiform ascospores are a good fit for the genus.

Based on a megablast search of NCBI GenBank nucleotide database, the ITS sequence had distant, partial hits to *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831569.1; Identities = 269/299 (90 %), 6 gaps (2 %)), *Setoseptoria phragmitis* (strain CBS 114966, GenBankKF251250.1; Identities = 346/388 (89 %), 8 gaps (2 %)), and *Setoseptoria englandensis* (strain MFLUCC 17-0778, GenBank MG828963.1; Identities = 342/383 (89 %), 9 gaps (2 %)). Closest hits using the LSU sequence are *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank NG_059506.1; Identities = 864/872 (99 %), 1 gap (0 %)), *Poaceascoma halophilum* (strain MFLUCC 15-0949, GenBankMF615399.1; Identities = 854/864 (99 %), 3 gaps (0 %)), and *Poaceascoma taiwanense* (strain MFLUCC 18-0083, GenBank MG831567.1; Identities = 837/849 (99 %), no gaps). Closest hits using the rpb2 sequence had highest similarity to *Poaceascoma aquaticum* (strain MFLUCC 14-0048, GenBank KT373846.1; Identities = 798/875 (91 %), no gaps), *Poaceascoma helicoides* (strain MFLUCC 11-0136, GenBankKP998460.1; Identities = 728/833 (87 %), no gaps), and *Wettsteinina lacustris* (strain AFTOL-ID 1592 = CBS 618.86, GenBank DQ677972.1; Identities = 741/889 (83 %), 5 gaps (0 %)). Closest hits using the tef1 sequence had highest similarity to *Darksidea zeta* (strain CBS 135640, GenBank KP184191.1; Identities = 324/407 (80 %), 24 gaps (5 %)), *Darksidea beta* (strain CBS 135637, GenBank KP184189.1; Identities = 323/366 (80 %), 25 gaps (6 %)), and *Darksidea gamma* (strain CBS 135633, GenBank KP184187.1; Identities = 315/396 (80 %), 25 gaps (6 %)). Closest hits using the tub2 sequence had highest similarity to *Pleurophoma acaciae* (strain CPC 29188, GenBank KY173612.1; Identities = 520/649 (80 %), 35 gaps (5 %)), *Crassiclypeus aquaticus* (strain KH 185, GenBank LC312616.1; Identities = 425/539 (79 %), 32 gaps (5 %)), and *Flabellascoma minimum* (strain KT 2040, GenBank LC312620.1; Identities = 424/540 (79 %), 36 gaps (6 %)).

**Colour illustrations.** Rainforest in Chiang Mai. Asci with spirally twisted ascospores. Scale bars = 10 μm.
Nothoseiridium podocarpi
Fungal Planet 1044 – 29 June 2020

**Notoseiridium** Crous, *gen. nov.*

**Etymology.** Name refers to the fact that it is related to *Seiridium*, but morphologically distinct from that genus.

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

Plant pathogenic. *Conidiomata* black, round, flattened, acervular; wall of several layers of brown *textura epidermoidea*. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic. *Conidia* fusoid, slightly curved, smooth-walled, gilutulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric, 7–10 μm long; basal appendage filiform, flexuous, unbranched, excentric, 6–7 μm long.

*Culture characteristics. — Colonies spreading, with moderate aereal mycelium and smooth, lobate margin, covering dish after 2 wk at 25 °C. On MEA surface pale olivaceous grey.

**Notes.** *Seimatosporium* and allied genera have recently been revised (Bonthond et al. 2018, Liu et al. 2019), with 23 genera being accepted in *Sporocadaceae*. *Notoseiridium podocarpi* is allied to *Seiridium* (5-septate, appenedged conidia) and *Nonappendiculata* (3-septate, non-appenched conidia), but is distinct in having 4-septate, fusoid conidia with unbranched, excentric apical and basal appendages. *Notoseiridium* is further characterised by forming submerged acervuli that break through the epidermis with a saucer-like appearance, being associated with prominent leaf spots. It is not possible to distinguish *Notoseiridium* from *Seiridium* based on LSU sequence data.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Seimatosporium lichenicola* (*Discostroma fuscellum*; strain GSAA-0182, GenBank JF320818.1; Identities = 542/571 (95 %), 7 gaps (1 %)), *Sporocadus rosarum* (*Seimatosporium pseudorosarum*; strain MFLUCC 14-0466, GenBank KT284775.1; Identities = 561/592 (95 %), 4 gaps (0 %)), *Seimatosporium lichenicola* (strain CBS 160.25, GenBank MH854829.1; Identities = 561/592 (95 %), 6 gaps (1 %)) and *Millesimonycetes rhoicissi* (strain CPC 35297, GenBank NR_166350.1; Identities = 566/598 (95 %), 12 gaps (2 %)). Closest hits using the LSU sequence are *Seiridium unicorne* (strain CBS 320.51, GenBank MH868398.1; Identities = 870/870 (100 %), no gaps), *Seiridium pseuocardinale* (strain CBS 122613, GenBank MH554206.1; Identities = 834/834 (100 %), no gaps), and *Seiridium phylace* (strain CPC 19962, GenBank NG_042759.1; Identities = 870/871 (99 %), 1 gap (0 %)). Closest hits using the rp2 sequence had highest similarity to *Seiridium cardinale* (strain CPC 23791, GenBank LT853119.1; Identities = 721/838 (86 %), no gaps), *Seiridium unicorne* (strain CBS 143873, GenBank MK058473.1; Identities = 636/741 (86 %), no gaps), and *Seiridium aquaticum* (voucher MFLU 18-1627, GenBank MN156531.1; Identities = 642/748 (86 %), no gaps). Closest hits using the tef1 sequence had highest similarity to *Seiridium marginatum* (strain CBS 140403, GenBank LT853191.1; Identities = 344/417 (82 %), 30 gaps (7 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853200.1; Identities = 332/404 (82 %), 22 gaps (5 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853198.1; Identities = 331/403 (82 %), 31 gaps (7 %)). Closest hits using the tub2 sequence had highest similarity to *Seiridium cypressi* (strain CBS 224.55, GenBank LT853230.1; Identities = 652/791 (82 %), 46 gaps (5 %)), *Seiridium papillatum* (strain CBS 340.97, GenBank LT853250.1; Identities = 636/771 (82 %), 31 gaps (4 %)), and *Seiridium podocarpi* (strain CBS 137995, GenBank LT853248.1; Identities = 638/777 (82 %), 39 gaps (5 %)).

**Notoseiridium podocarpi** Crous, *sp. nov.*

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

Associated with brown leaf spots. *Conidiomata* (on *Podocarpus* leaves and on SNA), black, round, flattened, acervular, 300–400 μm diam; wall of several layers of brown *textura epidermoidea*, splitting open all along outer margin, appearing saucer-shaped on leaf. *Conidiophores* reduced to conidiogenous cells, arising from basal layers of stroma, hyaline, smooth, subcylindrical to ampulliform, annellidic, 5–10 × 2.5–3 μm. *Conidia* fusoid, slightly curved, smooth-walled, gilutulate, pale brown, unequally 4-euseptate; basal cell obconic with truncate hilum, hyaline; median cells pale brown; apical cell obtuse, hyaline; apical and basal appendage filiform, flexuous, unbranched, excentric, 7–10 μm long; basal appendage filiform, flexuous, unbranched, excentric, 6–7 μm long.

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

**Typus.** SOUTHERN AFRICA, Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (*Podocarpaceae*), Nov. 2018, M.J. Wingfield, HPC 2710 (holotype CBS H-24362, culture ex-type CPC 36967 = CBS 146690; ITS, LSU, rpb2, tef1 and tub2 sequences GenBank MT373363.1, MT373346.1, MT375099.1, MT375109.1 and MT375119.1, MycoBank MB835397).

**Notes.** *Seimatosporium* and allied genera have recently been revised (Bonthond et al. 2018, Liu et al. 2019), with 23 genera being accepted in *Sporocadaceae*. *Notoseiridium podocarpi* is allied to *Seiridium* (5-septate, appenedged conidia) and *Nonappendiculata* (3-septate, non-appenched conidia), but is distinct in having 4-septate, fusoid conidia with unbranched, excentric apical and basal appendages. *Notoseiridium* is further characterised by forming submerged acervuli.

Colour illustrations. Leaf spot on *Podocarpus latifolius* with *Notoseiridium podocarpi* and *Coleophoma podocarpi*. Conidialoma on PNA; conidialoma on OA; conidigenous cells; conidia. Scale bars: conidiomata = 400 μm, all others = 10 μm.

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

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

Francisco Roets, Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch 7600, South Africa; e-mail: frg@sun.ac.za

Wijnand J. Swart, Department of Plant Sciences (Division of Plant Pathology), University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa; e-mail: Swartwj@ufs.ac.za

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Fungal Planet 1045 – 29 June 2020

Coleophoma podocarpi Crous, sp. nov.

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

Classification — Dermatraceae, Helotiales, Leotiomyctes.
Associated with prominent brown leaf spots. Conidiomata pycnidal, grey-brown, 200–300 μm diam, with central ostiole. Conidiophores lining the inner cavity, intermingled among paraphyses, 0–2–septate, 20–35 × 5–7 μm, or reduced to conidiogenous cells, hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 μm. Paraphyses intermingled among conidiophores, hyaline, smooth, cylindrical, asperate, 3–6 (–6) μm diam, up to 30 μm long, with age becoming multisepate and with intercalary conidiogenous cells. Conidigenous cells hyaline, smooth, guttulate, doliiform to ampulliform, 7–10 × 3–4 μm, phialidic, with minute periclinal thickening. Conidia aseptate, hyaline, smooth, guttulate, subcylindrical to fusoid to irregular, straight to somewhat curved, apex subobtuse, base truncate, (9–)14–22 (–25) × (3.5–)4–5 (–7) μm.

Culture characteristics — Colonies flat, spreading, with moderately aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA and PDA surface brick, reverse vinaceous with diffuse vinaceous pigment. On OA surface brick.

Typus. SOUTH AFRICA, Western Cape Province, Knysna, on leaf spots of Podocarpus latifolius (Podocarpaceae), Nov, 2018, F. Roets, HPC 2697 (holotype CBS H-24347, culture ex-type CPC 373864.1, MT373347.1, MT375110.1 and MT375120.1, MycoBank MB835398).

Notes — Coleophoma includes species that are plant pathogenic or saprobic, occurring on a wide range of plant hosts (Crous et al. 2019b, 2020b). The genus was revised by Crous & Groenewald (2016), and shown to reside in the Dermatraceae (Leotiomyctes), with morphologically similar taxa also occurring in Dothideomycetes.

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Coleophoma parafusiformis (strain CBS 132692, GenBank NR_154807.1; Identities = 525/550 (95 %), 3 gaps (0 %)). Coleophoma eucalypticola (strain CBS 10974, GenBank NR_154805.1; Identities = 523/549 (95 %), no gaps), and Coleophoma xanthosiae (strain CPC 29214, GenBank NR_154838.1; Identities = 523/549 (95 %), 2 gaps (0 %)). Closest hits using the LSU sequence are Coleophoma paracylindrospora (strain CBS 109074, GenBank KU728531.1; Identities = 847/864 (98 %), no gaps), Coleophoma parafusiformis (strain CBS 132692, GenBank KU728534.1; Identities = 846/864 (98 %), no gaps), and Coleophoma proteae (strain CBS 132532, GenBank NG_042679.1; Identities = 845/864 (98 %), no gaps). Closest hits using the tef1 sequence had highest similarity to Coleophoma ericicol a (strain CBS 301.72, GenBank KU728566.1; Identities = 428/500 (86 %), 22 gaps (4 %)). Coleophoma parafusiformis (strain CBS 132692, GenBank KU728573.1; Identities = 411/489 (84 %), 30 gaps (6 %)), and Coleophoma eucalyptorum (strain CPC 19865, GenBank KU728569.1; Identities = 402/483 (83 %), 31 gaps (6 %)). Closest hits using the tub2 sequence had highest similarity to Coleophoma xanthosiae (strain CPC 29214, GenBank KY173598.1; Identities = 399/449 (89 %), 2 gaps (0 %)). Coleophoma eucalyptorum (strain KU728605.1, GenBank KU728605.1; Identities = 383/439 (87 %), 5 gaps (1 %)), and Coleophoma proteae (strain CBS 132532, GenBank KU728613.1; Identities = 384/442 (87 %), 9 gaps (2 %)).

Colour illustrations. Knysna forest with waterfall. Conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 μm.

The first of two equally most parsimonious trees obtained from a phylogenetic analysis of the Coleophoma ITS/actA/tef1/tub2 alignment (24 strains including the outgroup; 1324 characters including alignment gaps analysed: 766 constant, 126 variable and parsimony-uninformative and 432 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The novel species was added to the alignment of Crous & Groenewald (2016), where also the GenBank accession numbers of the reference sequences can be found. The tree was rooted to two strains of Davidhawksworthia illicola and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 70 % are shown at the nodes (PBS/NJBS) and the novel species is highlighted in bold. Type status is indicated in superscript. Branches present in the strict consensus tree are thickened. Tree statistics: TL = 1501, CI = 0.640, RI = 0.745, RC = 0.477. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Hamatocanthoscypha podocarpi
**Fungal Planet 1046 – 29 June 2020**

**Hamatocanthoscypha podocarpi** Crous, sp. nov.

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

*Classification.* — *Hamatocanthoscyphaceae, Helotiales, Leotiomyctes.*

*Mycelium.* Consisting of hyaline, branched, 1.5–2 µm diam hyphae. *Conidiophores* smooth, pale to medium brown, erect, solitary or in clusters, subcylindrical, branched below, 0–4-septate, 12–60 × 3–5 µm. *Conidiogenous cells* 13–40 × 3–4 µm, integrated, terminal and intercalary, subcylindrical, pale brown, smooth, base tapering to long cylindrical, apical venter, 3–9 µm long, slightly flared or not, 2–3 µm diam. *Conidia* in long unbranched chains, aseptate, hyaline, smooth, guttulate, subcylindrical with truncate ends, (6–)7–8(–9) × (1.5–)2 µm.

*Culture characteristics.* — Colonies flat, spreading, with folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, folded surface, moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam after 2 wk at 25 °C. On MEA, surface honey, reverse cinnamon. On PDA surface honey with isabelline in outer region, reverse isabelline. On OA surface honey.

*Typus.* **SOUTH AFRICA,** Western Cape Province, Knysna, on leaf spots of *Podocarpus latifolius* (Podocarpaceae), Nov. 2018, M.J. Wingfield, HPC 2710 (holotype CBS H-24349, culture ex-type CPC 37055 = CBS 146626; ITF, LSU, actA and rpb2 sequences GenBank MT373365.1, MT373348.1, MT375095.1 and MT375100.1, MycoBank MB835399).

Notes — The genus *Chalara* as circumscribed by Nag Raj & Kendrick (1976) is polyphyletic and awaits revision. *Hamatocanthoscypha podocarpi* is phylogenetically allied to the type species of *Hamatocanthoscypha, H. laricionis* (Svrček 1977), and placed in this genus based on DNA similarity. Several species of *'Chalara' have been described from *Podocarpus,* namely *C. brevipes* (conidia (6–)18.9(–12) × 1.5–2 µm), *C. novae-zealandiae* (conidia (5–)6.4(–8) × 1.5–2 µm), *C. cylindrosperma* (conidia (5.5–)11(–17) × (1.5–)1.9(–2.5) µm), *C. fusidioides* (conidia (4.5–)7.7(–12) × (1.5–)2.1(–3.5) µm), *C. acuaria* (conidia (12–)16(–20) × (2–)2.7(–3.5) µm) and *C. biicolor* (conidia 7-septate, (45–)50–60(–71) × 5.5–6 µm) (Nag Raj & Kendrick 1975). Of these, *H. podocarpi* is most similar to *C. brevipes,* but can be distinguished in having smaller conidiogenous cells, and conidiophores that are aggregated in clusters.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to numerous sequences wrongly labelled as ‘*Infundichalara microchona*’ (e.g., strain KRP75-5, GenBank HM036588.1; Identities = 531/537 (99 %), 2 gaps (0 %)), *Chalara holubovae* (strain CCF 3978, GenBank NR_154760.1; Identities = 483/501 (96 %), 3 gaps (0 %)), and *Hamatocanthoscypha laricionis* (voucher TNS-F13530, GenBank JN033441.1; Identities = 540/567 (95 %), 4 gaps (0 %)). Closest hits using the LSU sequence are *Leptodontidium beavervioides* (strain CBS 672.76, GenBank MH872794.1; Identities = 836/840 (99 %), no gaps), *Tricladium caudatum* (strain CCM F-13498, GenBank GQ477318.1; Identities = 833/837 (99 %), no gaps), and *Chalara constricta* (strain CBS 248.76, GenBank FJ176258.1; Identities = 825/829 (99 %), no gaps). No significant hits were obtained when the actA and rpb2 sequences were used in blastn and megablast searches.

*Colour illustrations.* Walkway in the Knysna forest. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
**Myrmecridium phragmiticola** Crous & Akulov, *sp. nov.*

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

*Classification.* — *Myrmecridiaceae, Myrmecridiales, Sordariomycetes.*

On SNA: *Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. *Conidiophores* unbranched, erect, straight, medium brown, thick-walled, 2–4-septate, up to 70 µm tall, 3–3.5 µm diam; basal cell 4–6 µm diam. *Conidiogenous cells* terminal, integrated, subcylindrical, 25–35 µm long, pale brown, forming a rachis with pimple-shaped denticles less than 1 µm long and 0.5 µm diam; slightly thickened. *Conidia* solitary, aseptate, pale brown, thin-walled, smooth, guttulate, with or without a wing-like gelatinous sheath, ellipsoid to fusoid, (7–)8–9 × (2.5–)3 µm; hilum unthickened nor darkened, 0.5 µm diam.

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 isabelline, reverse hazel. On PDA surface and reverse greyish sepia. On OA surface isabelline.

**Typus.** Ukraine, Sumy region, bank of Vorskla river, NNP Hetmanskyi, Klymentove village, on leaves of *Phragmites australis* (Poaceae), 5 Aug. 2018, A. Akulov. HPC 2554, AS 6809 (holotype CBS H-24351, culture ex-type CPC 36367 = CBS 146628; ITS and LSU sequences GenBank MT373366.1 and MT373349.1, MycoBank MB835400).

Notes — Arzanlou et al. (2007) established the genus *Myrmecridium* to accommodate taxa with hyaline mycelium, pigmented, solitary conidiophores with pimple-like denticles, and 0–1-septate, ellipsoid conidia with a mucoid sheath. *Myrmecridium phragmiticola* should be compared to *M. phragmites* (*Phragmites australis*, Netherlands), which has 0–1-septate conidia, (6.5–)7–8(–9) × (2.5–)3(–3.5) µm (Crous et al. 2011). Although the conidia are similar in size, those of *M. phragmiticola* are aseptate.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Myrmecridium phragmites* (strain CBS 131311, GenBank NR_137782.1; Identities = 531/552 (96 %), 6 gaps (1 %)), *Myrmecridium sparti* (strain CBS 140006, GenBank NR_155376.1; Identities = 523/543 (96 %), 4 gaps (0 %)), and *Myrmecridium banksiae* (strain CBS 132536, GenBank NR_111762.1; Identities = 522/546 (96 %), 4 gaps (0 %)). Closest hits using the *LSU* sequence are *Myrmecridium schulzeri* (strain CBS 188.96, GenBank EU041829.1; Identities = 855/860 (99 %), no gaps), *Myrmecridium banksiae* (strain CBS 132536, GenBank NG_042684.1; Identities = 862/870 (99 %), no gaps), and *Myrmecridium flexuosum* (strain CBS 398.76, GenBank EU041825.1; Identities = 852/860 (99 %), no gaps).

*Colour illustrations.* *Phragmites australis* along the bank of the Vorskla river. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.
Fungal Planet 1048 – 29 June 2020

**Diabolocovidia** Crous, gen. nov.

*Etymology.* This fungus was described during the coronavirus pandemic, April 2020. Name composed of *diabolicus* = devilish and *covid*, referring to COVID-19.

*Classification.* — *Xylariaceae*, *Xylariales*, *Sordariomycetes*.

*Mycelium* consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid, (7–)8–9–(11) × (4–)5–6–(7) µm; conidia remaining attached in chains of 8–12 propagules, disarticulating at maturity into single propagules or shorter chains.

*Type species.* *Diabolocovidia claustri* Crous. MycoBank MB835401.

**Diabolocovidia claustri** Crous, sp. nov.

*Etymology.* Name refers to the closure or lockdown experienced in many countries during the COVID-19 pandemic.

*Mycelium* consisting of branched, septate, hyaline to pale brown, smooth to finely roughened, 2–3 µm diam hyphae. *Conidiophores* solitary, erect, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* pale brown, smooth, subcylindrical to slightly clavate, 8–10 × 3–4 µm, proliferating via single apical blastic locus, and remaining attached to acropetal chain of conidia that remain attached to one another via narrow isthmus. *Conidia* brown, thin-walled, smooth, guttulate, granular, ellipsoid to obovoid, (7–)8–9–(11) × (4–)5–6–(7) µm; conidia remaining attached in chains of 8–12 propagules, disarticulating at maturity into single propagules or shorter chains.

*Culture characteristics.* — Colonies flat, spreading, with sparse to moderate aerial mycelium and feathery, lobate margin, reaching 30 mm diam after 2 wk at 25 °C. On MEA surface and reverse cinnamon. On PDA surface and reverse hazel to brown vinaceous. On OA surface hazel.

*Typus.* USA, Florida, Gainesville, on leaves of *Serenoa repens* (Arecaceae), 28 Feb. 2018, M.J. Wingfield, HPC 2792 (holotype CBS H-24353, culture ex-type CPC 37593 = CBS 146630; ITS and LSU sequences GenBank MT373387.1 and MT373350.1, MycoBank MB835402).

Notes — *Diabolocovidia* is reminiscent of genera such as *Ampullifera* (but conidiophores different and hyphopodia present) and *Junctospora* (but conidiophores sparingly branched, subhyaline; Seifert et al. 2011). Phylogenetically, it is allied to *Vamsapriya*, which is characterised by having brown, synnematos conidiophores, mono- to polytretic conidiogenous cells, and dark brown, septate conidia arranged in acropetal chains (Dai et al. 2014). Based on these differences, *Diabolocovidia* is herewith introduced as a new genus.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the *ITS* sequence had highest similarity to *Vamsapriya khunkonensis* (voucher MFLU 13-0367, GenBank NR_154499.1; Identities = 427/464 (92 %), 5 gaps (1 %)), *Didymobotryum rigidum* (strain JCM 8837, GenBank LC228650.1; Identities = 517/561 (92 %), 7 gaps (1 %)), and *Vamsapriya bambusicola* (voucher MFLU 13-0368, GenBank NR_154500.1; Identities = 533/605 (88 %), 37 gaps (6 %)). Closest hits using the *LSU* sequence are *Vamsapriya bambusicola* (strain MFLUCC 11-0477, GenBank NG_067527.1; Identities = 849/864 (98 %), no gaps), *Fasciatispora petrakii* (strain HKUCC 207, GenBank AY083828.1; Identities = 832/848 (98 %), 1 gap (0 %)), and *Vamsapriya indica* (strain MFLUCC 12-0544, GenBank KM462840.1; Identities = 815/831 (98 %), no gaps).

*Colour illustrations.* Leaves of *Serenoa repens*. Conidiophores with conidiogenous cells giving rise to chains of conidia. Scale bars = 10 µm.

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

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

Jason Smith, School of Forest Resources and Conservation University of Florida, Gainesville, FL 32611-0410 USA; e-mail: jasons@ufl.edu

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Juncomyces californiensis
**Juncomyces** Crous, gen. nov.

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

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

*Mycelium* consisting of brown, smooth to warty, septate, branch- ed. *Conidiophores* solitary, subcylindrical, mostly unbranched, erect, thick-walled, brown, verruculose, warty, multisep- tate, rarely forming from a brown stroma, with a few fasciculate conidiophores. *Conidiogenous* cells integrated, terminal, straight to geniculate-sinuous, proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, thickened, darkened and refractive, septate.

*Type species.* *Juncomyces californiensis* Crous. MycoBank MB835403.

**Juncomyces californiensis** Crous, sp. nov.

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

*Mycelium* consisting of brown, smooth to warty, septate, branch- ed, 2–3 µm diam hyphae. *Conidiophores* solitary, subcylindri- cal, mostly unbranched, erect, 80–180 × 5–7 µm, thick-walled, brown, verruculose, warty, multisep- tate, rarely forming from a brown stroma, up to 120 µm diam, with 1–3 fasciculate conidiophores, up to 60 µm tall. *Conidiogenous cells* integrated, terminal, straight to geniculate-sinuous, 35–60 × 5–7 µm; proliferating sympodially with several apical loci, flattened, thickened, darkened, and refractive, 4.5–5.5 µm diam. *Conidia* solitary, acicular to slightly obclavate, mostly thick-walled, verruculose, guttulate, apex subobtuse, base truncate, 4.5–5 µm diam, thickened, darkened and refractive, 3(–6)-septate, (65–)70–85(–90) × (7–)8(–9) µm.

*In vivo:* *Conidiophores* on culms erect, solitary, rarely in fasci- cles of 2–3, straight, 2–6-septate, subcylindrical, rejuvenating percurrenty, 50–110 × 5–7 µm, arising from immersed, brown, weakly developed stroma, 20–40 µm diam. *Conidiogenous cells* integrated, terminal and intercalary, medium brown, smooth, 10–45 × 5–6 µm with one to several loci, round, thickened, refractive, 3–4 µm diam. *Conidia* solitary, arranged in clusters on conidiophores, obclavate, slightly curved to straight, apex subobtuse, base truncate, 3–7-septate, at times constricted at some of the septa, thick-walled, medium brown, verrucu- lose, hilum thickened, darkened, refractive, 4–5 µm diam, (45–)55–70(–75) × (6–)7(–8) µm.

*Culture characteristics —* Colonies erumpent, spreading, with sparse aerial mycelium and smooth, feathery, even margin, reaching 12 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron-grey.

**Notes —** *Juncomyces* is closely related to *Graminopassalora*, which was introduced to accommodate *Passalora graminis*, a widespread pathogen occurring on a broad range of grass (*Poaceae*) hosts (Videira et al. 2017). *Juncomyces* differs from *Graminopassalora* by chiefly having solitary conidiophores (rarely fascicles of 2–3), and multisep- tate, obclavate conidia.

**Colour illustrations.** *Juncus effusus* growing in California. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.
Beltraniella podocarpi
Fungal Planet 1050 – 29 June 2020

**Beltraniella podocarpi** Crous, *sp. nov.*

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

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

*Setae* solitary to aggregated, erect, flexuous, arising from a lobate basal cell, 15–25 µm diam, dark brown, warty, chiefly unbranched, up to 20-septate, thick-walled with large central guttules, tapering in upper part to acute apex, 120–300 × 5–8 µm. *Conidiophores* arranged in dense clusters around the base of setae, brown, smooth, subcylindrical, frequently branched at basal cell, 1–2-septate, 10–30 × 6–8 µm. *Conidiogenous cells* integrated, terminal and intercalary, 7–12 × 6–7 µm, pale brown, smooth, obclavate, tapering toward 1–3 denticulate loci, 1–1.5 µm long, 1 µm diam. *Conidia* obovoid to narrowly turbinate, tapering toward base, apex rounded to subtruncate, asetate, finely verrucose, guttulate, pale brown, (25–)27–28(–33) × (7–)8 µm.

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

**Typus.** **South Africa,** Western Cape Province, Knysna, on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 30 Nov. 2018, M.J. Wingfield, HPC 2710 (holotype CBS H-24354; culture ex-type CPC 36783 = CBS 146633; ITS and LSU sequences GenBank MT373370.1 and MT373353.1, MycoBank MB835406).

Notes — *Beltraniella* is characterised by brown, unbranched setae, setiform conidiophores, polyblastic, denticulate conidiogenous cells, and turbinate conidia with a distinct hyaline transverse band (Rajeshkumar et al. 2016). *Beltraniella podocarpi* is closely related to several species that tend to have some overlap in conidial length, but have narrower conidia (Rajeshkumar et al. 2016, Crous et al. 2019a). Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Beltraniella portoricensis* (strain BCRC 34590, GenBank GU905993.1; **Identities** = 479/487 (98 %), 6 gaps (1 %)), *Beltraniella ramosiphora* (strain LCG 10-2, GenBank MG717500.1; **Identities** = 527/536 (98 %), 4 gaps (0 %)), and *Beltraniella pseudopor toricensis* (strain CBS 145547, GenBank NR_165552.1; **Identities** = 578/591 (98 %), 5 gaps (0 %)). Closest hits using the LSU sequence are *Beltraniella pseudopor toricensis* (strain CBS 145547, GenBank NG_067875.1; **Identities** = 821/825 (99 %)), *Beltraniella acaciae* (strain CPC 29498, GenBank NG_066374.1; **Identities** = 786/790 (99 %)), and *Beltraniella portoricensis* (strain CBS 856.70, GenBank MH871777.1; **Identities** = 842/848 (99 %), 1 gap).

Colour illustrations. Rainforest in Knysna, South Africa. Setae and conidiophores on PNA; dichotomously branched setae; conidiophores with conidiogenous cells; conidia with separating cell. Scale bars = 10 µm.
Neofabraea eucalyptorum
Neofabraea eucalyptorum Crous, sp. nov.

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

Classification — Dermateaceae, Helotiales, Leotiomycetes. Associated with brown, amphigenous leaf spots, 3–5 mm diam. Conidiomata 200–300 µm diam, acervular, erumpent, associated with dark brown, amphigenous leaf spots. Conidiophores hyaline, smooth, branched, septate, subcylindrical, phialidic, up to 80 µm long, 3–5 µm diam. Conidiogenous cells hyaline, smooth, subcylindrical, terminal and intercalary with visible periclinal thickening, 10–18 × 3–4 µm. Conidia subcylindrical to fusoid-ellipsoid, variously curved, hyaline, smooth, guttulate, apex subobtuse, base with flattened hilum, aseptate, but becoming up to 3-septate in older cultures, (25–)30–35–(40) × (6.5–)7–8(–9) µm.

Culture characteristics — Colonies spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 22 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface honey, reverse hazel. On OA surface honey.

Typus. USA, California, UC Davis, on leaves of Eucalyptus macrandra (Myrtaceae), 30 Apr. 2019, P.W. Crous, HPC 2889 (holotype CBS H-24355, culture ex-type CPC 37985 = CBS 146834; ITS, LSU and tub2 sequences GenBank MT373371.1, MT373354.1 and MT375121.1, MycoBank MB835407).

Notes — The Neofabraea generic complex was revised by Chen et al. (2016), and Neofabraea eucalypti was subsequently placed in Coleophoma (Crous & Groenewald 2016). Neofabraea eucalyptorum is thus the first confirmed species of the genus associated with leaf spots on Eucalyptus (Crous et al. 2019b).

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Neofabraea alba (strain UASWS0614, GenBank HQ166388.1; Identities = 485/499 (97 %), 3 gaps (0 %)), Neofabraea brunneipila (voucher MFLU 15-0231, GenBank MK584984.1; Identities = 490/505 (97 %), 1 gap (0 %)), and Neofabraea inaequalis (strain CBS 326.75, GenBank NR_155470.1; Identities = 490/505 (97 %), 1 gap (0 %)). Closest hits using the LSU sequence are Neofabraea brasiliensis (voucher CNPUV499, GenBank KR107002.1; Identities = 857/865 (99 %), no gaps), Pseudofabraea citricarpa (strain CBS 130297, GenBank KR859073.1; Identities = 844/852 (99 %), no gaps), and Neofabraea kienholzii (strain CBS 318.77, GenBank KR858874.1; Identities = 854/863 (99 %), no gaps). No significant hits were obtained when the tub2 sequence was used in blastn and megablast searches.

Colour illustrations. Leaf spots on Eucalyptus macrandra. Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.

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

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Ypsilina buttingtonensis
Fungal Planet description sheets

Fungal Planet 1052 – 29 June 2020

Ypsilina buttingtonensis Crous, Wainhouse & Brian Douglas, sp. nov.

Etymology. Name refers to the collection site, Buttington, Wales, UK, where it was collected.

Classification — Ploettnerulaceae, Helotiales, Leotiomy- cetes.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae. Conidiophores integrated, subcylindrical, hyaline, smooth, septate, sparingly branched, mostly terminal on hyphal ends, 30–100 × 4–6 µm. Conidiogenous cells integrated, terminal and intercalary, subcylindrical, smooth, 12–25 × 4–6 µm; proliferating sympodially. Conidia solitary but aggregating in mucoid mass, Y-shaped, smooth, hyaline; central cell obclavate, base with truncate hilum, 2 µm diam, apex subobtuse, (8–)15–20(–25) × 2(–2.5) µm.

Culture characteristics — Colonies erumpent, spreading, 2(–2.5) µm. Classification characteristics — Colonies erumpent, spreading, 2(–2.5) µm.

Notes — Although the ecology of Ypsilina remains unknown, Y. graminea has been isolated from freshwater foam, roots and leaves of various plants (Descals et al. 1998). Ypsilina buttingtonensis was isolated from an ancient pedunculate oak Quercus robur in Buttington, Wales (longitude and latitude: 52.678236, -3.1108743). The tree, known as the Buttington Oak, was an open-grown lapsed pollard. At the time when the tree fell in February 2018, it had a trunk girth of 11.03 m at breast height and was believed to be the second oldest oak tree in Wales. The tree had a 1.5 m diam hollow through centre where brown cubical rot could be seen, attributed to Fistulina hepatica. The significance of the tree was realised in 2009 when it was 'discovered'.

Cores of wood were extracted from the tree with a 5.5 mm increment bore. Wood chips were taken from the 30 cm cores at 1 cm intervals and placed on low pH 2 % malt agar Petri dishes and incubated at 20 °C in the dark. Ypsilina buttingtonensis was cultured from a chip 30 cm into the heartwood.

In addition to Ypsilina buttingtonensis, Fistulina hepatica, and eight species of ascomycete were also cultured from the wood chips including Cryphonectria radicalis, a close relative of the aggressive canker pathogen Cryphonectria parasitica, responsible for chestnut blight.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Helgardia anguioides (strain CBS 496.80, GenBank NR_158522.1; Identities = 522/533 (98 %), no gaps), Oculimacula acuformis (strain CBS 495.80, GenBank MH661289.1; Identities = 516/535 (96 %), 2 gaps (0 %)), and Oculimacula aestiva (strain CBS 114730, GenBank MG934454.1; Identities = 516/535 (96 %), 2 gaps (0 %)). Closest hits using the LSU sequence are Ypsilina graminea (strain CBS 114630, GenBank MH874529.1; Identities = 877/880 (99 %), 1 gap (0 %)), Helgardia anguioides (strain CBS 496.80, GenBank MH873055.1; Identities = 876/880 (99 %), no gaps), and Rhynchosporium orthosporum (strain 04CH-Bar-A.1.1.3, GenBank KU844335.1; Identities = 870/874 (99 %), no gaps).

Colour illustrations. The Buttington Oak (background photo credit: @thetreehunter Rob McBride). Conidiophores with conidiogenous cells; conidia. Scale bars = 10 µm.
Psuedopezicula betulae
Fungal Planet description sheets

Fungal Planet 1053 – 29 June 2020

Pseudopezicula betulae Crous, sp. nov.

Etymology. Name refers to Betula.

Classification — Discinellaceae, Helotiales, Leotiomycetes. Conidiomata sporodochial, superficial, round, 200–300 µm diam, white, composed of tightly aggregated conidiophores. Conidiophores hyaline, smooth, subcylindrical, extensively branched, septate, 3–4 µm diam, up to 90 µm long. Conidigenous cells hyaline, smooth, phialidic, subcylindrical to fusoid, apex with periclinal thickening, at times with percurrent proliferation and indistinct flared colarette (2–3 µm long). 4–13 x 2–5 µm. Conidia solitary, asperate, guttulate, hyaline, smooth, aggregating in mucoid mass, subcylindrical, straight to curved, apex obtuse, base truncate, with minute marginal frill, (5–)7–10(–17) x 2–2.5 µm.

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

Typus. USA, California, Yosemite, on brown, amphigenous leaf spots of Populus tremuloides (Salicaceae), 2019, S. Denman (holotype CBS H-24357, culture ex-type CPC 36499 = CBS 146683; ITS, LSU, rpb2, and tef1 sequences GenBank MT373373.1, MT373356.1, MT375102.1 and MT375116.1; MycoBank MB835409).

Pseudopezicula tracheiphila (Müll.-Thurg.) Korf & W.Y. Zhuang, Mycotaxon 26: 464. 1986

Basionym. Pseudopeziza tracheiphila Müll.-Thurg., Centrabil. Bakteriol. Parasitenk., 1. Abt. 10: 57. 1903.

Synonyms. Botrytis tracheiphila Sacc. & D. Sacc., Syll. Fung. (Abellini) 18: 157. 1906.

Phialophora tracheiphila (Sacc. & D. Sacc.) Korf, Mycotaxon 26: 464. 1986.

Typus. Neotype: SWITZERLAND, Seemühle, Walenstadt, on leaves of Vitis vinifera cv. ‘Blauburgunder’, H. Schüepp & M. Bodmer, CUP-061784 (designated in Korf et al. 1986). Epitype: LUXEMBOURG, on leaf of Vitis vinifera, coll. Sept. 1985, R. Pearson, isol. W.-Y. Zhuang (epitype designated here CUP 61766, MBT392064, culture ex-epitype CBS 308.86; ITS and LSU sequences GenBank MT373374.1 and MT373357.1).

Notes — Pseudopezicula accommodates two species of apothecial ascomycetes that cause angular leaf scorch on Vitis vinifera. An epitype is here designated for one of these, namely P. tracheiphila. In culture they produce phialophora-like asexual morphs (Korf et al. 1986), that resemble the phialidic asexual morph isolated in the present study. Although Pseudopezicula betulae was associated with prominent leaf spots, its occurrence was inconsistent, and therefore it is unknown whether it is a primary pathogen.

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Gyoerffyella entomobryoides (strain CBS 268.63, GenBank NR_145302.1; Identities = 512/529 (97 %), 1 gap (0 %)), Gyoerffyella rotula (strain 272Jb14, GenBank KU516477.1; Identities = 514/533 (96 %), 1 gap (0 %)), and Fontanospora eccentrica (strain UMB-881.11, GenBank KF730812.1; Identities = 495/514 (96 %), 2 gaps (0 %)). Closest hits using the LSU sequence are Lemonniera aquatica (strain CBS 167.46, GenBank MH867676.1; Identities = 831/837 (99 %), no gaps), Margaritispora aquatica (strain CBS 603.66, GenBank MH870561.1; Identities = 836/843 (99 %), 1 gap (0 %)), and Gyoerffyella entomobryoides (strain CBS 268.63, GenBank MH869886.1; Identities = 833/842 (99 %), no gaps). Closest hits using the rpb2 sequence had highest similarity to Gyoerffyella rotula (strain CCM F-400, GenBank MK241434.1; Identities = 704/863 (82 %), 2 gaps (0 %)), Lachnum virgineum (strain AFLT-ID 49 = voucher OSC 100002, GenBank DQ470877.1; Identities = 705/880 (80 %), 13 gaps (1 %)), and Lachnellula hyalina (strain CBS 185.66, GenBank XM_031145866.1; Identities = 699/877 (80 %), 11 gaps (1 %)). No significant hits were obtained when the tef1 sequence was used in blastn and megablast searches.

Colour illustrations. Amphigenous leaf spots on Populus tremuloides. Conidiomata on PDA; conidiophores with conidigenous cells; conidia. Scale bars = 300 µm (conidiomata), 10 µm (all others).
Gyrothrix encephalarti
**Gyrothrix encephalarti** Crous, sp. nov.

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

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

Culture sterile, morphology based on sporulation on dead leaf spots. *Mycelium* consisting of brown, smooth, septate, branched, 1.5–2 μm diam hyphae. *Setae* erect, 80–130 μm long, 3–4 μm diam, brown, multisepitate, thick-walled, verrucose, subcylindrical with apical taper, base bulbous, 5–6 μm diam, apex spirally twisted with twisted lateral branches in apical region. *Conidiophores* reduced to conidiogenous cells around base of setae, ampulliform to subcylindrical, pale brown, smooth, 6–10 × 3–4 μm, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, aseptate, fusoid, subcylindrical, apices subobtuse, base truncate, (7–)10–12(–14) × 3(–3.5) μm.

**Culture characteristics** — Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 55 mm diam after 2 wk at 25 °C. On MEA surface buff, reverse cinnamon. On PDA surface buff, reverse rosy buff. On OA surface rosy buff.

**Typus. SOUTH AFRICA, Northern Province, Tzaneen, on leaves of *Encephalartos* sp. (Zamiaceae), 2015, P.W. Crous, HPC 2486 (holotype CBS H-24364, culture ex-type CPC 35966 = CBS 146684; ITS, LSU and tef1 sequences GenBank MT373376.1, MT373358.1 and MT375117.1, MycoBank MB835410).

Notes — *Gyrothrix encephalarti* is closely related to *G. eucalypti* (*Eucalyptus* sp., South Africa; conidia (8–)10–13(–15) × (2–)12.5 μm, setae 100–180 μm tall, 4–5 μm diam at base; Crous et al. 2019c), but has wider conidia and shorter setae. DNA sequences of *G. eucalypti* and *G. encephalarti* are related to the type sequence deposited for *Neoanthostomella viticola* (NG_067792.1), which has a completely different asexual morph. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Neoanthostomella viticola* (strain MFLUCC 16-0243, GenBank NR_165511.1; Identities = 503/537 (94 %), 22 gaps (4 %)), *Gyrothrix eucalypti* (strain CPC 36066, GenBank NR_166315.1; Identities = 540/581 (93 %), 8 gaps (1 %)), and *Calceomyces lacunosus* (strain CBS 633.88, GenBank KY610397.1; Identities = 524/588 (89 %), 22 gaps (3 %)). Closest hits using the LSU sequence are *Gyrothrix eucalypti* (strain CPC 35992, GenBank MN567618.1; Identities = 869/880 (99 %), no gaps), and *Torula ficus* (strain MFLUCC 18-0112, GenBank MH260322.1; Identities = 792/803 (99 %), no gaps). Closest hits using the tef1 (second part) sequence had highest similarity to *Gyrothrix ramosa* (strain MUCL54061, GenBank KJ476975.1; Identities = 447/472 (95 %), no gaps), *Gyrothrix inops* (strain BE108, GenBank KJ476974.1; Identities = 447/472 (95 %), no gaps), and *Metarhizium globosum* (strain ARSEF 2596, GenBank EU248846.1; Identities = 438/470 (93 %), no gaps).

**Colour illustrations.** Leaves of *Encephalartos* sp. Setae and conidiogenous cells; conidia. Scale bars = 10 μm.
Satchmopsis metrosideri
Fungal Planet 1055 – 29 June 2020

Satchmopsis metrosideri Crous, sp. nov.

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

Classification — Cochlearomycetaceae, Lectiales, Leotiomycetes.

Conidiomata cupulate, superficial, 100–140 µm diam at apex, 130–180 µm deep, brown, attached to a basal stroma of dark brown cells that occupy the stomatal chamber; wall consisting of two regions, the lower region having thick-walled dark brown cells up to 5 layers thick; upper region on thin-walled paler cells, cylindrical, 10–17 × 3–4 µm, with even, smooth flat edge. In culture conidiomata are paler in colour and much larger, flattened, cupulate, and margins have cells that are lobate due to expanding growth (not flat as in vivo). Conidiogenous cells restricted to lower part of basal wall, 3–7 × 2–3 µm, doliform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. Conidia hyaline, smooth, aseptate, guttulate, subcylindrical, predominantly straight with obtuse ends, (15–)16–17(–19) × 1–1.5 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, reaching 60 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of sepia, reverse umber.

Typus. SOUTH AFRICA, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of Metrosideros excelsa (Myrtaceae), 2015, M.J. Wingfield, HPC 2754 (holotype CBS H-24359, culture ex-type CPC 37378 = CBS 146686; ITS, LSU, actA, rpb2, tef1 and tub2 sequences GenBank MT375337.1, MT375338.1, MT432194.1, MT375103.1, MT375111.1 and MT375122.1, MycoBank MB835411).

Additional material examined. SOUTH AFRICA, Eastern Cape Province, Haga Haga, Amathole, on leaf litter of M. excelsa, 2015, M.J. Wingfield, HPC 2754, culture CPC 37376; ITS, actA, rpb2, tef1 and tub2 sequences GenBank MT432187.1, MT432188.1, MT432189.1, MT432190.1 and MT432190.1.

Notes — The genus Satchmopsis, based on S. brasiliensis (Eucalyptus paniculata, Brazil; conidia 11.5–15.5 µm × 1–1.5 µm) (Sutton 1975) was introduced for a genus of cupulate coelomycetes with aseptate conidia. Satchmopsis is commonly isolated from eucalypt leaf litter in South America (Crous et al. 2006). The present collection, from Metrosideros excelsa leaf litter collected in South Africa, differs from S. brasiliensis in being phylogenetically distinct, and also having longer conidia. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to Satchmopsis brasiliensis (strain CPC 11017, GenBank DQ195786.1; Identities = 506/507 (99%), no gaps), Capturomyces luteus (strain CBS 144839, GenBank NR_165905.1; Identities = 474/511 (93%), 12 gaps (2%)), and Capturomyces funiculosus (strain CBS 144840, GenBank NR_165904.1; Identities = 471/512 (92%), 13 gaps (2%)). Closest hits using the LSU sequence are Satchmopsis brasiliensis (strain CPC 11017, GenBank DQ195798.1; Identities = 857/858 (99%), no gaps), Cochlearomyces eucalypti (strain CBS 142622, GenBank NG_059052.1; Identities = 828/862 (96%), 4 gaps (0%)), and Pallidophorina paarla (strain GLMC 791, GenBank MK314612.1; Identities = 824/863 (95%), 10 gaps (1 %)). Closest hits using the rpb2 sequence had highest similarity to Chlorociboria spathulata (strain D1822, GenBank JN985530.1; Identities = 695/887 (78%), 8 gaps (0%)), Moellerodiscus lentus (strain 10544, GenBank MT729344.1; Identities = 693/887 (78%), 18 gaps (2%)), and Microsystyla ellipsis (voucher KUS-F52489, GenBank JN086683.1; Identities = 687/890 (77%), 16 gaps (1%)). No significant hits were obtained when the actA, tef1 and tub2 sequences were used in blastn and megablast searches. The ITS, actA, rpb2 and tef1 sequences of CPC 37378 and 37376 were identical; ITS: 508/508, actA: 644/644, rpb2: 911/911, and tef1: 552/552; and tub2 almost identical: 695/701.

Erysiphe pisi genome GenBank GCA_000208805.1

Eucalyptus brassiana Malaysia

Satchmopsis brasiliensis

Eucalyptus grandis x camaldulensis Australia

Satchmopsis pini sp. nov.

Pinus tecunumanii Malaysia

Satchmopsis metrosideri sp. nov.

Notes — The single most parsimonious tree obtained from a phylogenetic analysis of the Satchmopsis ITS/rpb2/tef1/tub2 alignment (7 strains including the outgroup; 3220 characters including alignment gaps analysed: 1911 constant, 935 variable and parsimony-uninformative and 374 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The tree was rooted to Erysiphe pisi (genome GenBank GCA_000208805.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 49 % are shown at the nodes and the novel species are highlighted in bold. Type status is indicated in superscript. Tree statistics: TL = 1572, CI = 0.964, RI = 0.880, RC = 0.849. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

Note on host. The type was collected in South Africa, Haga Haga, with Metrosideros in background. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidia. Scale bars = 140 µm (conidiomata), 10 µm (all others).

The single most parsimonious tree obtained from a phylogenetic analysis of the Satchmopsis ITS/actA/rpb2/tef1/tub2 alignment (7 strains including the outgroup; 3220 characters including alignment gaps analysed: 1911 constant, 935 variable and parsimony-uninformative and 374 parsimony-informative). PAUP v. 4.0b10 (Swofford 2003) was used to analyse the data. The tree was rooted to Erysiphe pisi (genome GenBank GCA_000208805.1) and the scale bar indicates the number of changes. Parsimony bootstrap support values higher than 49 % are shown at the nodes and the novel species are highlighted in bold. Type status is indicated in superscript. Tree statistics: TL = 1572, CI = 0.964, RI = 0.880, RC = 0.849. The alignment and tree were deposited in TreeBASE (Submission ID S26166).

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

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

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Satchmopsis pini
**Satchmopsis pini** Crous, sp. nov.

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

**Classification.** *Cochlearomycetaceae, Leotiales, Leotiomycetes.*

*Conidiomata* cupulate, superficial, 140–200 µm diam, and 120–160 µm deep, dark brown, attached centrally to a brown stroma via a dark brown stalk, up to 150 µm tall, 50 µm wide; conidiomatal wall of two regions, the upper region of cylindrical cells with flat to obtuse edge, 3–7 × 2–3 µm; terminal 5–13 cell layers are prominently thick-walled, darker brown, and can give rise to hyphal outgrowths on outside of conidiomatal margin. *Conidiogenous cells* restricted to lower part of basal wall, 4–10 × 2–3 µm, doliiform to lageniform, phialidic with periclinal thickening, hyaline with indistinct collarette. *Conidia* hyaline, smooth, aseptate, guttulate, subcylindrical, straight with obtuse ends, (11–)12–14(–15) × 1–1.5 µm.

**Culture characteristics.** Colonies flat, spreading, with sparse aerial mycelium and feathery, lobate margin, covering dish after 2 wk at 25 °C. On MEA, PDA and OA surfaceumber with patches of sepia, reverseumber.

**Typus.** **MALAYSIA,** on dead needles of *Pinus tecunumanii* (Pinaceae), 31 Oct. 2010, M.J. Wingfield, HPC 2657 (holotype CBS H-24360, culture ex-type CPC 36649 = CBS 146687; ITS, LSU, actA, rpb2, tef1 and tub2 sequences GenBank MT373378.1, MT373360.1, MT375096.1, MT375104.1, MT375112.1 and MT375123.1, MycoBank MB835412).

**Additional material examined.** **MALAYSIA,** on dead needles of *P. tecunumanii*, 31 Oct. 2010, M.J. Wingfield, HPC 2657, culture CPC 36729; ITS, actA, rpb2 and tef1 sequences GenBank MT37379.1, MT375097.1, MT375105.1 and MT375113.1.

**Notes.** *Satchmopsis pini* is morphologically distinct from *S. brasiliensis* and *S. metrosideri* in having cupulate conidiomata with a prominently thick-walled, darker brown upper region, giving rise to hyphal outgrowths on outside of conidiomatal margin. Furthermore, conidiomata are centrally attached to a brown stroma via a long, dark brown stalk, which is absent in *S. brasiliensis* and *S. metrosideri.*

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195784.1; Identities = 507/507 (100 %), no gaps), *Massarina corticola* (strain 4607, GenBank FR668004.1; Identities = 420/451 (93 %), 9 gaps (1 %)), and *Capturomyces luteus* (strain CBS 144839, GenBank NR_165905.1; Identities = 473/510 (93 %), 11 gaps (2 %)). Closest hits using the LSU sequence are *Satchmopsis brasiliensis* (strain CBS 420.93, GenBank DQ195796.1; Identities = 873/873 (100 %), no gaps), *Cochlearomyces eucalypti* (strain CBS 142622, GenBank NG_059052.1; Identities = 840/877 (96 %), 4 gaps (0 %)), and *Pragmopora cf. bacillifera* (voucher G.M. 2019-04-30.1, GenBank MK900749.1; Identities = 843/883 (95 %), 10 gaps (1 %)). No significant hits were obtained when the actA, rpb2, tef1 and tub2 sequences were used in blastn and megablast searches. The ITS, actA, rpb2 and tef1 sequences of CPC 36649 and 36729 were identical; ITS: 507/507, actA: 596/596, rpb2: 879/879 and tef1: 405/405.

**Colour illustrations.** Beach area in Malaysia. Conidioma on OA; conidioma on SNA; conidiomatal wall; conidiogenous cells; conidia. Scale bars = 200 µm (conidiomata), 10 µm (all others).
Hymenotorrendiella communis
**Hymenotorrendiella communis** Croust & P.R. Johnst., sp. nov.

Etymology: Name refers to the common occurrence of this species.

Classification — *Helotiaceae, Helotiales, Leotiomycetes.*

Apothecia scattered on leaves, at times aggregated in clusters of 2–3, erumpent, stipitate, arising from a subepidermal brown stroma. Disc plane to convex, greyish brown to olivaceous, smooth, 0.4–1.0 mm diam. Receptacle cupulate, usually darker than the hymenium, bearing dark brown setae. Stipe central, smooth, brown, 0.2–0.6 mm high, 180–200 µm diam. Setae 40–100 per apothecium, 150–300 µm long, smooth. Dark brown, thick-walled, multisepalate, tip subobtusely rounded (2.5–3 µm diam), swollen at base, 9–15 µm diam. Asci cylindrical-clavate, apex conical-rounded, apical mechanism bluing slightly in Melzer’s reagent, croziers present, 8-spored, 90–115 × 7–9 µm. Ascospores fusoid, asette, tapering towards ends, guttulate, hyaline with mucoid caps at each end, (16–)20–21(–22) × (3.5–)4 µm. Paraphyses simple or branched near base, obtuse, hyaline, somewhat inflated, 2.5–3 µm diam at apex.

Culture characteristics — Colonies flat, spreading, with even smooth margin and sparse to moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA surface cinnamon with patches of hazel, reverse sienna toumber. On PDA surface amber to ochreous, reverse amber. On OA surface ochreous with patches of cinnamon.

**Typus. Australia,** New South Wales, La Trobe State Forest, on leaf litter of *Eucalyptus bicostata* (Myrtaceae), 30 Nov. 2015, P.W. Crous, HPC 1871 (holotype CBS H-24367, culture type CPC 32835 = CBS 146703; ITS sequence GenBank MT373382.1, MycoBank MB835413).

Notes — The phylogeny and morphology of *Torrendiella* and *Hymenotorrendiella* was discussed in detail by Johnston et al. (2014). Although the name *Torrendiella eucalypti* has commonly been used for the species occurring on *Eucalyptus* leaf litter (Crous et al. 2006), Johnston et al. (2014) showed that the type of *T. eucalypti* occurred on fallen phylloides of an *Acacia* sp. (Tasmania, Australia), which then became the type species of the new genus *Hymenotorrendiella.* However, this resulted in the common endophyte and sapore occurring on eucalypt leaf litter not having a name. Several collections from *Eucalyptus* leaf litter were investigated in the present study, and two taxa were found to be present. The first, described here as *H. communis,* occurred in a clade with isolates from Australia, Colombia, Spain, and South Africa. Morphologically, however, the South African isolates differ from others in this clade based on macromorphology. Apothecia have shorter stalks, 100–200 µm high; setae vary from 60–80 per apothecium, but are much shorter, and wider that those from other collections in this clade, being 70–150 µm long, with obtuse apices, 4(–5) µm diam, and slightly inflated bases, 4–7 µm diam. Asci are similar however, being 85–110 × 6–8 µm, as well as ascospores, (15–)19–21 × (3.5–)4 µm. *Hymenotorrendiella communis* can be distinguished from the second species, *H. indonesiana* (ascospores 17–25 × 3–4 µm), which occurs in Indonesia, by its shorter and wider ascospores.

Based on a megablast search of NCBI's nucleotide database, the closest hits using the ITS sequence had highest similarity to *Hymenotorrendiella indonesiana* (as *Torrendiella eucalypti*), strain 4876, GenBank FR686015.1; Identities = 522/527 (99 %), 5 gaps (0 %), *Hymenotorrendiella andina* (as *Torrendiella andina*) strain PRJ-SA193, GenBank KJ606682.1; Identities = 447/459 (97 %), no gaps), and *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*) voucher PDD 58572, GenBank AY755336.1; Identities = 420/433 (97 %), 1 gap (0 %).

**Hymenotorrendiella indonesiana** Croust & P.R. Johnst., sp. nov.

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

Description. Illustration & Discussion — See Crous et al. (2006), Stud. Mycol. 55: 61. 2006.

**Typus. Indonesia,** on *Eucalyptus urophylla* leaf litter, Mar. 2004, M.J. Wingfield (holotype CBS H-18041, single-ascospore cultures ex-type, CPC 11049 = CBS 115326, CPC 11050–11051; ITS, LSU and SSU sequences GenBank DQ195787.1–DQ195789.1, DQ195799.1–DQ195800.1 and DQ195810.1–DQ195811.1, MycoBank MB835414).

Notes — Based on a megablast search of NCBI's nucleotide database, the closest hits using the ITS sequence of CPC 11049 had highest similarity to *Hymenotorrendiella andina* (as *Torrendiella andina*) strain PRJ-SA193, GenBank KJ606682.1; Identities = 480/501 (96 %), 7 gaps (1 %)). *Hymenotorrendiella eucalypti* (voucher PDD 70105, GenBank MH578483.1; Identities = 470/495 (97 %), 7 gaps (1 %)), and *Hymenotorrendiella cannibalensis* (as *Torrendiella cannibalensis*); strain ICMP 18818, GenBank JN225947.1; Identities = 475/502 (95 %), 9 gaps (1 %)). The ITS sequences of CPC 11049, 11050 and 11051 are identical (498/498 bp). Closest hits using the LSU sequence of CPC 11049 are *Endoscypha perforans* (voucher PDD 102231, GenBank MK039717.1; Identities = 851/860 (99 %), no gaps), *Hymenotorrendiella madsenii* (as *Torrendiella madsenii*); strain PRJ-D672, GenBank KJ606676.1; Identities = 817/829 (99 %), no gaps), and *Roesleria subterranea* (strain CBS 201.25, GenBank MH866343.1; Identities = 839/853 (98 %), no gaps).

Supplementary material

FP1057 & 1058-1 Additional materials examined - *Hymenotorrendiella communis*

FP1057 & 1058-2 Additional materials examined - *Hymenotorrendiella indonesiana*

FP1057 & 1058-3 The first of 28 equally most parsimonious trees obtained from a phylogenetic analysis of the *Hymenotorrendiella*
**Fungal Planet description sheets**

**Absidia pararepens** Jurjević, M. Kolařík & Hubka, *sp. nov.*

**Etymology.** Refers to the phylogenetic proximity and phenotypic similarity to *A. repens*.

**Classification.** *Cunninghamellaceae*, *Mucorales*, *Mucoromycotina*.

**Micromorphology.** (on malt extract agar; MEA): Hyphae hyaline to brownish, coenocytic, smooth, finely roughened to definitely roughened near crustaceous, 3–13 μm diam. *Sporangioles* hyaline to brown near dark brown, simple or branched, arising solitarily, occasionally in pairs, never grouped in whorls, arising from aerial hyphae or substrate, most commonly 10–150 × 3–6 μm; smooth, finely roughened to definitely roughened near crustaceous walls, with a single septum below the sporangium and rarely with additional septum at the base. *Sporangia* hyaline to brown to dark greyish brown, most commonly pyriform, (10–)14–24(–26) μm diam, smooth-walled. *Apophyses* funnel-shaped, smooth-walled. *Columnellae* globose, hemispherical, with a short collarette, occasionally with one projection, smooth-walled, (6–)12–17(–22) μm diam. *Sporangiospores* of two types: sub-globulo to globoso, hyaline, smooth-walled, and oval, occasionally slightly irregular, brown, rough-walled (formed in the different sporangia), (3.3–)3.5–5(–9) × (3.3–)3.5–6 μm. *Chlamydospores* (terminal and intercalary) occasionally present in the aerial mycelia. Zygosporas not observed.

**Culture characteristics.** — (in darkness, 25 °C after 3 d / 7 d): Colonies on MEA 39–45/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown (light mouse grey to mouse grey, R51; Ridgway (1912)), abundant sporulation, reverse colonial buff to deep colonial buff (R30), smooth and wavy zonate. Colonies on potato dextrose agar (PDA 39–44/>90 mm diam, cottony, mycelium at first white, then becoming grey to grey-brown (R51), very good sporulation, reverse grey to grey with buttkhorn brown shades (R15), radially sulcate. Colonies on OA 35–40/>90 mm diam, cottony, mycelium at first white, then becoming light mouse grey to mouse grey (R51), good sporulation. Colony diam at 30 °C (in mm after 7 d): MEA 4–37; PDA 4–48; OA 5–48. No growth on MEA, PDA and OA at 32 °C.

**Typus.** USA, New York, Jericho, bathroom, air, 12 Dec. 2015, Ž. Jurjević (holotype BPI 911217, cultures ex-type CCF 6352 = CBS 146002 = ESM 3235, ITS and LSU sequences GenBank MT193669 and MT192308, MycoBank MB834983).

**Additional materials examined.** USA, Maryland, Parkton, bedroom, air, 16 Nov. 2015, Ž. Jurjević, culture CCF 6351 = ESM 3145 (ITS and LSU sequences GenBank MT193670 and MT192307); New Jersey, Tinton Falls, basement, air, 08 Mar. 2016, Ž. Jurjević, culture CCF 6353 = ESM 3556 (ITS sequence GenBank MT193671); New York, Massapequa Park, basement, swab, 09 Aug. 2016, Ž. Jurjević, culture CCF 6354 = ESM 3570 (ITS sequence GenBank MT193672); Ohio, hospital, air, 26 Sept. 2016, Ž. Jurjević, culture CCF 6355 = ESM 3656 (ITS sequence GenBank MT193673); New Jersey, Marlton, basement, concrete floor, swab, 04 Apr. 2017, Ž. Jurjević, culture CCF 6356 = ESM 4142 (ITS sequence GenBank MT193674).

**Notes.** BLAST analyses with the ITS and LSU sequences of *A. pararepens* showed greatest similarity with *A. repens* ex-type CBS 115583 (~87 % and ~95 % similarity, respectively). The American isolates KAS 3611 (GenBank FJ849793), FSU 939 (GenBank AY944891), CBS 101.32 = FSU 5891 (GenBank EF030527), CBS 102.32 = FSU 5892 (GenBank EF030528), NRRL 1336 (GenBank AF113448) and 14849A (GenBank AY234881) also represent *A. pararepens*, while European isolates CBS 115583 (GenBank EU484281, HM849706) and FSU 4726 (GenBank EU484288) represent *A. repens* s.str. However, this geographic pattern should be confirmed by analysis of additional strains.

Hesseltine & Ellis (1966) invalidly designated a neotype for *A. repens*. In conflict with Art. 8.4 (Turland et al. 2018), the authors selected a living culture, NRRL 1336. This culture originated from a collection of A.F. Blakeslee, and was probably isolated in America. However, as pointed out by Hoffmann et al. (2009) and Hoffmann (2010), there are large genetic differences between European and American isolates of ‘*A. repens*’. Consequently, the neotype of *A. repens* should be selected from among European strains in accordance with the original description of Van Tieghem (1878), who collected *A. repens* on fruit of *Bertholletia excelsa* lying on a layer of moist Sphagnum in France. The specimen CBS 115583 originating from England, UK, was mentioned as isotype of *A. repens* by Hoffmann et al. (2009) and Hoffmann (2010), but formal typification has never been published.

To formalize the typification, we designate here a lectotype of *A. repens* (illustration from the original material): pl. 12, f. 55–63 (not paginated) in P. van Tieghem, *Annales des Sciences Naturelles Botanique* Ser. 6, Vol. 4. 1878 [1876]. MycoBank typification no. is MBT392665. Epitype designated here: specimen CBS 115583 (preserved in metabolically inactive state), ex-epitype culture CBS 115583. MycoBank typification no. is MBT392666.

*Absidia pararepens* has on average shorter sporangiophores (10–150 × 3–6 μm), and larger sporangiospores ((3.3–)3.5–5(–9) × (3.3–)3.5–6 μm) than the closely related *A. repens* ((50–)140–250(–450) × 2.5–6 μm), and (2.8–5.5(–6.5) × 2–3 μm), respectively.

**Supplementary material.** FP1059 A best scoring maximum likelihood tree based on the ITS region sequences shows the relationships of *Absidia pararepens* sp. nov. with other species.
Annulohypoxylon spougei
**Fungal Planet 1060 – 29 June 2020**

**Annulohypoxylon spougei** Suwannasai, M.P. Martín, Phosri & Whalley, sp. nov.

**Etimology.** Named after the American bioinformatician John L. Spouge who contributed to the discovery of this species, and for his efforts to implement tools for DNA barcoding analyses within the genus Annulohypoxylon.

**Classification — Hypoxylaceae, Xylariiales, Sordariomycetes.**

**Stromata** glomerate to hemispherical, effused-pulvinate, with perithelial mounds 1/4 to 2/3 exposed and not covered by the outermost stromatal layer, 0.3–6 cm long x 0.3–3 cm broad and 1–1.6 mm thick; surface dark brown vinaceous, becoming black with reddish brown hues, finally black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny; black and 1–1.6 mm thick; surface dark brown vinaceous, becoming black and shiny.

**Perithecia** spherical, 0.5–0.7 mm diam. Oстioles conical papillate, surrounded by a flattened bөvev-type disc, 0.2–0.5 mm diam. Ascospores pale brown, unicellular, ellipsoid-inequalateral with narrowly rounded ends, 6–10.5 × 3.4–4.5 (–5.5) µm with straight germ slit along the full length of the spore; perisephe dehiscent in 10 % KOH, epispore smooth.

**Culture characteristics —** Colonies on potato dextrose agar (PDA) covering Petri dish in 2 wk, at first white, becoming hazel to dull green, azonate, with diffuse margins, with scattered black patches; reverse dull green to dark brown. *Conidiogenous structure* nodulisporium-like, brown. *Conidia* hyaline, smooth, ellipsoid, 3.5–4.5 × 2–3 µm.

**Type.** Thailand, Phitsanulok Province, Khao Kra' Yang Forest Planation, on corticated wood, Sept. 2006, C. Phosri & N. Suwannasai H099 (holotype SWUF-H099, ITS, α-actin and β-tubulin sequences GenBank FN252419, FR875158 and KP134519, MycoBank MB811164).

**Additional materials examined.** Herbarium number is indicated, as well as the ITS, α-actin, β-tubulin and EF-1α GenBank sequences between brackets, absent sequences are indicated with ‘–’. *Annulohypoxylon spougei* THAILAND, Phitsanulok Province, Dipterocarpaceae forest, Sept. 2006, C. Phosri & N. Suwannasai SWUF-H087 (FN252418, KP134506, FR875164, –); SWUF-H181 (FN252420, KP134507, KP134520, –); SWUF-H203 (FN252421, FR875159, FR875165, –); SWUF-H215 (FN252422, KP134508, KP134521, –); SWUF-H254 (FN252423, FR875160, FR875166, –); Nakhon Ratchasima Province, Dipterocarpaceae forest, July 2003, N. Suwannasai SUT081 (DQ332210, –, –); Trad Ratchasima Province, Dipterocarpaceae forest, Aug. 2003, C. Phosri & N. Suwannasai SUT236 (DQ332210, –, –, –); SUT242 (DQ332210, –, –, –); SUT244 (DQ332210, –, –, –, –); Kanchanaburi Province, Dipterocarpaceae forest, Aug. 2003, N. Suwannasai SUT285 (DQ332210, –, –, –); Chaiyaphum Province, Dipterocarpaceae forest, June 2009, C. Phosri & N. Suwannasai PK09007 (KP134526, KP134509, KP134522, KP134499); PK09026 (KP134527, KP134510, –, KP134500); PK09029 (KP134529, KP134512, –, –, –); *Annulohypoxylon nitens* THAILAND, Chiang Rai Province, Dipterocarpaceae forest, Sept. 2006, C. Phosri & N. Suwannasai SWUF-H154 (FM209453, FR875161, KP134513, –); SWUF-H157 (FM209455, FR875162, KP134514, –); Phitsanulok Province, Dipterocarpaceae forest, Sept. 2006, C. Phosri & N. Suwannasai SWUF-H189 (FM209459, KP134502, FR875167, –); SWUF-H197 (FM209461, FR875163, KP134515, –); Chaiyaphum Province, Dipterocarpaceae forest, June 2009, C. Phosri & N. Suwannasai PK121044 (KP134523, KP134503, KP134516, KP134496); KP121063 (KP134524, KP134504, KP134517, KP134498); KP121086 (KP134525, KP134505, KP134518, KP134497).

Notes — During extensive studies of the Hypoxylaceae in Thailand over a period of almost 20 yr, problems were encountered in the identification of several taxa, especially *A. nitens*. A previous study on species of Hypoxylon and Annulohypoxylon using morphology and ITS rDNA sequences (Suwannasai et al. 2013) indicated that this taxon was not monophyletic but could be separated into *A. nitens* and another species. Twenty-eight fungal specimens of *A. nitens* and a cryptic species collected from Thailand, previously named ‘*A. nitens*’ in our study (Suwannasai et al. 2013), were carefully re-analysed based on morphological and asexual morph characters. The comparison of morphological characters between *A. nitens* and a cryptic species showed unclear distinction of these species. The cryptic species, here named as *A. spougei* possesses spherical perithecia (0.5–0.7 mm diam), which are slightly narrower than those of *A. nitens* described by Ju & Rogers (1996) ((0.4–)0.5–1(–1.2) mm). The ostiole discs of both species groups are bөvev-type and have the same dimensions of 0.2–0.5 mm. Ascospore sizes of *A. nitens* and the cryptic species are 7.5–9 × 2.8–4.2 µm and 6–10.5 × 3.4–5.5 µm, respectively. These are similar to the species description for *A. nitens* (as *H. nitens*) (6.5–10(–11) × 3–4.5 µm) from Ju & Rogers (1996). The cultural and asexual morph characters were observed from both PDA and oatmeal agar. Colonies of *A. spougei* are white at first becoming hazel and dull green with scattered black patches. The asexual morph is nodulisporium-like and conidial size (3.5–4.5 × 2–3 µm) is similar to *A. nitens* (4–5 × 2.5–3 µm). With those similar features, it is very difficult to separate the *A. spougei* from *A. nitens* by using only morphological and asexual morph characters. However, although morphological data for all of the collections initially identified as *A. nitens* failed to provide clear separation of the two entities, there are clear supporting DNA data for their separation. In the present study based on α-actin, β-tubulin and elongation factor 1-α sequences, we confirm the separation of two taxa mentioned in Suwannasai et al. (2013).

**Colour illustrations.** Thailand, Chaiyaphum Province, Phu Khiao Wildlife Sanctuary, where the specimens were collected. From top to bottom: stromata with ostiolar discs (SWUF-H099); ascospores under SEM (SWUF-H099); fungal culture on PDA (SWUF-H099); nodulisporium-like anamorph (SWUF-H099); ascospores with apical apparatus (SWUF-H099). Scale bars = 0.5 mm (stromata), 5 µm (ascospores SEM), 1 cm (fungal culture), 15 µm (asexual morph), 5 µm (ascospores).

**Supplementary material**

**FP1060** UPGMA reconstruction based on k2P distances of α-actin, β-tubulin and EF-1α sequences of *Annulohypoxylon nitens* and *A. spougei* specimens using PAUP*+ v. 4.0b10 (Swofford 2003).

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Aspergillus banksianus
Aspergillus banksianus Pitt, sp. nov.

Etymology. Named for the Australian endemic tree Banksia integrifolia, from the rhizosphere of which this species was isolated.

Classification — Aspergillaceae, Eurotiales, Eurotiomycetes.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 25–30 mm diam, low and dense, plane or irregularly wrinkled, with narrow margins of white mycelium; conidiogenesis moderate to heavy, dark grey to dark grey blue (M. 24–25D–E2–3); exudate absent, soluble pigment brown; reverse Deep Green (M. 29F3–4). MEA, 25 °C, 7 d: Colonies 40–45 mm diam, low and plane, with wide uncoloured margins, light to heavily sporing, coloured as on CYA or slightly greener (M. 26D3); exudate and soluble pigment absent; reverse centra-ly Dark Green (M. 27F5), paler towards the margins. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies up to 5 mm diam, of white mycelium. 37 °C, CYA, 7 d: Colonies 40–45 mm diam, heavily sporing, dull green to grey green; reverse dark green, greyish green or black. Conidiophores borne from aerial hyphae, sometimes unbranch-ed, and then (5–)50–120 × 2.5–3 µm, sometimes bearing a short lateral stipe 10–40 µm long as well; broadening slowly to spathulate vesicles, 5–15 × 15 µm diam, fertile area character-isti-cally hemispherical but sometimes asymmetrical to give a ‘nodding’ appearance. Phialides short and stout, 3.5–6 × 2.5–3 µm, with narrow bases and very short narrow necks, sometimes almost ellipsoidal. Conidia 2.5–3 µm diam, smooth to finely roughened, borne in short disordered chains, separat-ing in wet mounts.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kornerup & Wanscher (1978).

Conidiophores

Phialides

Conidia

Colour illustrations. A specimen tree of the endemic species Banksia integrifolia, planted on a street in Collaroy, NSW, from under which a soil sample included A. banksianus. Colonies grown on CYA (upper) and malt extract agar (MEA) (lower) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 µm (fruiting structures) and 5 µm (conidia).

Fungal Planet description sheets

Cover image: A specimen tree of Banksia integrifolia, planted on a street in Collaroy, NSW, from which A. banksianus was isolated.

Typus: Australia, New South Wales, Collaroy, from rhizosphere soil beneath a specimen tree of the endemic species Banksia integrifolia (Pro-teaceae), 2004, A.-L. Markovina (holotype DAR 85042, cultures ex-type FRR 6047 = MST FP2248; ITS, BenA, CaM and RPB2 sequences GenBank MH280013, MT184780, MT184786, MT184792, MycoBank MB835223).

Notes — Aspergillus banksianus clusters in Aspergillus sub-genus Fumigati, in a small clade that includes A. brevipes and A. duricaulis, with which it shares slow growth at 25 °C, green conidal colouration and intermittent production of asymmetrical fruiting structures. Colonies of A. banksianus on CYA have a deep green reverse colour, in contrast with A. duricaulis, ‘colourless to pinkish drab’ or A. brevipes ‘becoming purple-red’ (Raper & Fennell 1965). Molecularly, A. banksianus is particularly close to A. quadricinctus, from which the most obvious difference is lack of the Neosartorya sexual morph. Aspergillus banksianus when grown on agar, liquid media or grain, displays a unique chemotaxonomic profile comprising banksialactones A–I, and banksiamarins A and B, which are not present in the closely related species A. quadricinctus and A. duricaulis (Chaudhary et al. 2018). Aspergillus banksianus also produces known metabolites clearanol and dothideomynone A, together with the pigments endocrocin and questin previously reported from other Aspergillus species.

John I. Pitt & Ernest Lacey, Microbial Screening Technologies, 28 Percival Rd, Smithfield, NSW 2164, Australia; e-mail: jipitt@microbialscreening.com & elacey@microbialscreening.com
Cameron L.M. Gilchrist & Yit-Heng Chooi, School of Chemistry and Biochemistry, University of Western Australia, Perth, WA 6009, Australia; e-mail: cameron.gilchrist@research.uwa.edu.au & yitheng.chooi@uwa.edu.au

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Aspergillus oxumiae
Aspergillus oxumiae C.N. Figueiredo, L.S. Sales, Y.F. Figueiredo, J.P. Andrade & J.T. De Souza, sp. nov.

Etymology. oxumiae, in honour of Oxum, a female African deity from the Yoruba religion.

Classification. Aspergillaceae, Eurotiales, Eurotiomyces.

Conidial heads radiate. Conidiophores uniseriate. Stipes smooth, frequently septate 48–890 (931) x 2–5 (7) μm, sometimes with subterminal branches and mycelial coils occasionally present. Vesicles pyriform to subglobe, pigmented, 8–20 (30) x 6.5–21 (30) μm (av. 12 ± 3.6 x 11 ± 3.2), phialides 4–13 (20) x 2–8 μm (av. 8 ± 2.7 x 4 ± 1.0) covering half to upper half of vesicle. Conidia globose to subglobe, 3–7 x 3.5–7 μm (av. 5 ± 0.77 x 5 ± 0.81), brown to greyish brown, with coarsely roughened to echinulate surface, average width/length = 1 ± 0.03, n = 74. Sclerotia observed.

Culture characteristics — Colonies on Czapek yeast autoly-sate agar (CYA46–47 mm diam at 25 °C in 7-d-old, lanose to floccose, radially and concentrically wrinkled, mycelium white (ISSC-NBS No. 263), sporulation poor to abundant, dark greyish yellowish brown (No. 81) to black (No. 267), sclerotia absent, white, globose, no exudate, no soluble pigment, reverse brownish pink (No. 33), yellowish white (No. 92), dark grey olive (No. 111). Colonies on Blakeslee’s malt extract agar (ME-Abl) 53–54 mm, floccose, radially and concentrically wrinkled, mycelium white (No. 263), sporulation moderate to abundant, dark olive brown (No. 96), olive black (No. 114), sclerotia moderate, white, globose, no exudate, no soluble pigment, reverse pale yellow (No. 89), greyish yellow (No. 90). Colonies on yeast extract sucrose agar (YES) 27–28 mm, lanose, irregularly wrinkled, mycelium white (No. 263), sporulation moderate, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse light greenish yellow (No. 101). Colonies on oatmeal agar (OA) 46–48 mm, floccose, low, plane, mycelium white (No. 263), sporulation poor to moderate, dark grey (No. 266), black (267), sclerotia abundant, white, globose, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on Czapek’s agar (CZ) 50–52 mm, floccose, low, plane, mycelium yellowish white (No. 92), sporulation poor, black (No. 267), sclerotia absent, no exudate, no soluble pigment, reverse yellowish white (No. 92). Colonies on CYA with 5 % NaCl (CYAS) 23–25 mm, floccose, irregularly wrinkled, mycelium white (No. 263), sporulation poor to abundant, dark yellowish brown (No. 78), sclerotia absent, no exudate, no soluble pigment, reverse yellowish brown (No. 89), dark greyish yellow (No. 91). Colonies on creatine sucrose agar (CREA) 19–22 mm, moderate mycelial growth, sclerotia absent, no acid production. The isolate did not grow in CYA at 10, 37 and 42 °C, but grows at 15 °C 20–22 mm, 20 °C 33–34 mm, 30 °C 32–33 mm and 33 °C 29–31.

Typus. Brazil, Bahia, municipality of Campo Formoso, S10°30′ W40°19′, in soil cultivated with Agave sisalana, 20 Oct. 2007. J.R.Q. Silva (holotype HURB 22369 - dried culture on MEAbl; culture ex-type CCDCA 11546 = UFLA115; ITS, LSU, CaM, benA and RPB2 sequences GenBank MN431165.1, MN508996, MN513842, MN521386 and MN521389, MycoBank MB832766).

Notes — Aspergillus oxumiae is phylogenetically related to the species A. serratalhadensis included in sect. Nigri, but it is clearly a different species. The morphological characteristics distinguishing A. oxumiae from A. serratalhadensis are: A. oxumiae grows slower on CYA and YES 25 °C and grows faster on OA 25 °C. Aspergillus oxumiae does not produce acid on CREA, the stipes and phialides are bigger and the vesicles are smaller. All macroscopic and microscopic measurements were done twice, independently, for isolate CCDCA 11546.

Colour illustrations. Agave sisalana. Seven-day-old colonies growing at 25 °C, top row left to right, obverse CYA, MEAbl and CREA; bottom row left to right, reverse CYA, MEAbl and obverse OA; conidiophores, conidia and coating of mycelia. Scale bars = 10 μm.

Cristiane Nascimento Figueiredo & Lucas Souza Sales, Federal University of Recôncavo da Bahia, Bahia, Brazil; e-mail: cristianefigueiredoo@gmail.com & lucassales@hotmail.com
Jackeline Pereira Andrade, Universidade Estadual de Feira de Santana, Bahia, Brazil, and Faculdades Integradas de Sergipe, Sergipe, Brazil; e-mail: jacklineandrade@hotmail.com
Yasmim Freitas Figueiredo & Jorge Teodoro De Souza, Federal University of Lavras, Minas Gerais, Brazil; e-mail: yasmim_f@hotmail.com & jorge.souza@ufla.br

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Aspergillus kumbius
**Aspergillus kumbius** Pitt, sp. nov.

*Etymology.* Named for the small town of Kumbia, South Burnett District, Queensland, Australia, near where this species was collected.

*Classification.* — *Aspergillaceae, Eurotiiales, Eurotiomycetes.*

*Conidiophores* borne from aerial hyphae, stipes 300–400(–600) × 5–6 μm, uncoloured to pale brown, smooth walled. Vesicles spherical, 15–25 μm diam, fertile over the upper hemisphere or two thirds; metulae 6–8 × 2.5–3.0 μm; phialides aceroset, 7–8 × 2.0–2.2 μm. *Conidia* spherical, 2.2–2.5 μm diam, walls smooth to finally roughened, borne in disordered chains.

*Culture characteristics.* — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane, sparse and velutinous; margins subsurface, entire; mycelium inconspicuous, white to pale yellow brown; reverse uncoloured. Czapek yeast extract agar (CYA), smooth to finally roughened, borne in disordered chains. Sparse, lightly sulcate, velutinous; margins entire, wide; mycelium white to pale yellow; abundant sclerotia borne on the agar surface, white at first, at maturity pale orange to orange grey (M. 5A–B3), spherical or near, 400–800 μm diam; conidial production sparse, pale yellow brown (M. 4–5A3); clear to pale brown exudate produced; soluble pigment absent; reverse pale yellow. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane, sparse and velutinous; margins subsurface, entire; mycelium inconspicuous, white to pale yellow brown; sclerotia moderately abundant, as on CYA except sometimes enveloped in fine white hyphae; conidial production light, yellow brown (M. 4A–B3), exudate and soluble pigment not produced; reverse uncoloured to pale orange. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 26–30 mm diam, of white mycelium; reverse uncoloured. 37 °C, CYA, 7 d: Colonies 6–12 mm diam, of white mycelium, reverse pale.

A maximum likelihood tree inferred from the combined ITS, *BenA* and *CaM* sequences of taxa within *Aspergillus* sect. *Circumdati*. The tree was constructed using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The HKY model was used for ITS sequences, K80+G4 for *BenA* and K80 for *CaM*. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S26813).

**Colour illustrations.** A scene of pasture near Kumbia, Queensland, similar to the one from which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 20 μm (fruiting structures) and 5 μm (conidia).

Media formulations are from Pitt & Hocking (2009); (M.) capitalised colours and notations are from Konerup & Wanscher (1978).

**Type.** AUSTRALIA, Queensland, Kumbia, from rhizosphere soil beneath pasture, 2004. J.I. Pitt (holotype DAR 85044, cultures ex-type FRR 6049 = MST FP2250 = CBS 146722; ITS, *BenA*, *CaM* and *RPB2* sequences GenBank MT179307, MT184782, MT184788 and MT184794, MycoBank MB835225).

*Notes.* — *Aspergillus kumbius* belongs in *Aspergillus* subgenus *Circumdati* sect. *Circumdati*. Moleurally, it is very close to *Aspergillus bridgeri* and *A. subramanianii*. It is distinguished by rapid growth at 25 °C with abundant buff coloured spherical sclerotia. When grown on agar, liquid media or grain, *A. kumbius* displays a unique chemotaxonomic profile including kumbicins A–D, which are not present in the closely related species *A. bridgeri, A. subramanianii, A. salwaensis, A. persii* or *A. sclerotiorum*. *Aspergillus kumbius* also produces known metabolites asterrinquolin D dimethyl ether, petromurins C and D, aspochraccin, JBIR-15, and neohydroxyaspergilllic acid, compounds previously reported from other *Aspergillus* species.

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Aspergillus luteorubrus
Aspergillus luteorubrus Pitt, sp. nov.

**Etymology.** Named for the colony colours on CYA plates: Latin *luteus*, yellow and *ruber*, red.

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

Conidiophores borne from aerial hyphae, slender, (40–)100–200(–300) × 2–2.5 µm, with thin smooth walls, enlarging slowly to very small spathulate vesicles, 4–6(–7) µm diam; bearing few short phialides, 5–7 × 2.5–3 µm. *Conidia* spherical, 2–2.5 µm diam, smooth-walled, borne in short disordered chains.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 38–42 mm diam, dense and velutinous, plane or lightly wrinkled; margins low to moderately deep, entire; mycelium pale yellow (M. 3–4A2–3); sporulation very light, inconspicuous or pale brown (M. near 4B3); exudate absent, soluble pigment sometimes produced, pale yellow; reverse bright yellow at the margins, otherwise intensely coloured, Cadmium Orange to Brownish Red (M. 5–8A–C8). Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–60 mm diam, plane, dense and velutinous to floccose; mycelium white to very pale yellow, in age becoming bright yellow (M. 4A3) centrally; sporulation inconspicuous; exudate and soluble pigment absent; reverse centrally Cadmium Orange (M. 5–6A–B7–8), paler yellow (M. 4A4–4A8) towards the margins. 37 °C, CYA, 7 d: Colonies 55–60 mm diam, of white or pale yellow mycelium; reverse Amber to Yolk Yellow (M. between 3 and 4B7–8).

**Media formulations** are from Pitt & Hocking (2009); (M.) capitalised colours and notation are from Kornerup & Wanscher (1978).

**Typus. AUSTRALIA,** Queensland, White Mountains National Park, from soil in a dry creek bed, 2004, J.J. Pitt (holotype DAR 85045, cultures ex-type FRR 5427 = MST FP2246 = CBS 146723; ITS, BenA, CaM and RPB2 sequences MT179305, MT184781, MT184787 and MT184793, MycoBank MB835226).

**Notes — Aspergillus luteorubrus** clusters in *Aspergillus* subg. *Fumigati*, near *A. fennelliae*. This heterothallic species produces cleistothecia and ascospores characteristic of the sexual genus *Neosartorya*. As only a single strain of *A. luteobrunneus* is known, it is not clear whether this is an asexual species or, perhaps more likely, heterothallic. *Aspergillus luteorubrus* differs from this and other closely related species in colony colours, conidial size, shape and ornamentation. Differences also exist in molecular phylogeny and chemistry (unpubl. data).

A maximum likelihood tree inferred from the combined BenA, CaM and actin sequences of taxa within *Aspergillus* sect. *Fumigati*. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the corrected Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The K80+G4 was used for BenA sequences, K80+G4 for CaM and TPM+I for actin. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 10 000 bootstrap replicates. Alignment in TreeBASE (study S25915).
Aspergillus malvicolor
**Fungal Planet 1065 – 29 June 2020**

**Aspergillus malvicolor** A.D. Hocking, *sp. nov.*

*Etymology.* Named for the distinctive colour of the conidia. Latin *malvi-*color, mauve.

*Classification — Aspergillaceae, Eurotiales, Eurotiomycetes.*

Conidiophores borne from subsurface or surface hyphae, stipes non-septate, 700–1000 × 8–10 µm, with thick, pale brown walls, often finely roughened, with small and undistinguished footcells. Vesicles 35–50 µm diam, sometimes with pinkish walls, bearing metulae and phialides over the entire surface area. *Metulae* mostly 8–10(–20) × 3–3.5(–5) µm; phialides closely packed, acerose, 8–10 × 2–2.5 µm. *Conidia* spherical, small, 2–2.2(–2.5) µm diam, with smooth to finely roughened walls, borne in radiate heads.

*Culture characteristics —* Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies 35–40 mm diam, plane or lightly radially sulcate, low to moderately deep; margins low, entire; mycelium inconspicuous; conidiogenesis heavy, coloured pink at the margins, grading to Greyish Magenta (M. 13C3) at the centres; colourless exudate sometimes produced; soluble pigment absent; reverse brown or pinkish brown. Malt extract agar (MEA), 25 °C, 7 d: Colonies 50–55 mm diam, low, plane and relatively sparse; margins subsurface to entire, low; mycelium pink or brown; sporulation heavy, coloured as on CYA; exudate and soluble pigment absent; reverse yellow brown. 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 20–25 mm diam, low and dense, mycelium inconspicuous, moderately sporing in pink shades, reverse pinkish brown. 37 °C, CYA, 7 d: Colonies 15–20 mm diam, of pinkish brown mycelium, reverse pale to brown.

*Media formulations* are from Pitt & Hocking (2009); (M.) colour is from Kermerup & Wanscher (1978).

*Typus. Australia,* Queensland, Kingaroy, from rhizosphere soil beneath a commercial crop of peanuts (*Arachis hypogaea*), 1979, A.D. Hocking (holo-type DAR 85046; cultures ex-type FRR 2383 = MST FP2244 = CBS 146724; ITS, BenA, CaM, RPB2 sequences GenBank MT179308, MT184764, MT184790, MT184796, MycoBank MB835227).

*Notes —* Aspergillus malvicolor clusters in *Aspergillus* subg. *Circumdati,* sect. *Circumdati,* where it is related to *A. ochraceus.* It differs from all described species of *Aspergillus* by the mauve colour of its conidia. Phylogenetically, the nearest related species is *A. neobridgeri,* from which it is distinguished by conidial colour, by growth rate at 37 °C, and in metabolite production (unpubl. data).

*Colour illustrations.* A commercial peanut crop, near Kingaroy, Queensland, similar to the one from under which this species was described. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 50 µm (fruiting structures) and 5 µm (conidia).

A maximum likelihood tree inferred from the combined ITS, BenA, CaM and RPB2 sequences of taxa within *Aspergillus* sect. *Circumdati.* The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TrNef+I model was used for ITS sequences, K80+G4 for BenA, TrNef+G for CaM and RPB2. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1 000 bootstrap replicates. Alignment available in TreeBASE (study S25914).

John I. Pitt & Ernest Lacey, Microbial Screening Technologies, 28 Percival Rd, Smithfield, NSW 2164, Australia; e-mail: jipitt@micascreening.com & elacey@micascreening.com

Ailsa D. Hocking, CSIRO Agriculture and Food, North Ryde, NSW 2113, Australia; e-mail: Ailsa.Hocking@csiro.au

Cameron L.M. Gilchrist & Yi-Heng Chooi, School of Chemistry and Biochemistry, University of Western Australia, Perth, WA 6009, Australia; e-mail: cameron.gilchrist@research.uwa.edu.au & yi-heng.chooi@uwa.edu.au

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Aspergillus nanangensis Pitt, sp. nov.

Etymology. Named for the town of Nanango, South Burnett District, Queensland, Australia, near which this species was collected.

Classification — Aspergillaceae, Eurotiaceae, Eurotiales, Eurotiomycetes.

Conidiophores borne from surface hyphae, 200–400 μm x 7–9 μm, with thick, smooth, pale yellow walls, bearing very small vesicles. Vesicles 9–12 μm diam, ellipsoidal to somewhat irregular, bearing metulae and phialides over almost all of the vesicle surface, but sometimes bent to form only a hemispherical head; metulae 7–8 × 2.2–2.5 μm; phialides ampulliform 7–8 × 2.2–2.5 μm. Conidia spherical, 2.8–3.5 μm diam, with walls varying from almost smooth to conspicuously spiny, borne in compact spherical heads, even at age.

Culture characteristics — Czapek yeast extract agar (CYA), 25 °C, 7 d: Colonies growing slowly, 13–17 mm diam, rather sparse, lightly floccose; margins narrow and entire; mycelium white to off white; conidial production light, pale greenish grey (M. 25–26C3); exudate and soluble pigment absent; reverse greyish orange (M. 5B3–4). Malt extract agar (MEA), 25 °C, 7 d: Colonies growing slowly, 10–14 mm diam, low, dense and velutinous; margins narrow, entire; mycelium white; conidial production heavy, dark green near Bottle Green (M. 26F3–4); exudate and soluble pigment absent; reverse brownish orange (M. 5C3). 25 % Glycerol nitrate agar (G25N), 25 °C, 7 d: Colonies 3–5 mm diam, of white mycelium only. 37 °C, CYA, 7 d: No growth.

Media formulations are from Pitt & Hocking (2009); (M.) colours are from Kermerup & Wanscher (1978).

Typus. AUSTRALIA, Queensland, Nanango, from undisturbed forest soil, 2004, J.I. Pitt (holotype DAR 84903, cultures ex-type CBS 146238 = FRR 6048 = MST FP2251; ITS, BenA, CaM and RPB2 sequences GenBank MK379278, MT184753, MT184759 and MT184796, MycoBank MB863001).

Notes — Aspergillus nanangensis clusters in Aspergillus clade Jani, a small clade within Aspergillus subg. Circumdati, but is molecularly distinct. It is close to Aspergillus janus and Aspergillus brevijanus, but differs from both by lack of the larger white conidial heads that characterise these species. Culturally, growth rates of A. nanangensis on standard media are much slower. Microscopically, A. nanangensis produces smaller vesicles, fertile over a reduced area. When grown on agar, liquid media or grain, A. nanangensis displays a unique chemotaxonomic profile comprising isonanangenine B and D, nanangelenin, nanangenic acid, nanangenines A–H and nanoxepin not present in the closely related species A. janus and A. brevijanus (Lacey et al. 2019). Aspergillus nanangensis also produces known metabolites asperphenamate, benzomalvin B and C, cytochalasin E and WIN 68306, compounds previously reported from other Aspergillus species.

Colour illustrations. Woodland near Nanango, Queensland, dominated by Eucalyptus species showing undisturbed soil from which A. nanangensis was collected. Colonies grown on CYA (left) and MEA (right) for 7 d at 25 °C; fruiting structures and conidia. Scale bars = 10 μm (fruiting structures) and 5 μm (conidia).

A maximum likelihood tree inferred from the combined ITS, BenA, CaM and RPB2 sequences of taxa within Aspergillus sect. Jani. The combined sequence alignment was partitioned by marker; substitution models for each partition were chosen according to the Bayesian Information Criteria using ModelTest-NG v. 0.1.6 (Darriba et al. 2020). The TPM2uf+G4 model was used for ITS sequences, K80+I+G4 for BenA, TrNef+G4 for CaM and RPB2. The tree was constructed using RAxML-NG v. 0.9.0 (Kozlov et al. 2019). Bootstrap support values are derived from 1000 bootstrap replicates. Alignment available in TreeBASE (study S25916).
Calvatia baixaverdensis
Calvatia baikaverdensis R.L. Oliveira, R.J. Ferreira, P. Marinho, M.P. Martín & Baseia, sp. nov.

Etymology. In reference to the region where this species was collected, Baixa Verde, João Câmara, RN, Brazil.

Classification — Agaricales, Agaricomycetes. Basidiomata growing solitary, epigeous, incrustations in the rooting base, subglobose and 31–36 mm wide × 16–28 mm high. Exoperidium < 0.1 mm thick, fragile, slightly tomentose, evanescent, white to yellowish white (3A1, 3A2; Kornerup & Wanscher 1978). Mesoperidium < 0.1 mm thick, fragile, membranaceous, persistent at the base, smooth with senescence, greyish brown to brown (4C4, 6D3, 6E4, 7F4). Endoperidium < 0.3 mm thick, fragile and brittle at the apex, resistant and persistent at the base, papyraceous, olive brown to brown (4D6, 6E4). Rhizomorphs not seen. Subgingle reduced, woolly, compact, brownish beige (6E3). Gleba powdery, not persistent, brownish beige, brown to dark brown (6E3, 6E4, 6F4), at maturity. Exoperidium hyphal, 2.0–5.3 µm diam, intertwined, frequent and non-regular septa, double V branching, walls ≤ 1.1 µm thin, straight for curves, hyaline, dextrinoid, low reaction and cyanophilic. Mesoperidium compacted, collapsed, hyaline, not dextrinoid and cyanophilic. Endoperidium apical composed of two layers of hyphae continuous, all brown, not dextrinoid and cyanophilic, hyphae 2.4–6.6 µm diam, frequent and non-regular true septa, double V branching, and mycosclereids globose, dextrinoid and cyanophilic. Exoperidium basal hyphal, 1.9–3.9 µm diam, rare and non-regular true septa, V-shaped branches, single and double, and in T, walls < 1.0 µm thin, tortuous and regular, brown, dextrinoid, and cyanophilic. Subgingle hyphal, 1.5–3.8 µm diam, rare true septa, branching V, single and double, and in T, cyanophilic nodes frequent, regular walls ≤ 1.0 µm thin, straight for curves, hyphae 2.4–6.6 µm diam, frequent and non-regular true septa, double V branching, and mycosclereids globose, dextrinoid and cyanophilic. Subgingle hyphal, 1.5–3.8 µm diam, rare true septa, branching V, single and double, and in T, cyanophilic nodes frequent, regular walls ≤ 1.0 µm thin, straight for curves, reddish brown, not dextrinoid and cyanophilic. Paracapillitium absent. Capillitium Calvatia-type, 1.9–3.5 µm diam, hyaline to light brown, dextrinoid and cyanophilic; septa frequent and non-regular, V-branching, single and double, and in T, fragmenting in any part of the capillitium or frequent in the septa; walls ≤ 0.8 µm thin and regular, straight, with large and numerous conspicuous pits (1–3 µm wide). Basidiospores globose to subglobose, 3.4–5.3 µm wide × 3.3–5.0 µm high (χ = 4.1 ± 0.3 × 3.9 ± 0.3; Q(0) (medium coefficient) = 1.05; n (measurement numbers) = 30), verrucose, ornamentation < 1 µm length; pedicels present in some basidiospores ≤ 0.7 µm in length.

Habit & Habitat — Basidiomata growing solitary on moist soil.

Typus. BRAZIL, Rio Grande do Norte, João Câmara, Serra do Torrão, 17 Feb. 2017, R.L. Oliveira (holotype UFRN-Fungos 3027); ITS sequence GenBank MT152990, MycoBank MB827690.

Additional materials examined. BRAZIL, Rio Grande do Norte, João Câmara, Serra do Torrão, 17 Feb. 2017, R.L. Oliveira (UFRN-Fungos 3027); ibid., 17 Feb. 2017, R.L. Oliveira (UFRN-Fungos 3028); ibid., 5 Mar. 2019, R.L. Oliveira (UFRN-Fungos 3117); ibid., 5 Mar. 2019, R.L. Oliveira (UFRN-Fungos 3118).

Notes — Calvatia baikaverdensis is morphologically related to species of sect. Calvatia: C. craniiformis, C. subtomentosa, C. rugosa, C. nodulata, and C. holothurioideae. Calvatia craniiformis, C. rugosa and C. subtomentosa have a capillitium with large conspicuous pits (1–3 µm wide) similar to C. baikaverdensis. However, C. craniiformis presents subglobose to globose basidiospores with punctate ornamentation, and well-developed cellular subgingle. Calvatia rugosa has exoperidium granulose, furfuraceous to subvelutinous, endoperidium smooth, membranous, very thin (< 0.5 mm), subgingle well-developed and lanose to cellular (Reid 1977). Calvatia subtomentosa has basidiospores 3.6–4.4 µm diam, and capillitium 3.6–5.8 µm branched, septate, rather short segments (Dissing & Lange 1962), but is easily distinguished from C. baikaverdensis in the ornamentation of the basidiospores, equinulate, and in the absence of pedicels, besides the absence of large pits in the capillitium and nodules in the hyphae of subgingle in C. subtomentosa. Calvatia nodulata and C. holothurioideae are other morphologically close species to C. baikaverdensis mainly by the basidiospores 3–5 µm diam and capillitium 2–4 µm diam; however, C. nodulata has exoperidium granulose to pilose, subgingle occupying half of the basidiomata, and capillitium with spaced nodules (Alfredo et al. 2014), and C. holothurioideae has subgingle prominent, cellular, capillitium with pores up to 2 µm diam (Rebriev 2013).

Supplementary material

FP1067 The ITS nrDNA consensus phylogenetic tree was obtained with a Bayesian analysis using MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003) under T92+G+I evolutionary for 5 M generations.
Candida pellucida
**Candida pellucida** A.M. Glushakova, M.A. Tomashevskaya & Kachalkin, *sp. nov.*

**Etymology.** The name refers to *Exomias pellucidus* from which the ex-type strain was isolated.

**Classification — Debaryomycetaceae, Saccharomycetales, Saccharomyces.**

On glucose peptone yeast extract agar (GPYA) and 5 % malt extract agar (MEA), after 7 d at 25 °C, streak is white-cream, semi-glistening, with a smooth surface and entire margin. Cells are ovoid to elongate (2–6 × 5–8 μm) and occur singly or in pairs, dividing by polar and multilateral budding. Rare pseudohyphae are produced on potato dextrose agar (PDA) and cornmeal agar (CMA). Aconidial spores and true hyphae have not been observed during 4 wk at 10 and 25 °C in culture (pure cultures and in mating test) grown on GPYA, MEA, PDA, CMA and yeast nitrogen base with 0.5 % glucose (YNB) agar. Fermentation of glucose, galactose (delayed weak), trehalose and maltose (delayed) are positive, but negative for sucrose, lactose and raffinose. Glucose, sucrose, galactose, maltose, cellulobiose, trehalose, melezitose, methyl alpha-D-glucoside, D-xylose, L-arabinose, D-glucosamine, ethanol, glycerol (weak), ribitol, D-mannitol, D-glucitol, salicin (weak), DL-lactic acid (weak), succinic acid (weak), citric acid, 2-keto-D-gluconate, arbutin are assimilated; no growth occurs on lactose, melibiose, raffinose, soluble starch, inulin, D-arabinose, D-ribose, L-sorbos, L-rhamnose, galactitol, erythritol, myo-inositol, 5-keto-D-gluconate, D-glucuronate and methanol. Nitrogen compounds: ammonium sulfate, potassium nitrate (weak), creatinine, creatine, L-lysine, D-glucosamine (weak) are assimilated. Growth on vitamin-free medium, on MEA with 10 % NaCl and on 50 % w/w glucose / yeast extract (0.5 %) agar is positive. Growth with 0.01 % and 0.1 % cycloheximide is weak. Starch-like compounds are not produced. Gelatin liquefaction and casein hydrolysis tests are positive. Diazonium blue B colour and urease reactions are negative. Maximum growth temperature is 42–44 °C.

**Typus.** RUSSIA, Moscow, Park Tsaritsyno, from *Exomias pellucidus* (Curculionidae), Oct. 2018, A.M. Glushakova, Ins-19-21 (holotype KBP Y-6457 pre- served in a metabolically inactive state, ex-type culture VKM Y-3050 = DSM 110120 = CBS 16171; SSU, ITS-D1/D2 domains of LSU nrDNA, TEF1 and RPB1 sequences GenBank MN908677, MN908679, LR745525 and LR745526, MycoBank MB854513).

**Additional materials examined.** RUSSIA, Moscow, Park Tsaritsyno, from *E. pellucidus*, Oct. 2018, A.M. Glushakova, KBP Y-6456, KBP Y-6456 and KBP Y-6466; ITS-D1/D2 domains of LSU nrDNA sequences GenBank MN908680, MN908681 and MN908682, Moscow, as endophyte from almond seeds bought on local market, Oct. 2019, A.M. Glushakova, KBP Y-6679; ITS-D1/D2 domains of LSU nrDNA sequence GenBank MT013027.

**Colour illustrations.** Russia, Moscow, Park Tsaritsyno, meadows with herbaceous flowering plants (the habitat of *Exomias pellucidus*). Candida pellucida KBP Y-6457. Growth of yeast colonies on MEA, yeast cells on MEA (after 7 d at 25 °C). Scale bar = 10 μm.

Notes — Analysis of the ITS-D1/D2 regions of the surveyed yeasts suggested that they were conspecific and represented a hitherto undescribed species of the *Candida/Lodderomyces* clade. Based on the NCBI GenBank nucleotide database, the best hits using the ITS sequence are *Candida viswanathii* CBS 7889 (GenBank KY102513; 90.24 % similar, 18 subst. and 23 gaps) and *Candida viswanathii* ATCC 22981T (GenBank NR_138345; 88.07 % similar, 24 subst. and 36 gaps), using LSU it is *Candida viswanathii* CBS 4024T (GenBank KY106885; 98.20 % similar, 9 subst.), using *SSU* it is *Candida labiduridarum* NRRL Y-27940T (GenBank NG_063271; 99.88 % similar, 2 subst.), using *TEF1* it is *Candida dubliniensis* CD36T (GenBank XM_002417390; 95.67 % similar, 19 subst.) and using *RPB1* it is *Candida viswanathii* CBS 4024T (GenBank AY497714; 88.83 % similar, 66 subst.). In compliance with a recent phylogenetic analysis of the genus (Zhai et al. 2019), the placement of the new species is demonstrated using the combined ITS and LSU rDNA phylogeny. *Candida pellucida* can be differentiated from the phylogenetically most close species *C. viswanathii* based on its ability to grow on vitamin-free medium, good growth at the temperature 42 °C, and negative growth on soluble starch.
**Cladophialophora cabanerensis** Maciá-Vicente, sp. nov.

*Etymology. Named after the Cabañeros National Park in central Spain, where the soil sample was collected.*

*Classification — Herpotrichiellaceae, Chaetothyriales, Eurotiomycetes.*

**Mycelium** consisting of hyaline, branched, septate hyphae, (0.5–)0.7–1.3(–1.6) µm diam, forming hyphal strands. **Conidiophores** mostly single, sympodial, erect, subcylindrical, hyaline, smooth, bearing one phialide, often reduced to a conidiogenous cell. **Conidiogenous cells** phialidic, hyaline, smooth, fusiform with one locus at the apex that leaves a scar, (2.8–)3.6–6.2(–7.6) × (1.3–)1.7–2.6(–2.9) µm. **Conidia** aseptate, produced in mass, hyaline, smooth, globose with a scar, (1.7–)1.9–2.3(–2.4) µm diam (n = 40). **Chlamydospores** absent. **Sexual morph** unknown.

**Culture characteristics — Colonies** slow-growing, reaching 11–14 mm diam on malt extract agar (MEA), 13–17 mm diam on potato-dextrose agar (PDA), and 9–12 mm diam on cornmeal agar (CMA) after 7 d at 25 °C. Colonies velvety, white, becoming light earthy after 3–4 wk, with a compact and suede-like surface; reverse white-cream.

**Typus. Span.** Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland (‘trampal’), N39.35 W4.36, 725 m asl, 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 (holotype FR 0214084, ex-type culture CBS 146781 = P6481; ITS and LSU sequences GenBank MN310213 and MN308512, MycoBank MB834845).

**Additional materials examined. Span.** Ciudad Real, Cabañeros National Park, from rhizospheric soil from a wet heathland (‘trampal’), N39.35 W4.36, 725 m asl, isolated from surface-sterilised, asymptomatic roots of an *A. 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, culture P6476; ITS and LSU sequences GenBank MT179621 and MN308510, MycoBank MB834845.

**Notes —** The three isolates examined have identical morphologies and partial ITS and LSU sequences. Since they originate from the same soil sample, they likely represent clonal isolates. Based on a megablast search of NCBI GenBank nucleotide database, the ITS sequence has low similarity with several unidentified *Chaetothyriales* strains (e.g., GenBank KX822488.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %); GenBank KF614863.1, identities 566/690 (82 %), 43 gaps (6 %)) and with *Cladophialophora immunda* (GenBank MH864254.1, identities 580/715 (81 %), 57 gaps (7 %)). However, the low identity values result from a long insert at the 3’ end of the 18S rDNA gene, similarly to what has been found in other fungi (e.g., Tedersoo et al. 2015, Cross et al. 2017), but that is not present in most GenBank records. When analysing only the partial ITS1 region (nt 551–679) that is homologous to other sequences in GenBank, the megablast search yields highest similarity with 15 environmental sequences originating from a single study (e.g., GenBank MF793689.1, identities 129/129 (100 %), no gaps; and to two unidentified fungi (GenBank MG592689.1, identities 129/129 (100 %), no gaps; GenBank GQ996076.1, identities 127/129 (98 %), 1 gap (0 %)) and two *Cladophialophora* sp. isolates (GenBank LC189029.1, identities 129/129 (100 %), no gaps; and GenBank LC229675.1, identities 127/129 (98 %), 1 gap (0 %)). The closest hits using the LSU sequence are an unidentified fungus (GenBank GU552546.1, identities 675/676 (99 %), 1 gap (0 %)), *Cladophialophora* sp. (GenBank MF588895.1, identities 669/676 (99 %), 1 gap (0 %)), unidentified *Chaetothyriales* (GenBank KF614869.1, identities 666/676 (99 %), 1 gap (0 %)), and *Cladophialophora carrionii* (GenBank AF050262.1, identities 665/676 (98 %), 1 gap (0 %)).

The genus *Cladophialophora* is polyphyletic, including species that are commonly isolated from soil and living plants, but also found as causal agents of human infections. *Cladophialophora cabanerensis* is phylogenetically placed outside the *Carrionii* and *Bantiana* clades defined by Badalí et al. (2008) that contain most species pathogenic to humans. All the closest hits in the megablast search using the insert-free ITS1 sequence originate from fungi associated with plant roots, like the type specimen of *C. cabanerensis*, suggesting a preference of the species toward this habitat.

**Colour illustrations.** Wet heathland (‘trampal’) located in the Cabañeros National Park, Ciudad Real, Spain. Seven-day-old colonies growing at 25 °C on PDA; from top to bottom, overview of mycelium bearing conidiophores under phase-contrast microscopy; conidiophores under light microscopy; loose conidia under light microscopy. Scale bars = 10 µm (mycelium) and 5 µm (conidiophores and conidia).

**Supplementary material**

FP1069 Maximum likelihood phylogenetic tree inferred from concatenated ITS and LSU rDNA sequences using RAxML v. 8.2.12 (Stamatakis 2014) with the GTR+I+G model.

Jose G. Maciá-Vicente, Institute of Ecology, Evolution and Diversity, Goethe University Frankfurt, Max-von-Laue-Str. 13, 60438, Frankfurt am Main, Germany; e-mail: maciavicente@em.uni-frankfurt.de

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
**Cladosporium arenosum** C. Gil-Durán & L. Sanhueza, *sp. nov.*

*Etyymology.* *arenosum* means sandy, referring to substrate (sea sand) from which the fungus was isolated.

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

*Mycelium* scarcely submerged and superficial; hyphae sinuous, unbranched, smooth, 1.6–3 μm wide, septate, not constricted at septa, subhyaline to olive brown. *Conidiophores* smooth, occasionally geniculate, multiseptate, erect to slightly flexuous, oblong, proliferating sympodially; macroconidiospores arising terminally or laterally from hyphae, up to 80 μm long, 3.1–4 μm wide; semimacronematous conidiospores arising terminally or laterally from hyphae, 1.3–1.6 μm wide, pale olive brown, with a single apical scar; micromonocnidiose conidiospore arising laterally from hyphae, 3.1–3.5 μm wide. *Ramoconidia* straight, smooth, concolourous, subcylindrical, 7.0–13.2 × 2.9–4.3 μm, 1-septate. *Secondary ramoconidia* ellipsoid to subcylindrical, smooth, 7.2–12.3 × 3.1–4.2 μm, 0–1-septate in the middle, with 2–3 distal hila, proliferating sympodially. *Conidia* numerous, catenated, dichotomously branched in all directions, straight, smooth, with up to 7 conidia; small terminal conidia obovoid, 2.5–5.8 × 1.4–2.8 μm; intercalary conidia ovoid or limoniform, 6–8.2 × 2.3–4.1 μm; microcyclic conidogenesis not observed.

*Culture characteristics —* (after 2 wk at 20 °C in the dark): On potato dextrose agar (PDA), colonies reach 44–47 mm diam, round shape, flat, dark olive green, dusty, aerial mycelium absent, profuse sporulation, margin white and glabrous, exudates (blackish droplets) produced mainly on the outermost colony surface; reverse olive green to olive black. On malt extract agar (MEA), colonies reach 44–47 mm, irregular flat growth, elevated centre, dusty, olive green to yellowish green, aerial mycelium absent, exudates absent, white flocculent margin; reverse, irregular olive-black. On synthetic nutrient-poor agar (SNA), colonies reach a 28–30 mm diam, irregular flat growth, dusty, olive-green, profuse sporulation mainly in the centre of the colony, exudates absent; reverse olive grey with white flocculent margin. On oatmeal agar (OA), colonies reach 40–45 mm diam, round shape, flat, olive-green, abundant velvety aerial mycelium, absent on the outermost colony surface, profuse sporulation, exudates absent, margin grey-green, narrow and glabrous.

*Cardinal temperature for growth —* Optimum 20 °C, maximum 25 °C, minimum 0 °C.

*Typus. AntArctica*, South Shetland archipelago, King George Island, Fildey Bay, from marine sediment sand, 24 Feb. 2018, L. Sanhueza LS-2 (holotype CHFCA-863 586 stored in a metabolically inactive state in Chilean Fungal Collection; ITS, LSU, actA and tef1 sequences GenBank MN879328, MT015967, MN890008 and MN900117, MycoBank MB834365).

*Notes —* Based on the combined analysis of ITS, actA and tef1 markers, *Cladosporium arenosum* belongs to the *C. cladosporioides* complex (Bensch et al. 2015) and is phylogenetically related to *Cladosporium asperulatum*. However, *C. asperulatum* exhibits asperulate surface ornamentation of its conidia, conidiophores and mycelium (Bensch et al. 2010), characters not found in *C. arenosum*. In addition, *C. asperulatum* has longer conidiosephores ((15–)45–210(–360) × (2–)3–4(–5) μm) and ramoconidia (15–50 × 3–4 μm) (Bensch et al. 2010). Finally, *C. arenosum* produces exudates on PDA, limoniform conidia, and its colonies have a characteristic yellowish green colour after 2 wk at 20 °C on MEA, characters not found in *C. asperulatum* (Bensch et al. 2010).

Based on a megablast search of NCBI GenBank nucleotide database, the closest hits using the *ITS* sequence are *Cladosporium perangustum* ID58 (GenBank MN511354.1; Identities 551/551 (100 %), no gaps), *Cladosporium globisporum* DTO 220-D4 (GenBank KP701967.1; Identities 551/551 (100 %), no gaps), and *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834357.1; Identities 551/551 (100 %), no gaps). The closest hits using the *LSU* sequence are *Cladosporium cladosporioides* CBS 129108 (GenBank MH876646.1; Identities 608/608 (100 %), no gaps), *Cladosporium herbarum* CBS 129088 (GenBank MH876640.1; Identities 608/608 (100 %), no gaps), and *Cladosporium tenuissimum* CBS 125995 (GenBank MH876286.1; Identities 608/608 (100 %), no gaps). The closest hits using the *actA* sequence are *Cladosporium asperulatum* UTHSC DI-13-216 (GenBank LN834541.1; Identities 218/227 (96 %), 1 gap (0 %)); *Cladosporium myrtacearum* CBS 126350 (GenBank HM148606.1; Identities 204/227 (90 %), 4 gaps (1 %)), and *Cladosporium longicaudatum* CPC 17189 (GenBank KT600598.1; Identities 202/224 (90 %), 5 gaps (2 %)). The closest hits with the *tef1* sequence are *Cladosporium asperulatum* BP312 (GenBank KU605784.1; Identities 242/242 (100 %), no gaps), *Cladosporium angustiterminale* CPC 15564 (GenBank KT600476.1; Identities 222/243 (91 %), 5 gaps (2 %)), and *Cladosporium lycoperdinum* CBS 126347 (GenBank HM148356.1; Identities 213/245 (87 %), 3 gaps (1 %)).

Phylogram obtained by combined analysis of ITS, actA and tef1 sequences of *C. arenosum* and related species from the *C. cladosporioides* complex (Bensch et al. 2018). Analyses were done in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001) under GTR + G model for 5 M generations. Posterior probability values > 0.84 are shown at the nodes. *Cercospora beticola* CBS 116456 was used as outgroup.

Carlos Gil-Durán, Gloria Levicién & Renato Chávez, Facultad de Química y Biología, Universidad de Santiago de Chile (USACH), Alameda 3378, Estación Central, 9170022, Santiago, Chile; e-mail: cagild@gmail.com; gloria.levicien@usach.cl & renato.chavez@usach.cl

Loreto Sanhueza & Alonso Ferrer, Facultad de Estudios Interdisciplinarios, Nucleo de Química y Bioquímica, Universidad Mayor, Santiago, Chile; e-mail: loreto.sanhueza@umayor.cl & alonso.ferrer@umayor.cl

**Fig. 1.** *C. arenosum sp. nov.* from South Shetland Islands, King George Island. A, Colony on PDA; B, Colony on OA; C, RS on OA; D, RS on MEA; E, RS on malt extract agar (MEA); F, Conidiophores on OA; G, Conidiophores on PDA; H, Conidia on OA; I, Conidia on OA; J, Conidia on OA; K, Conidia on OA; L, Conidia on OA. Scale bars = 10 μm.

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Cortinarius balteatoindicus
**Cortinarius balteatoindicus** Dima, Semwal, V. Papp, Brandrud & V.K. Bhatt, *sp. nov.*

**Etymology.** The first part of the epithet (‘balteato’) refers to the relationship with *C. balteatocumatilis*, the second part (‘indicus’) refers to India where the species occurs.

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

*Pileus* up to 75 mm diam, plano-convex to appinate, slightly glutinous when young, reddish golden to greyish orange (6B7–6B5); margin smooth or slightly innately fibrillose, incurved. *Lamellae* emarginate, moderately crowded, up to 6 mm broad, greyish when young, later greyish orange (6B4–6B6), lamellulae present, of various lengths. *Stipe* 65 × 17 mm, cylindrical, with slightly clavate base, up to 25 mm broad, greyish orange to brownish orange (6B5–6B6). *Context* dull lilac (15C3) to purplish in pileus and in stipe base. *Odour* distinct, earth-like. *Taste* indistinct. *Spore* print light brown (6D8). *Basidiospores* (9.4–)9.7–10.3 (–10.7) × 5.9–6.1 μm, av. = 10.07 × 5.7 μm, Q = (1.65–)1.73–1.80 (–1.85), Qav = 1.77, n = 50, amygdaloid, verrucose. *Basidia* 4-spored, 26–32 × 6–8 μm, clavate. *Pileipellis* more or less simplex (1-layered); strongly coloured in KOH. *Epicutis* purplish in pileus and in stipe base. *Lulae* present, of various lengths.

Notes — *Cortinarius balteatoindicus* is a member of sect. *Phleogmacioides* based on morphological and molecular (nrDNA ITS and LSU regions) data, belonging to the /balteatocumatilis clade. It forms a well-supported (BS = 99 %) lineage with three sequences known from the Americas: USA, Tennessee (GenBank MF773626), USA, Minnesota (GenBank KY964808) and Mexico (GenBank EU569251). The closest sequence is the one from Minnesota: they differ by 5 nucleotide and indel positions, but only in the ITS1 region. Further studies are needed to unravel whether this sequence belongs to *C. balteatoindicus* with such a disjunct distribution. The other North American sequence from Tennessee differs by 8 nucleotide and indel positions, so it might well represent a separate species. The phylogenetically more distant European species of this clade have more robust basidiomata too, e.g., *C. balteatocumatilis*, *C. balteatobulbosus*, *C. pseudonebulas*, and the recently described *C. hemicacereus* (Brotzu et al. 2019; ITS sequence GenBank MT152622) and have slightly larger spores. The special ecology and the unique ITS sequence are, however, the best delimiting characters for the time being.

**Typus.** India, Uttarakhand, Pauri Garhwal, Teka, 1965 m asl, N30°6′21″, 4 Sept. 2015, K. C. Semwal (holotype KCS 2509; ITS and LSU sequences GenBank MT137516 and MT241937, MycoBank MB834802). Colour illustrations. India, Uttarakhand, Pauri Garhwal, Teka, type locality. Spores and basidiomata (from KCS 2509, holotype). Scale bar = 10 μm (spores).

Phylogenetic tree derived from Maximum Likelihood analysis based on nrITS1-5.8S-ITS2 and binary data from indel coding with FastGap v. 1.2 (Borchsenius 2009). Analysis was performed in raxmlGUI v. 1.5.2 (Silvestro & Michalak 2012) using the GTR+GAMMA substitution model for the partitioned (ITS1-5.8S-ITS2) nucleotide data and the default setting for binary (indel) data. ML bootstrap support (BS) values shown at the nodes (BS > 70 %). Sequences generated for this study are highlighted in bold face. HT and NT abbreviations refer to holotype and neotype sequences, respectively.
Cortinarius ulhagarhiensis
Fungal Planet 1072 – 29 June 2020

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

Etymology. The epithet refers to the type locality at Ulkhagarhi which is named after the temple of the goddess Ulkheshwari in Uttarakhand, India.

Classification — Cortinariaceae, Agaricales, Agaricomycetes.

Pileus up to 110 mm diam, plano-convex to planar, slightly inflated at centre, surface glabrous, slimy when young, slightly bluish greyish when young, but soon becoming reddish golden to light brown (6C8–6D8); margin smooth, fairly undulate. Lamellae emarginate, crowded, greyish when young, later greyish orange (6B4), brownish orange (6C5) when mature, lamellulae present, of various lengths. Stipe 60–90 × 10–22 mm, prominently clavate at the base, bulb up to 30 mm wide, pale brown, becoming brownish orange to reddish orange (6D5, 6B7–7B7) with greyish lilac (15B4-3) tinge throughout the stipe, especially at apex. Context greyish to bluish lilac. Odour and taste not recorded. Spore print brown (8E8). Basidiospores (10.2–)10.6–11.3(–11.7) × (5.7–)5.9–6.6(–6.8) μm, av. = 10.97 × 6.2 μm, Q = (1.63–)1.71–1.83(–1.94), Qav = 1.77, n = 50, amygdaloid, verrucose. Basidia 4-spored, 25–30 × 5–7 μm, clavate. Pleipellis more or less simplex (1-layered); rather weakly coloured in KOH. Epicutis at surface of narrow, 2–5 μm diam, loosely erect-entangled, gelatinous, pale yellow hyphae; below a few layers of slightly wider, 3–8 μm diam hyphae with slightly thickened yellow walls, a few with pale, weakly encrusted wall pigment; the basal part of epicutis of hyphae up to approx. 10 μm diam, with distinctly thickened, yellow walls, forming tightly cemented bundles which in surface view forms a zig-pattern.

Habitat & Distribution — Caespitose, occurring among leaf litter of Quercus leucotrichophora, on humicolous soil, in temperate broadleaved forests dominated by mainly Q. leucotrichophora, Rhododendron arboreum, and Myrica esculenta.

Typos. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, 2025 m asl, N30°09′36″ E78°50′53″, 31 Aug. 2015, K.C. Semwal (holotype, KCS 2490; ITS and LSU sequences GenBank MT137517 and MT241839, MycoBank MB834804).

Notes — Cortinarius ulkhagarhiensis belongs to sect. Phlegmacioides based on both morphological and molecular (nrDNA ITS and LSU regions) data. Within the section it belongs to the /daulnoyae clade, where it forms a close sister species of the European C. caesiocolor. They differ by 5 nucleotide and indel positions, and in morphological characters. The spores of C. ulkhagarhiensis are significantly larger than those of C. caesiocolor (av. 10.97 × 6.2 μm vs 9.85 × 5.8 μm, respectively), and they are also longer (Qav = 1.77 vs 1.70). Macromorphologically they are rather similar, with e.g., bluish context. Another closely related species is the European C. daulnoyae (syn.: C. chromataphilus and C. sabuletorum) which has a strong earth-like smell, yellowing, never bluish context, and phylogenetically is more distant. Morphologically, other species in sect. Phlegmacioides might also resemble C. ulkhagarhiensis, but the ecology and ITS sequence data will be helpful in identification.

For phylogenetic tree see FP1071.

Colour illustrations. India, Uttarakhand, Pauri Garhwal, Ulkhagarhi, type locality. Spores and basidiomata (from KCS 2490, holotype). Scale bar = 10 μm (spores).

Bálint Dima, Department of Plant Anatomy, Institute of Biology, Eötvös Loránd University, Pázmány Péter sétány 1/C, H-1117, Budapest, Hungary; e-mail: cortinarius1@gmail.com
Kamal C. Semwal, Department of Biology, College of Sciences, Eritrea Institute of Technology, Mai Nafti, Asmara, Eritrea; e-mail: kamalsemwal@gmail.com
Viktor Papp, Department of Botany, Faculty of Horticultural Science, Szent István University, P.O. Box 53, H-1518, Budapest, Hungary; e-mail: papp.viktor@kerk.szie.hu & agaricum@gmail.com
Tor Erik Brandrud, Norwegian Institute for Nature Research, Gaustadalléen 21, NO-0349 Oslo, Norway; e-mail: tor.brandrud@nina.no
Vinod K. Bhatt, Navdanya, 105, Rajpur Road, Dehradun, Uttarakhand, India; e-mail: vinodkbhatt@gmail.com

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Cortinarius paezii
Fungal Planet 1073 – 29 June 2020

**Cortinarius paezii** Garrido-Benavent, Ballarà, Liimat. & Mahiques, *sp. nov.*

**Etymology.** The species is named after the Spanish Jesuit missionary Pedro Pérez (1564–1622), who was the first European that visited the Blue Nile source in Ethiopia and described the natural history of this country.

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

Basidiomata rather small. **Pileus** 10–25(–35) mm diam, at first hemispheric, later convex with a persistent, obnute, rounded and low umbo; margin first very incurved and highly lobulate and later extended and slightly serrate, retaining whitish veil remnants; surface hygrophanous, smooth to fibrous, dark grey, dark grey-brown (Caill. T31, T30; Caillé 1981) to ochreous, pale ochraceous or reddish brown (Caill. M49, M35, M25) when dry; mature pilei with necropigments. **Lamellae** moderately dense, uncinated, pale ochraceous to beige ochraceous (Caill. M29, N30); lamellae edges slightly paler, and slightly mustard brown with age; lamellulae present. **Stipe** (15–)20–35(–45) mm long and 3–6(–8) mm wide, cylindrical to clavulate or subglobose at the base; surface white, later pale beige, with universal veil fugacious, not forming an annular area. **Context** generally fibrous, pale ochraceous, and brownish in the stipe cortex. **Taste mild and smell indistinguishable.**

*Macrochemical reactions —* Negative to KOH, guaiac tincture, Ph.A. and methol. **Basidiospores** broadly ellipsoid in front and side view, (10–)11–11.8–12.5(–13) × (6.25–)7–7.3–7.5(–8) µm in size, with a Q (length/width ratio) = (1.5–)1.55–1.61–1.73(–1.8), and with a marked apical depression; spore surface densely ornamented with projecting warts of moderate size. **Basidia** 36–45 × 9–12 µm, 4-spored; lamellar edge with basidia and some claviform cells, 26–34 × 9–11 µm. **Pileipellis** a cutis formed by a layer of 4–8 µm wide, clamped, more or less cylindrical hyphae, with scattered pale ochraceous incrusted wall pigment; **subcutis** composed of short and irregularly-arranged, septate hyphae, 30–75 × 20–32 µm; hyphae of the veil remnants 2–3 µm diam.

**Habitat & Distribution —** Restricted to the alpine belt (＞2000 m asl) in association with *Dryas octopetala*. So far found in the Pre-Pyrenees (north-eastern Iberian Peninsula). The existence of an ITS sequence in GenBank (FR852009) identical to the ones obtained in the present study suggests the presence of *C. paezii* in the Hycranian forests of Iran.

**Typus.** **Spain**, Catalonia, Barcelona province, Berguedà, Salides, Serra d’Encija, Creu de Ferro, N42°16’26” E1°76’59”, 2250 m asl, associated with *Dryas octopetala* on calcareous soil, 26 Aug. 2018, J. Ballarà JB-9511-18 (holotype MA-90461; ITS sequence GenBank MT184886, MycoBank MB833243).

**Colour illustrations.** Spain, Catalonia, Serra d’Encija, prairie with *Dryas octopetala* in the alpine belt, ＞2000 m asl, where the holotype of *Cortinarius paezii* was collected (MA-90461). Basidiomata in upper photos correspond with the holotype; bottom left photo corresponds with MA-90460; holotype basidiospores. Scale bar = 10 µm.

Notes — Cortinarius paezii is a rather small telamonioid species with relatively large spores that we initially considered to conform to the morphological variability of *C. casimiri* due to the general size, habitat and pigmentation. However, basidiomata of the latter species are in general slenderer than those of *C. paezii*, and show reddish and somewhat lilaceous tinged, their smell is more or less raphanoid, and the spores are smaller, 10–11.5 × 6–7 µm (Brandrud et al. 1998). *Cortinarius paezii* produces hygrophanous pilei that are very dark when hydrated, without lilaceous traces, and instead shows pale ochraceous to reddish brown tinges with time. Furthermore, *C. casimiri* distributes preferentially in altimontane-subalpine habitats, and more rarely forms mycorrhizal associations with *Salix* spp. in the alpine belt. Considering other species growing in the alpine belt, *C. cavipes* would share two additional characters with *C. paezii*: the evident change in colour of pilei after drying and the clavate stipe (Favre 1955). As indicated by its epithet, however, *C. cavipes* has a hollow stipe; additionally, it shows lilaceous traces in the stipe apex and context (as in *C. casimiri*), and produces smaller, less ornamented spores.

Two additional alpine species described by Favre (1955) were *C. levipileus* and *C. rusticellus*. The former differs from *C. paezii* in producing smaller basidiomata, with a finely granulose pileus cuticle, with the surface dark to reddish brown, and by the less abundant veil remnants and the slightly smaller, more ovoid spores (lower Q value). Lamoure (1978) obtained similar values for spore size in *C. levipileus* and provided further evidence of its habitat on calcareous soils in the alpine belt. *Cortinarius rusticellus* produces spores more similar in size to those of the new species but has smaller basidiomata, pilei are more umbonate and fibrous to felly, lamellae are darker, and there is an abundant and persistent veil forming an evident annulus on the stipe.

The two ITS sequences obtained for the new species were 19 bp (plus four indels), 16 bp (plus eight indels), and 19 bp (plus six indels) different from those of *C. casimiri/Subtipes, C. levipileus* and *C. rusticellus* respectively. The phylogenetic tree revealed *C. tateinsis* as a close relative of *C. paezii*. This species was described from *Salix* and *Dryas* communities in the alpine belt of the Belaer Tatars, in northern Slovakia (Felinger & Landa 1993). Apart from the similar habitat, *C. paezii* and *C. tateinsis* share the general habitat of basidiomata, the hygrophanity of pilei and their pigmentation, and the spores, which the authors described as broadly ovoid, (10–)10.5–12.5 × (6.5–)7–8.5 µm. However, lilaceous to vinaceous tinges were originally noticed in the surface of the stipe base and in the stipe context of *C. tateinsis* while these characters are absent in *C. paezii*. Additionally, the stipe in *C. tateinsis* is described as ‘cylindrical, slightly narrowing towards the base’, whereas in the new species it is markedly clavate. The ITS sequence of *C. tateinsis* is provided for the first time in the present work, and shows five different nucleotides from *C. paezii* at the ITS1 region.

**Supplementary material**

FP1073-1 Additional materials examined.

FP1073-2 Phylogram depicting the evolutionary relationships of *Cortinarius paezii* and their relatives based on ITS sequence data.

Isaac Garrido-Benavent, Department of Biogeochemistry and Microbiological Ecology, National Museum of Natural Sciences, CSIC, E-28002, Madrid, Spain; e-mail: igbenavent@mncn.csic.es

Josep Ballarà, C/ Tossalet de les Forques, 44, E-08600, Berga, Catalonia, Spain; e-mail: josep.cortinarius@gmail.com

Kare Liimatainen, Jodrell Laboratory, Royal Botanic Gardens, Kew, Surrey TW9 3AB, UK; e-mail: k.liimatainen@kew.org

Rafael Mahiques, C/ Dr. Climent, 26, E-46837, Quatretondeta, València, Spain; e-mail: rmahiquessean@gmail.com

© 2020 Naturalis Biodiversity Center & Westerdijk Fungal Biodiversity Institute
Cylindrium magnoliae